Supplemental spectra and MALDI TOF MS identification information for Table 1

Annotated spectra for Table 1: 209 differentially expressed proteins identified by PMF and the combination results of PMF.

Spot numbers of the **209** proteins correspond to the proteins that listed in Table 1.

CID: collision induced desorption

MALDI TOF:

matrix assisted laser desorption/ionization time of flight

MS: mass spectrometry

PMF: peptide mass fingerprinting

Spot No.: **1**

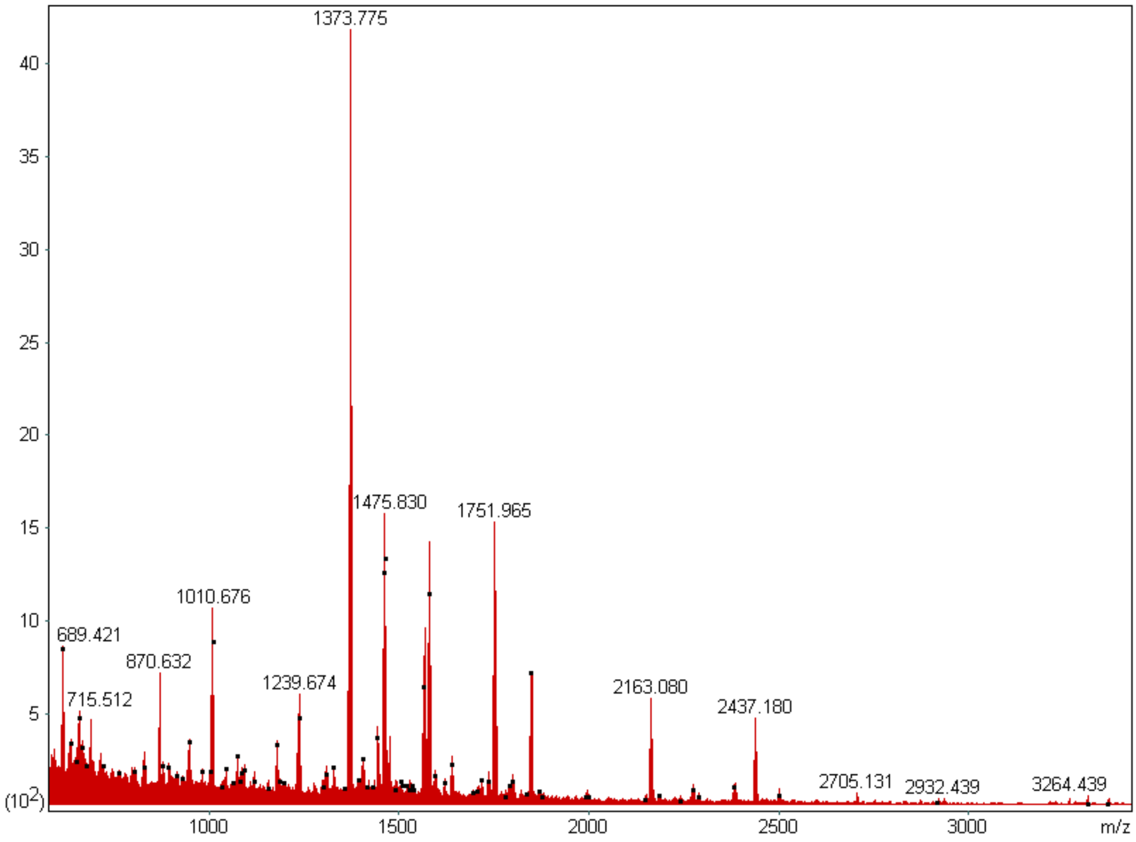
Mascot score: **114**   Sequence coverage %: **22**

NCBI accession No.: **gi| 15233779**

Matched peptides No.: **15**   Total peptides No.: **31**

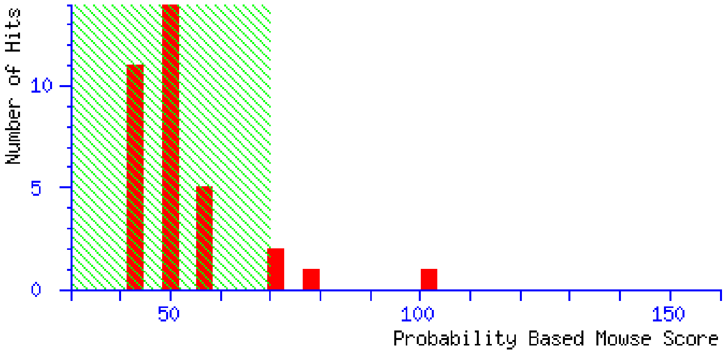
Calculated Mr: **76575**   Calculated p*I*: **5.07**

Annotated PMF **spectra:**

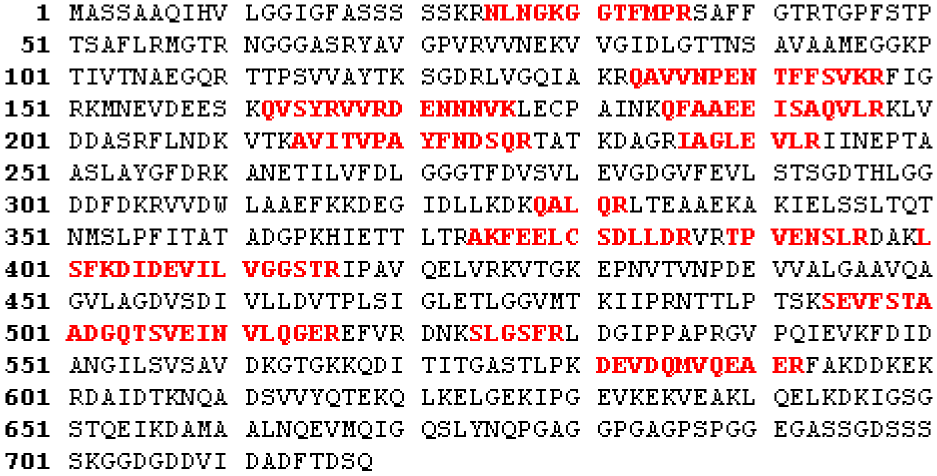


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

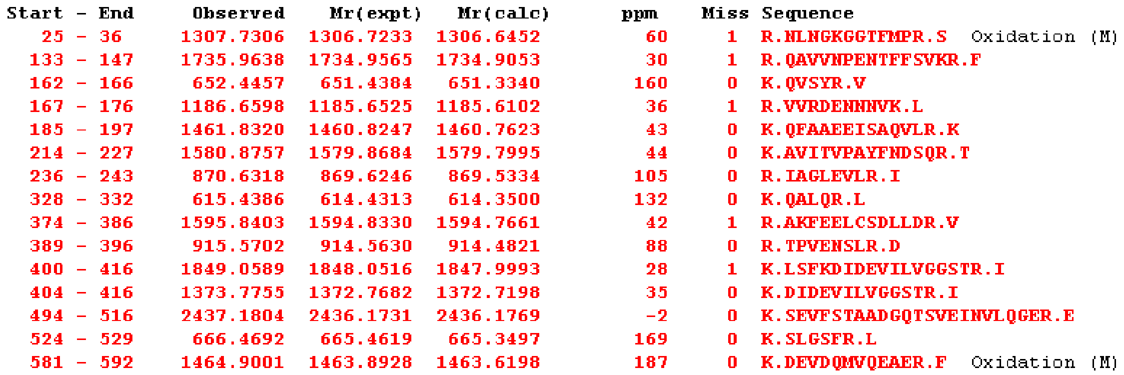


Matched peptide sequences: shown in Bold Red



1 MASSAAQIHV LGGIGFASSS SSKR**NLNGKG** **GTFMPR**SAFF GTRTGPFSTP
51 TSAFLRMGTR NGGGASRYAV GPVRVVNEKV VGIDLGTTNS AVAAMEGGKP
101 TIVTNAEGQR TTPSVVAYTK SGDRLVGQIA KR**QAVVNPEN** **TFFSVKR**FIG
151 RKMNEVDEES K**QVSYRVVRD** **ENNNVK**LECP AINK**QFAAEE** **ISAQVLR**KLV
201 DDASRFLNDK VTK**AVITVPA** **YFNDSQR**TAT KDAGR**IAGLE** **VLR**IINEPTA
251 ASLAYGFDRK ANETILVFDL GGGTFDVSVL EVGDGVFEVL STSGDTHLGG
301 DDFDKRVVDW LAAEFKKDEG IDLLKDK**QAL** **QR**LTEAAEKA KIELSSLTQT
351 NMSLPFITAT ADGPKHIETT LTR**AKFEELC** **SDLLDR**VR**TP** **VENSLR**DAK**L**
401 **SFKDIDEVIL** **VGGSTR**IPAV QELVRKVTGK EPNVTVNPDE VVALGAAVQA
451 GVLAGDVSDI VLLDVTPLSI GLETLGGVMT KIIPRNTTLP TSK**SEVFSTA**
501 **ADGQTSVEIN** **VLQGER**EFVR DNK**SLGSFR**L DGIPPAPRGV PQIEVKFDID
551 ANGILSVSAV DKGTGKKQDI TITGASTLPK **DEVDQMVQEA** **ER**FAKDDKEK
601 RDAIDTKNQA DSVVYQTEKQ LKELGEKIPG EVKEKVEAKL QELKDKIGSG
651 STQEIKDAMA ALNQEVMQIG QSLYNQPGAG GPGAGPSPGG EGASSGDSSS
701 SKGGDGDDVI DADFTDSQ

Matched peptides information:



```
Start - End      Observed   Mr(expt)   Mr(calc)        ppm    Miss Sequence
   25 - 36      1307.7306  1306.7233  1306.6452         60      1  R.NLNGKGGTFMPR.S  Oxidation (M)
  133 - 147     1735.9638  1734.9565  1734.9053         30      1  R.QAVVNPENTFFSVKR.F
  162 - 166      652.4457   651.4384   651.3340        160      0  K.QVSYR.V
  167 - 176     1186.6598  1185.6525  1185.6102         36      1  R.VVRDENNNVK.L
  185 - 197     1461.8320  1460.8247  1460.7623         43      0  K.QFAAEEISAQVLR.K
  214 - 227     1580.8757  1579.8684  1579.7995         44      0  K.AVITVPAYFNDSQR.T
  236 - 243      870.6318   869.6246   869.5334        105      0  R.IAGLEVLR.I
  328 - 332      615.4386   614.4313   614.3500        132      0  K.QALQR.L
  374 - 386     1595.8403  1594.8330  1594.7661         42      1  R.AKFEELCSDLLDR.V
  389 - 396      915.5702   914.5630   914.4821         88      0  R.TPVENSLR.D
  400 - 416     1849.0589  1848.0516  1847.9993         28      1  K.LSFKDIDEVILVGGSTR.I
  404 - 416     1373.7755  1372.7682  1372.7198         35      0  K.DIDEVILVGGSTR.I
  494 - 516     2437.1804  2436.1731  2436.1769         -2      0  K.SEVFSTAADGQTSVEINVLQGER.E
  524 - 529      666.4692   665.4619   665.3497        169      0  K.SLGSFR.L
  581 - 592     1464.9001  1463.8928  1463.6198        187      0  K.DEVDQMVQEAER.F  Oxidation (M)
```

Spot No.: **2**

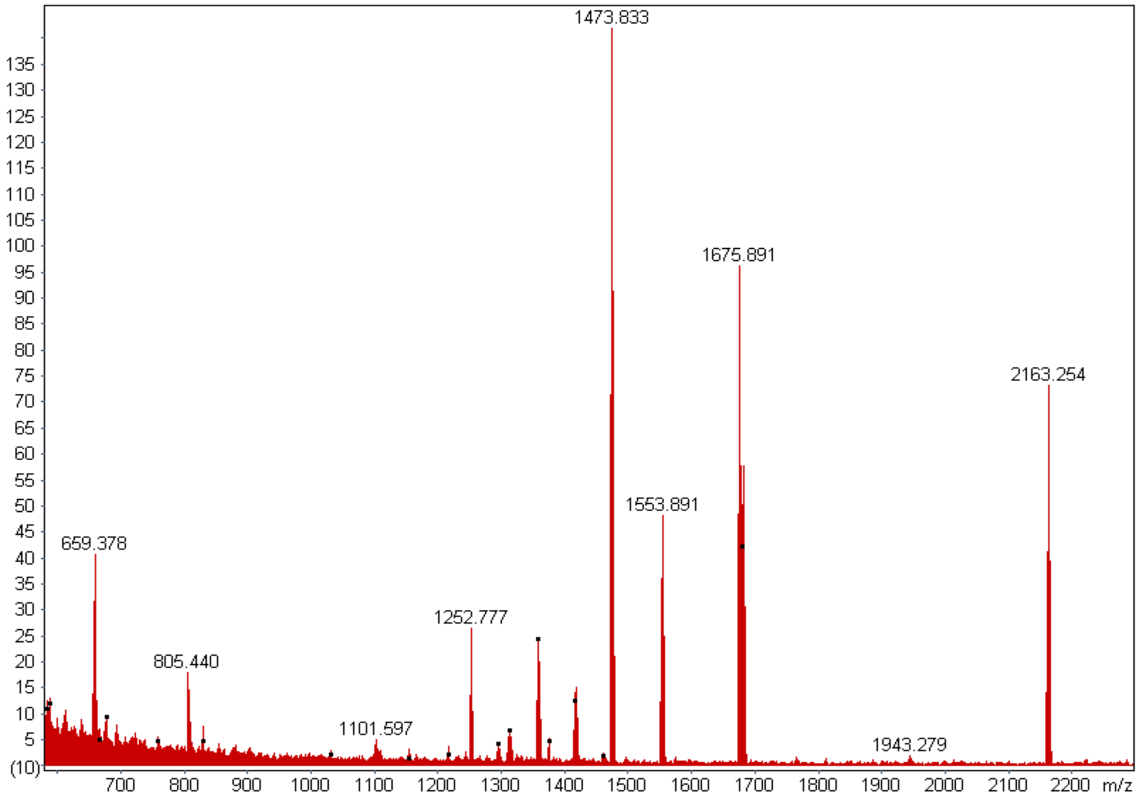
Mascot score: **86** Sequence coverage %: **16**

NCBI accession No.: **gi| 20559**

Matched peptides No.: **10** Total peptides No.: **19**

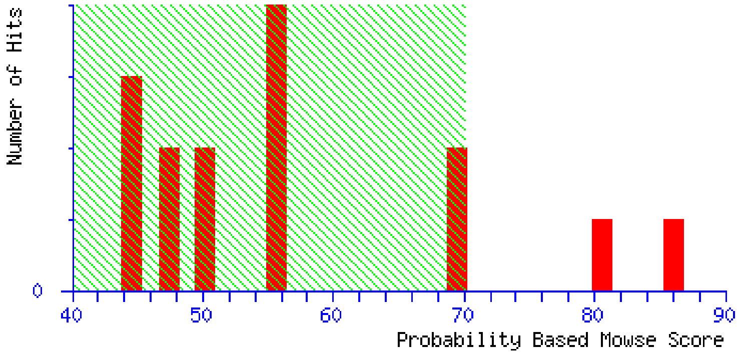
Calculated Mr: **71137** Calculated *p*I: **5.07**

Annotated PMF **spectra:**

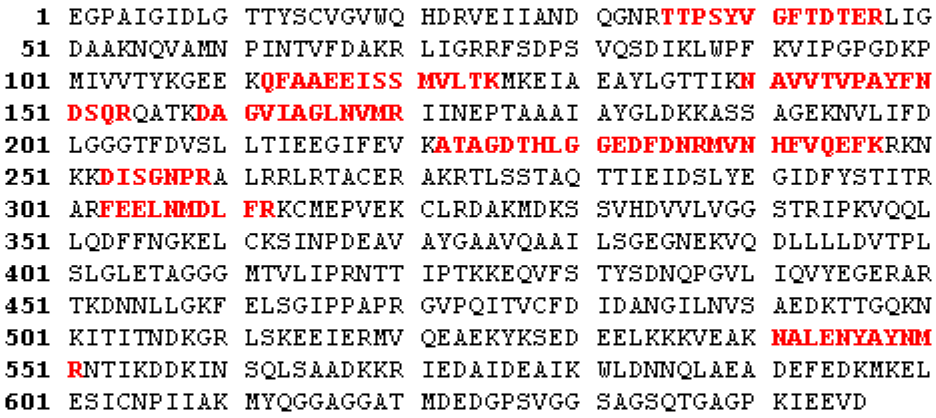


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

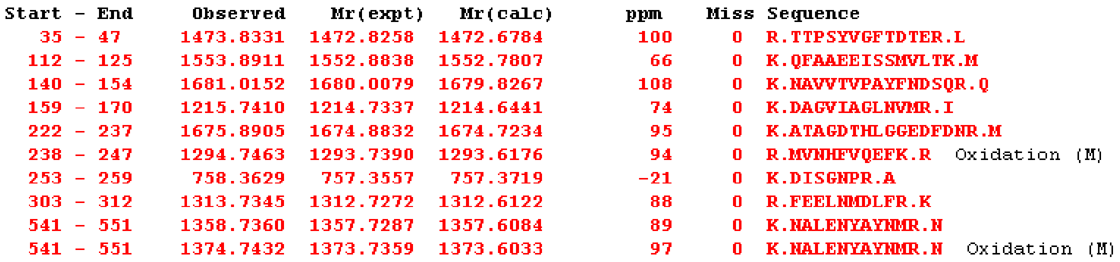


Matched peptide sequences: shown in Bold Red



1 EGPAIGIDLG TTYSCVGVWQ HDRVEIIAND QGNR**TTPSYV GFTDTER**LIG
51 DAAKNQVAMN PINTVFDAKR LIGRRFSDPS VQSDIKLWPF KVIPGPGDKP
101 MIVVTYKGEE K**QFAAEEISS MVLTK**MKEIA EAYLGTTIK**N AVVTVPAYFN**
151 **DSQR**QATK**DA GVIAGLNVMR** IINEPTAAAI AYGLDKKASS AGEKNVLIFD
201 LGGGTFDVSL LTIEEGIFEV K**ATAGDTHLG GEDFDNRMVN HFVQEFK**RKN
251 KK**DISGNPR**A LRRLRTACER AKRTLSSTAQ TTIEIDSLYE GIDFYSTITR
301 AR**FEELNMDL FR**KCMEPVEK CLRDAKMDKS SVHDVVLVGG STRIPKVQQL
351 LQDFFNGKEL CKSINPDEAV AYGAAVQAAI LSGEGNEKVQ DLLLLDVTPL
401 SLGLETAGGG MTVLIPRNTT IPTKKEQVFS TYSDNQPGVL IQVYEGERAR
451 TKDNNLLGKF ELSGIPPAPR GVPQITVCFD IDANGILNVS AEDKTTGQKN
501 KITITNDKGR LSKEEIERMV QEAEKYKSED EELKKKVEAK **NALENYAYNM**
551 **R**NTIKDDKIN SQLSAADKKR IEDAIDEAIK WLDNNQLAEA DEFEDKMKEL
601 ESICNPIIAK MYQGGAGGAT MDEDGPSVGG SAGSQTGAGP KIEEVD

Matched peptides information:



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Start - End      Observed    Mr(expt)    Mr(calc)       ppm    Miss Sequence
   35 - 47      1473.8331   1472.8258   1472.6784       100      0  R.TTPSYVGFTDTER.L
  112 - 125     1553.8911   1552.8838   1552.7807        66      0  K.QFAAEEISSMVLTK.M
  140 - 154     1681.0152   1680.0079   1679.8267       108      0  K.NAVVTVPAYFNDSQR.Q
  159 - 170     1215.7410   1214.7337   1214.6441        74      0  K.DAGVIAGLNVMR.I
  222 - 237     1675.8905   1674.8832   1674.7234        95      0  K.ATAGDTHLGGEDFDNR.M
  238 - 247     1294.7463   1293.7390   1293.6176        94      0  R.MVNHFVQEFK.R  Oxidation (M)
  253 - 259      758.3629    757.3557    757.3719       -21      0  K.DISGNPR.A
  303 - 312     1313.7345   1312.7272   1312.6122        88      0  R.FEELNMDLFR.K
  541 - 551     1358.7360   1357.7287   1357.6084        89      0  K.NALENYAYNMR.N
  541 - 551     1374.7432   1373.7359   1373.6033        97      0  K.NALENYAYNMR.N  Oxidation (M)
```

Spot No.: **3**

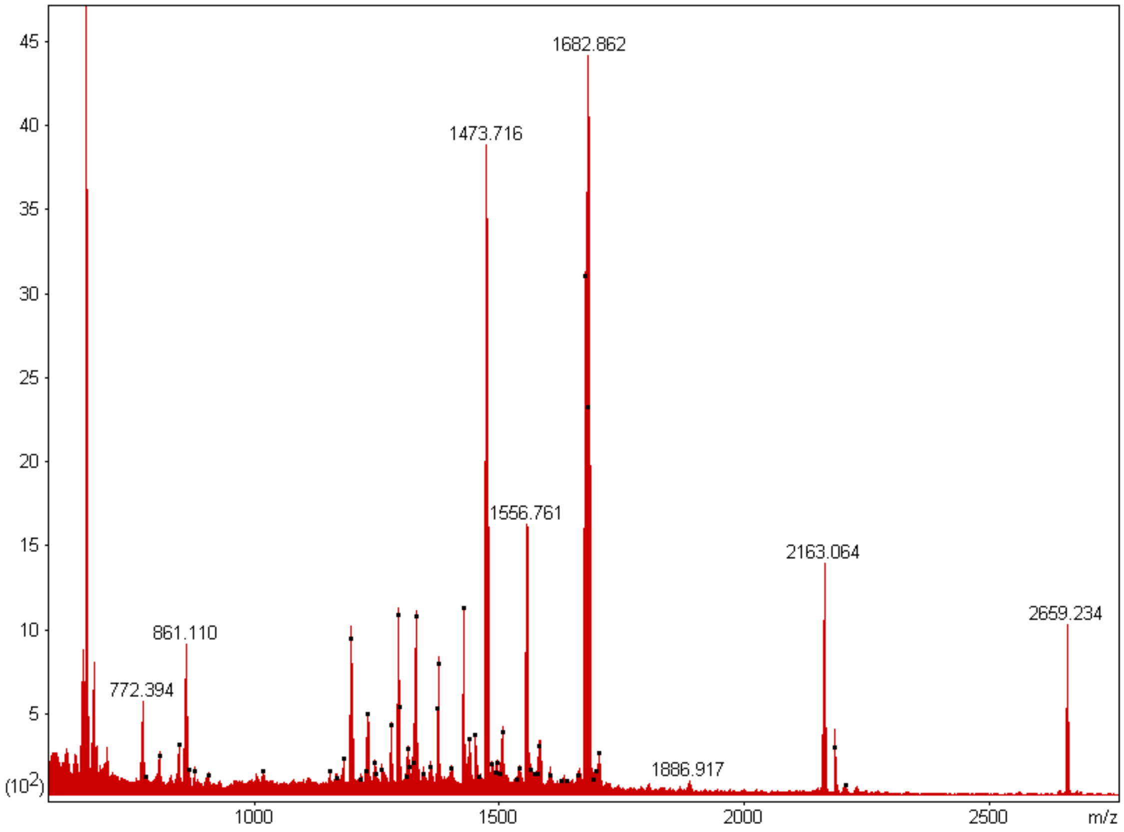
Mascot score: **99**   Sequence coverage %: **22**

NCBI accession No.: **gi| 3962377**

Matched peptides No.: **20**   Total peptides No.: **53**

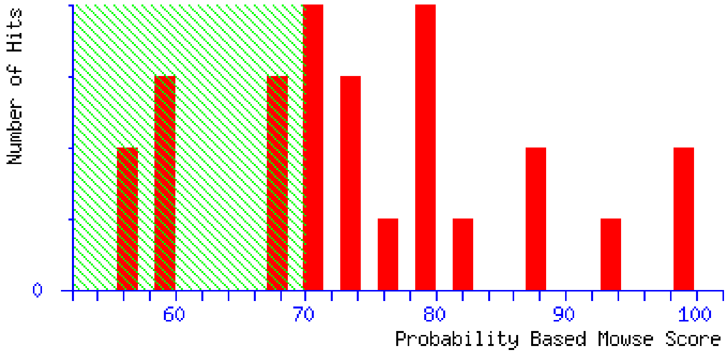
Calculated Mr: **71408**   Calculated *p*I: **5.14**

Annotated PMF **spectra:**

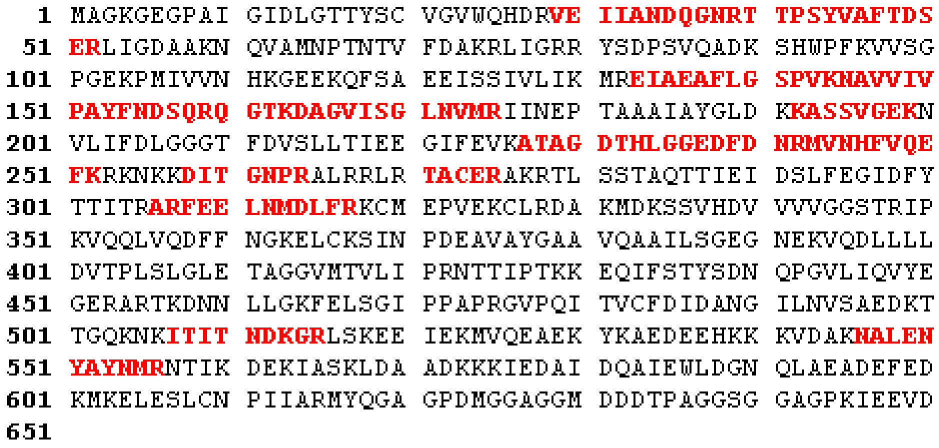


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

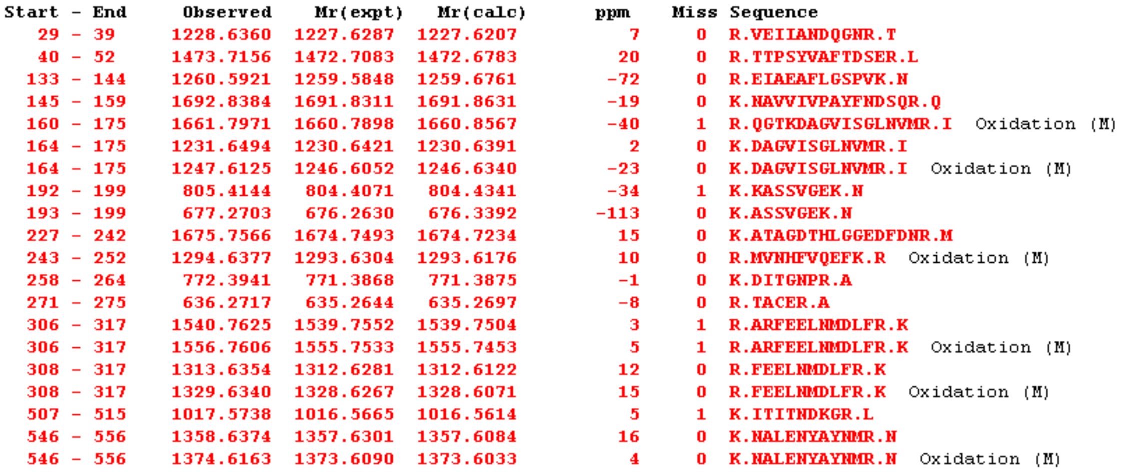


Matched peptide sequences: shown in Bold Red



1 MAGKGEGPAI GIDLGTTYSC VGVWQHDR**VE** **IIANDQGNRT** **TPSYVAFTDS**
51 **ER**LIGDAAKN QVAMNPTNTV FDAKRLIGRR YSDPSVQADK SHWPFKVVSG
101 PGEKPMIVVN HKGEEKQFSA EEISSIVLIK MR**EIAEAFLG** **SPVKNAVVIV**
151 **PAYFNDSQRQ** **GTKDAGVISG** **LNVMR**IINEP TAAAIAYGLD K**KASSVGEK**N
201 VLIFDLGGGT FDVSLLTIEE GIFEVK**ATAG** **DTHLGGEDFD** **NRMVNHFVQE**
251 **FK**RKNKK**DIT** **GNPR**ALRRLR **TACER**AKRTL SSTAQTTIEI DSLFEGIDFY
301 TTITR**ARFEE** **LNMDLFR**KCM EPVEKCLRDA KMDKSSVHDV VVVGGSTRIP
351 KVQQLVQDFF NGKELCKSIN PDEAVAYGAA VQAAILSGEG NEKVQDLLLL
401 DVTPLSLGLE TAGGVMTVLI PRNTTIPTKK EQIFSTYSDN QPGVLIQVYE
451 GERARTKDNN LLGKFELSGI PPAPRGVPQI TVCFDIDANG ILNVSAEDKT
501 TGQKNK**ITIT** **NDKGR**LSKEE IEKMVQEAEK YKAEDEEHKK KVDAK**NALEN**
551 **YAYNMR**NTIK DEKIASKLDA ADKKKIEDAI DQAIEWLDGN QLAEADEFED
601 KMKELESLCN PIIARMYQGA GPDMGGAGGM DDDTPAGGSG GAGPKIEEVD
651

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
29 - 39	1228.6360	1227.6287	1227.6207	7	0	R.VEIIANDQGNR.T	
40 - 52	1473.7156	1472.7083	1472.6783	20	0	R.TTPSYVAFTDSER.L	
133 - 144	1260.5921	1259.5848	1259.6761	-72	0	R.EIAEAFLGSPVK.N	
145 - 159	1692.8384	1691.8311	1691.8631	-19	0	K.NAVVIVPAYFNDSQR.Q	
160 - 175	1661.7971	1660.7898	1660.8567	-40	1	R.QGTKDAGVISGLNVMR.I	Oxidation (M)
164 - 175	1231.6494	1230.6421	1230.6391	2	0	K.DAGVISGLNVMR.I	
164 - 175	1247.6125	1246.6052	1246.6340	-23	0	K.DAGVISGLNVMR.I	Oxidation (M)
192 - 199	805.4144	804.4071	804.4341	-34	1	K.KASSVGEK.N	
193 - 199	677.2703	676.2630	676.3392	-113	0	K.ASSVGEK.N	
227 - 242	1675.7566	1674.7493	1674.7234	15	0	K.ATAGDTHLGGEDFDNR.M	
243 - 252	1294.6377	1293.6304	1293.6176	10	0	R.MVNHFVQEFK.R	Oxidation (M)
258 - 264	772.3941	771.3868	771.3875	-1	0	K.DITGNPR.A	
271 - 275	636.2717	635.2644	635.2697	-8	0	R.TACER.A	
306 - 317	1540.7625	1539.7552	1539.7504	3	1	R.ARFEELNMDLFR.K	
306 - 317	1556.7606	1555.7533	1555.7453	5	1	R.ARFEELNMDLFR.K	Oxidation (M)
308 - 317	1313.6354	1312.6281	1312.6122	12	0	R.FEELNMDLFR.K	
308 - 317	1329.6340	1328.6267	1328.6071	15	0	R.FEELNMDLFR.K	Oxidation (M)
507 - 515	1017.5738	1016.5665	1016.5614	5	1	K.ITITNDKGR.L	
546 - 556	1358.6374	1357.6301	1357.6084	16	0	K.NALENYAYNMR.N	
546 - 556	1374.6163	1373.6090	1373.6033	4	0	K.NALENYAYNMR.N	Oxidation (M)

Spot No.: **4**

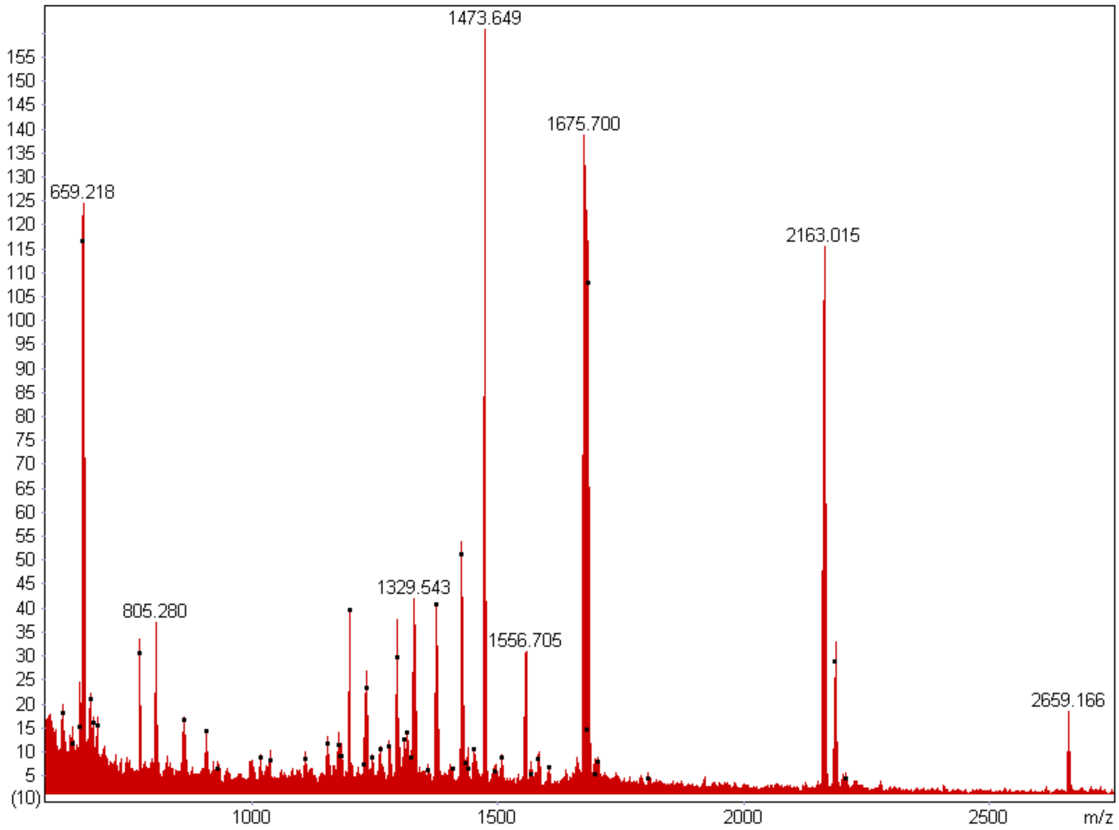
Mascot score: **100**   Sequence coverage %: **22**

NCBI accession No.: **gi| 15230534**

Matched peptides No.: **17**   Total peptides No.: **37**

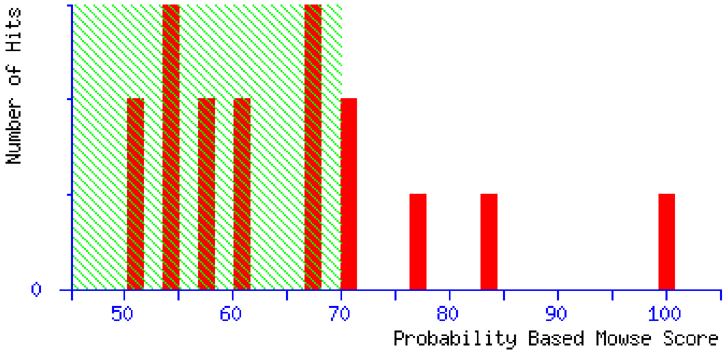
Calculated Mr: **71456**   Calculated *p*I: **5.14**

Annotated PMF **spectra:**

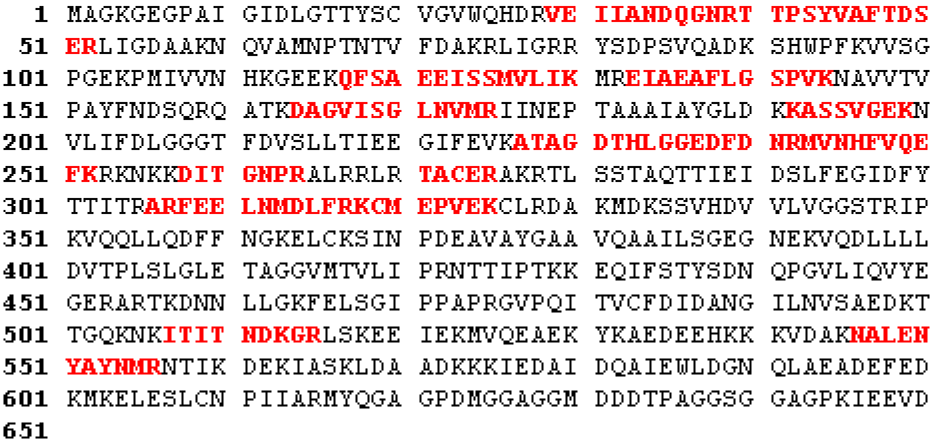


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant ($p<0.05$).

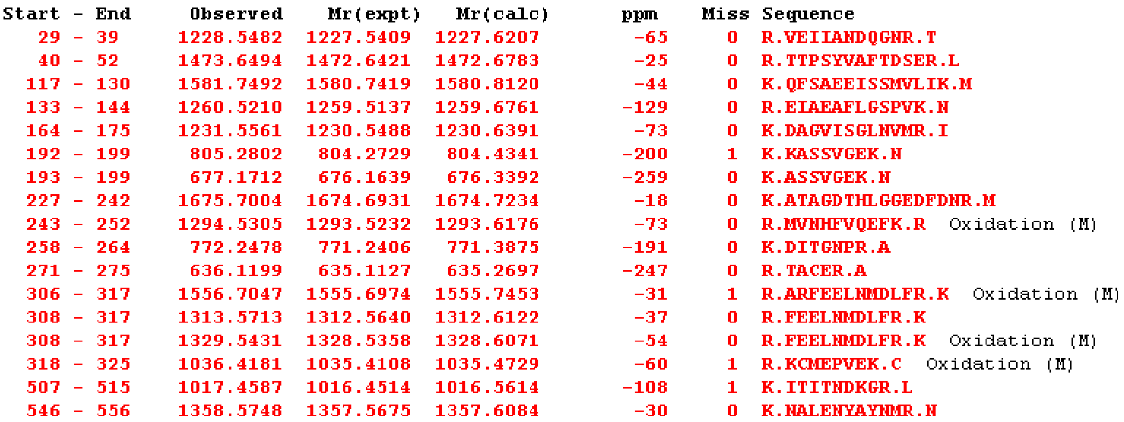


Matched peptide sequences: shown in Bold Red



1 MAGKGEGPAI GIDLGTTYSC VGVWQHDR**VE** **IIANDQGNRT** **TPSYVAFTDS**
51 **ER**LIGDAAKN QVAMNPTNTV FDAKRLIGRR YSDPSVQADK SHWPFKVVSG
101 PGEKPMIVVN HKGEEK**QFSA** **EEISSMVLIK** MR**EIAEAFLG** **SPVK**NAVVTV
151 PAYFNDSQRQ ATK**DAGVISG** **LNVMR**IINEP TAAAIAYGLD K**KASSVGEK**N
201 VLIFDLGGGT FDVSLLTIEE GIFEVK**ATAG** **DTHLGGEDFD** **NRMVNHFVQE**
251 **FK**RKNKK**DIT** **GNPR**ALRRLR **TACER**AKRTL SSTAQTTIEI DSLFEGIDFY
301 TTITR**ARFEE** **LNMDLFRKCM** **EPVEK**CLRDA KMDKSSVHDV VLVGGSTRIP
351 KVQQLLQDFF NGKELCKSIN PDEAVAYGAA VQAAILSGEG NEKVQDLLLL
401 DVTPLSLGLE TAGGVMTVLI PRNTTIPTKK EQIFSTYSDN QPGVLIQVYE
451 GERARTKDNN LLGKFELSGI PPAPRGVPQI TVCFDIDANG ILNVSAEDKT
501 TGQKNK**ITIT** **NDKGR**LSKEE IEKMVQEAEK YKAEDEEHKK KVDAK**NALEN**
551 **YAYNMR**NTIK DEKIASKLDA ADKKKIEDAI DQAIEWLDGN QLAEADEFED
601 KMKELESLCN PIIARMYQGA GPDMGGAGGM DDDTPAGGSG GAGPKIEEVD
651

Matched peptides information:



Start	-	End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
29	-	39	1228.5482	1227.5409	1227.6207	-65	0	R.VEIIANDQGNR.T
40	-	52	1473.6494	1472.6421	1472.6783	-25	0	R.TTPSYVAFTDSER.L
117	-	130	1581.7492	1580.7419	1580.8120	-44	0	K.QFSAEEISSMVLIK.M
133	-	144	1260.5210	1259.5137	1259.6761	-129	0	R.EIAEAFLGSPVK.N
164	-	175	1231.5561	1230.5488	1230.6391	-73	0	K.DAGVISGLNVMR.I
192	-	199	805.2802	804.2729	804.4341	-200	1	K.KASSVGEK.N
193	-	199	677.1712	676.1639	676.3392	-259	0	K.ASSVGEK.N
227	-	242	1675.7004	1674.6931	1674.7234	-18	0	K.ATAGDTHLGGEDFDNR.M
243	-	252	1294.5305	1293.5232	1293.6176	-73	0	R.MVNHFVQEFK.R Oxidation (M)
258	-	264	772.2478	771.2406	771.3875	-191	0	K.DITGNPR.A
271	-	275	636.1199	635.1127	635.2697	-247	0	R.TACER.A
306	-	317	1556.7047	1555.6974	1555.7453	-31	1	R.ARFEELNMDLFR.K Oxidation (M)
308	-	317	1313.5713	1312.5640	1312.6122	-37	0	R.FEELNMDLFR.K
308	-	317	1329.5431	1328.5358	1328.6071	-54	0	R.FEELNMDLFR.K Oxidation (M)
318	-	325	1036.4181	1035.4108	1035.4729	-60	1	R.KCMEPVEK.C Oxidation (M)
507	-	515	1017.4587	1016.4514	1016.5614	-108	1	K.ITITNDKGR.L
546	-	556	1358.5748	1357.5675	1357.6084	-30	0	K.NALENYAYNMR.N

Spot No.: **5**

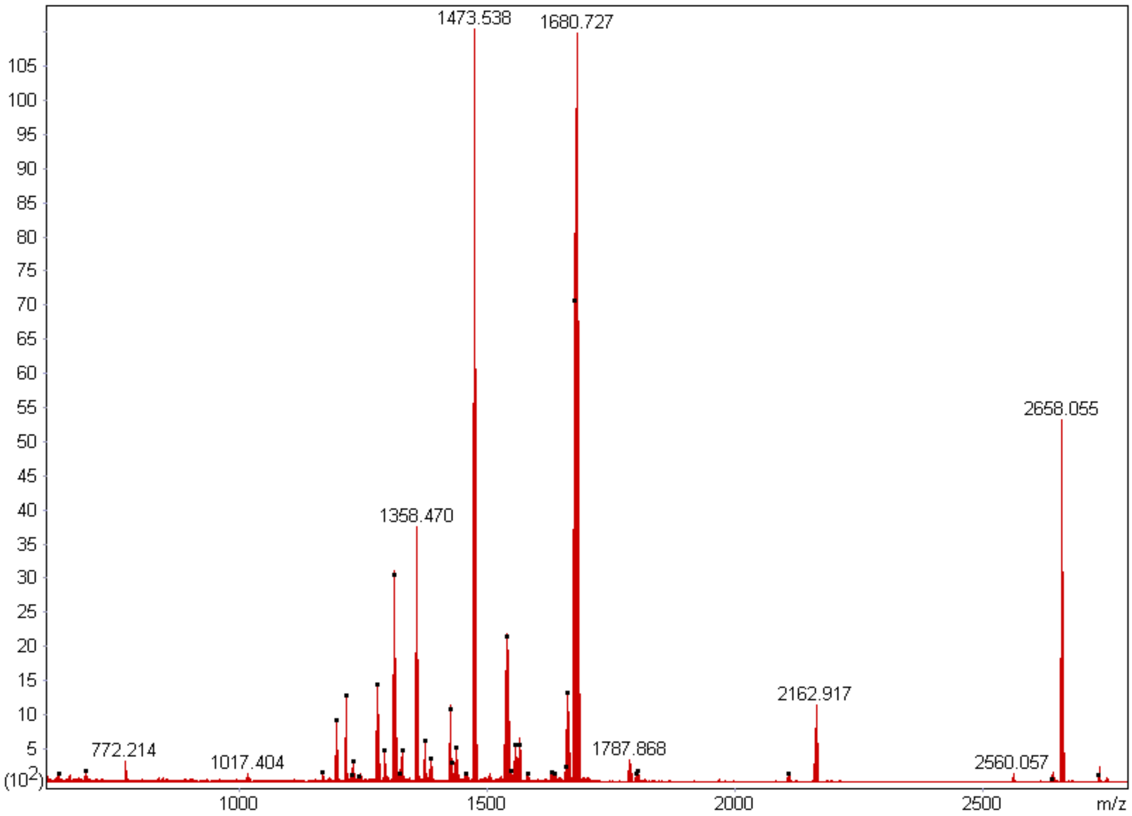
Mascot score: **201** Sequence coverage %: **43**

NCBI accession No.: **gi| 15241849**

Matched peptides No.: **27** Total peptides No.: **37**

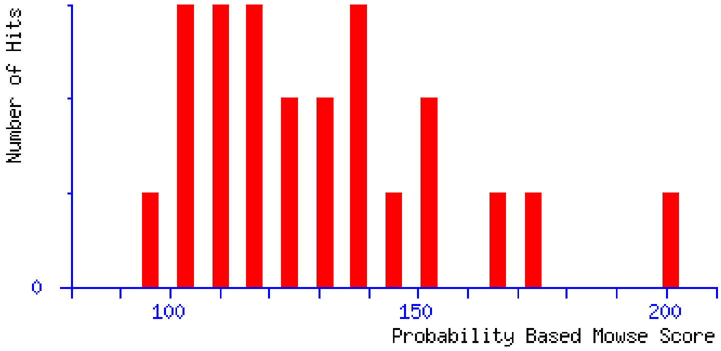
Calculated Mr: **71712** Calculated p*I*: **5.03**

Annotated PMF **spectra:**

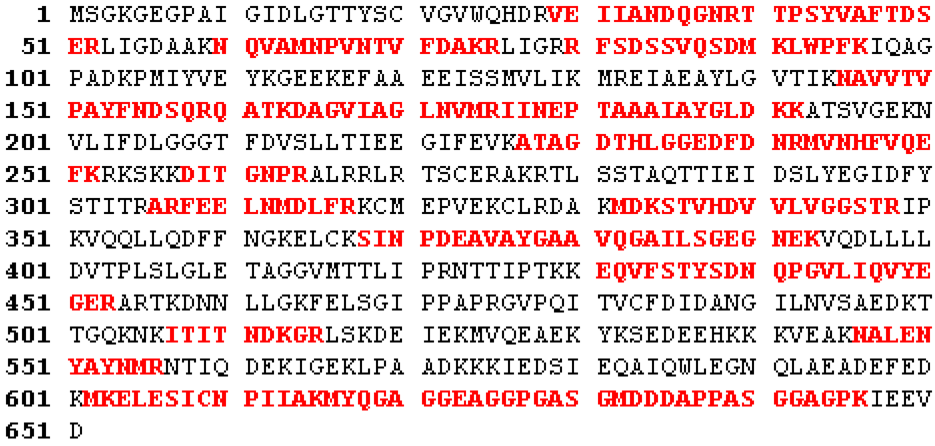


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red



```
  1 MSGKGEGPAI GIDLGTTYSC VGVWQHDRVE IIANDQGNRT TPSYVAFTDS
 51 ERLIGDAAKN QVAMNPVNTV FDAKRLIGRR FSDSSVQSDM KLWPFKIQAG
101 PADKPMIYVE YKGEEKEFAA EEISSMVLIK MREIAEAYLG VTIKNAVVTV
151 PAYFNDSQRQ ATKDAGVIAG LNVMRIINEP TAAAIAYGLD KKATSVGEKN
201 VLIFDLGGGT FDVSLLTIEE GIFEVKATAG DTHLGGEDFD NRMVNHFVQE
251 FKRKSKKDIT GNPRALRRLR TSCERAKRTL SSTAQTTIEI DSLYEGIDFY
301 STITRARFEE LNMDLFRKCM EPVEKCLRDA KMDKSTVHDV VLVGGSTRIP
351 KVQQLLQDFF NGKELCKSIN PDEAVAYGAA VQGAILSGEG NEKVQDLLLL
401 DVTPLSLGLE TAGGVMTTLI PRNTTIPTKK EQVFSTYSDN QPGVLIQVYE
451 GERARTKDNN LLGKFELSGI PPAPRGVPQI TVCFDIDANG ILNVSAEDKT
501 TGQKNKITIT NDKGRLSKDE IEKMVQEAEK YKSEDEEHKK KVEAKNALEN
551 YAYNMRNTIQ DEKIGEKLPA ADKKKIEDSI EQAIQWLEGN QLAEADEFED
601 KMKELESICN PIIAKMYQGA GGEAGGPGAS GMDDDAPPAS GGAGPKIEEV
651 D
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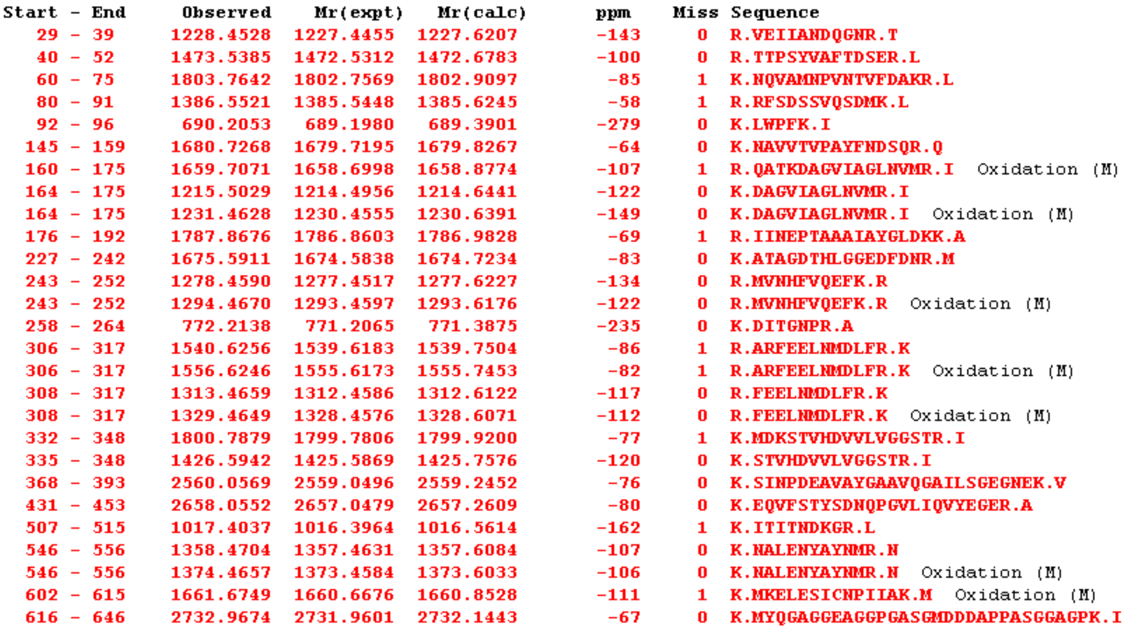
Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   29 - 39     1228.4528  1227.4455  1227.6207     -143     0  R.VEIIANDQGNR.T
   40 - 52     1473.5385  1472.5312  1472.6783     -100     0  R.TTPSYVAFTDSER.L
   60 - 75     1803.7642  1802.7569  1802.9097      -85     1  K.NQVAMNPVNTVFDAKR.L
   80 - 91     1386.5521  1385.5448  1385.6245      -58     1  R.RFSDSSVQSDMK.L
   92 - 96      690.2053   689.1980   689.3901     -279     0  K.LWPFK.I
  145 - 159    1680.7268  1679.7195  1679.8267      -64     0  K.NAVVTVPAYFNDSQR.Q
  160 - 175    1659.7071  1658.6998  1658.8774     -107     1  R.QATKDAGVIAGLNVMR.I  Oxidation (M)
  164 - 175    1215.5029  1214.4956  1214.6441     -122     0  K.DAGVIAGLNVMR.I
  164 - 175    1231.4628  1230.4555  1230.6391     -149     0  K.DAGVIAGLNVMR.I  Oxidation (M)
  176 - 192    1787.8676  1786.8603  1786.9828      -69     1  R.IINEPTAAAIAYGLDKK.A
  227 - 242    1675.5911  1674.5838  1674.7234      -83     0  K.ATAGDTHLGGEDFDNR.M
  243 - 252    1278.4590  1277.4517  1277.6227     -134     0  R.MVNHFVQEFK.R
  243 - 252    1294.4670  1293.4597  1293.6176     -122     0  R.MVNHFVQEFK.R  Oxidation (M)
  258 - 264     772.2138   771.2065   771.3875     -235     0  K.DITGNPR.A
  306 - 317    1540.6256  1539.6183  1539.7504      -86     1  R.ARFEELNMDLFR.K
  306 - 317    1556.6246  1555.6173  1555.7453      -82     1  R.ARFEELNMDLFR.K  Oxidation (M)
  308 - 317    1313.4659  1312.4586  1312.6122     -117     0  R.FEELNMDLFR.K
  308 - 317    1329.4649  1328.4576  1328.6071     -112     0  R.FEELNMDLFR.K  Oxidation (M)
  332 - 348    1800.7879  1799.7806  1799.9200      -77     1  K.MDKSTVHDVVLVGGSTR.I
  335 - 348    1426.5942  1425.5869  1425.7576     -120     0  K.STVHDVVLVGGSTR.I
  368 - 393    2560.0569  2559.0496  2559.2452      -76     0  K.SINPDEAVAYGAAVQGAILSGEGNEK.V
  431 - 453    2658.0552  2657.0479  2657.2609      -80     0  K.EQVFSTYSDNQPGVLIQVYEGER.A
  507 - 515    1017.4037  1016.3964  1016.5614     -162     1  K.ITITNDKGR.L
  546 - 556    1358.4704  1357.4631  1357.6084     -107     0  K.NALENYAYNMR.N
  546 - 556    1374.4657  1373.4584  1373.6033     -106     0  K.NALENYAYNMR.N  Oxidation (M)
  602 - 615    1661.6749  1660.6676  1660.8528     -111     1  K.MKELESICNPIIAK.M  Oxidation (M)
  616 - 646    2732.9674  2731.9601  2732.1443      -67     0  K.MYQGAGGEAGGPGASGMDDDAPPASGGAGPK.I
```

Spot No.: **6**

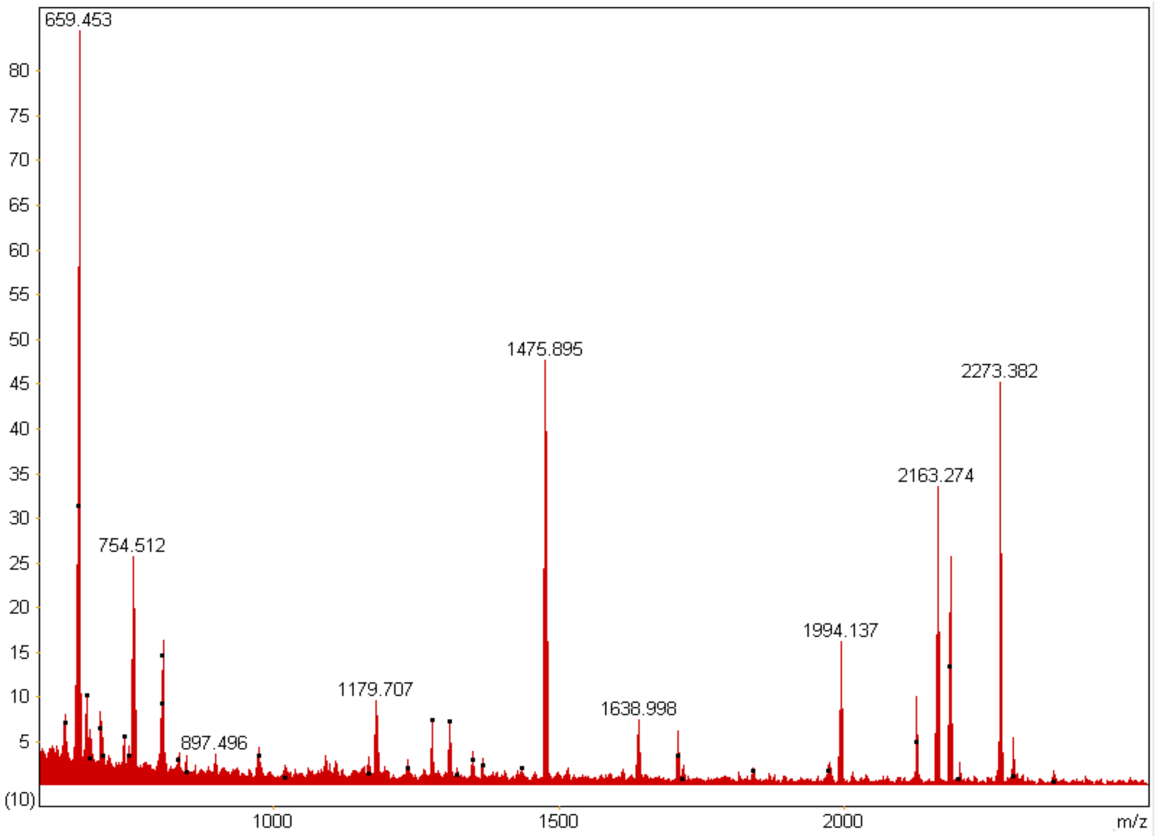
Mascot score: **93**   Sequence coverage %: **19**

NCBI accession No.: **gi| 1695717**

Matched peptides No.: **11**   Total peptides No.: **21**

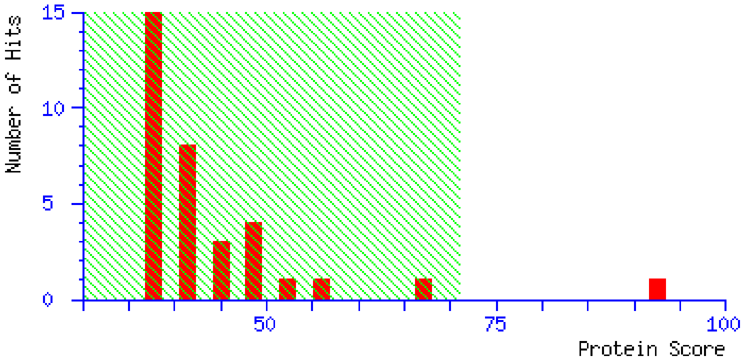
Calculated Mr: **73862**   Calculated *p*I: **5.08**

Annotated PMF **spectra:**

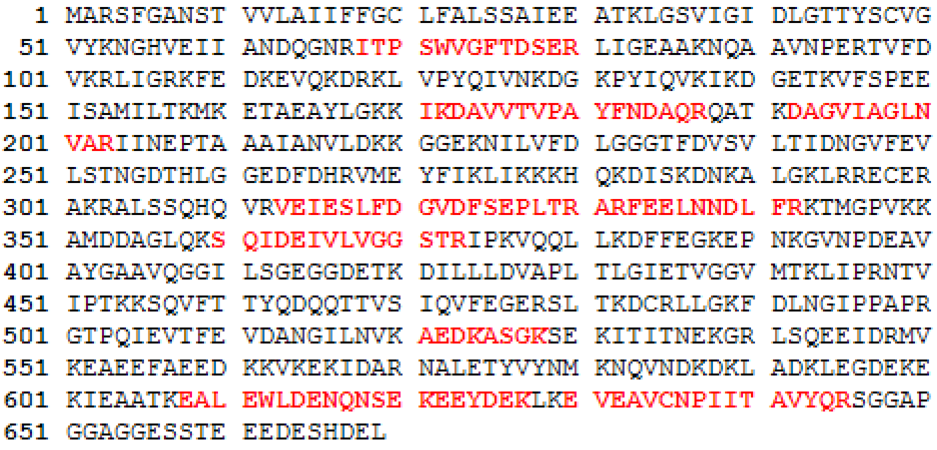


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

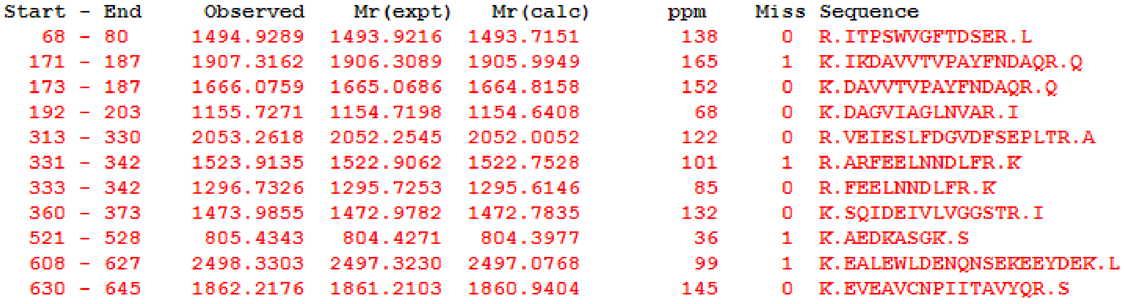


Matched peptide sequences: shown in **Bold Red**



1 MARSFGANST VVLAIIFFGC LFALSSAIEE ATKLGSVIGI DLGTTYSCVG
51 VYKNGHVEII ANDQGNR**ITP** **SWVGFTDSER** LIGEAAKNQA AVNPERTVFD
101 VKRLIGRKFE DKEVQKDRKL VPYQIVNKDG KPYIQVKIKD GETKVFSPEE
151 ISAMILTKMK ETAEAYLGKK **IKDAVVTVPA** **YFNDAQR**QAT K**DAGVIAGLN**
201 **VAR**IINEPTA AAIANVLDKK GGEKNILVFD LGGGTFDVSV LTIDNGVFEV
251 LSTNGDTHLG GEDFDHRVME YFIKLIKKKH QKDISKDNKA LGKLRRECER
301 AKRALSSQHQ VR**VEIESLFD** **GVDFSEPLTR** **ARFEELNNDL** **FR**KTMGPVKK
351 AMDDAGLQK**S** **QIDEIVLVGG** **STR**IPKVQQL LKDFFEGKEP NKGVNPDEAV
401 AYGAAVQGGI LSGEGGDETK DILLLDVAPL TLGIETVGGV MTKLIPRNTV
451 IPTKKSQVFT TYQDQQTTVS IQVFEGERSL TKDCRLLGKF DLNGIPPAPR
501 GTPQIEVTFE VDANGILNVK **AEDKASGK**SE KITITNEKGR LSQEEIDRMV
551 KEAEEFAEED KKVKEKIDAR NALETYVYNM KNQVNDKDKL ADKLEGDEKE
601 KIEAATK**EAL** **EWLDENQNSE** **KEEYDEK**LKE **VEAVCNPIIT** **AVYQR**SGGAP
651 GGAGGESSTE EEDESHDEL

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
68 - 80	1494.9289	1493.9216	1493.7151	138	0	R.ITPSWVGFTDSER.L
171 - 187	1907.3162	1906.3089	1905.9949	165	1	K.IKDAVVTVPAYFNDAQR.Q
173 - 187	1666.0759	1665.0686	1664.8158	152	0	K.DAVVTVPAYFNDAQR.Q
192 - 203	1155.7271	1154.7198	1154.6408	68	0	K.DAGVIAGLNVAR.I
313 - 330	2053.2618	2052.2545	2052.0052	122	0	R.VEIESLFDGVDFSEPLTR.A
331 - 342	1523.9135	1522.9062	1522.7528	101	1	R.ARFEELNNDLFR.K
333 - 342	1296.7326	1295.7253	1295.6146	85	0	R.FEELNNDLFR.K
360 - 373	1473.9855	1472.9782	1472.7835	132	0	K.SQIDEIVLVGGSTR.I
521 - 528	805.4343	804.4271	804.3977	36	1	K.AEDKASGK.S
608 - 627	2498.3303	2497.3230	2497.0768	99	1	K.EALEWLDENQNSEKEEYDEK.L
630 - 645	1862.2176	1861.2103	1860.9404	145	0	K.EVEAVCNPIITAVYQR.S

Spot No.: **7**

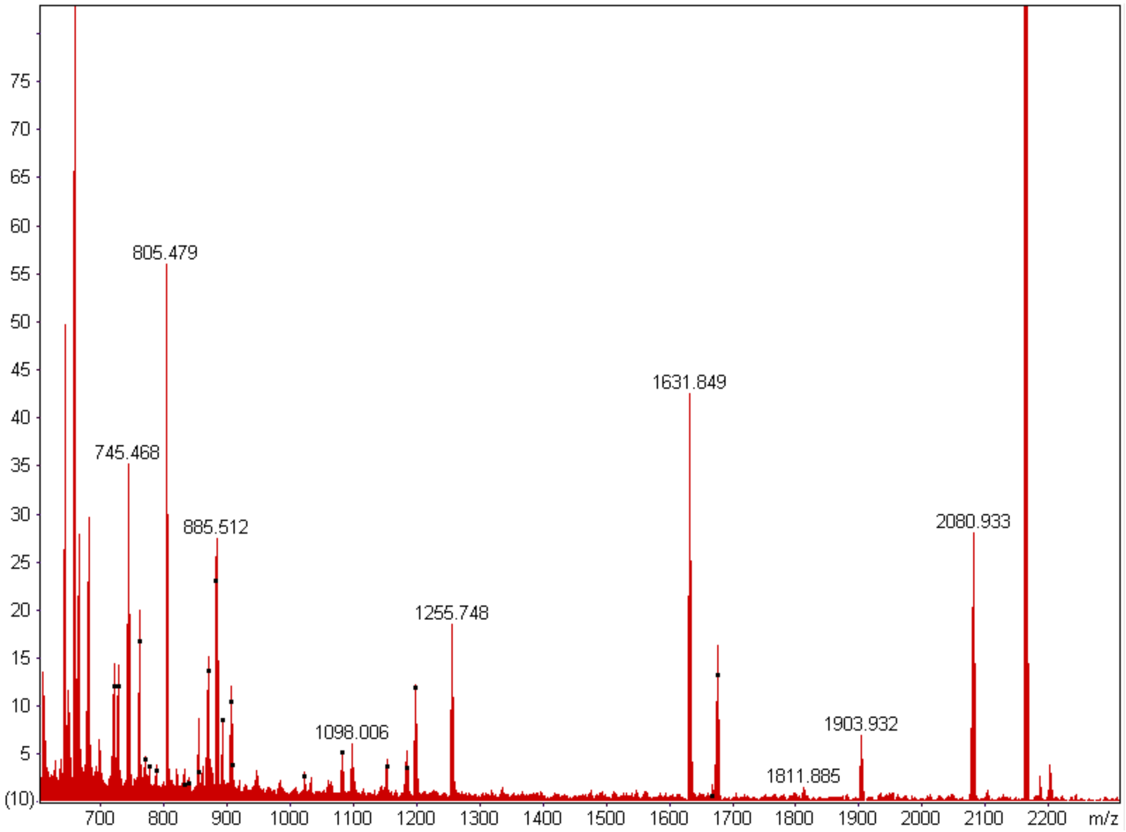
Mascot score: **99**   Sequence coverage %: **20**

NCBI accession No.: **gi| 2493122**

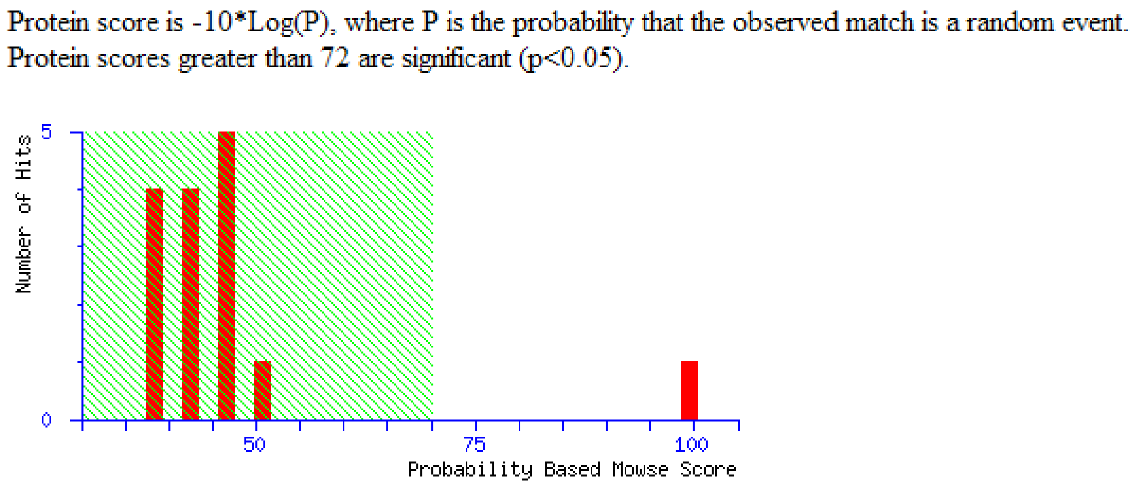
Matched peptides No.: **11**   Total peptides No.: **27**

Calculated Mr: **69030**   Calculated *p*I: **5.19**

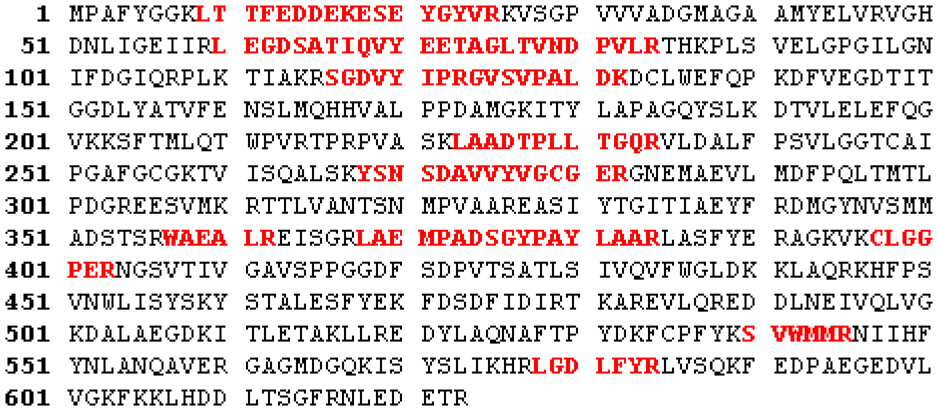
Annotated PMF **spectra:**



Probability Based Mowse Score:

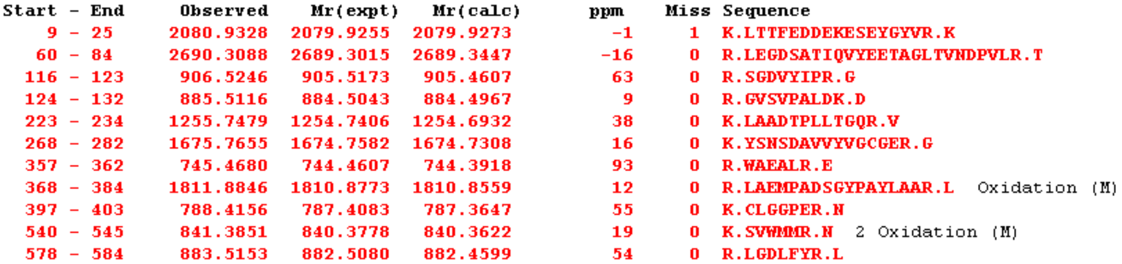

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

Matched peptide sequences: shown in Bold Red



1 MPAFYGGK**LT TFEDDEKESE YGYVR**KVSGP VVVADGMAGA AMYELVRVGH
51 DNLIGEIIR**L EGDSATIQVY EETAGLTVND PVLR**THKPLS VELGPGILGN
101 IFDGIQRPLK TIAKR**SGDVY IPRGVSVPAL DK**DCLWEFQP KDFVEGDTIT
151 GGDLYATVFE NSLMQHHVAL PPDAMGKITY LAPAGQYSLK DTVLELEFQG
201 VKKSFTMLQT WPVRTPRPVA SK**LAADTPLL TGQR**VLDALF PSVLGGTCAI
251 PGAFGCGKTV ISQALSK**YSN SDAVVYVGCG ER**GNEMAEVL MDFPQLTMTL
301 PDGREESVMK RTTLVANTSN MPVAAREASI YTGITIAEYF RDMGYNVSMM
351 ADSTSR**WAEA LR**EISGR**LAE MPADSGYPAY LAAR**LASFYE RAGKVK**CLGG**
401 **PER**NGSVTIV GAVSPPGGDF SDPVTSATLS IVQVFWGLDK KLAQRKHFPS
451 VNWLISYSKY STALESFYEK FDSDFIDIRT KAREVLQRED DLNEIVQLVG
501 KDALAEGDKI TLETAKLLRE DYLAQNAFTP YDKFCPFYK**S VWMMR**NIIHF
551 YNLANQAVER GAGMDGQKIS YSLIKHR**LGD LFYR**LVSQKF EDPAEGEDVL
601 VGKFKKLHDD LTSGFRNLED ETR

Matched peptides information:



```
Start - End      Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    9 - 25      2080.9328  2079.9255  2079.9273       -1      1  K.LTTFEDDEKESEYGYVR.K
   60 - 84      2690.3088  2689.3015  2689.3447      -16      0  R.LEGDSATIQVYEETAGLTVNDPVLR.T
  116 - 123      906.5246   905.5173   905.4607       63      0  R.SGDVYIPR.G
  124 - 132      885.5116   884.5043   884.4967        9      0  R.GVSVPALDK.D
  223 - 234     1255.7479  1254.7406  1254.6932       38      0  K.LAADTPLLTGQR.V
  268 - 282     1675.7655  1674.7582  1674.7308       16      0  K.YSNSDAVVYVGCGER.G
  357 - 362      745.4680   744.4607   744.3918       93      0  R.WAEALR.E
  368 - 384     1811.8846  1810.8773  1810.8559       12      0  R.LAEMPADSGYPAYLAAR.L   Oxidation (M)
  397 - 403      788.4156   787.4083   787.3647       55      0  K.CLGGPER.N
  540 - 545      841.3851   840.3778   840.3622       19      0  K.SVWMMR.N  2 Oxidation (M)
  578 - 584      883.5153   882.5080   882.4599       54      0  R.LGDLFYR.L
```

Spot No.: **8**

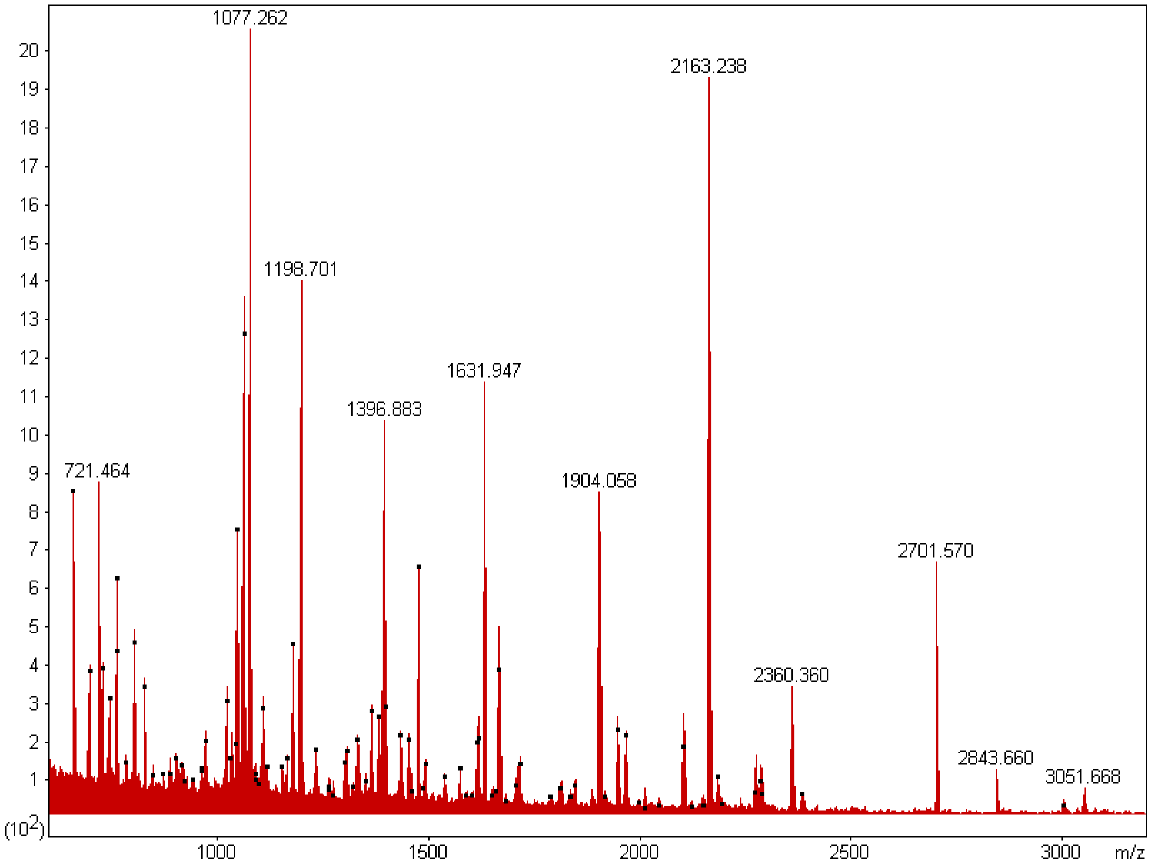
Mascot score: **129** Sequence coverage %: **36**

NCBI accession No.: **gi| 312282199**

Matched peptides No.: **24** Total peptides No.: **64**

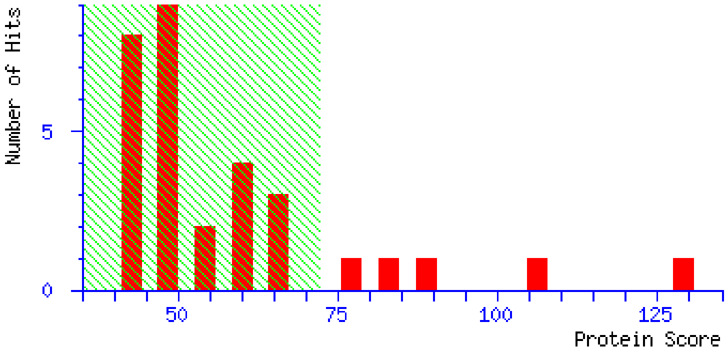
Calculated Mr: **74860** Calculated *p*I: **6.13**

Annotated PMF **spectra:**

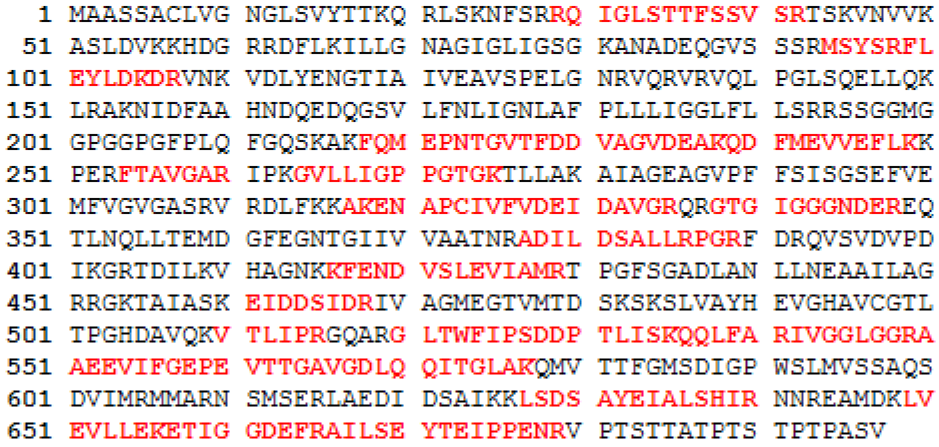


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

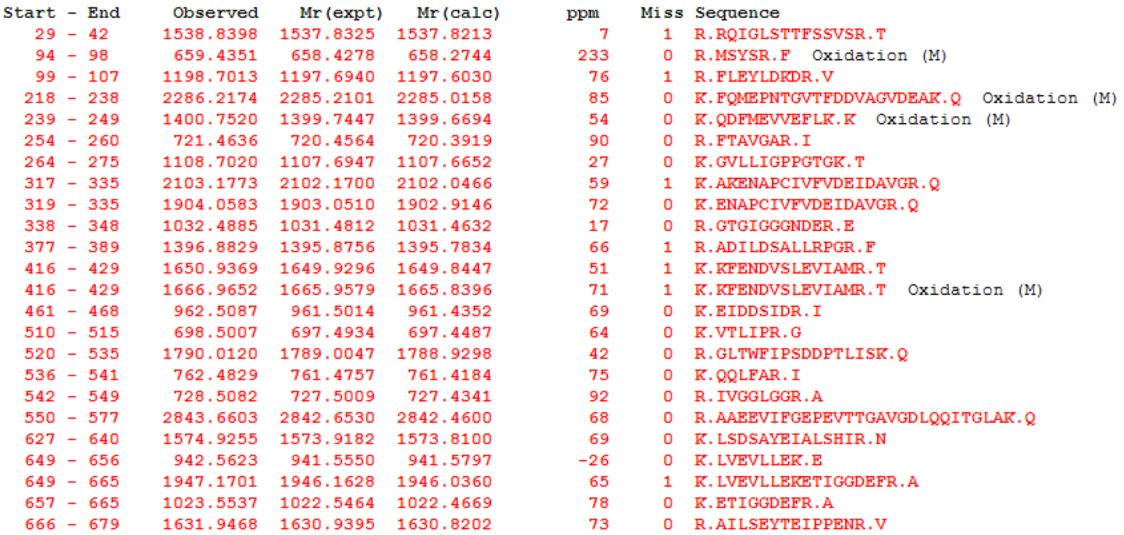


Matched peptide sequences: shown in Bold Red



1 MAASSACLVG NGLSVYTTKQ RLSKNFSR**RQ** **IGLSTTFSSV** **SR**TSKVNVVK
51 ASLDVKKHDG RRDFLKILLG NAGIGLIGSG KANADEQGVS SSR**MSYSRFL**
101 **EYLDKDR**VNK VDLYENGTIA IVEAVSPELG NRVQRVRVQL PGLSQELLQK
151 LRAKNIDFAA HNDQEDQGSV LFNLIGNLAF PLLLIGGLFL LSRRSSGGMG
201 GPGGPGFPLQ FGQSKAK**FQM** **EPNTGVTFDD** **VAGVDEAKQD** **FMEVVEFLK**K
251 PER**FTAVGAR** IPK**GVLLIGP** **PGTGK**TLLAK AIAGEAGVPF FSISGSEFVE
301 MFVGVGASRV RDLFKK**AKEN** **APCIVFVDEI** **DAVGR**QR**GTG** **IGGGNDER**EQ
351 TLNQLLTEMD GFEGNTGIIV VAATNR**ADIL** **DSALLRPGR**F DRQVSVDVPD
401 IKGRTDILKV HAGNK**KFEND** **VSLEVIAMR**T PGFSGADLAN LLNEAAILAG
451 RRGKTAIASK **EIDDSIDR**IV AGMEGTVMTD SKSKSLVAYH EVGHAVCGTL
501 TPGHDAVQK**V** **TLIPR**GQAR**G** **LTWFIPSDDP** **TLISKQQLFA** **RIVGGLGGRA**
551 **AEEVIFGEPE** **VTTGAVGDLQ** **QITGLAK**QMV TTFGMSDIGP WSLMVSSAQS
601 DVIMRMMARN SMSERLAEDI DSAIKK**LSDS** **AYEIALSHIR** NNREAMDK**LV**
651 **EVLLEKETIG** **GDEFRAILSE** **YTEIPPENR**V PTSTTATPTS TPTPASV

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)     ppm   Miss Sequence
   29 - 42     1538.8398  1537.8325  1537.8213       7     1  R.RQIGLSTTFSSVSR.T
   94 - 98      659.4351   658.4278   658.2744     233     0  R.MSYSR.F   Oxidation (M)
   99 - 107    1198.7013  1197.6940  1197.6030      76     1  R.FLEYLDKDR.V
  218 - 238    2286.2174  2285.2101  2285.0158      85     0  K.FQMEPNTGVTFDDVAGVDEAK.Q  Oxidation (M)
  239 - 249    1400.7520  1399.7447  1399.6694      54     0  K.QDFMEVVEFLK.K  Oxidation (M)
  254 - 260     721.4636   720.4564   720.3919      90     0  R.FTAVGAR.I
  264 - 275    1108.7020  1107.6947  1107.6652      27     0  K.GVLLIGPPGTGK.T
  317 - 335    2103.1773  2102.1700  2102.0466      59     1  K.AKENAPCIVFVDEIDAVGR.Q
  319 - 335    1904.0583  1903.0510  1902.9146      72     0  K.ENAPCIVFVDEIDAVGR.Q
  338 - 348    1032.4885  1031.4812  1031.4632      17     0  R.GTGIGGGNDER.E
  377 - 389    1396.8829  1395.8756  1395.7834      66     1  R.ADILDSALLRPGR.F
  416 - 429    1650.9369  1649.9296  1649.8447      51     1  K.KFENDVSLEVIAMR.T
  416 - 429    1666.9652  1665.9579  1665.8396      71     1  K.KFENDVSLEVIAMR.T  Oxidation (M)
  461 - 468     962.5087   961.5014   961.4352      69     0  K.EIDDSIDR.I
  510 - 515     698.5007   697.4934   697.4487      64     0  K.VTLIPR.G
  520 - 535    1790.0120  1789.0047  1788.9298      42     0  R.GLTWFIPSDDPTLISK.Q
  536 - 541     762.4829   761.4757   761.4184      75     0  K.QQLFAR.I
  542 - 549     728.5082   727.5009   727.4341      92     0  R.IVGGLGGR.A
  550 - 577    2843.6603  2842.6530  2842.4600      68     0  R.AAEEVIFGEPEVTTGAVGDLQQITGLAK.Q
  627 - 640    1574.9255  1573.9182  1573.8100      69     0  K.LSDSAYEIALSHIR.N
  649 - 656     942.5623   941.5550   941.5797     -26     0  K.LVEVLLEK.E
  649 - 665    1947.1701  1946.1628  1946.0360      65     1  K.LVEVLLEKETIGGDEFR.A
  657 - 665    1023.5537  1022.5464  1022.4669      78     0  K.ETIGGDEFR.A
  666 - 679    1631.9468  1630.9395  1630.8202      73     0  R.AILSEYTEIPPENR.V
```

Spot No.: **9**

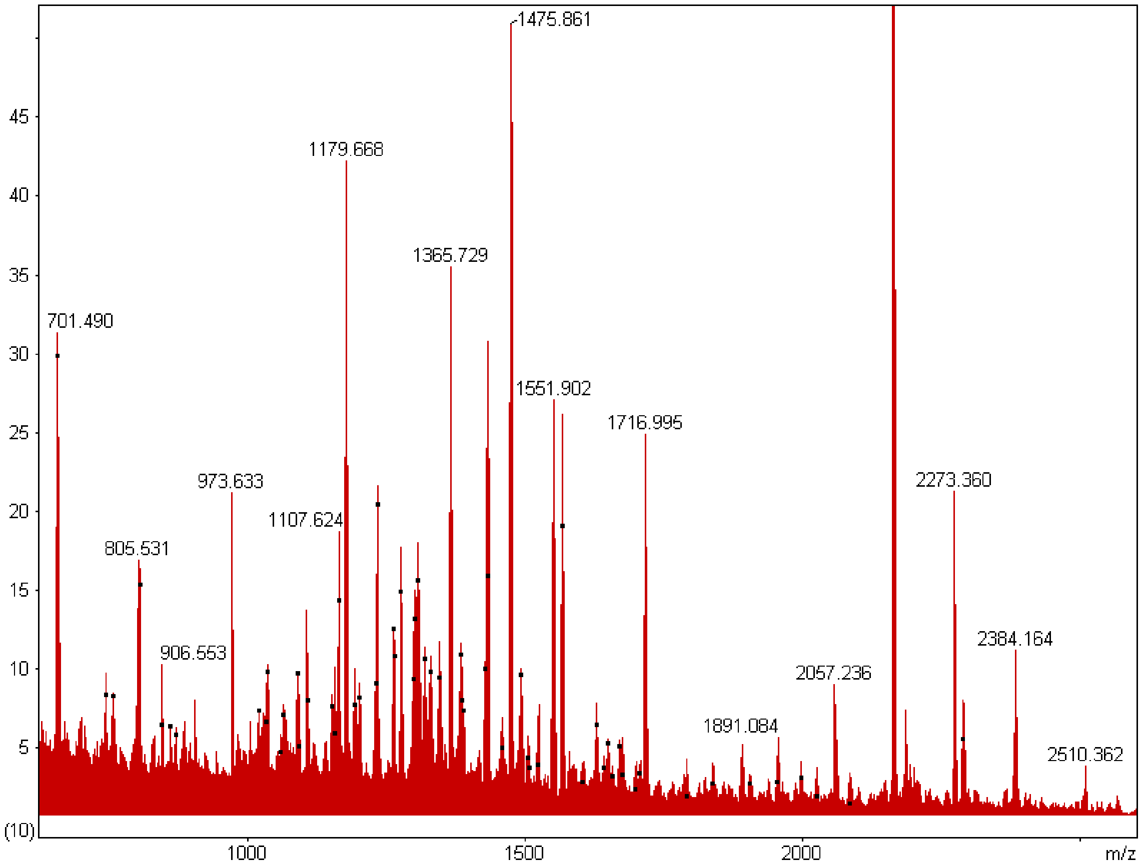
Mascot score: **90** Sequence coverage %: **29**

NCBI accession No.: **gi| 20467991**

Matched peptides No.: **18** Total peptides No.: **58**

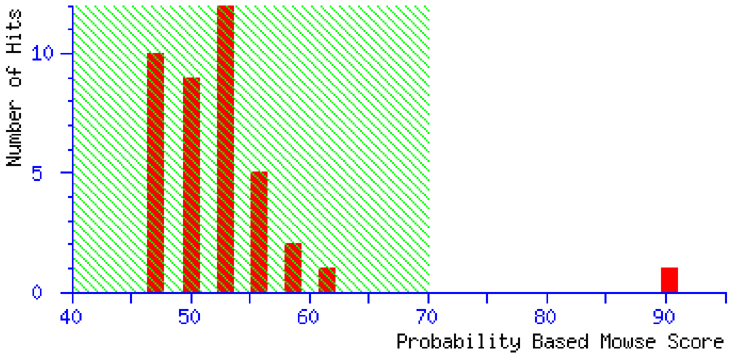
Calculated Mr: **74547** Calculated *p*I: **6.75**

Annotated PMF **spectra:**

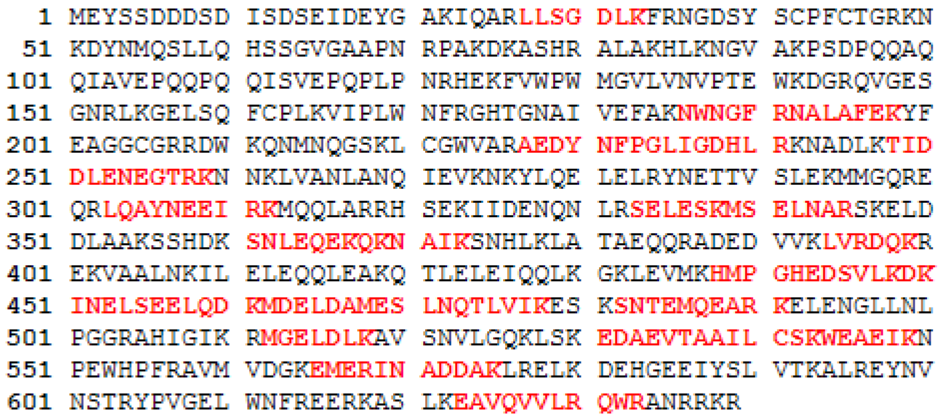


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

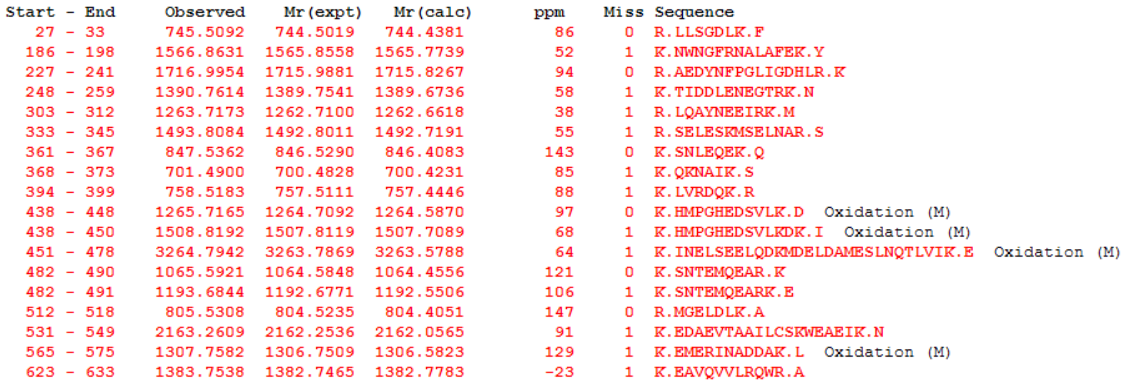


Matched peptide sequences: shown in Bold Red



1 MEYSSDDDSD ISDSEIDEYG AKIQAR**LLSG** **DLK**FRNGDSY SCPFCTGRKN
51 KDYNMQSLLQ HSSGVGAAPN RPAKDKASHR ALAKHLKNGV AKPSDPQQAQ
101 QIAVEPQQPQ QISVEPQPLP NRHEKFVWPW MGVLVNVPTE WKDGRQVGES
151 GNRLKGELSQ FCPLKVIPLW NFRGHTGNAI VEFAK**NWNGF** **RNALAFEK**YF
201 EAGGCGRRDW KQNMNQGSKL CGWVAR**AEDY** **NFPGLIGDHL** **R**KNADLK**TID**
251 **DLENEGTRK**N NKLVANLANQ IEVKNKYLQE LELRYNETTV SLEKMMGQRE
301 QR**LQAYNEEI** **RK**MQQLARRH SEKIIDENQN LR**SELESKMS** **ELNAR**SKELD
351 DLAAKSSHDK **SNLEQEKQKN** **AIK**SNHLKLA TAEQQRADED VVK**LVRDQK**R
401 EKVAALNKIL ELEQQLEAKQ TLELEIQQLK GKLEVMK**HMP** **GHEDSVLKDK**
451 **INELSEELQD** **KMDELDAMES** **LNQTLVIK**ES K**SNTEMQEAR** **K**ELENGLLNL
501 PGGRAHIGIK R**MGELDLK**AV SNVLGQKLSK **EDAEVTAAIL** **CSKWEAEIK**N
551 PEWHPFRAVM VDGK**EMERIN** **ADDAK**LRELK DEHGEEIYSL VTKALREYNV
601 NSTRYPVGEL WNFREERKAS LK**EAVQVVLR** **QWR**ANRRKR

Matched peptides information:



```
 Start - End      Observed     Mr(expt)    Mr(calc)       ppm    Miss Sequence
    27 - 33       745.5092     744.5019    744.4381        86      0  R.LLSGDLK.F
   186 - 198     1566.8631    1565.8558   1565.7739        52      1  K.NWNGFRNALAFEK.Y
   227 - 241     1716.9954    1715.9881   1715.8267        94      0  R.AEDYNFPGLIGDHLR.K
   248 - 259     1390.7614    1389.7541   1389.6736        58      1  K.TIDDLENEGTRK.N
   303 - 312     1263.7173    1262.7100   1262.6618        38      1  R.LQAYNEEIRK.M
   333 - 345     1493.8084    1492.8011   1492.7191        55      1  R.SELESKMSELNAR.S
   361 - 367      847.5362     846.5290    846.4083       143      0  K.SNLEQEK.Q
   368 - 373      701.4900     700.4828    700.4231        85      1  K.QKNAIK.S
   394 - 399      758.5183     757.5111    757.4446        88      1  K.LVRDQK.R
   438 - 448     1265.7165    1264.7092   1264.5870        97      0  K.HMPGHEDSVLK.D   Oxidation (M)
   438 - 450     1508.8192    1507.8119   1507.7089        68      1  K.HMPGHEDSVLKDK.I   Oxidation (M)
   451 - 478     3264.7942    3263.7869   3263.5788        64      1  K.INELSEELQDKMDELDAMESLNQTLVIK.E   Oxidation (M)
   482 - 490     1065.5921    1064.5848   1064.4556       121      0  K.SNTEMQEAR.K
   482 - 491     1193.6844    1192.6771   1192.5506       106      1  K.SNTEMQEARK.E
   512 - 518      805.5308     804.5235    804.4051       147      0  R.MGELDLK.A
   531 - 549     2163.2609    2162.2536   2162.0565        91      1  K.EDAEVTAAILCSKWEAEIK.N
   565 - 575     1307.7582    1306.7509   1306.5823       129      1  K.EMERINADDAK.L   Oxidation (M)
   623 - 633     1383.7538    1382.7465   1382.7783       -23      1  K.EAVQVVLRQWR.A
```

Spot No.: **10**

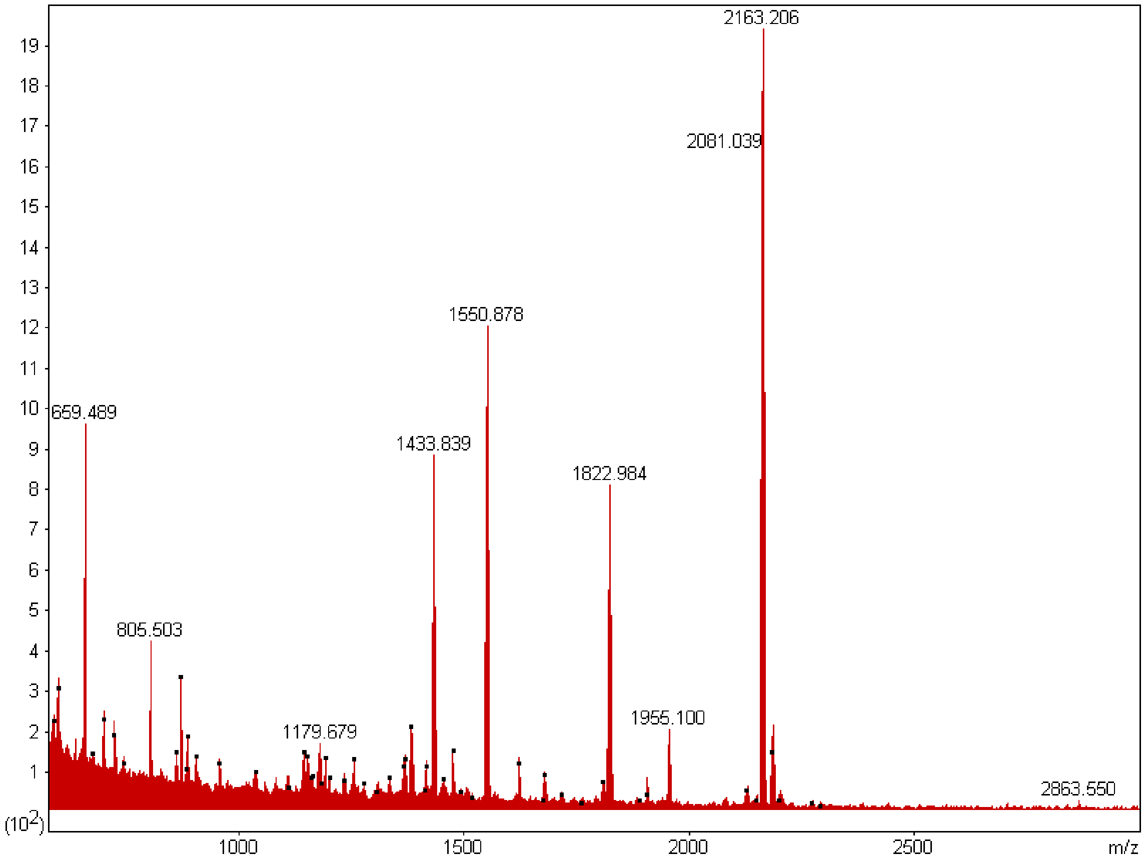
Mascot score: **95** Sequence coverage %: **22**

NCBI accession No.: **gi| 312283065**

Matched peptides No.: **16** Total peptides No.: **35**

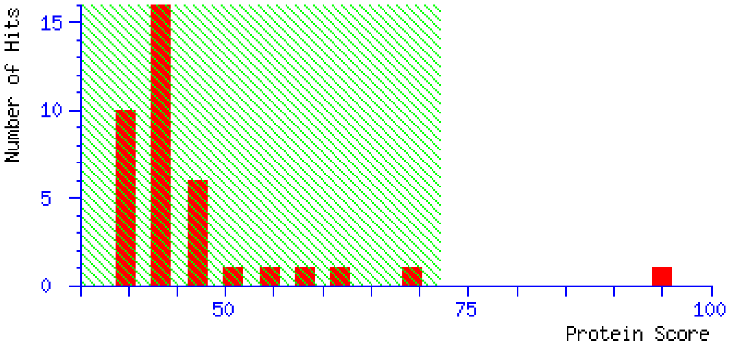
Calculated Mr: **73489** Calculated *p*I: **5.72**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in **Bold Red**

1 **MATAALLR**SI RRREVASTPF SAYKCLSSSG KISFNGSYLG QNWRSFSRAF
51 SSKPAGNDVI GIDLGTTNSC VAVMEGKNPK **VIENAEGAR**T TPSVVAFNPK
101 GELLVGTPAK RQAVTNPTNT VFGTKRLIGR KFDDPQTQKE MKMVPYKIVR
151 APNGDAWVEA NGQQYSPSQV GAFVLTK**MKE** **TAEAYLGK**SV KK**AVVTVPAY**
201 **FNDAQR**QATK DAGR**IAGLDV** **ERIINEPTAA** **ALSYGMTNK**E GLIAVFDLGG
251 GTFDISVLEI SNGVFEVKAT NGDTFLGGED FDNALLDFLV NEFKTTEGID
301 LAKDR**LALQR** LREAAEKAKI ELSSTSQTEI NLPFITADAS GAKHFNITLT
351 RSR**FETLVNH** **LIER**TRDPCK NCLKDAGISA K**EVDEVLLVG** **GMTR**VPK**VQS**
401 **VVSEIFGK**TP SK**GVNPDEAV** **AMGAALQGGI** **LR**GDVKELLL LDVTPLSLGI
451 ETLGGVFTRL ISRNTTIPTK KSQVFSTAAD NQTQVGIR**VL** **QGER**EMATDN
501 KLLGEFDLVG IPPSPRGIPQ IEVTFDIDAN GIVTVSAKDK TTGK**EQQITI**
551 **R**SSGGLSEDD IQKMVREAEL HAQKDKERKD LIDTKNTADT TIYSIEK**SLG**
601 **EYR**EKIPSEV AK**EIEDAVSD** **LR**SATSGDDL NEIKAKIDAA NKAVSKIGEH
651 MSNGGSGGGS APGGGAQKGS DEAPEAEYEE VKK

Matched peptides information:

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
1 - 8	862.5249	861.5176	861.4742	50	0	-.MATAALLR.S Oxidation (M)
81 - 89	958.5598	957.5525	957.4879	67	0	K.VIENAEGAR.T
178 - 188	1256.7208	1255.7135	1255.6118	81	1	K.MKETAEAYLGK.S Oxidation (M)
193 - 206	1550.8776	1549.8703	1549.7889	53	0	K.AVVTVPAYFNDAQR.Q
215 - 222	872.5613	871.5540	871.4763	89	0	R.IAGLDVER.I
223 - 239	1809.9646	1808.9573	1808.8978	33	0	R.IINEPTAAALSYGMTNK.E Oxidation (M)
306 - 310	600.4723	599.4650	599.3755	149	0	R.LALQR.L
354 - 364	1370.7903	1369.7830	1369.7354	35	0	R.FETLVNHLIER.T
382 - 394	1417.8149	1416.8076	1416.7283	56	0	K.EVDEVLLVGGMTR.V
382 - 394	1433.8390	1432.8317	1432.7232	76	0	K.EVDEVLLVGGMTR.V Oxidation (M)
398 - 408	1192.7085	1191.7012	1191.6499	43	0	K.VQSVVSEIFGK.T
413 - 432	1955.1000	1954.0927	1953.9942	50	0	K.GVNPDEAVAMGAALQGGILR.G Oxidation (M)
489 - 494	701.4826	700.4753	700.3868	126	0	R.VLQGER.E
545 - 551	887.5645	886.5572	886.4872	79	0	K.EQQITIR.S
598 - 603	724.4592	723.4520	723.3551	134	0	K.SLGEYR.E
613 - 622	1146.6350	1145.6277	1145.5564	62	0	K.EIEDAVSDLR.S

Spot No.: **11**

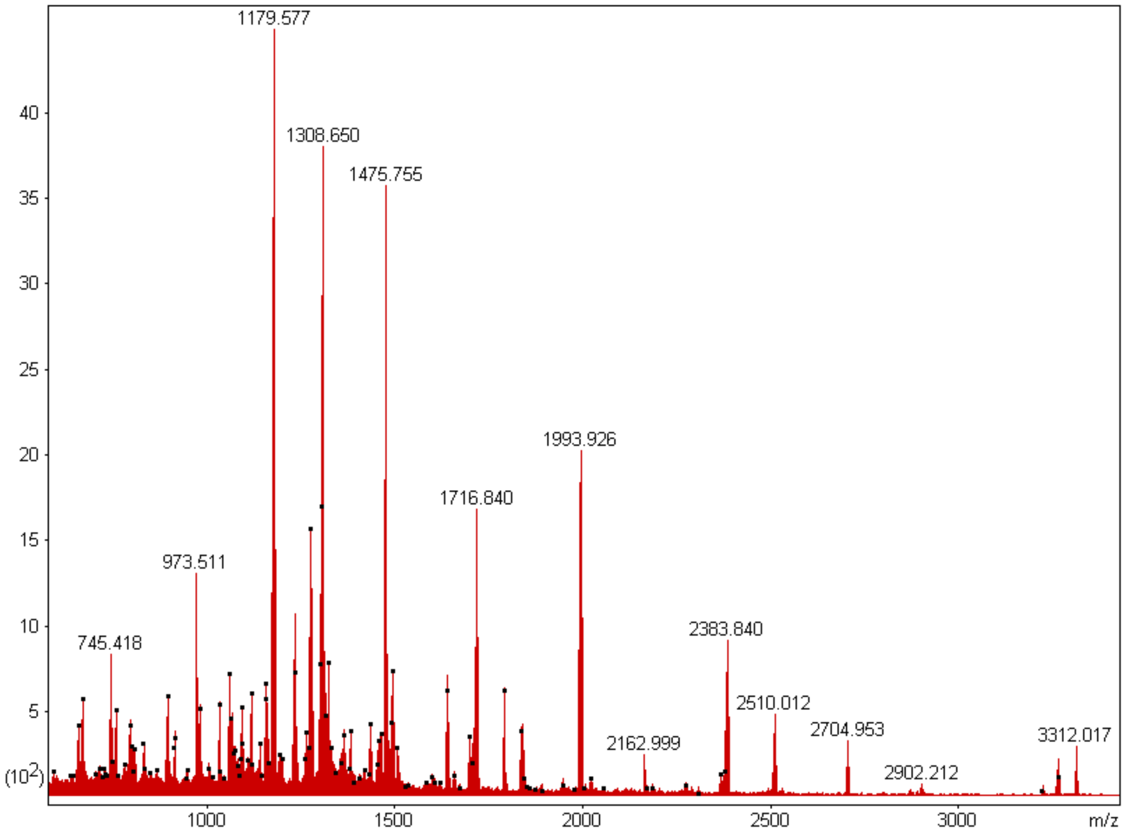
Mascot score: **146** Sequence coverage %: **43**

NCBI accession No.: **gi| 312282567**

Matched peptides No.: **15** Total peptides No.: **29**

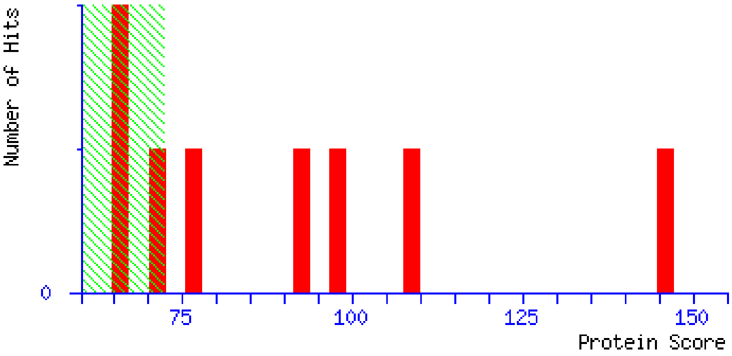
Calculated Mr: **42944** Calculated *p*I: **7.59**

Annotated PMF **spectra:**

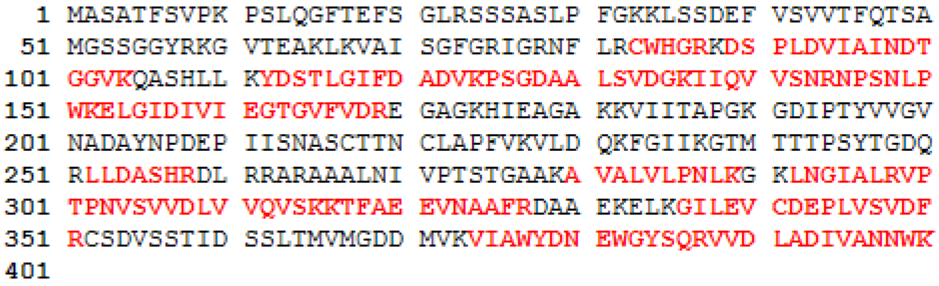


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

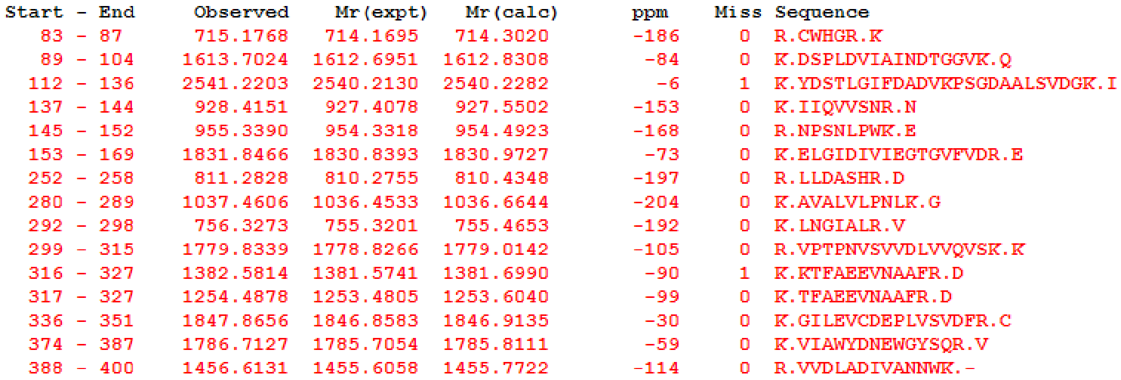


Matched peptide sequences: shown in Bold Red



1 MASATFSVPK PSLQGFTEFS GLRSSSASLP FGKKLSSDEF VSVVTFQTSA
51 MGSSGGYRKG VTEAKLKVAI SGFGRIGRNF LR**CWHGR**K**DS** **PLDVIAINDT**
101 **GGVK**QASHLL K**YDSTLGIFD** **ADVKPSGDAA** **LSVDGKIIQV** **VSNRNPSNLP**
151 **WKELGIDIVI** **EGTGVFVDR**E GAGKHIEAGA KKVIITAPGK GDIPTYVVGV
201 NADAYNPDEP IISNASCTTN CLAPFVKVLD QKFGIIKGTM TTTPSYTGDQ
251 R**LLDASHR**DL RRARAAALNI VPTSTGAAK**A** **VALVLPNLK**G K**LNGIALRVP**
301 **TPNVSVVDLV** **VQVSKKTFAE** **EVNAAFR**DAA EKELK**GILEV** **CDEPLVSVDF**
351 **R**CSDVSSTID SSLTMVMGDD MVK**VIAWYDN** **EWGYSQRVVD** **LADIVANNWK**
401

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
83 - 87	715.1768	714.1695	714.3020	-186	0	R.CWHGR.K
89 - 104	1613.7024	1612.6951	1612.8308	-84	0	K.DSPLDVIAINDTGGVK.Q
112 - 136	2541.2203	2540.2130	2540.2282	-6	1	K.YDSTLGIFDADVKPSGDAALSVDGK.I
137 - 144	928.4151	927.4078	927.5502	-153	0	K.IIQVVSNR.N
145 - 152	955.3390	954.3318	954.4923	-168	0	R.NPSNLPWK.E
153 - 169	1831.8466	1830.8393	1830.9727	-73	0	K.ELGIDIVIEGTGVFVDR.E
252 - 258	811.2828	810.2755	810.4348	-197	0	R.LLDASHR.D
280 - 289	1037.4606	1036.4533	1036.6644	-204	0	K.AVALVLPNLK.G
292 - 298	756.3273	755.3201	755.4653	-192	0	K.LNGIALR.V
299 - 315	1779.8339	1778.8266	1779.0142	-105	0	R.VPTPNVSVVDLVVQVSK.K
316 - 327	1382.5814	1381.5741	1381.6990	-90	1	K.KTFAEEVNAAFR.D
317 - 327	1254.4878	1253.4805	1253.6040	-99	0	K.TFAEEVNAAFR.D
336 - 351	1847.8656	1846.8583	1846.9135	-30	0	K.GILEVCDEPLVSVDFR.C
374 - 387	1786.7127	1785.7054	1785.8111	-59	0	K.VIAWYDNEWGYSQR.V
388 - 400	1456.6131	1455.6058	1455.7722	-114	0	R.VVDLADIVANNWK.-

Spot No.: **12**

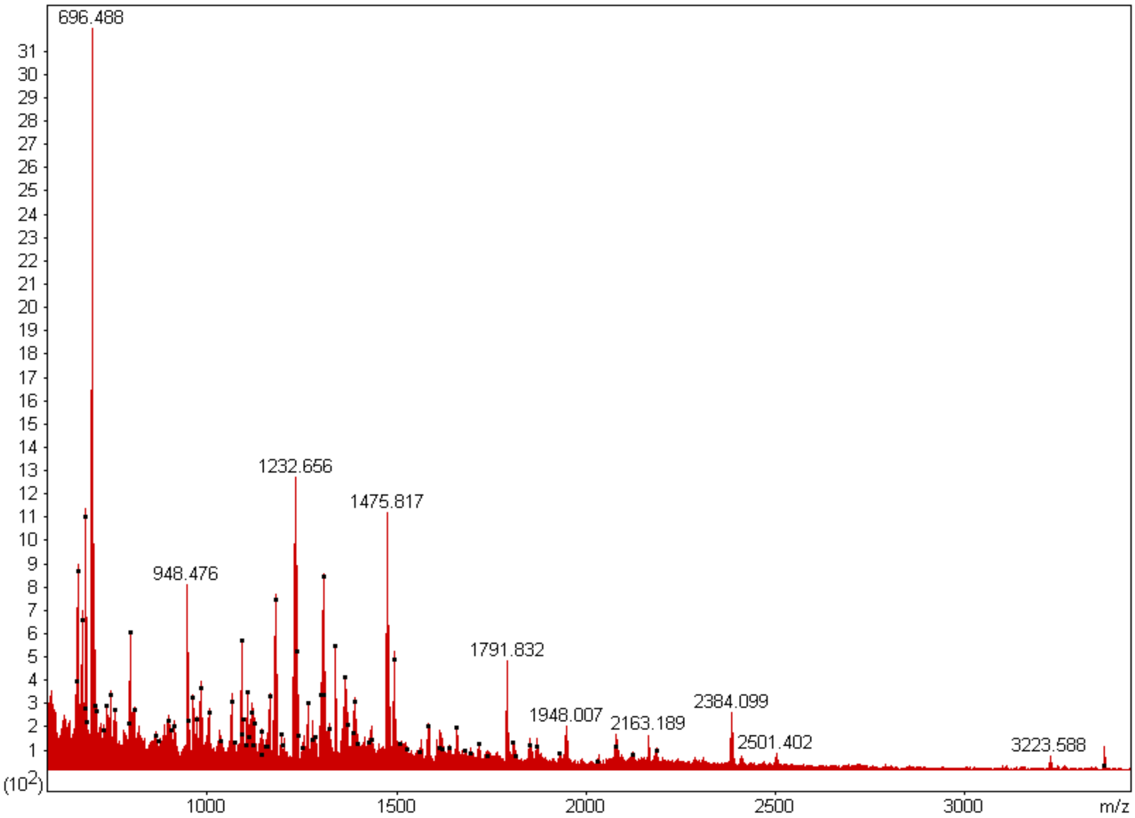
Mascot score: **85** Sequence coverage %: **35**

NCBI accession No.: **gi| 619894**

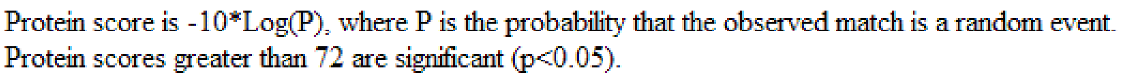
Matched peptides No.: **16** Total peptides No.: **94**

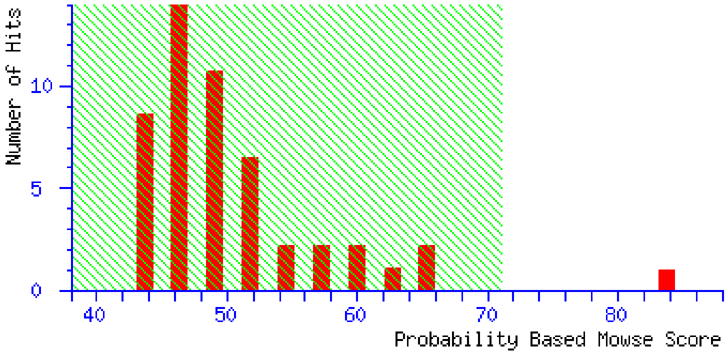
Calculated Mr: **46805** Calculated p*I*: **8.71**

Annotated PMF **spectra:**

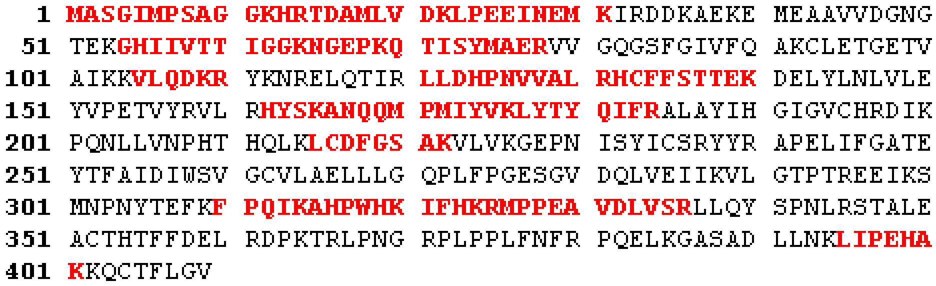


Probability Based Mowse Score:


Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

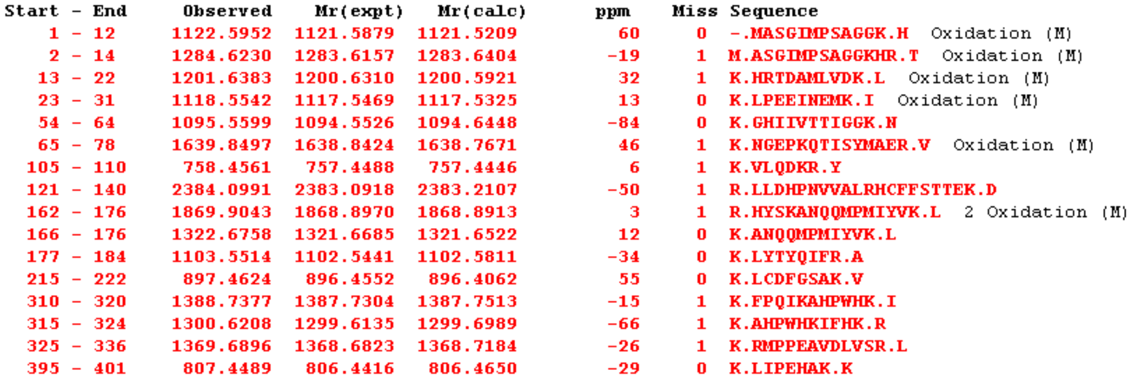


Matched peptide sequences: shown in Bold Red



```
  1 MASGIMPSAG GKHRTDAMLV DKLPEEINEM KIRDDKAEKE MEAAVVDGNG
 51 TEKGHIIVTT IGGKNGEPKQ TISYMAERVV GQGSFGIVFQ AKCLETGETV
101 AIKKVLQDKR YKNRELQTIR LLDHPNVVAL RHCFFSTTEK DELYLNLVLE
151 YVPETVYRVL RHYSKANQQM PMIYVKLYTY QIFRALAYIH GIGVCHRDIK
201 PQNLLVNPHT HQLKLCDFGS AKVLVKGEPN ISYICSRYYR APELIFGATE
251 YTFAIDIWSV GCVLAELLLG QPLFPGESGV DQLVEIIKVL GTPTREEIKS
301 MNPNYTEFKF PQIKAHPWHK IFHKRMPPEA VDLVSRLLQY SPNLRSTALE
351 ACTHTFFDEL RDPKTRLPNG RPLPPLFNFR PQELKGASAD LLNKLIPEHA
401 KKQCTFLGV
```

Matched peptides information:



Start	-	End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
1	-	12	1122.5952	1121.5879	1121.5209	60	0	-.MASGIMPSAGGK.H Oxidation (M)
2	-	14	1284.6230	1283.6157	1283.6404	-19	1	M.ASGIMPSAGGKHR.T Oxidation (M)
13	-	22	1201.6383	1200.6310	1200.5921	32	1	K.HRTDAMLVDK.L Oxidation (M)
23	-	31	1118.5542	1117.5469	1117.5325	13	0	K.LPEEINEMK.I Oxidation (M)
54	-	64	1095.5599	1094.5526	1094.6448	-84	0	K.GHIIVTTIGGK.N
65	-	78	1639.8497	1638.8424	1638.7671	46	1	K.NGEPKQTISYMAER.V Oxidation (M)
105	-	110	758.4561	757.4488	757.4446	6	1	K.VLQDKR.Y
121	-	140	2384.0991	2383.0918	2383.2107	-50	1	R.LLDHPNVVALRHCFFSTTEK.D
162	-	176	1869.9043	1868.8970	1868.8913	3	1	R.HYSKANQQMPMIYVK.L 2 Oxidation (M)
166	-	176	1322.6758	1321.6685	1321.6522	12	0	K.ANQQMPMIYVK.L
177	-	184	1103.5514	1102.5441	1102.5811	-34	0	K.LYTYQIFR.A
215	-	222	897.4624	896.4552	896.4062	55	0	K.LCDFGSAK.V
310	-	320	1388.7377	1387.7304	1387.7513	-15	1	K.FPQIKAHPWHK.I
315	-	324	1300.6208	1299.6135	1299.6989	-66	1	K.AHPWHKIFHK.R
325	-	336	1369.6896	1368.6823	1368.7184	-26	1	K.RMPPEAVDLVSR.L
395	-	401	807.4489	806.4416	806.4650	-29	0	K.LIPEHAK.K

Spot No.: **13**

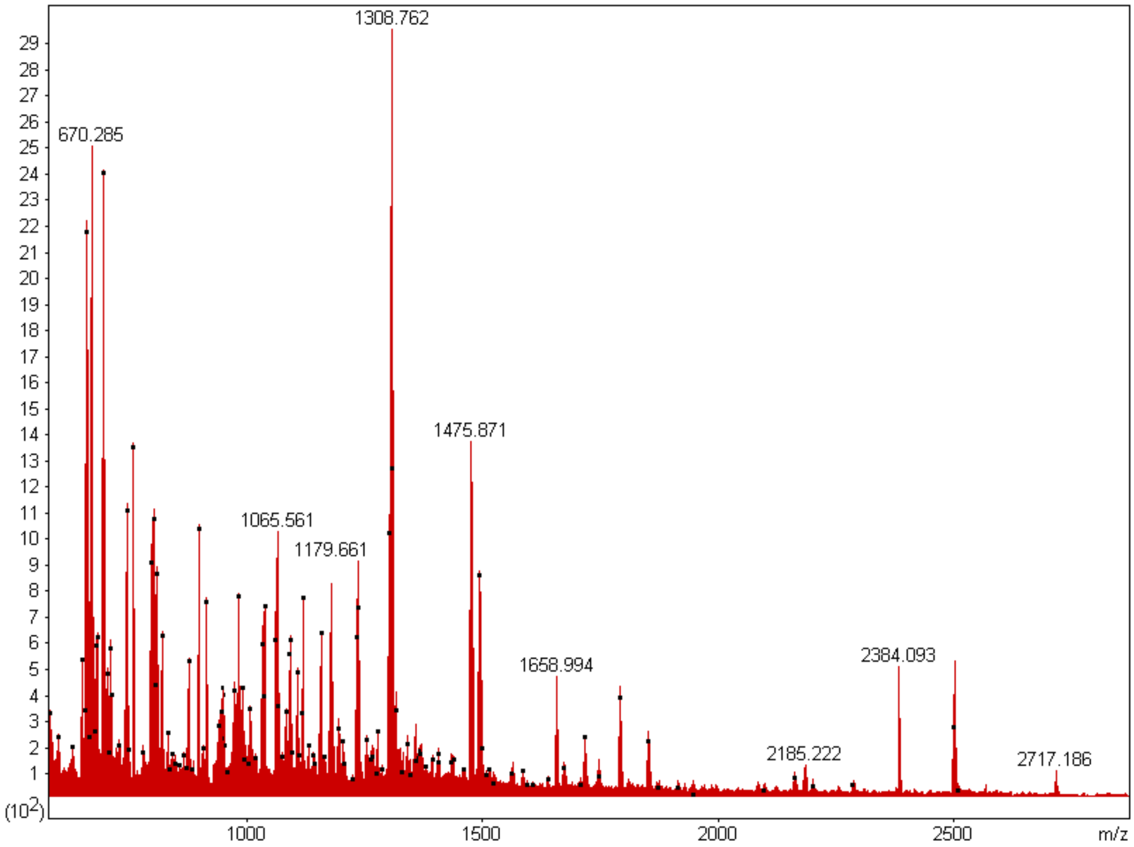
Mascot score: **81**   Sequence coverage %: **21**

NCBI accession No.: **gi| 116055771**

Matched peptides No.: **12**   Total peptides No.: **126**

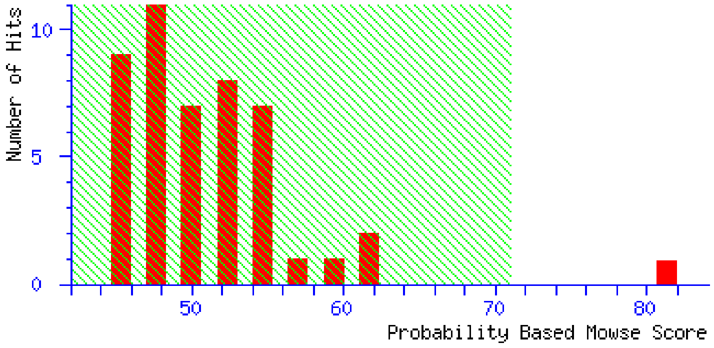
Calculated Mr: **63246**   Calculated *p*I: **9.35**

Annotated PMF **spectra:**

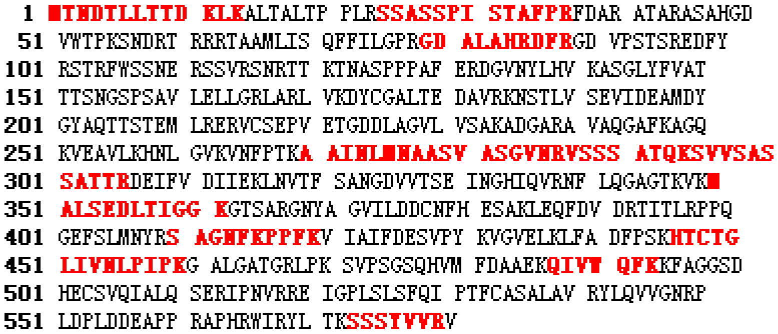


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red



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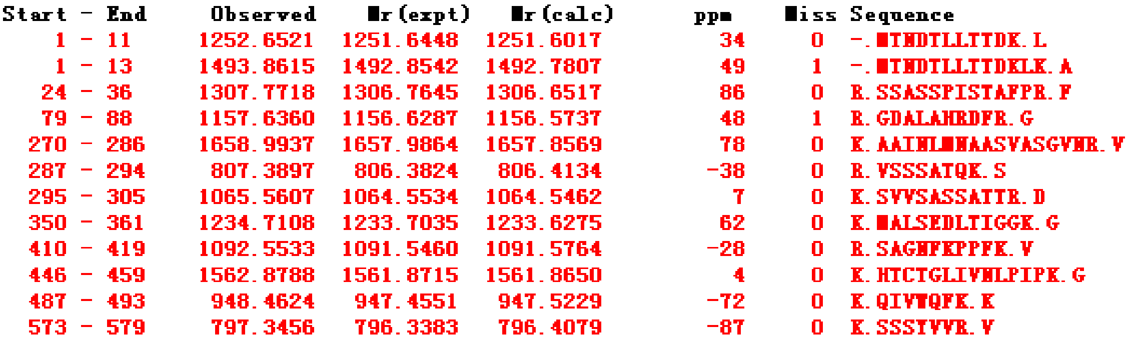
  1 MTNDTLLTTD KLKALTALTP PLRSSASSPI STAFPRFDAR ATARASAHGD
 51 VWTPKSNDRT RRRTAAMLIS QFFILGPRGD ALAHRDFRGD VPSTSREDFY
101 RSTRFWSSNE RSSVRSNRTT KTNASPPPAF ERDGVNYLHV KASGLYFVAT
151 TTSNGSPSAV LELLGRLARL VKDYCGALTE DAVRKNSTLV SEVIDEAMDY
201 GYAQTTSTEM LRERVCSEPV ETGDDLAGVL VSAKADGARA VAQGAFKAGQ
251 KVEAVLKHNL GVKVNFPTKA AINLMNAASV ASGVNRVSSS ATQESVVSAS
301 SATTRDEIFV DIIEKLNVTF SANGDVVTSE INGHIQVRNF LQGAGTKVKM
351 ALSEDLTIGG KGTSARGNYA GVILDDCNFH ESAKLEQFDV DRTITLRPPQ
401 GEFSLMNYRS AGNFKPPFKV IAIFDESVPY KVGVELKLFA DFPSKHTCTG
451 LIVNLPIPKG ALGATGRLPK SVPSGSQHVM FDAAEKQIVW QFKKFAGGSD
501 HECSVQIALQ SERIPNVRRE IGPLSLSFQI PTFCASALAV RYLQVVGNRP
551 LDPLDDEAPP RAPHRWIRYL TKSSSYVVRV
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    1 - 11     1252.6521  1251.6448  1251.6017      34      0  -.MTNDTLLTTDK.L
    1 - 13     1493.8615  1492.8542  1492.7807      49      1  -.MTNDTLLTTDKLK.A
   24 - 36     1307.7718  1306.7645  1306.6517      86      0  R.SSASSPISTAFPR.F
   79 - 88     1157.6360  1156.6287  1156.5737      48      1  R.GDALAHRDFR.G
  270 - 286    1658.9937  1657.9864  1657.8569      78      0  K.AAINLMNAASVASGVNR.V
  287 - 294     807.3897   806.3824   806.4134     -38      0  R.VSSSATQK.S
  295 - 305    1065.5607  1064.5534  1064.5462       7      0  K.SVVSASSATTR.D
  350 - 361    1234.7108  1233.7035  1233.6275      62      0  K.MALSEDLTIGGK.G
  410 - 419    1092.5533  1091.5460  1091.5764     -28      0  R.SAGNFKPPFK.V
  446 - 459    1562.8788  1561.8715  1561.8650       4      0  K.HTCTGLIVNLPIPK.G
  487 - 493     948.4624   947.4551   947.5229     -72      0  K.QIVWQFK.K
  573 - 579     797.3456   796.3383   796.4079     -87      0  K.SSSYVVR.V
```

Spot No.: **14**

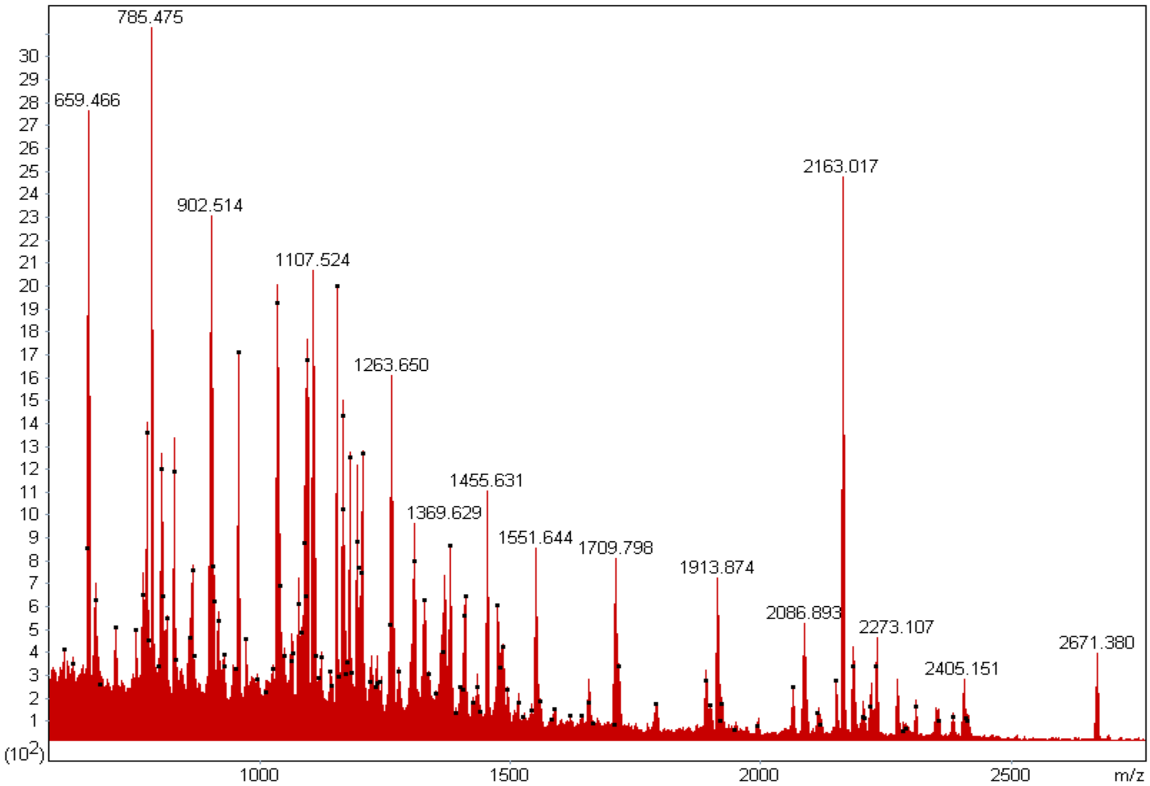
Mascot score: **84**   Sequence coverage %: **27**

NCBI accession No.: **gi| 147826444**

Matched peptides No.: **23**   Total peptides No.: **81**

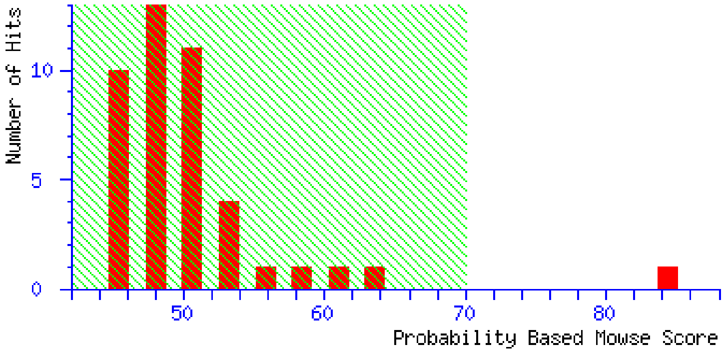
Calculated Mr: **100047**   Calculated *p*I: **9.49**

Annotated PMF **spectra:**

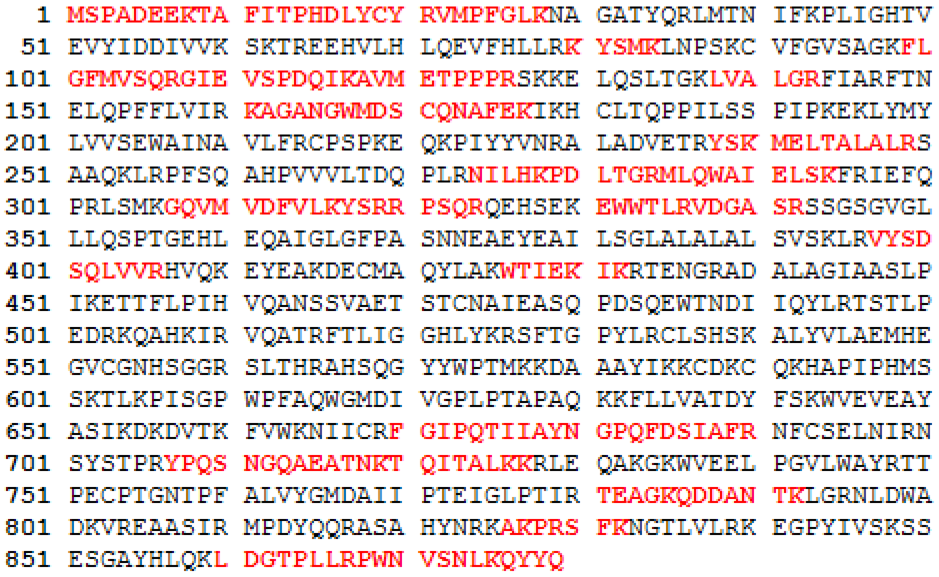


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

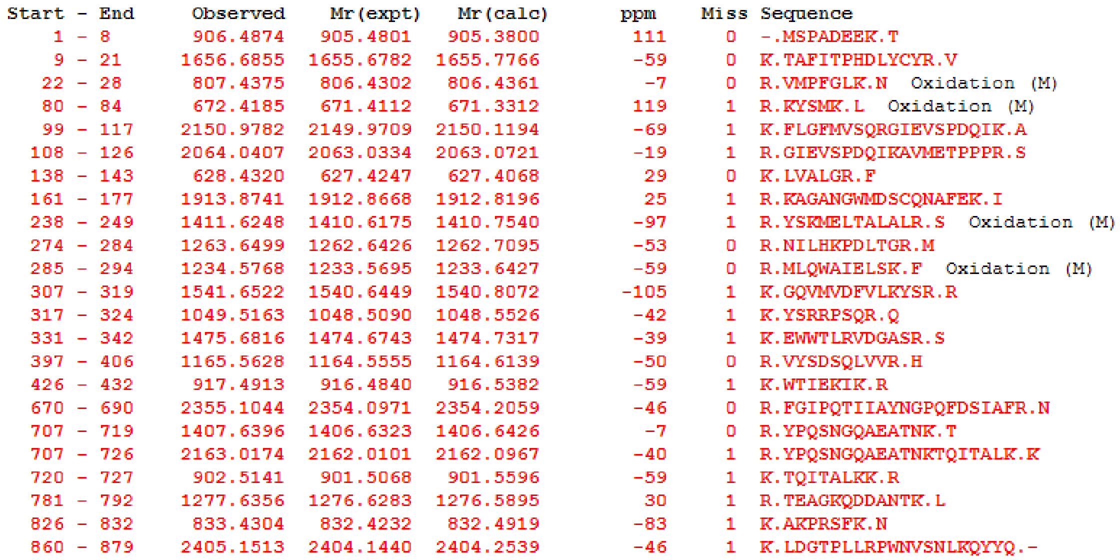


Matched peptide sequences: shown in Bold Red



1 **MSPADEEKTA** **FITPHDLYCY** **RVMPFGLK**NA GATYQRLMTN IFKPLIGHTV
51 EVYIDDIVVK SKTREEHVLH LQEVFHLLR**K** **YSMK**LNPSKC VFGVSAGK**FL**
101 **GFMVSQRGIE** **VSPDQIKAVM** **ETPPPR**SKKE LQSLTGK**LVA** **LGR**FIARFTN
151 ELQPFFLVIR **KAGANGWMDS** **CQNAFEK**IKH CLTQPPILSS PIPKEKLYMY
201 LVVSEWAINA VLFRCPSPKE QKPIYYVNRA LADVETR**YSK** **MELTALALR**S
251 AAQKLRPFSQ AHPVVVLTDQ PLR**NILHKPD** **LTGRMLQWAI** **ELSK**FRIEFQ
301 PRLSMK**GQVM** **VDFVLKYSRR** **PSQR**QEHSEK **EWWTLRVDGA** **SR**SSGSGVGL
351 LLQSPTGEHL EQAIGLGFPA SNNEAEYEAI LSGLALALAL SVSKLR**VYSD**
401 **SQLVVR**HVQK EYEAKDECMA QYLAK**WTIEK** **IK**RTENGRAD ALAGIAASLP
451 IKETTFLPIH VQANSSVAET STCNAIEASQ PDSQEWTNDI IQYLRTSTLP
501 EDRKQAHKIR VQATRFTLIG GHLYKRSFTG PYLRCLSHSK ALYVLAEMHE
551 GVCGNHSGGR SLTHRAHSQG YYWPTMKKDA AAYIKKCDKC QKHAPIPHMS
601 SKTLKPISGP WPFAQWGMDI VGPLPTAPAQ KKFLLVATDY FSKWVEVEAY
651 ASIKDKDVTK FVWKNIICR**F** **GIPQTIIAYN** **GPQFDSIAFR** NFCSELNIRN
701 SYSTPR**YPQS** **NGQAEATNKT** **QITALKK**RLE QAKGKWVEEL PGVLWAYRTT
751 PECPTGNTPF ALVYGMDAII PTEIGLPTIR **TEAGKQDDAN** **TK**LGRNLDWA
801 DKVREAASIR MPDYQQRASA HYNRK**AKPRS** **FK**NGTLVLRK EGPYIVSKSS
851 ESGAYHLQK**L** **DGTPLLRPWN** **VSNLKQYYQ**

Matched peptides information:



```
Start - End      Observed    Mr(expt)    Mr(calc)      ppm    Miss Sequence
    1 - 8        906.4874    905.4801    905.3800      111     0   -.MSPADEEK.T
    9 - 21      1656.6855   1655.6782   1655.7766      -59     0   K.TAFITPHDLYCYR.V
   22 - 28       807.4375    806.4302    806.4361       -7     0   R.VMPFGLK.N  Oxidation (M)
   80 - 84       672.4185    671.4112    671.3312      119     1   R.KYSMK.L  Oxidation (M)
   99 - 117     2150.9782   2149.9709   2150.1194      -69     1   K.FLGFMVSQRGIEVSPDQIK.A
  108 - 126     2064.0407   2063.0334   2063.0721      -19     1   R.GIEVSPDQIKAVMETPPPR.S
  138 - 143      628.4320    627.4247    627.4068       29     0   K.LVALGR.F
  161 - 177     1913.8741   1912.8668   1912.8196       25     1   R.KAGANGWMDSCQNAFEK.I
  238 - 249     1411.6248   1410.6175   1410.7540      -97     1   R.YSKMELTALALR.S  Oxidation (M)
  274 - 284     1263.6499   1262.6426   1262.7095      -53     0   R.NILHKPDLTGR.M
  285 - 294     1234.5768   1233.5695   1233.6427      -59     0   R.MLQWAIELSK.F  Oxidation (M)
  307 - 319     1541.6522   1540.6449   1540.8072     -105     1   K.GQVMVDFVLKYSR.R
  317 - 324     1049.5163   1048.5090   1048.5526      -42     1   K.YSRRPSQR.Q
  331 - 342     1475.6816   1474.6743   1474.7317      -39     1   K.EWWTLRVDGASR.S
  397 - 406     1165.5628   1164.5555   1164.6139      -50     0   R.VYSDSQLVVR.H
  426 - 432      917.4913    916.4840    916.5382      -59     1   K.WTIEKIK.R
  670 - 690     2355.1044   2354.0971   2354.2059      -46     0   R.FGIPQTIIAYNGPQFDSIAFR.N
  707 - 719     1407.6396   1406.6323   1406.6426       -7     0   R.YPQSNGQAEATNK.T
  707 - 726     2163.0174   2162.0101   2162.0967      -40     1   R.YPQSNGQAEATNKTQITALK.K
  720 - 727      902.5141    901.5068    901.5596      -59     1   K.TQITALKK.R
  781 - 792     1277.6356   1276.6283   1276.5895       30     1   R.TEAGKQDDANTK.L
  826 - 832      833.4304    832.4232    832.4919      -83     1   K.AKPRSFK.N
  860 - 879     2405.1513   2404.1440   2404.2539      -46     1   K.LDGTPLLRPWNVSNLKQYYQ.-
```

Spot No.: **15**

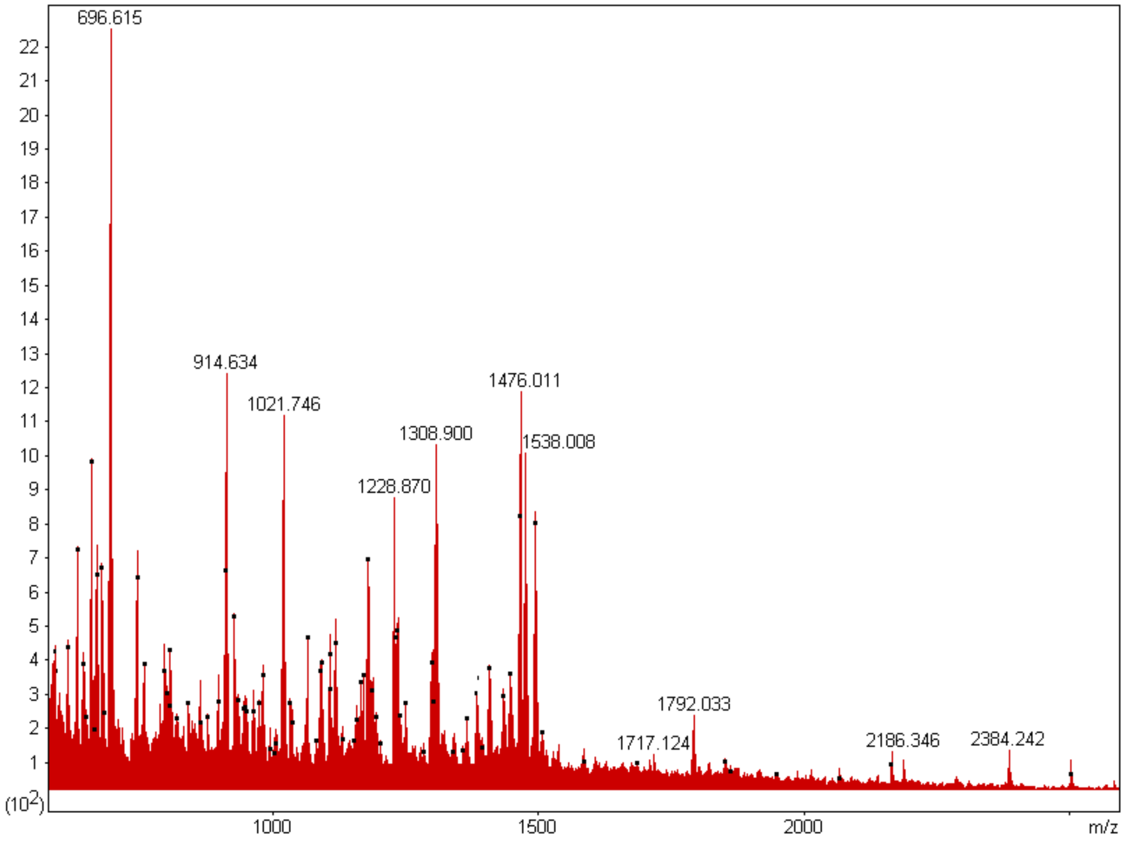
Mascot score: **102** Sequence coverage %: **33**

NCBI accession No.: **gi| 27752799**

Matched peptides No.: **18** Total peptides No.: **86**

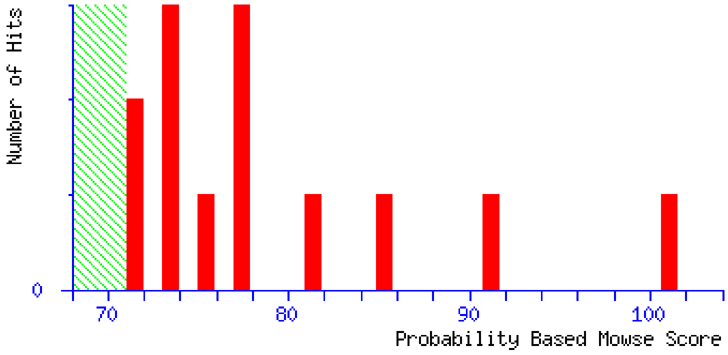
Calculated Mr: **47920** Calculated *p*I: **6.12**

Annotated PMF **spectra:**

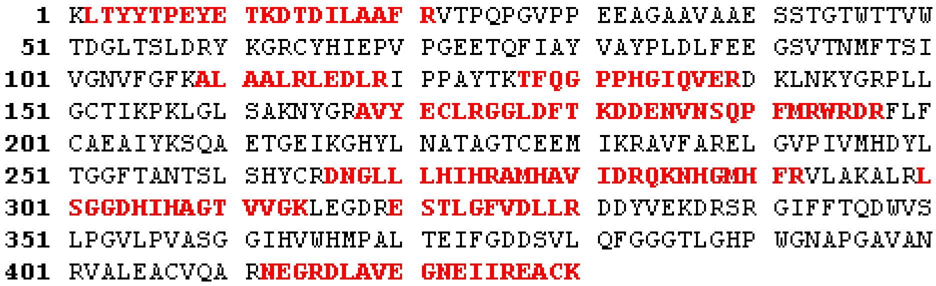


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red



1 K**LTYYTPEYE** **TKDTDILAAF** **R**VTPQPGVPP EEAGAAVAAE SSTGTWTTVW

51 TDGLTSLDRY KGRCYHIEPV PGEETQFIAY VAYPLDLFEE GSVTNMFTSI

101 VGNVFGFK**AL** **AALRLEDLR**I PPAYTK**TFQG** **PPHGIQVER**D KLNKYGRPLL

151 GCTIKPKLGL SAKNYGR**AVY** **ECLRGGLDFT** **KDDENVNSQP** **FMRWRDR**FLF

201 CAEAIYKSQA ETGEIKGHYL NATAGTCEEM IKRAVFAREL GVPIVMHDYL

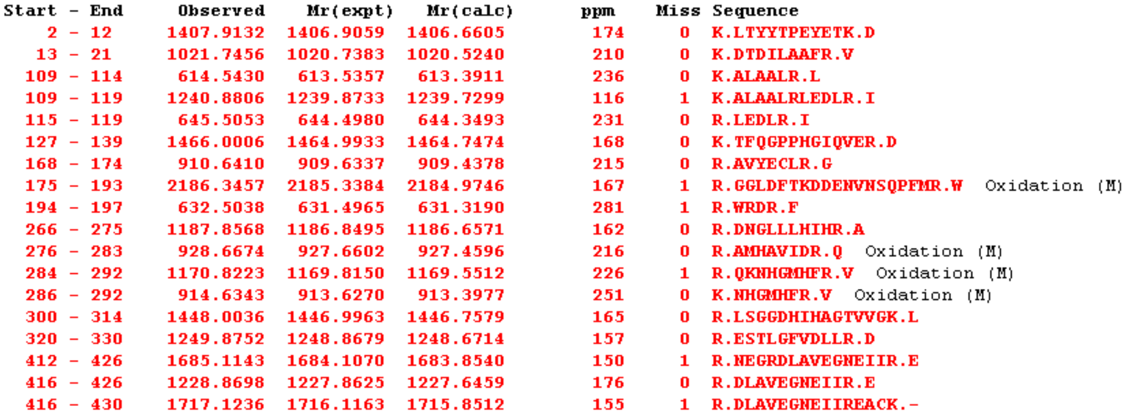
251 TGGFTANTSL SHYCR**DNGLL** **LHIHRAMHAV** **IDRQKNHGMH** **FR**VLAKALR**L**

301 **SGGDHIHAGT** **VVGK**LEGDR**E** **STLGFVDLLR** DDYVEKDRSR GIFFTQDWVS

351 LPGVLPVASG GIHVWHMPAL TEIFGDDSVL QFGGGTLGHP WGNAPGAVAN

401 RVALEACVQA R**NEGRDLAVE** **GNEIIREACK**

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    2 - 12     1407.9132  1406.9059  1406.6605      174      0  K.LTYYTPEYETK.D
   13 - 21     1021.7456  1020.7383  1020.5240      210      0  K.DTDILAAFR.V
  109 - 114     614.5430   613.5357   613.3911      236      0  K.ALAALR.L
  109 - 119    1240.8806  1239.8733  1239.7299      116      1  K.ALAALRLEDLR.I
  115 - 119     645.5053   644.4980   644.3493      231      0  R.LEDLR.I
  127 - 139    1466.0006  1464.9933  1464.7474      168      0  K.TFQGPPHGIQVER.D
  168 - 174     910.6410   909.6337   909.4378      215      0  R.AVYECLR.G
  175 - 193    2186.3457  2185.3384  2184.9746      167      1  R.GGLDFTKDDENVNSQPFMR.W  Oxidation (M)
  194 - 197     632.5038   631.4965   631.3190      281      1  R.WRDR.F
  266 - 275    1187.8568  1186.8495  1186.6571      162      0  R.DNGLLLHIHR.A
  276 - 283     928.6674   927.6602   927.4596      216      0  R.AMHAVIDR.Q  Oxidation (M)
  284 - 292    1170.8223  1169.8150  1169.5512      226      1  R.QKNHGMHFR.V  Oxidation (M)
  286 - 292     914.6343   913.6270   913.3977      251      0  K.NHGMHFR.V  Oxidation (M)
  300 - 314    1448.0036  1446.9963  1446.7579      165      0  R.LSGGDHIHAGTVVGK.L
  320 - 330    1249.8752  1248.8679  1248.6714      157      0  R.ESTLGFVDLLR.D
  412 - 426    1685.1143  1684.1070  1683.8540      150      1  R.NEGRDLAVEGNEIIR.E
  416 - 426    1228.8698  1227.8625  1227.6459      176      0  R.DLAVEGNEIIR.E
  416 - 430    1717.1236  1716.1163  1715.8512      155      1  R.DLAVEGNEIIREACK.-
```

Spot No.: **16**

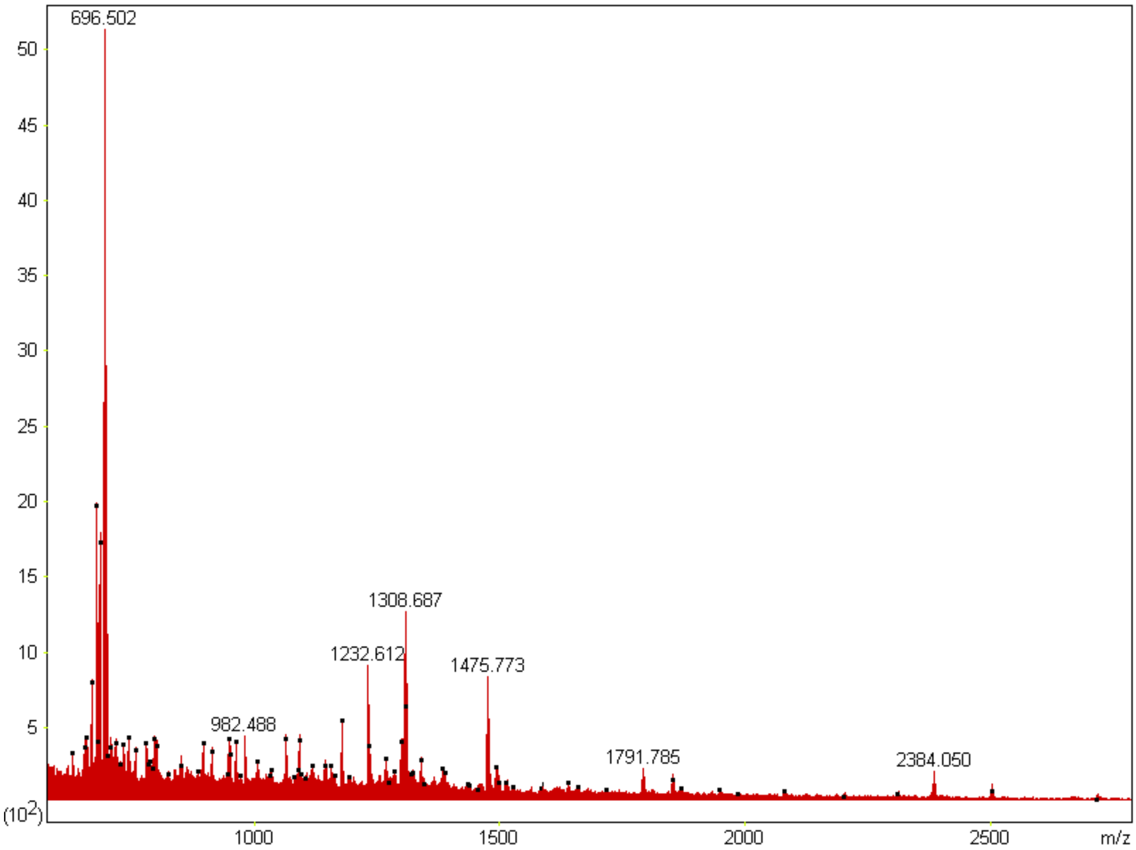
Mascot score: **82** Sequence coverage %: **21**

NCBI accession No.: **gi| 226463312**

Matched peptides No.: **28** Total peptides No.: **84**

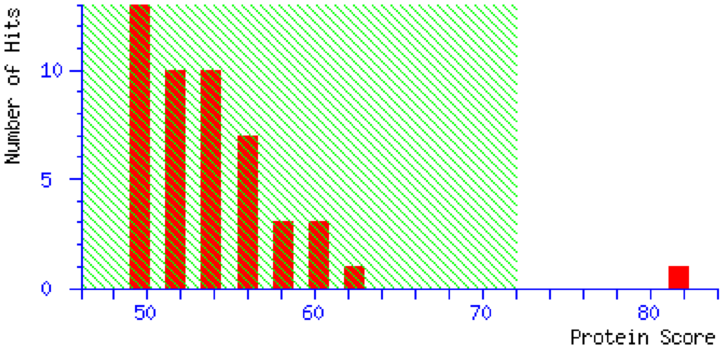
Calculated Mr: **111653** Calculated *p*I: **9.23**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 **MATTMTSSPL** **QDRSNDAK**LS PFSTRSKSVL GASAVAKSAL SKKSK**SVVYQ**
51 **DENAHATPTK** **SSKSSTSAAE** **K**SLDKVADEN DKLRDLNKRL LAELK**NARVS**
101 **AK**DAADAAAA NASASVENGE SVEKLTTQND ALR**ELNRKMI** **AHLKAAK**LEA
151 SSSAAEIDSL RAANEASSKE LAKALQKAET KYAFQIADAL TATAKAQEAA
201 AKANAHAADL RASADAERRD SATLKSLNDR ALAELKESRD AMESMNAAGA
251 TLSESMK**LAE** **SQR**DGLQATN ASLTTELRAA KKASAAAVAA AEANVLKKHA
301 KAMQEAKVAA AKENEMLREV NAKLVRTLKQ AQADSVGVAD AGDQLKALNA
351 K**LLAELK**KAR **AEANDAK**NSS EGSAKAAASA HEMLK**SVIHA** **RAELLAANAQ**
401 **ALSELQFMK**E ASEAHAAHAV DAAARLSDAE HQRDSLKALN VNVLNKLREA
451 K**AETAKAASD** **AAAALK**RHSE LAADR**ERVEE** **QR**ANLQELNR RLISEARRAR
501 AEFGRAELAR AQMEKAKEDA EASVKAHAAN AEALKAQVAE K**HAELAR**IEK
551 QTAKKIAEKE IAVAKAQAAE ADAEAKAAAA QLTMNGNLES QKKEAAGVLE
601 KVTQEKQALS SRLEIALQEL LEESAALKDA RESVK**SLDAK** **LHAAACELK**D
651 SCAGLTAASD ALVAAAEANA AKDKRVK**MLE** **KECVK**LTNAF AESEEIHRMD
701 LEAAVEAHAQ ETAKTEKLEN VLKMTKIAAT HKHEQHKATT AKLHGEIAGA
751 KKAEAAAKAL AR**AERDAAAD** **ATK**TRDAAAK EAARANDRAK AATADALAAK
801 AAAKEETAAA K**REIADAK**KN AARSAK**ASAA** **AAAAAAAAEK** **R**ACAAER**EMA**
851 **AAASRAAKAV** **KAAEDAATAK** **VAVADKR**LAQ TMAKHAASEH EAATQRAAAA
901 KLESALAAAN AALTTANAAN ATLREQDAKR HEK**ELARVVA** **K**ADAHVAELA
951 AELVAARATV NAANAELARR SNDLRRMKEI SGSVSRSLKA DASDAAARAD
1001 AMCVEVTGLE MRTESLESAL KAADAALAAA NREKCAAKRR EKFALFGLAI
1051 AAVRALLSAL AKARK

Matched peptides information:

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
1 - 13	1438.6840	1437.6767	1437.6592	12	0	-.MATTMTSSPLQDR.S
1 - 18	1985.9572	1984.9499	1984.8830	34	1	-.MATTMTSSPLQDRSNDAK.L 2 Oxidation (M)
2 - 13	1307.6766	1306.6693	1306.6187	39	0	M.ATTMTSSPLQDR.S
2 - 13	1323.6473	1322.6400	1322.6136	20	0	M.ATTMTSSPLQDR.S Oxidation (M)
46 - 60	1659.7658	1658.7585	1658.7900	-19	0	K.SVVYQDENAHATPTK.S
61 - 71	1082.5637	1081.5564	1081.5251	29	1	K.SSKSSTSAAEK.S
64 - 71	780.4469	779.4396	779.3661	94	0	K.SSTSAAEK.S
96 - 102	745.4670	744.4597	744.4242	48	1	K.NARVSAK.D
134 - 138	659.4297	658.4224	658.3762	70	1	R.ELNRK.M
139 - 144	728.4388	727.4316	727.4051	36	0	K.MIAHLK.A Oxidation (M)
139 - 147	982.4880	981.4807	981.5793	-100	1	K.MIAHLKAAK.L
258 - 263	703.4284	702.4211	702.3660	78	0	K.LAESQR.D
352 - 357	686.4757	685.4684	685.4374	45	0	K.LLAELK.K
361 - 367	718.4648	717.4575	717.3293	179	0	R.AEANDAK.N
386 - 391	682.4060	681.3988	681.3922	10	0	K.SVIHAR.A
392 - 409	1947.9517	1946.9444	1947.0135	-35	0	R.AELLAANAQALSELQFMK.E
452 - 466	1388.7027	1387.6954	1387.7307	-25	1	K.AETAKAASDAAAALK.R
476 - 482	945.5107	944.5034	944.4675	38	1	R.ERVEEQR.A
542 - 547	696.5019	695.4947	695.3714	177	0	K.HAELAR.I
636 - 649	1526.7733	1525.7660	1525.7922	-17	1	K.SLDAKLHAAACELK.D
678 - 685	1036.5406	1035.5333	1035.5093	23	1	K.MLEKECVK.L
763 - 773	1118.5438	1117.5365	1117.5363	0	1	R.AERDAAADATK.T
812 - 818	802.4746	801.4673	801.4344	41	1	K.REIADAK.K
827 - 841	1300.5774	1299.5701	1299.6894	-92	1	K.ASAAAAAAAAAAEKR.A
848 - 858	1092.5406	1091.5333	1091.5393	-5	1	R.EMAAAASRAAK.A Oxidation (M)
859 - 870	1145.5778	1144.5705	1144.6088	-33	1	K.AVKAAEDAATAK.V
871 - 877	758.4871	757.4798	757.4446	46	1	K.VAVADKR.L
934 - 941	885.4759	884.4686	884.5443	-86	1	K.ELARVVAK.A

Spot No.: **17**

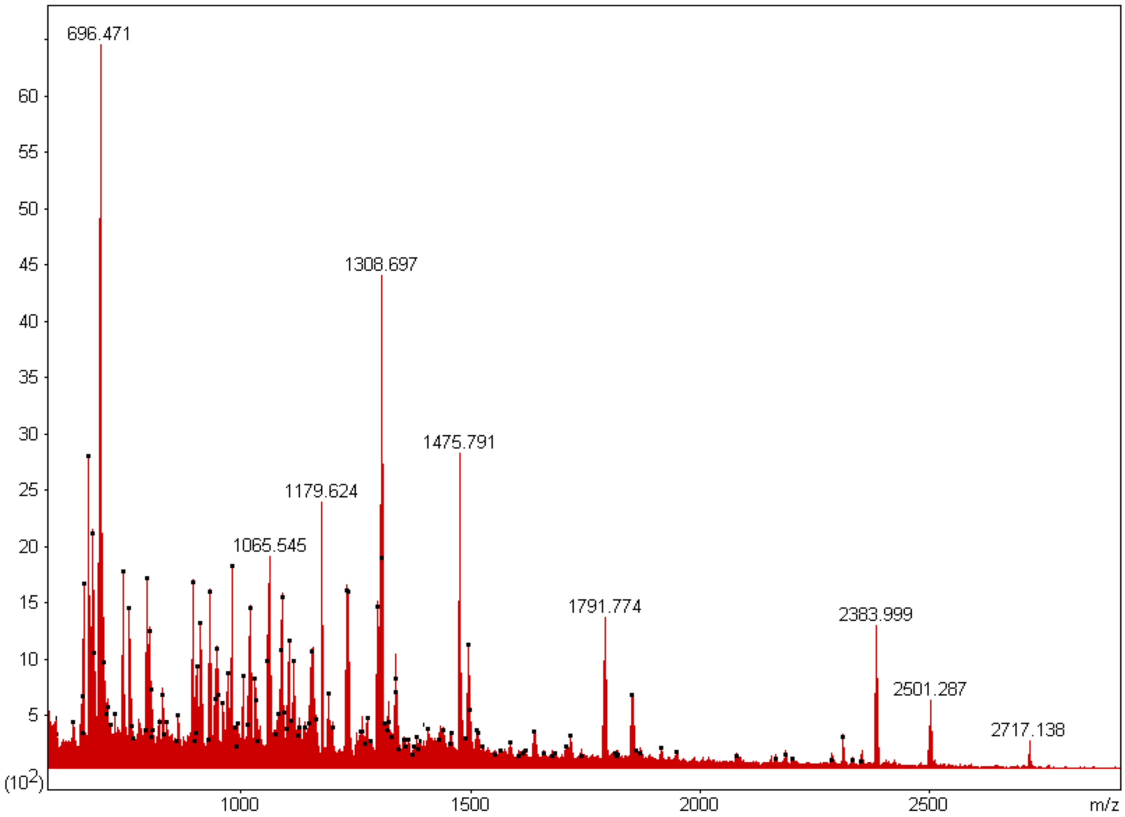
Mascot score: **84**   Sequence coverage %: **42**

NCBI accession No.: **gi| 159475545**

Matched peptides No.: **18**   Total peptides No.: **122**

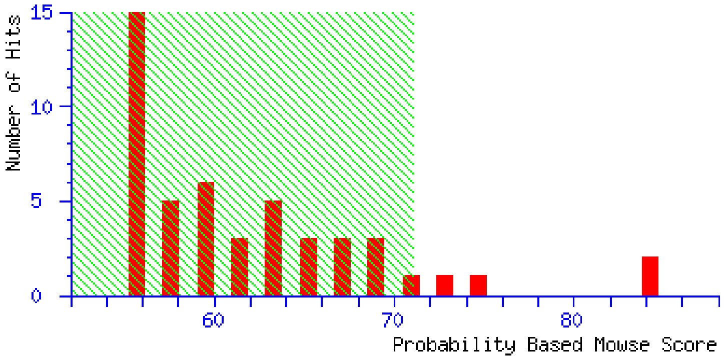
Calculated Mr: **40712**   Calculated *p*I: **8.87**

Annotated PMF **spectra:**

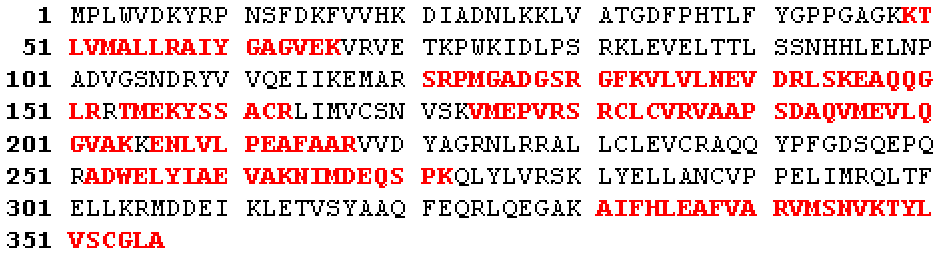


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

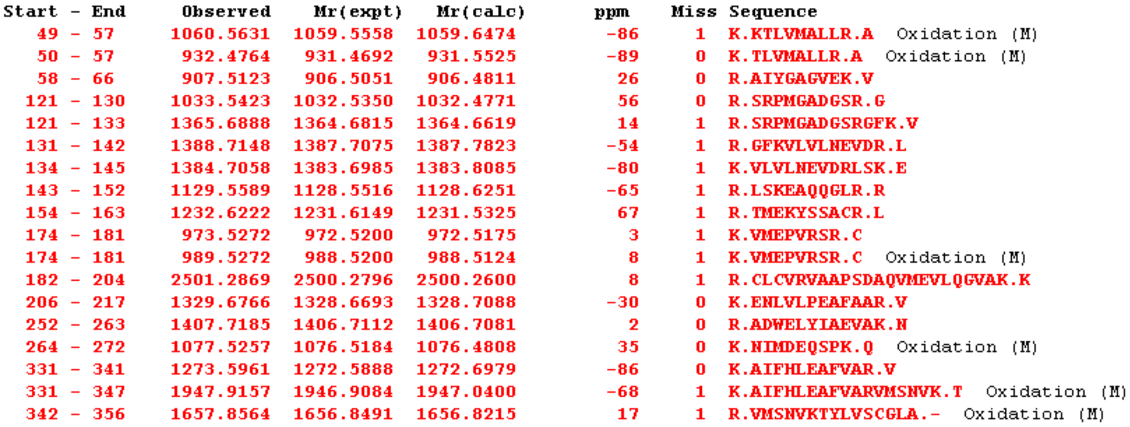


Matched peptide sequences: shown in Bold Red



```
  1 MPLWVDKYRP NSFDKFVVHK DIADNLKKLV ATGDFPHTLF YGPPGAGKKT
 51 LVMALLRAIY GAGVEKVRVE TKPWKIDLPS RKLEVELTTL SSNHHLELNP
101 ADVGSNDRYV VQEIIKEMAR SRPMGADGSR GFKVLVLNEV DRLSKEAQQG
151 LRRTMEKYSS ACRLIMVCSN VSKVMEPVRS RCLCVRVAAP SDAQVMEVLQ
201 GVAKKENLVL PEAFAARVVD YAGRNLRRAL LCLEVCRAQQ YPFGDSQEPQ
251 RADWELYIAE VAKNIMDEQS PKQLYLVRSK LYELLANCVP PELIMRQLTF
301 ELLKRMDDEI KLETVSYAAQ FEQRLQEGAK AIFHLEAFVA RVMSNVKTYL
351 VSCGLA
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
  49 - 57     1060.5631  1059.5558  1059.6474      -86      1  K.KTLVMALLR.A  Oxidation (M)
  50 - 57      932.4764   931.4692   931.5525      -89      0  K.TLVMALLR.A  Oxidation (M)
  58 - 66      907.5123   906.5051   906.4811       26      0  R.AIYGAGVEK.V
 121 - 130    1033.5423  1032.5350  1032.4771       56      0  R.SRPMGADGSR.G
 121 - 133    1365.6888  1364.6815  1364.6619       14      1  R.SRPMGADGSRGFK.V
 131 - 142    1388.7148  1387.7075  1387.7823      -54      1  R.GFKVLVLNEVDR.L
 134 - 145    1384.7058  1383.6985  1383.8085      -80      1  K.VLVLNEVDRLSK.E
 143 - 152    1129.5589  1128.5516  1128.6251      -65      1  R.LSKEAQQGLR.R
 154 - 163    1232.6222  1231.6149  1231.5325       67      1  R.TMEKYSSACR.L
 174 - 181     973.5272   972.5200   972.5175        3      1  K.VMEPVRSR.C
 174 - 181     989.5272   988.5200   988.5124        8      1  K.VMEPVRSR.C  Oxidation (M)
 182 - 204    2501.2869  2500.2796  2500.2600        8      1  R.CLCVRVAAPSDAQVMEVLQGVAK.K
 206 - 217    1329.6766  1328.6693  1328.7088      -30      0  K.ENLVLPEAFAAR.V
 252 - 263    1407.7185  1406.7112  1406.7081        2      0  R.ADWELYIAEVAK.N
 264 - 272    1077.5257  1076.5184  1076.4808       35      0  K.NIMDEQSPK.Q  Oxidation (M)
 331 - 341    1273.5961  1272.5888  1272.6979      -86      0  K.AIFHLEAFVAR.V
 331 - 347    1947.9157  1946.9084  1947.0400      -68      1  K.AIFHLEAFVARVMSNVK.T  Oxidation (M)
 342 - 356    1657.8564  1656.8491  1656.8215       17      1  R.VMSNVKTYLVSCGLA.-  Oxidation (M)
```

Spot No.: **18**

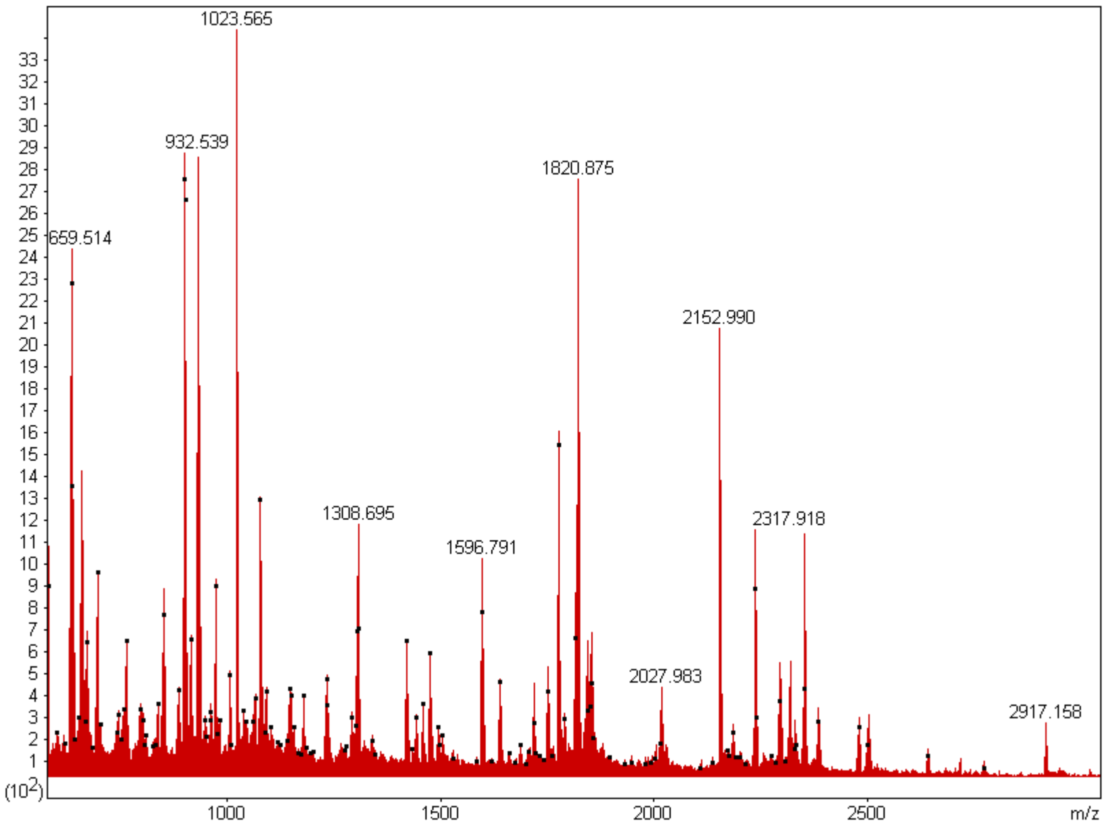
Mascot score: **107**   Sequence coverage %: **20**

NCBI accession No.: **gi| 4586021**

Matched peptides No.: **23**   Total peptides No.: **71**

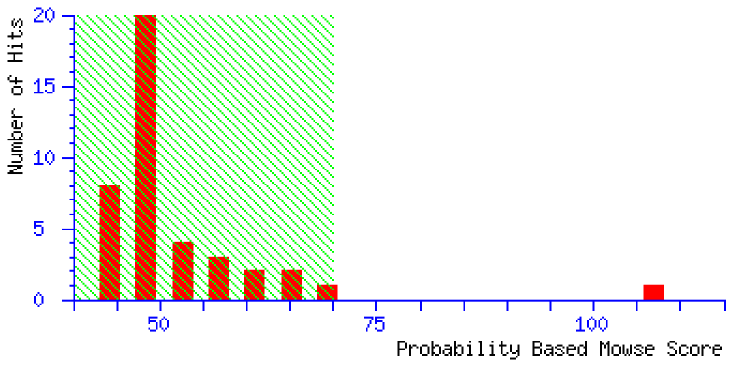
Calculated Mr: **98720**   Calculated *p*I: **5.79**

Annotated PMF **spectra:**

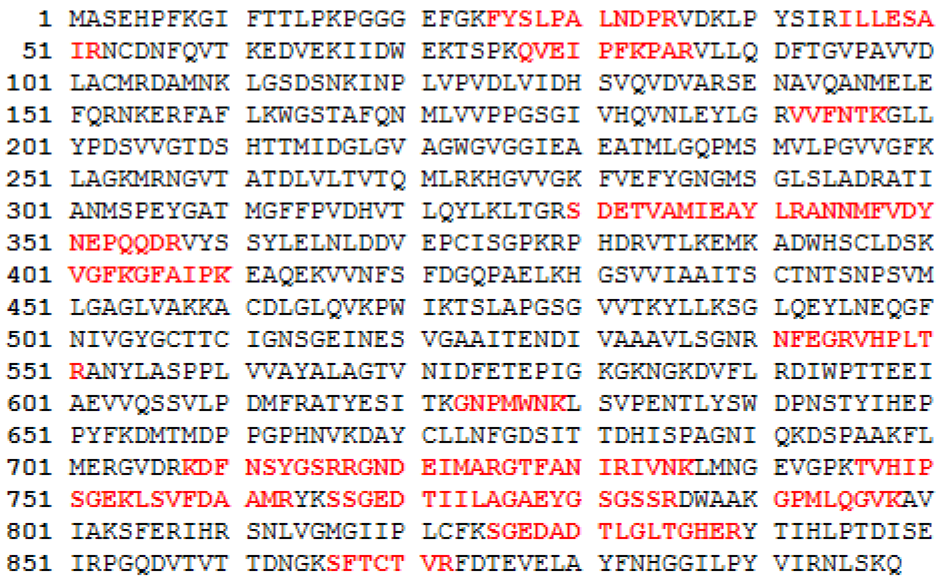


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

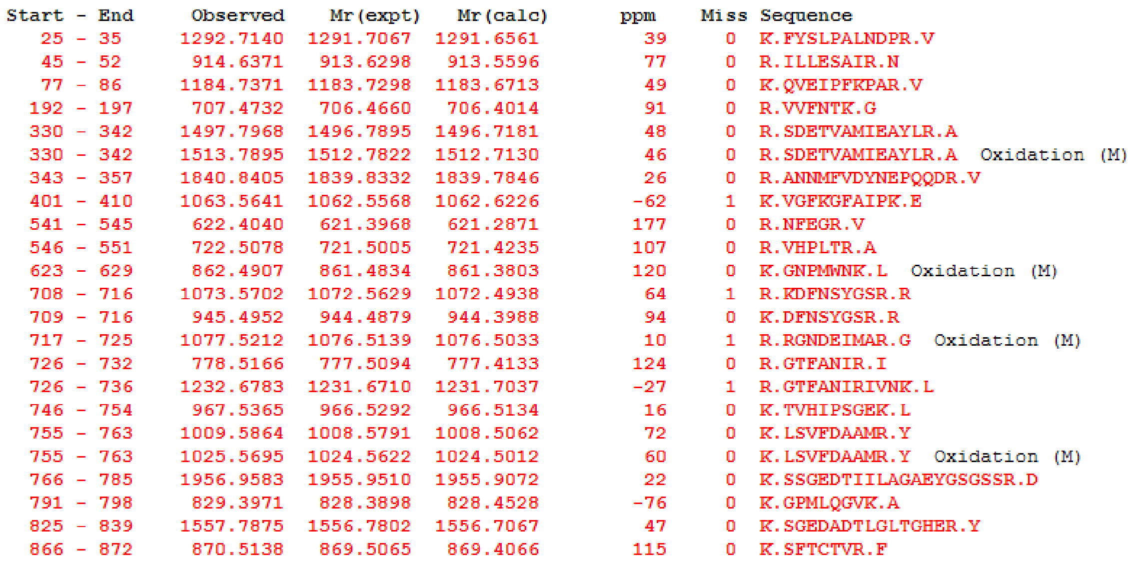


Matched peptide sequences: shown in **Bold Red**



1 MASEHPFKGI FTTLPKPGGG EFGK**FYSLPA** **LNDPR**VDKLP YSIR**ILLESA**
51 **IR**NCDNFQVT KEDVEKIIDW EKTSPK**QVEI** **PFKPAR**VLLQ DFTGVPAVVD
101 LACMRDAMNK LGSDSNKINP LVPVDLVIDH SVQVDVARSE NAVQANMELE
151 FQRNKERFAF LKWGSTAFQN MLVVPPGSGI VHQVNLEYLG R**VVFNTK**GLL
201 YPDSVVGTDS HTTMIDGLGV AGWGVGGIEA EATMLGQPMS MVLPGVVGFK
251 LAGKMRNGVT ATDLVLTVTQ MLRKHGVVGK FVEFYGNGMS GLSLADRATI
301 ANMSPEYGAT MGFFPVDHVT LQYLKLTGR**S** **DETVAMIEAY** **LRANNMFVDY**
351 **NEPQQDR**VYS SYLELNLDDV EPCISGPKRP HDRVTLKEMK ADWHSCLDSK
401 **VGFKGFAIPK** EAQEKVVNFS FDGQPAELKH GSVVIAAITS CTNTSNPSVM
451 LGAGLVAKKA CDLGLQVKPW IKTSLAPGSG VVTKYLLKSG LQEYLNEQGF
501 NIVGYGCTTC IGNSGEINES VGAAITENDI VAAAVLSGNR **NFEGRVHPLT**
551 **R**ANYLASPPL VVAYALAGTV NIDFETEPIG KGKNGKDVFL RDIWPTTEEI
601 AEVVQSSVLP DMFRATYESI TK**GNPMWNK**L SVPENTLYSW DPNSTYIHEP
651 PYFKDMTMDP PGPHNVKDAY CLLNFGDSIT TDHISPAGNI QKDSPAAKFL
701 MERGVDR**KDF** **NSYGSRRGND** **EIMARGTFAN** **IRIVNK**LMNG EVGPK**TVHIP**
751 **SGEKLSVFDA** **AMRYKSSGED** **TIILAGAEYG** **SGSSR**DWAAK **GPMLQGVK**AV
801 IAKSFERIHR SNLVGMGIIP LCFK**SGEDAD** **TLGLTGHER**Y TIHLPTDISE
851 IRPGQDVTVT TDNGK**SFTCT** **VR**FDTEVELA YFNHGGILPY VIRNLSKQ

Matched peptides information:



```
Start - End      Observed    Mr(expt)    Mr(calc)      ppm    Miss  Sequence
   25 - 35      1292.7140   1291.7067   1291.6561       39      0   K.FYSLPALNDPR.V
   45 - 52       914.6371    913.6298    913.5596       77      0   R.ILLESAIR.N
   77 - 86      1184.7371   1183.7298   1183.6713       49      0   K.QVEIPFKPAR.V
  192 - 197      707.4732    706.4660    706.4014       91      0   R.VVFNTK.G
  330 - 342     1497.7968   1496.7895   1496.7181       48      0   R.SDETVAMIEAYLR.A
  330 - 342     1513.7895   1512.7822   1512.7130       46      0   R.SDETVAMIEAYLR.A  Oxidation (M)
  343 - 357     1840.8405   1839.8332   1839.7846       26      0   R.ANNMFVDYNEPQQDR.V
  401 - 410     1063.5641   1062.5568   1062.6226      -62      1   K.VGFKGFAIPK.E
  541 - 545      622.4040    621.3968    621.2871      177      0   R.NFEGR.V
  546 - 551      722.5078    721.5005    721.4235      107      0   R.VHPLTR.A
  623 - 629      862.4907    861.4834    861.3803      120      0   K.GNPMWNK.L  Oxidation (M)
  708 - 716     1073.5702   1072.5629   1072.4938       64      1   R.KDFNSYGSR.R
  709 - 716      945.4952    944.4879    944.3988       94      0   K.DFNSYGSR.R
  717 - 725     1077.5212   1076.5139   1076.5033       10      1   R.RGNDEIMAR.G  Oxidation (M)
  726 - 732      778.5166    777.5094    777.4133      124      0   R.GTFANIR.I
  726 - 736     1232.6783   1231.6710   1231.7037      -27      1   R.GTFANIRIVNK.L
  746 - 754      967.5365    966.5292    966.5134       16      0   K.TVHIPSGEK.L
  755 - 763     1009.5864   1008.5791   1008.5062       72      0   K.LSVFDAAMR.Y
  755 - 763     1025.5695   1024.5622   1024.5012       60      0   K.LSVFDAAMR.Y  Oxidation (M)
  766 - 785     1956.9583   1955.9510   1955.9072       22      0   K.SSGEDTIILAGAEYGSGSSR.D
  791 - 798      829.3971    828.3898    828.4528      -76      0   K.GPMLQGVK.A
  825 - 839     1557.7875   1556.7802   1556.7067       47      0   K.SGEDADTLGLTGHER.Y
  866 - 872      870.5138    869.5065    869.4066      115      0   K.SFTCTVR.F
```

Spot No.: **19**

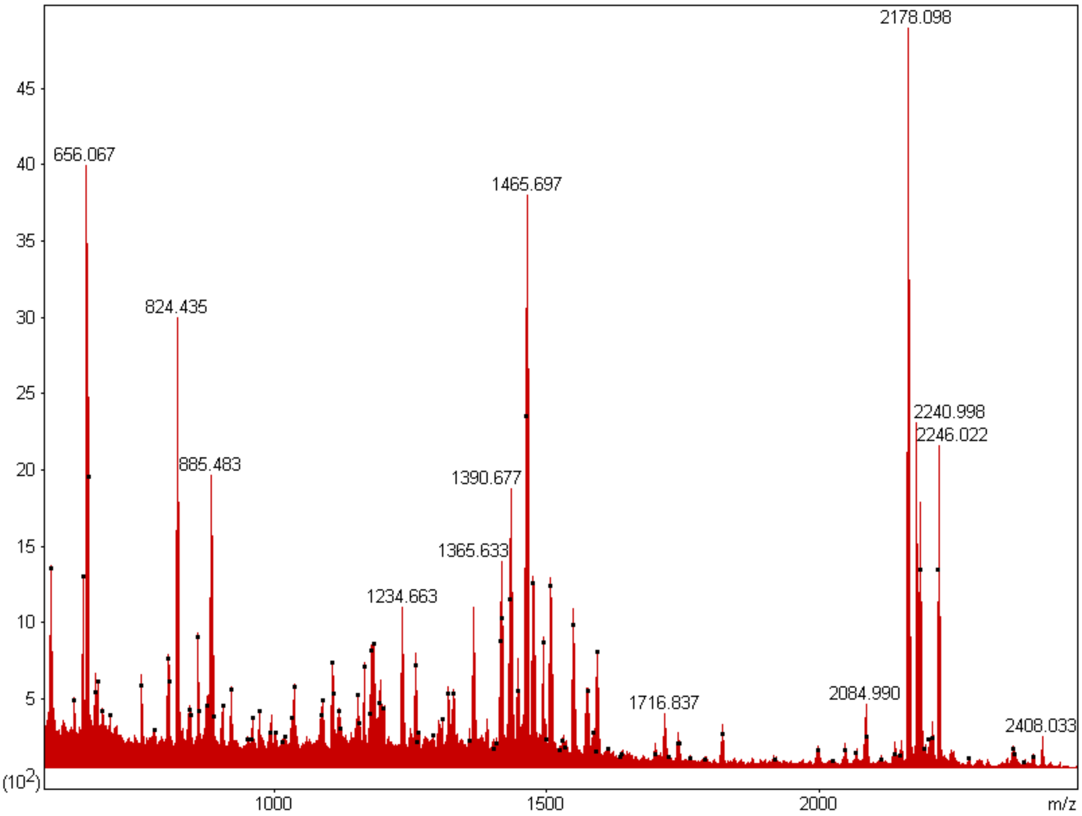
Mascot score: **155**   Sequence coverage %: **31**

NCBI accession No.: **gi| 18407650**

Matched peptides No.: **27**   Total peptides No.: **71**

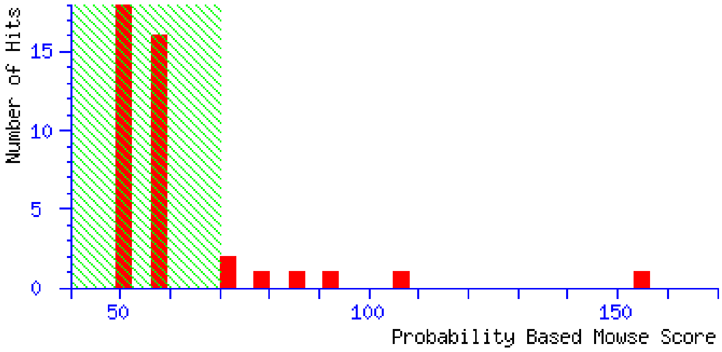
Calculated Mr: **86345**   Calculated *p*I: **5.43**

Annotated PMF **spectra:**

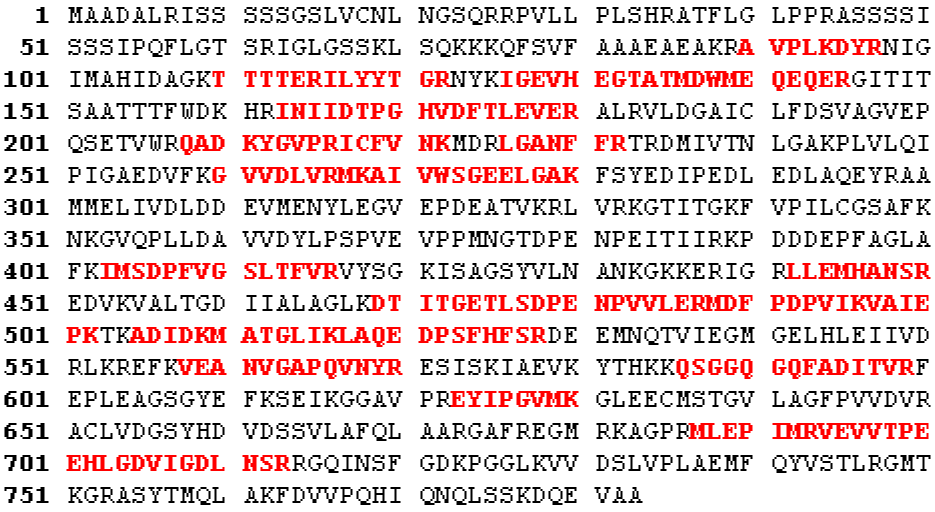


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red



1 MAADALRISS SSSGSLVCNL NGSQRRPVLL PLSHRATFLG LPPRASSSSI

51 SSSIPQFLGT SRIGLGSSKL SQKKKQFSVF AAAEAEAKR**A VPLKDYR**NIG

101 IMAHIDAGK**T TTTERILYYT GR**NYK**IGEVH EGTATMDWME QEQER**GITIT

151 SAATTTFWDK HR**INIIDTPG HVDFTLEVER** ALRVLDGAIC LFDSVAGVEP

201 QSETVWR**QAD KYGVPRICFV NK**MDR**LGANF FR**TRDMIVTN LGAKPLVLQI

251 PIGAEDVFK**G VVDLVRMKAI VWSGEELGAK** FSYEDIPEDL EDLAQEYRAA

301 MMELIVDLDD EVMENYLEGV EPDEATVKRL VRKGTITGKF VPILCGSAFK

351 NKGVQPLLDA VVDYLPSPVE VPPMNGTDPE NPEITIIRKP DDDEPFAGLA

401 FK**IMSDPFVG SLTFVR**VYSG KISAGSYVLN ANKGKKERIG R**LLEMHANSR**

451 EDVKVALTGD IIALAGLK**DT ITGETLSDPE NPVVLERMDF PDPVIKVAIE**

501 **PK**TK**ADIDKM ATGLIKLAQE DPSFHFSR**DE EMNQTVIEGM GELHLEIIVD

551 RLKREFK**VEA NVGAPQVNYR** ESISKIAEVK YTHKK**QSGGQ GQFADITVR**F

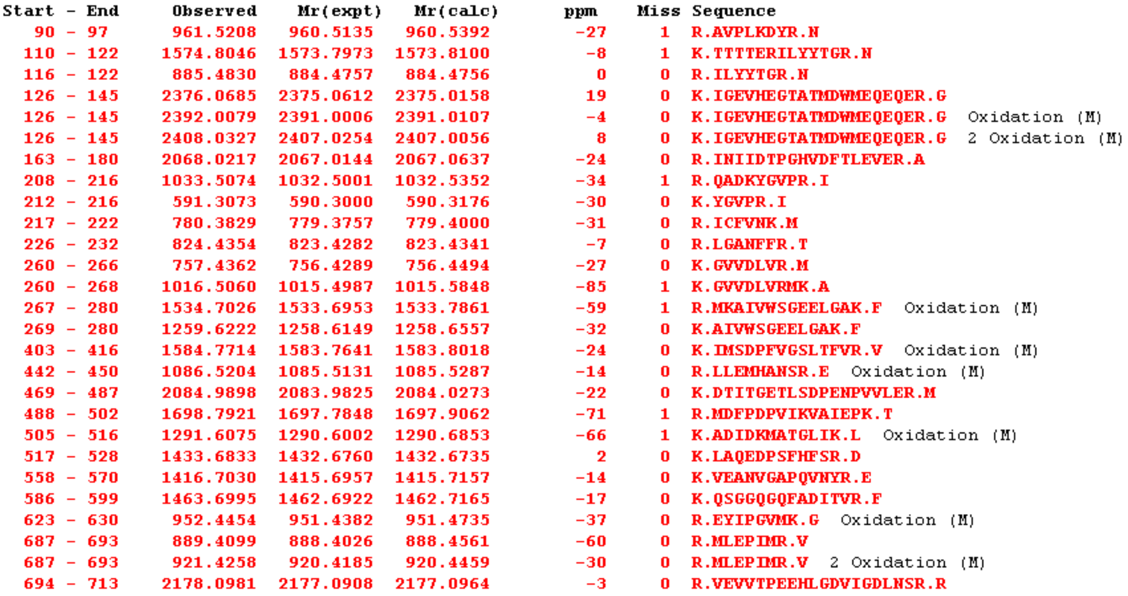
601 EPLEAGSGYE FKSEIKGGAV PR**EYIPGVMK** GLEECMSTGV LAGFPVVDVR

651 ACLVDGSYHD VDSSVLAFQL AARGAFREGM RKAGPR**MLEP IMRVEVVTPE**

701 **EHLGDVIGDL NSR**RGQINSF GDKPGGLKVV DSLVPLAEMF QYVSTLRGMT

751 KGRASYTMQL AKFDVVPQHI QNQLSSKDQE VAA

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
90 - 97	961.5208	960.5135	960.5392	-27	1	R.AVPLKDYR.N	
110 - 122	1574.8046	1573.7973	1573.8100	-8	1	K.TTTERILYYTGR.N	
116 - 122	885.4830	884.4757	884.4756	0	0	R.ILYYTGR.N	
126 - 145	2376.0685	2375.0612	2375.0158	19	0	K.IGEVHEGTATMDWMEQEQER.G	
126 - 145	2392.0079	2391.0006	2391.0107	-4	0	K.IGEVHEGTATMDWMEQEQER.G	Oxidation (M)
126 - 145	2408.0327	2407.0254	2407.0056	8	0	K.IGEVHEGTATMDWMEQEQER.G	2 Oxidation (M)
163 - 180	2068.0217	2067.0144	2067.0637	-24	0	R.INIIDTPGHVDFTLEVER.A	
208 - 216	1033.5074	1032.5001	1032.5352	-34	1	R.QADKYGVPR.I	
212 - 216	591.3073	590.3000	590.3176	-30	0	K.YGVPR.I	
217 - 222	780.3829	779.3757	779.4000	-31	0	R.ICFVNK.M	
226 - 232	824.4354	823.4282	823.4341	-7	0	R.LGANFFR.T	
260 - 266	757.4362	756.4289	756.4494	-27	0	K.GVVDLVR.M	
260 - 268	1016.5060	1015.4987	1015.5848	-85	1	K.GVVDLVRMK.A	
267 - 280	1534.7026	1533.6953	1533.7861	-59	1	R.MKAIVWSGEELGAK.F	Oxidation (M)
269 - 280	1259.6222	1258.6149	1258.6557	-32	0	K.AIVWSGEELGAK.F	
403 - 416	1584.7714	1583.7641	1583.8018	-24	0	K.IMSDPFVGSLTFVR.V	Oxidation (M)
442 - 450	1086.5204	1085.5131	1085.5287	-14	0	R.LLEMHANSR.E	Oxidation (M)
469 - 487	2084.9898	2083.9825	2084.0273	-22	0	K.DTITGETLSDPENPVVLER.M	
488 - 502	1698.7921	1697.7848	1697.9062	-71	1	R.MDFPDPVIKVAIEPK.T	
505 - 516	1291.6075	1290.6002	1290.6853	-66	1	K.ADIDKMATGLIK.L	Oxidation (M)
517 - 528	1433.6833	1432.6760	1432.6735	2	0	K.LAQEDPSFHFSR.D	
558 - 570	1416.7030	1415.6957	1415.7157	-14	0	K.VEANVGAPQVNYR.E	
586 - 599	1463.6995	1462.6922	1462.7165	-17	0	K.QSGGQGQFADITVR.F	
623 - 630	952.4454	951.4382	951.4735	-37	0	R.EYIPGVMK.G	Oxidation (M)
687 - 693	889.4099	888.4026	888.4561	-60	0	R.MLEPIMR.V	
687 - 693	921.4258	920.4185	920.4459	-30	0	R.MLEPIMR.V	2 Oxidation (M)
694 - 713	2178.0981	2177.0908	2177.0964	-3	0	R.VEVVTPEEHLGDVIGDLNSR.R	

Spot No.: **20**

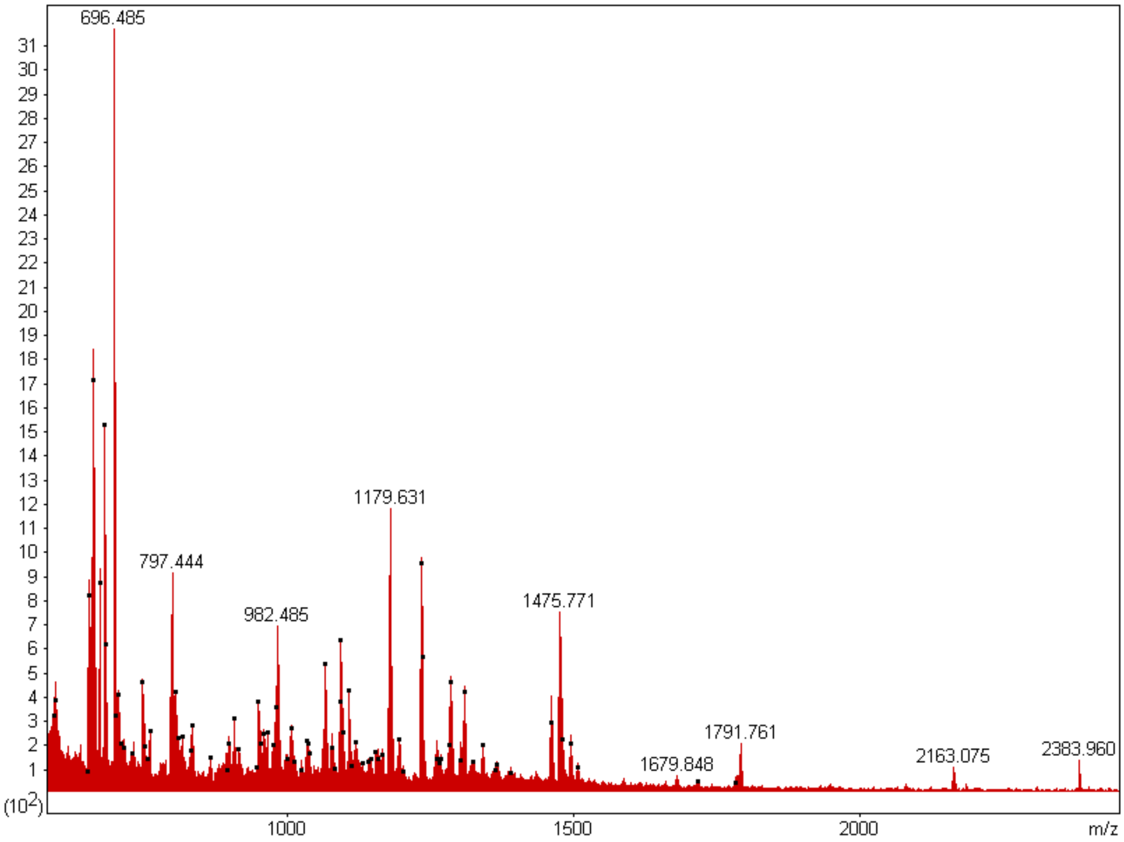
Mascot score: **94** Sequence coverage %: **19**

NCBI accession No.: **gi| 77548468**

Matched peptides No.: **24** Total peptides No.: **85**

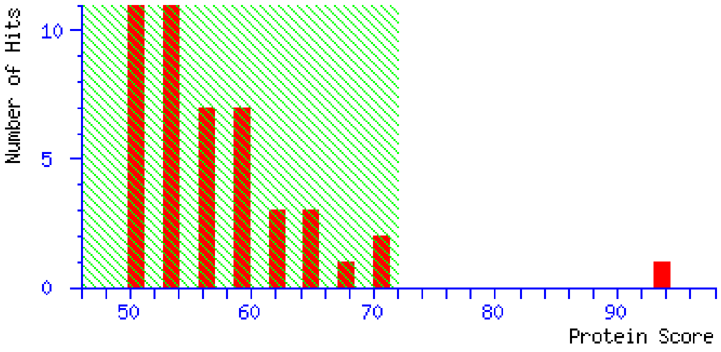
Calculated Mr: **115734** Calculated *p*I: **5.29**

Annotated PMF **spectra:**

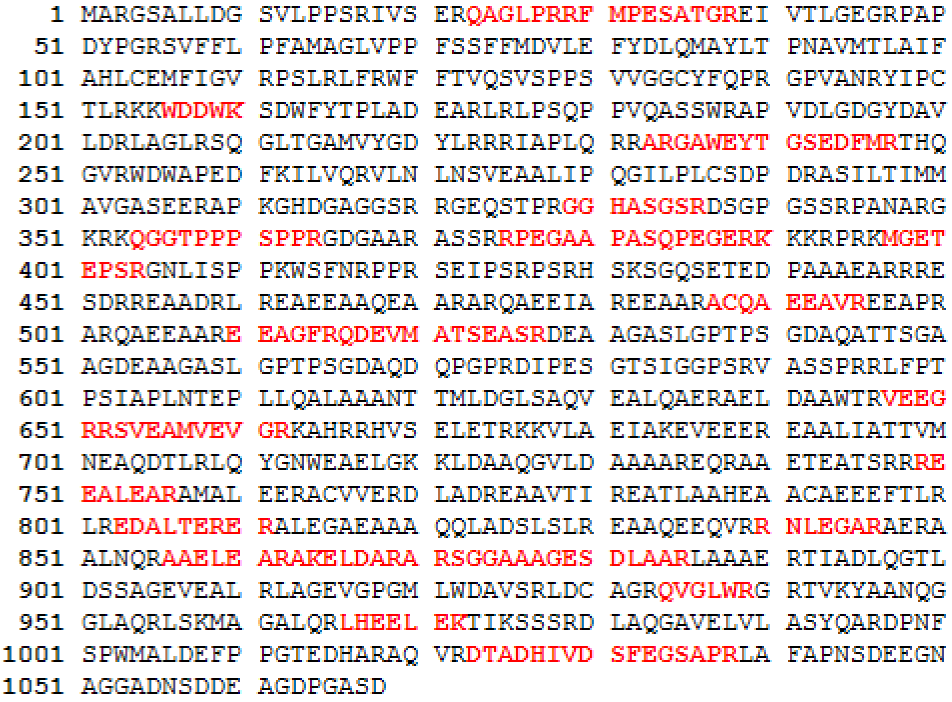


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red



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   1 MARGSALLDG SVLPPSRIVS ERQAGLPRRF MPESATGREI VTLGEGRPAP
  51 DYPGRSVFFL PFAMAGLVPP FSSFFMDVLE FYDLQMAYLT PNAVMTLAIF
 101 AHLCEMFIGV RPSLRLFRWF FTVQSVSPPS VVGGCYFQPR GPVANRYIPC
 151 TLRKKWDDWK SDWFYTPLAD EARLRLPSQP PVQASSWRAP VDLGDGYDAV
 201 LDRLAGLRSQ GLTGAMVYGD YLRRRIAPLQ RRARGAWEYT GSEDFMRTHQ
 251 GVRWDWAPED FKILVQRVLN LNSVEAALIP QGILPLCSDP DRASILTIMM
 301 AVGASEERAP KGHDGAGGSR RGEQSTPRGG HASGSRDSGP GSSRPANARG
 351 KRKQGGTPPP SPPRGDGAAR ASSRRPEGAA PASQPEGERK KKRPRKMGET
 401 EPSRGNLISP PKWSFNRPPR SEIPSRPSRH SKSGQSETED PAAAEARRRE
 451 SDRREAADRL REAEEAAQEA ARARQAEEIA REEAARACQA EEAVREEAPR
 501 ARQAEEAARE EAGFRQDEVM ATSEASRDEA AGASLGPTPS GDAQATTSGA
 551 AGDEAAGASL GPTPSGDAQD QPGPRDIPES GTSIGGPSRV ASSPRRLFPT
 601 PSIAPLNTEP LLQALAAANT TMLDGLSAQV EALQAERAEL DAAWTRVEEG
 651 RRSVEAMVEV GRKAHRRHVS ELETRKKVLA EIAKEVEEER EAALIATTVM
 701 NEAQDTLRLQ YGNWEAELGK KLDAAQGVLD AAAAREQRAA ETEATSRRRE
 751 EALEARAMAL EERACVVERD LADREAAVTI REATLAAHEA ACAEEEFTLR
 801 LREDALTERE RALEGAEAAA QQLADSLSLR EAAQEEQVRR NLEGARAERA
 851 ALNQRAAELE ARAKELDARA RSGGAAAGES DLAARLAAAE RTIADLQGTL
 901 DSSAGEVEAL RLAGEVGPGM LWDAVSRLDC AGRQVGLWRG RTVKYAANQG
 951 GLAQRLSKMA GALQRLHEEL EKTIKSSSRD LAQGAVELVL ASYQARDPNF
1001 SPWMALDEFP PGTEDHARAQ VRDTADHIVD SFEGSAPRLA FAPNSDEEGN
1051 AGGADNSDDE AGDPGASD
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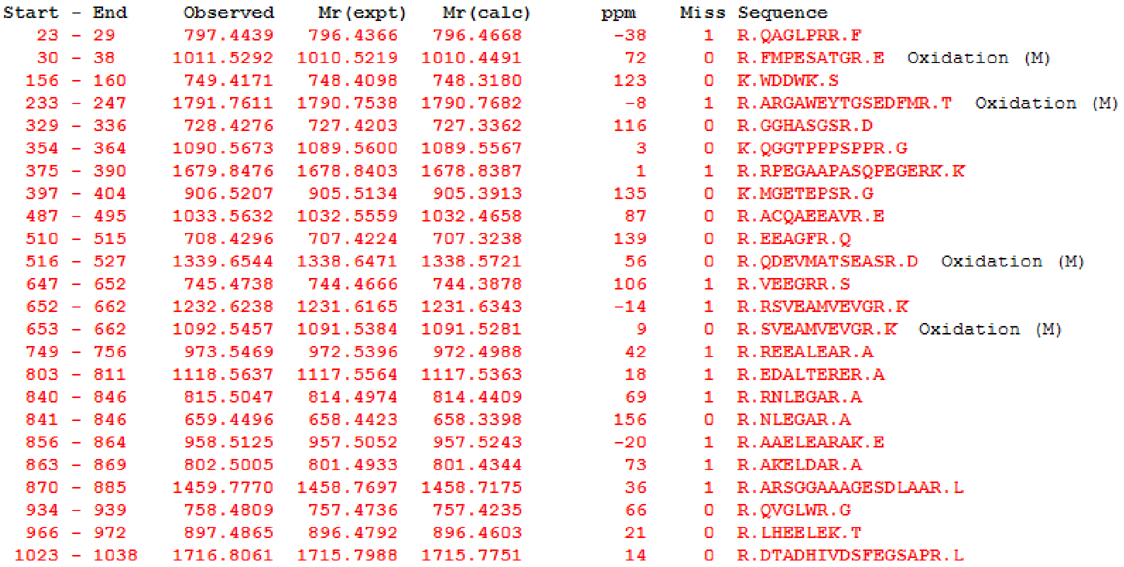
Matched peptides information:



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Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   23 - 29      797.4439   796.4366   796.4668      -38      1  R.QAGLPRR.F
   30 - 38     1011.5292  1010.5219  1010.4491       72      0  R.FMPESATGR.E  Oxidation (M)
  156 - 160     749.4171   748.4098   748.3180      123      0  K.WDDWK.S
  233 - 247    1791.7611  1790.7538  1790.7682       -8      1  R.ARGAWEYTGSEDFMR.T  Oxidation (M)
  329 - 336     728.4276   727.4203   727.3362      116      0  R.GGHASGSR.D
  354 - 364    1090.5673  1089.5600  1089.5567        3      0  K.QGGTPPPSPPR.G
  375 - 390    1679.8476  1678.8403  1678.8387        1      1  R.RPEGAAPASQPEGERK.K
  397 - 404     906.5207   905.5134   905.3913      135      0  K.MGETEPSR.G
  487 - 495    1033.5632  1032.5559  1032.4658       87      0  R.ACQAEEAVR.E
  510 - 515     708.4296   707.4224   707.3238      139      0  R.EEAGFR.Q
  516 - 527    1339.6544  1338.6471  1338.5721       56      0  R.QDEVMATSEASR.D  Oxidation (M)
  647 - 652     745.4738   744.4666   744.3878      106      1  R.VEEGRR.S
  652 - 662    1232.6238  1231.6165  1231.6343      -14      1  R.RSVEAMVEVGR.K
  653 - 662    1092.5457  1091.5384  1091.5281        9      0  R.SVEAMVEVGR.K  Oxidation (M)
  749 - 756     973.5469   972.5396   972.4988       42      1  R.REEALEAR.A
  803 - 811    1118.5637  1117.5564  1117.5363       18      1  R.EDALTERER.A
  840 - 846     815.5047   814.4974   814.4409       69      1  R.RNLEGAR.A
  841 - 846     659.4496   658.4423   658.3398      156      0  R.NLEGAR.A
  856 - 864     958.5125   957.5052   957.5243      -20      1  R.AAELEARAK.E
  863 - 869     802.5005   801.4933   801.4344       73      1  R.AKELDAR.A
  870 - 885    1459.7770  1458.7697  1458.7175       36      1  R.ARSGGAAAGESDLAAR.L
  934 - 939     758.4809   757.4736   757.4235       66      0  R.QVGLWR.G
  966 - 972     897.4865   896.4792   896.4603       21      0  R.LHEELEK.T
 1023 - 1038   1716.8061  1715.7988  1715.7751       14      0  R.DTADHIVDSFEGSAPR.L
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Spot No.: **21**

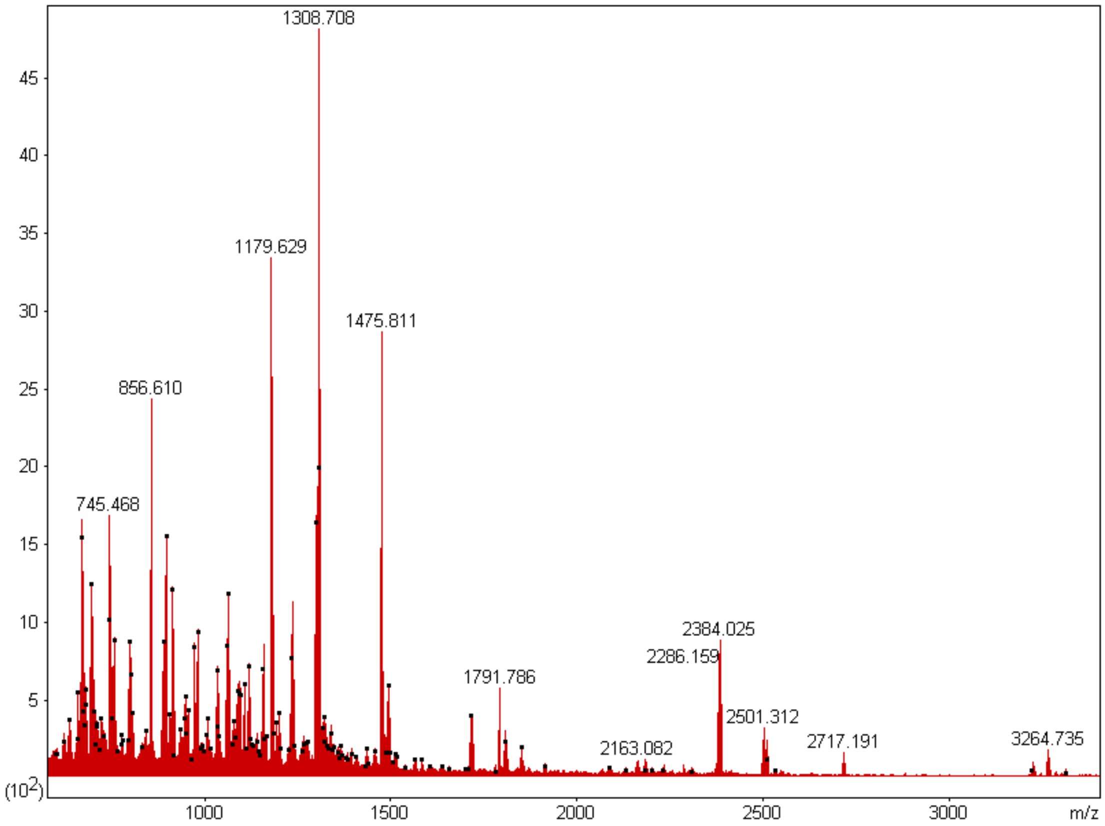
Mascot score: **90** Sequence coverage %: **23**

NCBI accession No.: **gi| 303276186**

Matched peptides No.: **44** Total peptides No.: **126**

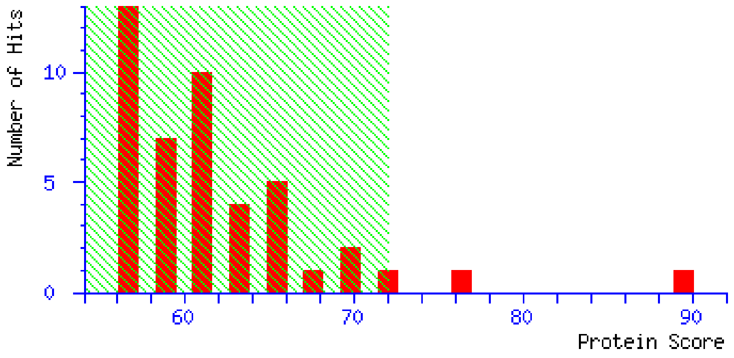
Calculated Mr: **188682** Calculated *p*I: **6.11**

Annotated PMF **spectra:**



Probability Based Mowse Score:

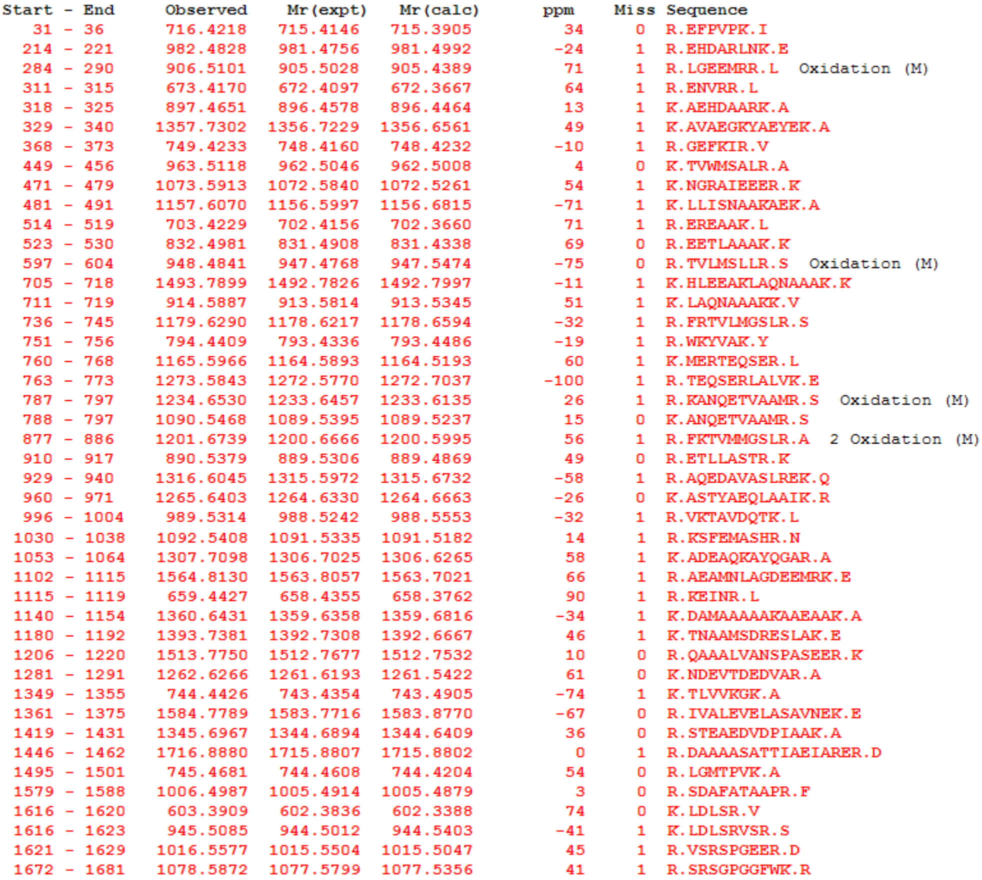
Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 MPVSKERTVP ITSWANAELE VSERLRRSER **EFPVPK**IPEL ARERSRSAPE
51 TAAPRSPARE TSTSTSGGAR ERSPDHLLTK RRGNPFGFGF AIDVHALLDK
101 LPKPGRRAPP SPARRPASEN DATSSENSHS SPSPAKENAL VAAGLATPPP
151 TKTPDADAML ASSPDADAML ASSPAPTWTP KHLDSANKLN AELHAKLVRE
201 QEKAREAIKN LKR**EHDARLN** **K**ERGERKEEV RRMNEQHEAR AKKREEEASR
251 EREKREDERE RARERDADDL KRLNERLEEK ATR**LGEEMRR** LCDEHEARLK
301 KHDDERKAER **ENVRR**LK**AEH** **DAARK**ADK**AV** **AEGKYAEYEK** AVALGKLEME
351 DLARQLEKDR RELRTER**GEF** **KIR**VRRFQED HDLMESELDE TQTNAQMMLR
401 EAQAEIIALK NTAQRIEAEW EVTKLEQAAV AAEKEKERAR QKVELRFK**TV**
451 **WMSALR**ASFV RWKSESRRIK **NGRAIEEER**K **LLISNAAKAE** **K**ALEEESARG
501 AAMLEAAREE AKR**EREAAK**L QR**EETLAAAK** KDLNDAEAAK KAAIKKMEDA
551 LKAQTEATIR AQNQLEEAEL NQAAAARAAS VAALGRLEQR AALRFR**TVLM**
601 **SLLR**SSFTRW KNETSLSRVE RVERAEMLEH KAAKERAEQA LEDARASQEK
651 MIEGMKAKHE ESVDAIKTEH SRAVETIKAE HSEAVSKLED ALRKSNEEIS
701 TAKK**HLEEAK** **LAQNAAAKK**V EVAARERAAQ TATLR**FRTVL** **MGSLR**SSFVR
751 **WKYVAK**YQK**M** **ERTEQSERLA** **LVK**EKEKAEN ELAEAR**KANQ** **ETVAAMR**SKQ
801 AETLQIIEDA KQSIAKQVQE KQDSTIKKLE EALEKQTNAT LRAQKQFDDA
851 ELARAAAVQA AKIAATERAL QKAALR**FKTV** **MMGSLR**ASFQ RWKYAAKFMR
901 RDREADAER**E** **TLLASTR**KAG RELEDARR**AQ** **EDAVASLREK** QRKEKQRLEE
951 QHAAAAEQK**A** **STYAEQLAAI** **K**REAAAALAS AREEELDSTA DIERR**VKTAV**
1001 **DQTK**LELGSS VDQLRAQLAS LEIKLTASR**K** **SFEMASHR**NA TLEDEVDAAN
1051 RK**ADEAQKAY** **QGAR**AAAAFM EADADEMKQV LDQVNEAHAL ALEDERRKLA
1101 R**AEAMNLAGD** **EEMRKEINR**L HSELEEQKLL VAAASKATK**D** **AMAAAAAKAA**
1151 **EAAK**AESEAA RARESMLLSD AASSAEMAK**T** **NAAMSDRESL** **AK**ECEQLRLE
1201 LAAAR**QAAAL** **VANSPASEER** KRTSARKASP SPAPAGSASS SKKKSARQRG
1251 TITVDEHEEA IALLRGEIQV LVSRLGDVGK **NDEVTDEDVA** **R**ARSKAAKDL
1301 DLAIQLTEDW EEEPRTPRGA NDDDGSESGS ESDDDHVETV VKLNNRCK**TL**
1351 **VVKGK**AALAR **IVALEVELAS** **AVNEK**ESATA WALACTRRAK GAEEAAMFAK
1401 DEARDLKLRT RDIRLGKR**ST** **EAEDVDPIAA** **K**AAIERLEVE LSEAR**DAAAA**
1451 **SATTIAEIAR** **ER**DVLKRELV GYERRKKAGG DFDELISGSN VIER**LGMTPV**
1501 **K**AKEEPEPEE EEEEEGFFAW LTTPSRQPDV EEKAKKKEED DEPGFFRTLF
1551 GLTPSKDAAG EGGARPAASE KSDSSASR**SD** **AFATAAPR**FR SGASVTSGDD
1601 AATRNLANTP PSIPK**LDLSR** **VSRSPGEER**D RGGREGARSD ADADAESDAE
1651 SDAASGDARR VAGEASESDA R**SRSGPGGFW** **K**RVAGDDADF SDSDSVESVS
1701 GQL

Matched peptides information:



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Start - End     Observed    Mr(expt)   Mr(calc)      ppm    Miss Sequence
   31 - 36      716.4218    715.4146   715.3905       34      0  R.EFPVPK.I
  214 - 221     982.4828    981.4756   981.4992      -24      1  R.EHDARLNK.E
  284 - 290     906.5101    905.5028   905.4389       71      1  R.LGEEMRR.L   Oxidation (M)
  311 - 315     673.4170    672.4097   672.3667       64      1  R.ENVRR.L
  318 - 325     897.4651    896.4578   896.4464       13      1  K.AEHDAARK.A
  329 - 340    1357.7302   1356.7229  1356.6561       49      1  K.AVAEGKYAEYEK.A
  368 - 373     749.4233    748.4160   748.4232      -10      1  R.GEFKIR.V
  449 - 456     963.5118    962.5046   962.5008        4      0  K.TVWMSALR.A
  471 - 479    1073.5913   1072.5840  1072.5261       54      1  K.NGRAIEEER.K
  481 - 491    1157.6070   1156.5997  1156.6815      -71      1  K.LLISNAAKAEK.A
  514 - 519     703.4229    702.4156   702.3660       71      1  R.EREAAK.L
  523 - 530     832.4981    831.4908   831.4338       69      0  R.EETLAAAK.K
  597 - 604     948.4841    947.4768   947.5474      -75      0  R.TVLMSLLR.S   Oxidation (M)
  705 - 718    1493.7899   1492.7826  1492.7997      -11      1  K.HLEEAKLAQNAAAK.K
  711 - 719     914.5887    913.5814   913.5345       51      1  K.LAQNAAAKK.V
  736 - 745    1179.6290   1178.6217  1178.6594      -32      1  R.FRTVLMGSLR.S
  751 - 756     794.4409    793.4336   793.4486      -19      1  R.WKYVAK.Y
  760 - 768    1165.5966   1164.5893  1164.5193       60      1  K.MERTEQSER.L
  763 - 773    1273.5843   1272.5770  1272.7037     -100      1  R.TEQSERLALVK.E
  787 - 797    1234.6530   1233.6457  1233.6135       26      1  R.KANQETVAAMR.S   Oxidation (M)
  788 - 797    1090.5468   1089.5395  1089.5237       15      0  K.ANQETVAAMR.S
  877 - 886    1201.6739   1200.6666  1200.5995       56      1  R.FKTVMMGSLR.A  2 Oxidation (M)
  910 - 917     890.5379    889.5306   889.4869       49      0  R.ETLLASTR.K
  929 - 940    1316.6045   1315.5972  1315.6732      -58      1  R.AQEDAVASLREK.Q
  960 - 971    1265.6403   1264.6330  1264.6663      -26      0  K.ASTYAEQLAAIK.R
  996 - 1004    989.5314    988.5242   988.5553      -32      1  R.VKTAVDQTK.L
 1030 - 1038   1092.5408   1091.5335  1091.5182       14      1  R.KSFEMASHR.N
 1053 - 1064   1307.7098   1306.7025  1306.6265       58      1  K.ADEAQKAYQGAR.A
 1102 - 1115   1564.8130   1563.8057  1563.7021       66      1  R.AEAMNLAGDEEMRK.E
 1115 - 1119    659.4427    658.4355   658.3762       90      1  R.KEINR.L
 1140 - 1154   1360.6431   1359.6358  1359.6816      -34      1  K.DAMAAAAAKAAEAAK.A
 1180 - 1192   1393.7381   1392.7308  1392.6667       46      1  K.TNAAMSDRESLAK.E
 1206 - 1220   1513.7750   1512.7677  1512.7532       10      0  R.QAAALVANSPASEER.K
 1281 - 1291   1262.6266   1261.6193  1261.5422       61      0  K.NDEVTDEDVAR.A
 1349 - 1355    744.4426    743.4354   743.4905      -74      1  K.TLVVKGK.A
 1361 - 1375   1584.7789   1583.7716  1583.8770      -67      0  R.IVALEVELASAVNEK.E
 1419 - 1431   1345.6967   1344.6894  1344.6409       36      0  R.STEAEDVDPIAAK.A
 1446 - 1462   1716.8880   1715.8807  1715.8802        0      1  R.DAAAASATTIAEIARER.D
 1495 - 1501    745.4681    744.4608   744.4204       54      0  R.LGMTPVK.A
 1579 - 1588   1006.4987   1005.4914  1005.4879        3      0  R.SDAFATAAPR.F
 1616 - 1620    603.3909    602.3836   602.3388       74      0  K.LDLSR.V
 1616 - 1623    945.5085    944.5012   944.5403      -41      1  K.LDLSRVSR.S
 1621 - 1629   1016.5577   1015.5504  1015.5047       45      1  R.VSRSPGEER.D
 1672 - 1681   1078.5872   1077.5799  1077.5356       41      1  R.SRSGPGGFWK.R
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Spot No.: **22**

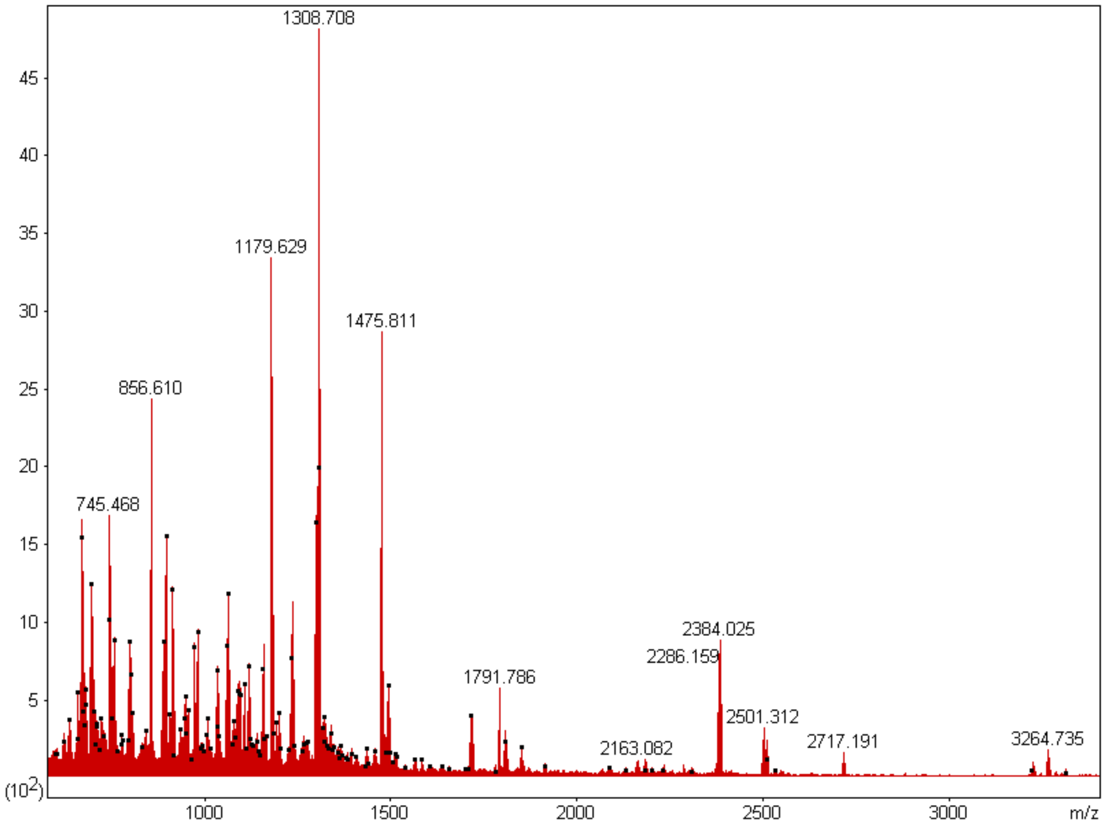
Mascot score: **90** Sequence coverage %: **25**

NCBI accession No.: **gi| 294460288**

Matched peptides No.: **12** Total peptides No.: **71**

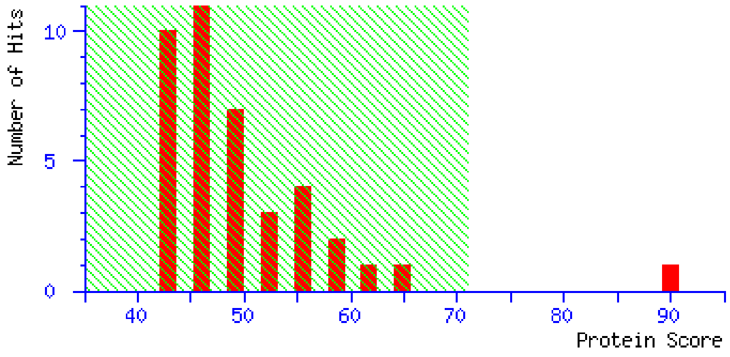
Calculated Mr: **52848** Calculated p*I*: **5.97**

Annotated PMF **spectra:**

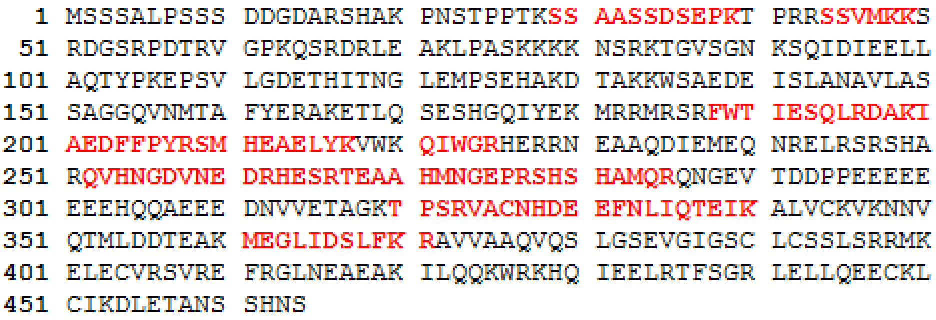


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

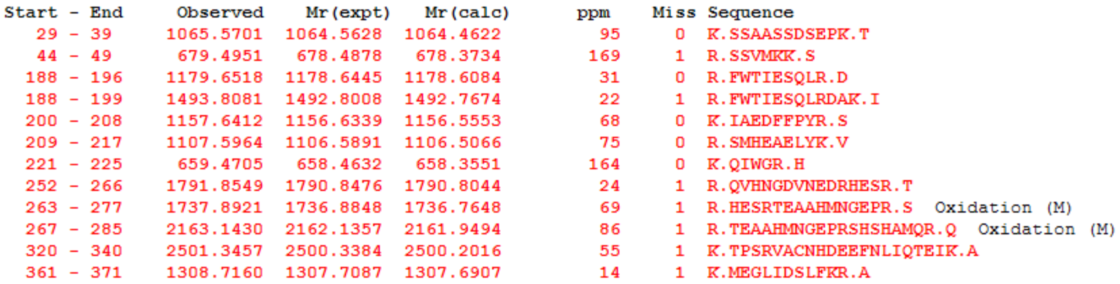


Matched peptide sequences: shown in Bold Red



```
  1 MSSSALPSSS DDGDARSHAK PNSTPPTKSS AASSDSEPKT PRRSSVMKKS
 51 RDGSRPDTRV GPKQSRDRLE AKLPASKKKK NSRKTGVSGN KSQIDIEELL
101 AQTYPKEPSV LGDETHITNG LEMPSEHAKD TAKKWSAEDE ISLANAVLAS
151 SAGGQVNMTA FYERAKETLQ SESHGQIYEK MRRMRSRFWT IESQLRDAKI
201 AEDFFPYRSM HEAELYKVWK QIWGRHERRN EAAQDIEMEQ NRELRSRSHA
251 RQVHNGDVNE DRHESRTEAA HMNGEPRSHS HAMQRQNGEV TDDPPEEEEE
301 EEEHQQAEEE DNVVETAGKT PSRVACNHDE EFNLIQTEIK ALVCKVKNNV
351 QTMLDDTEAK MEGLIDSLFK RAVVAAQVQS LGSEVGIGSC LCSSLSRRMK
401 ELECVRSVRE FRGLNEAEAK ILQQKWRKHQ IEELRTFSGR LELLQEECKL
451 CIKDLETANS SHNS
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   29 - 39     1065.5701  1064.5628  1064.4622       95      0  K.SSAASSDSEPK.T
   44 - 49      679.4951   678.4878   678.3734      169      1  R.SSVMKK.S
  188 - 196    1179.6518  1178.6445  1178.6084       31      0  R.FWTIESQLR.D
  188 - 199    1493.8081  1492.8008  1492.7674       22      1  R.FWTIESQLRDAK.I
  200 - 208    1157.6412  1156.6339  1156.5553       68      0  K.IAEDFFPYR.S
  209 - 217    1107.5964  1106.5891  1106.5066       75      0  R.SMHEAELYK.V
  221 - 225     659.4705   658.4632   658.3551      164      0  K.QIWGR.H
  252 - 266    1791.8549  1790.8476  1790.8044       24      1  R.QVHNGDVNEDRHESR.T
  263 - 277    1737.8921  1736.8848  1736.7648       69      1  R.HESRTEAAHMNGEPR.S  Oxidation (M)
  267 - 285    2163.1430  2162.1357  2161.9494       86      1  R.TEAAHMNGEPRSHSHAMQR.Q  Oxidation (M)
  320 - 340    2501.3457  2500.3384  2500.2016       55      1  K.TPSRVACNHDEEFNLIQTEIK.A
  361 - 371    1308.7160  1307.7087  1307.6907       14      1  K.MEGLIDSLFKR.A
```

Spot No.: **23**

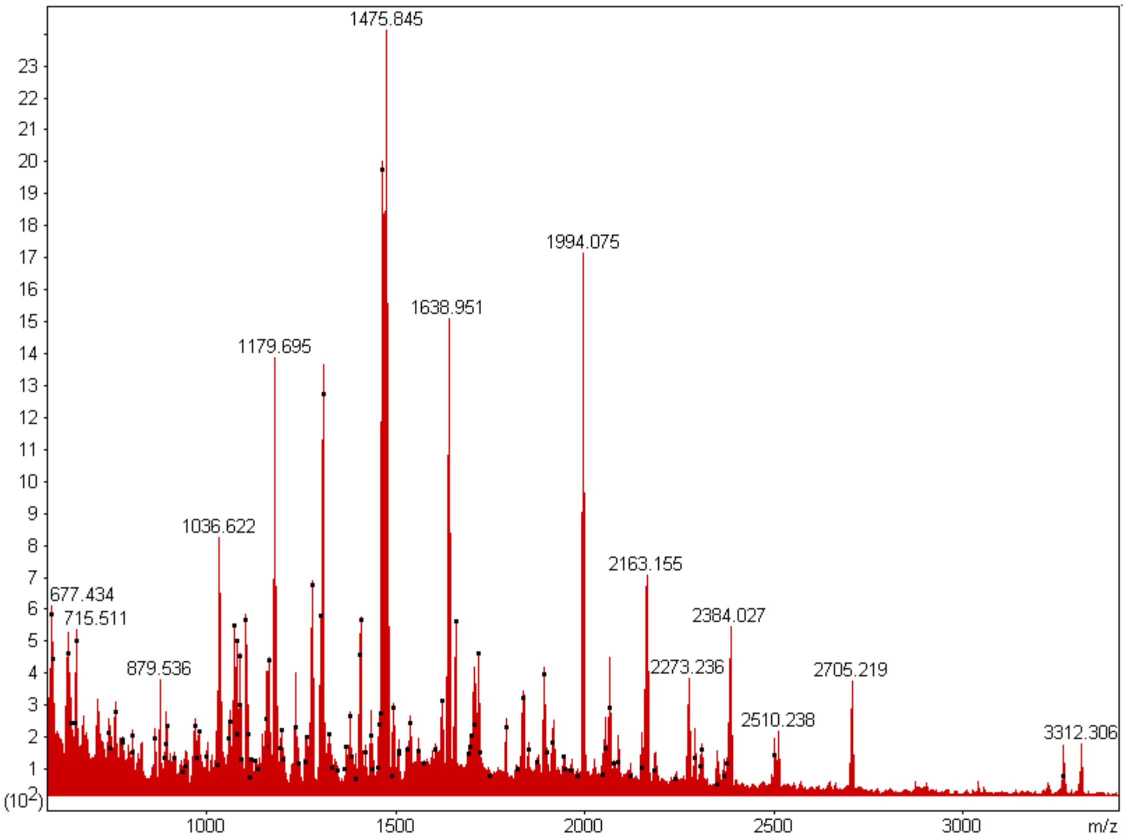
Mascot score: **81**   Sequence coverage %: **34**

NCBI accession No.: **gi| 125575959**

Matched peptides No.: **12**   Total peptides No.: **111**

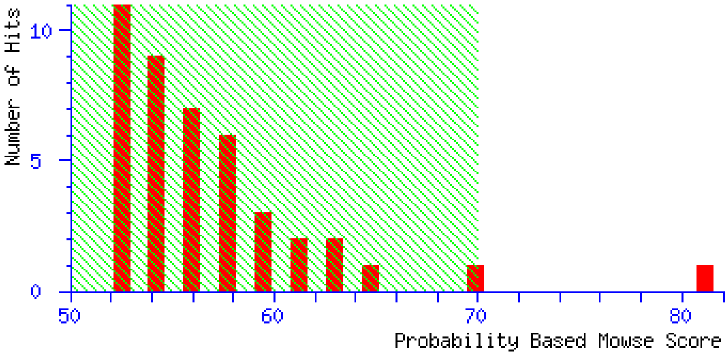
Calculated Mr: **29568**   Calculated *p*I: **5.53**

Annotated PMF **spectra:**

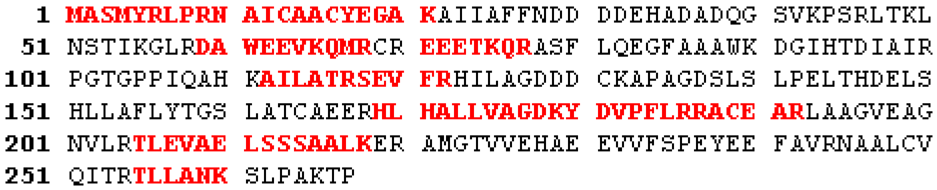


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

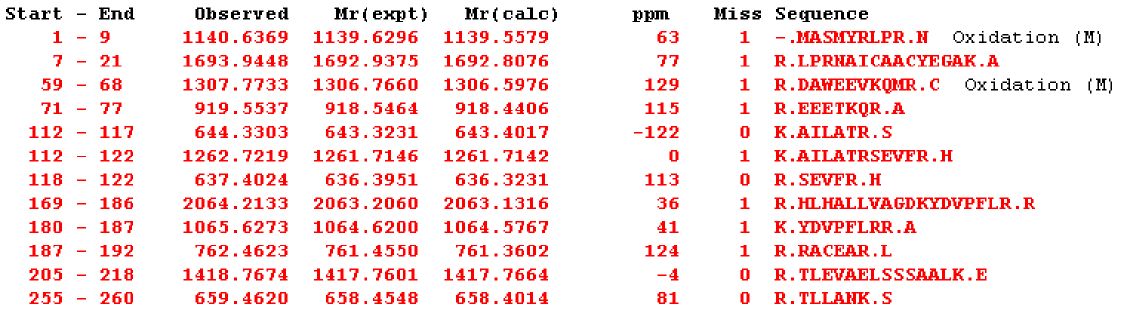


Matched peptide sequences: shown in Bold Red



1 **MASMYRLPRN** **AICAACYEGA** **K**AIIAFFNDD DDEHADADQG SVKPSRLTKL
51 NSTIKGLR**DA** **WEEVKQMR**CR **EEETKQR**ASF LQEGFAAAWK DGIHTDIAIR
101 PGTGPPIQAH K**AILATRSEV** **FR**HILAGDDD CKAPAGDSLS LPELTHDELS
151 HLLAFLYTGS LATCAEER**HL** **HALLVAGDKY** **DVPFLRRACE** **AR**LAAGVEAG
201 NVLR**TLEVAE** **LSSSAALK**ER AMGTVVEHAE EVVFSPEYEE FAVRNAALCV
251 QITR**TLLANK** SLPAKTP

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss Sequence
    1 - 9      1140.6369  1139.6296  1139.5579       63     1  -.MASMYRLPR.N  Oxidation (M)
    7 - 21     1693.9448  1692.9375  1692.8076       77     1  R.LPRNAICAACYEGAK.A
   59 - 68     1307.7733  1306.7660  1306.5976      129     1  R.DAWEEVKQMR.C  Oxidation (M)
   71 - 77      919.5537   918.5464   918.4406      115     1  R.EEETKQR.A
  112 - 117     644.3303   643.3231   643.4017     -122     0  K.AILATR.S
  112 - 122    1262.7219  1261.7146  1261.7142        0     1  K.AILATRSEVFR.H
  118 - 122     637.4024   636.3951   636.3231      113     0  R.SEVFR.H
  169 - 186    2064.2133  2063.2060  2063.1316       36     1  R.HLHALLVAGDKYDVPFLR.R
  180 - 187    1065.6273  1064.6200  1064.5767       41     1  K.YDVPFLRR.A
  187 - 192     762.4623   761.4550   761.3602      124     1  R.RACEAR.L
  205 - 218    1418.7674  1417.7601  1417.7664       -4     0  R.TLEVAELSSSAALK.E
  255 - 260     659.4620   658.4548   658.4014       81     0  R.TLLANK.S
```

Spot No.: **24**

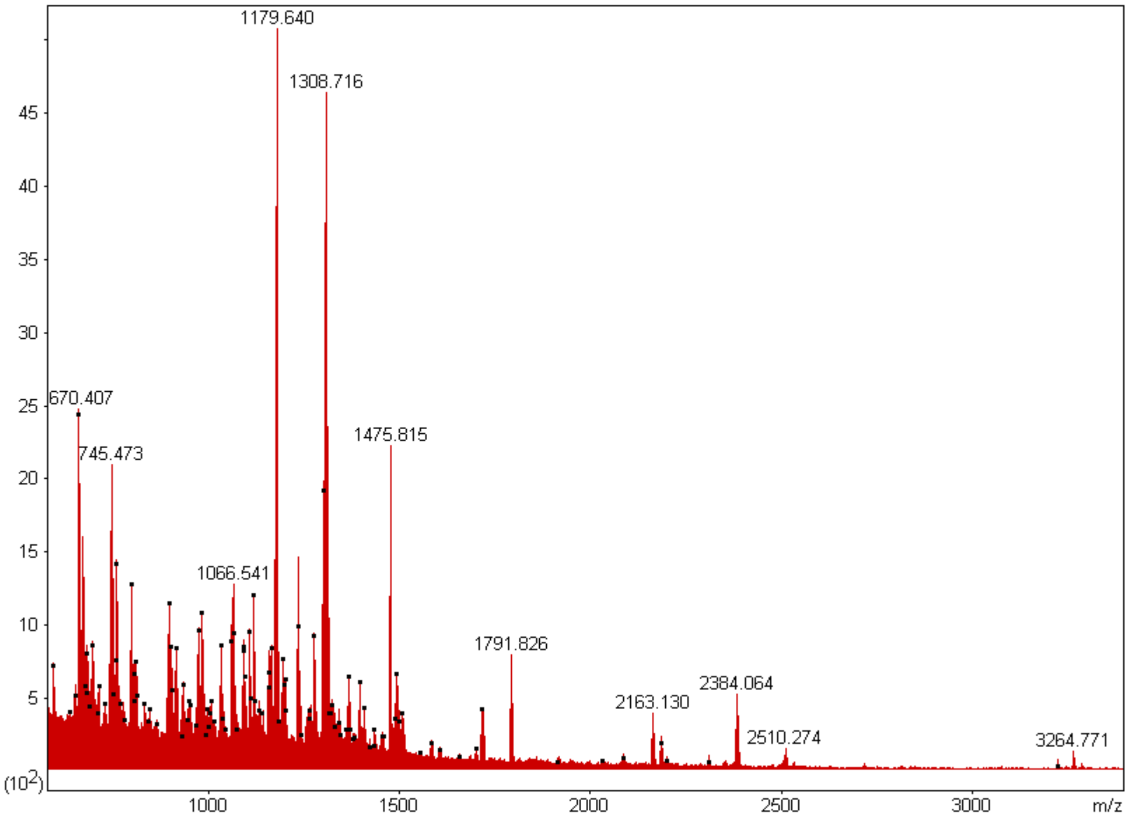
Mascot score: **82** Sequence coverage %: **26**

NCBI accession No.: **gi| 168036931**

Matched peptides No.: **17** Total peptides No.: **116**

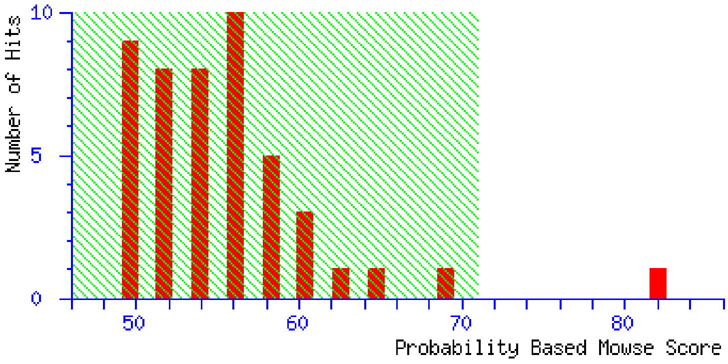
Calculated Mr: **49474** Calculated p*I*: **9.31**

Annotated PMF **spectra:**

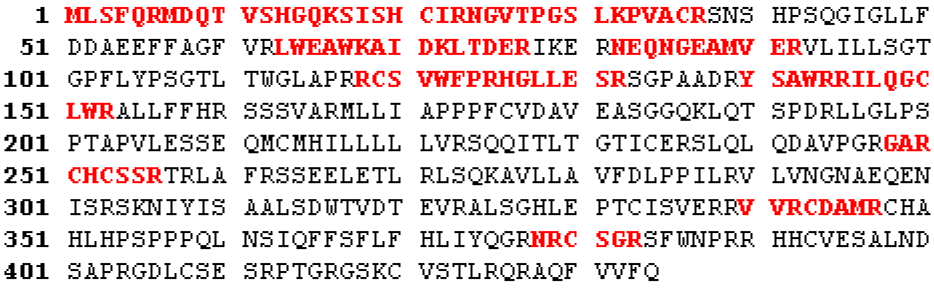


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

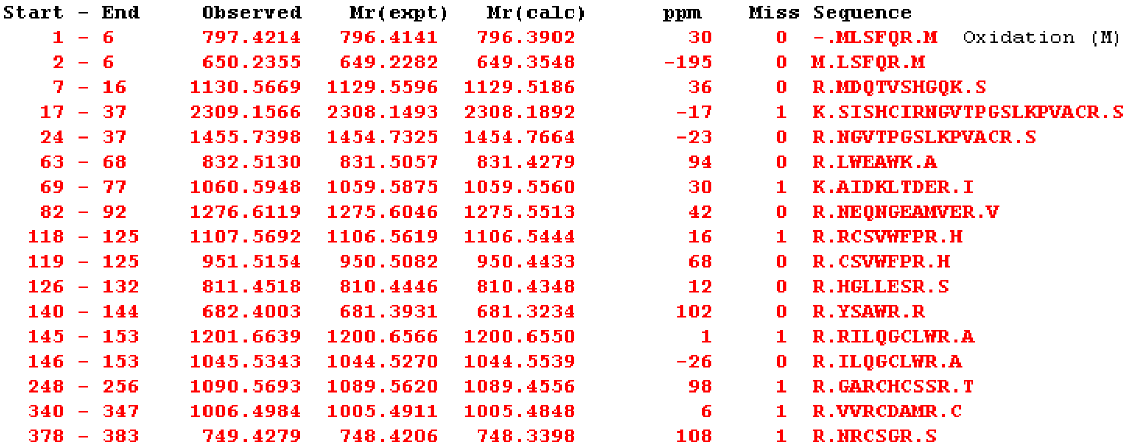


Matched peptide sequences: shown in Bold Red



1 **MLSFQRMDQT VSHGQKSISH CIRNGVTPGS LKPVACR**SNS HPSQGIGLLF
51 DDAEEFFAGF VR**LWEAWKAI DKLTDER**IKE R**NEQNGEAMV ER**VLILLSGT
101 GPFLYPSGTL TWGLAPR**RCS VWFPRHGLLE SR**SGPAADR**Y SAWRRILQGC**
151 **LWR**ALLFFHR SSSVARMLLI APPPFCVDAV EASGGQKLQT SPDRLLGLPS
201 PTAPVLESSE QMCMHILLLL LVRSQQITLT GTICERSLQL QDAVPGR**GAR**
251 **CHCSSR**TRLA FRSSEELETL RLSQKAVLLA VFDLPPILRV LVNGNAEQEN
301 ISRSKNIYIS AALSDWTVDT EVRALSGHLE PTCISVERR**V VRCDAMR**CHA
351 HLHPSPPPQL NSIQFFSFLF HLIYQGR**NRC SGR**SFWNPRR HHCVESALND
401 SAPRGDLCSE SRPTGRGSKC VSTLRQRAQF VVFQ

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
1 - 6	797.4214	796.4141	796.3902	30	0	-.MLSFQR.M Oxidation (M)
2 - 6	650.2355	649.2282	649.3548	-195	0	M.LSFQR.M
7 - 16	1130.5669	1129.5596	1129.5186	36	0	R.MDQTVSHGQK.S
17 - 37	2309.1566	2308.1493	2308.1892	-17	1	K.SISHCIRNGVTPGSLKPVACR.S
24 - 37	1455.7398	1454.7325	1454.7664	-23	0	R.NGVTPGSLKPVACR.S
63 - 68	832.5130	831.5057	831.4279	94	0	R.LWEAWK.A
69 - 77	1060.5948	1059.5875	1059.5560	30	1	K.AIDKLTDER.I
82 - 92	1276.6119	1275.6046	1275.5513	42	0	R.NEQNGEAMVER.V
118 - 125	1107.5692	1106.5619	1106.5444	16	1	R.RCSVWFPR.H
119 - 125	951.5154	950.5082	950.4433	68	0	R.CSVWFPR.H
126 - 132	811.4518	810.4446	810.4348	12	0	R.HGLLESR.S
140 - 144	682.4003	681.3931	681.3234	102	0	R.YSAWR.R
145 - 153	1201.6639	1200.6566	1200.6550	1	1	R.RILQGCLWR.A
146 - 153	1045.5343	1044.5270	1044.5539	-26	0	R.ILQGCLWR.A
248 - 256	1090.5693	1089.5620	1089.4556	98	1	R.GARCHCSSR.T
340 - 347	1006.4984	1005.4911	1005.4848	6	1	R.VVRCDAMR.C
378 - 383	749.4279	748.4206	748.3398	108	1	R.NRCSGR.S

Spot No.: **25**

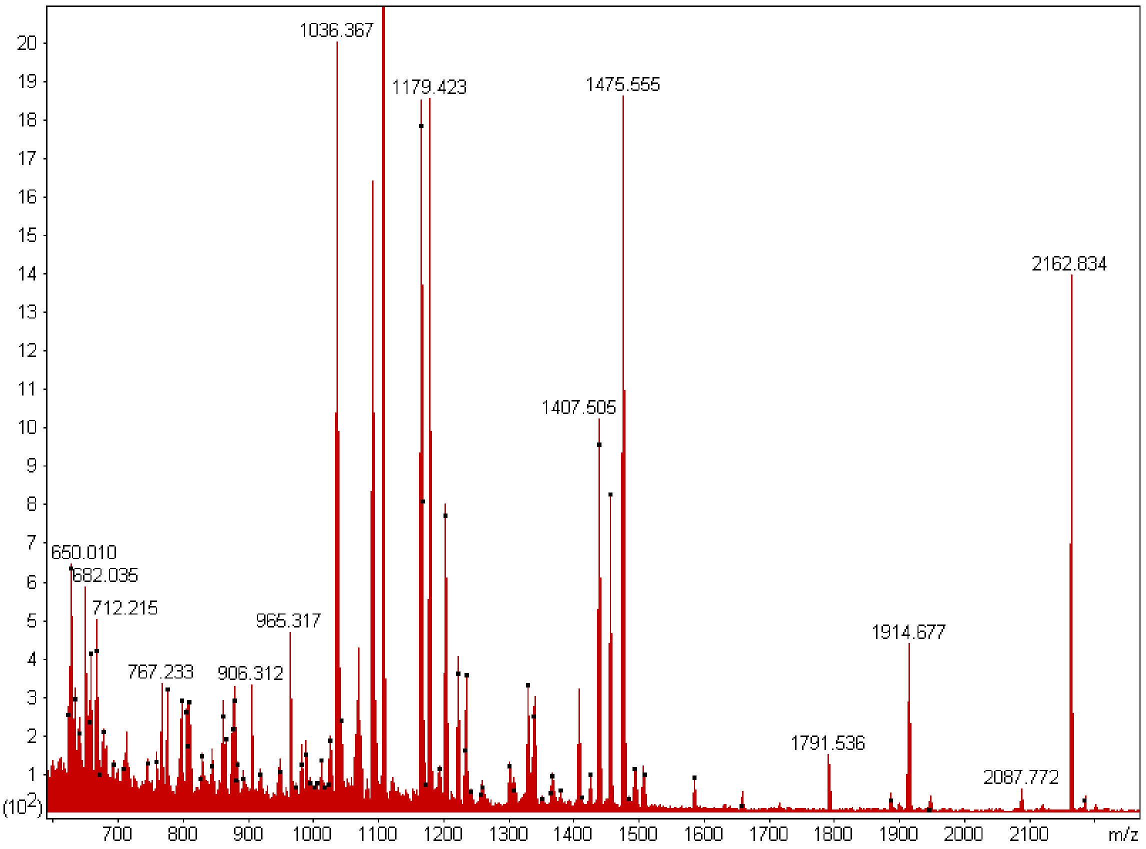
Mascot score: **96** Sequence coverage %: **26**

NCBI accession No.: **gi| 168037847**

Matched peptides No.: **20** Total peptides No.: **53**

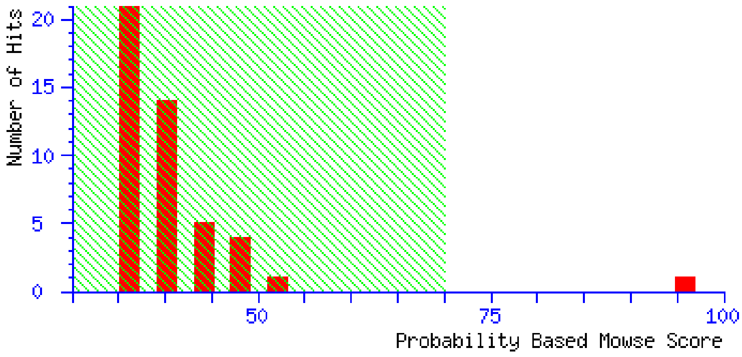
Calculated Mr: **70593** Calculated *p*I: **9.86**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 MGVQMFLCPV VK**LEHTLSK**M KHSPNAEQLR GAEVVKGRLN RTSR**SLQAAN**
51 **MIIAR**NPNPM GLSDMLDSTS DNLNGQNGNS SGLLGNNVK**Q** **GNETTR**EFKL
101 AECLKELASF QR**SVLEDPQE** **DYPMQPK**DLN TLFSAGIIQS KRVENADALS
151 AEAKGTVSED LGKAGCNVGA VKSTRRREVK AIQQKPWSFS TKTSVRQLKG
201 DAGVGKIERL IRMSKKSPVV GAKSR**QYVIH** **SNPLATGR**RL STASSKRR**DS**
251 **LELSPTK**CKR MSNSPTLKPK SAEKKK**YGFG** **IQAANAGNR**K TCSNKEQMPT
301 LKGGKAENKA LKHTDRQKVI LK**RVMSSPVN** **GKK**KVLRETA SGLMSSVDLS
351 AAARRARR**LS** **QVLRSEHELK** HHNQQYAK**EA** **QQLRQQLAIK** EDEADRAQSA
401 SMLLRQICAN QAAELKSYKE AVPILMKELS EVREKYFKQE DDLQFELNAK
451 LGFQTEVSNL RDCVESLTND IQQTR**TVNTA** **LAKR**VHQYEK SVCTSCRLYI
501 NQKPMKK**EMS** **PMPSKTK**AGH PLKTPIRLRS DSNLGR**WNSP** **R**AALTSMKEM
551 ENSWQLENQK **LPFKSTGDVN** **QNPLK**DLEQH DFALQARCEN VSQGLSNSDC
601 PPVDALK**NRI** **SSLLFTASQA** **LENQHR**AM

Matched peptides information:

```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   13 - 19      827.2610   826.2537   826.4548      -243      0  K.LEHTLSK.M
   45 - 55     1203.4329  1202.4256  1202.6441      -182      0  R.SLQAANMIIAR.N  Oxidation (M)
   90 - 96      805.2733   804.2660   804.3726      -133      0  K.QGNETTR.E
  113 - 127    1791.5361  1790.5288  1790.8033      -153      0  R.SVLEDPQEDYPMQPK.D  Oxidation (M)
  226 - 238    1455.4855  1454.4782  1454.7630      -196      0  R.QYVIHSNPLATGR.R
  249 - 257     989.3113   988.3040   988.5077      -206      0  R.DSLELSPTK.C
  277 - 289    1338.4622  1337.4549  1337.6476      -144      0  K.YGFGIQAANAGNR.K
  323 - 332    1074.3601  1073.3528  1073.5652      -198      1  K.RVMSSPVNGK.K
  323 - 332    1090.3556  1089.3483  1089.5601      -194      1  K.RVMSSPVNGK.K  Oxidation (M)
  324 - 333    1062.3337  1061.3264  1061.5539      -214      1  R.VMSSPVNGKK.K  Oxidation (M)
  359 - 370    1438.4935  1437.4862  1437.7939      -214      1  R.LSQVLRSEHELK.H
  379 - 390    1425.5013  1424.4940  1424.8099      -222      1  K.EAQQLRQQLAIK.E
  476 - 484     973.3445   972.3373   972.5716      -241      1  R.TVNTALAKR.V
  508 - 515     906.3123   905.3050   905.3987      -103      0  K.EMSPMPSK.T
  508 - 517    1167.4913  1166.4840  1166.5311       -40      1  K.EMSPMPSKTK.A  2 Oxidation (M)
  537 - 541     659.2599   658.2526   658.3187      -100      0  R.WNSPR.A
  561 - 575    1657.5952  1656.5879  1656.8835      -178      1  K.LPFKSTGDVNQNPLK.D
  565 - 575    1172.3409  1171.3336  1171.5833      -213      0  K.STGDVNQNPLK.D
  608 - 626    2184.8768  2183.8695  2184.1399      -124      1  K.NRISSLLFTASQALENQHR.A
  610 - 626    1914.6770  1913.6697  1913.9959      -170      0  R.ISSLLFTASQALENQHR.A
```

Spot No.: **26**

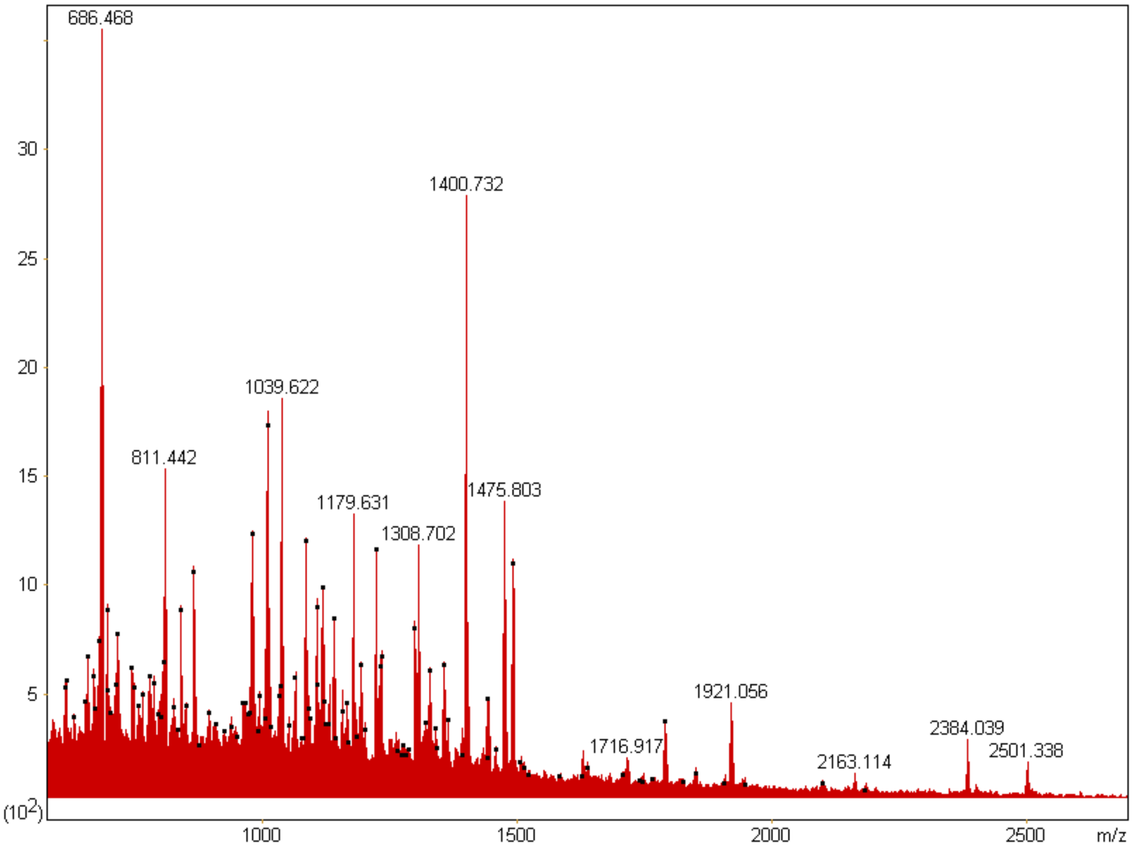
Mascot score: **81**   Sequence coverage %: **36**

NCBI accession No.: **gi| 168014980**

Matched peptides No.: **14**   Total peptides No.: **115**

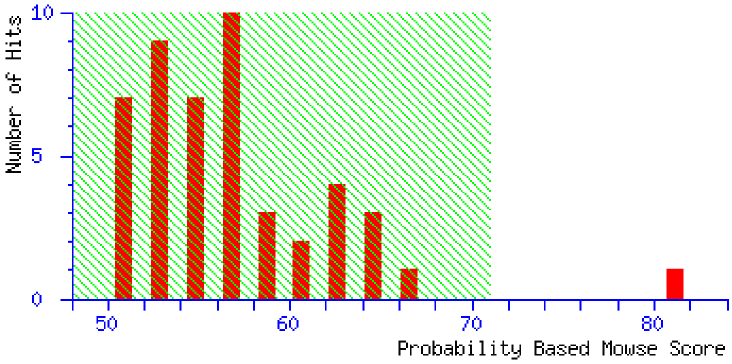
Calculated Mr: **29082**   Calculated *p*I: **9.53**

Annotated PMF **spectra:**

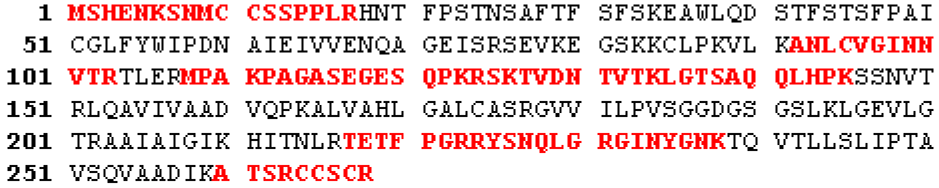


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

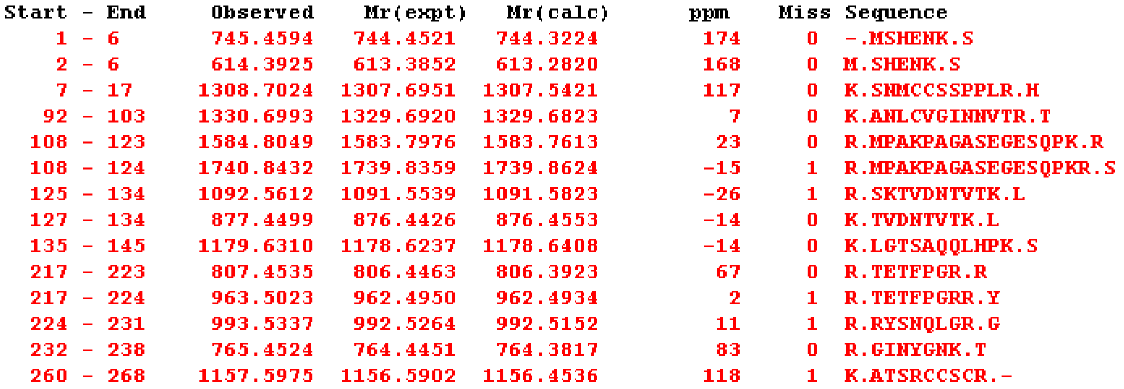


Matched peptide sequences: shown in Bold Red



```
  1 MSHENKSNMC CSSPPLRHNT FPSTNSAFTF SFSKEAWLQD STFSTSFPAI
 51 CGLFYWIPDN AIEIVVENQA GEISRSEVKE GSKKCLPKVL KANLCVGINN
101 VTRTLERMPA KPAGASEGES QPKRSKTVDN TVTKLGTSAQ QLHPKSSNVT
151 RLQAVIVAAD VQPKALVAHL GALCASRGVV ILPVSGGDGS GSLKLGEVLG
201 TRAAIAIGIK HITNLRTETF PGRRYSNQLG RGINYGNKTQ VTLLSLIPTA
251 VSQVAADIKA TSRCCSCR
```

Matched peptides information:



```
Start - End     Observed    Mr(expt)    Mr(calc)      ppm   Miss Sequence
    1 - 6       745.4594    744.4521    744.3224      174     0  -.MSHENK.S
    2 - 6       614.3925    613.3852    613.2820      168     0  M.SHENK.S
    7 - 17     1308.7024   1307.6951   1307.5421      117     0  K.SNMCCSSPPLR.H
   92 - 103    1330.6993   1329.6920   1329.6823        7     0  K.ANLCVGINNVTR.T
  108 - 123    1584.8049   1583.7976   1583.7613       23     0  R.MPAKPAGASEGESQPK.R
  108 - 124    1740.8432   1739.8359   1739.8624      -15     1  R.MPAKPAGASEGESQPKR.S
  125 - 134    1092.5612   1091.5539   1091.5823      -26     1  R.SKTVDNTVTK.L
  127 - 134     877.4499    876.4426    876.4553      -14     0  K.TVDNTVTK.L
  135 - 145    1179.6310   1178.6237   1178.6408      -14     0  K.LGTSAQQLHPK.S
  217 - 223     807.4535    806.4463    806.3923       67     0  R.TETFPGR.R
  217 - 224     963.5023    962.4950    962.4934        2     1  R.TETFPGRR.Y
  224 - 231     993.5337    992.5264    992.5152       11     1  R.RYSNQLGR.G
  232 - 238     765.4524    764.4451    764.3817       83     0  R.GINYGNK.T
  260 - 268    1157.5975   1156.5902   1156.4536      118     1  K.ATSRCCSCR.-
```

Spot No.: **27**

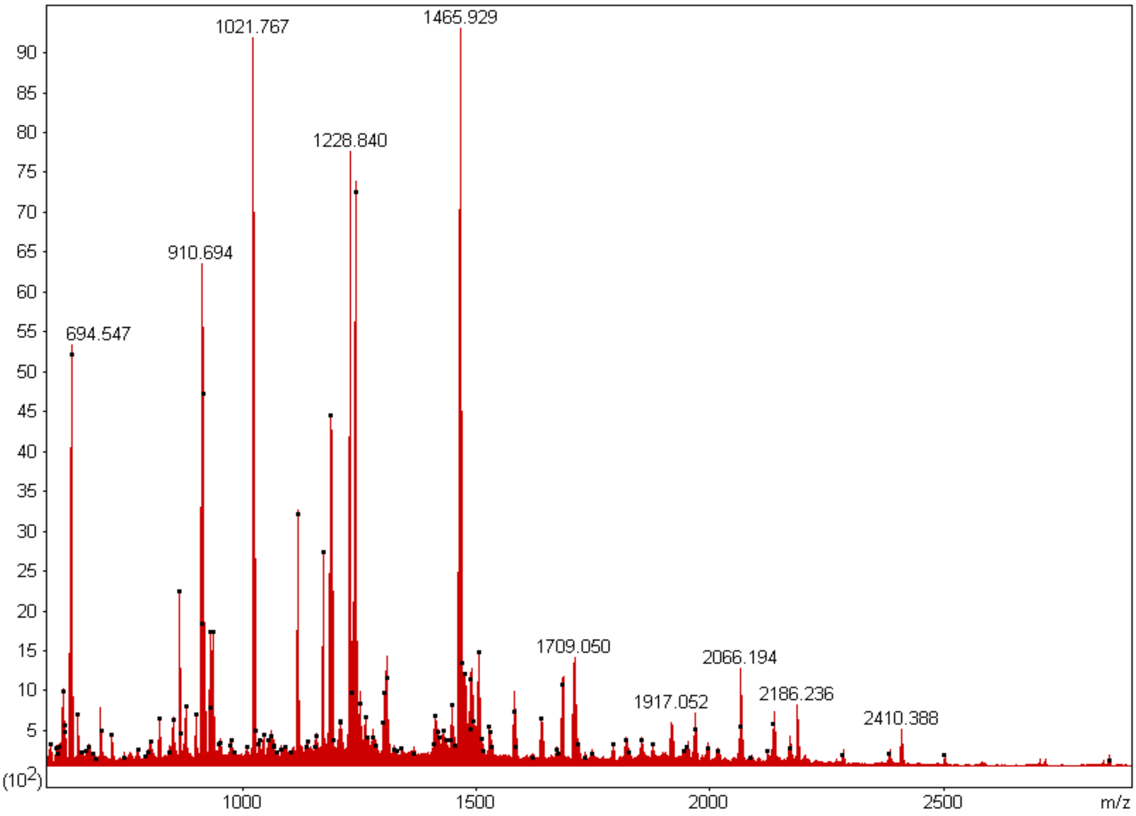
Mascot score: **145**   Sequence coverage %: **42**

NCBI accession No.: **gi| 27752799**

Matched peptides No.: **26**   Total peptides No.: **106**

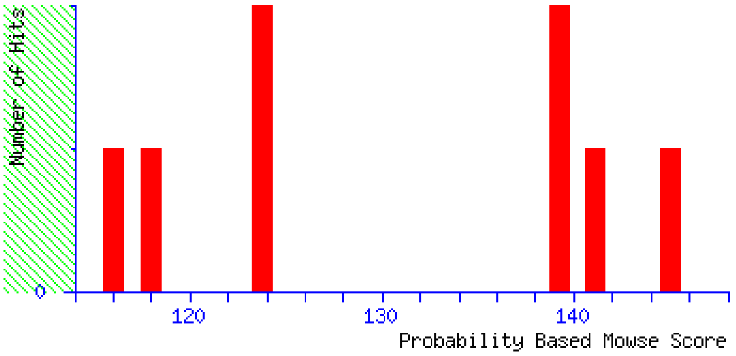
Calculated Mr: **47920**   Calculated p*I*: **6.12**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

```
  1 KLTYYTPEYE TKDTDILAAF RVTPQPGVPP EEAGAAVAAE SSTGTWTTVW
 51 TDGLTSLDRY KGRCYHIEPV PGEETQFIAY VAYPLDLFEE GSVTNMFTSI
101 VGNVFGFKAL AALRLEDLRI PPAYTKTFQG PPHGIQVERD KLNKYGRPLL
151 GCTIKPKLGL SAKNYGRAVY ECLRGGLDFT KDDENVNSQP FMRWRDRFLF
201 CAEAIYKSQA ETGEIKGHYL NATAGTCEEM IKRAVFAREL GVPIVMHDYL
251 TGGFTANTSL SHYCRDNGLL LHIHRAMHAV IDRQKNHGMH FRVLAKALRL
301 SGGDHIHAGT VVGKLEGDRE STLGFVDLLR DDYVEKDRSR GIFFTQDWVS
351 LPGVLPVASG GIHVWHMPAL TEIFGDDSVL QFGGGTLGHP WGNAPGAVAN
401 RVALEACVQA RNEGRDLAVE GNEIIREACK
```

Matched peptides information:

```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    2 - 21     2410.3885  2409.3812  2409.1740       86      1  K.LTYYTPEYETKDTDILAAFR.V
   13 - 21     1021.7666  1020.7593  1020.5240      231      0  K.DTDILAAFR.V
  109 - 119    1240.9356  1239.9283  1239.7299      160      1  K.ALAALRLEDLR.I
  115 - 126    1415.9373  1414.9300  1414.7820      105      1  R.LEDLRIPPAYTK.T
  120 - 126     789.6769   788.6697   788.4432      287      0  R.IPPAYTK.T
  127 - 139    1465.9295  1464.9222  1464.7474      119      0  K.TFQGPPHGIQVER.D
  127 - 141    1709.0495  1708.0422  1707.8693      101      1  K.TFQGPPHGIQVERDK.L
  168 - 174     910.6939   909.6867   909.4378      274      0  R.AVYECLR.G
  175 - 193    2170.1670  2169.1597  2168.9797       83      1  R.GGLDFTKDDENVNSQPFMR.W
  175 - 193    2186.2364  2185.2291  2184.9746      116      1  R.GGLDFTKDDENVNSQPFMR.W  Oxidation (M)
  217 - 233    1951.0774  1950.0701  1949.9087       83      1  K.GHYLNATAGTCEEMIKR.A
  217 - 233    1967.1414  1966.1341  1965.9037      117      1  K.GHYLNATAGTCEEMIKR.A  Oxidation (M)
  266 - 275    1187.8508  1186.8435  1186.6571      157      0  R.DNGLLLHIHR.A
  276 - 283     912.7179   911.7106   911.4647      270      0  R.AMHAVIDR.Q
  276 - 283     928.6998   927.6925   927.4596      251      0  R.AMHAVIDR.Q  Oxidation (M)
  284 - 292    1154.7452  1153.7379  1153.5563      157      1  R.QKNHGMHFR.V
  284 - 292    1170.8137  1169.8064  1169.5512      218      1  R.QKNHGMHFR.V  Oxidation (M)
  286 - 292     898.6489   897.6416   897.4028      266      0  K.NHGMHFR.V
  286 - 292     914.6479   913.6406   913.3977      266      0  K.NHGMHFR.V  Oxidation (M)
  300 - 314    1447.9304  1446.9231  1446.7579      114      0  R.LSGGDHIHAGTVVGK.L
  315 - 330    1820.1394  1819.1321  1818.9476      101      1  K.LEGDRESTLGFVDLLR.D
  320 - 330    1249.8421  1248.8348  1248.6714      131      0  R.ESTLGFVDLLR.D
  402 - 411    1116.8063  1115.7990  1115.5757      200      0  R.VALEACVQAR.N
  412 - 426    1685.0548  1684.0475  1683.8540      115      1  R.NEGRDLAVEGNEIIR.E
  416 - 426    1228.8397  1227.8324  1227.6459      152      0  R.DLAVEGNEIIR.E
  416 - 430    1717.0479  1716.0406  1715.8512      110      1  R.DLAVEGNEIIREACK.-
```

Spot No.: **28**

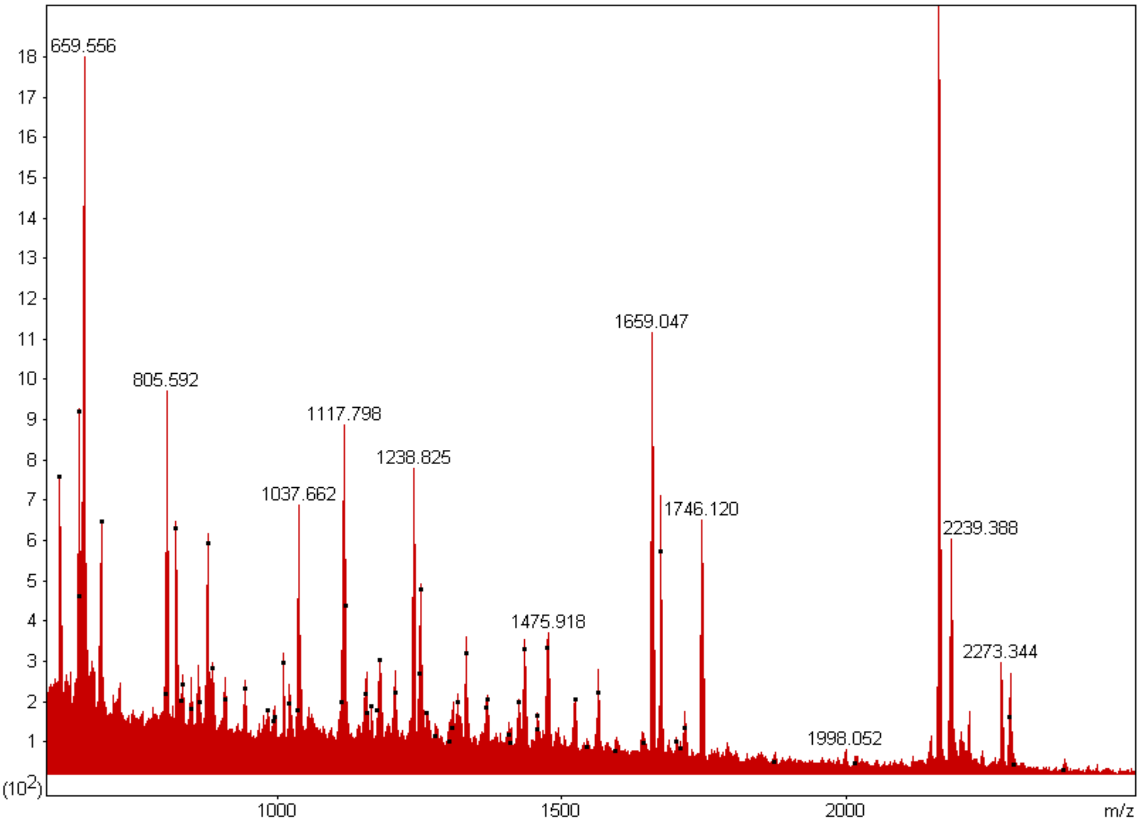
Mascot score: **104** Sequence coverage %: **24**

NCBI accession No.: **gi| 2623298**

Matched peptides No.: **21** Total peptides No.: **56**

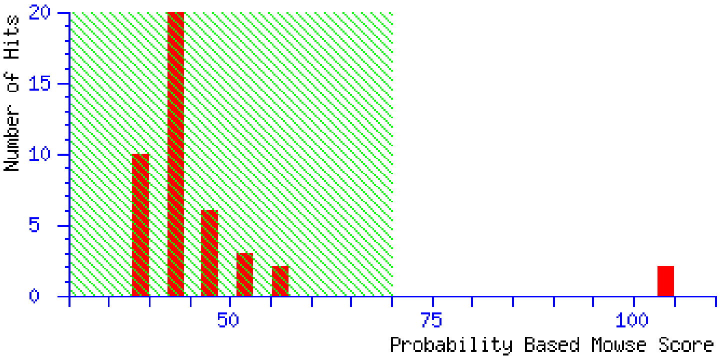
Calculated Mr: **86044** Calculated *p*I: **5.57**

Annotated PMF **spectra:**

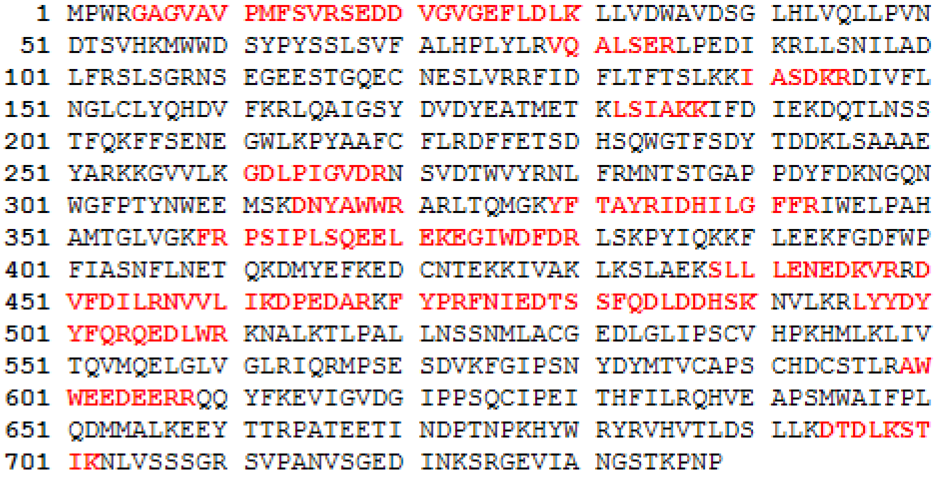


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

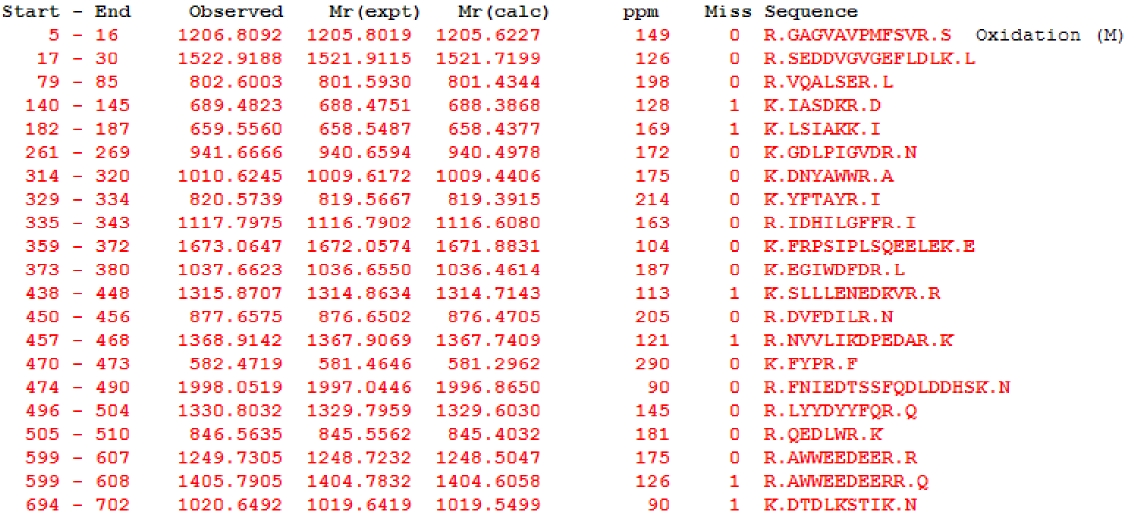


Matched peptide sequences: shown in Bold Red



```
  1 MPWRGAGVAV PMFSVRSEDD VGVGEFLDLK LLVDWAVDSG LHLVQLLPVN
 51 DTSVHKMWWD SYPYSSLSVF ALHPLYLRVQ ALSERLPEDI KRLLSNILAD
101 LFRSLSGRNS EGEESTGQEC NESLVRRFID FLTFTSLKKI ASDKRDIVFL
151 NGLCLYQHDV FKRLQAIGSY DVDYEATMET KLSIAKKIFD IEKDQTLNSS
201 TFQKFFSENE GWLKPYAAFC FLRDFFETSD HSQWGTFSDY TDDKLSAAAE
251 YARKKGVVLK GDLPIGVDRN SVDTWVYRNL FRMNTSTGAP PDYFDKNGQN
301 WGFPTYNWEE MSKDNYAWWR ARLTQMGKYF TAYRIDHILG FFRIWELPAH
351 AMTGLVGKFR PSIPLSQEEL EKEGIWDFDR LSKPYIQKKF LEEKFGDFWP
401 FIASNFLNET QKDMYEFKED CNTEKKIVAK LKSLAEKSLL LENEDKVRRD
451 VFDILRNVVL IKDPEDARKF YPRFNIEDTS SFQDLDDHSK NVLKRLYYDY
501 YFQRQEDLWR KNALKTLPAL LNSSNMLACG EDLGLIPSCV HPKHMLKLIV
551 TQVMQELGLV GLRIQRMPSE SDVKFGIPSN YDYMTVCAPS CHDCSTLRAW
601 WEEDEERRQQ YFKEVIGVDG IPPSQCIPEI THFILRQHVE APSMWAIFPL
651 QDMMALKEEY TTRPATEETI NDPTNPKHYW RYRVHVTLDS LLKDTDLKST
701 IKNLVSSSGR SVPANVSGED INKSRGEVIA NGSTKPNP
```

Matched peptides information:



```
Start - End      Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   5 - 16      1206.8092  1205.8019  1205.6227      149     0  R.GAGVAVPMFSVR.S  Oxidation (M)
  17 - 30      1522.9188  1521.9115  1521.7199      126     0  R.SEDDVGVGEFLDLK.L
  79 - 85       802.6003   801.5930   801.4344      198     0  R.VQALSER.L
 140 - 145      689.4823   688.4751   688.3868      128     1  K.IASDKR.D
 182 - 187      659.5560   658.5487   658.4377      169     1  K.LSIAKK.I
 261 - 269      941.6666   940.6594   940.4978      172     0  K.GDLPIGVDR.N
 314 - 320     1010.6245  1009.6172  1009.4406      175     0  K.DNYAWWR.A
 329 - 334      820.5739   819.5667   819.3915      214     0  K.YFTAYR.I
 335 - 343     1117.7975  1116.7902  1116.6080      163     0  R.IDHILGFFR.I
 359 - 372     1673.0647  1672.0574  1671.8831      104     0  K.FRPSIPLSQEELEK.E
 373 - 380     1037.6623  1036.6550  1036.4614      187     0  K.EGIWDFDR.L
 438 - 448     1315.8707  1314.8634  1314.7143      113     1  K.SLLLENEDKVR.R
 450 - 456      877.6575   876.6502   876.4705      205     0  R.DVFDILR.N
 457 - 468     1368.9142  1367.9069  1367.7409      121     1  R.NVVLIKDPEDAR.K
 470 - 473      582.4719   581.4646   581.2962      290     0  K.FYPR.F
 474 - 490     1998.0519  1997.0446  1996.8650       90     0  R.FNIEDTSSFQDLDDHSK.N
 496 - 504     1330.8032  1329.7959  1329.6030      145     0  R.LYYDYYFQR.Q
 505 - 510      846.5635   845.5562   845.4032      181     0  R.QEDLWR.K
 599 - 607     1249.7305  1248.7232  1248.5047      175     0  R.AWWEEDEER.R
 599 - 608     1405.7905  1404.7832  1404.6058      126     1  R.AWWEEDEERR.Q
 694 - 702     1020.6492  1019.6419  1019.5499       90     1  K.DTDLKSTIK.N
```

Spot No.: **29**

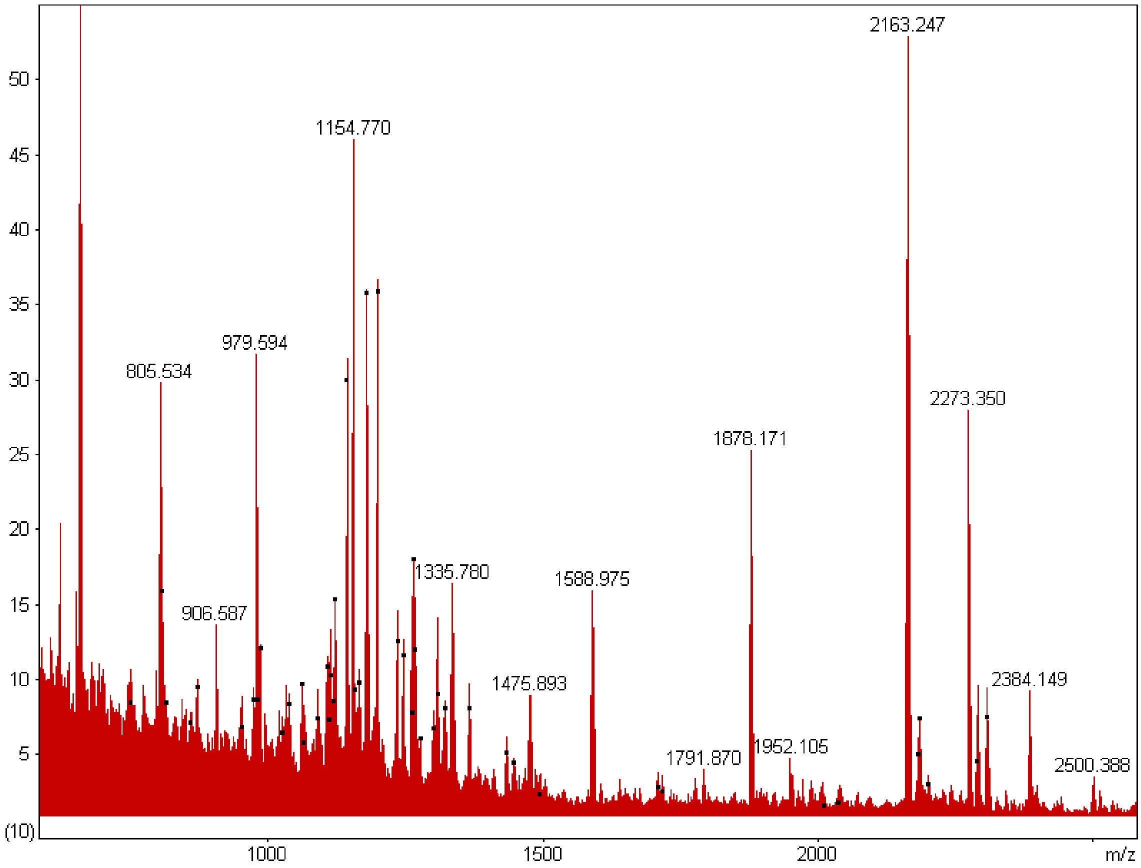
Mascot score: **110** Sequence coverage %: **24**

NCBI accession No.: **gi| 312283107**

Matched peptides No.: **17** Total peptides No.: **42**

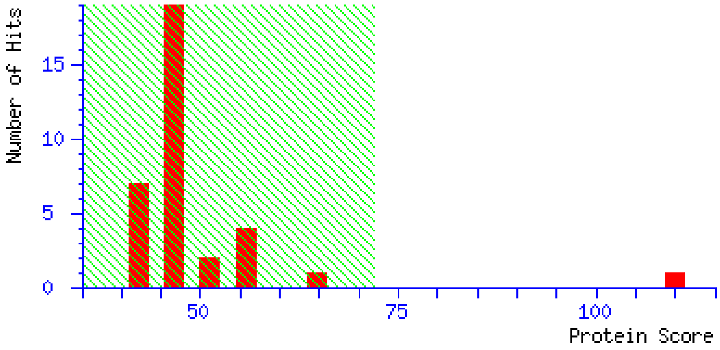
Calculated Mr: **78095** Calculated *p*I: **5.74**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 MEELDRSRAF AKDVKRIVVK VGTAVVTGKG GRLALGRLGA LCEQLAELNS
51 DGFEVILVSS GAVGLGRQRL RYRQLVNSSF ADLQKPQSEL DGKACAGVGQ
101 SSLMAYYETM FDQLDVTAAQ LLVNDSSFR**D** **KDFR**KQLNET VKSMLDLR**VI**
151 **PIFNENDAIS** **TR**RAPYQDSS GIFWDNDSLA ALLALELKAD LLILLSDVEG
201 LYTGPPSDPN SKLIHTFIK**E** **KHQDEITFGD** **K**SR**LGRGGMT** **AKVK**AAVNAA
251 YAGIPVIITS GYSAENIDKV LRGLR**VGTLF** **HQDARQWAPI** **TDSTARDMAV**
301 **AAR**ESSRKLQ ALSSEDRKQI LYNIADALEA NEKTIRDENE LDVSAAQEAG
351 FEESLVARLV MTPAKISSLA ASVRKLADME DPIGRVLKKT EVADGLVLEK
401 TSSPLGVLLI VFESRPDALV QIASLAIRSG NGLLLKGGKE ARRSNAILHK
451 VITDAIPETV GGK**LIGLVTS** **R**EEIPDLLK**L** **DDVIDLVIPR** GSNKLVSQIK
501 NTTKIPVLGH ADGICHVYVD KSCNLDMAKR IISDAKLDYP AACNAMETLL
551 VHKDLEQNGL NELIFVLQSN GVTVYGGPR**A** **SAILNIPEAR** SFNYEYCSK**A**
601 **CTVEVVEDVY** **GAIDHIHRHG** **SAHTDCIVTE** **DTEVAELFLR** QVDSAAVFHN
651 ASTR**FSDGAR** **FGLGAEVGIS** **TGR**IHAR**GPV** **GVEGLLTTRW** **LMR**GKGQVVD
701 GDNGIAYTHQ DIPIQS

Matched peptides information:

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
130 - 134	680.4588	679.4515	679.3289	180	1	R.DKDFR.K
149 - 162	1588.9751	1587.9678	1587.8257	90	0	R.VIPIFNENDAISTR.R
220 - 231	1446.8472	1445.8399	1445.6787	112	1	K.EKHQDEITFGDK.S
234 - 242	906.5870	905.5797	905.4753	115	1	R.LGRGGMTAK.V Oxidation (M)
237 - 244	807.4981	806.4908	806.4320	73	1	R.GGMTAKVK.A Oxidation (M)
276 - 285	1143.7019	1142.6946	1142.5833	97	0	R.VGTLFHQDAR.Q
286 - 296	1245.7168	1244.7095	1244.6149	76	0	R.QWAPITDSTAR.D
297 - 303	749.4634	748.4562	748.3538	137	0	R.DMAVAAR.E Oxidation (M)
464 - 471	858.6027	857.5955	857.5334	72	0	K.LIGLVTSR.E
480 - 490	1267.8337	1266.8264	1266.7184	85	0	K.LDDVIDLVIPR.G
580 - 590	1154.7698	1153.7625	1153.6455	101	0	R.ASAILNIPEAR.S
600 - 618	2183.2279	2182.2206	2182.0477	79	0	K.ACTVEVVEDVYGAIDHIHR.H
619 - 640	2500.3880	2499.3807	2499.1700	84	0	R.HGSAHTDCIVTEDTEVAELFLR.Q
655 - 660	652.3950	651.3877	651.2976	138	0	R.FSDGAR.F
661 - 673	1263.7771	1262.7698	1262.6619	85	0	R.FGLGAEVGISTGR.I
678 - 689	1198.7764	1197.7691	1197.6718	81	0	R.GPVGVEGLLTTR.W
690 - 693	621.4161	620.4088	620.3104	159	0	R.WLMR.G Oxidation (M)

Spot No.: **30**

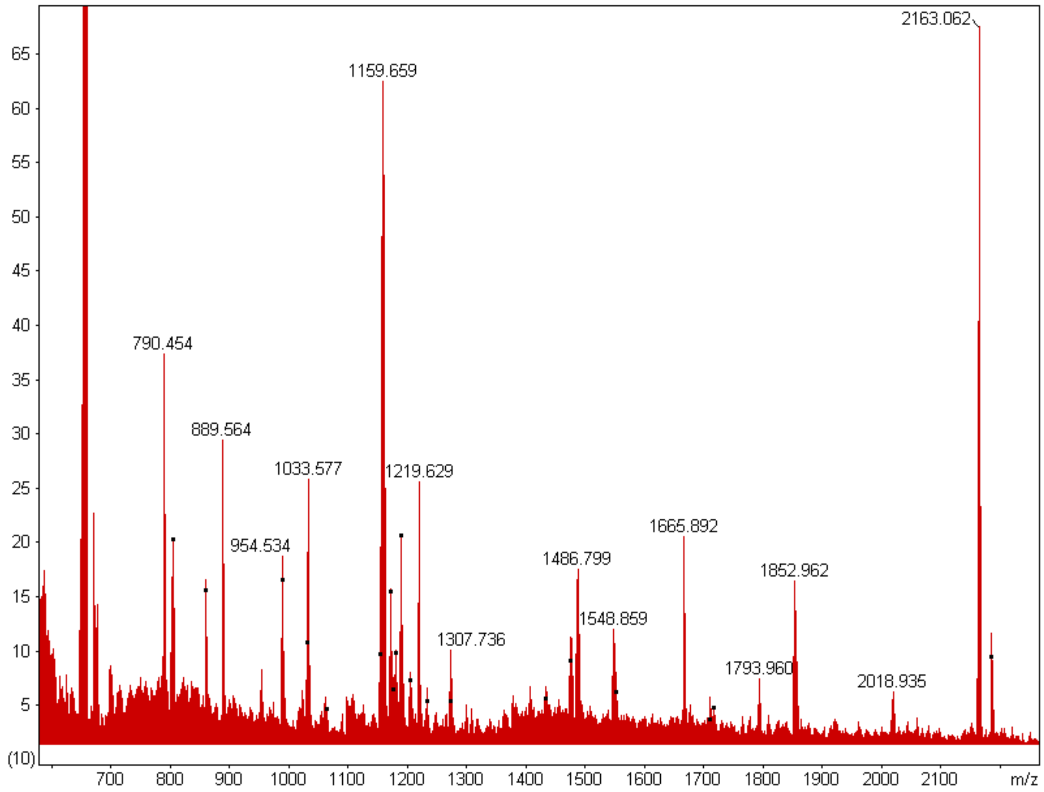
Mascot score: **102**   Sequence coverage %: **16**

NCBI accession No.: **gi| 157342076**

Matched peptides No.: **13**   Total peptides No.: **26**

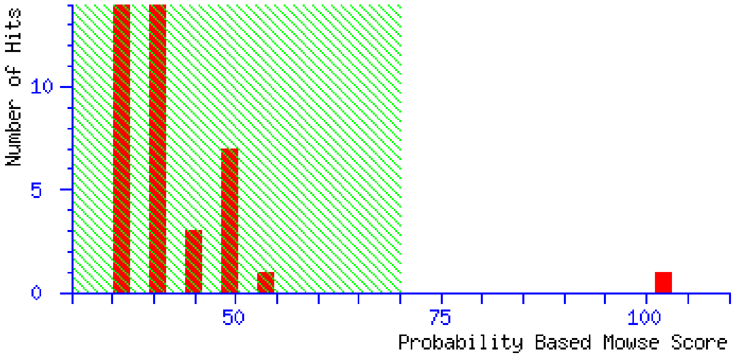
Calculated Mr: **78285**   Calculated *p*I: **4.98**

Annotated PMF **spectra:**

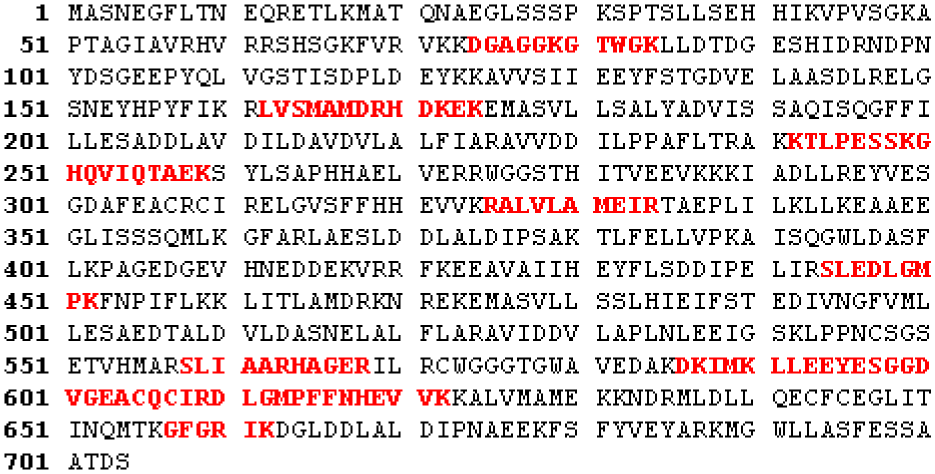


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

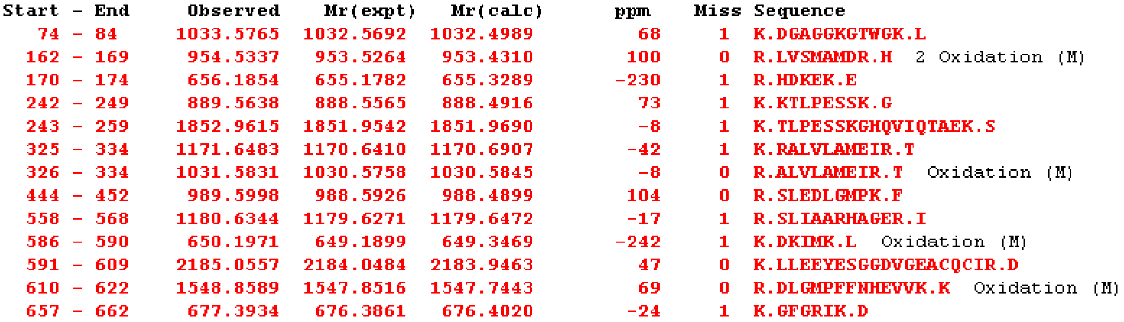


Matched peptide sequences: shown in Bold Red



1	MASNEGFLTN	EQRETLKMAT	QNAEGLSSSP	KSPTSLLSEH	HIKVPVSGKA
51	PTAGIAVRHV	RRSHSGKFVR	VKK**DGAGGKG**	**TWGK**LLDTDG	ESHIDRNDPN
101	YDSGEEPYQL	VGSTISDPLD	EYKKAVVSII	EEYFSTGDVE	LAASDLRELG
151	SNEYHPYFIK	R**LVSMAMDRH**	**DKEK**EMASVL	LSALYADVIS	SAQISQGFFI
201	LLESADDLAV	DILDAVDVLA	LFIARAVVDD	ILPPAFLTRA	K**KTLPESSKG**
251	**HQVIQTAEK**S	YLSAPHHAEL	VERRWGGSTH	ITVEEVKKKI	ADLLREYVES
301	GDAFEACRCI	RELGVSFFHH	EVVK**RALVLA**	**MEIR**TAEPLI	LKLLKEAAEE
351	GLISSSQMLK	GFARLAESLD	DLALDIPSAK	TLFELLVPKA	ISQGWLDASF
401	LKPAGEDGEV	HNEDDEKVRR	FKEEAVAIIH	EYFLSDDIPE	LIR**SLEDLGM**
451	**PK**FNPIFLKK	LITLAMDRKN	REKEMASVLL	SSLHIEIFST	EDIVNGFVML
501	LESAEDTALD	VLDASNELAL	FLARAVIDDV	LAPLNLEEIG	SKLPPNCSGS
551	ETVHMAR**SLI**	**AARHAGER**IL	RCWGGGTGWA	VEDAK**DKIMK**	**LLEEYESGGD**
601	**VGEACQCIRD**	**LGMPFFNHEV**	**VK**KALVMAME	KKNDRMLDLL	QECFCEGLIT
651	INQMTK**GFGR**	**IK**DGLDDLAL	DIPNAEEKFS	FYVEYARKMG	WLLASFESSA
701	ATDS				

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
74 - 84	1033.5765	1032.5692	1032.4989	68	1	K.DGAGGKGTWGK.L
162 - 169	954.5337	953.5264	953.4310	100	0	R.LVSMAMDR.H 2 Oxidation (M)
170 - 174	656.1854	655.1782	655.3289	-230	1	R.HDKEK.E
242 - 249	889.5638	888.5565	888.4916	73	1	K.KTLPESSK.G
243 - 259	1852.9615	1851.9542	1851.9690	-8	1	K.TLPESSKGHQVIQTAEK.S
325 - 334	1171.6483	1170.6410	1170.6907	-42	1	K.RALVLAMEIR.T
326 - 334	1031.5831	1030.5758	1030.5845	-8	0	R.ALVLAMEIR.T Oxidation (M)
444 - 452	989.5998	988.5926	988.4899	104	0	R.SLEDLGMPK.F
558 - 568	1180.6344	1179.6271	1179.6472	-17	1	R.SLIAARHAGER.I
586 - 590	650.1971	649.1899	649.3469	-242	1	K.DKIMK.L Oxidation (M)
591 - 609	2185.0557	2184.0484	2183.9463	47	0	K.LLEEYESGGDVGEACQCIR.D
610 - 622	1548.8589	1547.8516	1547.7443	69	0	R.DLGMPFFNHEVVK.K Oxidation (M)
657 - 662	677.3934	676.3861	676.4020	-24	1	K.GFGRIK.D

Spot No.: **31**

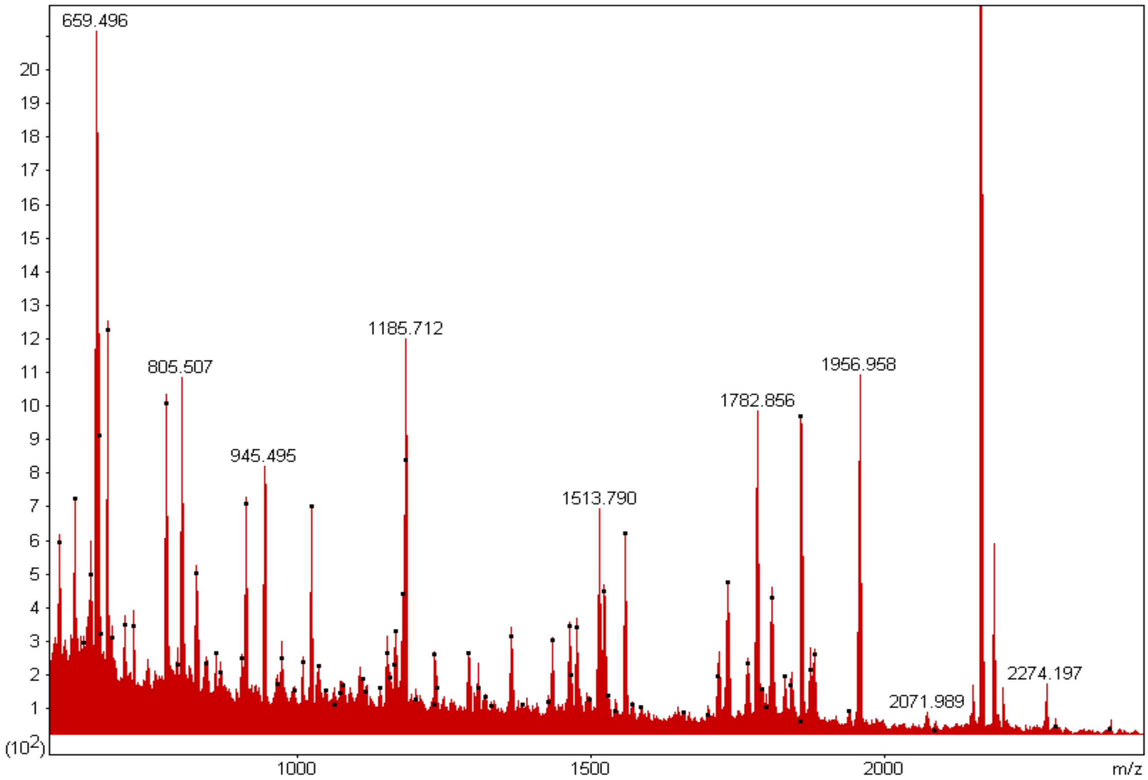
Mascot score: **98**   Sequence coverage %: **20**

NCBI accession No.: **gi| 4586021**

Matched peptides No.: **23**   Total peptides No.: **68**

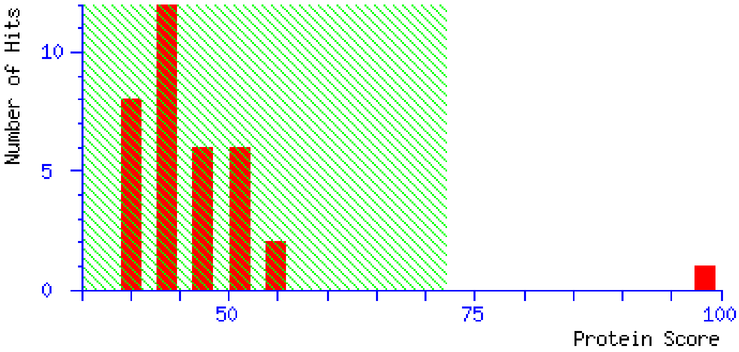
Calculated Mr: **98720**   Calculated *p*I: **5.79**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 MASEHPFKGI FTTLPKPGGG EFGK**FYSLPA LNDPR**VDKLP YSIR**ILLESA**
51 **IR**NCDNFQVT KEDVEKIIDW EKTSPK**QVEI PFKPAR**VLLQ DFTGVPAVVD
101 LACMRDAMNK LGSDSNKINP LVPVDLVIDH SVQVDVARSE NAVQANMELE
151 FQRNKERFAF LKWGSTAFQN MLVVPPGSGI VHQVNLEYLG R**VVFNTK**GLL
201 YPDSVVGTDS HTTMIDGLGV AGWGVGGIEA EATMLGQPMS MVLPGVVGFK
251 LAGKMRNGVT ATDLVLTVTQ MLRKHGVVGK FVEFYGNGMS GLSLADRATI
301 ANMSPEYGAT MGFFPVDHVT LQYLKLTGR**S DETVAMIEAY LRANNMFVDY**
351 **NEPQQDR**VYS SYLELNLDDV EPCISGPKRP HDRVTLKEMK ADWHSCLDSK
401 **VGFKGFAIPK** EAQEKVVNFS FDGQPAELKH GSVVIAAITS CTNTSNPSVM
451 LGAGLVAKKA CDLGLQVKPW IKTSLAPGSG VVTKYLLKSG LQEYLNEQGF
501 NIVGYGCTTC IGNSGEINES VGAAITENDI VAAAVLSGNR **NFEGRVHPLT**
551 **R**ANYLASPPL VVAYALAGTV NIDFETEPIG KGKNGKDVFL RDIWPTTEEI
601 AEVVQSSVLP DMFRATYESI TK**GNPMWNK**L SVPENTLYSW DPNSTYIHEP
651 PYFKDMTMDP PGPHNVKDAY CLLNFGDSIT TDHISPAGNI QKDSPAAKFL
701 MERGVDR**KDF NSYGSRRGND EIMARGTFAN IRIVNK**LMNG EVGPK**TVHIP**
751 **SGEKLSVFDA AMR**YK**SSGED TIILAGAEYG SGSSR**DWAAK **GPMLQGVK**AV
801 IAKSFERIHR SNLVGMGIIP LCFKSGEDAD TLGLTGHER**Y TIHLPTDISE**
851 **IR**PGQDVTVT TDNGK**SFTCT VR**FDTEVELA YFNHGGILPY VIRNLSKQ

Matched peptides information:

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
25 - 35	1292.7140	1291.7067	1291.6561	39	0	K.FYSLPALNDPR.V
45 - 52	914.6371	913.6298	913.5596	77	0	R.ILLESAIR.N
77 - 86	1184.7371	1183.7298	1183.6713	49	1	K.QVEIPFKPAR.V
192 - 197	707.4732	706.4660	706.4014	91	0	R.VVFNTK.G
330 - 342	1497.7968	1496.7895	1496.7181	48	0	R.SDETVAMIEAYLR.A
330 - 342	1513.7895	1512.7822	1512.7130	46	0	R.SDETVAMIEAYLR.A Oxidation (M)
343 - 357	1840.8405	1839.8332	1839.7846	26	0	R.ANNMFVDYNEPQQDR.V
401 - 410	1063.5641	1062.5568	1062.6226	-62	1	K.VGFKGFAIPK.E
541 - 545	622.4040	621.3968	621.2871	177	0	R.NFEGR.V
546 - 551	722.5078	721.5005	721.4235	107	0	R.VHPLTR.A
623 - 629	862.4907	861.4834	861.3803	120	0	K.GNPMWNK.L Oxidation (M)
708 - 716	1073.5702	1072.5629	1072.4938	64	1	R.KDFNSYGSR.R
709 - 716	945.4952	944.4879	944.3988	94	0	K.DFNSYGSR.R
717 - 725	1077.5212	1076.5139	1076.5033	10	1	R.RGNDEIMAR.G Oxidation (M)
726 - 732	778.5166	777.5094	777.4133	124	0	R.GTFANIR.I
726 - 736	1232.6783	1231.6710	1231.7037	-27	1	R.GTFANIRIVNK.L
746 - 754	967.5365	966.5292	966.5134	16	0	K.TVHIPSGEK.L
755 - 763	1009.5864	1008.5791	1008.5062	72	0	K.LSVFDAAMR.Y
755 - 763	1025.5695	1024.5622	1024.5012	60	0	K.LSVFDAAMR.Y Oxidation (M)
766 - 785	1956.9583	1955.9510	1955.9072	22	0	K.SSGEDTIILAGAEYGSGSSR.D
791 - 798	829.3971	828.3898	828.4528	-76	0	K.GPMLQGVK.A
840 - 852	1557.7875	1556.7802	1556.8198	-25	0	R.YTIHLPTDISEIR.P
866 - 872	870.5138	869.5065	869.4066	115	0	K.SFTCTVR.F

Spot No.: **32**

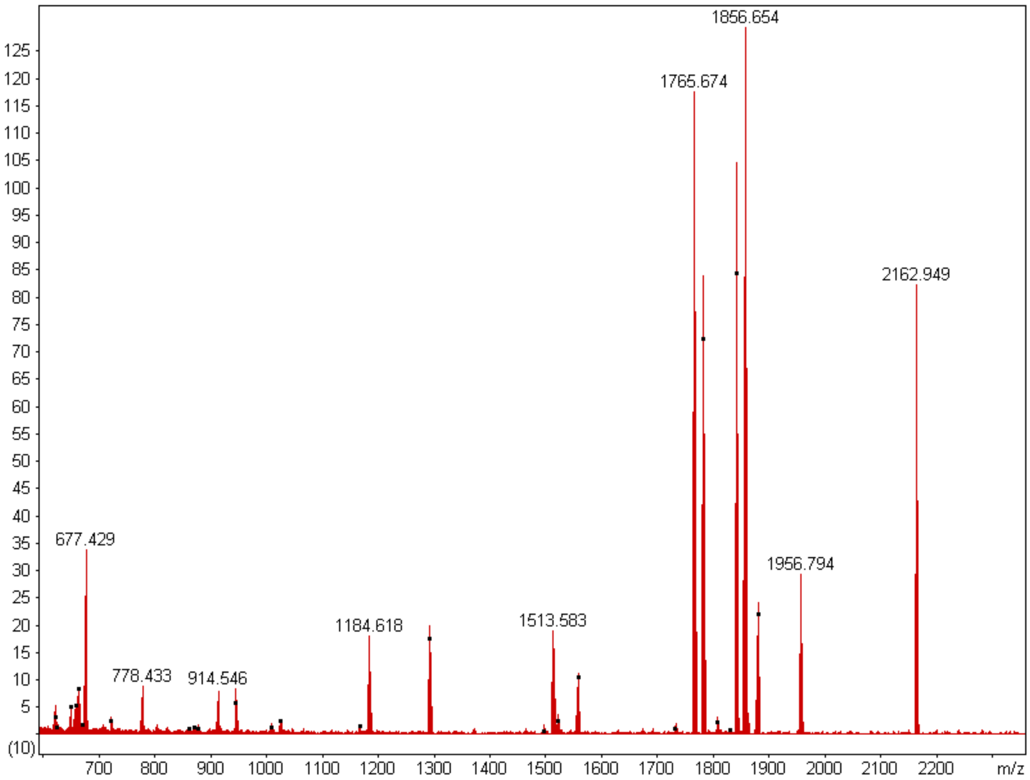
Mascot score: **123** Sequence coverage %: **16**

NCBI accession No.: **gi| 4586021**

Matched peptides No.: **18** Total peptides No.: **33**

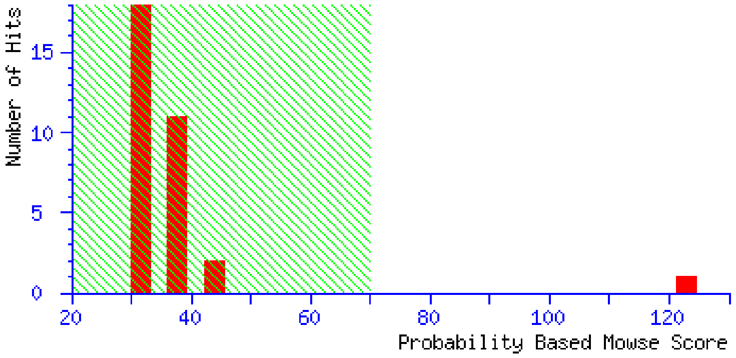
Calculated Mr: **98720** Calculated *p*I: **5.79**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 MASEHPFKGI FTTLPKPGGG EFGK**FYSLPA LNDPR**VDKLP YSIR**ILLESA**
51 **IR**NCDNFQVT KEDVEKIIDW EKTSPK**QVEI PFKPAR**VLLQ DFTGVPAVVD
101 LACMRDAMNK LGSDSNKINP LVPVDLVIDH SVQVDVAR**SE NAVQANMELE**
151 **FQR**NKER**FAF LK**WGSTAFQN MLVVPPGSGI VHQVNLEYLG RVVFNTKGLL
201 YPDSVVGTDS HTTMIDGLGV AGWGVGGIEA EATMLGQPMS MVLPGVVGFK
251 LAGKMRNGVT ATDLVLTVTQ MLRKHGVVGK FVEFYGNGMS GLSLADRATI
301 ANMSPEYGAT MGFFPVDHVT LQYLKLTGR**S DETVAMIEAY LRANNMFVDY**
351 **NEPQQDR**VYS SYLELNLDDV EPCISGPKRP HDRVTLKEMK ADWHSCLDSK
401 VGFKGFAIPK EAQEKVVNFS FDGQPAELKH GSVVIAAITS CTNTSNPSVM
451 LGAGLVAKKA CDLGLQVKPW IKTSLAPGSG VVTKYLLKSG LQEYLNEQGF
501 NIVGYGCTTC IGNSGEINES VGAAITENDI VAAAVLSGNR **NFEGR**VHPLT
551 RANYLASPPL VVAYALAGTV NIDFETEPIG KGKNGKDVFL RDIWPTTEEI
601 AEVVQSSVLP DMFRATYESI TKGNPMWNKL SVPENTLYSW DPNSTYIHEP
651 PYFKDMTMDP PGPHNVKDAY CLLNFGDSIT TDHISPAGNI QKDSPAAKFL
701 MERGVDRK**DF NSYGSR**RGND EIMAR**GTFAN IR**IVNKLMNG EVGPKTVHIP
751 SGEK**LSVFDA AMR**YK**SSGED TIILAGAEYG SGSSR**DWAAK GPMLQGVKAV
801 IAKSFERIHR SNLVGMGIIP LCFK**SGEDAD TLGLTGHER**Y TIHLPTDISE
851 IRPGQDVTVT TDNGK**SFTCT VR**FDTEVELA YFNHGGILPY VIRNLSKQ

Matched peptides information:

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
25 - 35	1292.5758	1291.5685	1291.6561	-68	0	**K.FYSLPALNDPR.V**	
45 - 52	914.5460	913.5388	913.5596	-23	0	**R.ILLESAIR.N**	
77 - 86	1184.6179	1183.6106	1183.6713	-51	0	**K.QVEIPFKPAR.V**	
139 - 153	1765.6744	1764.6671	1764.8101	-81	0	**R.SENAVQANMELEFQR.N**	
139 - 153	1781.6735	1780.6662	1780.8050	-78	0	**R.SENAVQANMELEFQR.N**	Oxidation (M)
158 - 162	625.3991	624.3918	624.3635	45	0	**R.FAFLK.W**	
330 - 342	1497.6232	1496.6159	1496.7181	-68	0	**R.SDETVAMIEAYLR.A**	
330 - 342	1513.5832	1512.5759	1512.7130	-91	0	**R.SDETVAMIEAYLR.A**	Oxidation (M)
343 - 357	1840.6524	1839.6451	1839.7846	-76	0	**R.ANNMFVDYNEPQQDR.V**	
343 - 357	1856.6539	1855.6466	1855.7795	-72	0	**R.ANNMFVDYNEPQQDR.V**	Oxidation (M)
541 - 545	622.3393	621.3321	621.2871	72	0	**R.NFEGR.V**	
709 - 716	945.3825	944.3752	944.3988	-25	0	**K.DFNSYGSR.R**	
726 - 732	778.4329	777.4256	777.4133	16	0	**R.GTFANIR.I**	
755 - 763	1009.4719	1008.4646	1008.5062	-41	0	**K.LSVFDAAMR.Y**	
755 - 763	1025.4610	1024.4537	1024.5012	-46	0	**K.LSVFDAAMR.Y**	Oxidation (M)
766 - 785	1956.7935	1955.7862	1955.9072	-62	0	**K.SSGEDTIILAGAEYGSGSSR.D**	
825 - 839	1557.5818	1556.5745	1556.7067	-85	0	**K.SGEDADTLGLTGHER.Y**	
866 - 872	870.4208	869.4135	869.4066	8	0	**K.SFTCTVR.F**	

Spot No.: **33**

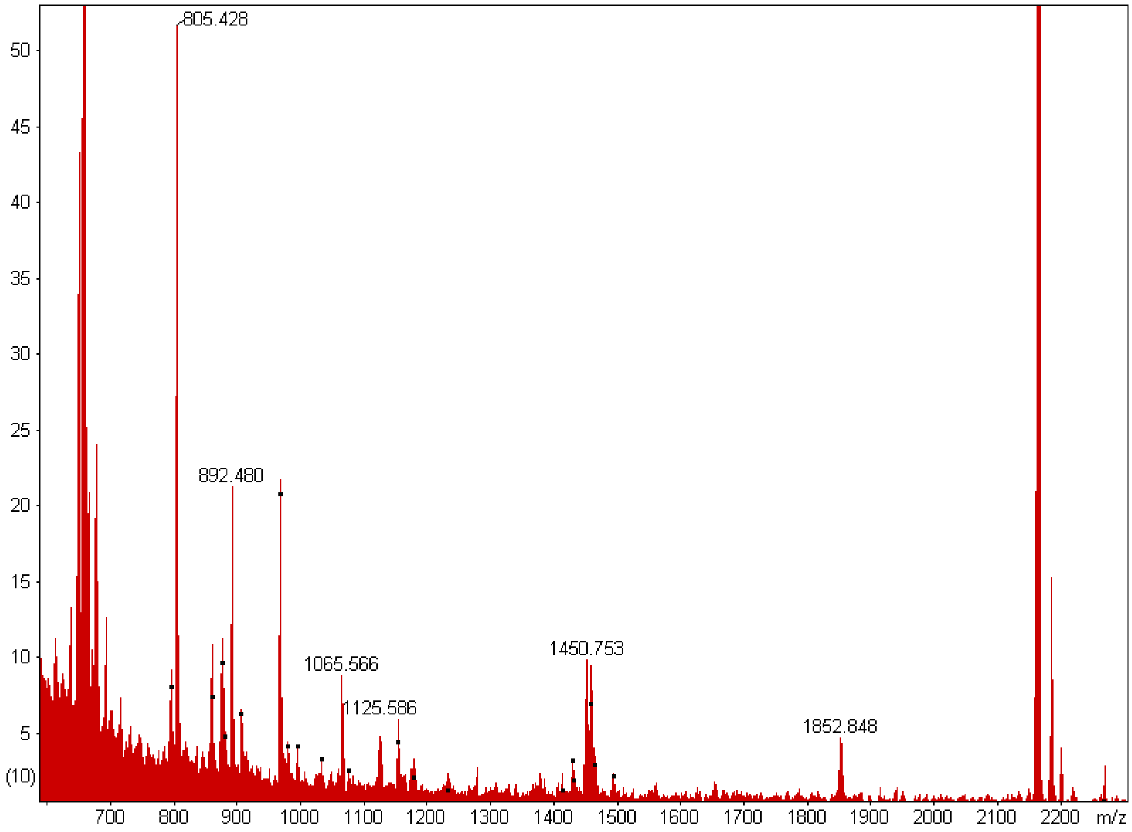
Mascot score: **93**   Sequence coverage %: **12**

NCBI accession No.: **gi| 15232704**

Matched peptides No.: **12**   Total peptides No.: **24**

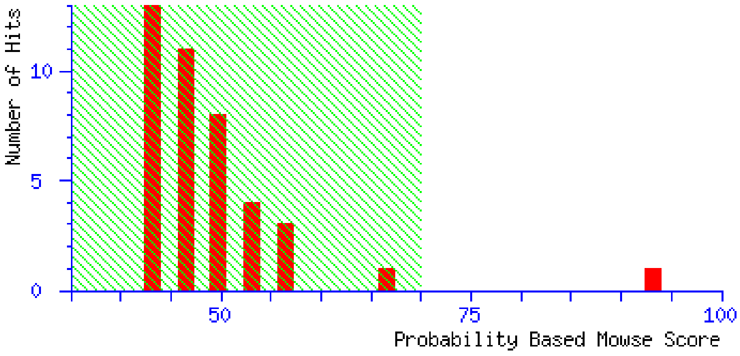
Calculated Mr: **95499**   Calculated *p*I: **5.79**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 MANANGKAAT SLPEKISAKA NPEADDATEI AGNIVYHAK**Y** **SPHFSPLK**FG
51 PEQALYATAE SLRDRLIQLW NETYVHFNKV DPKQTYYLSM EYLQGRALTN
101 AIGNLNLQGP YADALRTLGY ELEEIAEQEK DAALGNGGLG RLASCFLDSM
151 ATLNLPAWGY GLRYRHGLFK QIITKKGQEE IPEDWLEK**FS** **PWEIVRHDVV**
201 **FPVRFFGKVQ** **VNPDGSR**KWV DGDVVQALAY DVPIPGYGTK NTISLRLWEA
251 KARAEDLDLF QFNEGEYELA AQLHSRAQQI CTVLYPGDAT ENGKLLRLKQ
301 QFFLCSASLQ DIISRFHERS TTEGSRKWSE FPSKVAVQMN DTHPTLAIPE
351 LMRLLMDDNG LGWDEAWDVT SKTVAYTNHT VLPEALEK**WS** **QSLMWK**LLPR
401 **HMEIIEEIDK** **R**FVQTIRDTR VDLEDKISSL SILDNNPQKP VVRMANLCVV
451 SSHTVNGVAQ LHSDILKAEL FADYVSIWPN KFQNKTNGIT PRRWLRFCSP
501 ELSDIITKWL KTDKWITDLD LLTGLR**QFAD** **NEELQSEWAS** **AK**TANKKR**LA**
551 **QYIER**VTGVS IDPTSLFDIQ VKRIHEYKRQ LMNILGVVYR FKKLKEMKPE
601 ERKKTVPRTV MIGGKAFATY TNAKRIVKLV NDVGDVVNSD PEVNEYLKVV
651 FVPNYNVTVA EMLIPGSELS QHISTAGMEA SGTSNMKFAL NGCLIIGTLD
701 GANVEIREEV GEENFFLFGA TADQVPRLRK **EREDGLFKPD** **PRFEEAKQFV**
751 **K**SGVFGSYDY GPLLDSLEGN TGFGRGDYFL VGYDFPSYMD AQAK**VDEAYK**
801 **DR**KGWLKMSI LSTAGSGKFS SDRTIAQYAK EIWNIEACPV P

Matched peptides information:

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
40 - 48	1075.5512	1074.5439	1074.5498	-5	0	K.YSPHFSPLK.F	
189 - 196	1033.5047	1032.4974	1032.5393	-41	0	K.FSPWEIVR.H	
197 - 204	968.5232	967.5159	967.5240	-8	0	R.HDVVFPVR.F	
205 - 217	1450.7534	1449.7461	1449.7365	7	1	R.FFGKVQVNPDGSR.K	
389 - 396	1065.5662	1064.5589	1064.5113	45	0	K.WSQSLMWK.L	
401 - 411	1412.7476	1411.7403	1411.7129	19	1	R.HMEIIEEIDKR.F	
401 - 411	1428.7167	1427.7094	1427.7078	1	1	R.HMEIIEEIDKR.F	Oxidation (M)
527 - 542	1852.8476	1851.8403	1851.8275	7	0	R.QFADNEELQSEWASAK.T	
549 - 555	892.4796	891.4723	891.4814	-10	0	R.LAQYIER.V	
731 - 742	1458.7519	1457.7446	1457.7263	13	1	K.EREDGLFKPDPR.F	
743 - 751	1125.5863	1124.5790	1124.5866	-7	1	R.FEEAKQFVK.S	
795 - 802	995.5436	994.5364	994.4720	65	1	K.VDEAYKDR.K	

Spot No.: **34**

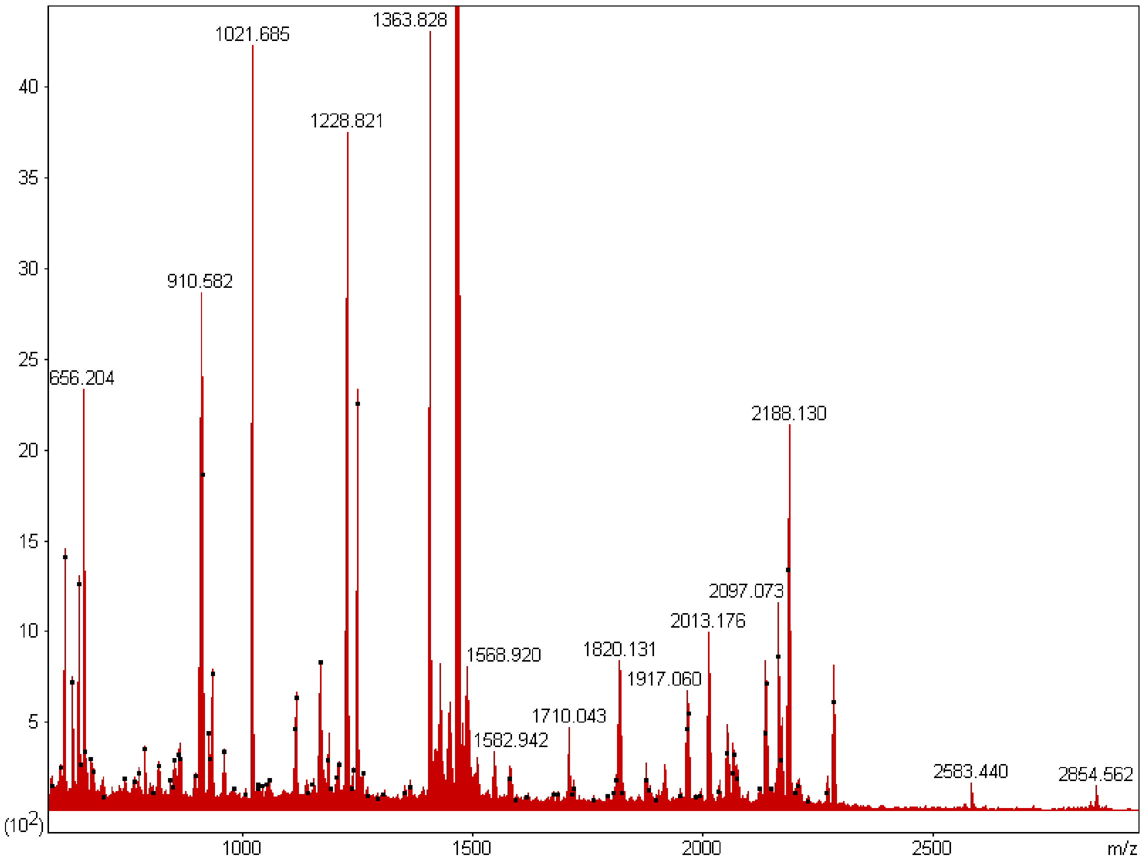
Mascot score: **240** Sequence coverage %: **49**

NCBI accession No.: **gi| 4185573**

Matched peptides No.: **35** Total peptides No.: **84**

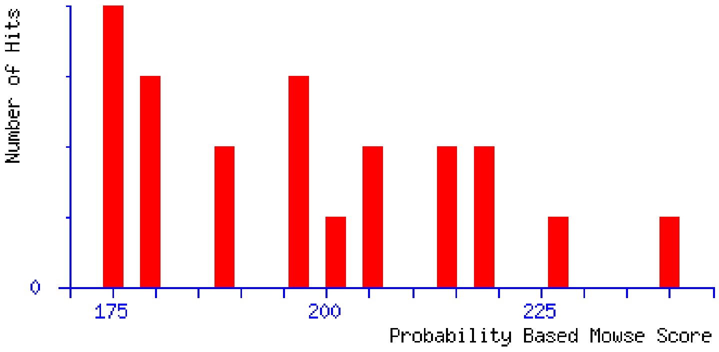
Calculated Mr: **52905** Calculated *p*I: **6.09**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

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  1 SVGFKAGVKE YKLTYYTPEY ETKDTDILAA FRVTPQPGVP PEEAGAAVAA
 51 ESSTGTWTTV WTDGLTSLDR YKGRCYGIEP VPGEENQYIA YVAYPLDLFE
101 EGSVTNMFTS IVGNVFGFKA LRALRLEDLR IPPAYTKTFQ GPPHGIQVER
151 DKLNKYGRPL LGCTIKPKLG LSAKNYGRAV YECLRGGLDF TKDDENVNSQ
201 PFMRWRDRFL FCAEAIYKSQ AETGEIKGHY LNATAGTCEE MIKRAVFARE
251 LGVPIVMHDY LTGGFTANTS LAHYCRDNGL LLHIHRAMHA VIDRQKNHGM
301 HFRVLAKALR LSGGDHIHAG TVVGKLEGDR ESTLGFVDLL RDDYIEKDRS
351 RGIFFTQDWV SLPGVLPVAS GGIHVWHMPA LTEIFGDDSV LQFGGGTLGH
401 PWGNAPGAVA NRVALEACVQ ARNEGRDLAV EGNEIIRQAS KWSPELAAAC
451 EVWKEIKFNF PTIDKLDGPV EKFD
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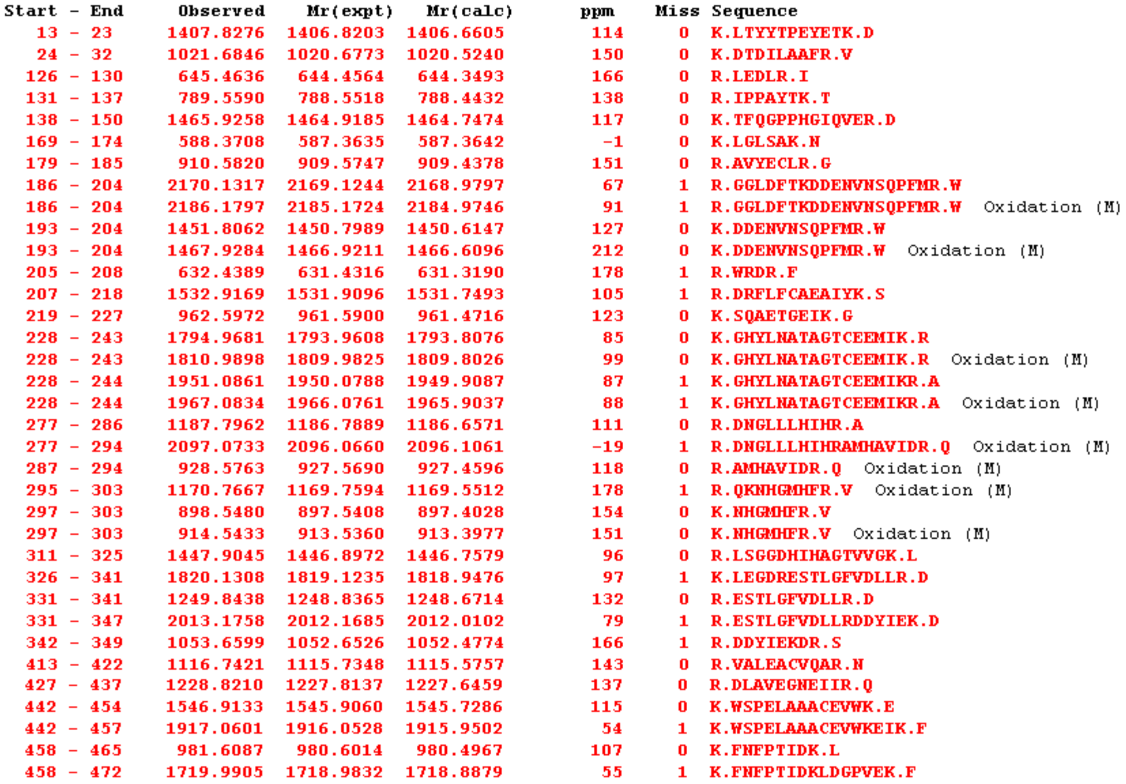
Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
13 - 23	1407.8276	1406.8203	1406.6605	114	0	K.LTYYTPEYETK.D	
24 - 32	1021.6846	1020.6773	1020.5240	150	0	K.DTDILAAFR.V	
126 - 130	645.4636	644.4564	644.3493	166	0	R.LEDLR.I	
131 - 137	789.5590	788.5518	788.4432	138	0	R.IPPAYTK.T	
138 - 150	1465.9258	1464.9185	1464.7474	117	0	K.TFQGPPHGIQVER.D	
169 - 174	588.3708	587.3635	587.3642	-1	0	K.LGLSAK.N	
179 - 185	910.5820	909.5747	909.4378	151	0	R.AVYECLR.G	
186 - 204	2170.1317	2169.1244	2168.9797	67	1	R.GGLDFTKDDENVNSQPFMR.W	
186 - 204	2186.1797	2185.1724	2184.9746	91	1	R.GGLDFTKDDENVNSQPFMR.W	Oxidation (M)
193 - 204	1451.8062	1450.7989	1450.6147	127	0	K.DDENVNSQPFMR.W	
193 - 204	1467.9284	1466.9211	1466.6096	212	0	K.DDENVNSQPFMR.W	Oxidation (M)
205 - 208	632.4389	631.4316	631.3190	178	1	R.WRDR.F	
207 - 218	1532.9169	1531.9096	1531.7493	105	1	R.DRFLFCAEAIYK.S	
219 - 227	962.5972	961.5900	961.4716	123	0	K.SQAETGEIK.G	
228 - 243	1794.9681	1793.9608	1793.8076	85	0	K.GHYLNATAGTCEEMIK.R	
228 - 243	1810.9898	1809.9825	1809.8026	99	0	K.GHYLNATAGTCEEMIK.R	Oxidation (M)
228 - 244	1951.0861	1950.0788	1949.9087	87	1	K.GHYLNATAGTCEEMIKR.A	
228 - 244	1967.0834	1966.0761	1965.9037	88	1	K.GHYLNATAGTCEEMIKR.A	Oxidation (M)
277 - 286	1187.7962	1186.7889	1186.6571	111	0	R.DNGLLLHIHR.A	
277 - 294	2097.0733	2096.0660	2096.1061	-19	1	R.DNGLLLHIHRAMHAVIDR.Q	Oxidation (M)
287 - 294	928.5763	927.5690	927.4596	118	0	R.AMHAVIDR.Q	Oxidation (M)
295 - 303	1170.7667	1169.7594	1169.5512	178	1	R.QKNHGMHFR.V	Oxidation (M)
297 - 303	898.5480	897.5408	897.4028	154	0	K.NHGMHFR.V	
297 - 303	914.5433	913.5360	913.3977	151	0	K.NHGMHFR.V	Oxidation (M)
311 - 325	1447.9045	1446.8972	1446.7579	96	0	R.LSGGDHIHAGTVVGK.L	
326 - 341	1820.1308	1819.1235	1818.9476	97	1	K.LEGDRESTLGFVDLLR.D	
331 - 341	1249.8438	1248.8365	1248.6714	132	0	R.ESTLGFVDLLR.D	
331 - 347	2013.1758	2012.1685	2012.0102	79	1	R.ESTLGFVDLLRDDYIEK.D	
342 - 349	1053.6599	1052.6526	1052.4774	166	1	R.DDYIEKDR.S	
413 - 422	1116.7421	1115.7348	1115.5757	143	0	R.VALEACVQAR.N	
427 - 437	1228.8210	1227.8137	1227.6459	137	0	R.DLAVEGNEIIR.Q	
442 - 454	1546.9133	1545.9060	1545.7286	115	0	K.WSPELAAACEVWK.E	
442 - 457	1917.0601	1916.0528	1915.9502	54	1	K.WSPELAAACEVWKEIK.F	
458 - 465	981.6087	980.6014	980.4967	107	0	K.FNFPTIDK.L	
458 - 472	1719.9905	1718.9832	1718.8879	55	1	K.FNFPTIDKLDGPVEK.F	

Spot No.: **35**

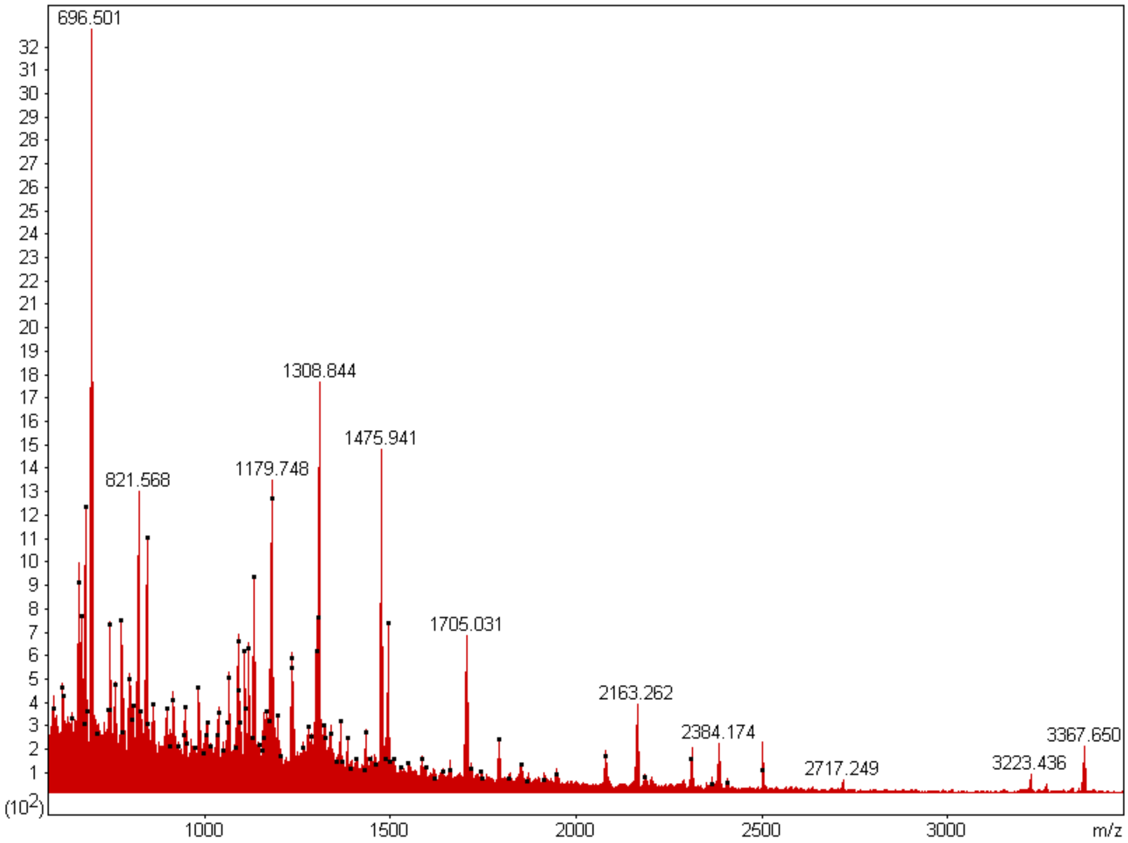
Mascot score: **87** Sequence coverage %: **27**

NCBI accession No.: **gi| 15226573**

Matched peptides No.: **19** Total peptides No.: **108**

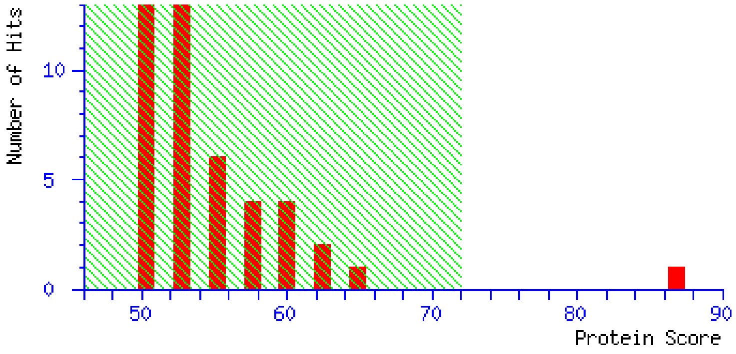
Calculated Mr: **65977** Calculated *p*I: **5.95**

Annotated PMF **spectra:**

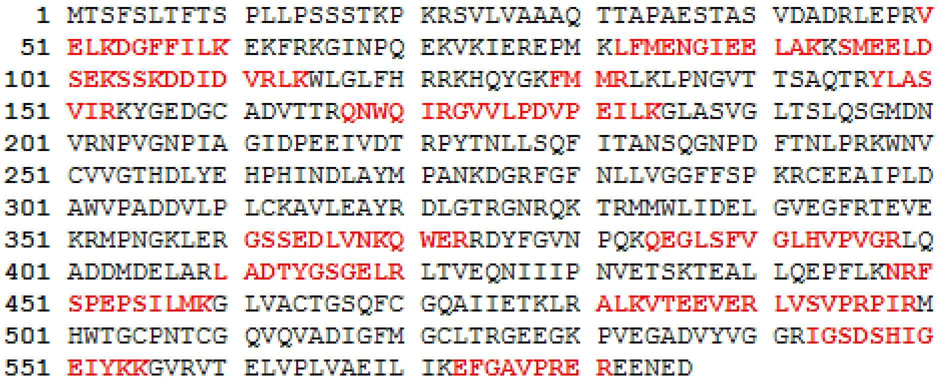


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant ($p<0.05$).

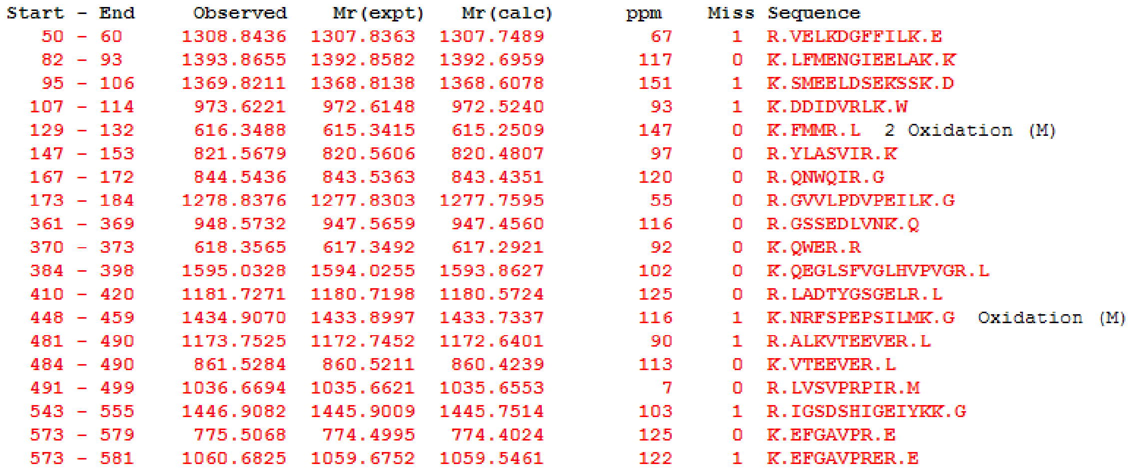


Matched peptide sequences: shown in **Bold Red**



1 MTSFSLTFTS PLLPSSSTKP KRSVLVAAAQ TTAPAESTAS VDADRLEPR**V**
51 **ELKDGFFILK** EKFRKGINPQ EKVKIEREPM K**LFMENGIEE LAK**K**SMEELD**
101 **SEKSSKDDID VRLK**WLGLFH RRKHQYGK**FM MR**LKLPNGVT TSAQTR**YLAS**
151 **VIR**KYGEDGC ADVTTR**QNWQ IRGVVLPDVP EILK**GLASVG LTSLQSGMDN
201 VRNPVGNPIA GIDPEEIVDT RPYTNLLSQF ITANSQGNPD FTNLPRKWNV
251 CVVGTHDLYE HPHINDLAYM PANKDGRFGF NLLVGGFFSP KRCEEAIPLD
301 AWVPADDVLP LCKAVLEAYR DLGTRGNRQK TRMMWLIDEL GVEGFRTEVE
351 KRMPNGKLER **GSSEDLVNKQ WER**RDYFGVN PQK**QEGLSFV GLHVPVGR**LQ
401 ADDMDELAR**L ADTYGSGELR** LTVEQNIIIP NVETSKTEAL LQEPFLK**NRF**
451 **SPEPSILMK**G LVACTGSQFC GQAIIETKLR **ALKVTEEVER LVSVPRPIR**M
501 HWTGCPNTCG QVQVADIGFM GCLTRGEEGK PVEGADVYVG GR**IGSDSHIG**
551 **EIYKK**GVRVT ELVPLVAEIL IK**EFGAVPRE R**EENED

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
50 - 60	1308.8436	1307.8363	1307.7489	67	1	R.VELKDGFFILK.E	
82 - 93	1393.8655	1392.8582	1392.6959	117	0	K.LFMENGIEELAK.K	
95 - 106	1369.8211	1368.8138	1368.6078	151	1	K.SMEELDSEKSSK.D	
107 - 114	973.6221	972.6148	972.5240	93	1	K.DDIDVRLK.W	
129 - 132	616.3488	615.3415	615.2509	147	0	K.FMMR.L	2 Oxidation (M)
147 - 153	821.5679	820.5606	820.4807	97	0	R.YLASVIR.K	
167 - 172	844.5436	843.5363	843.4351	120	0	R.QNWQIR.G	
173 - 184	1278.8376	1277.8303	1277.7595	55	0	R.GVVLPDVPEILK.G	
361 - 369	948.5732	947.5659	947.4560	116	0	R.GSSEDLVNK.Q	
370 - 373	618.3565	617.3492	617.2921	92	0	K.QWER.R	
384 - 398	1595.0328	1594.0255	1593.8627	102	0	K.QEGLSFVGLHVPVGR.L	
410 - 420	1181.7271	1180.7198	1180.5724	125	0	R.LADTYGSGELR.L	
448 - 459	1434.9070	1433.8997	1433.7337	116	1	K.NRFSPEPSILMK.G	Oxidation (M)
481 - 490	1173.7525	1172.7452	1172.6401	90	1	R.ALKVTEEVER.L	
484 - 490	861.5284	860.5211	860.4239	113	0	K.VTEEVER.L	
491 - 499	1036.6694	1035.6621	1035.6553	7	0	R.LVSVPRPIR.M	
543 - 555	1446.9082	1445.9009	1445.7514	103	1	R.IGSDSHIGEIYKK.G	
573 - 579	775.5068	774.4995	774.4024	125	0	K.EFGAVPR.E	
573 - 581	1060.6825	1059.6752	1059.5461	122	1	K.EFGAVPRER.E	

Spot No.: **36**

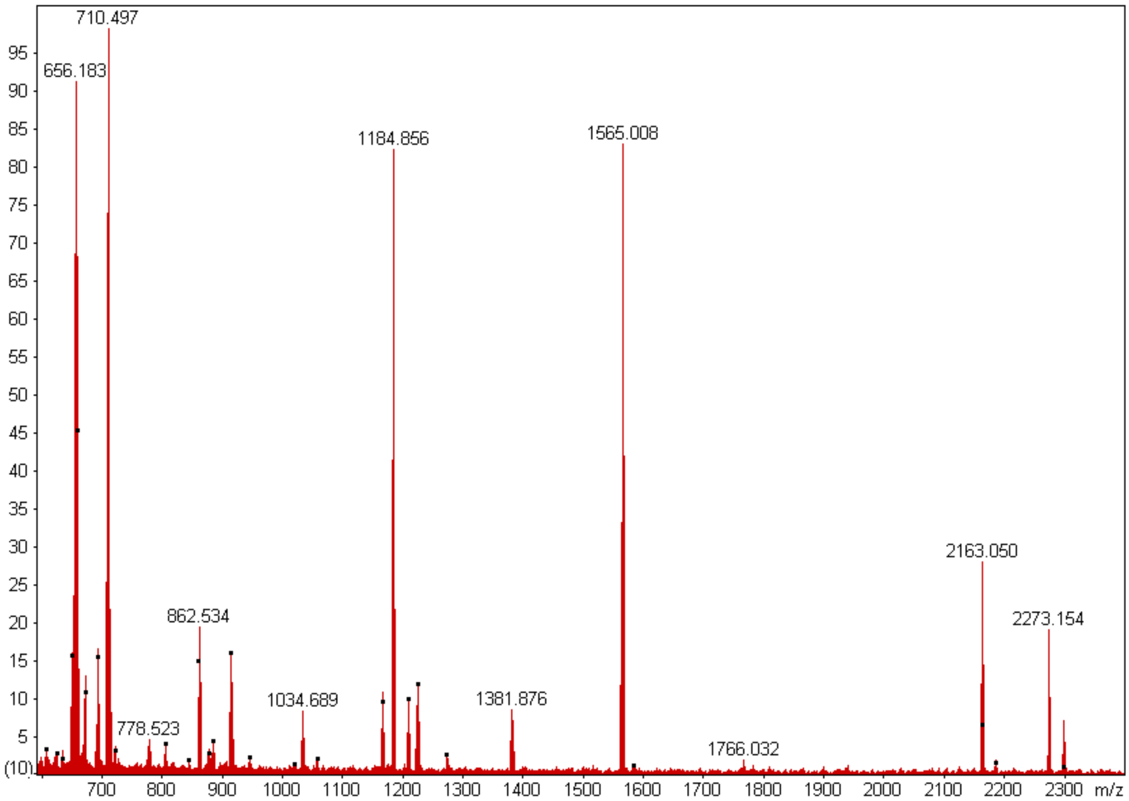
Mascot score: **107** Sequence coverage %: **15**

NCBI accession No.: **gi| 15233349**

Matched peptides No.: **15** Total peptides No.: **29**

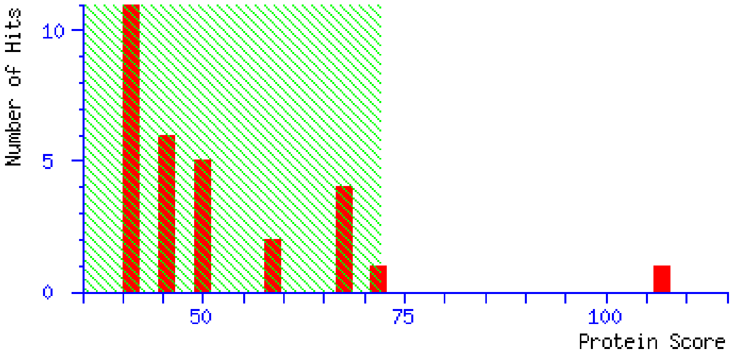
Calculated Mr: **98774** Calculated *p*I: **5.98**

Annotated PMF **spectra:**

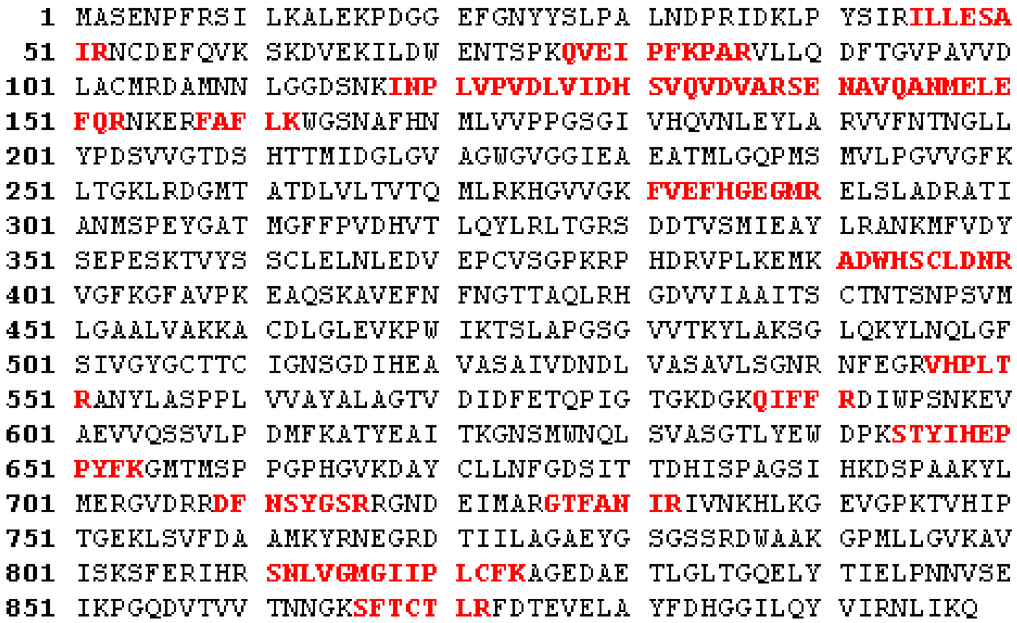


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red



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  1 MASENPFRSI LKALEKPDGG EFGNYYSLPA LNDPRIDKLP YSIRILLESA
 51 IRNCDEFQVK SKDVEKILDW ENTSPKQVEI PFKPARVLLQ DFTGVPAVVD
101 LACMRDAMNN LGGDSNKINP LVPVDLVIDH SVQVDVARSE NAVQANMELE
151 FQRNKERFAF LKWGSNAFHN MLVVPPGSGI VHQVNLEYLA RVVFNTNGLL
201 YPDSVVGTDS HTTMIDGLGV AGWGVGGIEA EATMLGQPMS MVLPGVVGFK
251 LTGKLRDGMT ATDLVLTVTQ MLRKHGVVGK FVEFHGEGMR ELSLADRATI
301 ANMSPEYGAT MGFFPVDHVT LQYLRLTGRS DDTVSMIEAY LRANKMFVDY
351 SEPESKTVYS SCLELNLEDV EPCVSGPKRP HDRVPLKEMK ADWHSCLDNR
401 VGFKGFAVPK EAQSKAVEFN FNGTTAQLRH GDVVIAAITS CTNTSNPSVM
451 LGAALVAKKA CDLGLEVKPW IKTSLAPGSG VVTKYLAKSG LQKYLNQLGF
501 SIVGYGCTTC IGNSGDIHEA VASAIVDNDL VASAVLSGNR NFEGRVHPLT
551 RANYLASPPL VVAYALAGTV DIDFETQPIG TGKDGKQIFF RDIWPSNKEV
601 AEVVQSSVLP DMFKATYEAI TKGNSMWNQL SVASGTLYEW DPKSTYIHEP
651 PYFKGMTMSP PGPHGVKDAY CLLNFGDSIT TDHISPAGSI HKDSPAAKYL
701 MERGVDRRDF NSYGSRRGND EIMARGTFAN IRIVNKHLKG EVGPKTVHIP
751 TGEKLSVFDA AMKYRNEGRD TIILAGAEYG SGSSRDWAAK GPMLLGVKAV
801 ISKSFERIHR SNLVGMGIIP LCFKAGEDAE TLGLTGQELY TIELPNNVSE
851 IKPGQDVTVV TNNGKSFTCT LRFDTEVELA YFDHGGILQY VIRNLIKQ
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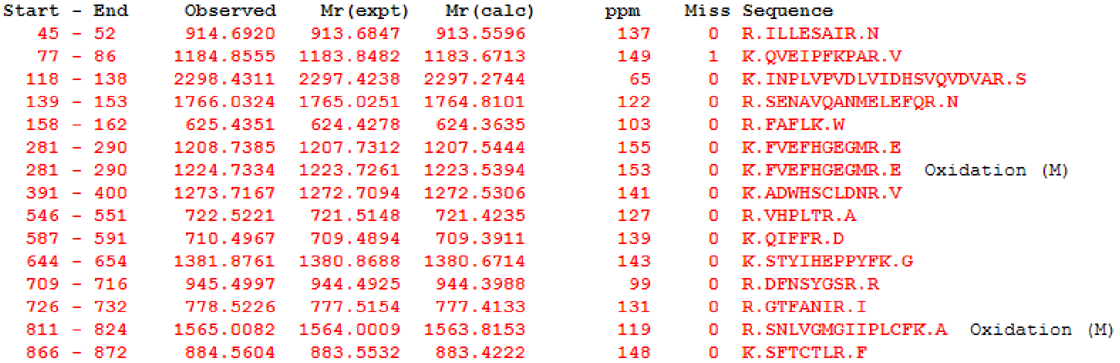
Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   45 - 52      914.6920   913.6847   913.5596      137     0   R.ILLESAIR.N
   77 - 86     1184.8555  1183.8482  1183.6713      149     1   K.QVEIPFKPAR.V
  118 - 138    2298.4311  2297.4238  2297.2744       65     0   K.INPLVPVDLVIDHSVQVDVAR.S
  139 - 153    1766.0324  1765.0251  1764.8101      122     0   R.SENAVQANMELEFQR.N
  158 - 162     625.4351   624.4278   624.3635      103     0   R.FAFLK.W
  281 - 290    1208.7385  1207.7312  1207.5444      155     0   K.FVEFHGEGMR.E
  281 - 290    1224.7334  1223.7261  1223.5394      153     0   K.FVEFHGEGMR.E  Oxidation (M)
  391 - 400    1273.7167  1272.7094  1272.5306      141     0   K.ADWHSCLDNR.V
  546 - 551     722.5221   721.5148   721.4235      127     0   R.VHPLTR.A
  587 - 591     710.4967   709.4894   709.3911      139     0   K.QIFFR.D
  644 - 654    1381.8761  1380.8688  1380.6714      143     0   K.STYIHEPPYFK.G
  709 - 716     945.4997   944.4925   944.3988       99     0   R.DFNSYGSR.R
  726 - 732     778.5226   777.5154   777.4133      131     0   R.GTFANIR.I
  811 - 824    1565.0082  1564.0009  1563.8153      119     0   R.SNLVGMGIIPLCFK.A  Oxidation (M)
  866 - 872     884.5604   883.5532   883.4222      148     0   K.SFTCTLR.F
```

Spot No.: **37**

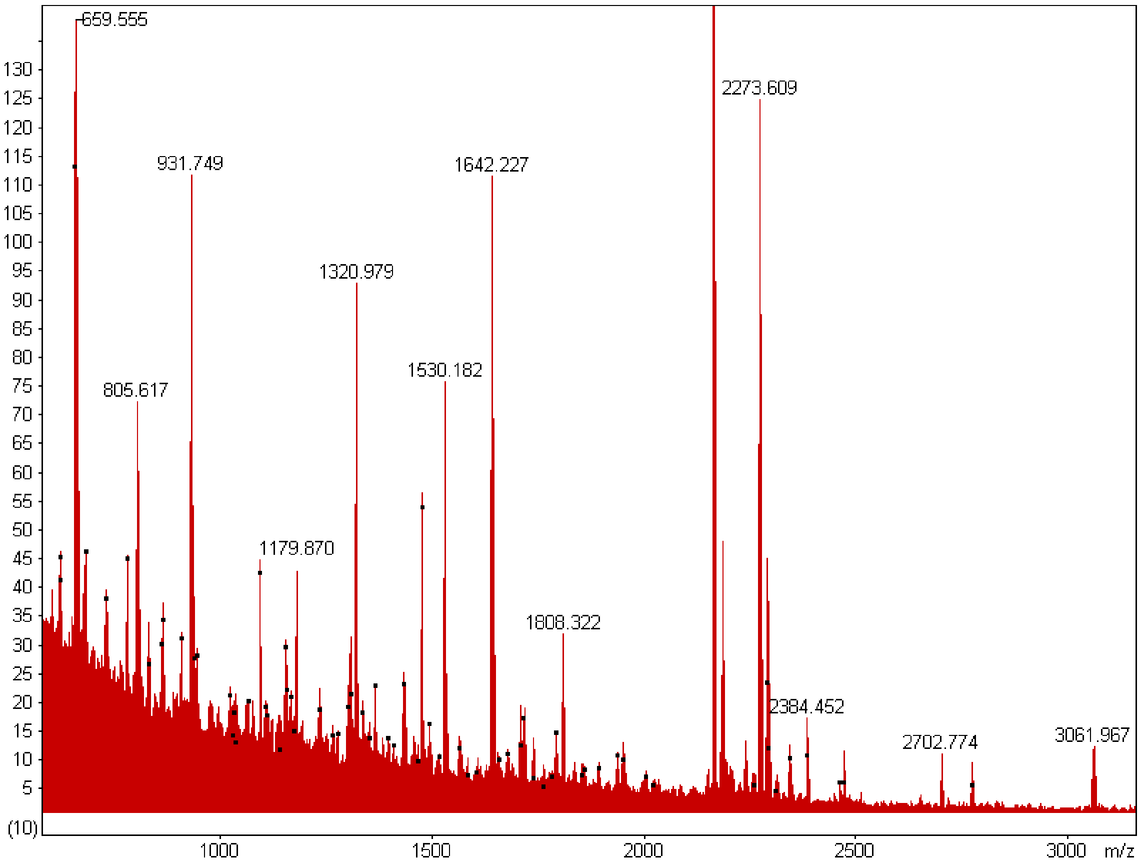
Mascot score: **94**   Sequence coverage %: **19**

NCBI accession No.: **gi| 14596025**

Matched peptides No.: **20**   Total peptides No.: **55**

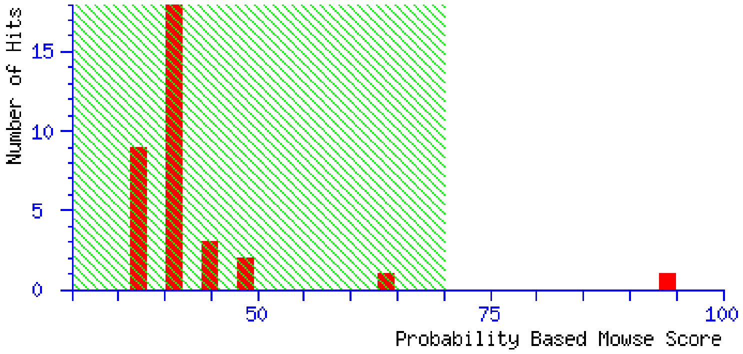
Calculated Mr: **113852**   Calculated *p*I: **6.51**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 MERARRLAYR GIVKRLVNDT KRHRNAETPH LVPHAPARYV SSLSPFISTP
51 RSVNHTAAFG RHQQTRSISV DAVKPSDTFP R**RHNSATPDE** **QTHMAK**FCGF
101 DHIDSLIDAT VPKSIRLDSM KFSK**FDAGLT** **ESQMIQHMVD** **LASKNK**VFKS
151 FIGMGYYNTH VPTVILRNIM ENPAWYTQYT PYQAEISQGR LESLLNFQTV
201 ITDLTGLPMS NASLLDEGTA AAEAMAMCNN ILKGKKKTFV IASNCHPQTI
251 DVCK**TRADGF** **DLK**VVTSDLK DIDYSSGDVC GVLVQYPGTE GEVLDYAEFV
301 KNAHANGVKV VMATDLLALT VLKPPGEFGA DIVVGSAQR**F** **GVPMGYGGPH**
351 **AAFLATSQEY** **KRMMPGRIIG** **ISVDSSGK**QA LRMAMQTR**EQ** **HIR**RDKATSN
401 ICTAQALLAN MAAMYAVYHG PAGLKSIAQR VHGLAGIFSL GLNK**LGVAEV**
451 **QELPFFDTVK** IKCSDAHAIA DAASK**SEINL** **R**VVDSTTITA SFDETTTLDD
501 VDKLFKVFAS GKPVPFTAES LAPEVQNSIP SSLTRESPYL THPIFNMYHT
551 EHELLRYIHK LQSKDLSLCH SMIPLGSCTM KLNATTEMMP VTWPSFTDIH
601 PFAPVEQAQG YQEMFENLGD LLCTITGFDS FSLQPNAGAA GEYAGLMVIR
651 **AYHMSRGDHH** **RNVCIIPVSA** **HGTNPASAAM** **CGMK**IITVGT DAKGNINIEE
701 VRKAAEANKD NLAALMVTYP STHGVYEEGI DEICNIIHEN GGQVYMDGAN
751 MNAQVGLTSP GFIGADVCHL NLHK**TFCIPH** **GGGGPGMGPI** **GVK**NHLAPFL
801 PSHPVIPTGG IPQPEKTAPL GAISAAPWGS ALILPISYTY IAMMGSGGLT
851 DASKIAILNA NYMAKRLEK**H** **YPVLFR**GVNG TVAHEFIIDL RGFKNTAGIE
901 PEDVAKRLMD YGFHGPTMSW PVPGTLMIEP TESESKAELD R**FCDALISIR**
951 EEIAQIEKGN ADVQNNVLKG APHPPSLLMA DTWKKPYSR**E** **YAAFPAPWLR**
1001 SSK**FWPTTGR** **VDNVYGDRK**L VCTLLPEEEQ VTAAVSA

Matched peptides information:

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
82 - 96	1739.1921	1738.1848	1737.7853	230	1	R.RHNSATPDEQTHMAK.F Oxidation (M)
83 - 96	1583.1333	1582.1260	1581.6842	279	0	R.HNSATPDEQTHMAK.F Oxidation (M)
125 - 146	2462.7650	2461.7577	2462.1934	-177	1	K.FDAGLTESQMIQHMVDLASKNK.V
255 - 263	1022.7491	1021.7418	1021.5193	218	1	K.TRADGFDLK.V
340 - 361	2344.5557	2343.5484	2343.0994	192	0	R.FGVPMGYGGPHAAFLATSQEYK.R Oxidation (M)
363 - 367	623.4294	622.4221	622.2567	266	0	R.MMPGR.I 2 Oxidation (M)
363 - 378	1680.2103	1679.2030	1678.8382	217	1	R.MMPGRIIGISVDSSGK.Q 2 Oxidation (M)
389 - 393	682.5155	681.5082	681.3558	224	0	R.EQHIR.R
445 - 460	1792.1327	1791.1254	1790.9455	100	0	K.LGVAEVQELPFFDTVK.I
476 - 481	731.5769	730.5697	730.3973	236	0	K.SEINLR.V
651 - 656	780.5345	779.5272	779.3384	242	0	R.AYHMSR.G Oxidation (M)
657 - 661	621.4541	620.4468	620.2779	272	0	R.GDHHR.N
662 - 684	2386.6096	2385.6023	2385.1062	208	0	R.NVCIIPVSAHGTNPASAAMCGMK.I
775 - 793	1855.2809	1854.2736	1853.8917	206	0	K.TFCIPHGGGGPGMGPIGVK.N Oxidation (M)
870 - 876	931.7489	930.7417	930.5076	252	0	K.HYPVLFR.G
942 - 950	1094.8137	1093.8064	1093.5590	226	0	R.FCDALISIR.E
990 - 1000	1320.9786	1319.9713	1319.6662	231	0	R.EYAAFPAPWLR.S
1004 - 1010	864.6285	863.6213	863.4290	223	0	K.FWPTTGR.V
1011 - 1018	937.6605	936.6532	936.4301	238	0	R.VDNVYGDR.K
1011 - 1019	1065.7593	1064.7520	1064.5251	213	1	R.VDNVYGDRK.L

Spot No.: **38**

Mascot score: **103**

Sequence coverage %: **51**

NCBI accession No.: **gi| 312281703**

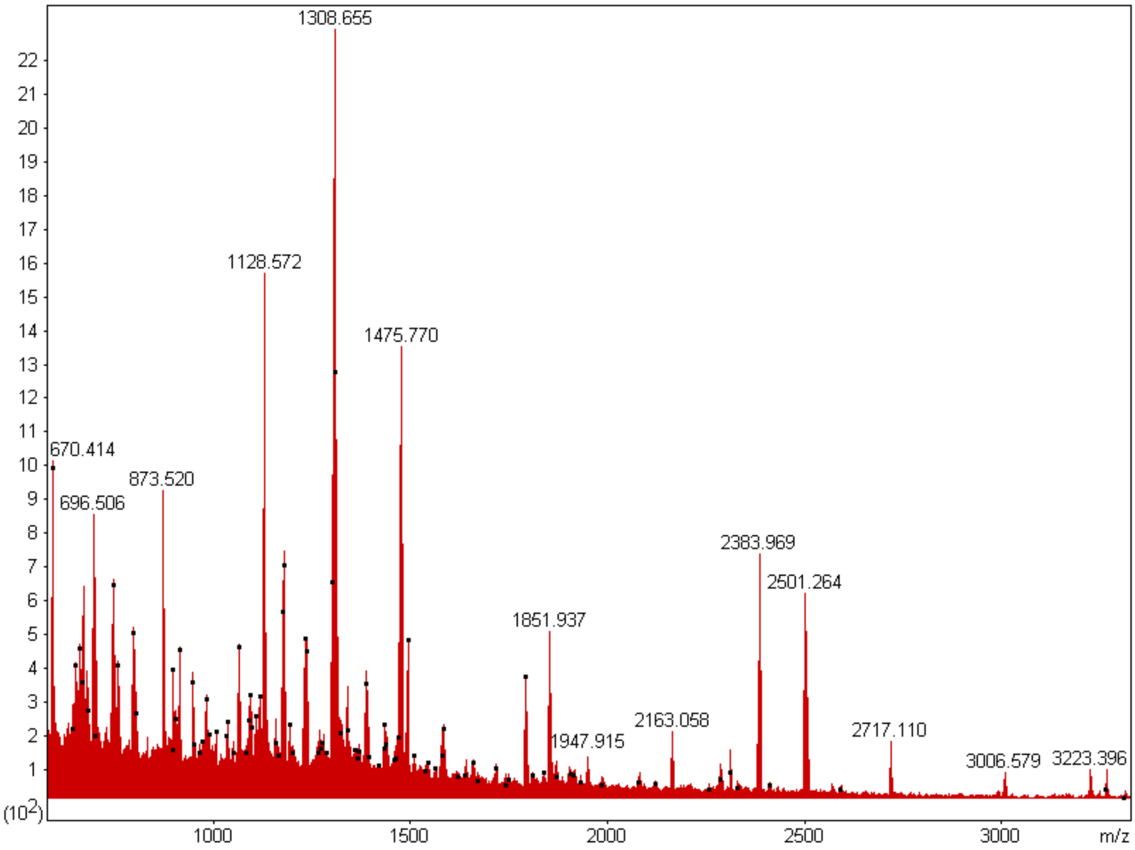
Matched peptides No.: **14**

Total peptides No.: **70**

Calculated Mr: **38065**

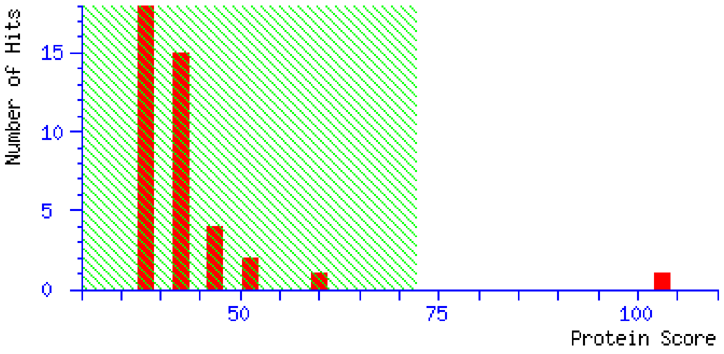
Calculated p*I*: **5.48**

Annotated PMF **spectra:**

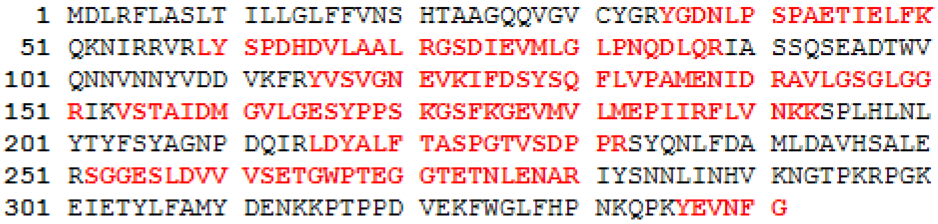


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

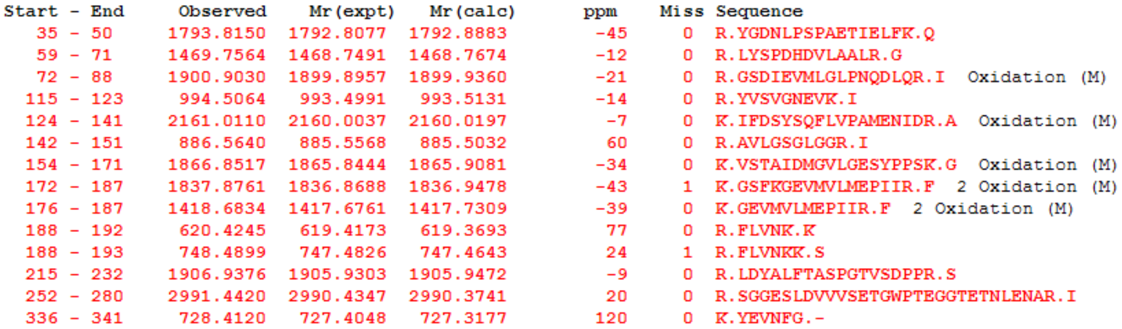


Matched peptide sequences: shown in Bold Red



```
  1 MDLRFLASLT ILLGLFFVNS HTAAGQQVGV CYGRYGDNLP SPAETIELFK
 51 QKNIRRVRLY SPDHDVLAAL RGSDIEVMLG LPNQDLQRIA SSQSEADTWV
101 QNNVNNYVDD VKFRYVSVGN EVKIFDSYSQ FLVPAMENID RAVLGSGLGG
151 RIKVSTAIDM GVLGESYPPS KGSFKGEVMV LMEPIIRFLV NKKSPLHLNL
201 YTYFSYAGNP DQIRLDYALF TASPGTVSDP PRSYQNLFDA MLDAVHSALE
251 RSGGESLDVV VSETGWPTEG GTETNLENAR IYSNNLINHV KNGTPKRPGK
301 EIETYLFAMY DENKKPTPPD VEKFWGLFHP NKQPKYEVNF G
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   35 - 50     1793.8150  1792.8077  1792.8883      -45      0  R.YGDNLPSPAETIELFK.Q
   59 - 71     1469.7564  1468.7491  1468.7674      -12      0  R.LYSPDHDVLAALR.G
   72 - 88     1900.9030  1899.8957  1899.9360      -21      0  R.GSDIEVMLGLPNQDLQR.I  Oxidation (M)
  115 - 123     994.5064   993.4991   993.5131      -14      0  R.YVSVGNEVK.I
  124 - 141    2161.0110  2160.0037  2160.0197       -7      0  K.IFDSYSQFLVPAMENIDR.A  Oxidation (M)
  142 - 151     886.5640   885.5568   885.5032       60      0  R.AVLGSGLGGR.I
  154 - 171    1866.8517  1865.8444  1865.9081      -34      0  K.VSTAIDMGVLGESYPPSK.G  Oxidation (M)
  172 - 187    1837.8761  1836.8688  1836.9478      -43      1  K.GSFKGEVMVLMEPIIR.F  2 Oxidation (M)
  176 - 187    1418.6834  1417.6761  1417.7309      -39      0  K.GEVMVLMEPIIR.F  2 Oxidation (M)
  188 - 192     620.4245   619.4173   619.3693       77      0  R.FLVNK.K
  188 - 193     748.4899   747.4826   747.4643       24      1  R.FLVNKK.S
  215 - 232    1906.9376  1905.9303  1905.9472       -9      0  R.LDYALFTASPGTVSDPPR.S
  252 - 280    2991.4420  2990.4347  2990.3741       20      0  R.SGGESLDVVVSETGWPTEGGTETNLENAR.I
  336 - 341     728.4120   727.4048   727.3177      120      0  K.YEVNFG.-
```

Spot No.: **39**

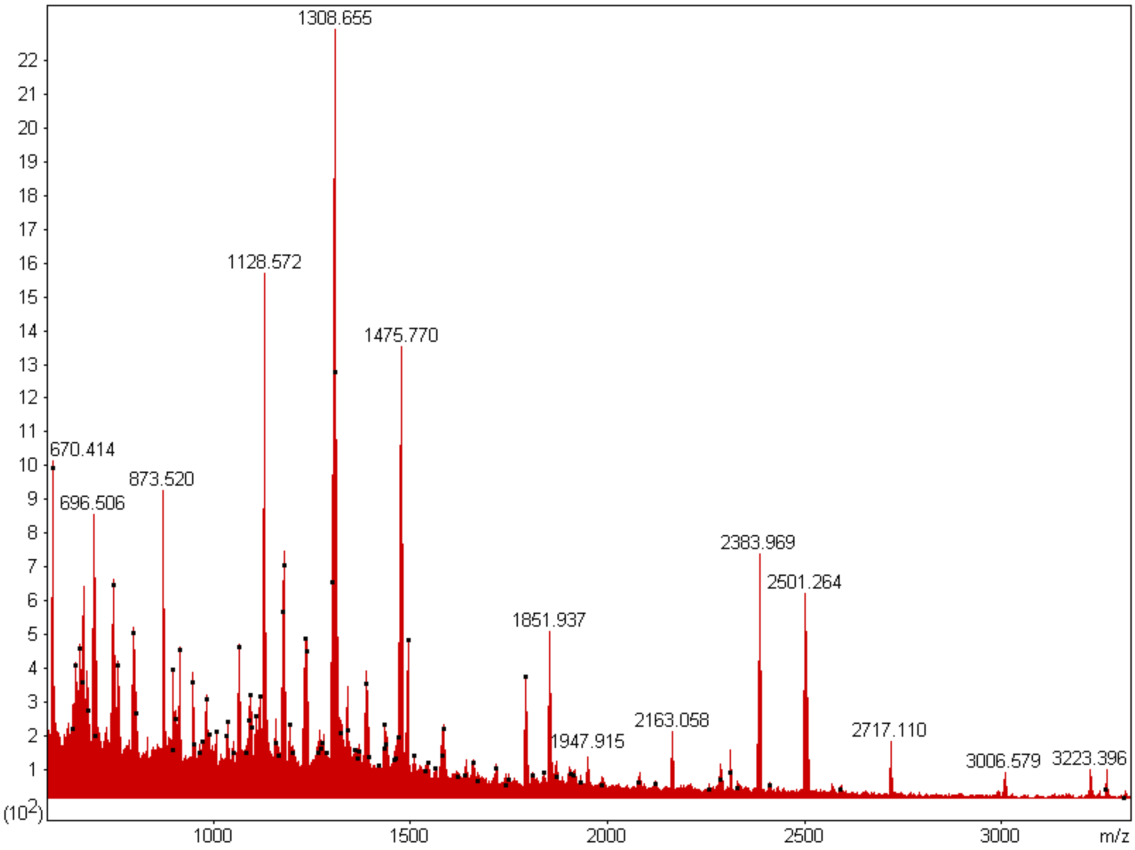
Mascot score: **86** Sequence coverage %: **43**

NCBI accession No.: **gi| 312281829**

Matched peptides No.: **15** Total peptides No.: **105**

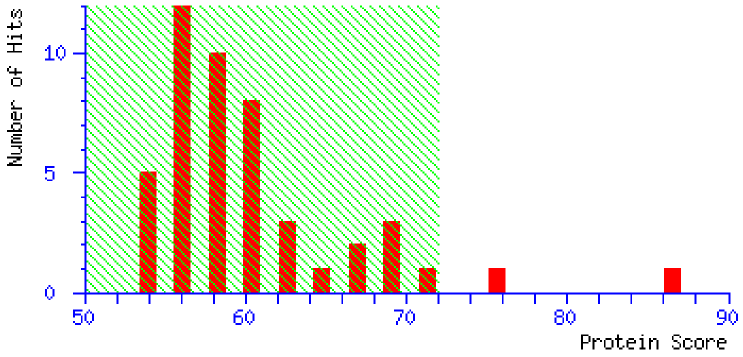
Calculated Mr: **43118** Calculated p*I*: **6.49**

Annotated PMF **spectra:**

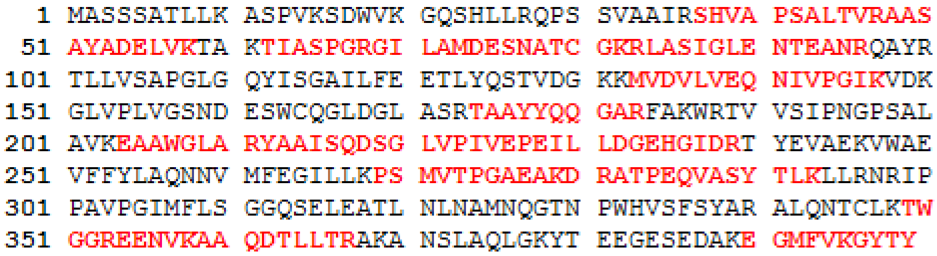


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).

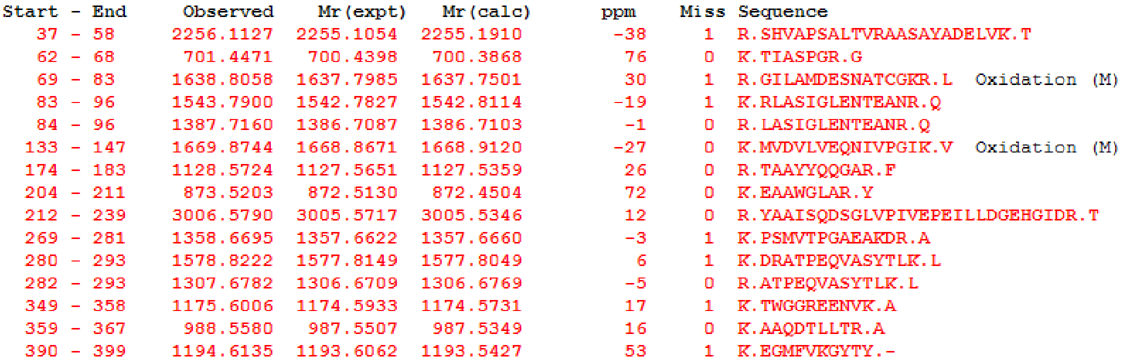


Matched peptide sequences: shown in Bold Red



```
  1 MASSSATLLK ASPVKSDWVK GQSHLLRQPS SVAAIRSHVA PSALTVRAAS
 51 AYADELVKTA KTIASPGRGI LAMDESNATC GKRLASIGLE NTEANRQAYR
101 TLLVSAPGLG QYISGAILFE ETLYQSTVDG KKMVDVLVEQ NIVPGIKVDK
151 GLVPLVGSND ESWCQGLDGL ASRTAAYYQQ GARFAKWRTV VSIPNGPSAL
201 AVKEAAWGLA RYAAISQDSG LVPIVEPEIL LDGEHGIDRT YEVAEKVWAE
251 VFFYLAQNNV MFEGILLKPS MVTPGAEAKD RATPEQVASY TLKLLRNRIP
301 PAVPGIMFLS GGQSELEATL NLNAMNQGTN PWHVSFSYAR ALQNTCLKTW
351 GGREENVKAA QDTLLTRAKA NSLAQLGKYT EEGESEDAKE GMFVKGYTY
```

Matched peptides information:



```
Start - End     Observed    Mr(expt)   Mr(calc)      ppm    Miss Sequence
   37 - 58     2256.1127  2255.1054  2255.1910      -38      1  R.SHVAPSALTVRAASAYADELVK.T
   62 - 68      701.4471   700.4398   700.3868       76      0  K.TIASPGR.G
   69 - 83     1638.8058  1637.7985  1637.7501       30      1  R.GILAMDESNATCGKR.L  Oxidation (M)
   83 - 96     1543.7900  1542.7827  1542.8114      -19      1  K.RLASIGLENTEANR.Q
   84 - 96     1387.7160  1386.7087  1386.7103       -1      0  R.LASIGLENTEANR.Q
  133 - 147    1669.8744  1668.8671  1668.9120      -27      0  K.MVDVLVEQNIVPGIK.V  Oxidation (M)
  174 - 183    1128.5724  1127.5651  1127.5359       26      0  R.TAAYYQQGAR.F
  204 - 211     873.5203   872.5130   872.4504       72      0  K.EAAWGLAR.Y
  212 - 239    3006.5790  3005.5717  3005.5346       12      0  R.YAAISQDSGLVPIVEPEILLDGEHGIDR.T
  269 - 281    1358.6695  1357.6622  1357.6660       -3      1  K.PSMVTPGAEAKDR.A
  280 - 293    1578.8222  1577.8149  1577.8049        6      1  K.DRATPEQVASYTLK.L
  282 - 293    1307.6782  1306.6709  1306.6769       -5      0  R.ATPEQVASYTLK.L
  349 - 358    1175.6006  1174.5933  1174.5731       17      1  K.TWGGREENVK.A
  359 - 367     988.5580   987.5507   987.5349       16      0  K.AAQDTLLTR.A
  390 - 399    1194.6135  1193.6062  1193.5427       53      1  K.EGMFVKGYTY.-
```

Spot No.: **40**

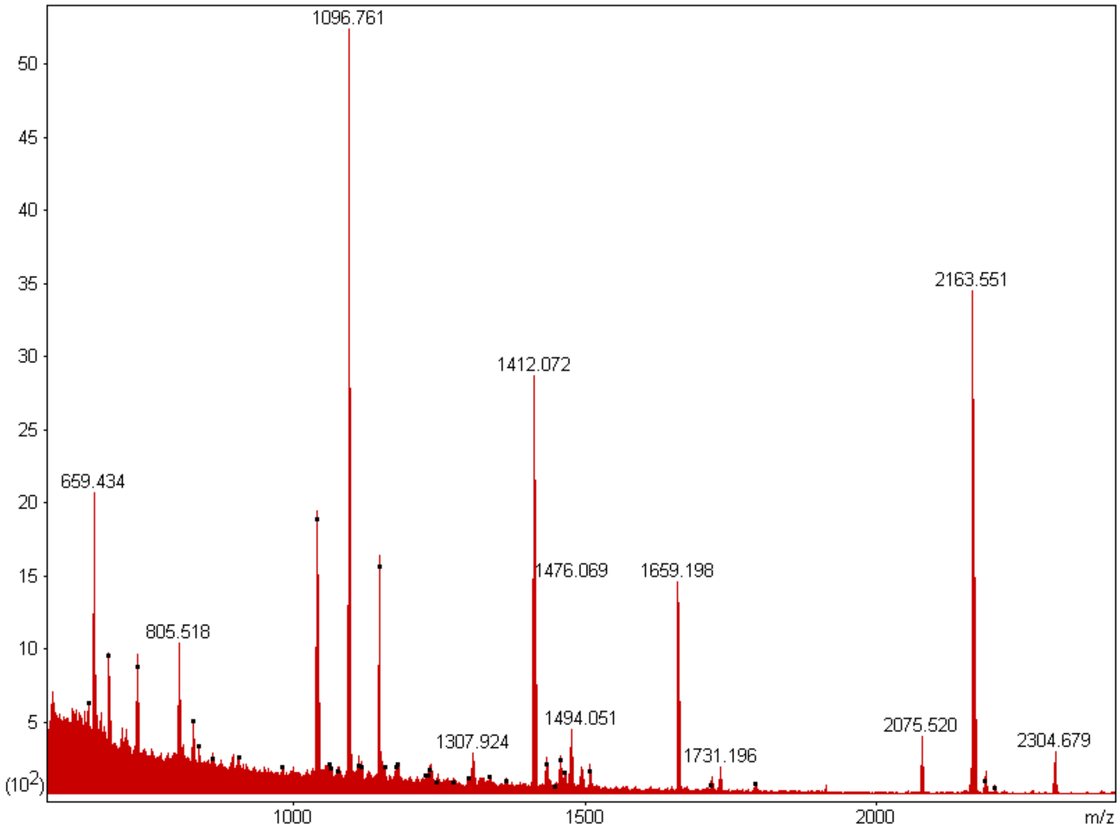
Mascot score: **86** Sequence coverage %: **15**

NCBI accession No.: **gi| 15238686**

Matched peptides No.: **12** Total peptides No.: **28**

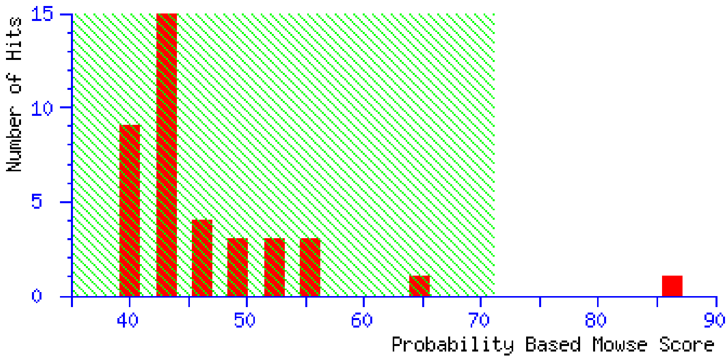
Calculated Mr: **84646** Calculated *p*I: **6.09**

Annotated PMF **spectra:**

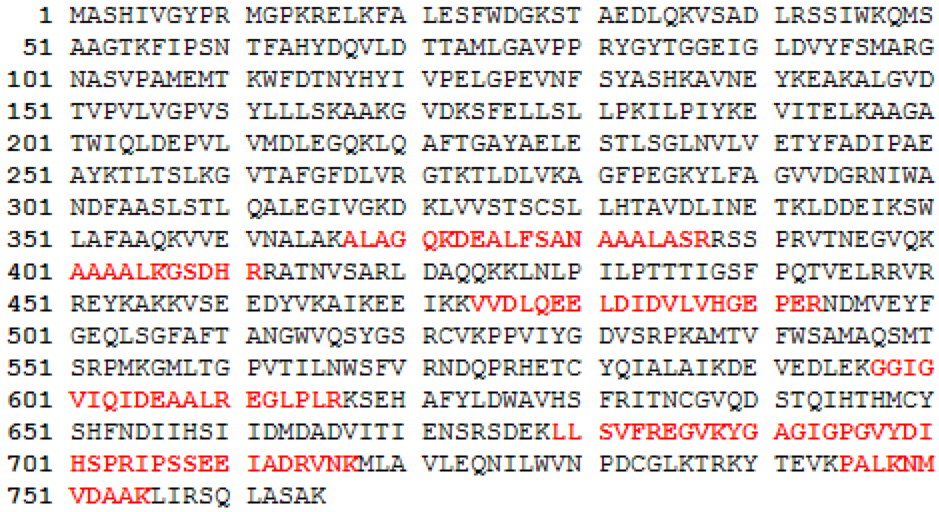


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant ($p<0.05$).

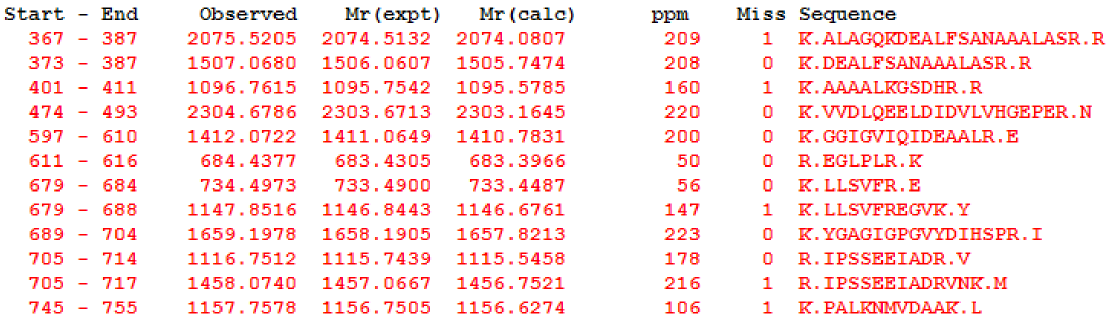


Matched peptide sequences: shown in Bold Red



```
  1 MASHIVGYPR MGPKRELKFA LESFWDGKST AEDLQKVSAD LRSSIWKQMS
 51 AAGTKFIPSN TFAHYDQVLD TTAMLGAVPP RYGYTGGEIG LDVYFSMARG
101 NASVPAMEMT KWFDTNYHYI VPELGPEVNF SYASHKAVNE YKEAKALGVD
151 TVPVLVGPVS YLLLSKAAKG VDKSFELLSL LPKILPIYKE VITELKAAGA
201 TWIQLDEPVL VMDLEGQKLQ AFTGAYAELE STLSGLNVLV ETYFADIPAE
251 AYKTLTSLKG VTAFGFDLVR GTKTLDLVKA GFPEGKYLFA GVVDGRNIWA
301 NDFAASLSTL QALEGIVGKD KLVVSTSCSL LHTAVDLINE TKLDDEIKSW
351 LAFAAQKVVE VNALAKALAG QKDEALFSAN AAALASRRSS PRVTNEGVQK
401 AAAALKGSDH RRATNVSARL DAQQKKLNLP ILPTTTIGSF PQTVELRRVR
451 REYKAKKVSE EDYVKAIKEE IKKVVDLQEE LDIDVLVHGE PERNDMVEYF
501 GEQLSGFAFT ANGWVQSYGS RCVKPPVIYG DVSRPKAMTV FWSAMAQSMT
551 SRPMKGMLTG PVTILNWSFV RNDQPRHETC YQIALAIKDE VEDLEKGGIG
601 VIQIDEAALR EGLPLRKSEH AFYLDWAVHS FRITNCGVQD STQIHTHMCY
651 SHFNDIIHSI IDMDADVITI ENSRSDEKLL SVFREGVKYG AGIGPGVYDI
701 HSPRIPSSEE IADRVNKMLA VLEQNILWVN PDCGLKTRKY TEVKPALKNM
751 VDAAKLIRSQ LASAK
```

Matched peptides information:



```
Start - End     Observed     Mr(expt)     Mr(calc)        ppm    Miss  Sequence
  367 - 387    2075.5205    2074.5132    2074.0807        209       1  K.ALAGQKDEALFSANAAALASR.R
  373 - 387    1507.0680    1506.0607    1505.7474        208       0  K.DEALFSANAAALASR.R
  401 - 411    1096.7615    1095.7542    1095.5785        160       1  K.AAAALKGSDHR.R
  474 - 493    2304.6786    2303.6713    2303.1645        220       0  K.VVDLQEELDIDVLVHGEPER.N
  597 - 610    1412.0722    1411.0649    1410.7831        200       0  K.GGIGVIQIDEAALR.E
  611 - 616     684.4377     683.4305     683.3966         50       0  R.EGLPLR.K
  679 - 684     734.4973     733.4900     733.4487         56       0  K.LLSVFR.E
  679 - 688    1147.8516    1146.8443    1146.6761        147       1  K.LLSVFREGVK.Y
  689 - 704    1659.1978    1658.1905    1657.8213        223       0  K.YGAGIGPGVYDIHSPR.I
  705 - 714    1116.7512    1115.7439    1115.5458        178       0  R.IPSSEEIADR.V
  705 - 717    1458.0740    1457.0667    1456.7521        216       1  R.IPSSEEIADRVNK.M
  745 - 755    1157.7578    1156.7505    1156.6274        106       1  K.PALKNMVDAAK.L
```

Spot No.: **41**

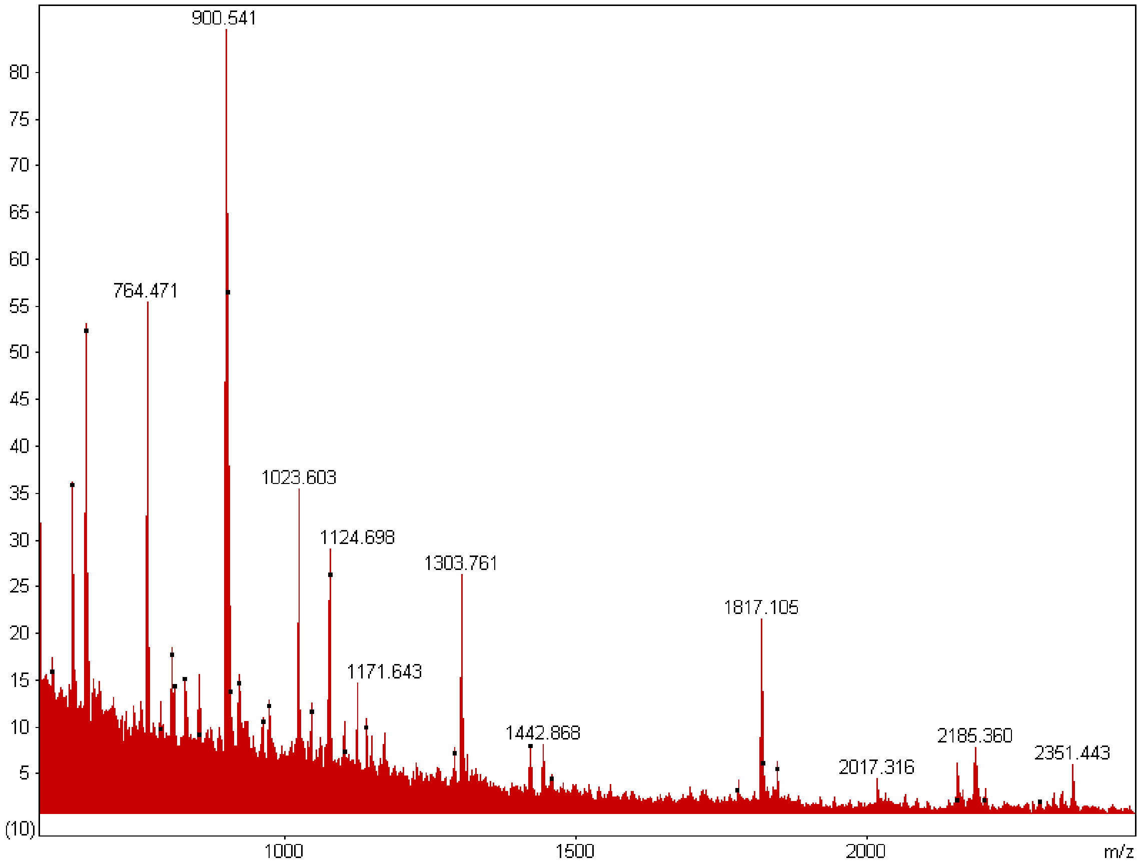
Mascot score: **93**   Sequence coverage %: **14**

NCBI accession No.: **gi| 146572852**

Matched peptides No.: **9**   Total peptides No.: **27**

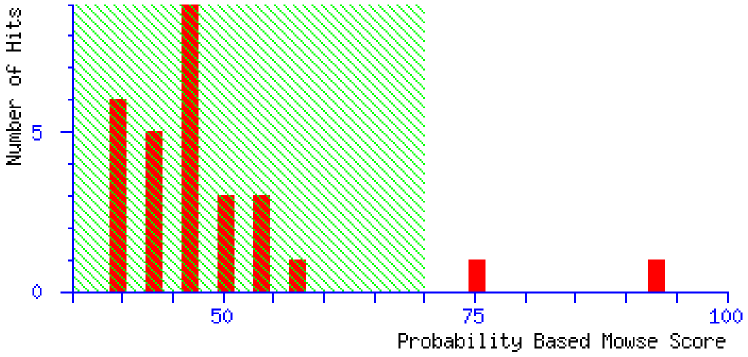
Calculated Mr: **61174**   Calculated p*I*: **6.27**

Annotated PMF **spectra:**

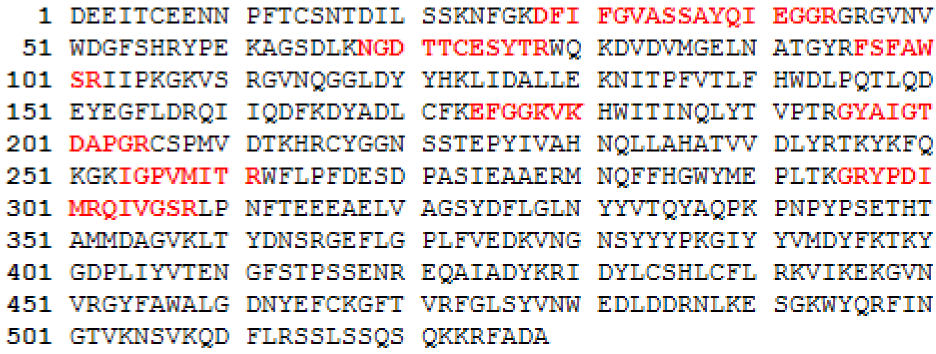


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

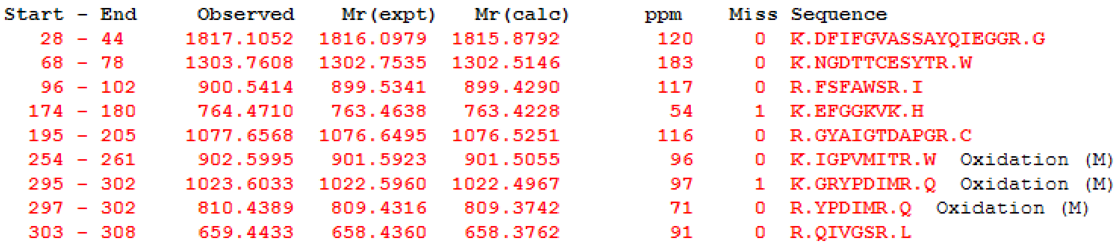


Matched peptide sequences: shown in Bold Red



```
  1 DEEITCEENN PFTCSNTDIL SSKNFGKDFI FGVASSAYQI EGGRGRGVNV
 51 WDGFSHRYPE KAGSDLKNGD TTCESYTRWQ KDVDVMGELN ATGYRFSFAW
101 SRIIPKGKVS RGVNQGGLDY YHKLIDALLE KNITPFVTLF HWDLPQTLQD
151 EYEGFLDRQI IQDFKDYADL CFKEFGGKVK HWITINQLYT VPTRGYAIGT
201 DAPGRCSPMV DTKHRCYGGN SSTEPYIVAH NQLLAHATVV DLYRTKYKFQ
251 KGKIGPVMIT RWFLPFDESD PASIEAAERM NQFFHGWYME PLTKGRYPDI
301 MRQIVGSRLP NFTEEEAELV AGSYDFLGLN YYVTQYAQPK PNPYPSETHT
351 AMMDAGVKLT YDNSRGEFLG PLFVEDKVNG NSYYYPKGIY YVMDYFKTKY
401 GDPLIYVTEN GFSTPSSENR EQAIADYKRI DYLCSHLCFL RKVIKEKGVN
451 VRGYFAWALG DNYEFCKGFT VRFGLSYVNW EDLDDRNLKE SGKWYQRFIN
501 GTVKNSVKQD FLRSSLSSQS QKKRFADA
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)     ppm    Miss Sequence
   28 - 44     1817.1052  1816.0979  1815.8792     120      0  K.DFIFGVASSAYQIEGGR.G
   68 - 78     1303.7608  1302.7535  1302.5146     183      0  K.NGDTTCESYTR.W
   96 - 102     900.5414   899.5341   899.4290     117      0  R.FSFAWSR.I
  174 - 180     764.4710   763.4638   763.4228      54      1  K.EFGGKVK.H
  195 - 205    1077.6568  1076.6495  1076.5251     116      0  R.GYAIGTDAPGR.C
  254 - 261     902.5995   901.5923   901.5055      96      0  K.IGPVMITR.W  Oxidation (M)
  295 - 302    1023.6033  1022.5960  1022.4967      97      1  K.GRYPDIMR.Q  Oxidation (M)
  297 - 302     810.4389   809.4316   809.3742      71      0  R.YPDIMR.Q  Oxidation (M)
  303 - 308     659.4433   658.4360   658.3762      91      0  R.QIVGSR.L
```

Spot No.: **42**

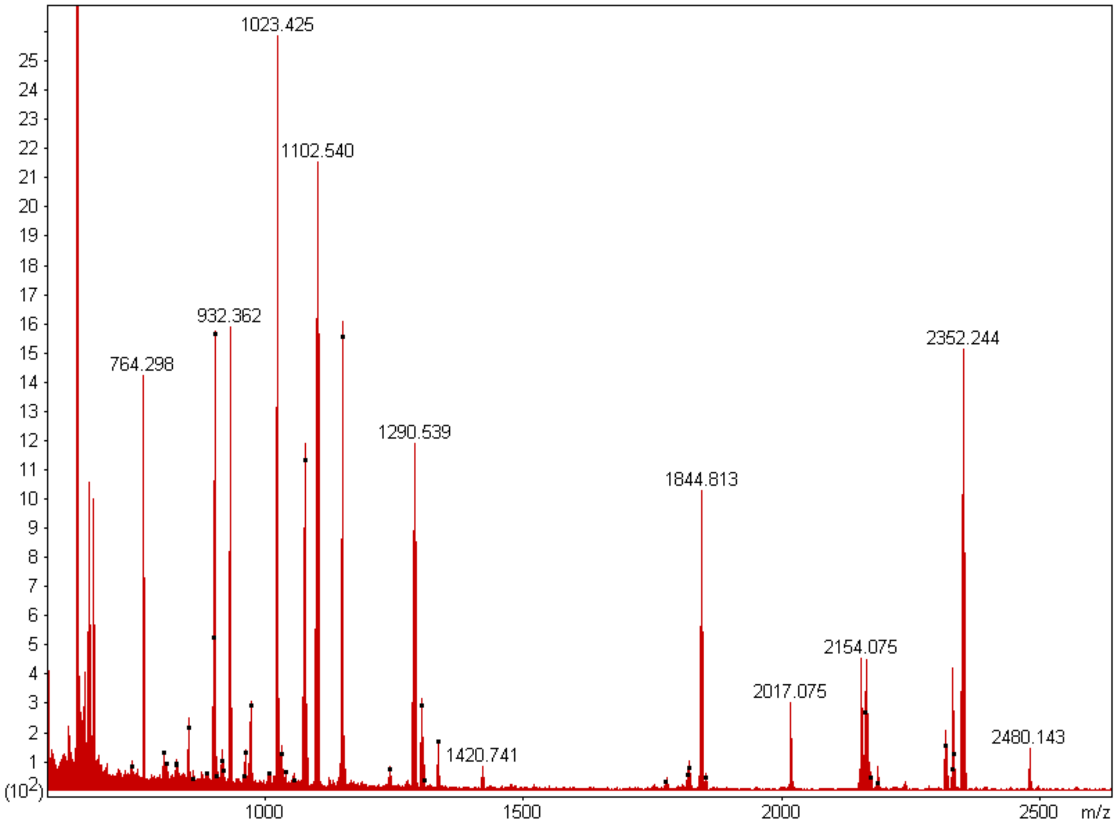
Mascot score: **87** Sequence coverage %: **17**

NCBI accession No.: **gi| 152207441**

Matched peptides No.: **13** Total peptides No.: **38**

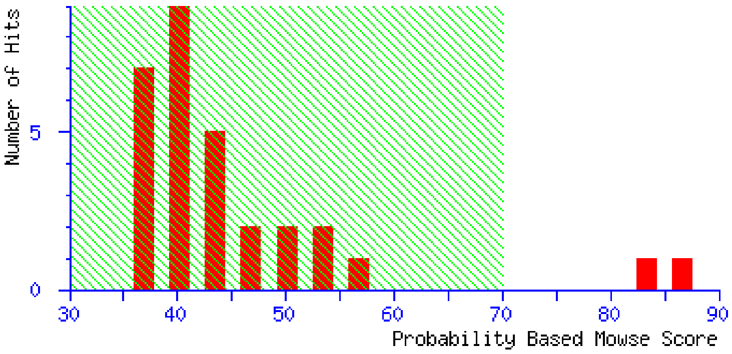
Calculated Mr: **62750** Calculated *p*I: **8.71**

Annotated PMF **spectra:**

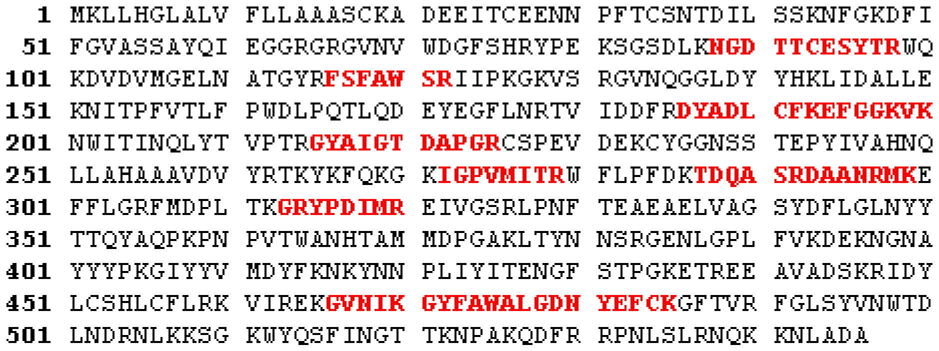


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).

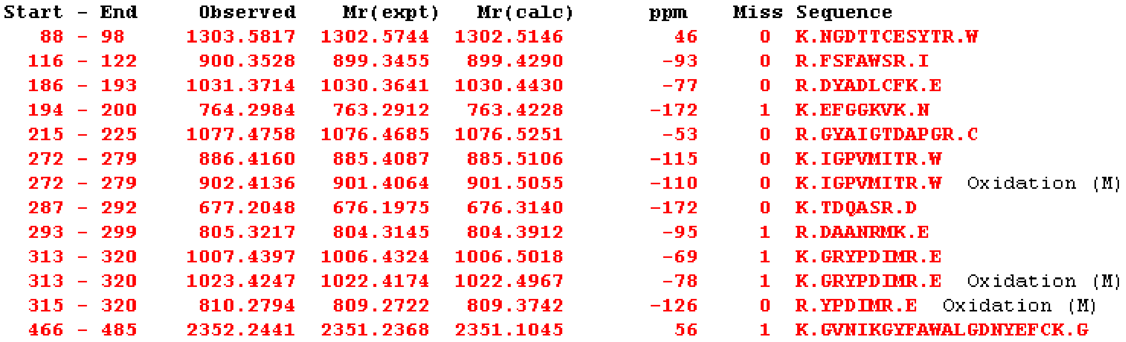


Matched peptide sequences: shown in Bold Red



1 MKLLHGLALV FLLAAASCKA DEEITCEENN PFTCSNTDIL SSKNFGKDFI
51 FGVASSAYQI EGGRGRGVNV WDGFSHRYPE KSGSDLK**NGD** **TTCESYTR**WQ
101 KDVDVMGELN ATGYR**FSFAW** **SR**IIPKGKVS RGVNQGGLDY YHKLIDALLE
151 KNITPFVTLF PWDLPQTLQD EYEGFLNRTV IDDFR**DYADL** **CFKEFGGKVK**
201 NWITINQLYT VPTR**GYAIGT** **DAPGR**CSPEV DEKCYGGNSS TEPYIVAHNQ
251 LLAHAAAVDV YRTKYKFQKG K**IGPVMITR**W FLPFDK**TDQA** **SRDAANRMK**E
301 FFLGRFMDPL TK**GRYPDIMR** EIVGSRLPNF TEAEAELVAG SYDFLGLNYY
351 TTQYAQPKPN PVTWANHTAM MDPGAKLTYN NSRGENLGPL FVKDEKNGNA
401 YYYPKGIYYV MDYFKNKYNN PLIYITENGF STPGKETREE AVADSKRIDY
451 LCSHLCFLRK VIREK**GVNIK** **GYFAWALGDN** **YEFCK**GFTVR FGLSYVNWTD
501 LNDRNLKKSG KWYQSFINGT TKNPAKQDFR RPNLSLRNQK KNLADA

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss Sequence
   88 - 98     1303.5817  1302.5744  1302.5146       46     0  K.NGDTTCESYTR.W
  116 - 122     900.3528   899.3455   899.4290      -93     0  R.FSFAWSR.I
  186 - 193    1031.3714  1030.3641  1030.4430      -77     0  R.DYADLCFK.E
  194 - 200     764.2984   763.2912   763.4228     -172     1  K.EFGGKVK.N
  215 - 225    1077.4758  1076.4685  1076.5251      -53     0  R.GYAIGTDAPGR.C
  272 - 279     886.4160   885.4087   885.5106     -115     0  K.IGPVMITR.W
  272 - 279     902.4136   901.4064   901.5055     -110     0  K.IGPVMITR.W  Oxidation (M)
  287 - 292     677.2048   676.1975   676.3140     -172     0  K.TDQASR.D
  293 - 299     805.3217   804.3145   804.3912      -95     1  R.DAANRMK.E
  313 - 320    1007.4397  1006.4324  1006.5018      -69     1  K.GRYPDIMR.E
  313 - 320    1023.4247  1022.4174  1022.4967      -78     1  K.GRYPDIMR.E  Oxidation (M)
  315 - 320     810.2794   809.2722   809.3742     -126     0  R.YPDIMR.E  Oxidation (M)
  466 - 485    2352.2441  2351.2368  2351.1045       56     1  K.GVNIKGYFAWALGDNYEFCK.G
```

Spot No.: **43**

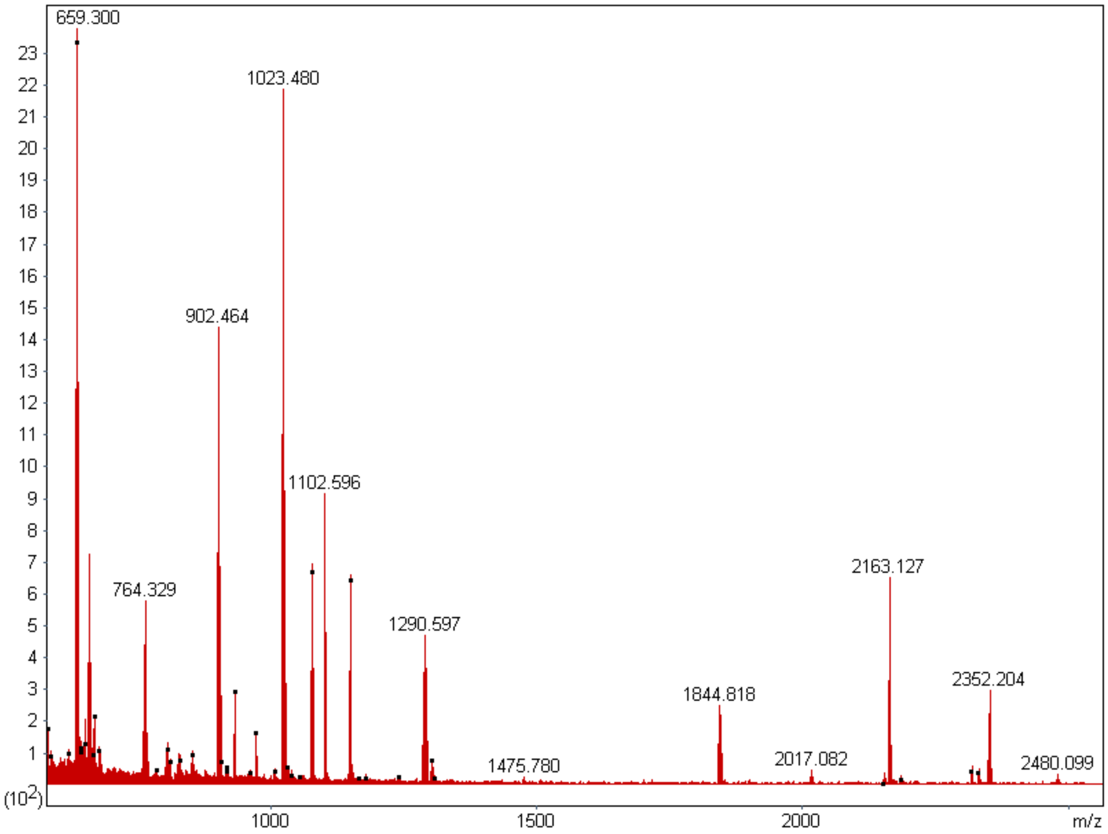
Mascot score: **86**   Sequence coverage %: **37**

NCBI accession No.: **gi| 78096539**

Matched peptides No.: **10**   Total peptides No.: **42**

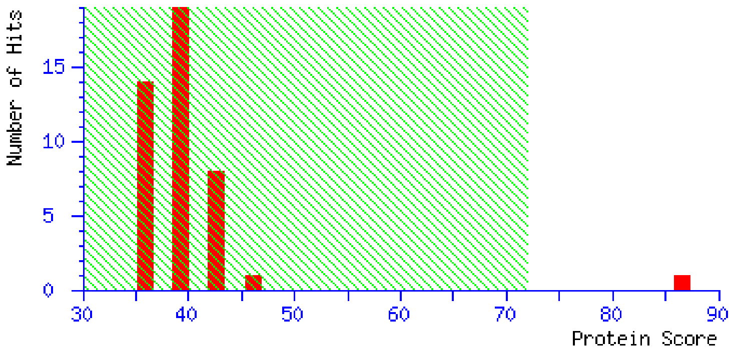
Calculated Mr: **23412**   Calculated *p*I: **9.37**

Annotated PMF **spectra:**

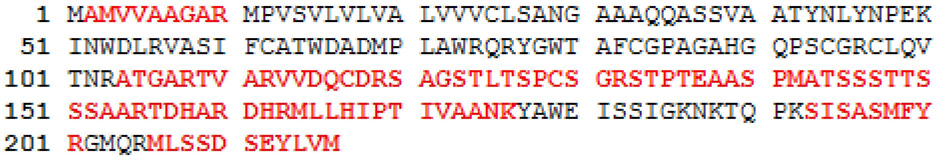


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant ($p<0.05$).

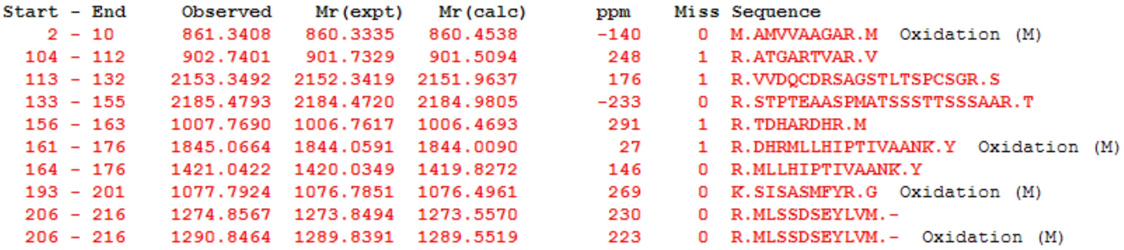


Matched peptide sequences: shown in Bold Red



```
  1 MAMVVAAGAR MPVSVLVLVA LVVVCLSANG AAAQQASSVA ATYNLYNPEK
 51 INWDLRVASI FCATWDADMP LAWRQRYGWT AFCGPAGAHG QPSCGRCLQV
101 TNRATGARTV ARVVDQCDRS AGSTLTSPCS GRSTPTEAAS PMATSSSTTS
151 SSAARTDHAR DHRMLLHIPT IVAANKYAWE ISSIGKNKTQ PKSISASMFY
201 RGMQRMLSSD SEYLVM
```

Matched peptides information:



```
Start - End      Observed    Mr(expt)    Mr(calc)       ppm    Miss Sequence
    2 - 10       861.3408    860.3335    860.4538      -140      0  M.AMVVAAGAR.M  Oxidation (M)
  104 - 112      902.7401    901.7329    901.5094       248      1  R.ATGARTVAR.V
  113 - 132     2153.3492   2152.3419   2151.9637       176      1  R.VVDQCDRSAGSTLTSPCSGR.S
  133 - 155     2185.4793   2184.4720   2184.9805      -233      0  R.STPTEAASPMATSSSTTSSSAAR.T
  156 - 163     1007.7690   1006.7617   1006.4693       291      1  R.TDHARDHR.M
  161 - 176     1845.0664   1844.0591   1844.0090        27      1  R.DHRMLLHIPTIVAANK.Y  Oxidation (M)
  164 - 176     1421.0422   1420.0349   1419.8272       146      0  R.MLLHIPTIVAANK.Y
  193 - 201     1077.7924   1076.7851   1076.4961       269      0  K.SISASMFYR.G  Oxidation (M)
  206 - 216     1274.8567   1273.8494   1273.5570       230      0  R.MLSSDSEYLVM.-
  206 - 216     1290.8464   1289.8391   1289.5519       223      0  R.MLSSDSEYLVM.-  Oxidation (M)
```

Spot No.: **44**

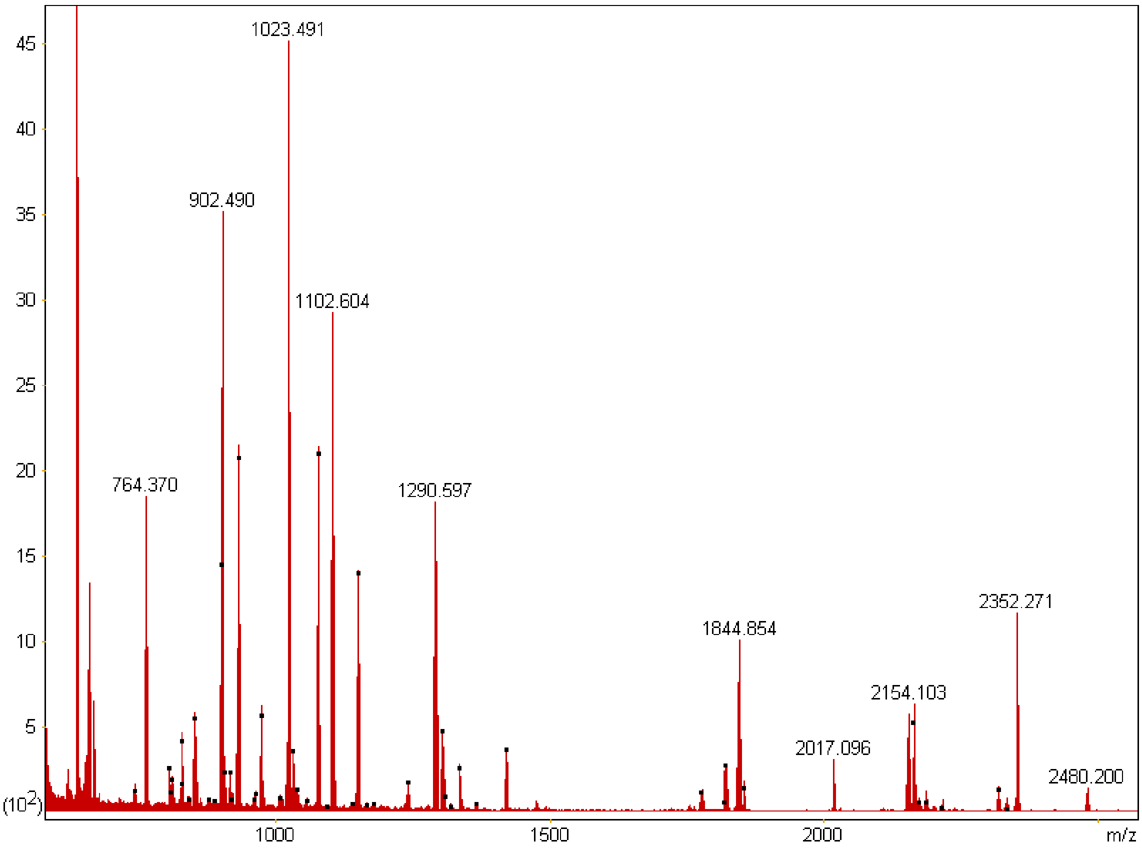
Mascot score: **84** Sequence coverage %: **20**

NCBI accession No.: **gi| 152207441**

Matched peptides No.: **14** Total peptides No.: **51**

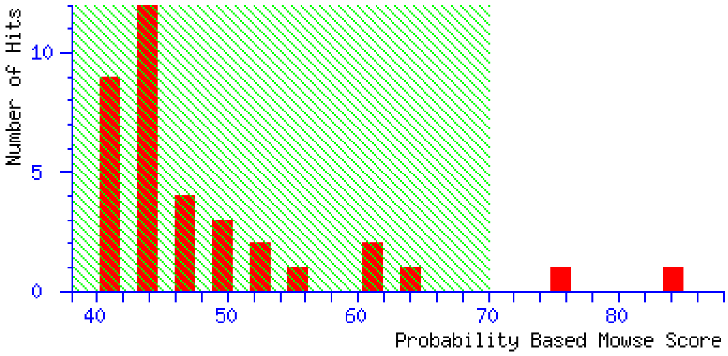
Calculated Mr: **62750** Calculated *p*I: **8.71**

Annotated PMF **spectra:**

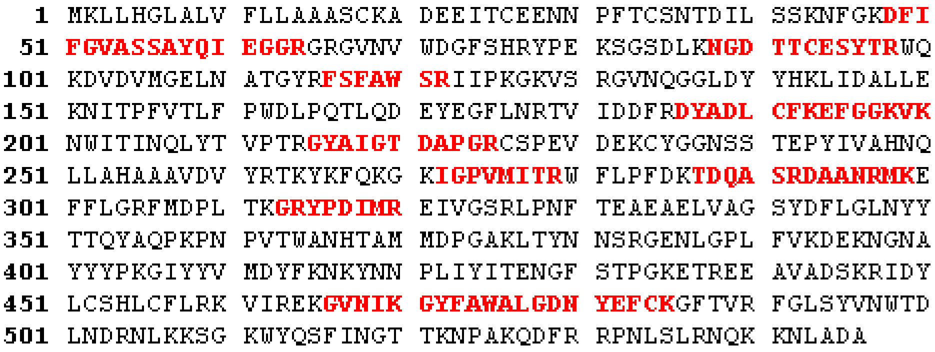


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

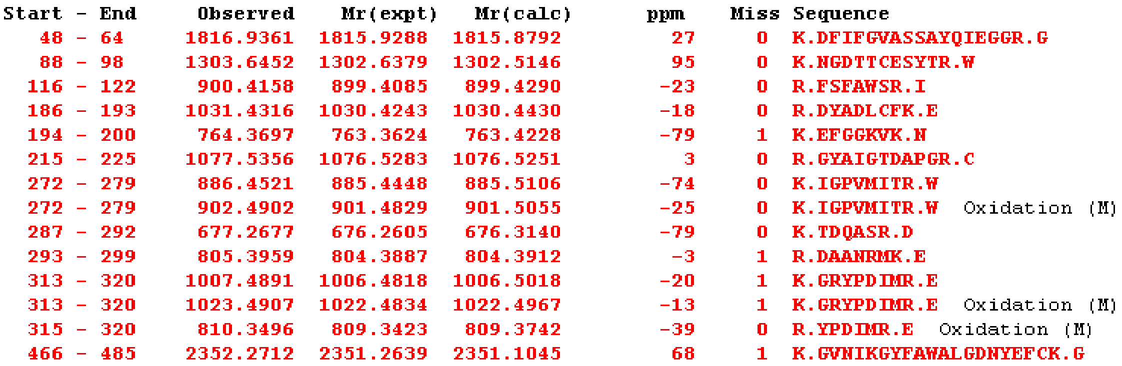


Matched peptide sequences: shown in Bold Red



```
  1 MKLLHGLALV FLLAAASCKA DEEITCEENN PFTCSNTDIL SSKNFGKDFI
 51 FGVASSAYQI EGGRGRGVNV WDGFSHRYPE KSGSDLKNGD TTCESYTRWQ
101 KDVDVMGELN ATGYRFSFAW SRIIPKGKVS RGVNQGGLDY YHKLIDALLE
151 KNITPFVTLF PWDLPQTLQD EYEGFLNRTV IDDFRDYADL CFKEFGGKVK
201 NWITINQLYT VPTRGYAIGT DAPGRCSPEV DEKCYGGNSS TEPYIVAHNQ
251 LLAHAAAVDV YRTKYKFQKG KIGPVMITRW FLPFDKTDQA SRDAANRMKE
301 FFLGRFMDPL TKGRYPDIMR EIVGSRLPNF TEAEAELVAG SYDFLGLNYY
351 TTQYAQPKPN PVTWANHTAM MDPGAKLTYN NSRGENLGPL FVKDEKNGNA
401 YYYPKGIYYV MDYFKNKYNN PLIYITENGF STPGKETREE AVADSKRIDY
451 LCSHLCFLRK VIREKGVNIK GYFAWALGDN YEFCKGFTVR FGLSYVNWTD
501 LNDRNLKKSG KWYQSFINGT TKNPAKQDFR RPNLSLRNQK KNLADA
```

Matched peptides information:



```
Start - End      Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   48 - 64      1816.9361  1815.9288  1815.8792       27      0  K.DFIFGVASSAYQIEGGR.G
   88 - 98      1303.6452  1302.6379  1302.5146       95      0  K.NGDTTCESYTR.W
  116 - 122      900.4158   899.4085   899.4290      -23      0  R.FSFAWSR.I
  186 - 193     1031.4316  1030.4243  1030.4430      -18      0  R.DYADLCFK.E
  194 - 200      764.3697   763.3624   763.4228      -79      1  K.EFGGKVK.N
  215 - 225     1077.5356  1076.5283  1076.5251        3      0  R.GYAIGTDAPGR.C
  272 - 279      886.4521   885.4448   885.5106      -74      0  K.IGPVMITR.W
  272 - 279      902.4902   901.4829   901.5055      -25      0  K.IGPVMITR.W  Oxidation (M)
  287 - 292      677.2677   676.2605   676.3140      -79      0  K.TDQASR.D
  293 - 299      805.3959   804.3887   804.3912       -3      1  R.DAANRMK.E
  313 - 320     1007.4891  1006.4818  1006.5018      -20      1  K.GRYPDIMR.E
  313 - 320     1023.4907  1022.4834  1022.4967      -13      1  K.GRYPDIMR.E  Oxidation (M)
  315 - 320      810.3496   809.3423   809.3742      -39      0  R.YPDIMR.E  Oxidation (M)
  466 - 485     2352.2712  2351.2639  2351.1045       68      1  K.GVNIKGYFAWALGDNYEFCK.G
```

Spot No.: **45**

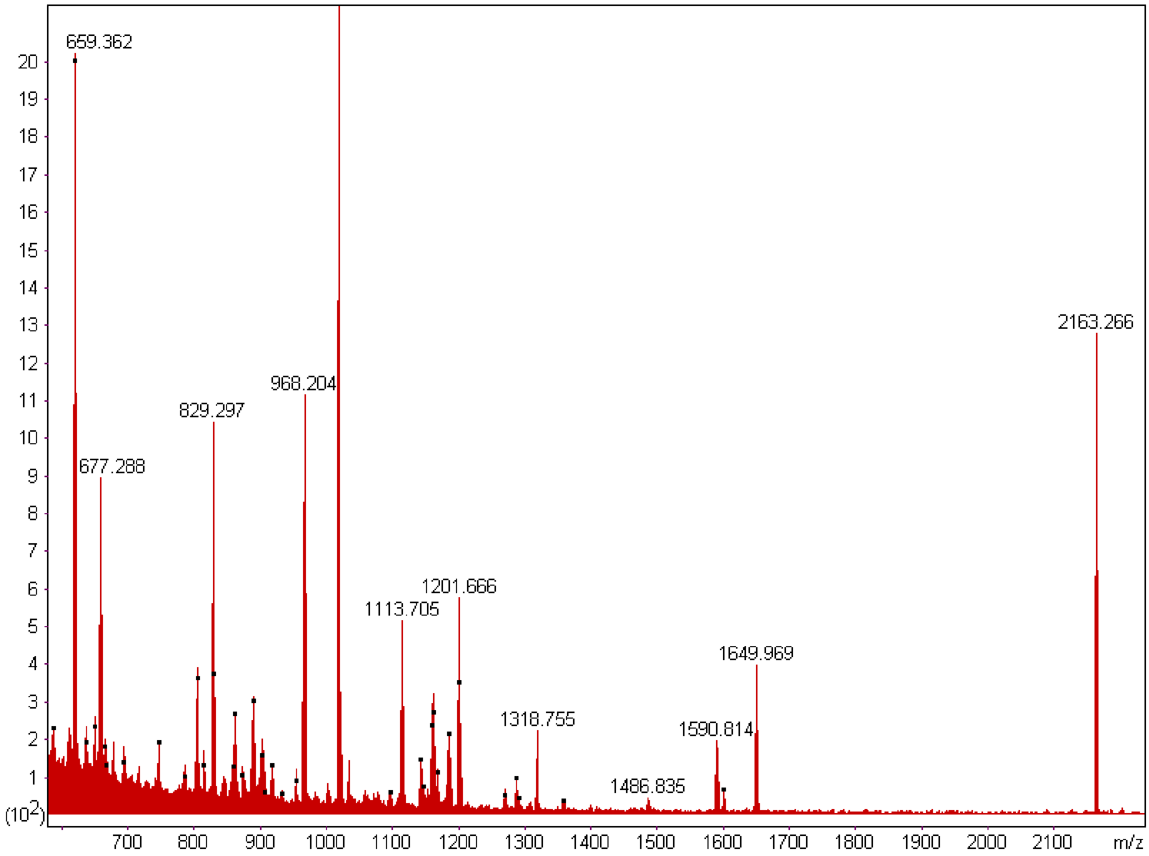
Mascot score: **85**   Sequence coverage %: **19**

NCBI accession No.: **gi| 10177293**

Matched peptides No.: **12**   Total peptides No.: **33**

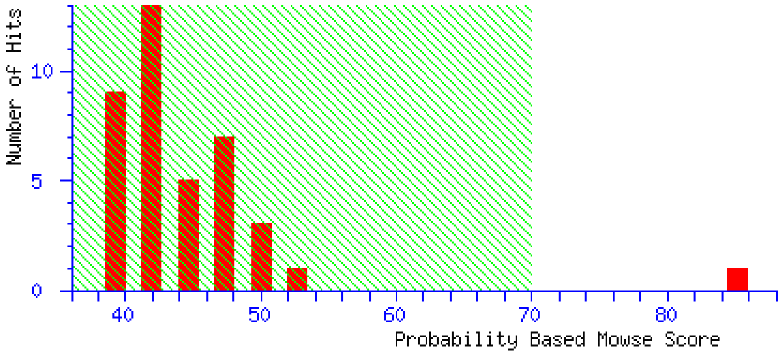
Calculated Mr: **61812**   Calculated *p*I: **9.60**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 MDPSAAPYNP RYTGGGGGYG PSPVMAGDNS GYNRYPSFQP PSGGFSVGRG
51 GGRGGYGQYG DRNGGGNWGG GGGRGGSSK**R** **ELDSVSLPK**Q NFGNLVHFEK
101 NFYVESPTVQ AMTEQDVAMY R**TERDISVEG** **RDVPKPMK**MF QDANFPDNIL
151 EAIAKLGFTE PTPIQAQGWP MALKGR**DLIG** **IAETGSGK**TL AYLLPALVHV
201 SAQPRLGQDD GPIVLILAPT RELAVQIQEE SR**KFGLR**SGV RSTCIYGGAP
251 K**GPQIRDLR**R GVEIVIATPG RLIDMLECQH TNLKRVTYLV LDEADRMLDM
301 GFEPQIRKIV SQIRPDR**QTL** **LWSATWPR**EV ETLARQFLRD PYK**AIIGSTD**
351 **LK**ANQSINQV IEIVPTPEKY NRLLTLLKQL MDGSKILIFV ETKRGCDQVT
401 RQLRMDGWPA LAIHGDKTQS ERDRVLAEFK SGRSPIMTAT DVAARGLDVK
451 DIKCVVNYDF PNTLEDYIHR **IGRTGR**AGAK **GMAFTFFTHD** **NAKFARELVK**
501 ILQEAGQVVP PTLSALVRSS GSGYGGSGGG RNFRPRGGGR GGGFGDKRSR
551 **STSNFVPHGG** **KR**TW

Matched peptides information:

Start – End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
80 – 89	1143.6475	1142.6402	1142.6295	9	1	K.RELDSVSLPK.Q	
122 – 131	1161.6444	1160.6371	1160.5786	50	1	R.TERDISVEGR.D	
132 – 138	830.5137	829.5064	829.4368	84	0	R.DVPKPMK.M	Oxidation (M)
177 – 188	1160.6395	1159.6322	1159.6085	20	0	R.DLIGIAETGSGK.T	
233 – 237	620.3546	619.3473	619.3806	-54	1	R.KFGLR.S	
252 – 259	954.5522	953.5449	953.5406	5	1	K.GPQIRDLR.R	
318 – 328	1358.7645	1357.7572	1357.7143	32	0	R.QTLLWSATWPR.E	
344 – 352	917.3328	916.3256	916.5229	-215	0	K.AIIGSTDLK.A	
471 – 476	659.3615	658.3542	658.3875	-50	1	R.IGRTGR.A	
481 – 493	1486.8347	1485.8274	1485.6711	105	0	K.GMAFTFFTHDNAK.F	
494 – 500	862.4368	861.4296	861.5072	-90	1	K.FARELVK.I	
551 – 562	1286.7560	1285.7487	1285.6527	75	1	R.STSNFVPHGGKR.T	

Spot No.: **46**

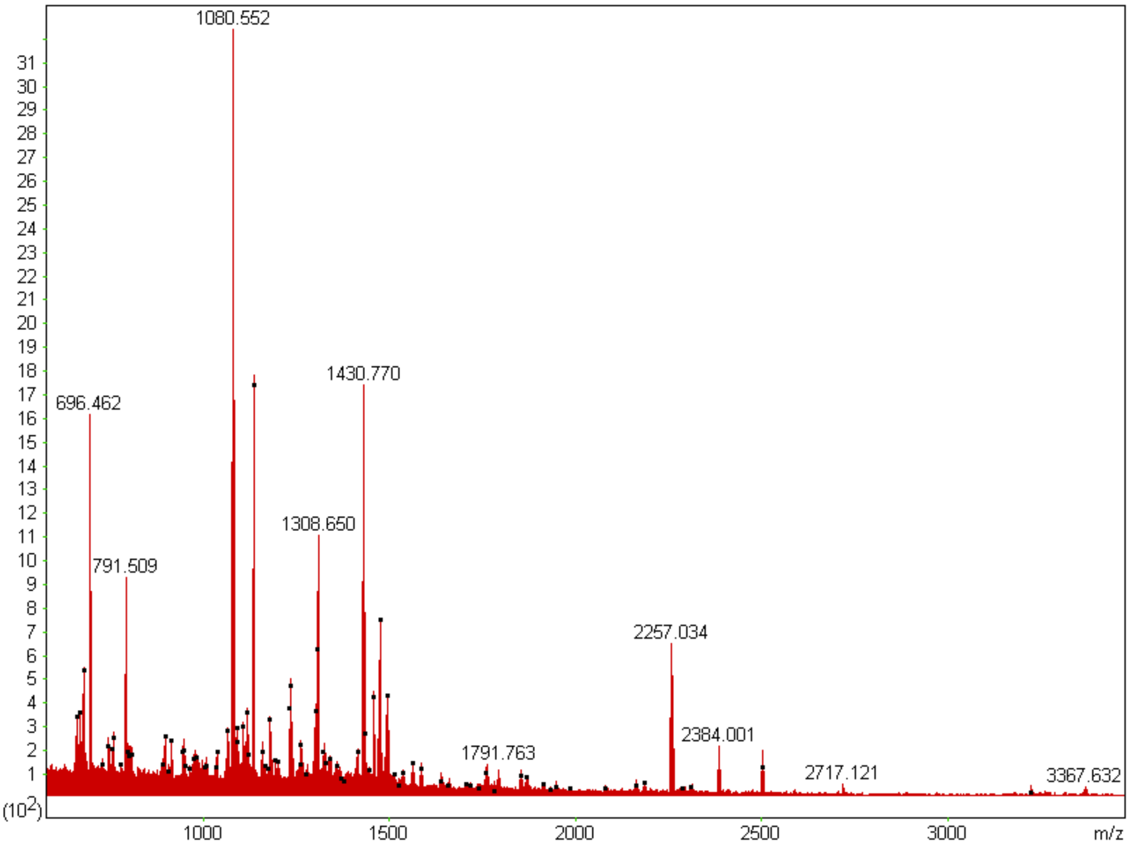
Mascot score: **84** Sequence coverage %: **24**

NCBI accession No.: **gi| 34849893**

Matched peptides No.: **20** Total peptides No.: **76**

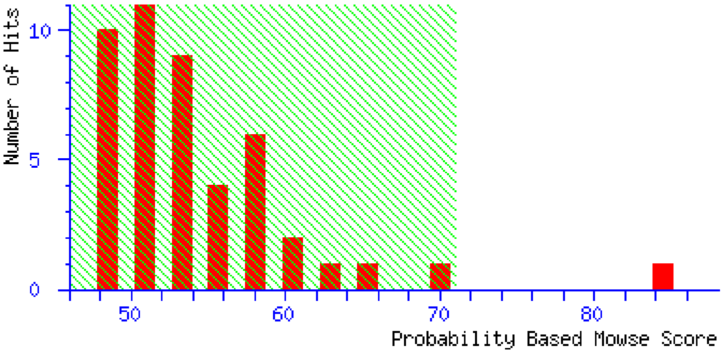
Calculated Mr: **89768** Calculated p*I*: **6.52**

Annotated PMF **spectra:**

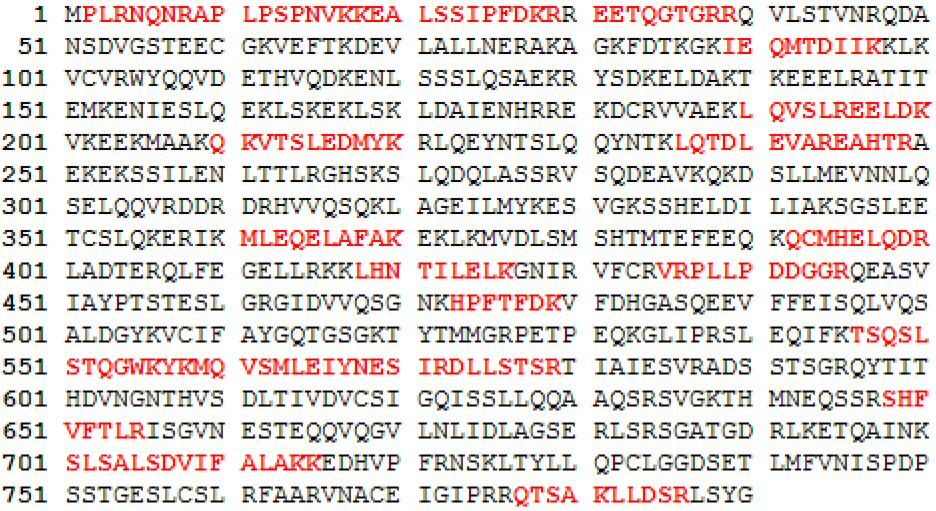


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

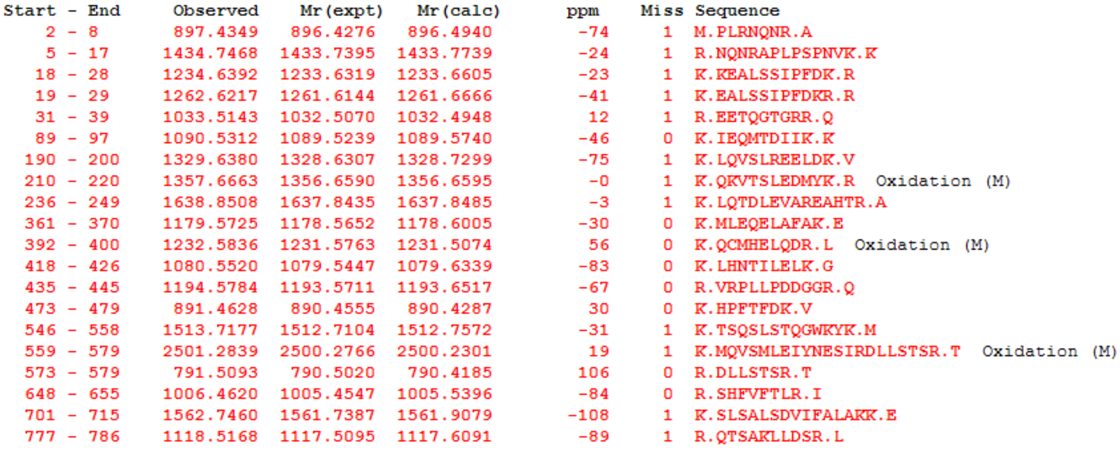


Matched peptide sequences: shown in Bold Red



```
  1 MPLRNQNRAP LPSPNVKKEA LSSIPFDKRR EETQGTGRRQ VLSTVNRQDA
 51 NSDVGSTEEC GKVEFTKDEV LALLNERAKA GKFDTKGKIE QMTDIIKKLK
101 VCVRWYQQVD ETHVQDKENL SSSLQSAEKR YSDKELDAKT KEEELRATIT
151 EMKENIESLQ EKLSKEKLSK LDAIENHRRE KDCRVVAEKL QVSLREELDK
201 VKEEKMAAKQ KVTSLEDMYK RLQEYNTSLQ QYNTKLQTDL EVAREAHTRA
251 EKEKSSILEN LTTLRGHSKS LQDQLASSRV SQDEAVKQKD SLLMEVNNLQ
301 SELQQVRDDR DRHVVQSQKL AGEILMYKES VGKSSHELDI LIAKSGSLEE
351 TCSLQKERIK MLEQELAFAK EKLKMVDLSM SHTMTEFEEQ KQCMHELQDR
401 LADTERQLFE GELLRKKLHN TILELKGNIR VFCRVRPLLP DDGGRQEASV
451 IAYPTSTESL GRGIDVVQSG NKHPFTFDKV FDHGASQEEV FFEISQLVQS
501 ALDGYKVCIF AYGQTGSGKT YTMMGRPETP EQKGLIPRSL EQIFKTSQSL
551 STQGWKYKMQ VSMLEIYNES IRDLLSTSRT IAIESVRADS STSGRQYTIT
601 HDVNGNTHVS DLTIVDVCSI GQISSLLQQA AQSRSVGKTH MNEQSSRSHF
651 VFTLRISGVN ESTEQQVQGV LNLIDLAGSE RLSRSGATGD RLKETQAINK
701 SLSALSDVIF ALAKKEDHVP FRNSKLTYLL QPCLGGDSET LMFVNISPDP
751 SSTGESLCSL RFAARVNACE IGIPRRQTSA KLLDSRLSYG
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss Sequence
    2 - 8       897.4349   896.4276   896.4940      -74      1 M.PLRNQNR.A
    5 - 17     1434.7468  1433.7395  1433.7739      -24      1 R.NQNRAPLPSPNVK.K
   18 - 28     1234.6392  1233.6319  1233.6605      -23      1 K.KEALSSIPFDK.R
   19 - 29     1262.6217  1261.6144  1261.6666      -41      1 K.EALSSIPFDKR.R
   31 - 39     1033.5143  1032.5070  1032.4948       12      1 R.EETQGTGRR.Q
   89 - 97     1090.5312  1089.5239  1089.5740      -46      0 K.IEQMTDIIK.K
  190 - 200    1329.6380  1328.6307  1328.7299      -75      1 K.LQVSLREELDK.V
  210 - 220    1357.6663  1356.6590  1356.6595       -0      1 K.QKVTSLEDMYK.R  Oxidation (M)
  236 - 249    1638.8508  1637.8435  1637.8485       -3      1 K.LQTDLEVAREAHTR.A
  361 - 370    1179.5725  1178.5652  1178.6005      -30      0 K.MLEQELAFAK.E
  392 - 400    1232.5836  1231.5763  1231.5074       56      0 K.QCMHELQDR.L  Oxidation (M)
  418 - 426    1080.5520  1079.5447  1079.6339      -83      0 K.LHNTILELK.G
  435 - 445    1194.5784  1193.5711  1193.6517      -67      0 R.VRPLLPDDGGR.Q
  473 - 479     891.4628   890.4555   890.4287       30      0 K.HPFTFDK.V
  546 - 558    1513.7177  1512.7104  1512.7572      -31      1 K.TSQSLSTQGWKYK.M
  559 - 579    2501.2839  2500.2766  2500.2301       19      1 K.MQVSMLEIYNESIRDLLSTSR.T  Oxidation (M)
  573 - 579     791.5093   790.5020   790.4185      106      0 R.DLLSTSR.T
  648 - 655    1006.4620  1005.4547  1005.5396      -84      0 R.SHFVFTLR.I
  701 - 715    1562.7460  1561.7387  1561.9079     -108      1 K.SLSALSDVIFALAKK.E
  777 - 786    1118.5168  1117.5095  1117.6091      -89      1 R.QTSAKLLDSR.L
```

Spot No.: **47**

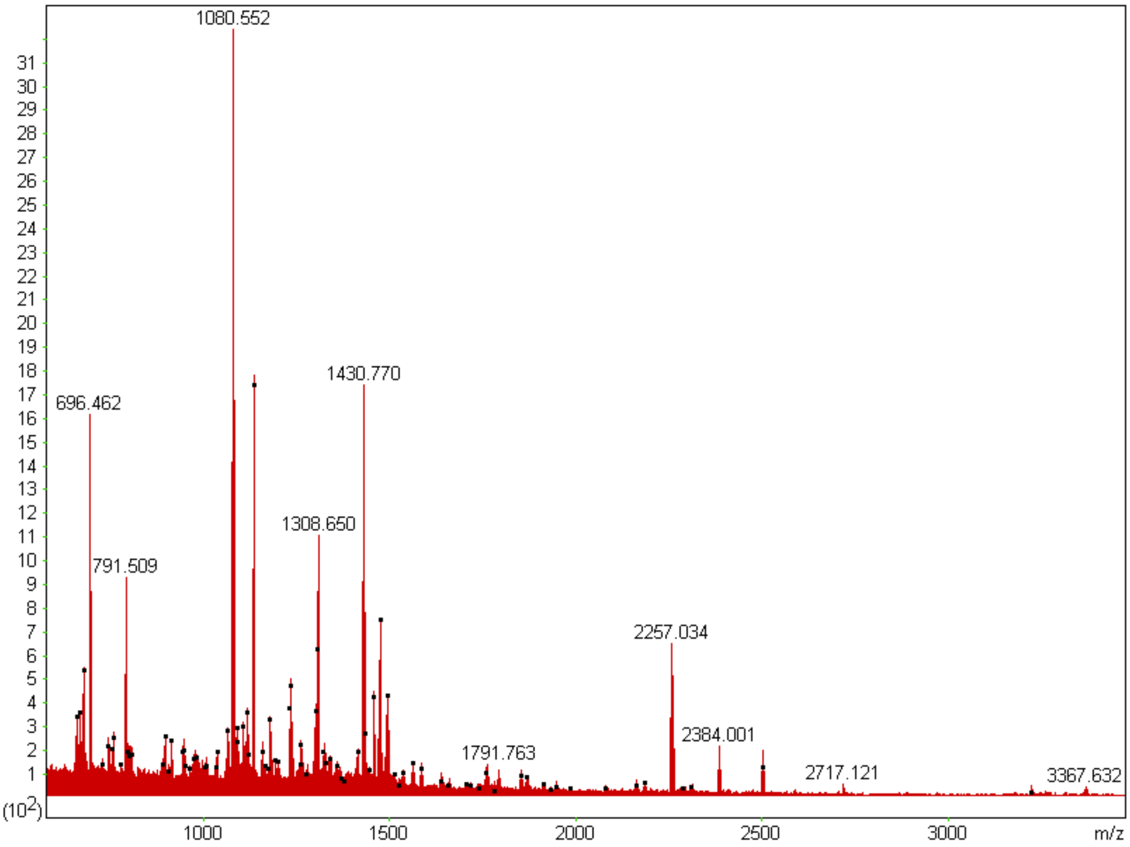
Mascot score: **171** Sequence coverage %: **39**

NCBI accession No.: **gi| 30959098**

Matched peptides No.: **25** Total peptides No.: **108**

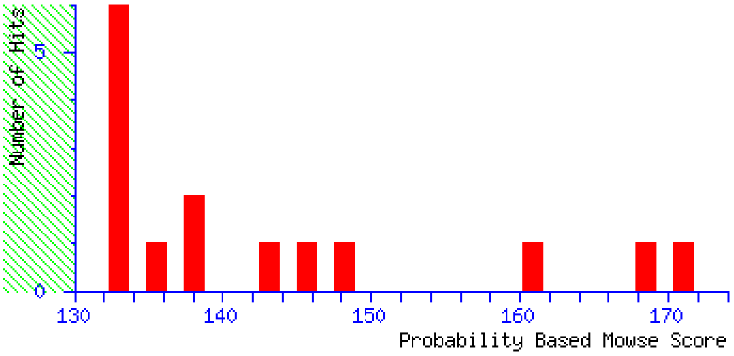
Calculated Mr: **49918** Calculated p*I*: **6.12**

Annotated PMF **spectra:**

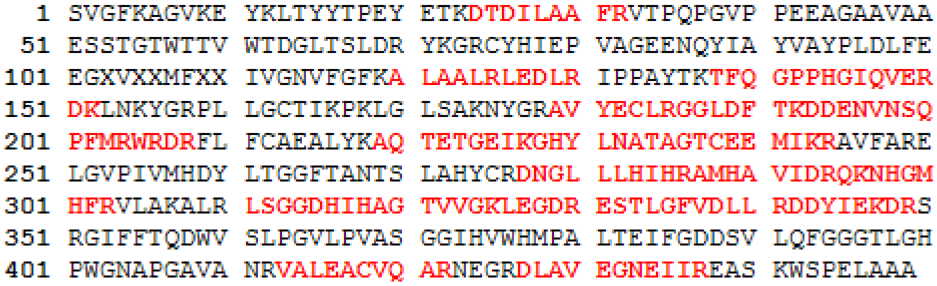


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).

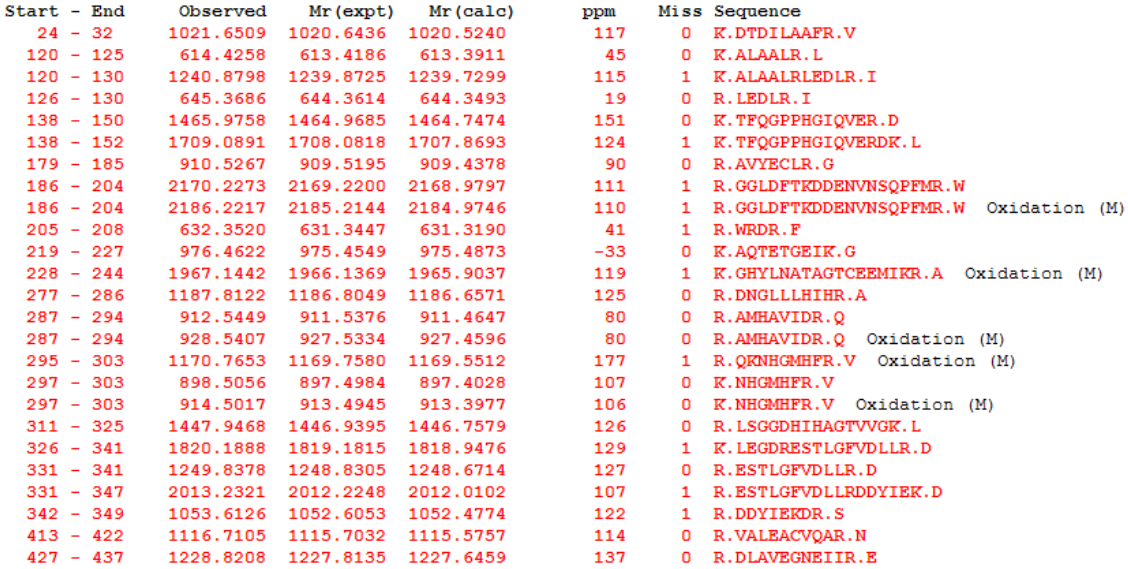


Matched peptide sequences: shown in Bold Red



1 SVGFKAGVKE YKLTYYTPEY ETK**DTDILAA** **FR**VTPQPGVP PEEAGAAVAA
51 ESSTGTWTTV WTDGLTSLDR YKGRCYHIEP VAGEENQYIA YVAYPLDLFE
101 EGXVXXMFXX IVGNVFGFK**A** **LAALRLEDLR** IPPAYTK**TFQ** **GPPHGIQVER**
151 **DK**LNKYGRPL LGCTIKPKLG LSAKNYGR**AV** **YECLRGGLDF** **TKDDENVNSQ**
201 **PFMRWRDR**FL FCAEALYK**AQ** **TETGEIKGHY** **LNATAGTCEE** **MIKR**AVFARE
251 LGVPIVMHDY LTGGFTANTS LAHYCR**DNGL** **LLHIHRAMHA** **VIDRQKNHGM**
301 **HFR**VLAKALR **LSGGDHIHAG** **TVVGKLEGDR** **ESTLGFVDLL** **RDDYIEKDR**S
351 RGIFFTQDWV SLPGVLPVAS GGIHVWHMPA LTEIFGDDSV LQFGGGTLGH
401 PWGNAPGAVA NR**VALEACVQ** **AR**NEGR**DLAV** **EGNEIIR**EAS KWSPELAAA

Matched peptides information:



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Start - End     Observed   Mr(expt)   Mr(calc)     ppm  Miss Sequence
   24 - 32     1021.6509  1020.6436  1020.5240     117    0  K.DTDILAAFR.V
  120 - 125     614.4258   613.4186   613.3911      45    0  K.ALAALR.L
  120 - 130    1240.8798  1239.8725  1239.7299     115    1  K.ALAALRLEDLR.I
  126 - 130     645.3686   644.3614   644.3493      19    0  R.LEDLR.I
  138 - 150    1465.9758  1464.9685  1464.7474     151    0  K.TFQGPPHGIQVER.D
  138 - 152    1709.0891  1708.0818  1707.8693     124    1  K.TFQGPPHGIQVERDK.L
  179 - 185     910.5267   909.5195   909.4378      90    0  R.AVYECLR.G
  186 - 204    2170.2273  2169.2200  2168.9797     111    1  R.GGLDFTKDDENVNSQPFMR.W
  186 - 204    2186.2217  2185.2144  2184.9746     110    1  R.GGLDFTKDDENVNSQPFMR.W  Oxidation (M)
  205 - 208     632.3520   631.3447   631.3190      41    1  R.WRDR.F
  219 - 227     976.4622   975.4549   975.4873     -33    0  K.AQTETGEIK.G
  228 - 244    1967.1442  1966.1369  1965.9037     119    1  K.GHYLNATAGTCEEMIKR.A  Oxidation (M)
  277 - 286    1187.8122  1186.8049  1186.6571     125    0  R.DNGLLLHIHR.A
  287 - 294     912.5449   911.5376   911.4647      80    0  R.AMHAVIDR.Q
  287 - 294     928.5407   927.5334   927.4596      80    0  R.AMHAVIDR.Q  Oxidation (M)
  295 - 303    1170.7653  1169.7580  1169.5512     177    1  R.QKNHGMHFR.V  Oxidation (M)
  297 - 303     898.5056   897.4984   897.4028     107    0  K.NHGMHFR.V
  297 - 303     914.5017   913.4945   913.3977     106    0  K.NHGMHFR.V  Oxidation (M)
  311 - 325    1447.9468  1446.9395  1446.7579     126    0  R.LSGGDHIHAGTVVGK.L
  326 - 341    1820.1888  1819.1815  1818.9476     129    1  K.LEGDRESTLGFVDLLR.D
  331 - 341    1249.8378  1248.8305  1248.6714     127    0  R.ESTLGFVDLLR.D
  331 - 347    2013.2321  2012.2248  2012.0102     107    1  R.ESTLGFVDLLRDDYIEK.D
  342 - 349    1053.6126  1052.6053  1052.4774     122    1  R.DDYIEKDR.S
  413 - 422    1116.7105  1115.7032  1115.5757     114    0  R.VALEACVQAR.N
  427 - 437    1228.8208  1227.8135  1227.6459     137    0  R.DLAVEGNEIIR.E
```

Spot No.: **48**

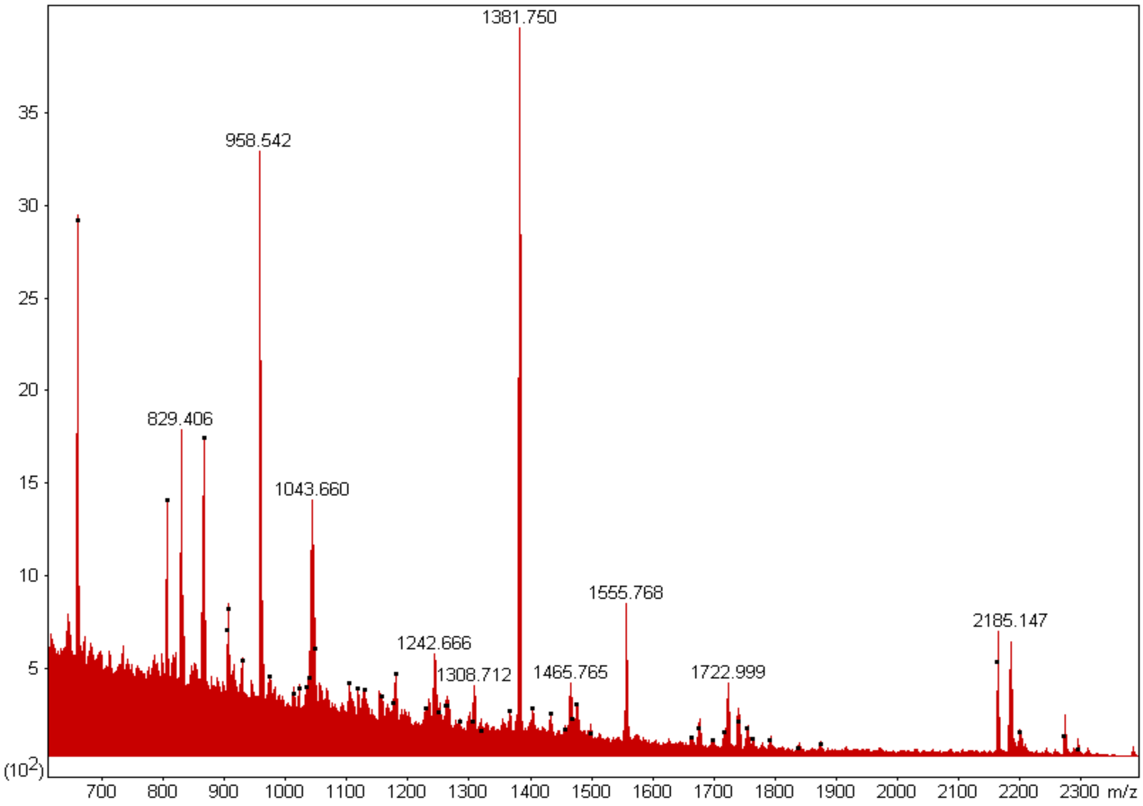
Mascot score: **87**   Sequence coverage %: **23**

NCBI accession No.: **gi| 312282657**

Matched peptides No.: **11**   Total peptides No.: **38**

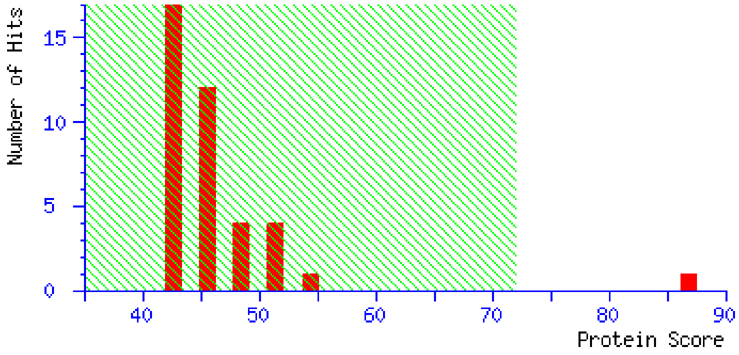
Calculated Mr: **53947**   Calculated *p*I: **6.43**

Annotated PMF **spectra:**

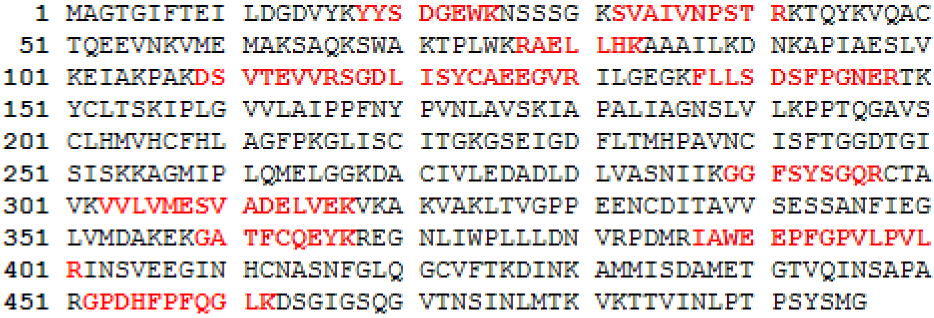


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

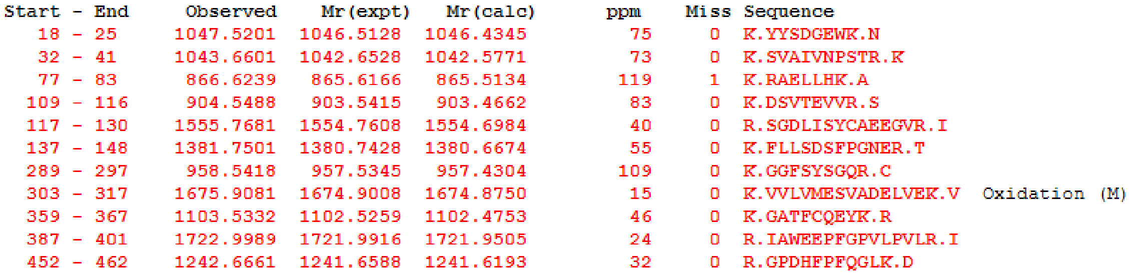


Matched peptide sequences: shown in Bold Red



```
  1 MAGTGIFTEI LDGDVYKYYS DGEWKNSSSG KSVAIVNPST RKTQYKVQAC
 51 TQEEVNKVME MAKSAQKSWA KTPLWKRAEL LHKAAAILKD NKAPIAESLV
101 KEIAKPAKDS VTEVVRSGDL ISYCAEEGVR ILGEGKFLLS DSFPGNERTK
151 YCLTSKIPLG VVLAIPPFNY PVNLAVSKIA PALIAGNSLV LKPPTQGAVS
201 CLHMVHCFHL AGFPKGLISC ITGKGSEIGD FLTMHPAVNC ISFTGGDTGI
251 SISKKAGMIP LQMELGGKDA CIVLEDADLD LVASNIIKGG FSYSGQRCTA
301 VKVVLVMESV ADELVEKVKA KVAKLTVGPP EENCDITAVV SESSANFIEG
351 LVMDAKEKGA TFCQEYKREG NLIWPLLLDN VRPDMRIAWE EPFGPVLPVL
401 RINSVEEGIN HCNASNFGLQ GCVFTKDINK AMMISDAMET GTVQINSAPA
451 RGPDHFPFQG LKDSGIGSQG VTNSINLMTK VKTTVINLPT PSYSMG
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   18 - 25     1047.5201  1046.5128  1046.4345       75     0   K.YYSDGEWK.N
   32 - 41     1043.6601  1042.6528  1042.5771       73     0   K.SVAIVNPSTR.K
   77 - 83      866.6239   865.6166   865.5134      119     1   K.RAELLHK.A
  109 - 116     904.5488   903.5415   903.4662       83     0   K.DSVTEVVR.S
  117 - 130    1555.7681  1554.7608  1554.6984       40     0   R.SGDLISYCAEEGVR.I
  137 - 148    1381.7501  1380.7428  1380.6674       55     0   K.FLLSDSFPGNER.T
  289 - 297     958.5418   957.5345   957.4304      109     0   K.GGFSYSGQR.C
  303 - 317    1675.9081  1674.9008  1674.8750       15     0   K.VVLVMESVADELVEK.V  Oxidation (M)
  359 - 367    1103.5332  1102.5259  1102.4753       46     0   K.GATFCQEYK.R
  387 - 401    1722.9989  1721.9916  1721.9505       24     0   R.IAWEEPFGPVLPVLR.I
  452 - 462    1242.6661  1241.6588  1241.6193       32     0   R.GPDHFPFQGLK.D
```

Spot No.: **49**

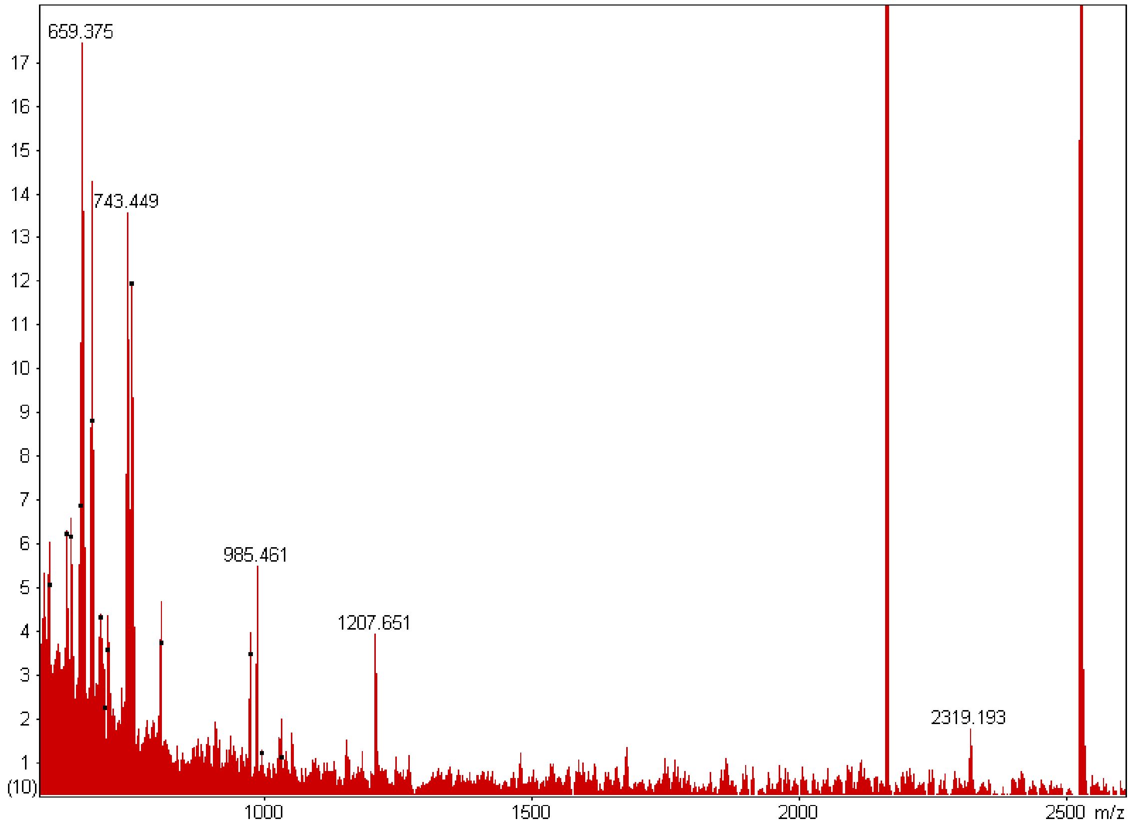
Mascot score: **82**   Sequence coverage %: **14**

NCBI accession No.: **gi| 4210334**

Matched peptides No.: **7**   Total peptides No.: **13**

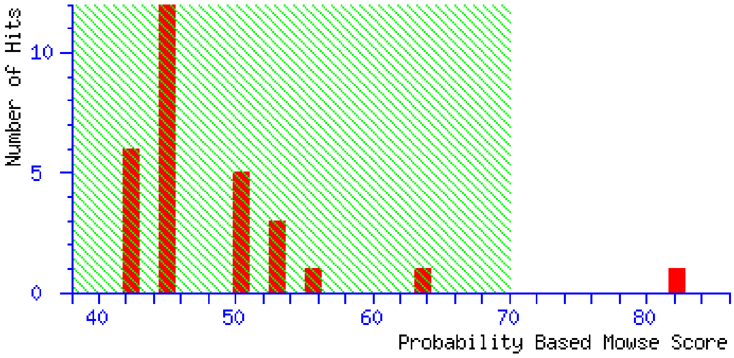
Calculated Mr: **50272**   Calculated *p*I: **6.00**

Annotated PMF **spectra:**

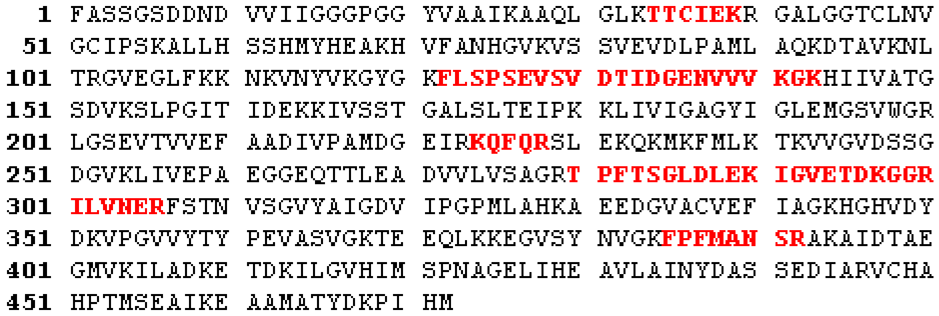


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).

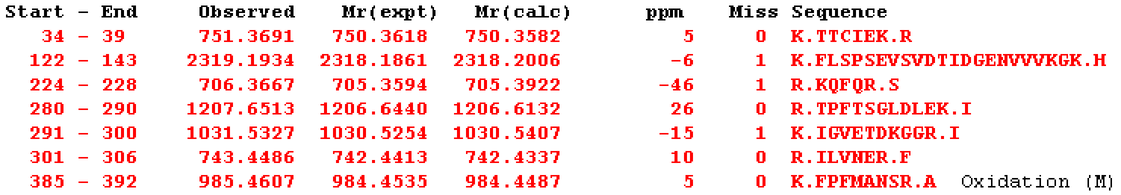


Matched peptide sequences: shown in Bold Red



1 FASSGSDDND VVIIGGGPGG YVAAIKAAQL GLK**TTCIEK**R GALGGTCLNV
51 GCIPSKALLH SSHMYHEAKH VFANHGVKVS SVEVDLPAML AQKDTAVKNL
101 TRGVEGLFKK NKVNYVKGYG K**FLSPSEVSV DTIDGENVVV KGK**HIIVATG
151 SDVKSLPGIT IDEKKIVSST GALSLTEIPK KLIVIGAGYI GLEMGSVWGR
201 LGSEVTVVEF AADIVPAMDG EIR**KQFQR**SL EKQKMKFMLK TKVVGVDSSG
251 DGVKLIVEPA EGGEQTTLEA DVVLVSAGR**T PFTSGLDLEK IGVETDKGGR**
301 **ILVNER**FSTN VSGVYAIGDV IPGPMLAHKA EEDGVACVEF IAGKHGHVDY
351 DKVPGVVYTY PEVASVGKTE EQLKKEGVSY NVGK**FPFMAN SR**AKAIDTAE
401 GMVKILADKE TDKILGVHIM SPNAGELIHE AVLAINYDAS SEDIARVCHA
451 HPTMSEAIKE AAMATYDKPI HM

Matched peptides information:



```
 Start - End      Observed   Mr(expt)   Mr(calc)      ppm   Miss Sequence
    34 - 39       751.3691   750.3618   750.3582        5      0 K.TTCIEK.R
   122 - 143     2319.1934  2318.1861  2318.2006       -6      1 K.FLSPSEVSVDTIDGENVVVKGK.H
   224 - 228      706.3667   705.3594   705.3922      -46      1 R.KQFQR.S
   280 - 290     1207.6513  1206.6440  1206.6132       26      0 R.TPFTSGLDLEK.I
   291 - 300     1031.5327  1030.5254  1030.5407      -15      1 K.IGVETDKGGR.I
   301 - 306      743.4486   742.4413   742.4337       10      0 R.ILVNER.F
   385 - 392      985.4607   984.4535   984.4487        5      0 K.FPFMANSR.A  Oxidation (M)
```

Spot No.: **50**

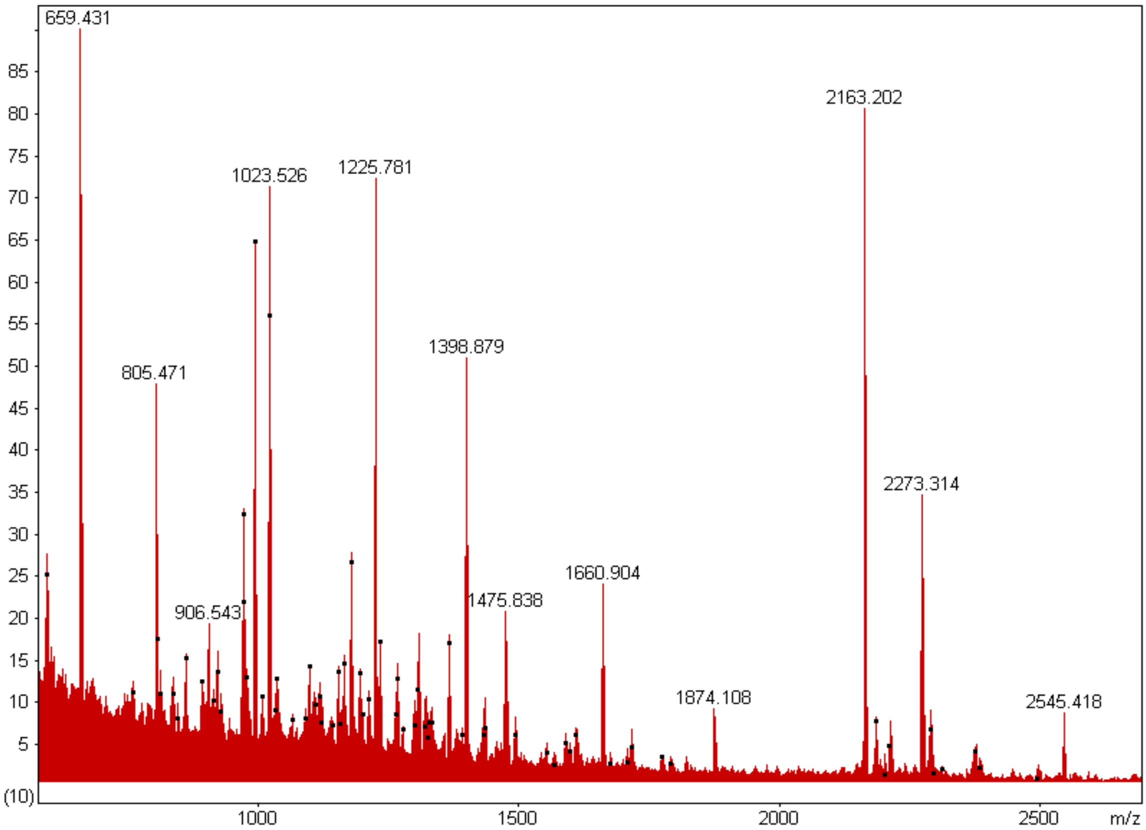
Mascot score: **150** Sequence coverage %: **39**

NCBI accession No.: **gi| 3033398**

Matched peptides No.: **18** Total peptides No.: **57**

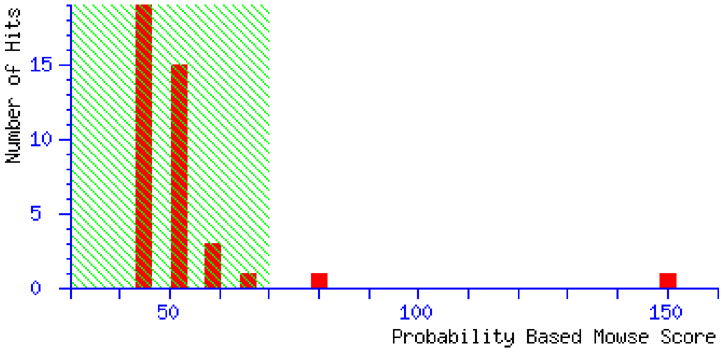
Calculated Mr: **59890** Calculated *p*I: **5.89**

Annotated PMF **spectra:**

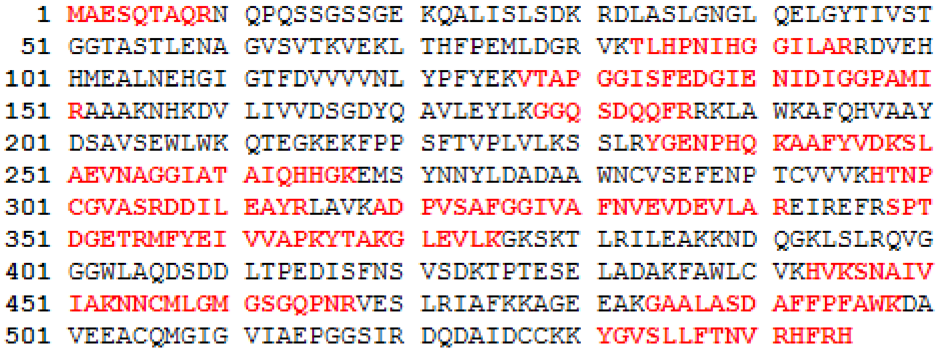


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

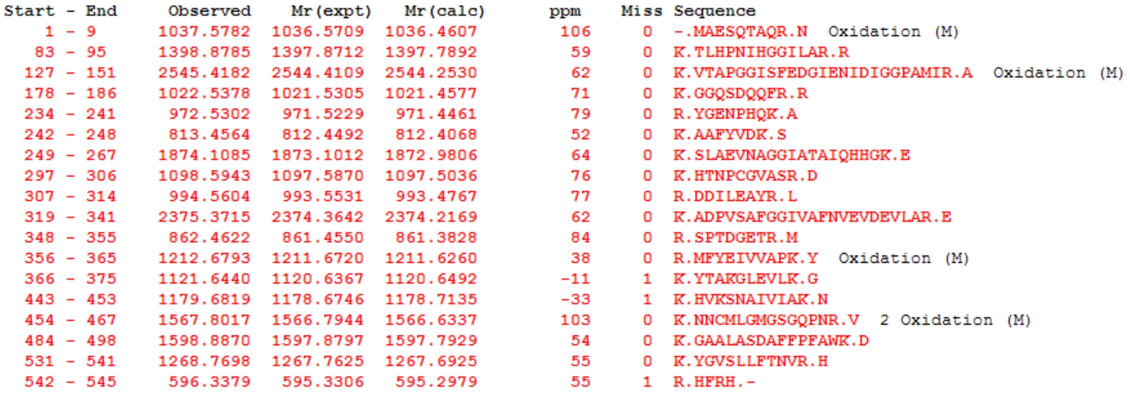


Matched peptide sequences: shown in Bold Red



```
  1 MAESQTAQRN QPQSSGSSGE KQALISLSDK RDLASLGNGL QELGYTIVST
 51 GGTASTLENA GVSVTKVEKL THFPEMLDGR VKTLHPNIHG GILARRDVEH
101 HMEALNEHGI GTFDVVVVNL YPFYEKVTAP GGISFEDGIE NIDIGGPAMI
151 RAAAKNHKDV LIVVDSGDYQ AVLEYLKGGQ SDQQFRRKLA WKAFQHVAAY
201 DSAVSEWLWK QTEGKEKFPP SFTVPLVLKS SLRYGENPHQ KAAFYVDKSL
251 AEVNAGGIAT AIQHHGKEMS YNNYLDADAA WNCVSEFENP TCVVVKHTNP
301 CGVASRDDIL EAYRLAVKAD PVSAFGGIVA FNVEVDEVLA REIREFRSPT
351 DGETRMFYEI VVAPKYTAKG LEVLKGKSKT LRILEAKKND QGKLSLRQVG
401 GGWLAQDSDD LTPEDISFNS VSDKTPTESE LADAKFAWLC VKHVKSNAIV
451 IAKNNCMLGM GSGQPNRVES LRIAFKKAGE EAKGAALASD AFFPFAWKDA
501 VEEACQMGIG VIAEPGGSIR DQDAIDCCKK YGVSLLFTNV RHFRH
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    1 - 9      1037.5782  1036.5709  1036.4607      106      0  -.MAESQTAQR.N  Oxidation (M)
   83 - 95     1398.8785  1397.8712  1397.7892       59      0  K.TLHPNIHGGILAR.R
  127 - 151    2545.4182  2544.4109  2544.2530       62      0  K.VTAPGGISFEDGIENIDIGGPAMIR.A  Oxidation (M)
  178 - 186    1022.5378  1021.5305  1021.4577       71      0  K.GGQSDQQFR.R
  234 - 241     972.5302   971.5229   971.4461       79      0  R.YGENPHQK.A
  242 - 248     813.4564   812.4492   812.4068       52      0  K.AAFYVDK.S
  249 - 267    1874.1085  1873.1012  1872.9806       64      0  K.SLAEVNAGGIATAIQHHGK.E
  297 - 306    1098.5943  1097.5870  1097.5036       76      0  K.HTNPCGVASR.D
  307 - 314     994.5604   993.5531   993.4767       77      0  R.DDILEAYR.L
  319 - 341    2375.3715  2374.3642  2374.2169       62      0  K.ADPVSAFGGIVAFNVEVDEVLAR.E
  348 - 355     862.4622   861.4550   861.3828       84      0  R.SPTDGETR.M
  356 - 365    1212.6793  1211.6720  1211.6260       38      0  R.MFYEIVVAPK.Y  Oxidation (M)
  366 - 375    1121.6440  1120.6367  1120.6492      -11      1  K.YTAKGLEVLK.G
  443 - 453    1179.6819  1178.6746  1178.7135      -33      1  K.HVKSNAIVIAK.N
  454 - 467    1567.8017  1566.7944  1566.6337      103      0  K.NNCMLGMGSGQPNR.V  2 Oxidation (M)
  484 - 498    1598.8870  1597.8797  1597.7929       54      0  K.GAALASDAFFPFAWK.D
  531 - 541    1268.7698  1267.7625  1267.6925       55      0  K.YGVSLLFTNVR.H
  542 - 545     596.3379   595.3306   595.2979       55      1  R.HFRH.-
```

Spot No.: **51**

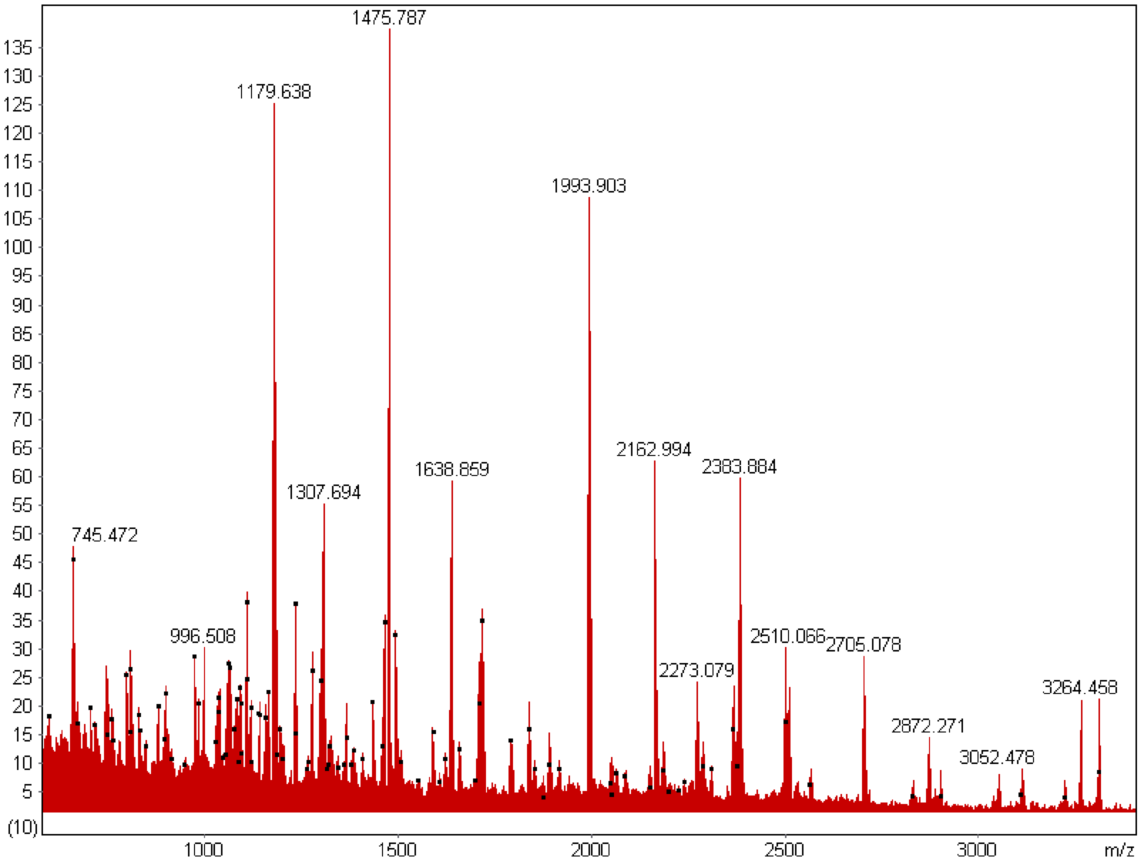
Mascot score: **111** Sequence coverage %: **34**

NCBI accession No.: **gi| 22417145**

Matched peptides No.: **15** Total peptides No.: **66**

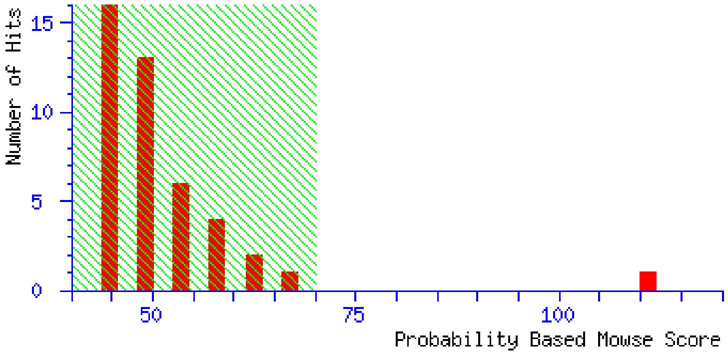
Calculated Mr: **41355** Calculated *p*I: **10.68**

Annotated PMF **spectra:**

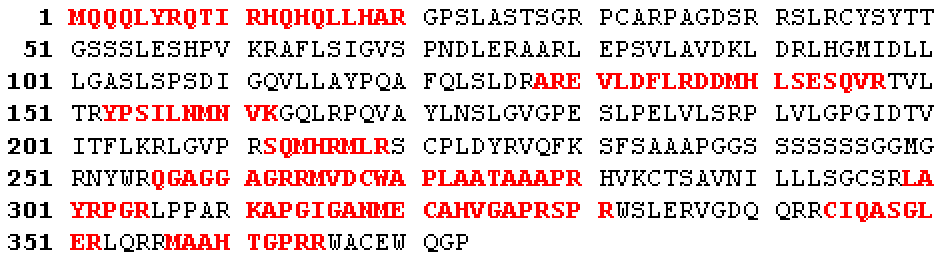


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

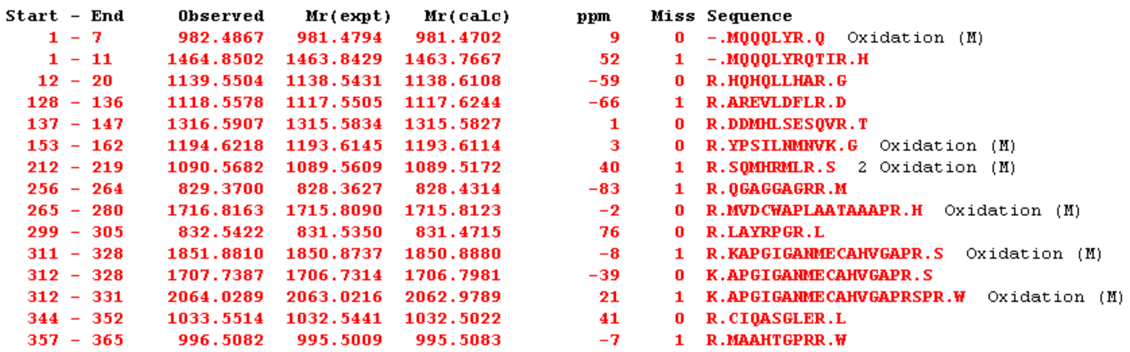


Matched peptide sequences: shown in Bold Red



1 **MQQQLYRQTI** **RHQHQLLHAR** GPSLASTSGR PCARPAGDSR RSLRCYSYTT
51 GSSSLESHPV KRAFLSIGVS PNDLERAARL EPSVLAVDKL DRLHGMIDLL
101 LGASLSPSDI GQVLLAYPQA FQLSLDR**ARE** **VLDFLRDDMH** **LSESQVR**TVL
151 TR**YPSILNMN** **VK**GQLRPQVA YLNSLGVGPE SLPELVLSRP LVLGPGIDTV
201 ITFLKRLGVP R**SQMHRMLR**S CPLDYRVQFK SFSAAAPGGS SSSSSSGGMG
251 RNYWR**QGAGG** **AGRRMVDCWA** **PLAATAAAPR** HVKCTSAVNI LLLSGCSR**LA**
301 **YRPGR**LPPAR **KAPGIGANME** **CAHVGAPRSP** **R**WSLERVGDQ QRR**CIQASGL**
351 **ER**LQRR**MAAH** **TGPRR**WACEW QGP

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
1 - 7	982.4867	981.4794	981.4702	9	0	-.MQQQLYR.Q Oxidation (M)
1 - 11	1464.8502	1463.8429	1463.7667	52	1	-.MQQQLYRQTIR.H
12 - 20	1139.5504	1138.5431	1138.6108	-59	0	R.HQHQLLHAR.G
128 - 136	1118.5578	1117.5505	1117.6244	-66	1	R.AREVLDFLR.D
137 - 147	1316.5907	1315.5834	1315.5827	1	0	R.DDMHLSESQVR.T
153 - 162	1194.6218	1193.6145	1193.6114	3	0	R.YPSILNMNVK.G Oxidation (M)
212 - 219	1090.5682	1089.5609	1089.5172	40	1	R.SQMHRMLR.S 2 Oxidation (M)
256 - 264	829.3700	828.3627	828.4314	-83	1	R.QGAGGAGRR.M
265 - 280	1716.8163	1715.8090	1715.8123	-2	0	R.MVDCWAPLAATAAAPR.H Oxidation (M)
299 - 305	832.5422	831.5350	831.4715	76	0	R.LAYRPGR.L
311 - 328	1851.8810	1850.8737	1850.8880	-8	1	R.KAPGIGANMECAHVGAPR.S Oxidation (M)
312 - 328	1707.7387	1706.7314	1706.7981	-39	0	K.APGIGANMECAHVGAPR.S
312 - 331	2064.0289	2063.0216	2062.9789	21	1	K.APGIGANMECAHVGAPRSPR.W Oxidation (M)
344 - 352	1033.5514	1032.5441	1032.5022	41	0	R.CIQASGLER.L
357 - 365	996.5082	995.5009	995.5083	-7	1	R.MAAHTGPRR.W

Spot No.: **52**

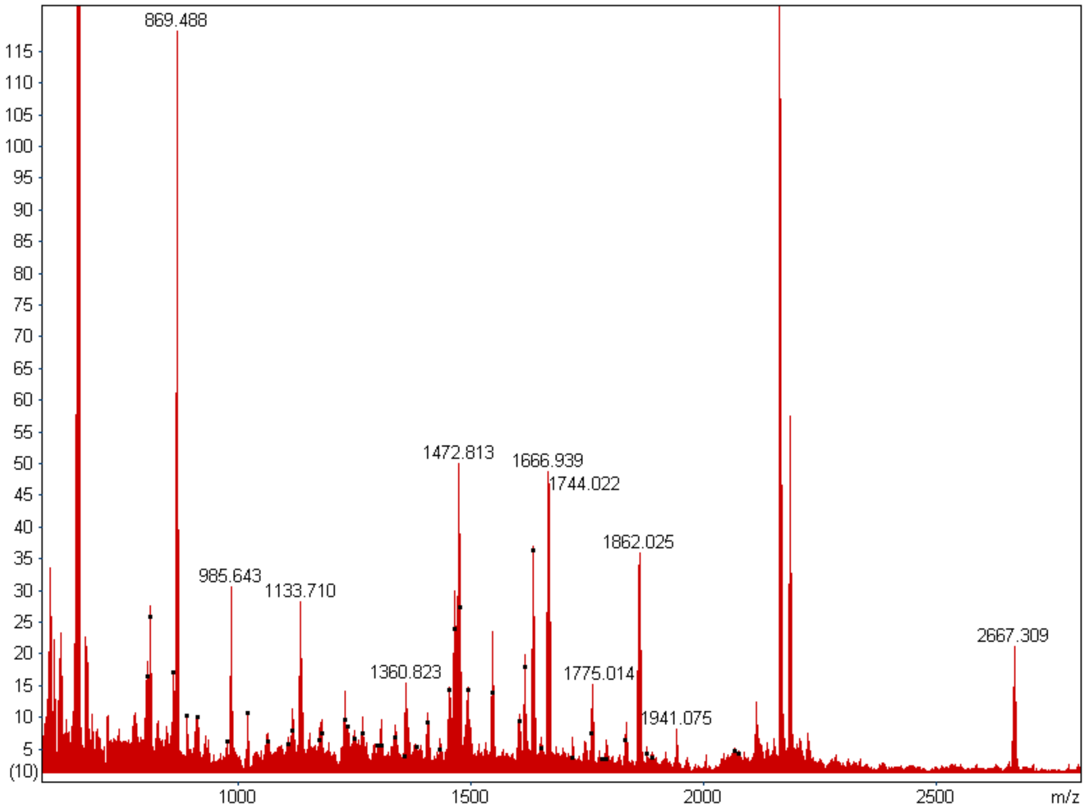
Mascot score: **92** Sequence coverage %: **17**

NCBI accession No.: **gi| 30693102**

Matched peptides No.: **12** Total peptides No.: **30**

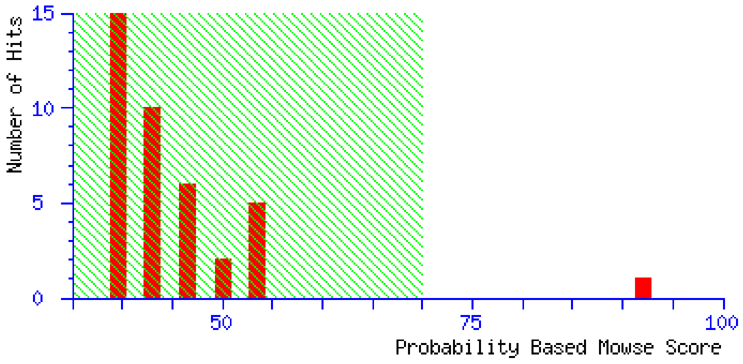
Calculated Mr: **82214** Calculated *p*I: **6.24**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 MGLGILASRT IRPASRLLQS QTSNFFLRTI VSKPELQSPE SAAVSEPEPP
51 TQILPPRNPV GGARVHFSNP EDAIEVFVDG YAVKVPKGFT VLQACEVAGV
101 DIPR**FCYHSR LSIAGNCR**MC LVEVEKSPKP VASCAMPALP GMKIKTDTPI
151 AKKAREGVME FLLMNHPLDC PICDQGGECD LQDQSMAFGS DRGRFTEMKR
201 **SVVDKNLGPL VK**TVMTRCIQ CTRCVRFASE VAGVQDLGIL GRGSGEEIGT
251 YVEKLMTSEL SGNVIDICPV GALTSKPFAF KARNWELKAT ETIDVSDAVG
301 SNIRVDSRGP EVMRIIPR**LN EDINEEWISD KTR**FCYDGLK RQRLSDPMIR
351 DSDGRFKAVS WRDALAVVGD IIHQVKPDEI VGVAGQLSDA ESMMVLK**DFV**
401 **NR**MGSDNVWC EGTAAGVDAD LRYSYLMNTS ISGLENADLF LLIGTQPR**VE**
451 **AAMVNAR**ICK TVRASNAKVG YVGPPAEFNY DCKHLGTGPD TLKEIAEGRH
501 PFCTALKNAK NPAIIVGAGL FNRTDKNAIL SSVESIAQAN NVVRPDWNGL
551 NFLLQYAAQA AALDLGLIQQ SAKALESAKF VYLMGADDVN VDKIPK**DAFV**
601 **VYQGHHGDK**A VYR**ANVILPA SAFTEKEGTY ENTEGFTQQT VPAVPTVGDA**
651 **R**DDWKIVRAL SEVSGVKLPY NSIEGVRSRI K**SVAPNLVHT DER**EPAAFGP
701 SLKPECKEAM STTPFQTVVE NFYMTNSITR ASK**IMAQCSA VLLK**K

Matched peptides information:

Start	–	End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
105	–	110	869.4882	868.4810	868.3650	134	0	R.FCYHSR.L	
111	–	118	890.5136	889.5063	889.4440	70	0	R.LSIAGNCR.M	
201	–	212	1268.7294	1267.7221	1267.7500	-22	1	R.SVVDKNLGPLVK.T	
319	–	331	1604.9052	1603.8979	1603.7365	101	0	R.LNEDINEEWISDK.T	
319	–	333	1862.0254	1861.0181	1860.8853	71	1	R.LNEDINEEWISDKTR.F	
398	–	402	650.3375	649.3302	649.3184	18	0	K.DFVNR.M	
449	–	457	976.6086	975.6014	975.4807	124	0	R.VEAAMVNAR.I	Oxidation (M)
597	–	609	1472.8129	1471.8056	1471.6844	82	0	K.DAFVVYQGHHGDK.A	
614	–	626	1360.8234	1359.8161	1359.7398	56	0	R.ANVILPASAFTEK.E	
627	–	651	2667.3086	2666.3013	2666.2460	21	0	K.EGTYENTEGFTQQTVPAVPTVGDAR.D	
682	–	693	1337.7721	1336.7648	1336.6735	68	0	K.SVAPNLVHTDER.E	
734	–	744	1249.7812	1248.7739	1248.6570	94	0	K.IMAQCSAVLLK.K	Oxidation (M)

Spot No.: **53**

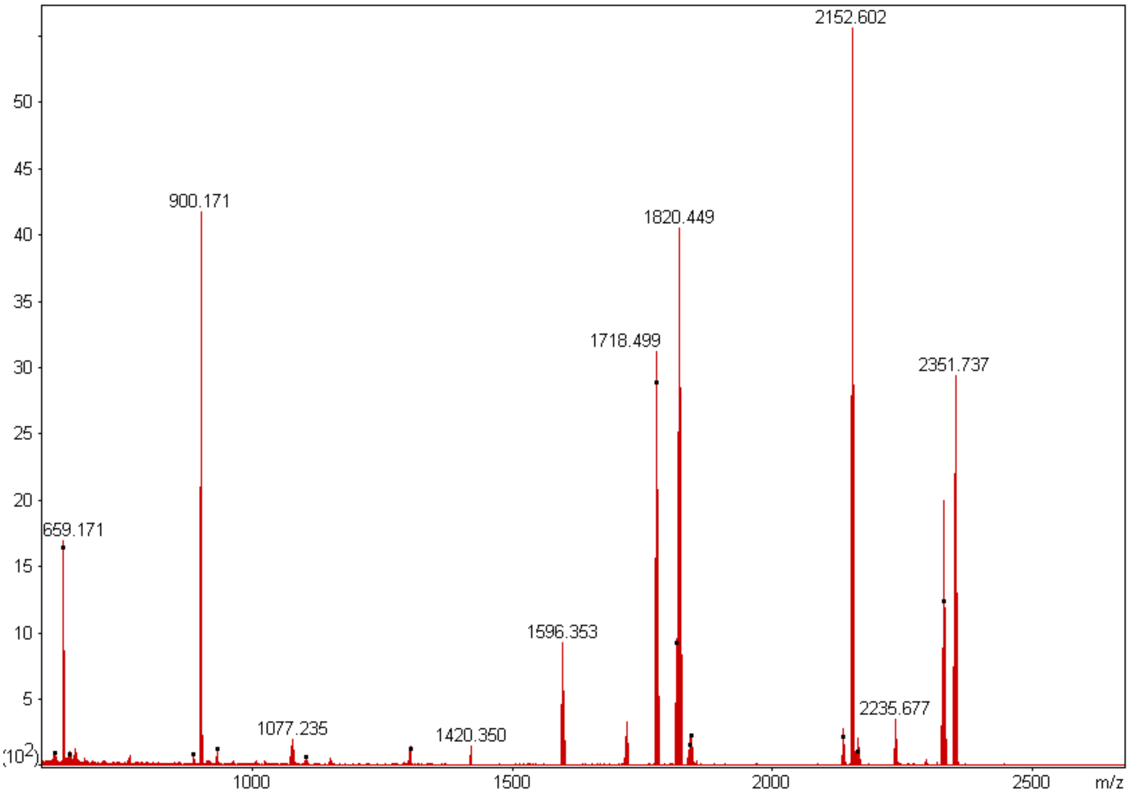
Mascot score: **85**   Sequence coverage %: **19**

NCBI accession No.: **gi| 152207441**

Matched peptides No.: **10**   Total peptides No.: **19**

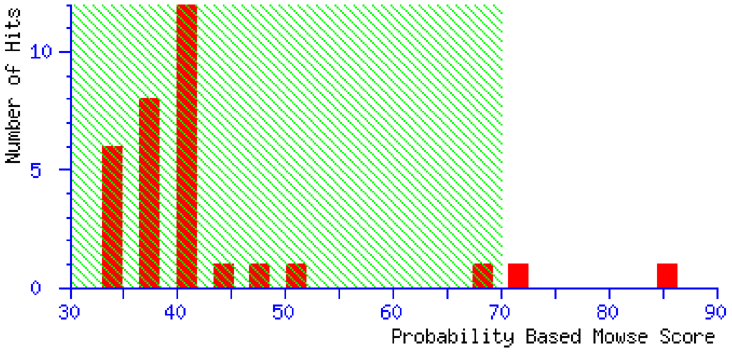
Calculated Mr: **62750**   Calculated *p*I: **8.71**

Annotated PMF **spectra:**

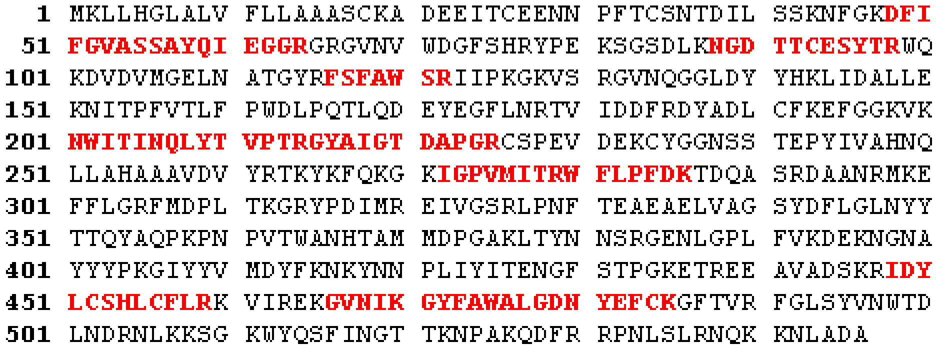


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

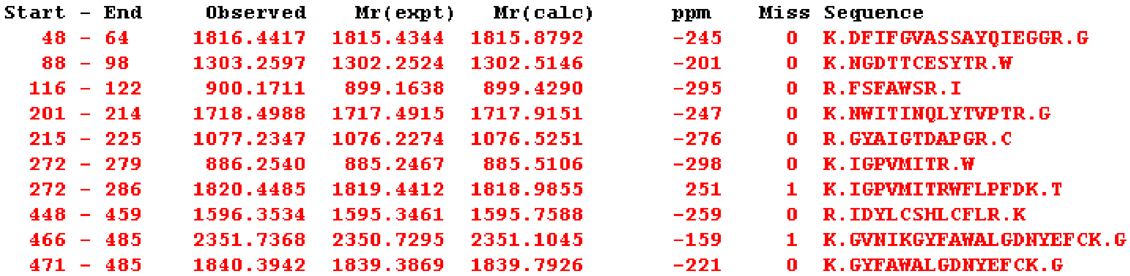


Matched peptide sequences: shown in Bold Red



```
  1 MKLLHGLALV FLLAAASCKA DEEITCEENN PFTCSNTDIL SSKNFGKDFI
 51 FGVASSAYQI EGGRGRGVNV WDGFSHRYPE KSGSDLKNGD TTCESYTRWQ
101 KDVDVMGELN ATGYRFSFAW SRIIPKGKVS RGVNQGGLDY YHKLIDALLE
151 KNITPFVTLF PWDLPQTLQD EYEGFLNRTV IDDFRDYADL CFKEFGGKVK
201 NWITINQLYT VPTRGYAIGT DAPGRCSPEV DEKCYGGNSS TEPYIVAHNQ
251 LLAHAAAVDV YRTKYKFQKG KIGPVMITRW FLPFDKTDQA SRDAANRMKE
301 FFLGRFMDPL TKGRYPDIMR EIVGSRLPNF TEAEAELVAG SYDFLGLNYY
351 TTQYAQPKPN PVTWANHTAM MDPGAKLTYN NSRGENLGPL FVKDEKNGNA
401 YYYPKGIYYV MDYFKNKYNN PLIYITENGF STPGKETREE AVADSKRIDY
451 LCSHLCFLRK VIREKGVNIK GYFAWALGDN YEFCKGFTVR FGLSYVNWTD
501 LNDRNLKKSG KWYQSFINGT TKNPAKQDFR RPNLSLRNQK KNLADA
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   48 - 64     1816.4417  1815.4344  1815.8792     -245     0  K.DFIFGVASSAYQIEGGR.G
   88 - 98     1303.2597  1302.2524  1302.5146     -201     0  K.NGDTTCESYTR.W
  116 - 122     900.1711   899.1638   899.4290     -295     0  R.FSFAWSR.I
  201 - 214    1718.4988  1717.4915  1717.9151     -247     0  K.NWITINQLYTVPTR.G
  215 - 225    1077.2347  1076.2274  1076.5251     -276     0  R.GYAIGTDAPGR.C
  272 - 279     886.2540   885.2467   885.5106     -298     0  K.IGPVMITR.W
  272 - 286    1820.4485  1819.4412  1818.9855      251     1  K.IGPVMITRWFLPFDK.T
  448 - 459    1596.3534  1595.3461  1595.7588     -259     0  R.IDYLCSHLCFLR.K
  466 - 485    2351.7368  2350.7295  2351.1045     -159     1  K.GVNIKGYFAWALGDNYEFCK.G
  471 - 485    1840.3942  1839.3869  1839.7926     -221     0  K.GYFAWALGDNYEFCK.G
```

Spot No.: **54**

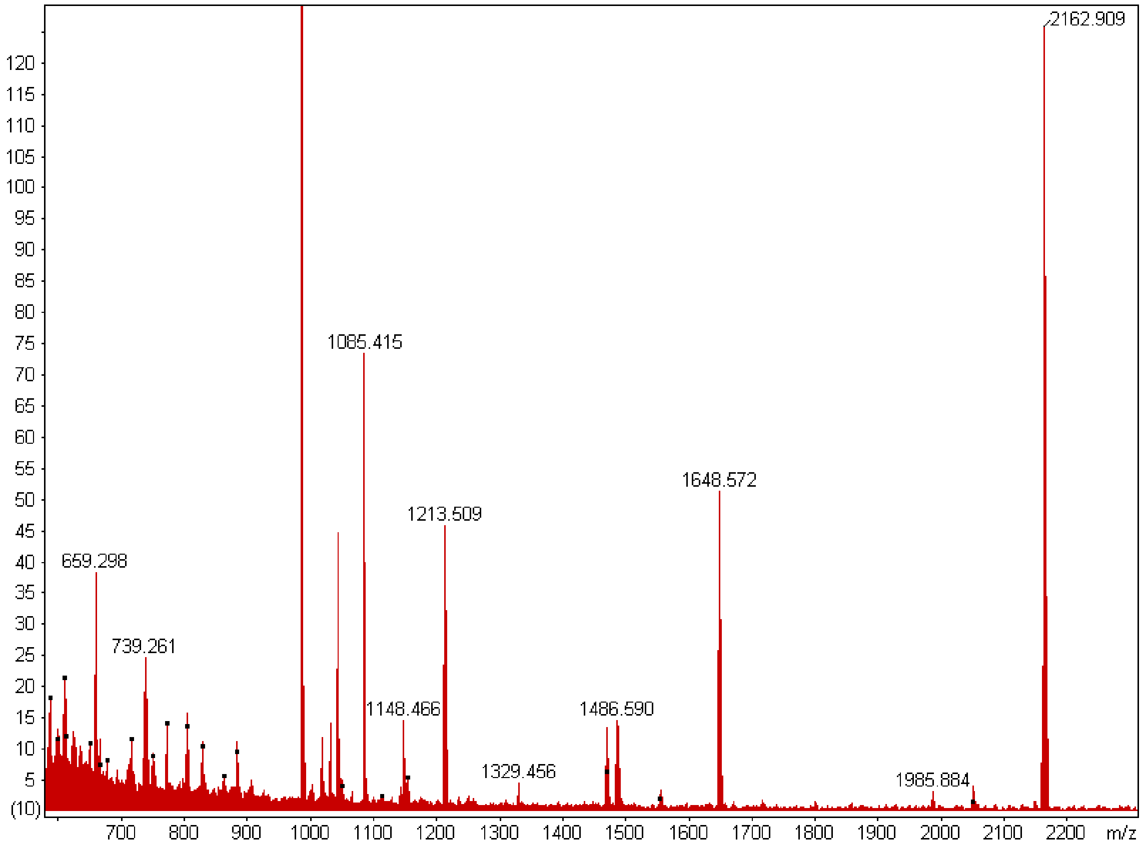
Mascot score: **122** Sequence coverage %: **21**

NCBI accession No.: **gi| 15226573**

Matched peptides No.: **16** Total peptides No.: **38**

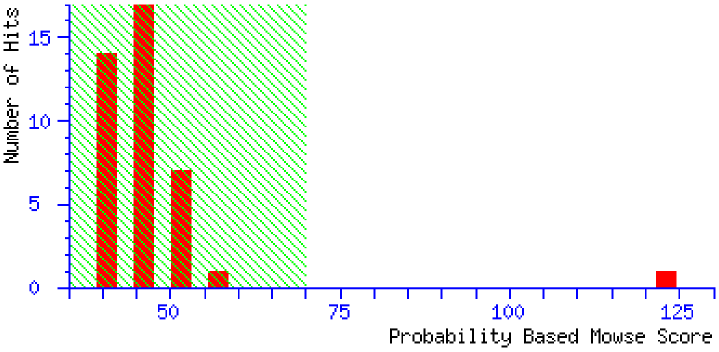
Calculated Mr: **65977** Calculated *p*I: **5.95**

Annotated PMF **spectra:**

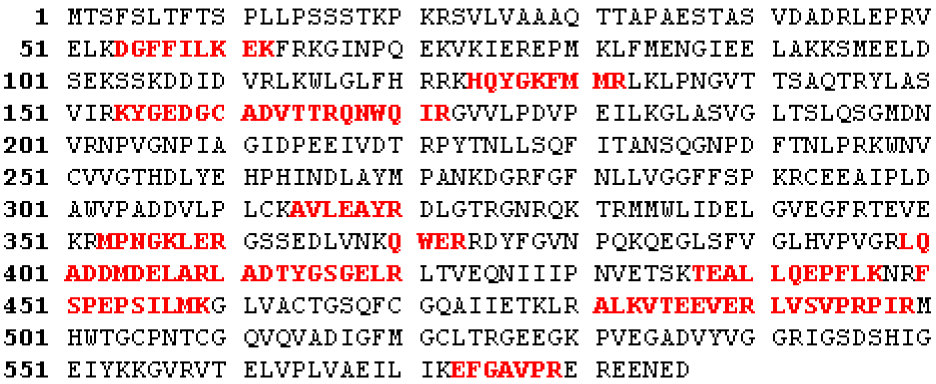


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

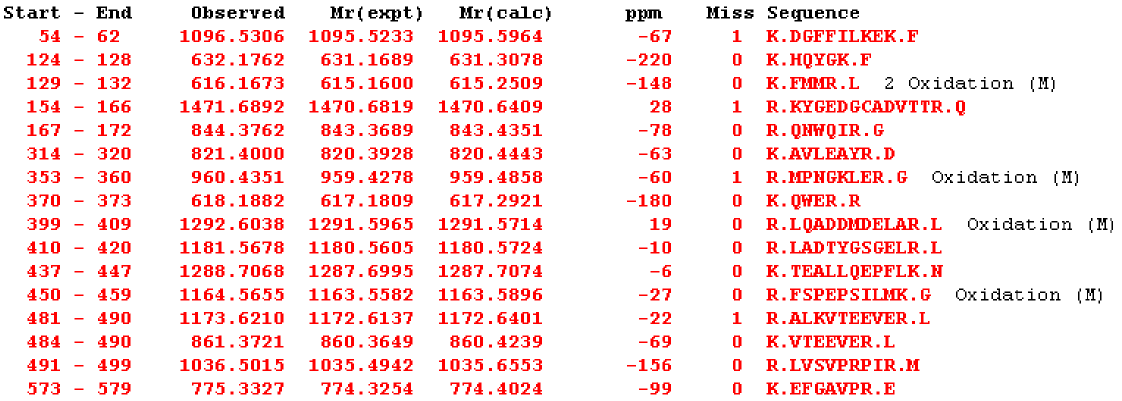


Matched peptide sequences: shown in Bold Red



1 MTSFSLTFTS PLLPSSSTKP KRSVLVAAAQ TTAPAESTAS VDADRLEPRV
51 ELK**DGFFILK** **EK**FRKGINPQ EKVKIEREPM KLFMENGIEE LAKKSMEELD
101 SEKSSKDDID VRLKWLGLFH RRK**HQYGKFM** **MR**LKLPNGVT TSAQTRYLAS
151 VIR**KYGEDGC** **ADVTTRQNWQ** **IR**GVVLPDVP EILKGLASVG LTSLQSGMDN
201 VRNPVGNPIA GIDPEEIVDT RPYTNLLSQF ITANSQGNPD FTNLPRKWNV
251 CVVGTHDLYE HPHINDLAYM PANKDGRFGF NLLVGGFFSP KRCEEAIPLD
301 AWVPADDVLP LCK**AVLEAYR** DLGTRGNRQK TRMMWLIDEL GVEGFRTEVE
351 KR**MPNGKLER** GSSEDLVNK**Q** **WER**RDYFGVN PQKQEGLSFV GLHVPVGR**LQ**
401 **ADDMDELARL** **ADTYGSGELR** LTVEQNIIIP NVETSK**TEAL** **LQEPFLK**NR**F**
451 **SPEPSILMK**G LVACTGSQFC GQAIIETKLR **ALKVTEEVER** **LVSVPRPIR**M
501 HWTGCPNTCG QVQVADIGFM GCLTRGEEGK PVEGADVYVG GRIGSDSHIG
551 EIYKKGVRVT ELVPLVAEIL IK**EFGAVPR**E REENED

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss Sequence
   54 - 62     1096.5306  1095.5233  1095.5964      -67     1  K.DGFFILKEK.F
  124 - 128     632.1762   631.1689   631.3078     -220     0  K.HQYGK.F
  129 - 132     616.1673   615.1600   615.2509     -148     0  K.FMMR.L  2 Oxidation (M)
  154 - 166    1471.6892  1470.6819  1470.6409       28     1  R.KYGEDGCADVTTR.Q
  167 - 172     844.3762   843.3689   843.4351      -78     0  R.QNWQIR.G
  314 - 320     821.4000   820.3928   820.4443      -63     0  K.AVLEAYR.D
  353 - 360     960.4351   959.4278   959.4858      -60     1  R.MPNGKLER.G  Oxidation (M)
  370 - 373     618.1882   617.1809   617.2921     -180     0  K.QWER.R
  399 - 409    1292.6038  1291.5965  1291.5714       19     0  R.LQADDMDELAR.L  Oxidation (M)
  410 - 420    1181.5678  1180.5605  1180.5724      -10     0  R.LADTYGSGELR.L
  437 - 447    1288.7068  1287.6995  1287.7074       -6     0  K.TEALLQEPFLK.N
  450 - 459    1164.5655  1163.5582  1163.5896      -27     0  R.FSPEPSILMK.G  Oxidation (M)
  481 - 490    1173.6210  1172.6137  1172.6401      -22     1  R.ALKVTEEVER.L
  484 - 490     861.3721   860.3649   860.4239      -69     0  K.VTEEVER.L
  491 - 499    1036.5015  1035.4942  1035.6553     -156     0  R.LVSVPRPIR.M
  573 - 579     775.3327   774.3254   774.4024      -99     0  K.EFGAVPR.E
```

Spot No.: **55**

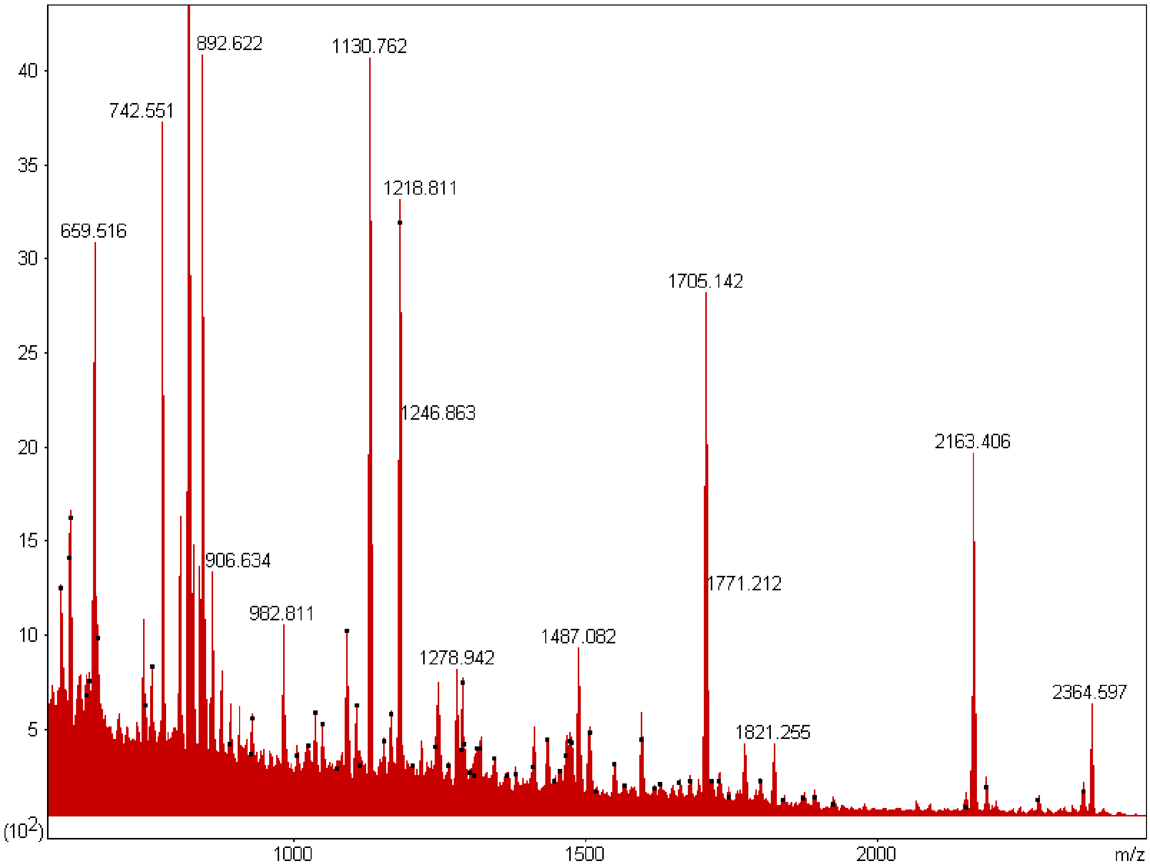
Mascot score: **143** Sequence coverage %: **34**

NCBI accession No.: **gi| 23397093**

Matched peptides No.: **22** Total peptides No.: **87**

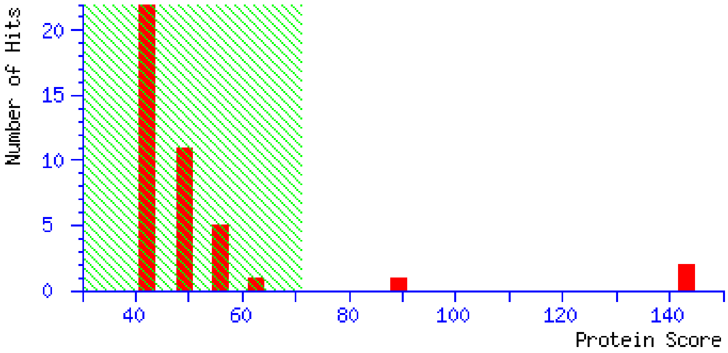
Calculated Mr: **65878** Calculated p*I*: **5.85**

Annotated PMF **spectra:**

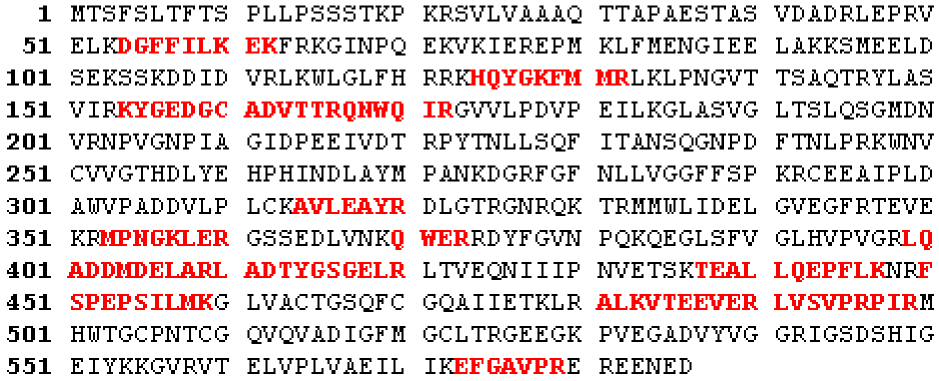


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

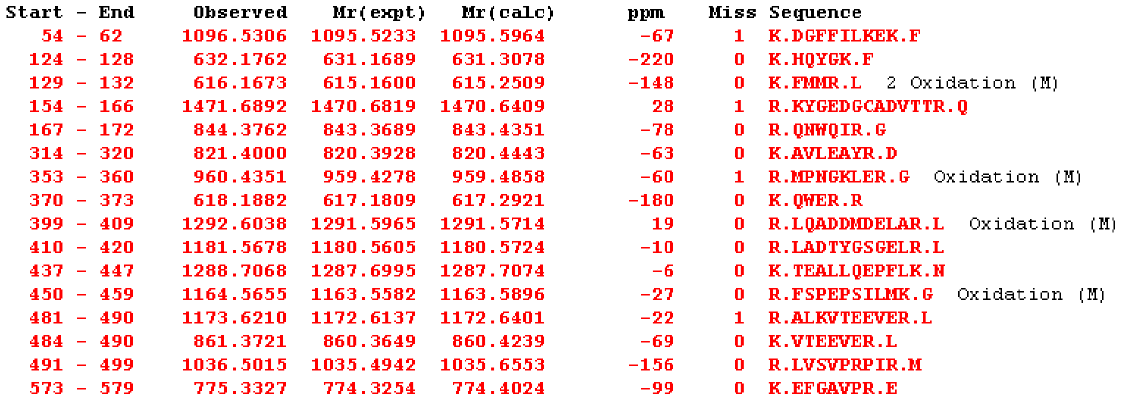


Matched peptide sequences: shown in Bold Red



```
  1 MTSFSLTFTS PLLPSSSTKP KRSVLVAAAQ TTAPAESTAS VDADRLEPRV
 51 ELKDGFFILK EKFRKGINPQ EKVKIEREPM KLFMENGIEE LAKKSMEELD
101 SEKSSKDDID VRLKWLGLFH RRKHQYGKFM MRLKLPNGVT TSAQTRYLAS
151 VIRKYGEDGC ADVTTRQNWQ IRGVVLPDVP EILKGLASVG LTSLQSGMDN
201 VRNPVGNPIA GIDPEEIVDT RPYTNLLSQF ITANSQGNPD FTNLPRKWNV
251 CVVGTHDLYE HPHINDLAYM PANKDGRFGF NLLVGGFFSP KRCEEAIPLD
301 AWVPADDVLP LCKAVLEAYR DLGTRGNRQK TRMMWLIDEL GVEGFRTEVE
351 KRMPNGKLER GSSEDLVNKQ WERRDYFGVN PQKQEGLSFV GLHVPVGRLQ
401 ADDMDELARL ADTYGSGELR LTVEQNIIIP NVETSKTEAL LQEPFLKNRF
451 SPEPSILMKG LVACTGSQFC GQAIIETKLR ALKVTEEVER LVSVPRPIRM
501 HWTGCPNTCG QVQVADIGFM GCLTRGEEGK PVEGADVYVG GRIGSDSHIG
551 EIYKKGVRVT ELVPLVAEIL IKEFGAVPRE REENED
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   54 - 62     1096.5306  1095.5233  1095.5964      -67      1  K.DGFFILKEK.F
  124 - 128     632.1762   631.1689   631.3078     -220      0  K.HQYGK.F
  129 - 132     616.1673   615.1600   615.2509     -148      0  K.FMMR.L  2 Oxidation (M)
  154 - 166    1471.6892  1470.6819  1470.6409       28      1  R.KYGEDGCADVTTR.Q
  167 - 172     844.3762   843.3689   843.4351      -78      0  R.QNWQIR.G
  314 - 320     821.4000   820.3928   820.4443      -63      0  K.AVLEAYR.D
  353 - 360     960.4351   959.4278   959.4858      -60      1  R.MPNGKLER.G  Oxidation (M)
  370 - 373     618.1882   617.1809   617.2921     -180      0  K.QWER.R
  399 - 409    1292.6038  1291.5965  1291.5714       19      0  R.LQADDMDELAR.L  Oxidation (M)
  410 - 420    1181.5678  1180.5605  1180.5724      -10      0  R.LADTYGSGELR.L
  437 - 447    1288.7068  1287.6995  1287.7074       -6      0  K.TEALLQEPFLK.N
  450 - 459    1164.5655  1163.5582  1163.5896      -27      0  R.FSPEPSILMK.G  Oxidation (M)
  481 - 490    1173.6210  1172.6137  1172.6401      -22      1  R.ALKVTEEVER.L
  484 - 490     861.3721   860.3649   860.4239      -69      0  K.VTEEVER.L
  491 - 499    1036.5015  1035.4942  1035.6553     -156      0  R.LVSVPRPIR.M
  573 - 579     775.3327   774.3254   774.4024      -99      0  K.EFGAVPR.E
```

Spot No.: **56**

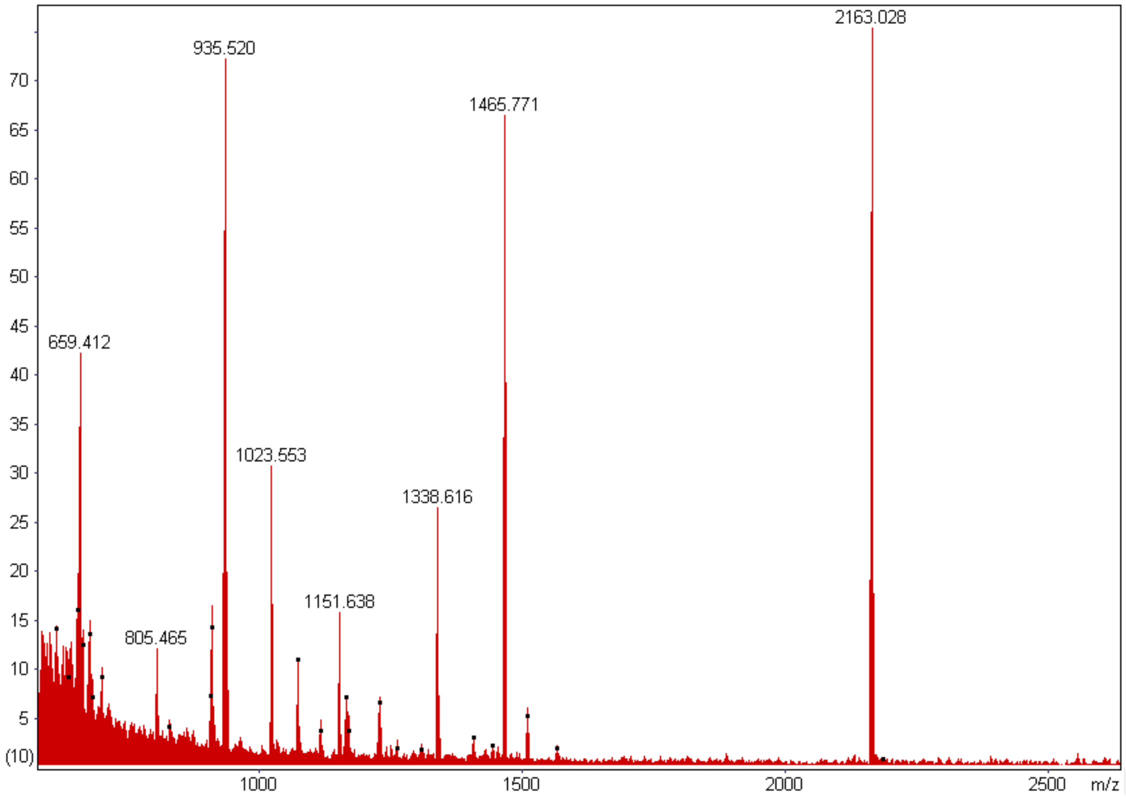
Mascot score: **98** Sequence coverage %: **21**

NCBI accession No.: **gi| 5817375**

Matched peptides No.: **9** Total peptides No.: **20**

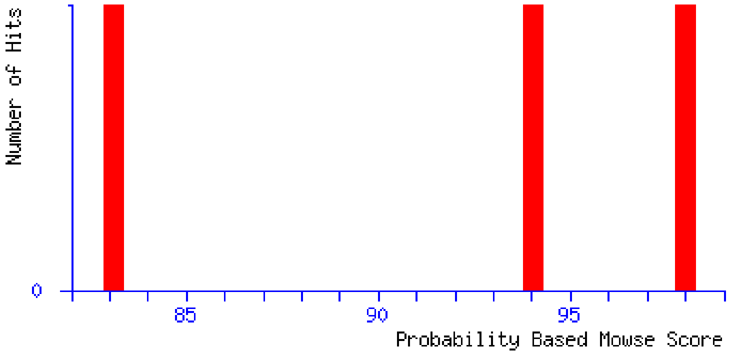
Calculated Mr: **49130** Calculated *p*I: **6.74**

Annotated PMF **spectra:**

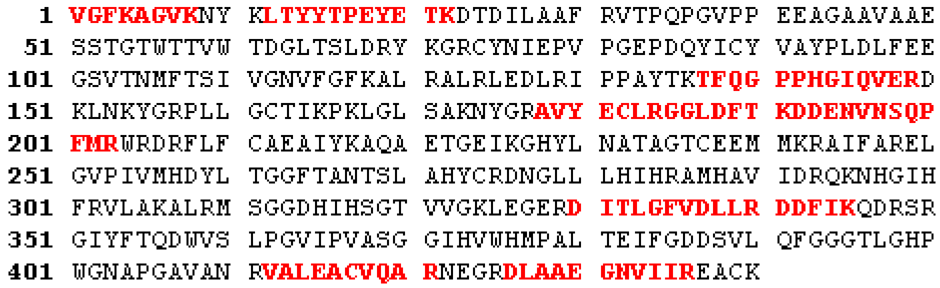


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

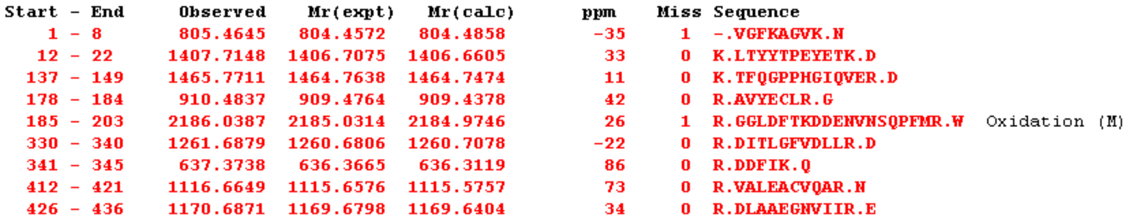


Matched peptide sequences: shown in Bold Red



```
  1 VGFKAGVKNY KLTYYTPEYE TKDTDILAAF RVTPQPGVPP EEAGAAVAAE
 51 SSTGTWTTVW TDGLTSLDRY KGRCYNIEPV PGEPDQYICY VAYPLDLFEE
101 GSVTNMFTSI VGNVFGFKAL RALRLEDLRI PPAYTKTFQG PPHGIQVERD
151 KLNKYGRPLL GCTIKPKLGL SAKNYGRAVY ECLRGGLDFT KDDENVNSQP
201 FMRWRDRFLF CAEAIYKAQA ETGEIKGHYL NATAGTCEEM MKRAIFAREL
251 GVPIVMHDYL TGGFTANTSL AHYCRDNGLL LHIHRAMHAV IDRQKNHGIH
301 FRVLAKALRM SGGDHIHSGT VVGKLEGERD ITLGFVDLLR DDFIKQDRSR
351 GIYFTQDWVS LPGVIPVASG GIHVWHMPAL TEIFGDDSVL QFGGGTLGHP
401 WGNAPGAVAN RVALEACVQA RNEGRDLAAE GNVIIREACK
```

Matched peptides information:



```
Start - End      Observed    Mr(expt)    Mr(calc)       ppm   Miss Sequence
    1 - 8        805.4645    804.4572    804.4858       -35    1   -.VGFKAGVK.N
   12 - 22      1407.7148   1406.7075   1406.6605        33    0   K.LTYYTPEYETK.D
  137 - 149     1465.7711   1464.7638   1464.7474        11    0   K.TFQGPPHGIQVER.D
  178 - 184      910.4837    909.4764    909.4378        42    0   R.AVYECLR.G
  185 - 203     2186.0387   2185.0314   2184.9746        26    1   R.GGLDFTKDDENVNSQPFMR.W  Oxidation (M)
  330 - 340     1261.6879   1260.6806   1260.7078       -22    0   R.DITLGFVDLLR.D
  341 - 345      637.3738    636.3665    636.3119        86    0   R.DDFIK.Q
  412 - 421     1116.6649   1115.6576   1115.5757        73    0   R.VALEACVQAR.N
  426 - 436     1170.6871   1169.6798   1169.6404        34    0   R.DLAAEGNVIIR.E
```

Spot No.: **57**

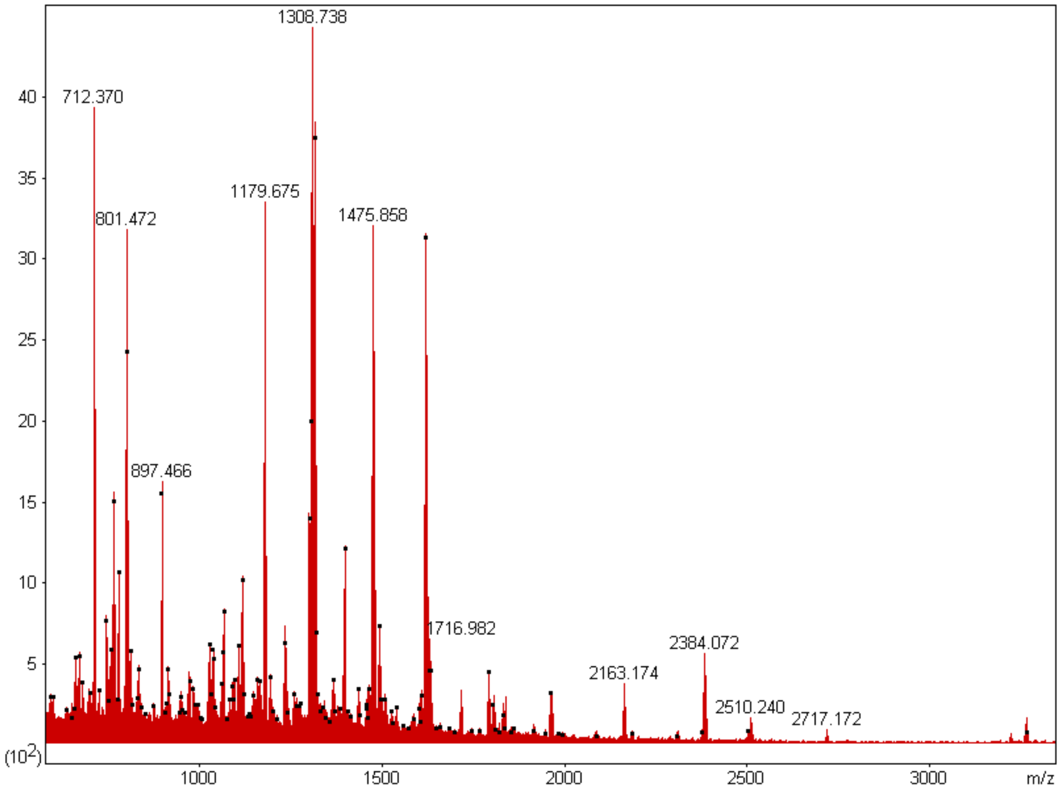
Mascot score: **112** Sequence coverage %: **43**

NCBI accession No.: **gi| 13431553**

Matched peptides No.: **19** Total peptides No.: **114**

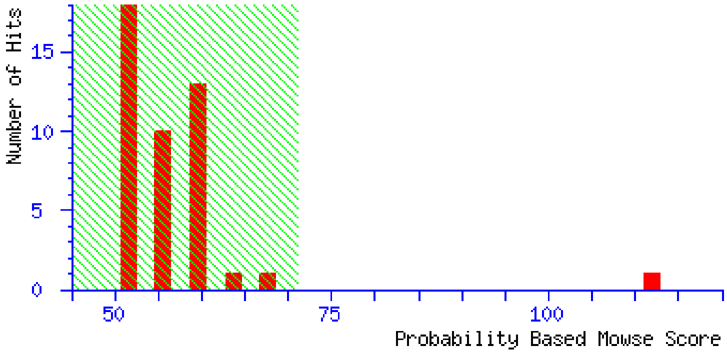
Calculated Mr: **44111** Calculated p*I*: **6.24**

Annotated PMF **spectra:**

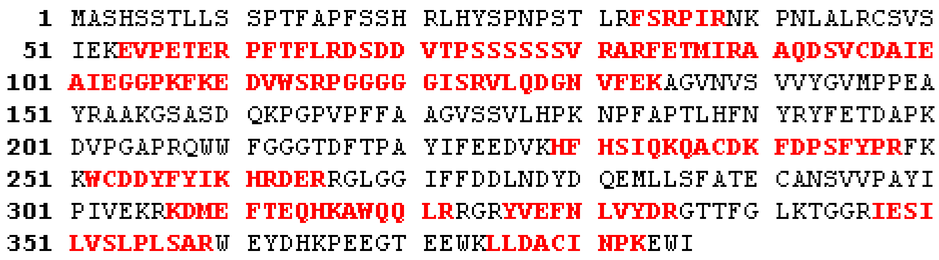


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

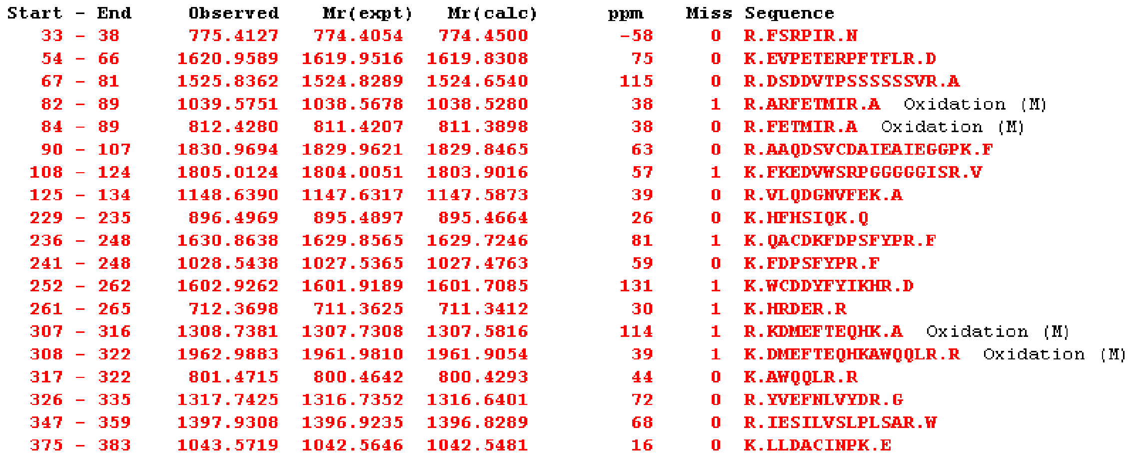


Matched peptide sequences: shown in Bold Red



1 MASHSSTLLS SPTFAPFSSH RLHYSPNPST LR**FSRPIR**NK PNLALRCSVS
51 IEK**EVPETER PFTFLRDSDD VTPSSSSSSV RARFETMIRA AQDSVCDAIE**
101 **AIEGGPKFKE DVWSRPGGGG GISRVLQDGN VFEK**AGVNVS VVYGVMPPEA
151 YRAAKGSASD QKPGPVPFFA AGVSSVLHPK NPFAPTLHFN YRYFETDAPK
201 DVPGAPRQWW FGGGTDFTPA YIFEEDVK**HF HSIQKQACDK FDPSFYPR**FK
251 K**WCDDYFYIK HRDER**RGLGG IFFDDLNDYD QEMLLSFATE CANSVVPAYI
301 PIVEKR**KDME FTEQHKAWQQ LR**RGR**YVEFN LVYDR**GTTFG LKTGGR**IESI**
351 **LVSLPLSAR**W EYDHKPEEGT EEWK**LLDACI NPK**EWI

Matched peptides information:



```
Start - End      Observed    Mr(expt)   Mr(calc)       ppm    Miss Sequence
   33 - 38       775.4127    774.4054   774.4500       -58      0  R.FSRPIR.N
   54 - 66      1620.9589   1619.9516  1619.8308        75      0  K.EVPETERPFTFLR.D
   67 - 81      1525.8362   1524.8289  1524.6540       115      0  R.DSDDVTPSSSSSSVR.A
   82 - 89      1039.5751   1038.5678  1038.5280        38      1  R.ARFETMIR.A  Oxidation (M)
   84 - 89       812.4280    811.4207   811.3898        38      0  R.FETMIR.A  Oxidation (M)
   90 - 107     1830.9694   1829.9621  1829.8465        63      0  R.AAQDSVCDAIEAIEGGPK.F
  108 - 124     1805.0124   1804.0051  1803.9016        57      1  K.FKEDVWSRPGGGGGISR.V
  125 - 134     1148.6390   1147.6317  1147.5873        39      0  R.VLQDGNVFEK.A
  229 - 235      896.4969    895.4897   895.4664        26      0  K.HFHSIQK.Q
  236 - 248     1630.8638   1629.8565  1629.7246        81      1  K.QACDKFDPSFYPR.F
  241 - 248     1028.5438   1027.5365  1027.4763        59      0  K.FDPSFYPR.F
  252 - 262     1602.9262   1601.9189  1601.7085       131      1  K.WCDDYFYIKHR.D
  261 - 265      712.3698    711.3625   711.3412        30      1  K.HRDER.R
  307 - 316     1308.7381   1307.7308  1307.5816       114      1  R.KDMEFTEQHK.A  Oxidation (M)
  308 - 322     1962.9883   1961.9810  1961.9054        39      1  K.DMEFTEQHKAWQQLR.R  Oxidation (M)
  317 - 322      801.4715    800.4642   800.4293        44      0  K.AWQQLR.R
  326 - 335     1317.7425   1316.7352  1316.6401        72      0  R.YVEFNLVYDR.G
  347 - 359     1397.9308   1396.9235  1396.8289        68      0  R.IESILVSLPLSAR.W
  375 - 383     1043.5719   1042.5646  1042.5481        16      0  K.LLDACINPK.E
```

Spot No.: **58**

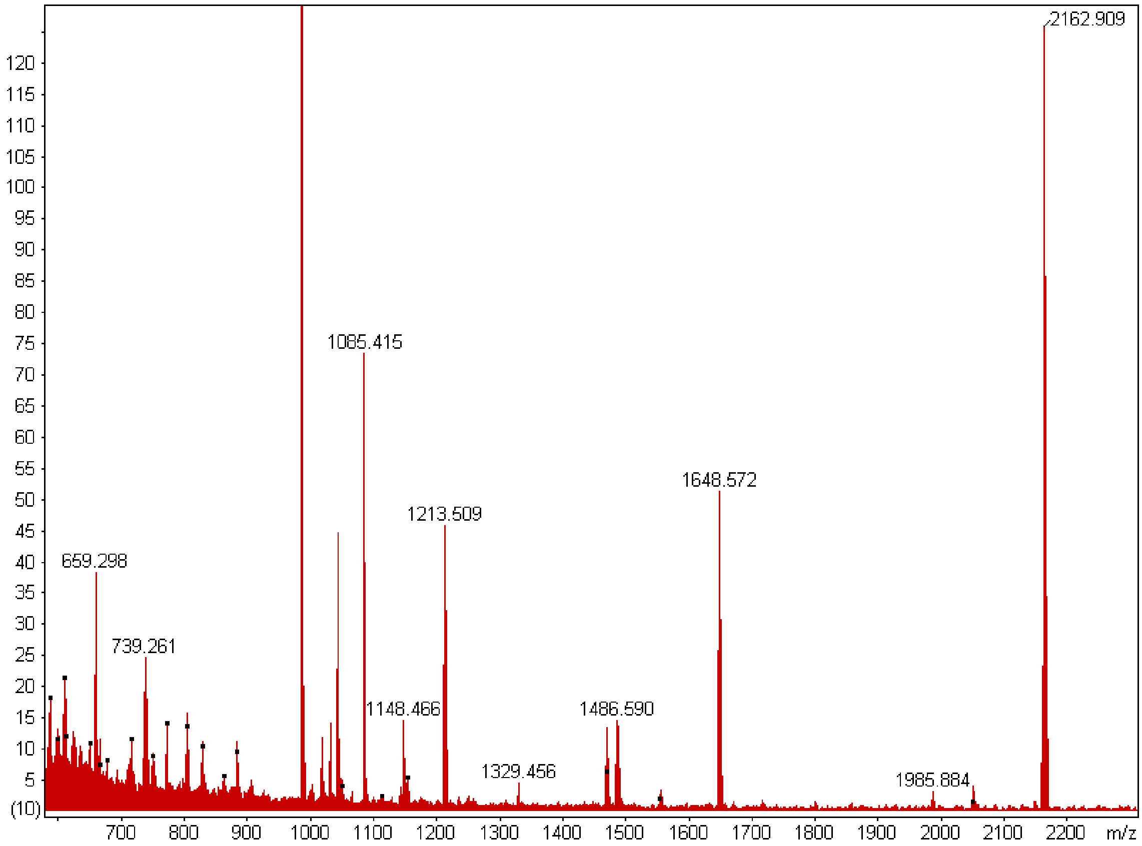
Mascot score: **146** Sequence coverage %: **23**

NCBI accession No.: **gi| 15223226**

Matched peptides No.: **15** Total peptides No.: **27**

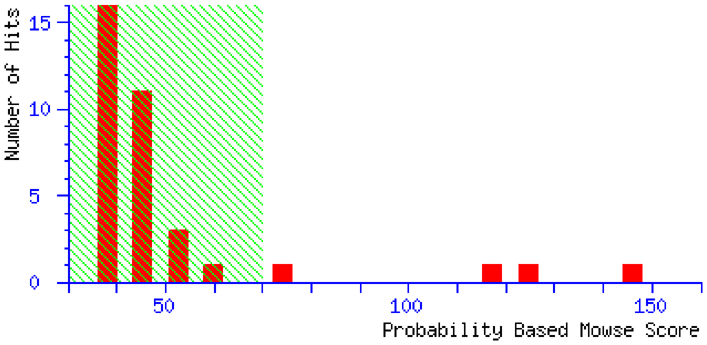
Calculated Mr: **63670** Calculated *p*I: **5.56**

Annotated PMF **spectra:**

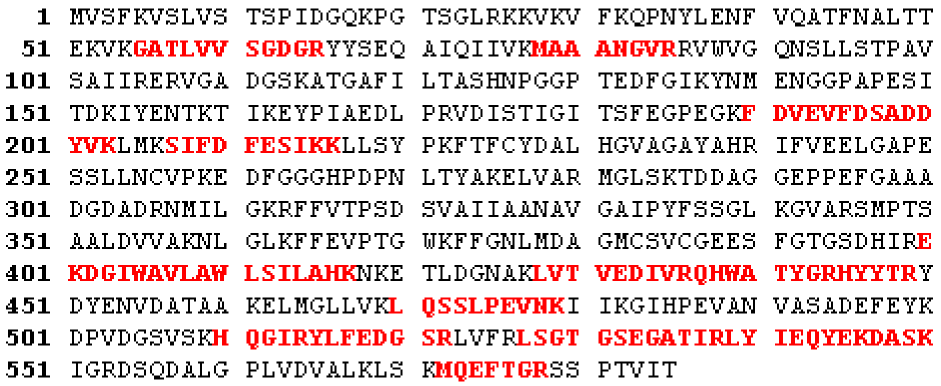


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

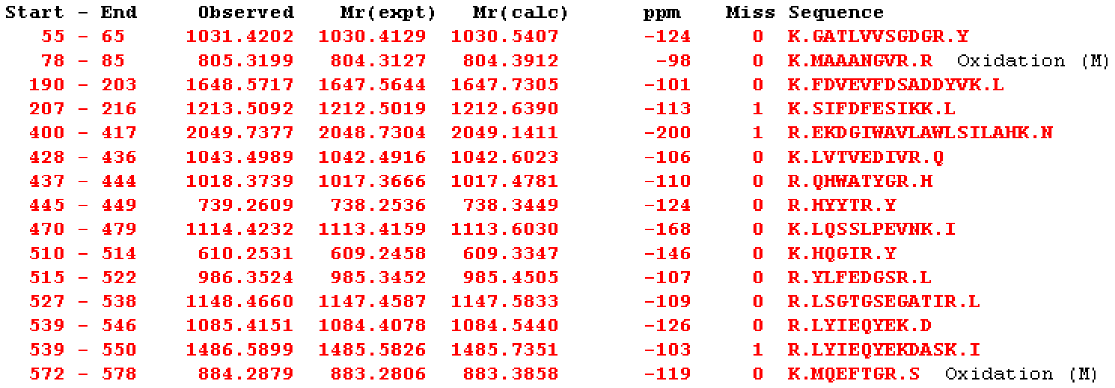


Matched peptide sequences: shown in Bold Red



1 MVSFKVSLVS TSPIDGQKPG TSGLRKKVKV FKQPNYLENF VQATFNALTT
51 EKVK**GATLVV SGDGR**YYSEQ AIQIIVK**MAA ANGVR**RVWVG QNSLLSTPAV
101 SAIIRERVGA DGSKATGAFI LTASHNPGGP TEDFGIKYNM ENGGPAPESI
151 TDKIYENTKT IKEYPIAEDL PRVDISTIGI TSFEGPEGK**F DVEVFDSADD**
201 **YVK**LMK**SIFD FESIKK**LLSY PKFTFCYDAL HGVAGAYAHR IFVEELGAPE
251 SSLLNCVPKE DFGGGHPDPN LTYAKELVAR MGLSKTDDAG GEPPEFGAAA
301 DGDADRNMIL GKRFFVTPSD SVAIIAANAV GAIPYFSSGL KGVARSMPTS
351 AALDVVAKNL GLKFFEVPTG WKFFGNLMDA GMCSVCGEES FGTGSDHIR**E**
401 **KDGIWAVLAW LSILAHK**NKE TLDGNAK**LVT VEDIVRQHWA TYGRHYYTR**Y
451 DYENVDATAA KELMGLLVK**L QSSLPEVNK**I IKGIHPEVAN VASADEFEYK
501 DPVDGSVSK**H QGIRYLFEDG SR**LVFR**LSGT GSEGATIRLY IEQYEKDASK**
551 IGRDSQDALG PLVDVALKLS K**MQEFTGR**SS PTVIT

Matched peptides information:



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Start - End      Observed    Mr(expt)   Mr(calc)       ppm    Miss  Sequence
  55 - 65       1031.4202   1030.4129  1030.5407      -124     0   K.GATLVVSGDGR.Y
  78 - 85        805.3199    804.3127   804.3912       -98     0   K.MAAANGVR.R  Oxidation (M)
 190 - 203      1648.5717   1647.5644  1647.7305      -101     0   K.FDVEVFDSADDYVK.L
 207 - 216      1213.5092   1212.5019  1212.6390      -113     1   K.SIFDFESIKK.L
 400 - 417      2049.7377   2048.7304  2049.1411      -200     1   R.EKDGIWAVLAWLSILAHK.N
 428 - 436      1043.4989   1042.4916  1042.6023      -106     0   K.LVTVEDIVR.Q
 437 - 444      1018.3739   1017.3666  1017.4781      -110     0   R.QHWATYGR.H
 445 - 449       739.2609    738.2536   738.3449      -124     0   R.HYYTR.Y
 470 - 479      1114.4232   1113.4159  1113.6030      -168     0   K.LQSSLPEVNK.I
 510 - 514       610.2531    609.2458   609.3347      -146     0   K.HQGIR.Y
 515 - 522       986.3524    985.3452   985.4505      -107     0   R.YLFEDGSR.L
 527 - 538      1148.4660   1147.4587  1147.5833      -109     0   R.LSGTGSEGATIR.L
 539 - 546      1085.4151   1084.4078  1084.5440      -126     0   R.LYIEQYEK.D
 539 - 550      1486.5899   1485.5826  1485.7351      -103     1   R.LYIEQYEKDASK.I
 572 - 578       884.2879    883.2806   883.3858      -119     0   K.MQEFTGR.S  Oxidation (M)
```

Spot No.: **59**

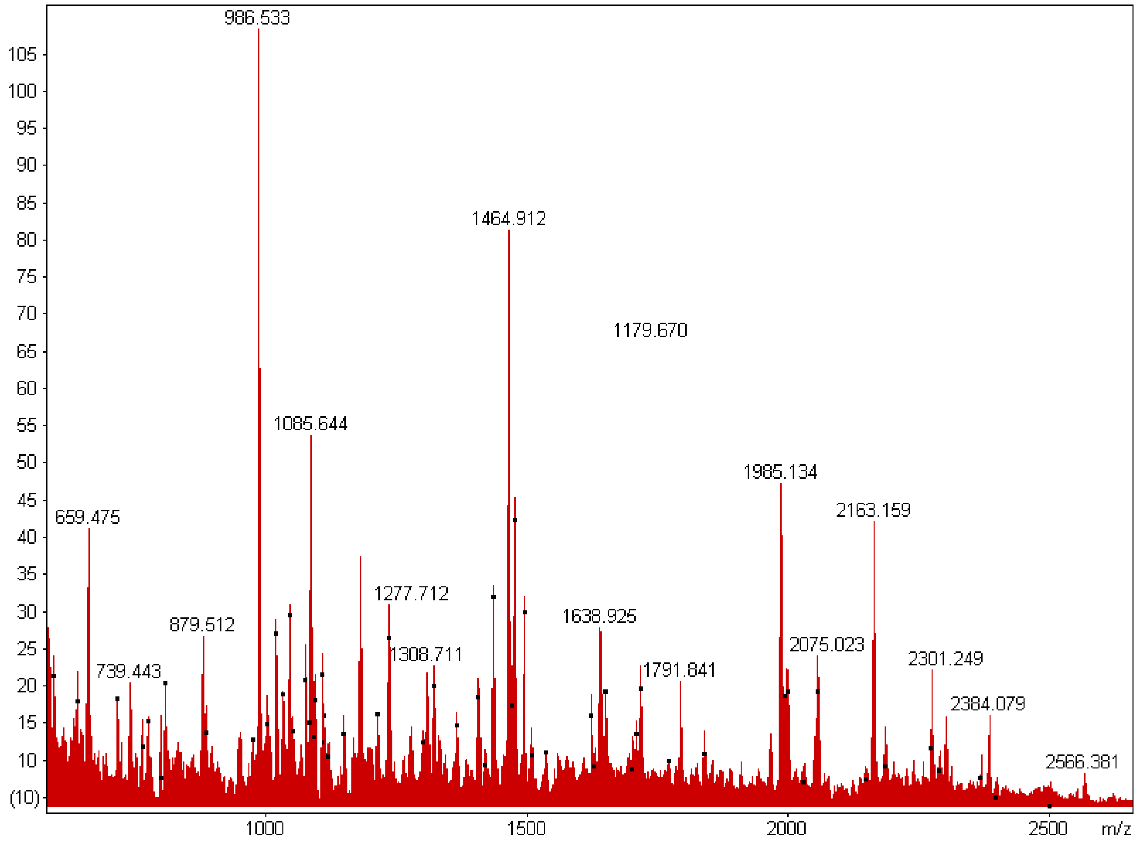
Mascot score: **124**   Sequence coverage %: **31**

NCBI accession No.: **gi| 15223226**

Matched peptides No.: **16**   Total peptides No.: **52**

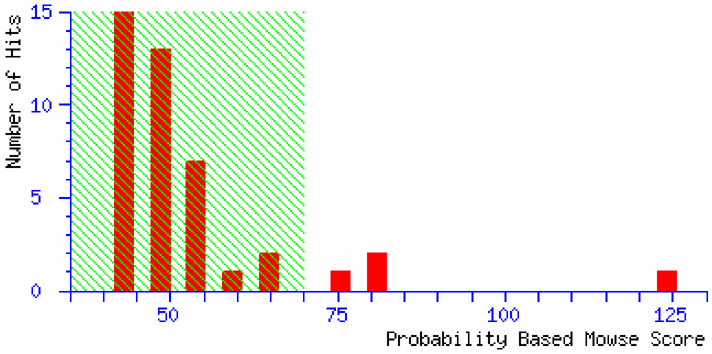
Calculated Mr: **63670**   Calculated *p*I: **5.56**

Annotated PMF **spectra:**

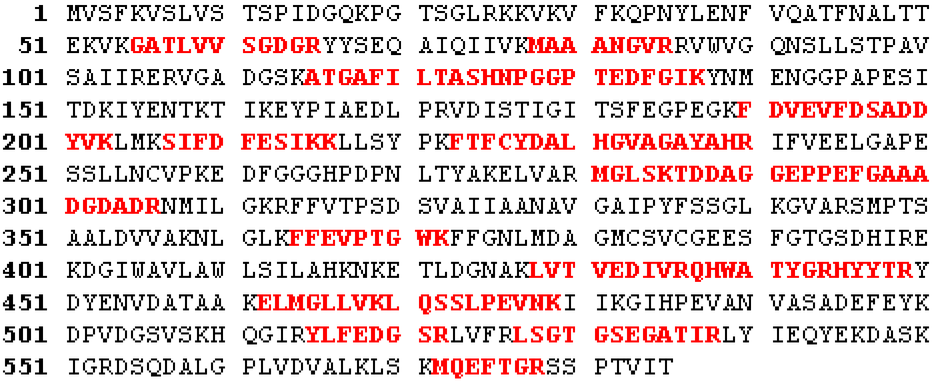


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

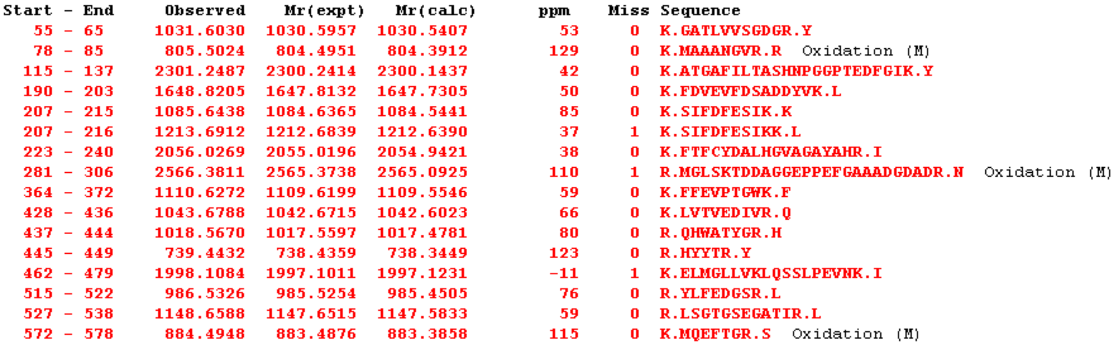


Matched peptide sequences: shown in Bold Red



```
  1 MVSFKVSLVS TSPIDGQKPG TSGLRKKVKV FKQPNYLENF VQATFNALTT
 51 EKVKGATLVV SGDGRYYSEQ AIQIIVKMAA ANGVRRVWVG QNSLLSTPAV
101 SAIIRERVGA DGSKATGAFI LTASHNPGGP TEDFGIKYNM ENGGPAPESI
151 TDKIYENTKT IKEYPIAEDL PRVDISTIGI TSFEGPEGKF DVEVFDSADD
201 YVKLMKSIFD FESIKKLLSY PKFTFCYDAL HGVAGAYAHR IFVEELGAPE
251 SSLLNCVPKE DFGGGHPDPN LTYAKELVAR MGLSKTDDAG GEPPEFGAAA
301 DGDADRNMIL GKRFFVTPSD SVAIIAANAV GAIPYFSSGL KGVARSMPTS
351 AALDVVAKNL GLKFFEVPTG WKFFGNLMDA GMCSVCGEES FGTGSDHIRE
401 KDGIWAVLAW LSILAHKNKE TLDGNAKLVT VEDIVRQHWA TYGRHYYTRY
451 DYENVDATAA KELMGLLVKL QSSLPEVNKI IKGIHPEVAN VASADEFEYK
501 DPVDGSVSKH QGIRYLFEDG SRLVFRLSGT GSEGATIRLY IEQYEKDASK
551 IGRDSQDALG PLVDVALKLS KMQEFTGRSS PTVIT
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   55 - 65     1031.6030  1030.5957  1030.5407       53      0  K.GATLVVSGDGR.Y
   78 - 85      805.5024   804.4951   804.3912      129      0  K.MAAANGVR.R  Oxidation (M)
  115 - 137    2301.2487  2300.2414  2300.1437       42      0  K.ATGAFILTASHNPGGPTEDFGIK.Y
  190 - 203    1648.8205  1647.8132  1647.7305       50      0  K.FDVEVFDSADDYVK.L
  207 - 215    1085.6438  1084.6365  1084.5441       85      0  K.SIFDFESIK.K
  207 - 216    1213.6912  1212.6839  1212.6390       37      1  K.SIFDFESIKK.L
  223 - 240    2056.0269  2055.0196  2054.9421       38      0  K.FTFCYDALHGVAGAYAHR.I
  281 - 306    2566.3811  2565.3738  2565.0925      110      1  R.MGLSKTDDAGGEPPEFGAAADGDADR.N  Oxidation (M)
  364 - 372    1110.6272  1109.6199  1109.5546       59      0  K.FFEVPTGWK.F
  428 - 436    1043.6788  1042.6715  1042.6023       66      0  K.LVTVEDIVR.Q
  437 - 444    1018.5670  1017.5597  1017.4781       80      0  R.QHWATYGR.H
  445 - 449     739.4432   738.4359   738.3449      123      0  R.HYYTR.Y
  462 - 479    1998.1084  1997.1011  1997.1231      -11      1  K.ELMGLLVKLQSSLPEVNK.I
  515 - 522     986.5326   985.5254   985.4505       76      0  R.YLFEDGSR.L
  527 - 538    1148.6588  1147.6515  1147.5833       59      0  R.LSGTGSEGATIR.L
  572 - 578     884.4948   883.4876   883.3858      115      0  K.MQEFTGR.S  Oxidation (M)
```

Spot No.: **60**

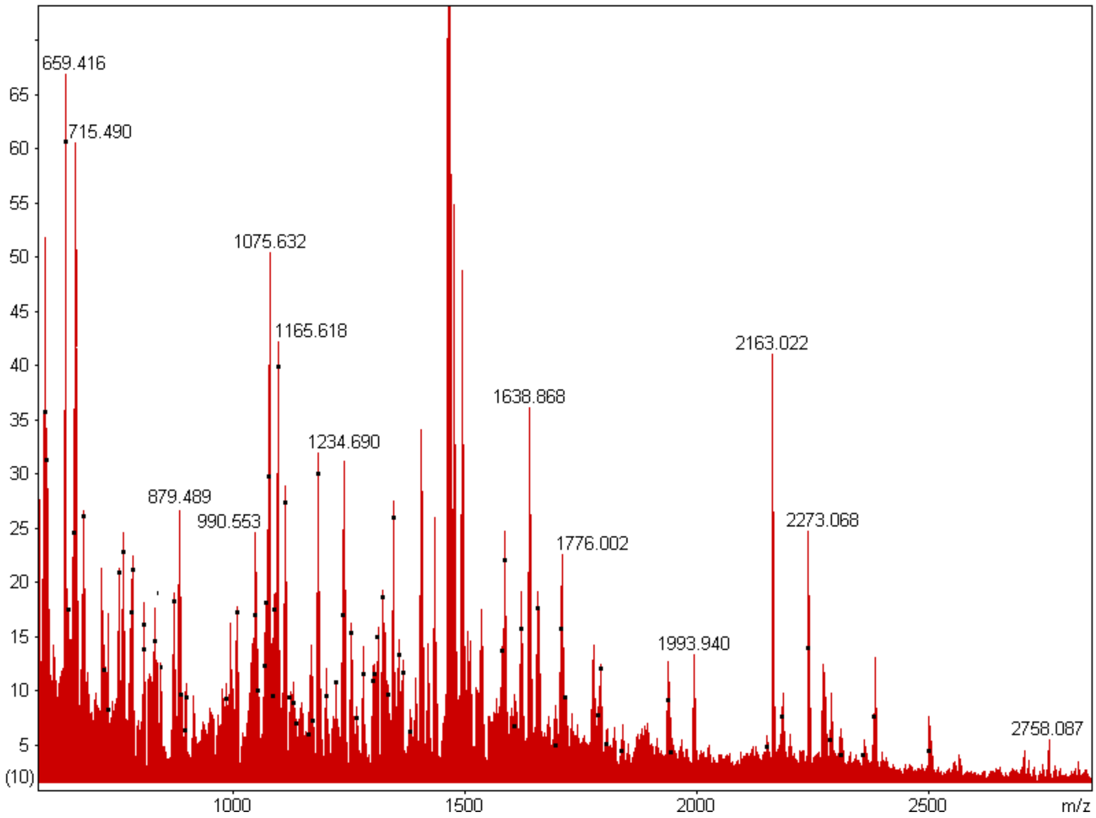
Mascot score: **93** Sequence coverage %: **24**

NCBI accession No.: **gi| 22328910**

Matched peptides No.: **14** Total peptides No.: **57**

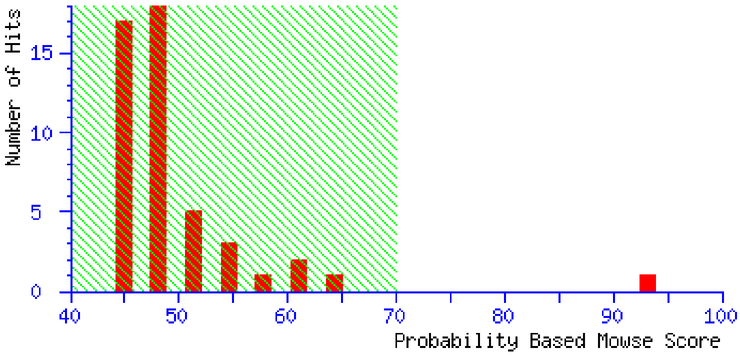
Calculated Mr: **54154** Calculated p*I*: **6.25**

Annotated PMF **spectra:**

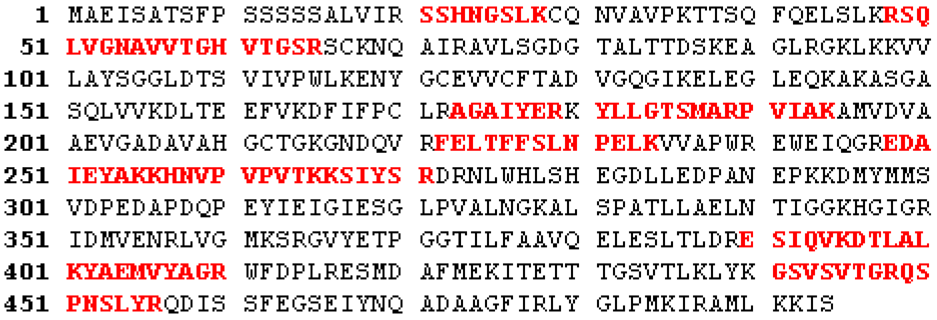


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant ($p<0.05$).

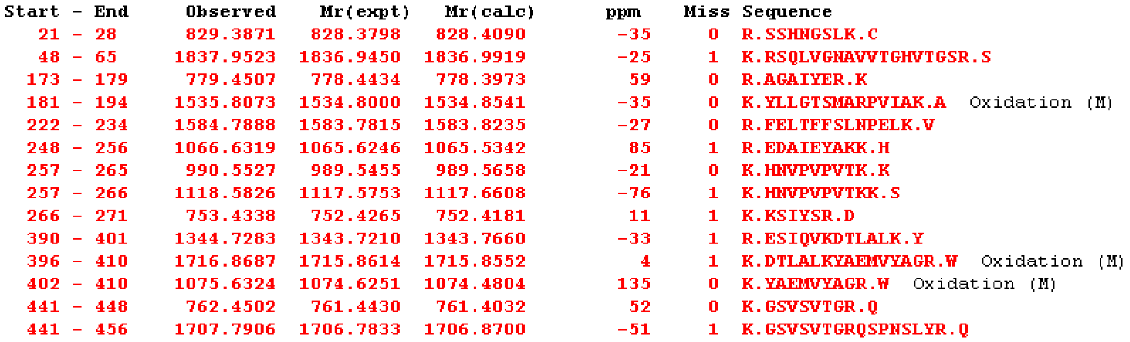


Matched peptide sequences: shown in Bold Red



1 MAEISATSFP SSSSSALVIR **SSHNGSLK**CQ NVAVPKTTSQ FQELSLK**RSQ**
51 **LVGNAVVTGH** **VTGSR**SCKNQ AIRAVLSGDG TALTTDSKEA GLRGKLKKVV
101 LAYSGGLDTS VIVPWLKENY GCEVVCFTAD VGQGIKELEG LEQKAKASGA
151 SQLVVKDLTE EFVKDFIFPC LR**AGAIYER**K **YLLGTSMARP** **VIAK**AMVDVA
201 AEVGADAVAH GCTGKGNDQV R**FELTFFSLN** **PELK**VVAPWR EWEIQGR**EDA**
251 **IEYAKKHNVP** **VPVTKKSIYS** **R**DRNLWHLSH EGDLLEDPAN EPKKDMYMMS
301 VDPEDAPDQP EYIEIGIESG LPVALNGKAL SPATLLAELN TIGGKHGIGR
351 IDMVENRLVG MKSRGVYETP GGTILFAAVQ ELESLTLDR**E** **SIQVKDTLAL**
401 **KYAEMVYAGR** WFDPLRESMD AFMEKITETT TGSVTLKLYK **GSVSVTGRQS**
451 **PNSLYR**QDIS SFEGSEIYNQ ADAAGFIRLY GLPMKIRAML KKIS

Matched peptides information:



```
Start - End     Observed    Mr(expt)   Mr(calc)      ppm    Miss Sequence
   21 - 28      829.3871    828.3798   828.4090      -35     0   R.SSHNGSLK.C
   48 - 65     1837.9523   1836.9450  1836.9919      -25     1   K.RSQLVGNAVVTGHVTGSR.S
  173 - 179     779.4507    778.4434   778.3973       59     0   R.AGAIYER.K
  181 - 194    1535.8073   1534.8000  1534.8541      -35     0   K.YLLGTSMARPVIAK.A  Oxidation (M)
  222 - 234    1584.7888   1583.7815  1583.8235      -27     0   R.FELTFFSLNPELK.V
  248 - 256    1066.6319   1065.6246  1065.5342       85     1   R.EDAIEYAKK.H
  257 - 265     990.5527    989.5455   989.5658      -21     0   K.HNVPVPVTK.K
  257 - 266    1118.5826   1117.5753  1117.6608      -76     1   K.HNVPVPVTKK.S
  266 - 271     753.4338    752.4265   752.4181       11     1   K.KSIYSR.D
  390 - 401    1344.7283   1343.7210  1343.7660      -33     1   R.ESIQVKDTLALK.Y
  396 - 410    1716.8687   1715.8614  1715.8552        4     1   K.DTLALKYAEMVYAGR.W  Oxidation (M)
  402 - 410    1075.6324   1074.6251  1074.4804      135     0   K.YAEMVYAGR.W  Oxidation (M)
  441 - 448     762.4502    761.4430   761.4032       52     0   K.GSVSVTGR.Q
  441 - 456    1707.7906   1706.7833  1706.8700      -51     1   K.GSVSVTGRQSPNSLYR.Q
```

Spot No.: **61**

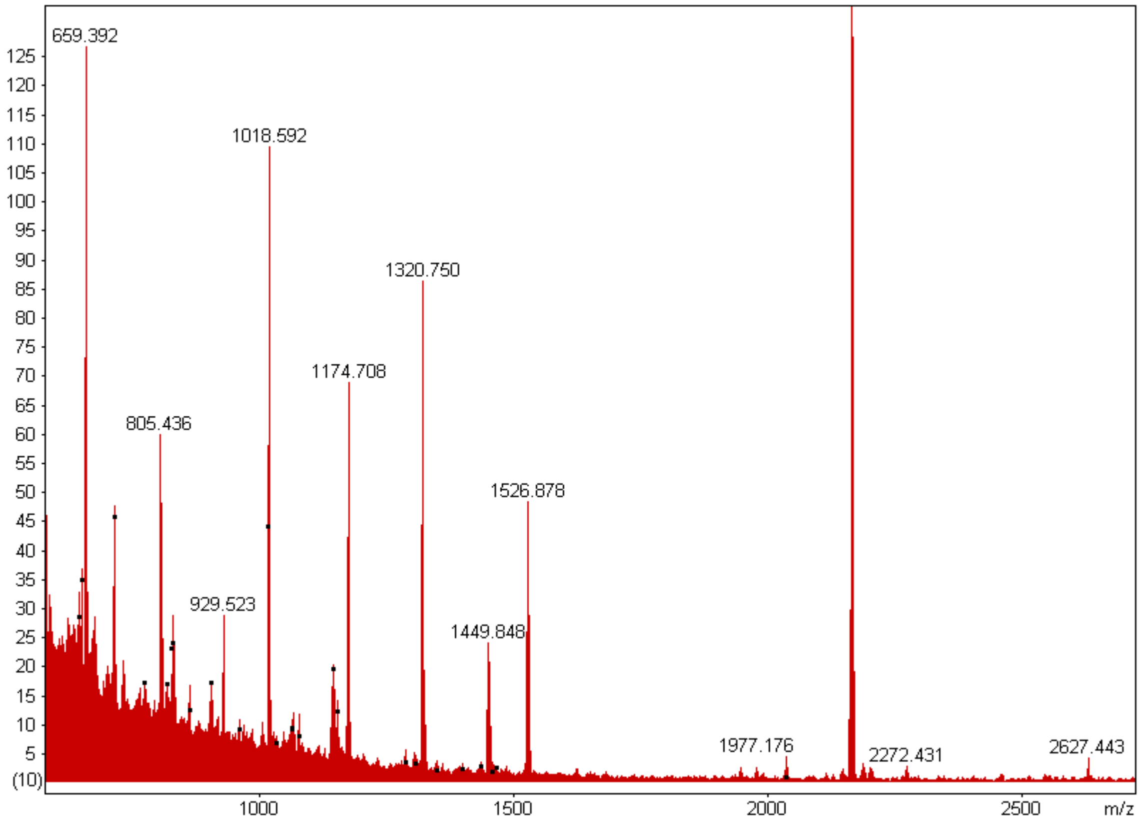
Mascot score: **112**   Sequence coverage %: **24**

NCBI accession No.: **gi| 15242093**

Matched peptides No.: **13**   Total peptides No.: **31**

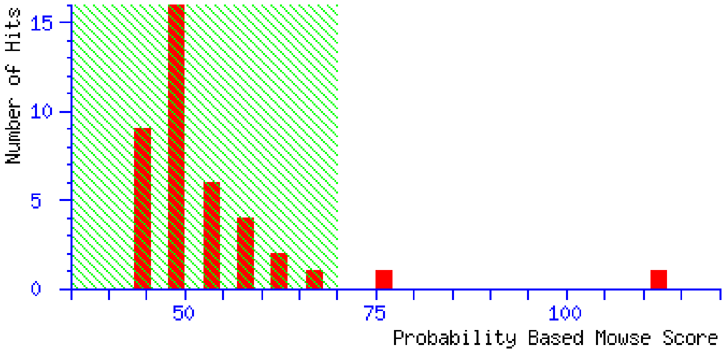
Calculated Mr: **57763**   Calculated *p*I: **5.59**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 MPIDKIFKDD ASEEKGERAR MASFVGAMAI SDLVKSTLGP KGMDK**ILQST**
51 **GR**GHAVTVTN DGATILK**SLH** **IDNPAAK**VLV DISK**VQDDEV** **GDGTTSVVVL**
101 **AGELLR**EAEK LVASK**IHPMT** **IIAGYR**MASE CAR**NALLKR**V IDNKDNAEKF
151 RSDLLKIAMT TLCSKILSQD KEHFAEMAVD AVFRLKGSTN LEAIQIIKKP
201 GGSLK**DSFLD** **EGFILDKK**IG IGQPKRIENA NILVANTAMD TDKVKIYGAR
251 VRVDSMTKVA EIEGAEKEKM KDKVKKIIGH GINCFVNRQL IYNFPEELFA
301 DAGILAIEHA DFEGIER**LGL** **VTGGEIASTF** **DNPESVK**LGH CK**LIEEIMIG**
351 **EDK**LIHFSGC EMGQACSIVL R**GASHHVLDE** **AER**SLHDALC VLSQTVNDTR
401 VLLGGGWPEM VMAKEVDELA RKTAGK**KSHA** **IEAFSR**ALVA IPTTIADNAG
451 LDSAELVAQL RAEHHTEGCN AGIDVITGAV GDMEER**GIYE** **AFK**VKQAVLL
501 SATEASEMIL RVDEIITCAP RRREDRM

Matched peptides information:

Start	–	End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
46	–	52	774.4096	773.4023	773.4395	-48	0	K.ILQSTGR.G	
68	–	77	1065.5784	1064.5711	1064.5614	9	0	K.SLHIDNPAAK.V	
85	–	106	2272.4307	2271.4234	2271.1595	116	0	K.VQDDEVGDGTTSVVVLAGELLR.E	
116	–	126	1287.8006	1286.7933	1286.6805	88	0	K.IHPMTIIAGYR.M	Oxidation (M)
134	–	139	714.4092	713.4020	713.4548	-74	1	R.NALLKR.V	
206	–	217	1398.7478	1397.7405	1397.6715	49	0	K.DSFLDEGFILDK.K	
206	–	218	1526.8776	1525.8703	1525.7664	68	1	K.DSFLDEGFILDKK.I	
318	–	337	2034.2125	2033.2052	2033.0317	85	0	R.LGLVTGGEIASTFDNPESVK.L	
343	–	353	1305.7513	1304.7440	1304.6533	70	0	K.LIEEIMIGEDK.L	Oxidation (M)
372	–	383	1320.7496	1319.7423	1319.6218	91	0	R.GASHHVLDEAER.S	
427	–	436	1145.6951	1144.6878	1144.5989	78	1	K.KSHAIEAFSR.A	
428	–	436	1017.5753	1016.5680	1016.5039	63	0	K.SHAIEAFSR.A	
487	–	493	827.4165	826.4092	826.4225	-16	0	R.GIYEAFK.V	

Spot No.: **62**

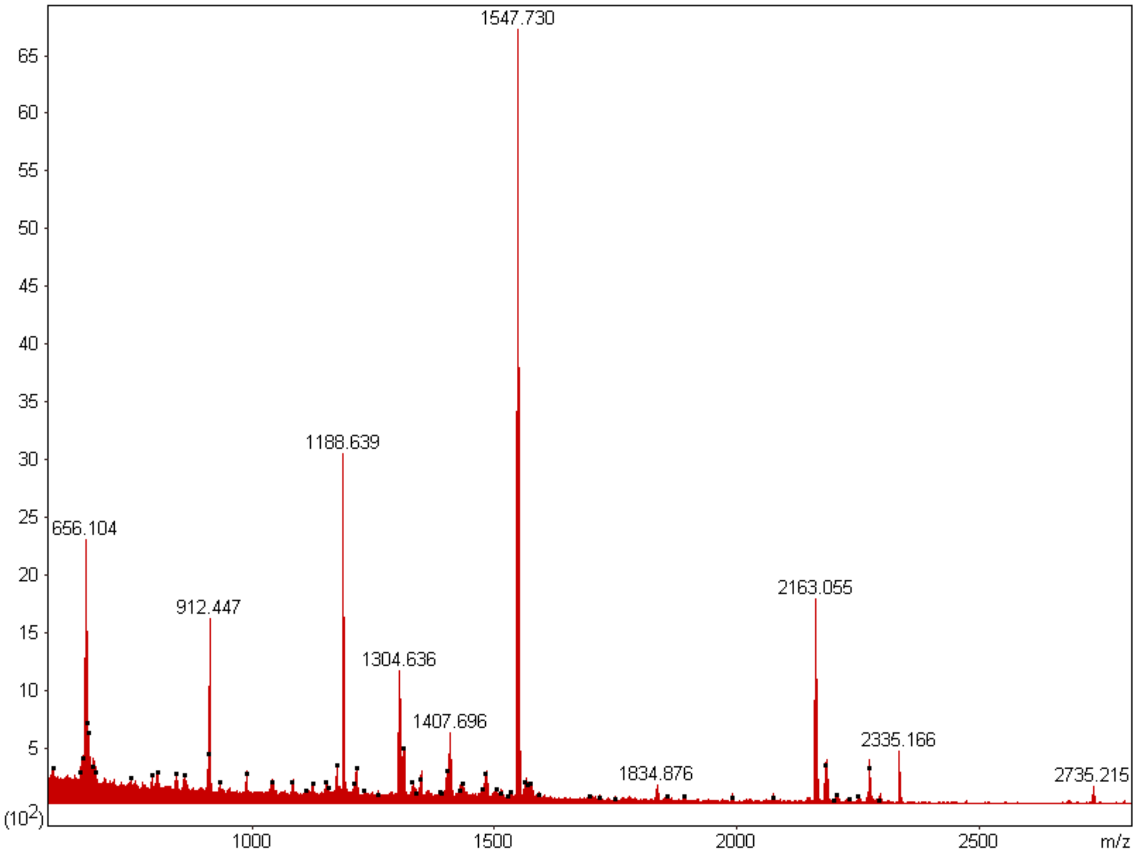
Mascot score: **145** Sequence coverage %: **31**

NCBI accession No.: **gi| 18391066**

Matched peptides No.: **18** Total peptides No.: **47**

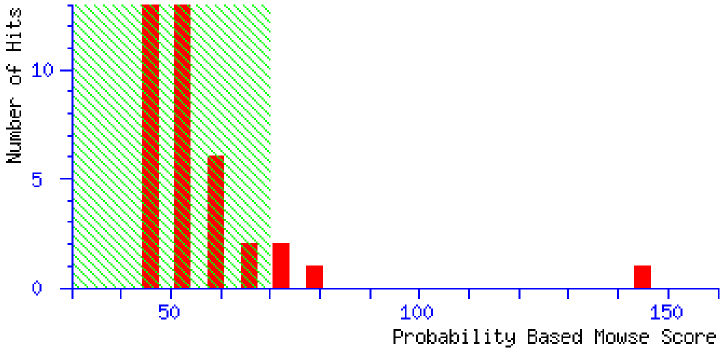
Calculated Mr: **60770** Calculated *p*I: **5.32**

Annotated PMF **spectra:**

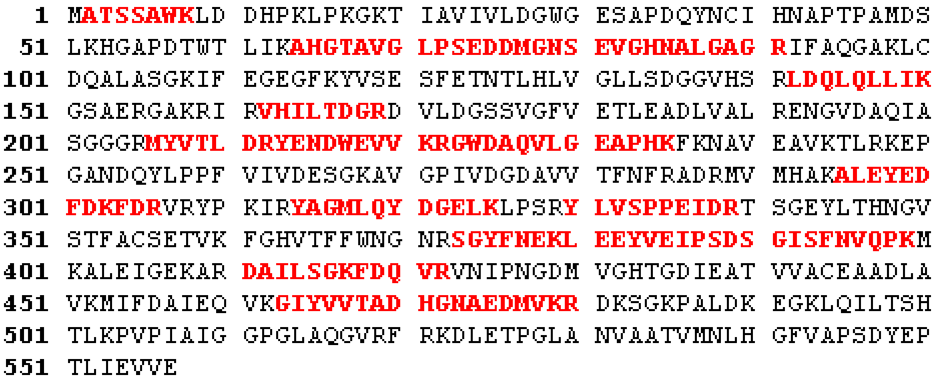


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

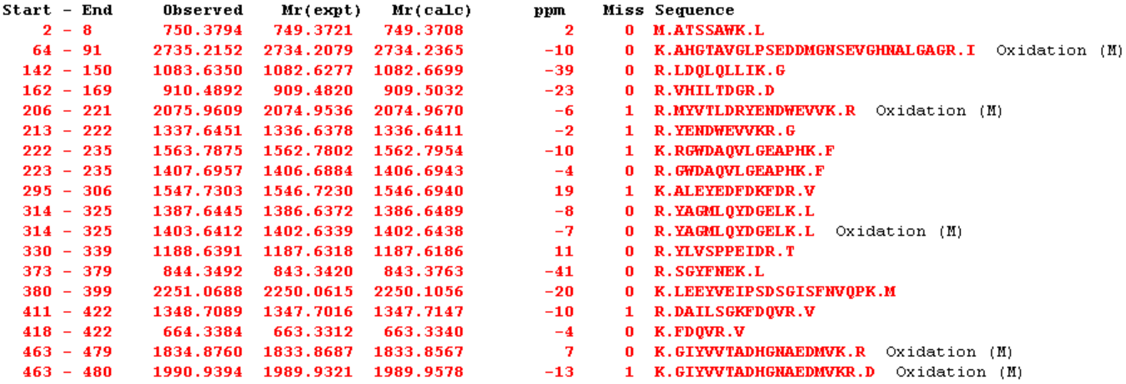


Matched peptide sequences: shown in Bold Red



1 M**ATSSAWK**LD DHPKLPKGKT IAVIVLDGWG ESAPDQYNCI HNAPTPAMDS
51 LKHGAPDTWT LIK**AHGTAVG** **LPSEDDMGNS** **EVGHNALGAG** **R**IFAQGAKLC
101 DQALASGKIF EGEGFKYVSE SFETNTLHLV GLLSDGGVHS R**LDQLQLLIK**
151 GSAERGAKRI R**VHILTDGR**D VLDGSSVGFV ETLEADLVAL RENGVDAQIA
201 SGGGR**MYVTL** **DRYENDWEVV** **KRGWDAQVLG** **EAPHK**FKNAV EAVKTLRKEP
251 GANDQYLPPF VIVDESGKAV GPIVDGDAVV TFNFRADRMV MHAK**ALEYED**
301 **FDKFDR**VRYP KIR**YAGMLQY** **DGELK**LPSR**Y** **LVSPPEIDR**T SGEYLTHNGV
351 STFACSETVK FGHVTFFWNG NR**SGYFNEKL** **EEYVEIPSDS** **GISFNVQPK**M
401 KALEIGEKAR **DAILSGKFDQ** **VR**VNIPNGDM VGHTGDIEAT VVACEAADLA
451 VKMIFDAIEQ VK**GIYVVTAD** **HGNAEDMVKR** DKSGKPALDK EGKLQILTSH
501 TLKPVPIAIG GPGLAQGVRF RKDLETPGLA NVAATVMNLH GFVAPSDYEP
551 TLIEVVE

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
2 - 8	750.3794	749.3721	749.3708	2	0	M.ATSSAWK.L	
64 - 91	2735.2152	2734.2079	2734.2365	-10	0	K.AHGTAVGLPSEDDMGNSEVGHNALGAGR.I	Oxidation (M)
142 - 150	1083.6350	1082.6277	1082.6699	-39	0	R.LDQLQLLIK.G	
162 - 169	910.4892	909.4820	909.5032	-23	0	R.VHILTDGR.D	
206 - 221	2075.9609	2074.9536	2074.9670	-6	1	R.MYVTLDRYENDWEVVK.R	Oxidation (M)
213 - 222	1337.6451	1336.6378	1336.6411	-2	1	R.YENDWEVVKR.G	
222 - 235	1563.7875	1562.7802	1562.7954	-10	1	K.RGWDAQVLGEAPHK.F	
223 - 235	1407.6957	1406.6884	1406.6943	-4	0	R.GWDAQVLGEAPHK.F	
295 - 306	1547.7303	1546.7230	1546.6940	19	1	K.ALEYEDFDKFDR.V	
314 - 325	1387.6445	1386.6372	1386.6489	-8	0	R.YAGMLQYDGELK.L	
314 - 325	1403.6412	1402.6339	1402.6438	-7	0	R.YAGMLQYDGELK.L	Oxidation (M)
330 - 339	1188.6391	1187.6318	1187.6186	11	0	R.YLVSPPEIDR.T	
373 - 379	844.3492	843.3420	843.3763	-41	0	R.SGYFNEK.L	
380 - 399	2251.0688	2250.0615	2250.1056	-20	0	K.LEEYVEIPSDSGISFNVQPK.M	
411 - 422	1348.7089	1347.7016	1347.7147	-10	1	R.DAILSGKFDQVR.V	
418 - 422	664.3384	663.3312	663.3340	-4	0	K.FDQVR.V	
463 - 479	1834.8760	1833.8687	1833.8567	7	0	K.GIYVVTADHGNAEDMVK.R	Oxidation (M)
463 - 480	1990.9394	1989.9321	1989.9578	-13	1	K.GIYVVTADHGNAEDMVKR.D	Oxidation (M)

Spot No.: **63**

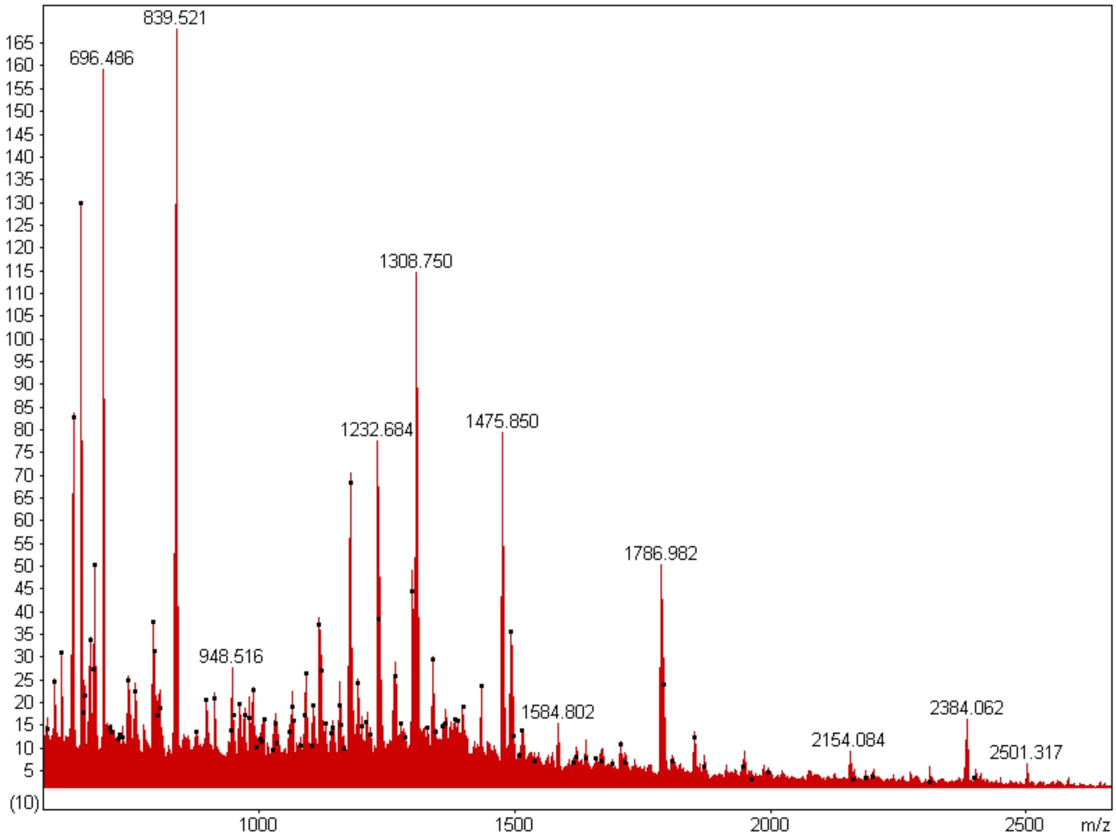
Mascot score: **87**   Sequence coverage %: **49**

NCBI accession No.: **gi| 30690323**

Matched peptides No.: **19**   Total peptides No.: **169**

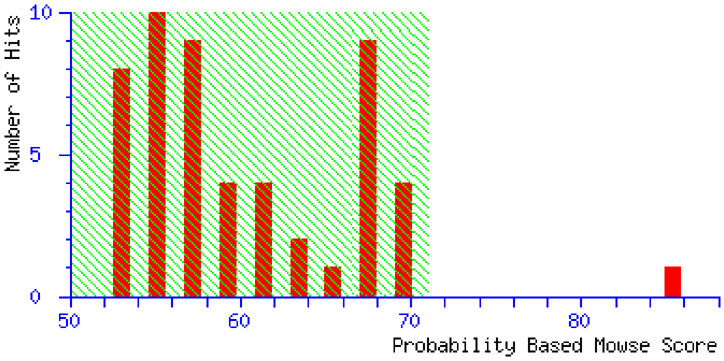
Calculated Mr: **39646**   Calculated p*I*: **9.44**

Annotated PMF **spectra:**

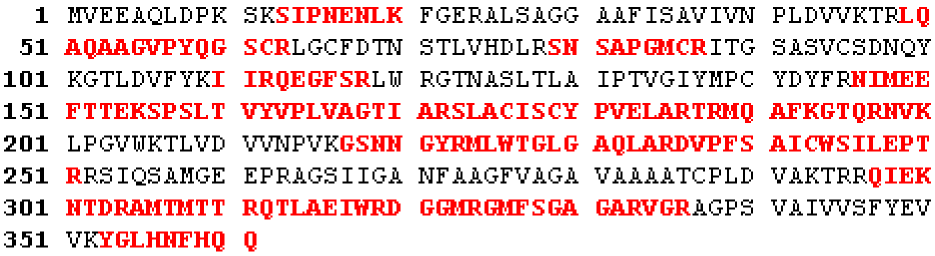


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

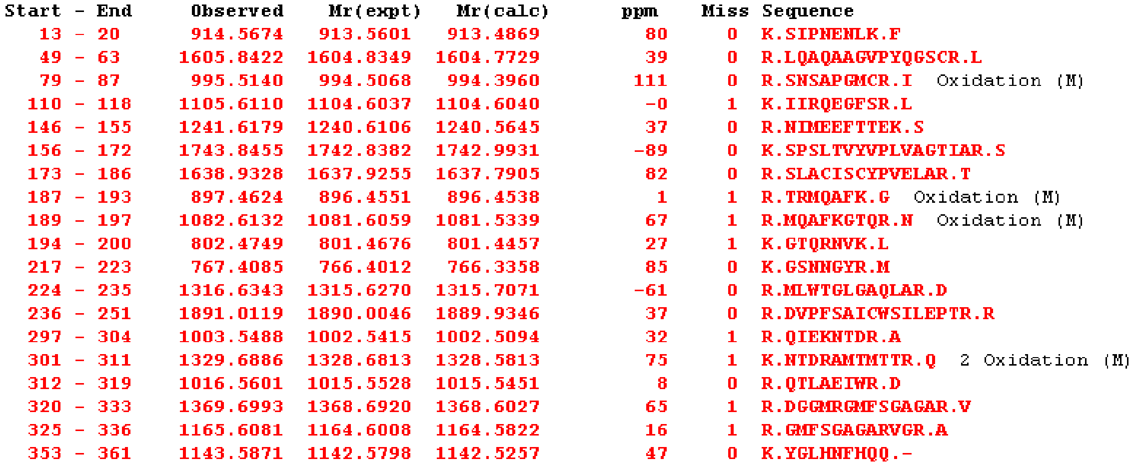


Matched peptide sequences: shown in Bold Red



1 MVEEAQLDPK SK**SIPNENLK** FGERALSAGG AAFISAVIVN PLDVVKTR**LQ**
51 **AQAAGVPYQG** **SCR**LGCFDTN STLVHDLR**SN** **SAPGMCR**ITG SASVCSDNQY
101 KGTLDVFYK**I** **IRQEGFSR**LW RGTNASLTLA IPTVGIYMPC YDYFR**NIMEE**
151 **FTTEKSPSLT** **VYVPLVAGTI** **ARSLACISCY** **PVELARTRMQ** **AFKGTQRNVK**
201 LPGVWKTLVD VVNPVK**GSNN** **GYRMLWTGLG** **AQLARDVPFS** **AICWSILEPT**
251 **R**RSIQSAMGE EPRAGSIIGA NFAAGFVAGA VAAAATCPLD VAKTRR**QIEK**
301 **NTDRAMTMTT** **RQTLAEIWRD** **GGMRGMFSGA** **GARVGR**AGPS VAIVVSFYEV
351 VK**YGLHNFHQ** **Q**

Matched peptides information:



```
Start - End      Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   13 - 20       914.5674   913.5601   913.4869       80      0  K.SIPNENLK.F
   49 - 63      1605.8422  1604.8349  1604.7729       39      0  R.LQAQAAGVPYQGSCR.L
   79 - 87       995.5140   994.5068   994.3960      111      0  R.SNSAPGMCR.I  Oxidation (M)
  110 - 118     1105.6110  1104.6037  1104.6040       -0      1  K.IIRQEGFSR.L
  146 - 155     1241.6179  1240.6106  1240.5645       37      0  R.NIMEEFTTEK.S
  156 - 172     1743.8455  1742.8382  1742.9931      -89      0  K.SPSLTVYVPLVAGTIAR.S
  173 - 186     1638.9328  1637.9255  1637.7905       82      0  R.SLACISCYPVELAR.T
  187 - 193      897.4624   896.4551   896.4538        1      1  R.TRMQAFK.G  Oxidation (M)
  189 - 197     1082.6132  1081.6059  1081.5339       67      1  R.MQAFKGTQR.N  Oxidation (M)
  194 - 200      802.4749   801.4676   801.4457       27      1  K.GTQRNVK.L
  217 - 223      767.4085   766.4012   766.3358       85      0  K.GSNNGYR.M
  224 - 235     1316.6343  1315.6270  1315.7071      -61      0  R.MLWTGLGAQLAR.D
  236 - 251     1891.0119  1890.0046  1889.9346       37      0  R.DVPFSAICWSILEPTR.R
  297 - 304     1003.5488  1002.5415  1002.5094       32      1  R.QIEKNTDR.A
  301 - 311     1329.6886  1328.6813  1328.5813       75      1  K.NTDRAMTMTTR.Q  2 Oxidation (M)
  312 - 319     1016.5601  1015.5528  1015.5451        8      0  R.QTLAEIWR.D
  320 - 333     1369.6993  1368.6920  1368.6027       65      1  R.DGGMRGMFSGAGAR.V
  325 - 336     1165.6081  1164.6008  1164.5822       16      1  R.GMFSGAGARVGR.A
  353 - 361     1143.5871  1142.5798  1142.5257       47      0  K.YGLHNFHQQ.-
```

Spot No.: **64**

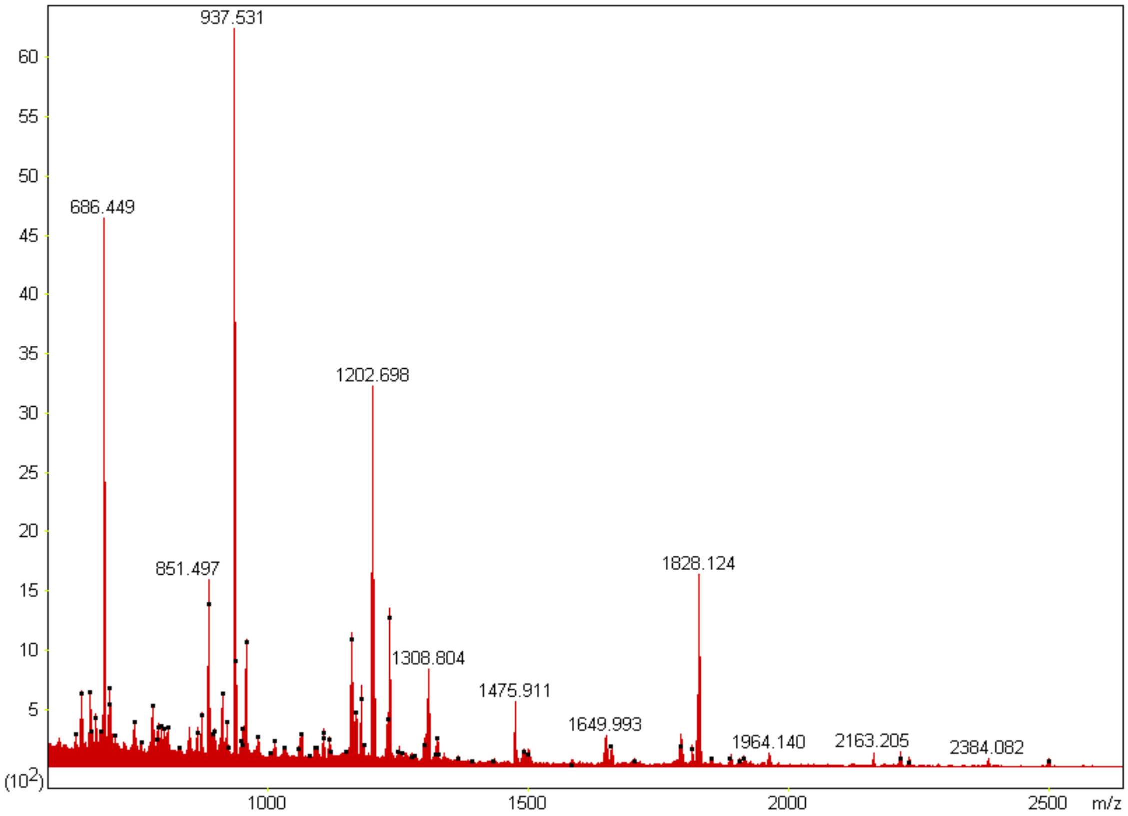
Mascot score: **108**   Sequence coverage %: **32**

NCBI accession No.: **gi| 15228194**

Matched peptides No.: **16**   Total peptides No.: **87**

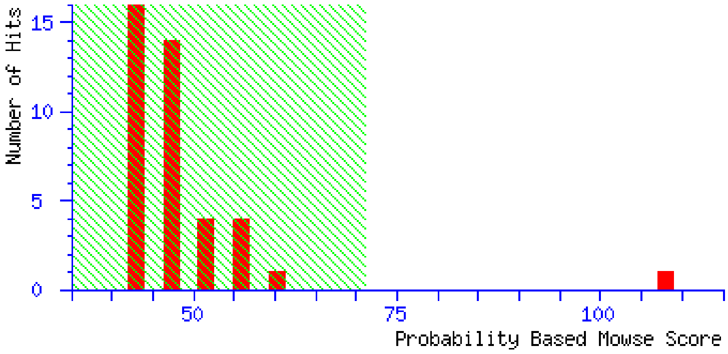
Calculated Mr: **42787**   Calculated p*I*: **6.17**

Annotated PMF **spectra:**

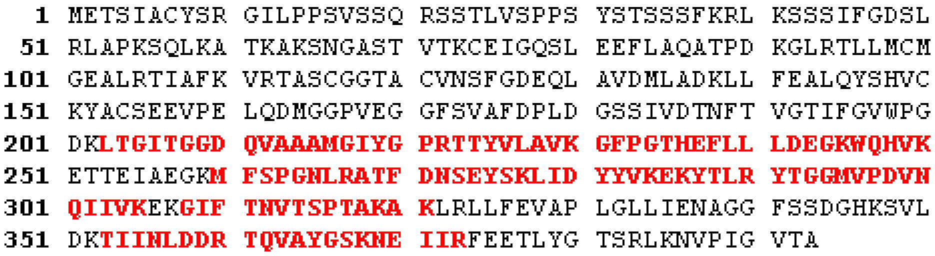


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

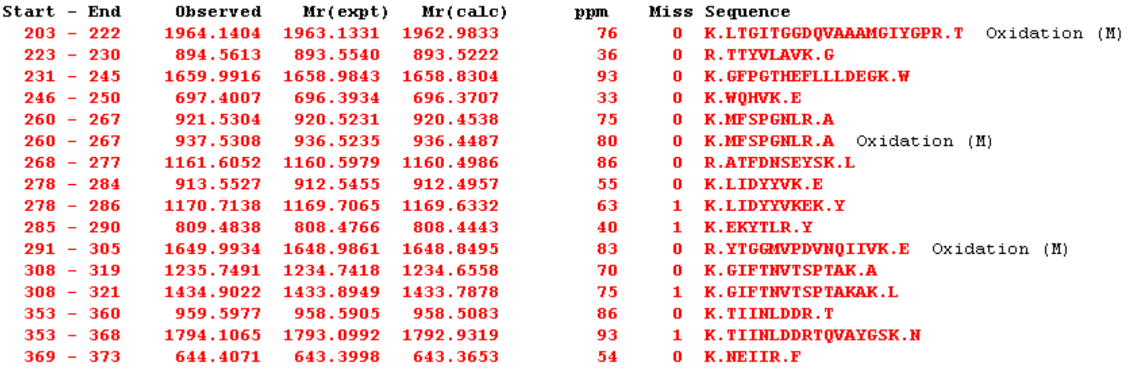


Matched peptide sequences: shown in Bold Red



1 METSIACYSR GILPPSVSSQ RSSTLVSPPS YSTSSSFKRL KSSSIFGDSL
51 RLAPKSQLKA TKAKSNGAST VTKCEIGQSL EEFLAQATPD KGLRTLLMCM
101 GEALRTIAFK VRTASCGGTA CVNSFGDEQL AVDMLADKLL FEALQYSHVC
151 KYACSEEVPE LQDMGGPVEG GFSVAFDPLD GSSIVDTNFT VGTIFGVWPG
201 DK**LTGITGGD QVAAAMGIYG PRTTYVLAVK GFPGTHEFLL LDEGKWQHVK**
251 ETTEIAEGK**M FSPGNLRATF DNSEYSKLID YYVKEKYTLR YTGGMVPDVN**
301 **QIIVK**EK**GIF TNVTSPTAKA K**LRLLFEVAP LGLLIENAGG FSSDGHKSVL
351 DK**TIINLDDR TQVAYGSKNE IIR**FEETLYG TSRLKNVPIG VTA

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss Sequence
  203 - 222    1964.1404  1963.1331  1962.9833       76      0 K.LTGITGGDQVAAAMGIYGPR.T  Oxidation (M)
  223 - 230     894.5613   893.5540   893.5222       36      0 R.TTYVLAVK.G
  231 - 245    1659.9916  1658.9843  1658.8304       93      0 K.GFPGTHEFLLLDEGK.W
  246 - 250     697.4007   696.3934   696.3707       33      0 K.WQHVK.E
  260 - 267     921.5304   920.5231   920.4538       75      0 K.MFSPGNLR.A
  260 - 267     937.5308   936.5235   936.4487       80      0 K.MFSPGNLR.A  Oxidation (M)
  268 - 277    1161.6052  1160.5979  1160.4986       86      0 R.ATFDNSEYSK.L
  278 - 284     913.5527   912.5455   912.4957       55      0 K.LIDYYVK.E
  278 - 286    1170.7138  1169.7065  1169.6332       63      1 K.LIDYYVKEK.Y
  285 - 290     809.4838   808.4766   808.4443       40      1 K.EKYTLR.Y
  291 - 305    1649.9934  1648.9861  1648.8495       83      0 R.YTGGMVPDVNQIIVK.E  Oxidation (M)
  308 - 319    1235.7491  1234.7418  1234.6558       70      0 K.GIFTNVTSPTAK.A
  308 - 321    1434.9022  1433.8949  1433.7878       75      1 K.GIFTNVTSPTAKAK.L
  353 - 360     959.5977   958.5905   958.5083       86      0 K.TIINLDDR.T
  353 - 368    1794.1065  1793.0992  1792.9319       93      1 K.TIINLDDRTQVAYGSK.N
  369 - 373     644.4071   643.3998   643.3653       54      0 K.NEIIR.F
```

Spot No.: **65**

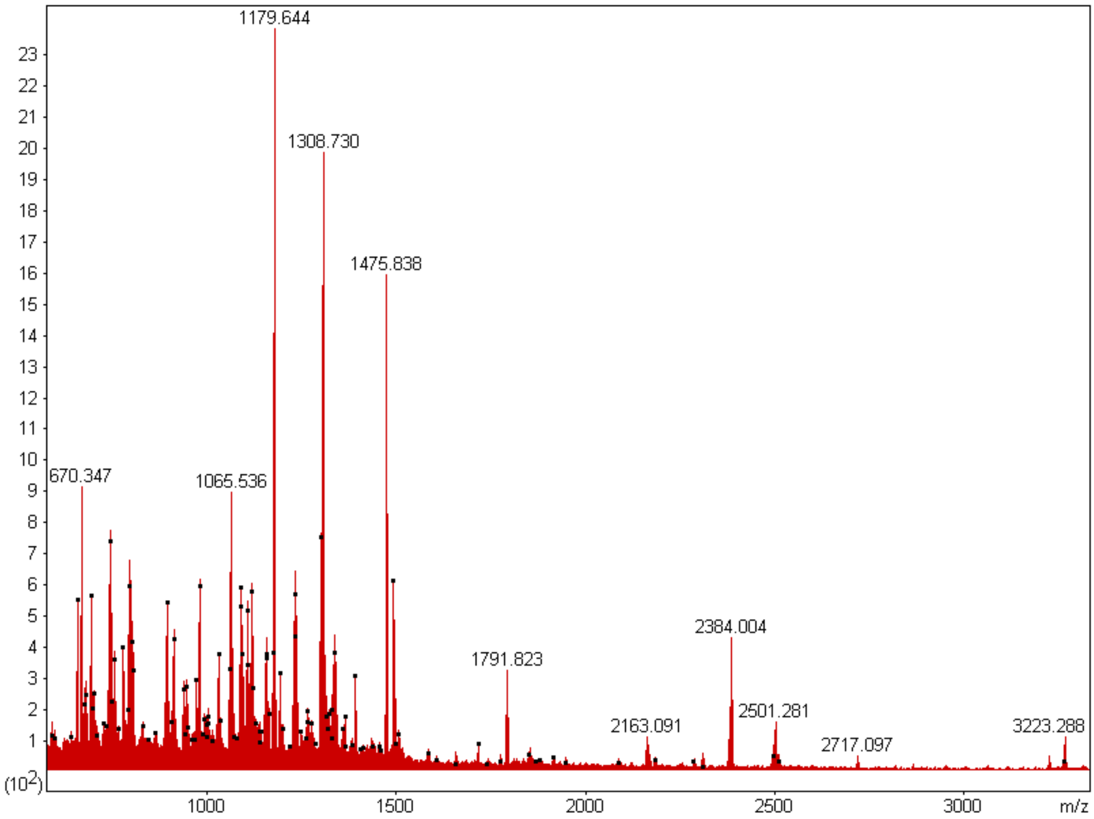
Mascot score: **84**   Sequence coverage %: **29**

NCBI accession No.: **gi| 15234171**

Matched peptides No.: **29**   Total peptides No.: **106**

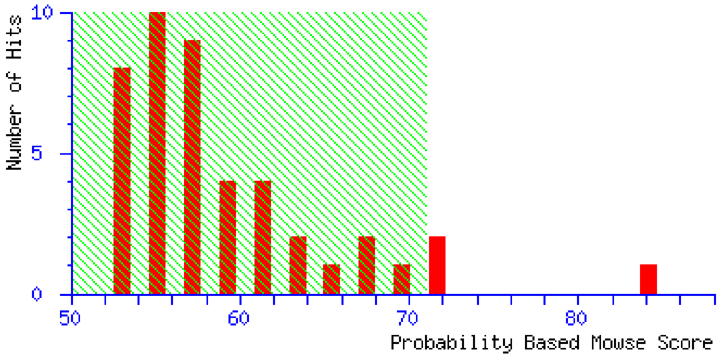
Calculated Mr: **87227**   Calculated p*I*: **5.06**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 MEDLKTTDAL SLPVVSDNGG IIEPELQLPQ AIPTELENNE EENGTIQQSQ
51 SEEDSAENGK **IYMDDTFLPS** **K**SQVKETQDS PTTPSFVSPS AEIVLPR**VNT**
101 **KYEAEGTTR**N AVSPRPLYSP RSIGSPRALL SPRFAGSSSP LSNGTPISMD
151 SFRDSIDTAS PFESVKEAVS K**FGGITDWKA** **HR**MKVLER**RN** **FVEQELDK**IQ
201 EEIPEYKKKS EMVEMSK**MLA** **VEELESTK**RL IEELKLNLEK **AETEEQQAK**Q
251 DSELAKLR**VQ** **EMEQGIADEA** **SVASK**AQLEV AQAR**HTSAIS** **ELESVK**EELQ
301 TLQNEYDALV K**EKDLAVK**EA EEAVIASKEV ERK**VEELTIE** **LIATK**ESLEC
351 AHSSHLEAEE HR**IGAAMLRD** **QETHR**WEKEL KQAEEELQRL KQHLVSTKEL
401 QVK**LEFASAL** **LLDLK**K**ELAD** **HK**ESSKVKEE TSETVVTNIE ISLQEK**TTDI**
451 **QKAVASAK**KE LEEVNANVEK ATSEVNCLKV ASSSLRLEID KEKSALDSLK
501 QREGMASVTV ASLEAEIDIT R**CEIALVK**SK EKETREEMVE LPKQLQQASQ
551 EADEAK**SFAE** **LAREELR**KSQ EEAEQAKAGA STMESRLFAA QK**EIEAIKAS**
601 **ERLALAAIKA** **LQESESSSK**E NAVDSPRTVT LTIEEYYELS KRAHEAEEAA
651 NAR**VAAAVSE** **VGEAK**ETEKR SLEKLEEVNK **EMVERK**ATLA GAMEKAEKAK
701 EGKLGVEQEL RKWREVSEKK RKNGSSHGKS IQGSKEKEAE TSVSNETETN
751 PIPQVNPVKK KKKLFPR**FFM** **FLMKK**KSHK

Matched peptides information:

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
61 - 71	1329.7001	1328.6928	1328.6322	46	0	K.IYMDDTFLPSK.S	
98 - 109	1368.6938	1367.6865	1367.6681	13	1	R.VNTKYEAEGTTR.N	
172 - 182	1287.6776	1286.6703	1286.6520	14	1	K.FGGITDWKAHR.M	
189 - 198	1277.6978	1276.6905	1276.6411	39	1	R.RNFVEQELDK.I	
190 - 198	1121.5666	1120.5593	1120.5400	17	0	R.NFVEQELDK.I	
218 - 228	1249.6508	1248.6435	1248.6271	13	0	K.MLAVEELESTK.R	
218 - 228	1265.6499	1264.6426	1264.6220	16	0	K.MLAVEELESTK.R	Oxidation (M)
241 - 249	1033.5272	1032.5199	1032.4723	46	0	K.AETEEQQAK.Q	
259 - 275	1791.8231	1790.8158	1790.8356	-11	0	R.VQEMEQGIADEASVASK.A	
285 - 296	1300.6140	1299.6067	1299.6670	-46	0	R.HTSAISELESVK.E	
312 - 318	802.4502	801.4429	801.4596	-21	1	K.EKDLAVK.E	
334 - 345	1358.7618	1357.7545	1357.7704	-12	0	K.VEELTIELIATK.E	
363 - 375	1497.8309	1496.8236	1496.7518	48	1	R.IGAAMLRDQETHR.W	
404 - 415	1332.6919	1331.6846	1331.7700	-64	0	K.LEFASALLLDLK.K	
417 - 422	712.3650	711.3577	711.3551	4	0	K.ELADHK.E	
447 - 458	1232.6332	1231.6259	1231.6772	-42	1	K.TTDIQKAVASAK.K	
522 - 528	832.4753	831.4680	831.4524	19	0	R.CEIALVK.S	
557 - 563	793.4058	792.3985	792.4130	-18	0	K.SFAELAR.E	
557 - 567	1320.6810	1319.6737	1319.6833	-7	1	K.SFAELAREELR.K	
593 - 602	1145.5637	1144.5564	1144.6087	-46	1	K.EIEAIKASER.L	
599 - 609	1142.5800	1141.5727	1141.6819	-96	1	K.ASERLALAAIK.A	
603 - 609	699.4271	698.4198	698.4690	-70	0	R.LALAAIK.A	
610 - 619	1065.5361	1064.5288	1064.4986	28	0	K.ALQESESSSK.E	
654 - 665	1130.5620	1129.5547	1129.5979	-38	0	R.VAAAVSEVGEAK.E	
681 - 685	679.3751	678.3678	678.3007	99	0	K.EMVER.K	Oxidation (M)
681 - 686	807.3885	806.3812	806.3956	-18	1	K.EMVERK.A	Oxidation (M)
768 - 774	963.4684	962.4612	962.4758	-15	0	R.FFMFLMK.K	
768 - 774	995.5084	994.5011	994.4656	36	0	R.FFMFLMK.K	2 Oxidation (M)
768 - 775	1107.5590	1106.5517	1106.5657	-13	1	R.FFMFLMKK.K	Oxidation (M)

Spot No.: **66**

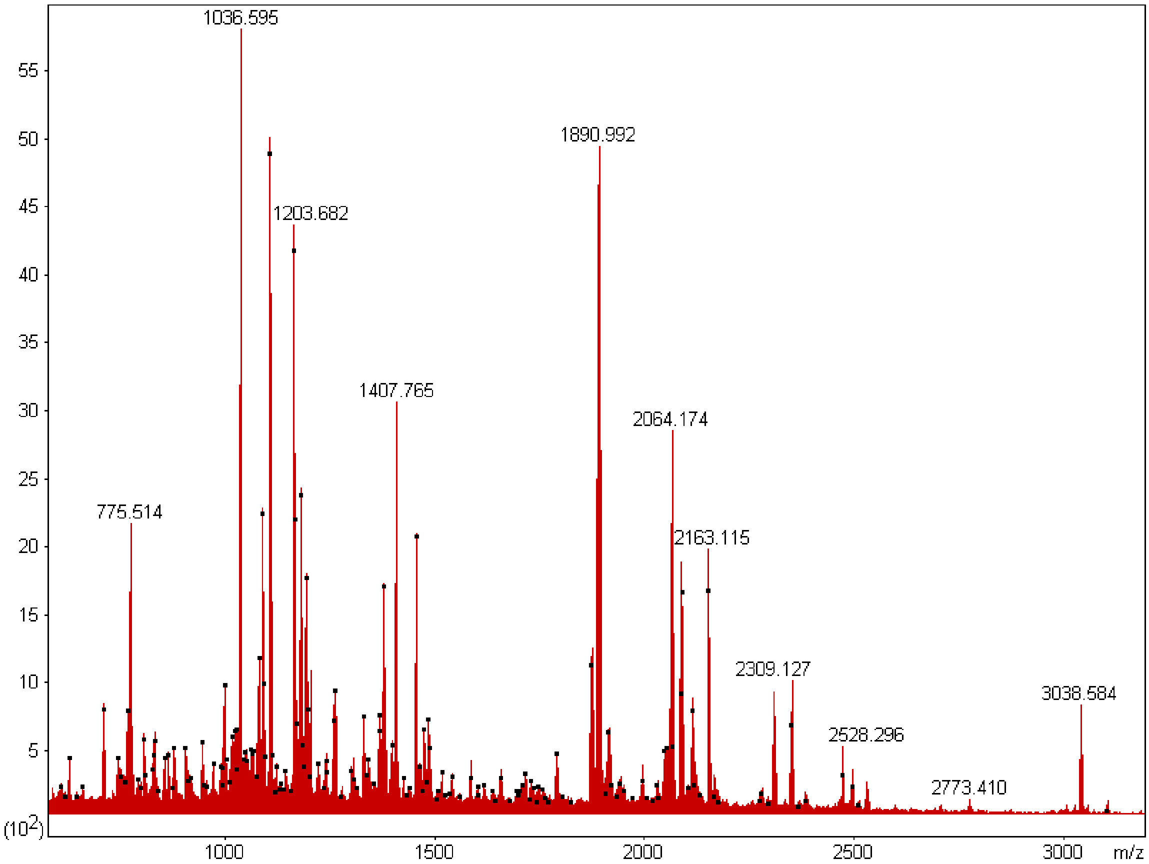
Mascot score: **82** Sequence coverage %: **40**

NCBI accession No.: **gi| 6093122**

Matched peptides No.: **19** Total peptides No.: **108**

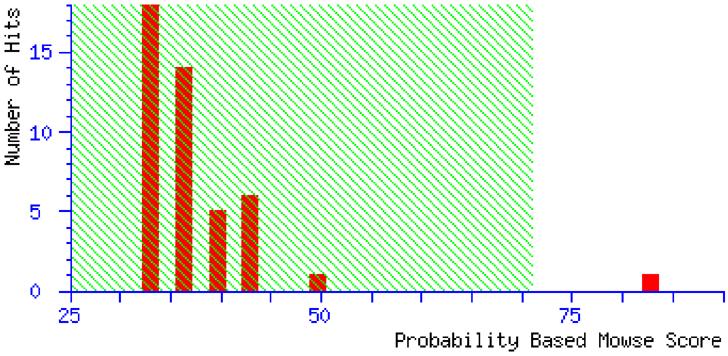
Calculated Mr: **65243** Calculated p*I*: **9.01**

Annotated PMF **spectra:**

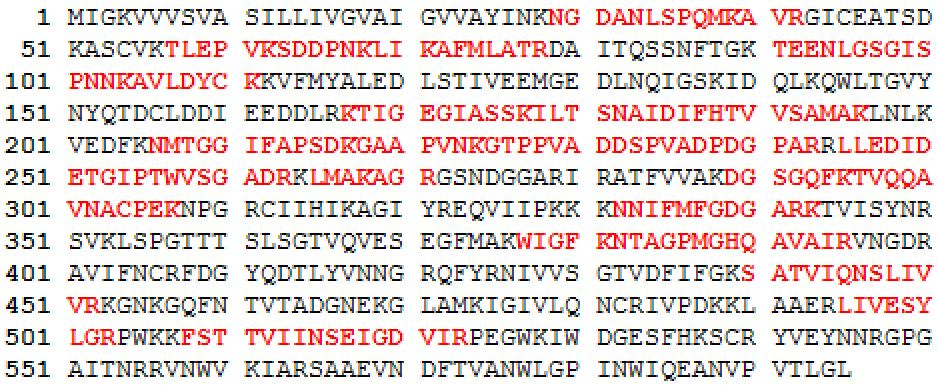


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red



```
  1 MIGKVVVSVA SILLIVGVAI GVVAYINKNG DANLSPQMKA VRGICEATSD
 51 KASCVKTLEP VKSDDPNKLI KAFMLATRDA ITQSSNFTGK TEENLGSGIS
101 PNNKAVLDYC KKVFMYALED LSTIVEEMGE DLNQIGSKID QLKQWLTGVY
151 NYQTDCLDDI EEDDLRKTIG EGIASSKILT SNAIDIFHTV VSAMAKLNLK
201 VEDFKNMTGG IFAPSDKGAA PVNKGTPPVA DDSPVADPDG PARRLLEDID
251 ETGIPTWVSG ADRKLMAKAG RGSNDGGARI RATFVVAKDG SGQFKTVQQA
301 VNACPEKNPG RCIIHIKAGI YREQVIIPKK KNNIFMFGDG ARKTVISYNR
351 SVKLSPGTTT SLSGTVQVES EGFMAKWIGF KNTAGPMGHQ AVAIRVNGDR
401 AVIFNCRFDG YQDTLYVNNG RQFYRNIVVS GTVDFIFGKS ATVIQNSLIV
451 VRKGNKGQFN TVTADGNEKG LAMKIGIVLQ NCRIVPDKKL AAERLIVESY
501 LGRPWKKFST TVIINSEIGD VIRPEGWKIW DGESFHKSCR YVEYNNRGPG
551 AITNRRVNWV KIARSAAEVN DFTVANWLGP INWIQEANVP VTLGL
```

Matched peptides information:

```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   29 - 42     1516.7710  1515.7637  1515.7464       11      1  K.NGDANLSPQMKAVR.G  Oxidation (M)
   57 - 68     1342.7524  1341.7451  1341.6776       50      1  K.TLEPVKSDDPNK.L
   63 - 71     1029.6295  1028.6222  1028.5502       70      1  K.SDDPNKLIK.A
   69 - 78     1179.6601  1178.6528  1178.6845      -27      1  K.LIKAFMLATR.D  Oxidation (M)
   72 - 78      809.4990   808.4917   808.4265       81      0  K.AFMLATR.D
   91 - 111    2309.1274  2308.1201  2308.1005        9      1  K.TEENLGSGISPNNKAVLDYCK.K
  167 - 177    1090.5915  1089.5842  1089.6030      -17      1  R.KTIGEGIASSK.I
  178 - 196    2047.0786  2046.0713  2046.0820       -5      0  K.ILTSNAIDIFHTVVSAMAK.L  Oxidation (M)
  206 - 224    1890.9918  1889.9845  1889.9305       29      1  K.NMTGGIFAPSDKGAAPVNK.G  Oxidation (M)
  218 - 243    2471.2484  2470.2411  2470.2088       13      1  K.GAAPVNKGTPPVADDSPVADPDGPAR.R
  245 - 263    2087.0282  2086.0209  2086.0219       -0      0  R.LLEDIDETGIPTWVSGADR.K
  265 - 271     746.4933   745.4861   745.4268       79      1  K.LMAKAGR.G
  289 - 307    2064.1742  2063.1669  2062.9742       93      1  K.DGSGQFKTVQQAVNACPEK.N
  332 - 342    1241.6377  1240.6304  1240.5659       52      0  K.NNIFMFGDGAR.K
  332 - 343    1369.7272  1368.7199  1368.6608       43      1  K.NNIFMFGDGARK.T
  377 - 395    2054.0916  2053.0843  2053.0680        8      1  K.WIGFKNTAGPMGHQAVAIR.V
  440 - 452    1399.7358  1398.7285  1398.8195      -65      0  K.SATVIQNSLIVVR.K
  495 - 503    1049.5827  1048.5754  1048.5917      -15      0  R.LIVESYLGR.P
  508 - 523    1763.8590  1762.8517  1762.9465      -54      0  K.FSTTVIINSEIGDVIR.P
```

Spot No.: **67**

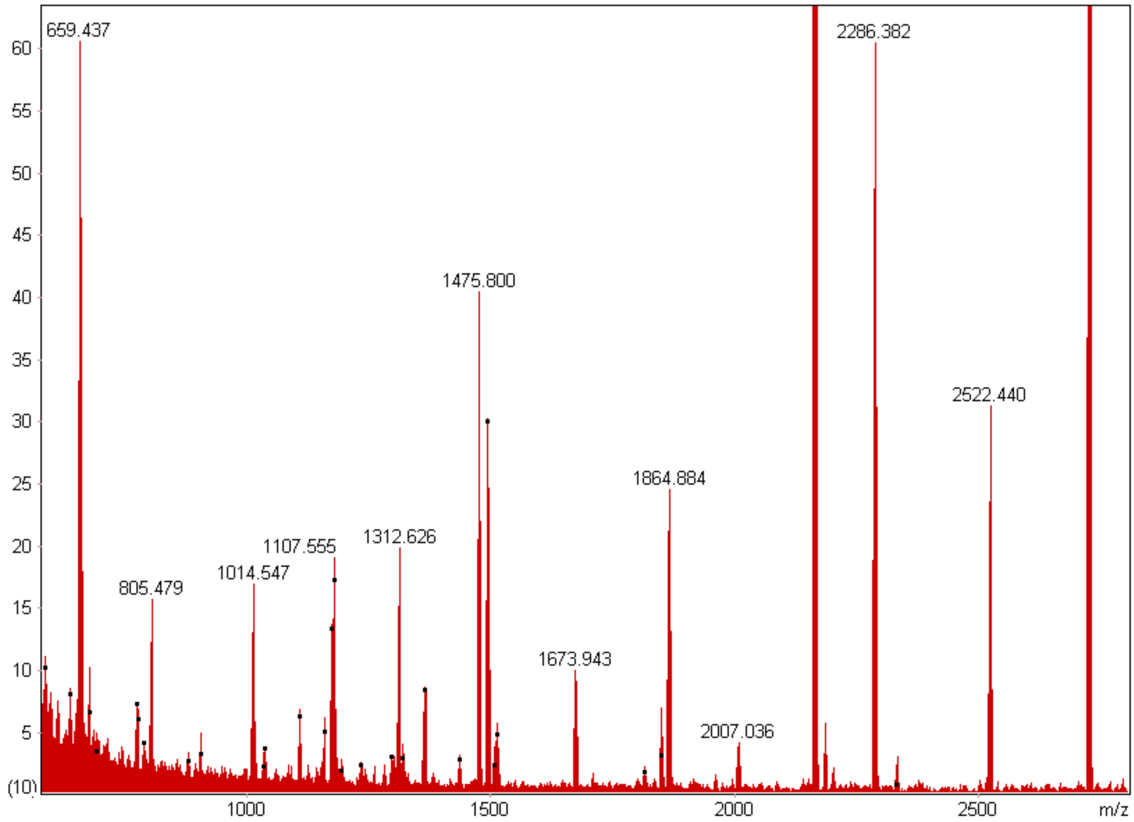
Mascot score: **81**   Sequence coverage %: **13**

NCBI accession No.: **gi| 302608108**

Matched peptides No.: **14**   Total peptides No.: **41**

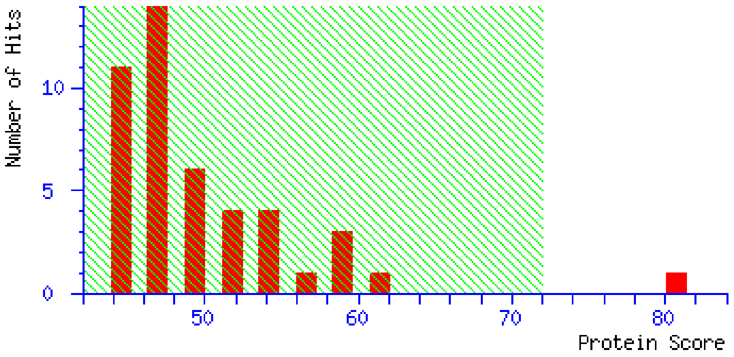
Calculated Mr: **109709**   Calculated *p*I: **5.88**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

```
  1 MASSERHHSI DAQVRNLAPG KVSEDDKLVE YDVLLMDRFL DILQDLHGPG
 51 IREFVQDCYE LSAEYEGDRN AARLKELGSR LASLAPADAI LVAGSIQHML
101 NLANLAEEVQ IAHRRRNKLK SGDFADEGSA TTESNIEETI KRLVDLGKSK
151 EEVFEALKNQ TVDLVLTAHP TQSVRRSLLQ KHARIRNCLT QLNAKDITDD
201 EKKEIDEDLH RAIQAAFRTD EIRRAQPTPQ DEMRYGMSYI HETIWKGVPK
251 FLRRVDTALK NIGIDERLPY NVPLIQFCSW MGGDRDGNPR VTPEVTRDVC
301 LLSRMMAANL YFSGLEDLMF ELSMWRCNDE LRARAQEIHS APKKAAKHYI
351 EFWKQIPLSE PYRVVLGNVR DKLYNTRERA RQLLTNEVSD IPEESVFSNV
401 QEFLEPLELC YKSLCESGDK TIADGSLLDF LRQVTAFGLS LVKLDIRQES
451 ERHTDVIDAI TTHIGIGSYR SWPEEKRQEW LLSELRGKRP LLAPDMPQTE
501 EIADVLGCFR VLAELPRDSF GPYIISMATA PSDVLAVELL QRECHVKEPL
551 PVVPLFERLA DLQNAPASME RLFSVDWYLE RINGKQQVMI GYSDSGKDAG
601 RLSAAWQLYR AQEELAQVAK RYSVKLTMFH GRGGTVGRGG GPSHLAILSQ
651 PPDTINGSIR VTVQGEVIEH SFGEEHLCFR TLERFTAATL EHGMHPPVSP
701 KPEWRKLMDE MAVVATEEYR SIVVREPRFV EYFRSATPET EYGKMNIGSR
751 PAKRKPQGGI TSLRAIPWIF SWTQTRFHLP VWLGVGAAFQ SAIKTDSKNI
801 QKLKEMYKEW PFFRVTIDLL EMVFAKGDPS IAALYDELLV ADDLKPFGEQ
851 LRNKYLETQQ FLLQIAGHKE ILEADPFLKQ SLRLRNPYIT TLNVFQAYTL
901 KLMRDPNFQV KKQPPLSKEF SDEKKPAGLV ELNPASEYAP GLEDTLILTM
951 KGIAAGMQNT G
```

Matched peptides information:

```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss Sequence
   28 - 38     1365.6647  1364.6574  1364.7010      -32     0  K.LVEYDVLLMDR.F
  149 - 158    1179.6158  1178.6085  1178.6183       -8     1  K.SKEEVFEALK.N
  327 - 334    1033.5170  1032.5097  1032.4771       32     1  R.CNDELRAR.A
  421 - 432    1320.6270  1319.6197  1319.7085      -67     0  K.TIADGSLLDFLR.Q
  453 - 476    2725.5368  2724.5295  2724.3507       66     1  R.HTDVIDAITTHIGIGSYRSWPEEK.R
  471 - 476     775.3743   774.3670   774.3548       16     0  R.SWPEEK.R
  586 - 597    1312.6262  1311.6189  1311.6129        5     0  K.QQVMIGYSDSGK.D
  602 - 610    1107.5548  1106.5475  1106.5873      -36     0  R.LSAAWQLYR.A
  702 - 705     587.2878   586.2806   586.2863      -10     0  K.PEWR.K
  745 - 750     677.3478   676.3405   676.3326       12     0  K.MNIGSR.P
  745 - 750     693.3537   692.3464   692.3275       27     0  K.MNIGSR.P  Oxidation (M)
  809 - 814     881.4321   880.4248   880.4232        2     0  K.EWPFFR.V
  870 - 879    1174.6735  1173.6662  1173.6281       32     0  K.EILEADPFLK.Q
  886 - 904    2286.3819  2285.3746  2285.2242       66     1  R.NPYITTLNVFQAYTLKLMR.D
```

Spot No.: **68**

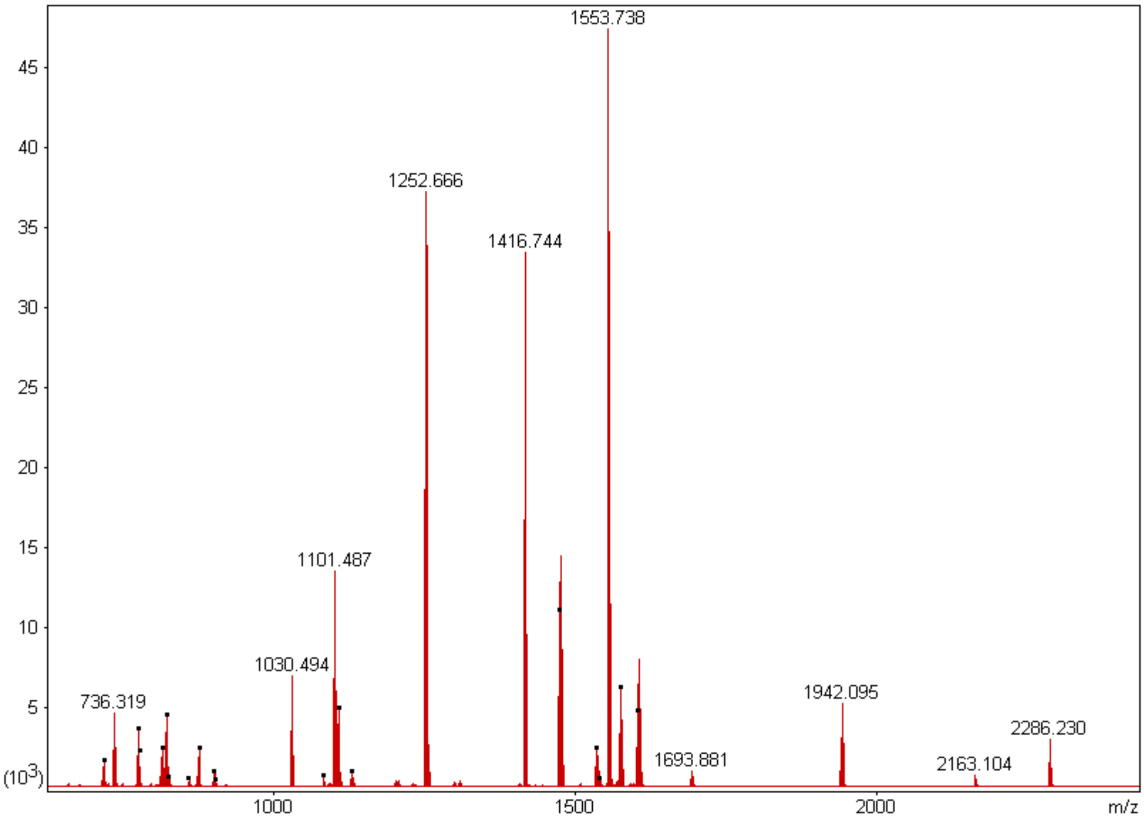
Mascot score: **236**   Sequence coverage %: **33**

NCBI accession No.: **gi| 7525018**

Matched peptides No.: **19**   Total peptides No.: **29**

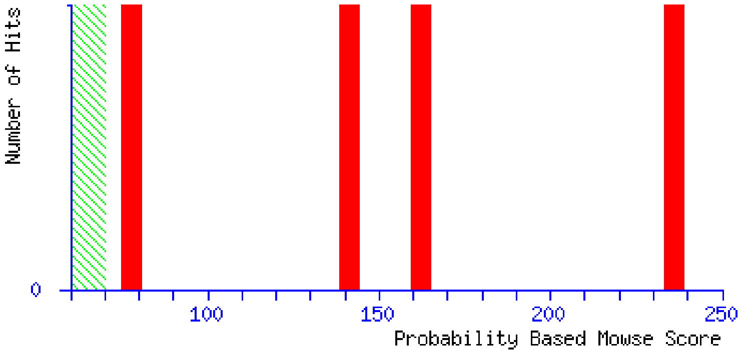
Calculated Mr: **55351**   Calculated *p*I: **5.19**

Annotated PMF **spectra:**

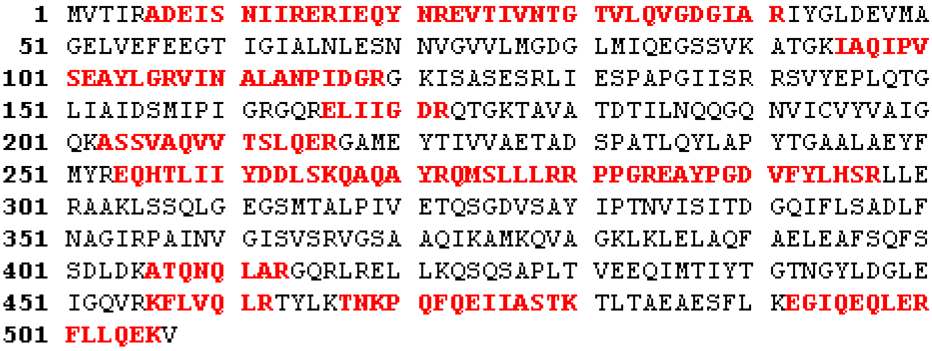


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

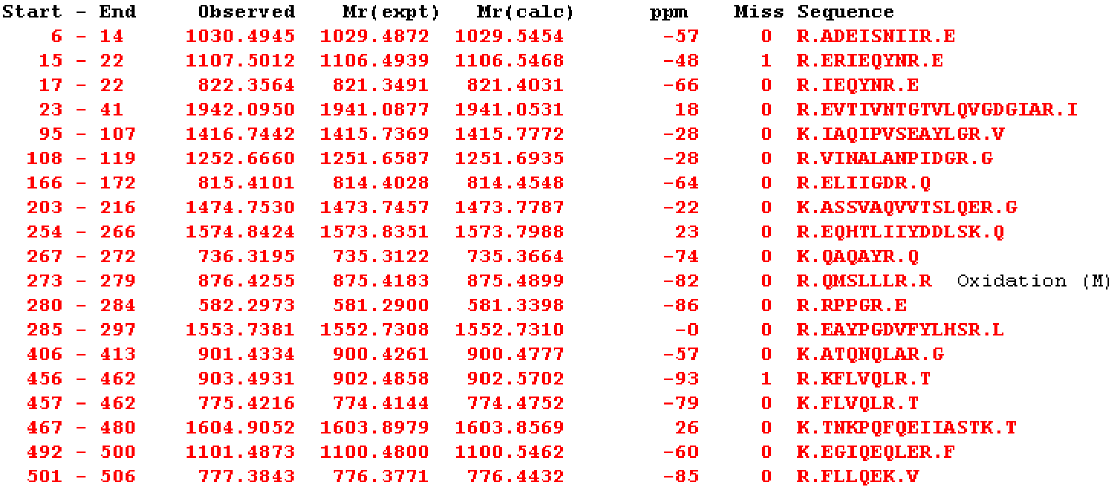


Matched peptide sequences: shown in Bold Red



```
  1 MVTIRADEIS NIIRERIEQY NREVTIVNTG TVLQVGDGIA RIYGLDEVMA
 51 GELVEFEEGT IGIALNLESN NVGVVLMGDG LMIQEGSSVK ATGKIAQIPV
101 SEAYLGRVIN ALANPIDGRG KISASESRLI ESPAPGIISR RSVYEPLQTG
151 LIAIDSMIPI GRGQRELIIG DRQTGKTAVA TDTILNQQGQ NVICVYVAIG
201 QKASSVAQVV TSLQERGAME YTIVVAETAD SPATLQYLAP YTGAALAEYF
251 MYREQHTLII YDDLSKQAQA YRQMSLLLRR PPGREAYPGD VFYLHSRLLE
301 RAAKLSSQLG EGSMTALPIV ETQSGDVSAY IPTNVISITD GQIFLSADLF
351 NAGIRPAINV GISVSRVGSA AQIKAMKQVA GKLKLELAQF AELEAFSQFS
401 SDLDKATQNQ LARGQRLREL LKQSQSAPLT VEEQIMTIYT GTNGYLDGLE
451 IGQVRKFLVQ LRTYLKTNKP QFQEIIASTK TLTAEAESFL KEGIQEQLER
501 FLLQEKV
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss Sequence
    6 - 14     1030.4945  1029.4872  1029.5454      -57    0   R.ADEISNIIR.E
   15 - 22     1107.5012  1106.4939  1106.5468      -48    1   R.ERIEQYNR.E
   17 - 22      822.3564   821.3491   821.4031      -66    0   R.IEQYNR.E
   23 - 41     1942.0950  1941.0877  1941.0531       18    0   R.EVTIVNTGTVLQVGDGIAR.I
   95 - 107    1416.7442  1415.7369  1415.7772      -28    0   K.IAQIPVSEAYLGR.V
  108 - 119    1252.6660  1251.6587  1251.6935      -28    0   R.VINALANPIDGR.G
  166 - 172     815.4101   814.4028   814.4548      -64    0   R.ELIIGDR.Q
  203 - 216    1474.7530  1473.7457  1473.7787      -22    0   K.ASSVAQVVTSLQER.G
  254 - 266    1574.8424  1573.8351  1573.7988       23    0   R.EQHTLIIYDDLSK.Q
  267 - 272     736.3195   735.3122   735.3664      -74    0   K.QAQAYR.Q
  273 - 279     876.4255   875.4183   875.4899      -82    0   R.QMSLLLR.R  Oxidation (M)
  280 - 284     582.2973   581.2900   581.3398      -86    0   R.RPPGR.E
  285 - 297    1553.7381  1552.7308  1552.7310       -0    0   R.EAYPGDVFYLHSR.L
  406 - 413     901.4334   900.4261   900.4777      -57    0   K.ATQNQLAR.G
  456 - 462     903.4931   902.4858   902.5702      -93    1   R.KFLVQLR.T
  457 - 462     775.4216   774.4144   774.4752      -79    0   K.FLVQLR.T
  467 - 480    1604.9052  1603.8979  1603.8569       26    0   K.TNKPQFQEIIASTK.T
  492 - 500    1101.4873  1100.4800  1100.5462      -60    0   K.EGIQEQLER.F
  501 - 506     777.3843   776.3771   776.4432      -85    0   R.FLLQEK.V
```

Spot No.: **69**

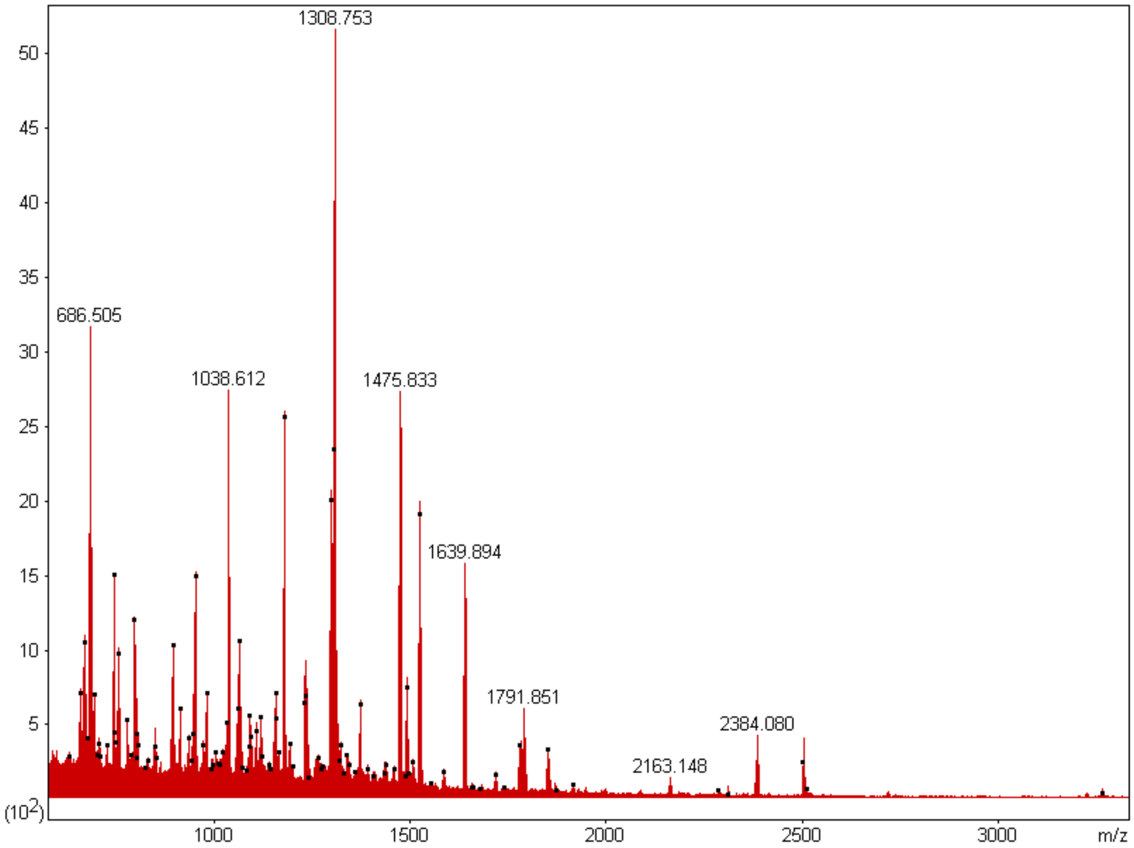
Mascot score: **82**   Sequence coverage %: **31**

NCBI accession No.: **gi| 157830716**

Matched peptides No.: **8**   Total peptides No.: **103**

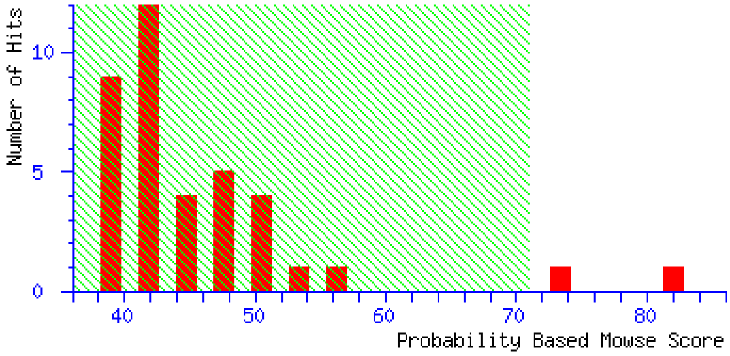
Calculated Mr: **27386**   Calculated *p*I: **6.23**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 **YPIFAQQNYE NPR**EATGRIV CANCHLASKP VDIEVPQAVL PDTVFEAVVK
51 **IPYDMQLK**QV LANGKKGALN VGAVLILPEG FELAPPDRIS PEMKEKIGNL
101 SFQNYRPNKK **NILVIGPVPG QK**YSEITFPI LAPDPATNKD VHFLK**YPIYV**
151 **GGNR**GRGQIY PDGSKSNNTV YNATAGGIIS KILRK**EKGGY EITIVDASNE**
201 **RQVIDIIPRG LELLVSEGES IK**LDQPLTSN PNVGGFGQGD AEIVLQDPLR
251

Matched peptides information:

```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    1 - 13     1639.8944  1638.8871  1638.7790       66      0  -.YPIFAQQNYENPR.E
   51 - 58     1023.5653  1022.5580  1022.5107       46      0  K.IPYDMQLK.Q   Oxidation (M)
  111 - 122    1234.6917  1233.6844  1233.7445      -49      0  K.NILVIGPVPGQK.Y
  146 - 154    1038.6123  1037.6050  1037.5294       73      0  K.YPIYVGGNR.G
  186 - 201    1780.9733  1779.9660  1779.8639       57      1  K.EKGGYEITIVDASNER.Q
  188 - 201    1523.8261  1522.8188  1522.7263       61      0  K.GGYEITIVDASNER.Q
  202 - 209     953.6410   952.6338   952.5706       66      0  R.QVIDIIPR.G
  210 - 222    1373.7862  1372.7789  1372.7449       25      0  R.GLELLVSEGESIK.L
```

Spot No.: **70**

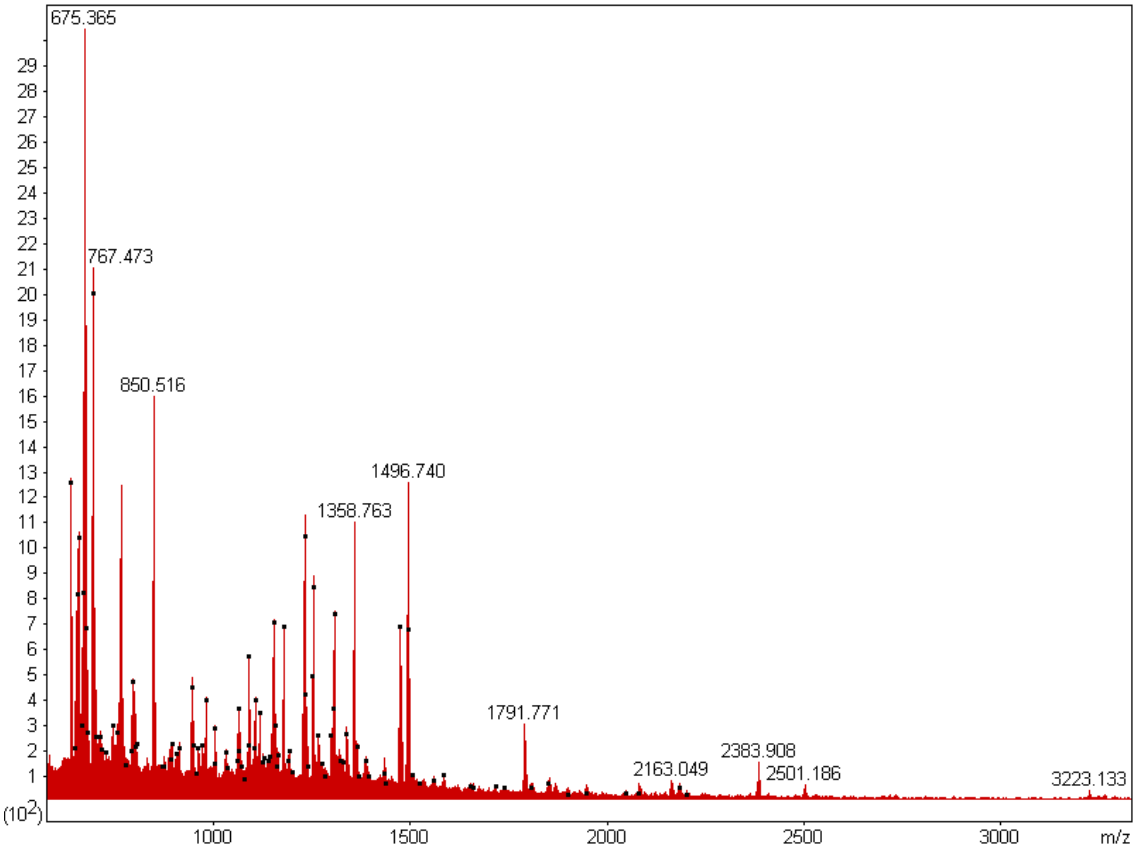
Mascot score: **84**   Sequence coverage %: **46**

NCBI accession No.: **gi| 222640350**

Matched peptides No.: **14**   Total peptides No.: **104**

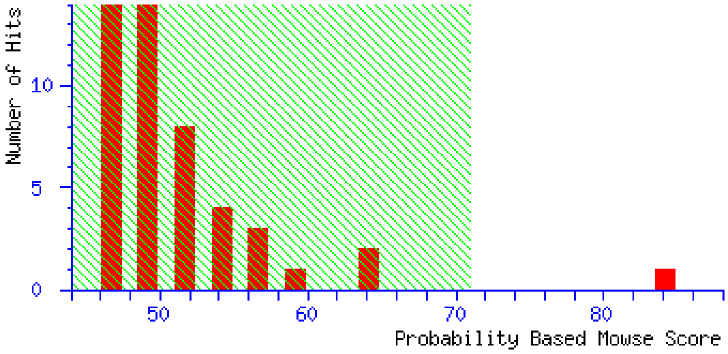
Calculated Mr: **23549**   Calculated p*I*: **11.42**

Annotated PMF **spectra:**

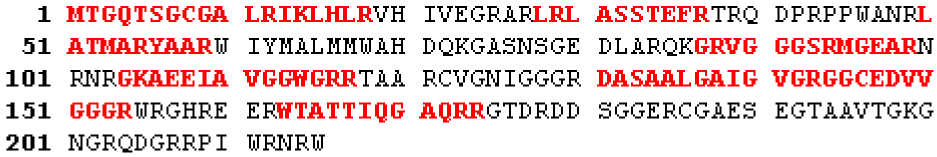


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

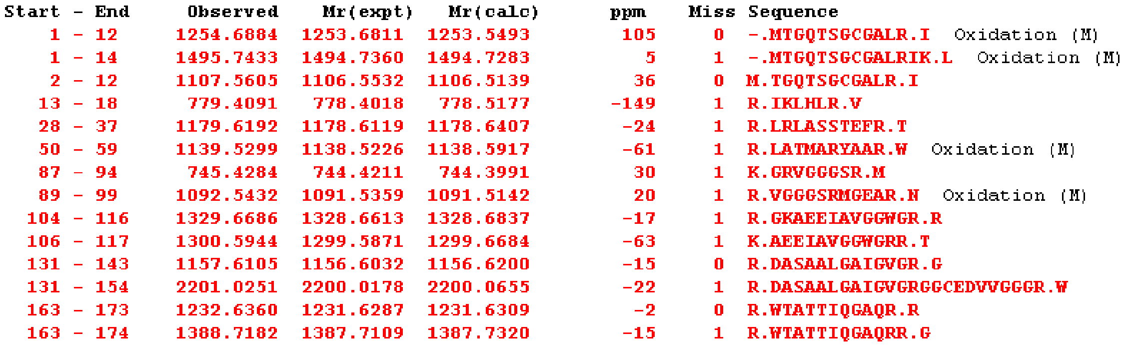


Matched peptide sequences: shown in Bold Red



```
  1 MTGQTSGCGA LRIKLHLRVH IVEGRARLRL ASSTEFRTRQ DPRPPWANRL
 51 ATMARYAARW IYMALMMWAH DQKGASNSGE DLARQKGRVG GGSRMGEARN
101 RNRGKAEEIA VGGWGRRTAA RCVGNIGGGR DASAALGAIG VGRGGCEDVV
151 GGGRWRGHRE ERWTATTIQG AQRRGTDRDD SGGERCGAES EGTAAVTGKG
201 NGRQDGRRPI WRNRW
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)     ppm   Miss Sequence
    1 - 12     1254.6884  1253.6811  1253.5493     105     0  -.MTGQTSGCGALR.I  Oxidation (M)
    1 - 14     1495.7433  1494.7360  1494.7283       5     1  -.MTGQTSGCGALRIK.L  Oxidation (M)
    2 - 12     1107.5605  1106.5532  1106.5139      36     0  M.TGQTSGCGALR.I
   13 - 18      779.4091   778.4018   778.5177    -149     1  R.IKLHLR.V
   28 - 37     1179.6192  1178.6119  1178.6407     -24     1  R.LRLASSTEFR.T
   50 - 59     1139.5299  1138.5226  1138.5917     -61     1  R.LATMARYAAR.W  Oxidation (M)
   87 - 94      745.4284   744.4211   744.3991      30     1  K.GRVGGGSR.M
   89 - 99     1092.5432  1091.5359  1091.5142      20     1  R.VGGGSRMGEAR.N  Oxidation (M)
  104 - 116    1329.6686  1328.6613  1328.6837     -17     1  R.GKAEEIAVGGWGR.R
  106 - 117    1300.5944  1299.5871  1299.6684     -63     1  K.AEEIAVGGWGRR.T
  131 - 143    1157.6105  1156.6032  1156.6200     -15     0  R.DASAALGAIGVGR.G
  131 - 154    2201.0251  2200.0178  2200.0655     -22     1  R.DASAALGAIGVGRGGCEDVVGGGR.W
  163 - 173    1232.6360  1231.6287  1231.6309      -2     0  R.WTATTIQGAQR.R
  163 - 174    1388.7182  1387.7109  1387.7320     -15     1  R.WTATTIQGAQRR.G
```

Spot No.: **71**

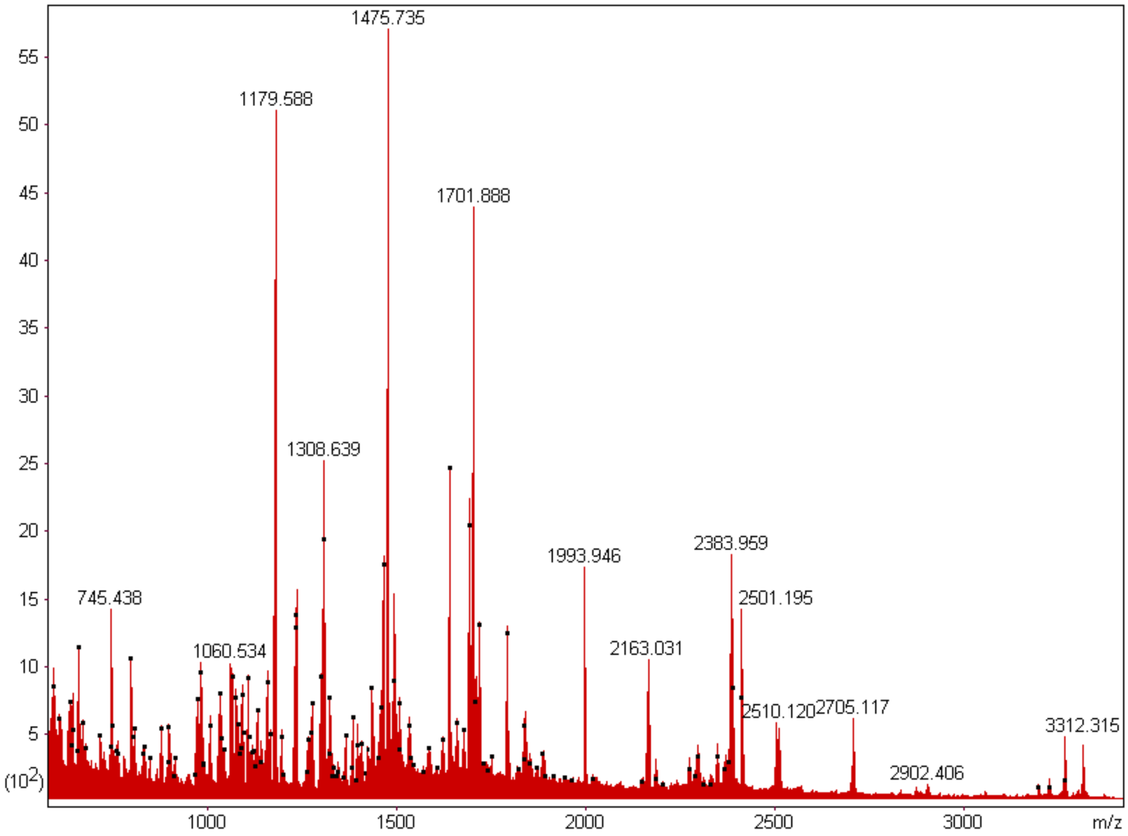
Mascot score: **81**	Sequence coverage %: **20**

NCBI accession No.: **gi| 44190501**

Matched peptides No.: **15**	Total peptides No.: **65**

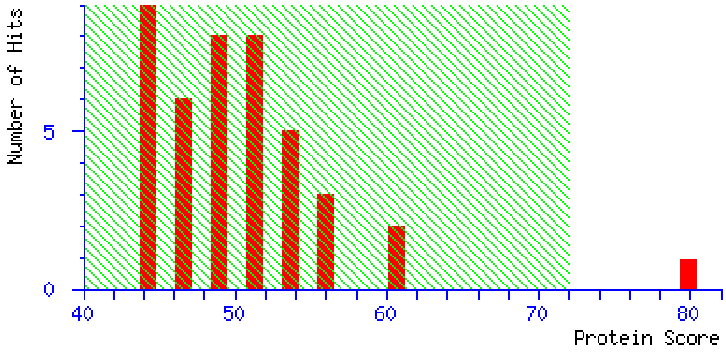
Calculated Mr: **84907**	Calculated *p*I: **5.69**

Annotated PMF **spectra:**

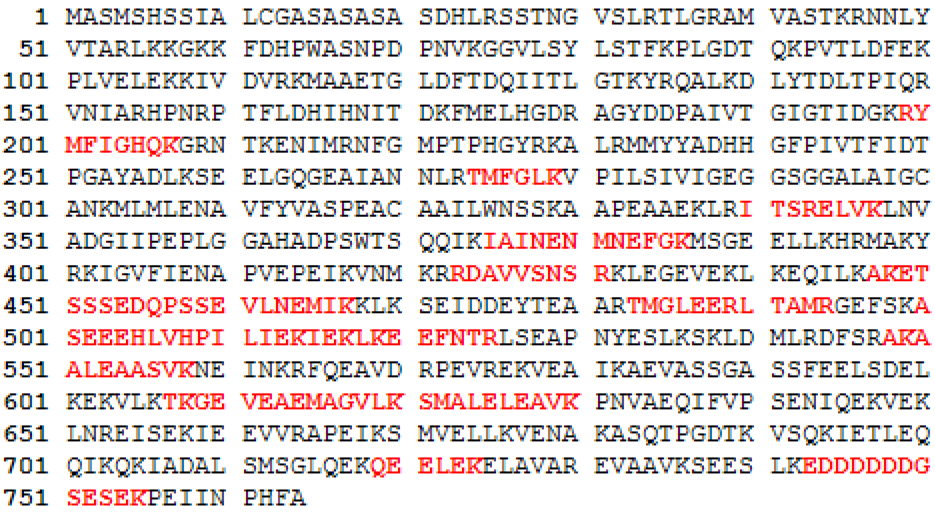


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

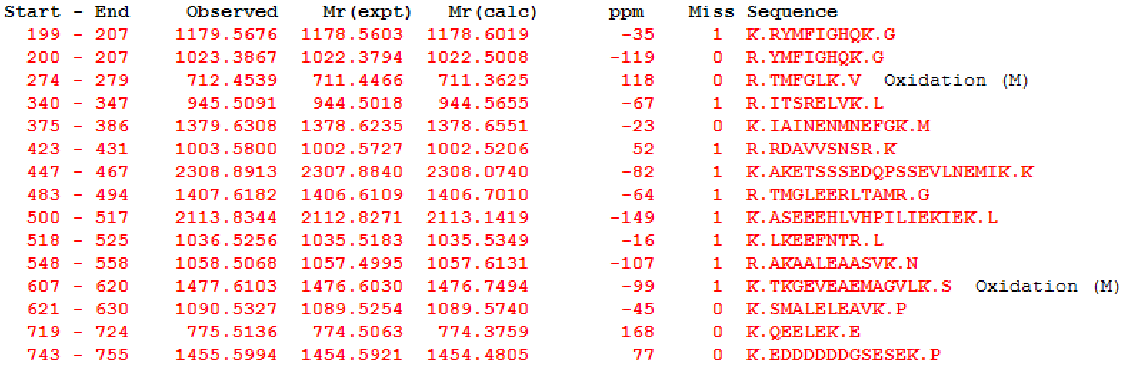


Matched peptide sequences: shown in Bold Red



```
  1 MASMSHSSIA LCGASASASA SDHLRSSTNG VSLRTLGRAM VASTKRNNLY
 51 VTARLKKGKK FDHPWASNPD PNVKGGVLSY LSTFKPLGDT QKPVTLDFEK
101 PLVELEKKIV DVRKMAAETG LDFTDQIITL GTKYRQALKD LYTDLTPIQR
151 VNIARHPNRP TFLDHIHNIT DKFMELHGDR AGYDDPAIVT GIGTIDGKRY
201 MFIGHQKGRN TKENIMRNFG MPTPHGYRKA LRMMYYADHH GFPIVTFIDT
251 PGAYADLKSE ELGQGEAIAN NLRTMFGLKV PILSIVIGEG GSGGALAIGC
301 ANKMLMLENA VFYVASPEAC AAILWNSSKA APEAAEKLRI TSRELVKLNV
351 ADGIIPEPLG GAHADPSWTS QQIKIAINEN MNEFGKMSGE ELLKHRMAKY
401 RKIGVFIENA PVEPEIKVNM KRRDAVVSNS RKLEGEVEKL KEQILKAKET
451 SSSEDQPSSE VLNEMIKKLK SEIDDEYTEA ARTMGLEERL TAMRGEFSKA
501 SEEEHLVHPI LIEKIEKLKE EFNTRLSEAP NYESLKSKLD MLRDFSRAKA
551 ALEAASVKNE INKRFQEAVD RPEVREKVEA IKAEVASSGA SSFEELSDEL
601 KEKVLKTKGE VEAEMAGVLK SMALELEAVK PNVAEQIFVP SENIQEKVEK
651 LNREISEKIE EVVRAPEIKS MVELLKVENA KASQTPGDTK VSQKIETLEQ
701 QIKQKIADAL SMSGLQEKQE ELEKELAVAR EVAAVKSEES LKEDDDDDDG
751 SESEKPEIIN PHFA
```

Matched peptides information:



```
Start - End      Observed    Mr(expt)   Mr(calc)      ppm    Miss  Sequence
  199 - 207     1179.5676   1178.5603  1178.6019      -35     1   K.RYMFIGHQK.G
  200 - 207     1023.3867   1022.3794  1022.5008     -119     0   R.YMFIGHQK.G
  274 - 279      712.4539    711.4466   711.3625      118     0   R.TMFGLK.V   Oxidation (M)
  340 - 347      945.5091    944.5018   944.5655      -67     1   R.ITSRELVK.L
  375 - 386     1379.6308   1378.6235  1378.6551      -23     0   K.IAINENMNEFGK.M
  423 - 431     1003.5800   1002.5727  1002.5206       52     1   R.RDAVVSNSR.K
  447 - 467     2308.8913   2307.8840  2308.0740      -82     1   K.AKETSSSEDQPSSEVLNEMIK.K
  483 - 494     1407.6182   1406.6109  1406.7010      -64     1   R.TMGLEERLTAMR.G
  500 - 517     2113.8344   2112.8271  2113.1419     -149     1   K.ASEEEHLVHPILIEKIEK.L
  518 - 525     1036.5256   1035.5183  1035.5349      -16     1   K.LKEEFNTR.L
  548 - 558     1058.5068   1057.4995  1057.6131     -107     1   R.AKAALEAASVK.N
  607 - 620     1477.6103   1476.6030  1476.7494      -99     1   K.TKGEVEAEMAGVLK.S   Oxidation (M)
  621 - 630     1090.5327   1089.5254  1089.5740      -45     0   K.SMALELEAVK.P
  719 - 724      775.5136    774.5063   774.3759      168     0   K.QEELEK.E
  743 - 755     1455.5994   1454.5921  1454.4805       77     0   K.EDDDDDDGSESEK.P
```

Spot No.: **72**

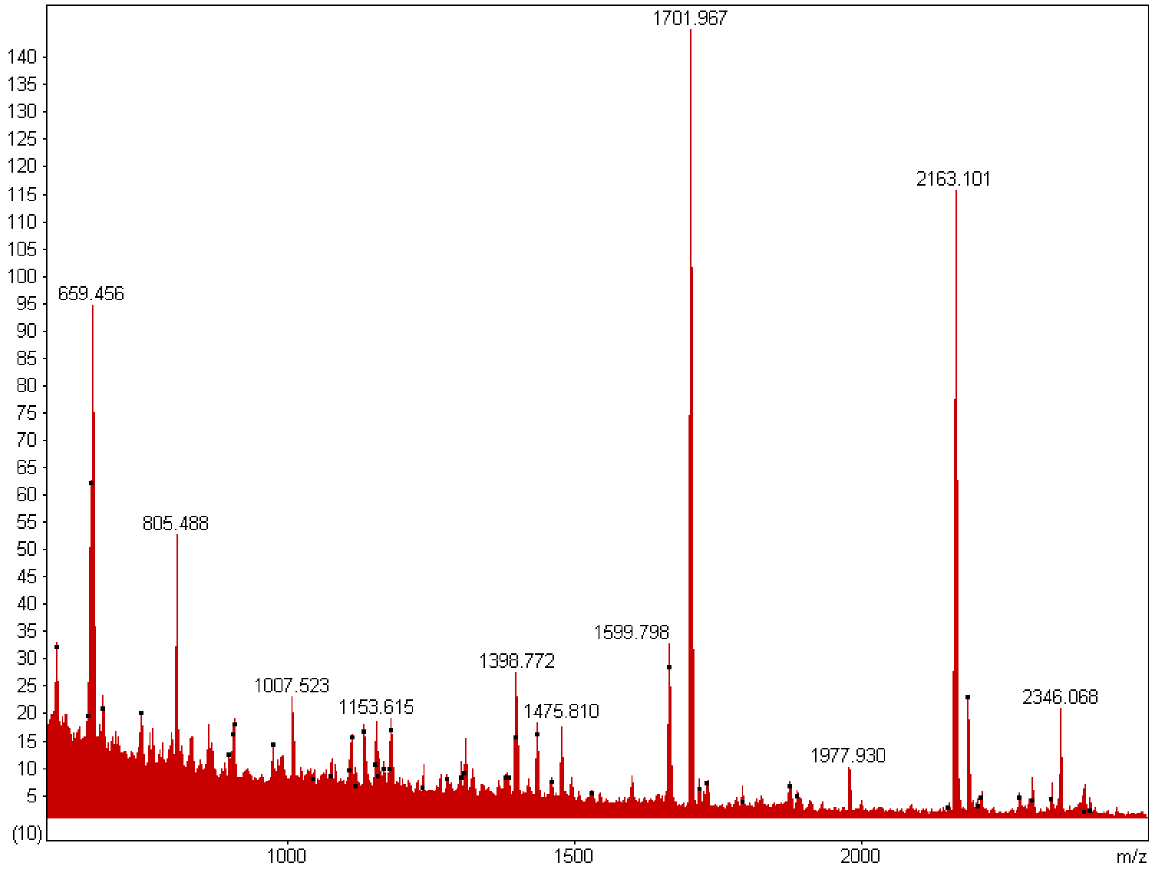
Mascot score: **102** Sequence coverage %: **28**

NCBI accession No.: **gi| 15220329**

Matched peptides No.: **11** Total peptides No.: **34**

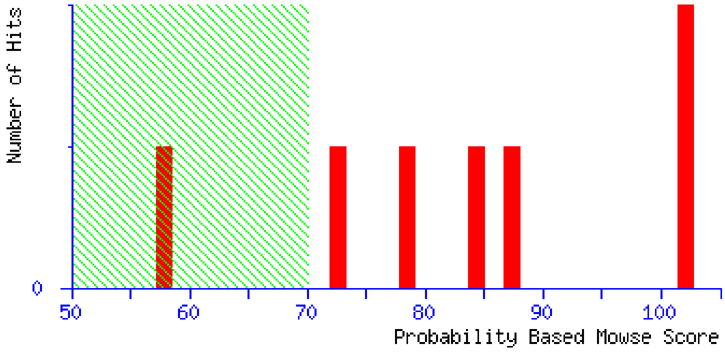
Calculated Mr: **50194** Calculated *p*I: **4.93**

Annotated PMF **spectra:**

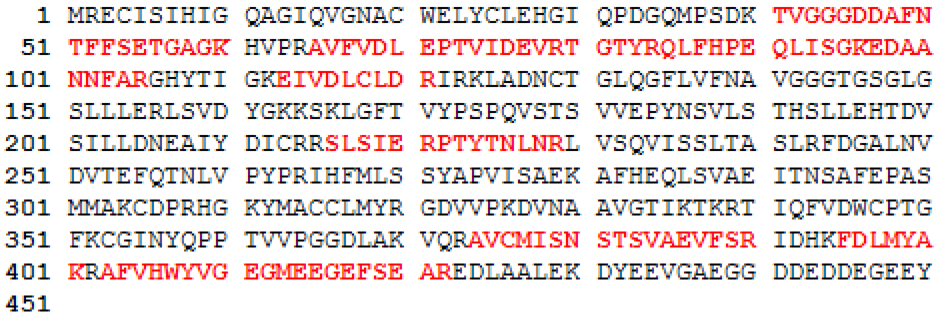


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

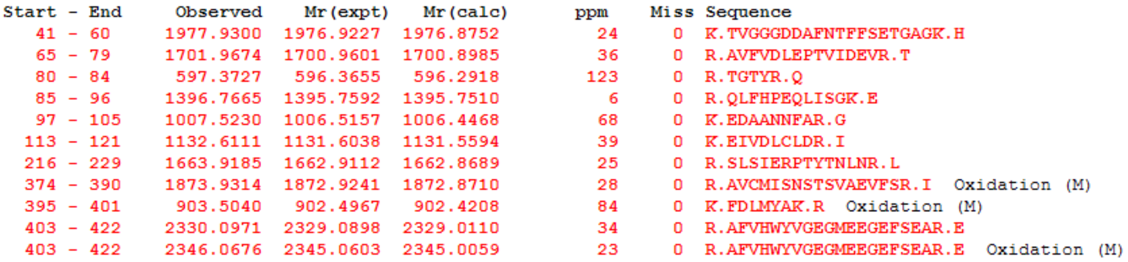


Matched peptide sequences: shown in Bold Red



```
  1 MRECISIHIG QAGIQVGNAC WELYCLEHGI QPDGQMPSDK TVGGGDDAFN
 51 TFFSETGAGK HVPRAVFVDL EPTVIDEVRT GTYRQLFHPE QLISGKEDAA
101 NNFARGHYTI GKEIVDLCLD RIRKLADNCT GLQGFLVFNA VGGGTGSGLG
151 SLLLERLSVD YGKKSKLGFT VYPSPQVSTS VVEPYNSVLS THSLLEHTDV
201 SILLDNEAIY DICRRSLSIE RPTYTNLNRL VSQVISSLTA SLRFDGALNV
251 DVTEFQTNLV PYPRIHFMLS SYAPVISAEK AFHEQLSVAE ITNSAFEPAS
301 MMAKCDPRHG KYMACCLMYR GDVVPKDVNA AVGTIKTKRT IQFVDWCPTG
351 FKCGINYQPP TVVPGGDLAK VQRAVCMISN STSVAEVFSR IDHKFDLMYA
401 KRAFVHWYVG EGMEEGEFSE AREDLAALEK DYEEVGAEGG DDEDDEGEEY
451
```

Matched peptides information:



```
Start - End     Observed    Mr(expt)   Mr(calc)      ppm    Miss Sequence
   41 - 60     1977.9300  1976.9227  1976.8752       24      0  K.TVGGGDDAFNTFFSETGAGK.H
   65 - 79     1701.9674  1700.9601  1700.8985       36      0  R.AVFVDLEPTVIDEVR.T
   80 - 84      597.3727   596.3655   596.2918      123      0  R.TGTYR.Q
   85 - 96     1396.7665  1395.7592  1395.7510        6      0  R.QLFHPEQLISGK.E
   97 - 105    1007.5230  1006.5157  1006.4468       68      0  K.EDAANNFAR.G
  113 - 121    1132.6111  1131.6038  1131.5594       39      0  K.EIVDLCLDR.I
  216 - 229    1663.9185  1662.9112  1662.8689       25      0  R.SLSIERPTYTNLNR.L
  374 - 390    1873.9314  1872.9241  1872.8710       28      0  R.AVCMISNSTSVAEVFSR.I  Oxidation (M)
  395 - 401     903.5040   902.4967   902.4208       84      0  K.FDLMYAK.R  Oxidation (M)
  403 - 422    2330.0971  2329.0898  2329.0110       34      0  R.AFVHWYVGEGMEEGEFSEAR.E
  403 - 422    2346.0676  2345.0603  2345.0059       23      0  R.AFVHWYVGEGMEEGEFSEAR.E  Oxidation (M)
```

Spot No.: **73**

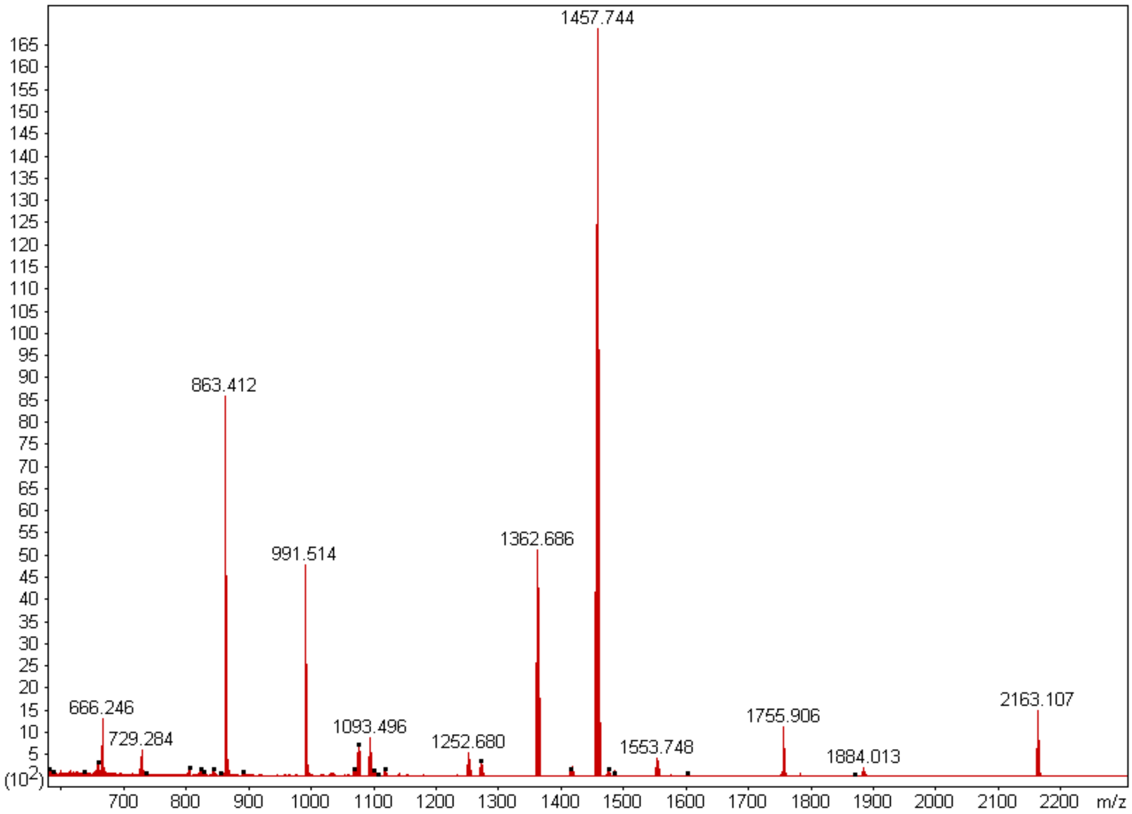
Mascot score: **82** Sequence coverage %: **15**

NCBI accession No.: **gi| 110738696**

Matched peptides No.: **11** Total peptides No.: **27**

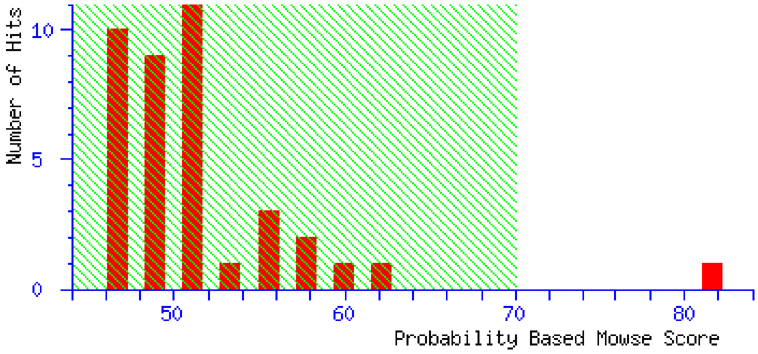
Calculated Mr: **71308** Calculated *p*I: **6.47**

Annotated PMF **spectra:**

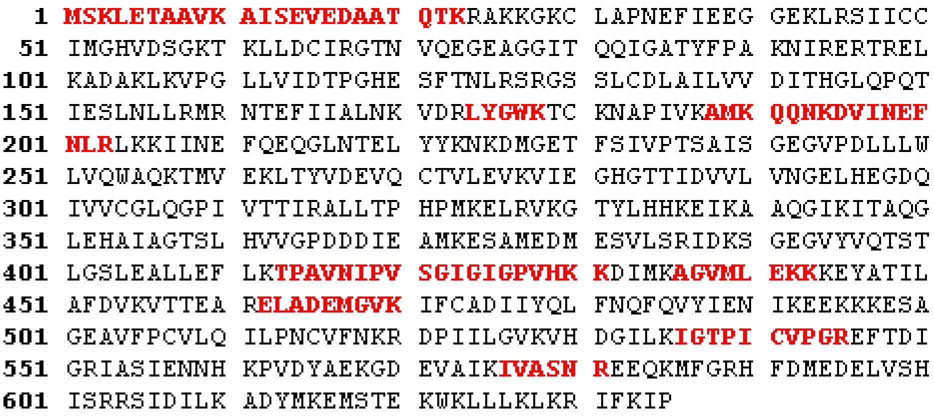


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).

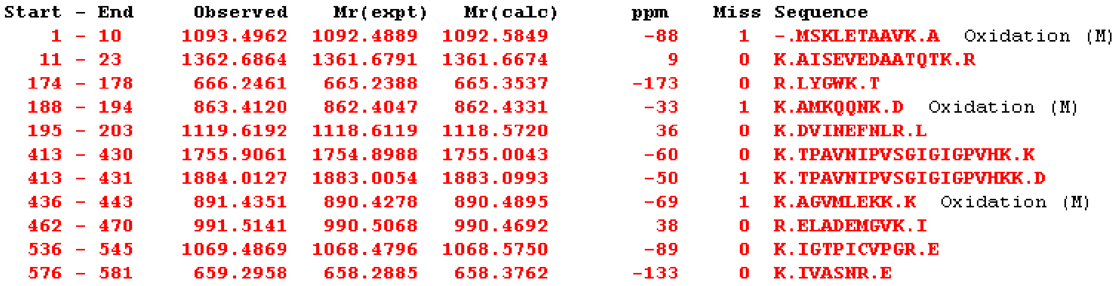


Matched peptide sequences: shown in Bold Red



```
  1 MSKLETAAVK AISEVEDAAT QTKRAKKGKC LAPNEFIEEG GEKLRSIICC
 51 IMGHVDSGKT KLLDCIRGTN VQEGEAGGIT QQIGATYFPA KNIRERTREL
101 KADAKLKVPG LLVIDTPGHE SFTNLRSRGS SLCDLAILVV DITHGLQPQT
151 IESLNLLRMR NTEFIIALNK VDRLYGWKTC KNAPIVKAMK QQNKDVINEF
201 NLRLKKIINE FQEQGLNTEL YYKNKDMGET FSIVPTSAIS GEGVPDLLLW
251 LVQWAQKTMV EKLTYVDEVQ CTVLEVKVIE GHGTTIDVVL VNGELHEGDQ
301 IVVCGLQGPI VTTIRALLTP HPMKELRVKG TYLHHKEIKA AQGIKITAQG
351 LEHAIAGTSL HVVGPDDDIE AMKESAMEDM ESVLSRIDKS GEGVYVQTST
401 LGSLEALLEF LKTPAVNIPV SGIGIGPVHK KDIMKAGVML EKKKEYATIL
451 AFDVKVTTEA RELADEMGVK IFCADIIYQL FNQFQVYIEN IKEEKKKESA
501 GEAVFPCVLQ ILPNCVFNKR DPIILGVKVH DGILKIGTPI CVPGREFTDI
551 GRIASIENNH KPVDYAEKGD EVAIKIVASN REEQKMFGRH FDMEDELVSH
601 ISRRSIDILK ADYMKEMSTE KWKLLLKLKR IFKIP
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss Sequence
    1 - 10     1093.4962  1092.4889  1092.5849      -88    1  -.MSKLETAAVK.A  Oxidation (M)
   11 - 23     1362.6864  1361.6791  1361.6674        9    0  K.AISEVEDAATQTK.R
  174 - 178     666.2461   665.2388   665.3537     -173    0  R.LYGWK.T
  188 - 194     863.4120   862.4047   862.4331      -33    1  K.AMKQQNK.D  Oxidation (M)
  195 - 203    1119.6192  1118.6119  1118.5720       36    0  K.DVINEFNLR.L
  413 - 430    1755.9061  1754.8988  1755.0043      -60    0  K.TPAVNIPVSGIGIGPVHK.K
  413 - 431    1884.0127  1883.0054  1883.0993      -50    1  K.TPAVNIPVSGIGIGPVHKK.D
  436 - 443     891.4351   890.4278   890.4895      -69    1  K.AGVMLEKK.K  Oxidation (M)
  462 - 470     991.5141   990.5068   990.4692       38    0  R.ELADEMGVK.I
  536 - 545    1069.4869  1068.4796  1068.5750      -89    0  K.IGTPICVPGR.E
  576 - 581     659.2958   658.2885   658.3762     -133    0  K.IVASNR.E
```

Spot No.: **74**

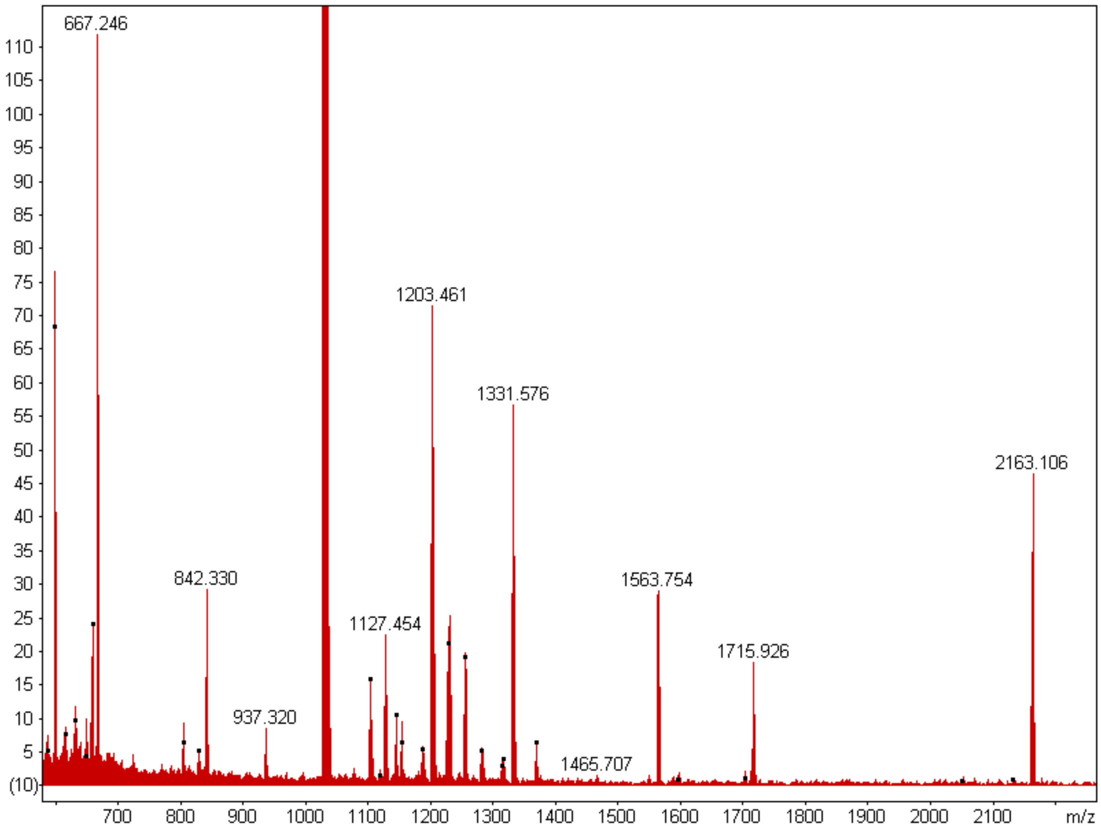
Mascot score: **170** Sequence coverage %: **32**

NCBI accession No.: **gi| 2493132**

Matched peptides No.: **17** Total peptides No.: **31**

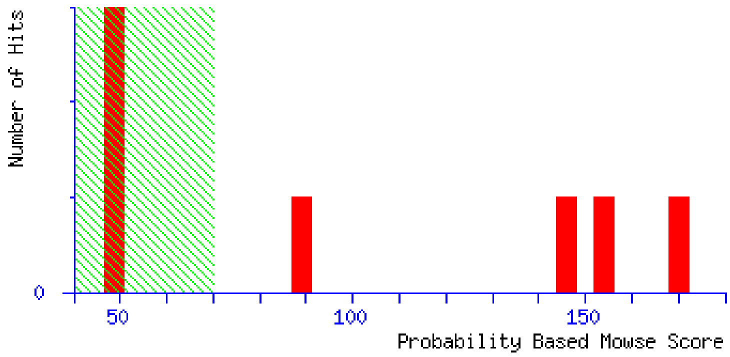
Calculated Mr: **53806** Calculated *p*I: **5.12**

Annotated PMF **spectra:**

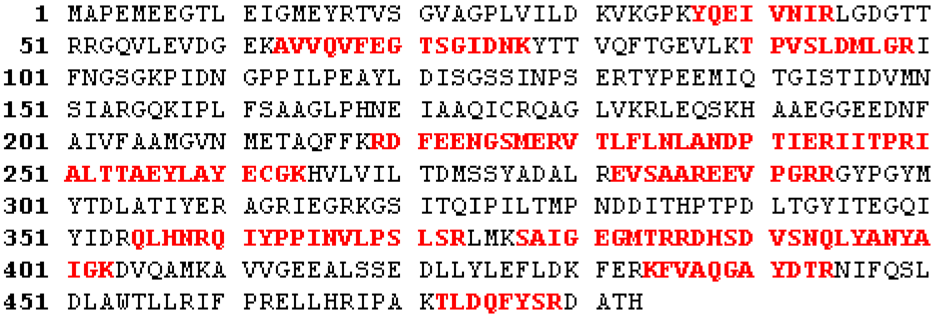


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

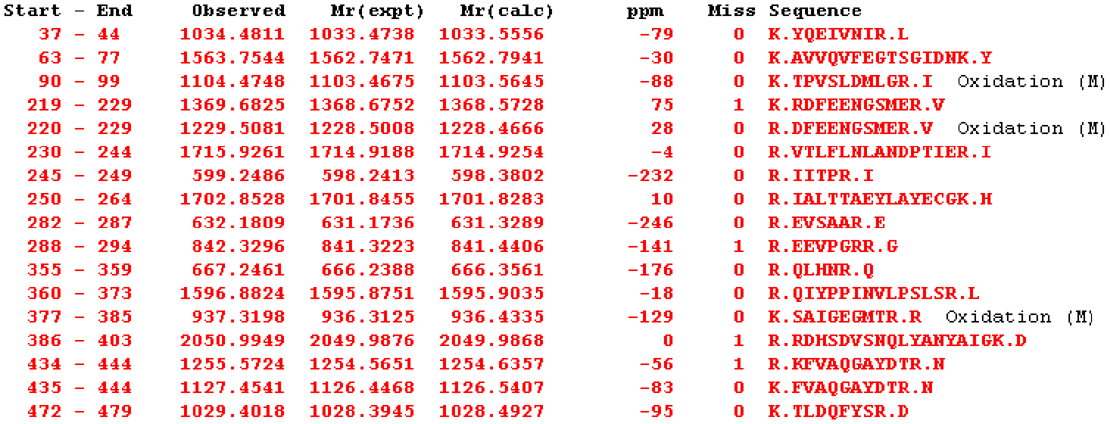


Matched peptide sequences: shown in Bold Red



```
  1 MAPEMEEGTL EIGMEYRTVS GVAGPLVILD KVKGPKYQEI VNIRLGDGTT
 51 RRGQVLEVDG EKAVVQVFEG TSGIDNKYTT VQFTGEVLKT PVSLDMLGRI
101 FNGSGKPIDN GPPILPEAYL DISGSSINPS ERTYPEEMIQ TGISTIDVMN
151 SIARGQKIPL FSAAGLPHNE IAAQICRQAG LVKRLEQSKH AAEGGEEDNF
201 AIVFAAMGVN METAQFFKRD FEENGSMERV TLFLNLANDP TIERIITPRI
251 ALTTAEYLAY ECGKHVLVIL TDMSSYADAL REVSAAREEV PGRRGYPGYM
301 YTDLATIYER AGRIEGRKGS ITQIPILTMP NDDITHPTPD LTGYITEGQI
351 YIDRQLHNRQ IYPPINVLPS LSRLMKSAIG EGMTRRDHSD VSNQLYANYA
401 IGKDVQAMKA VVGEEALSSE DLLYLEFLDK FERKFVAQGA YDTRNIFQSL
451 DLAWTLLRIF PRELLHRIPA KTLDQFYSRD ATH
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   37 - 44     1034.4811  1033.4738  1033.5556      -79     0  K.YQEIVNIR.L
   63 - 77     1563.7544  1562.7471  1562.7941      -30     0  K.AVVQVFEGTSGIDNK.Y
   90 - 99     1104.4748  1103.4675  1103.5645      -88     0  K.TPVSLDMLGR.I  Oxidation (M)
  219 - 229    1369.6825  1368.6752  1368.5728       75     1  K.RDFEENGSMER.V
  220 - 229    1229.5081  1228.5008  1228.4666       28     0  R.DFEENGSMER.V  Oxidation (M)
  230 - 244    1715.9261  1714.9188  1714.9254       -4     0  R.VTLFLNLANDPTIER.I
  245 - 249     599.2486   598.2413   598.3802     -232     0  R.IITPR.I
  250 - 264    1702.8528  1701.8455  1701.8283       10     0  R.IALTTAEYLAYECGK.H
  282 - 287     632.1809   631.1736   631.3289     -246     0  R.EVSAAR.E
  288 - 294     842.3296   841.3223   841.4406     -141     1  R.EEVPGRR.G
  355 - 359     667.2461   666.2388   666.3561     -176     0  R.QLHNR.Q
  360 - 373    1596.8824  1595.8751  1595.9035      -18     0  R.QIYPPINVLPSLSR.L
  377 - 385     937.3198   936.3125   936.4335     -129     0  K.SAIGEGMTR.R  Oxidation (M)
  386 - 403    2050.9949  2049.9876  2049.9868        0     1  R.RDHSDVSNQLYANYAIGK.D
  434 - 444    1255.5724  1254.5651  1254.6357      -56     1  R.KFVAQGAYDTR.N
  435 - 444    1127.4541  1126.4468  1126.5407      -83     0  K.FVAQGAYDTR.N
  472 - 479    1029.4018  1028.3945  1028.4927      -95     0  K.TLDQFYSR.D
```

Spot No.: **75**

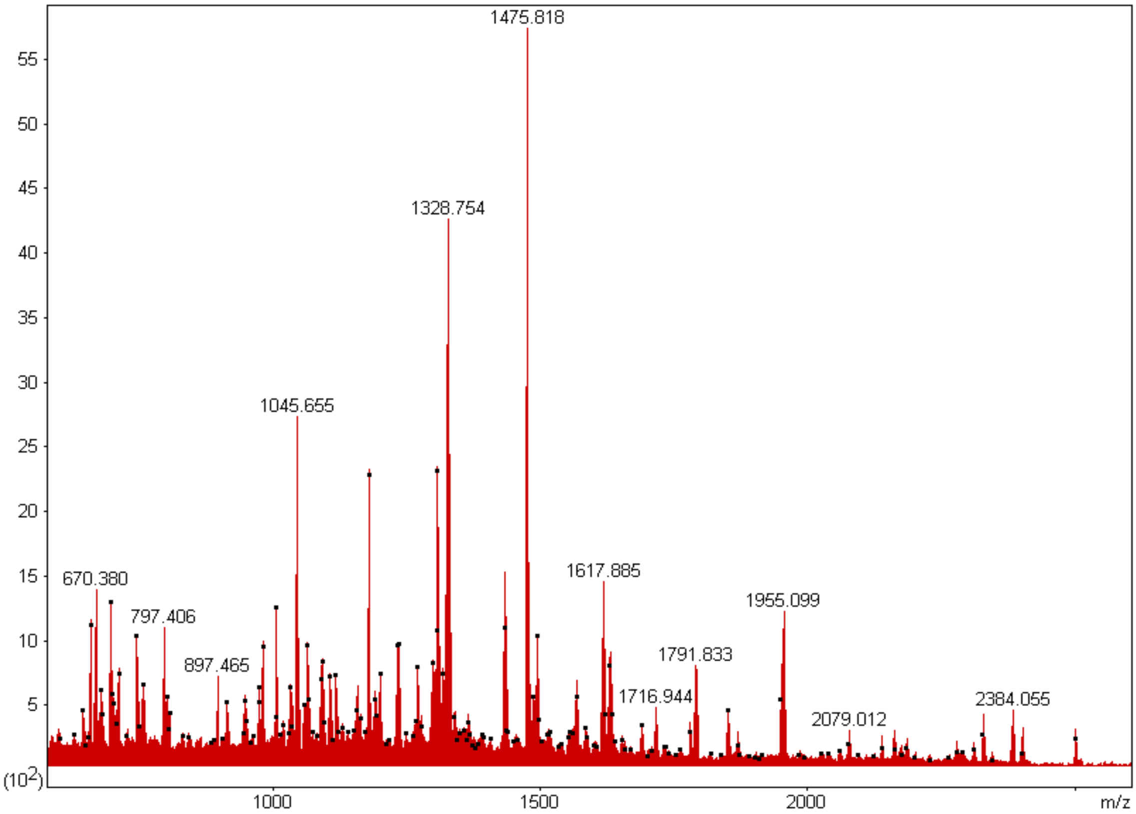
Mascot score: **109**   Sequence coverage %: **52**

NCBI accession No.: **gi| 7708185**

Matched peptides No.: **25**   Total peptides No.: **157**

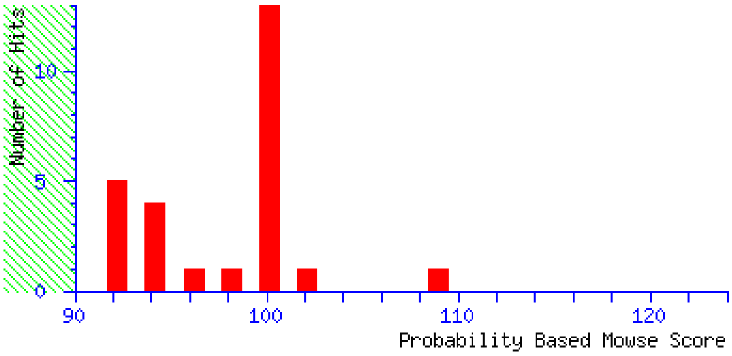
Calculated Mr: **52907**   Calculated *p*I: **5.21**

Annotated PMF **spectra:**

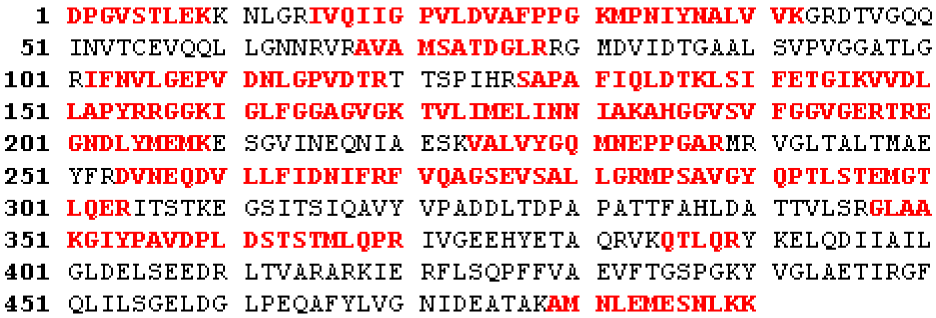


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

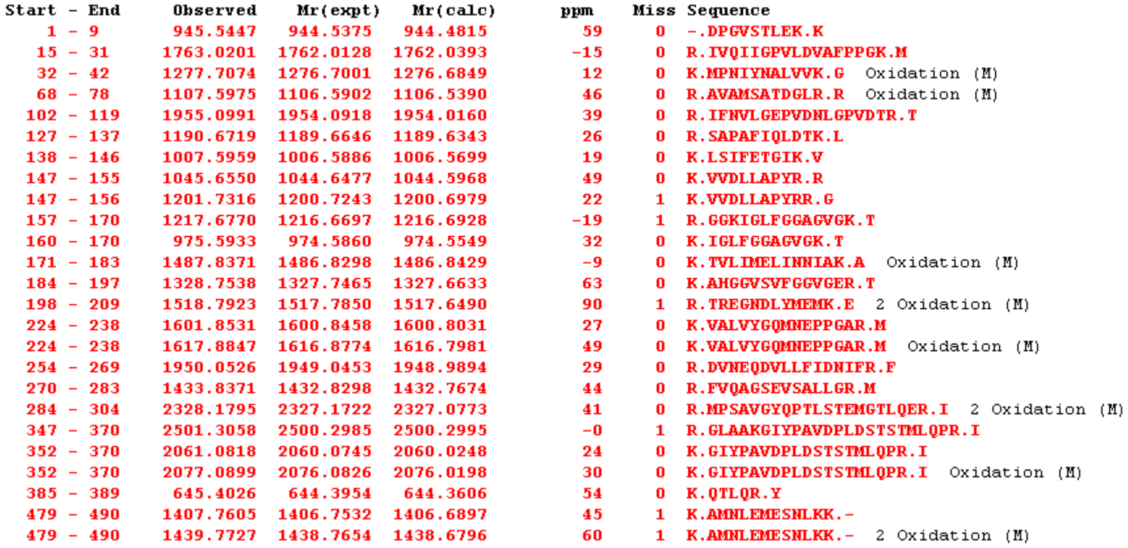


Matched peptide sequences: shown in Bold Red



1 **DPGVSTLEK**K NLGR**IVQIIG PVLDVAFPPG KMPNIYNALV VK**GRDTVGQQ
51 INVTCEVQQL LGNNRVR**AVA MSATDGLR**RG MDVIDTGAAL SVPVGGATLG
101 R**IFNVLGEPV DNLGPVDTR**T TSPIHR**SAPA FIQLDTKLSI FETGIKVVDL**
151 **LAPYRRGGKI GLFGGAGVGK TVLIMELINN IAKAHGGVSV FGGVGERTRE**
201 **GNDLYMEMK**E SGVINEQNIA ESK**VALVYGQ MNEPPGAR**MR VGLTALTMAE
251 YFR**DVNEQDV LLFIDNIFRF VQAGSEVSAL LGRMPSAVGY QPTLSTEMGT**
301 **LQER**ITSTKE GSITSIQAVY VPADDLTDPA PATTFAHLDA TTVLSR**GLAA**
351 **KGIYPAVDPL DSTSTMLQPR** IVGEEHYETA QRVK**QTLQR**Y KELQDIIAIL
401 GLDELSEEDR LTVARARKIE RFLSQPFFVA EVFTGSPGKY VGLAETIRGF
451 QLILSGELDG LPEQAFYLVG NIDEATAK**AM NLEMESNLKK**

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
1 - 9	945.5447	944.5375	944.4815	59	0	**-.DPGVSTLEK.K**
15 - 31	1763.0201	1762.0128	1762.0393	-15	0	**R.IVQIIGPVLDVAFPPGK.M**
32 - 42	1277.7074	1276.7001	1276.6849	12	0	**K.MPNIYNALVVK.G** Oxidation (M)
68 - 78	1107.5975	1106.5902	1106.5390	46	0	**R.AVAMSATDGLR.R** Oxidation (M)
102 - 119	1955.0991	1954.0918	1954.0160	39	0	**R.IFNVLGEPVDNLGPVDTR.T**
127 - 137	1190.6719	1189.6646	1189.6343	26	0	**R.SAPAFIQLDTK.L**
138 - 146	1007.5959	1006.5886	1006.5699	19	0	**K.LSIFETGIK.V**
147 - 155	1045.6550	1044.6477	1044.5968	49	0	**K.VVDLLAPYR.R**
147 - 156	1201.7316	1200.7243	1200.6979	22	1	**K.VVDLLAPYRR.G**
157 - 170	1217.6770	1216.6697	1216.6928	-19	1	**R.GGKIGLFGGAGVGK.T**
160 - 170	975.5933	974.5860	974.5549	32	0	**K.IGLFGGAGVGK.T**
171 - 183	1487.8371	1486.8298	1486.8429	-9	0	**K.TVLIMELINNIAK.A** Oxidation (M)
184 - 197	1328.7538	1327.7465	1327.6633	63	0	**K.AHGGVSVFGGVGER.T**
198 - 209	1518.7923	1517.7850	1517.6490	90	1	**R.TREGNDLYMEMK.E** 2 Oxidation (M)
224 - 238	1601.8531	1600.8458	1600.8031	27	0	**K.VALVYGQMNEPPGAR.M**
224 - 238	1617.8847	1616.8774	1616.7981	49	0	**K.VALVYGQMNEPPGAR.M** Oxidation (M)
254 - 269	1950.0526	1949.0453	1948.9894	29	0	**R.DVNEQDVLLFIDNIFR.F**
270 - 283	1433.8371	1432.8298	1432.7674	44	0	**R.FVQAGSEVSALLGR.M**
284 - 304	2328.1795	2327.1722	2327.0773	41	0	**R.MPSAVGYQPTLSTEMGTLQER.I** 2 Oxidation (M)
347 - 370	2501.3058	2500.2985	2500.2995	-0	1	**R.GLAAKGIYPAVDPLDSTSTMLQPR.I**
352 - 370	2061.0818	2060.0745	2060.0248	24	0	**K.GIYPAVDPLDSTSTMLQPR.I**
352 - 370	2077.0899	2076.0826	2076.0198	30	0	**K.GIYPAVDPLDSTSTMLQPR.I** Oxidation (M)
385 - 389	645.4026	644.3954	644.3606	54	0	**K.QTLQR.Y**
479 - 490	1407.7605	1406.7532	1406.6897	45	1	**K.AMNLEMESNLKK.-**
479 - 490	1439.7727	1438.7654	1438.6796	60	1	**K.AMNLEMESNLKK.-** 2 Oxidation (M)

Spot No.: **76**

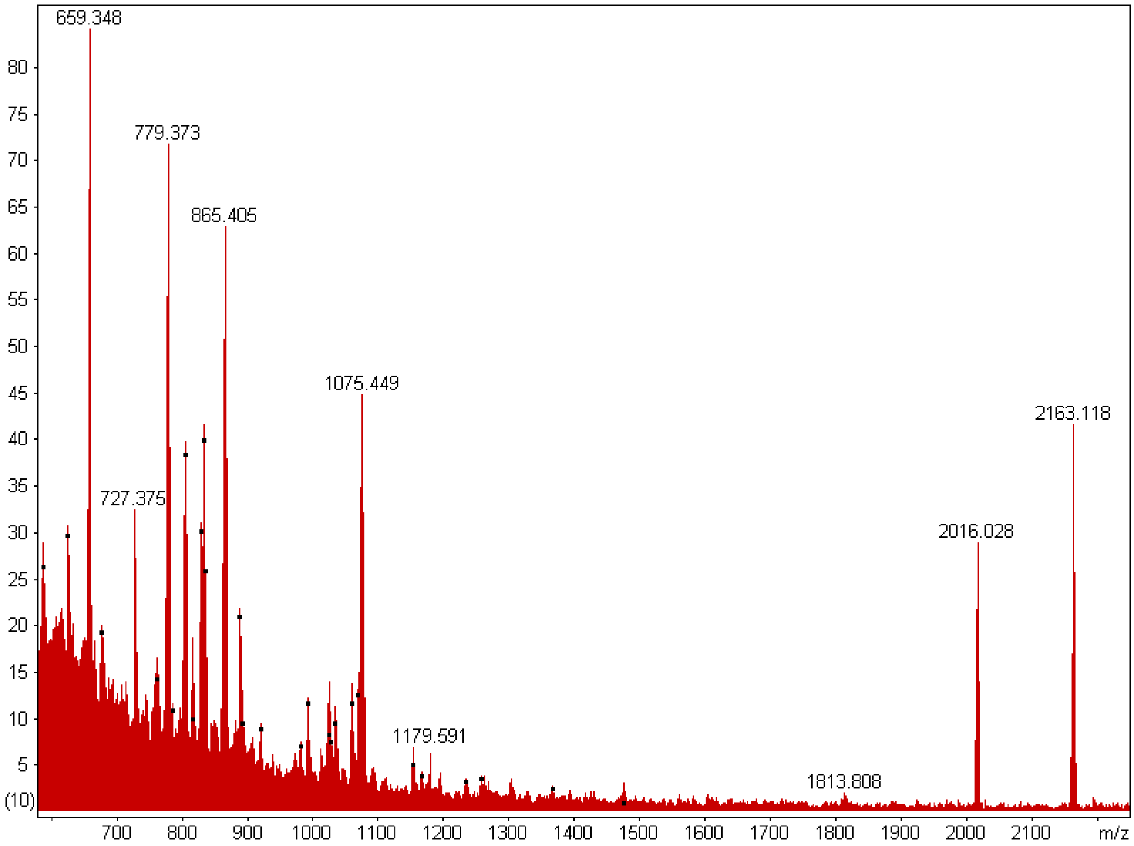
Mascot score: **81** Sequence coverage %: **12**

NCBI accession No.: **gi| 22328910**

Matched peptides No.: **10** Total peptides No.: **22**

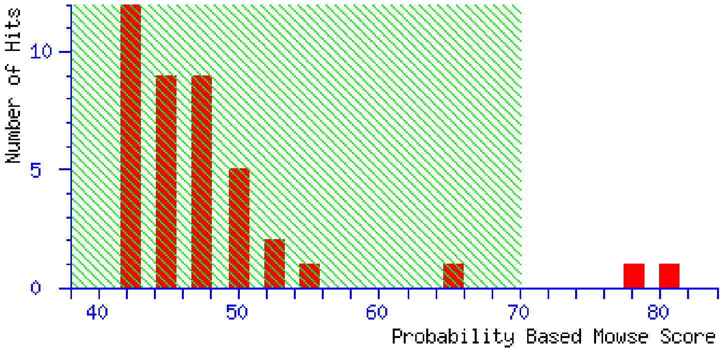
Calculated Mr: **54154** Calculated *p*I: **6.25**

Annotated PMF **spectra:**

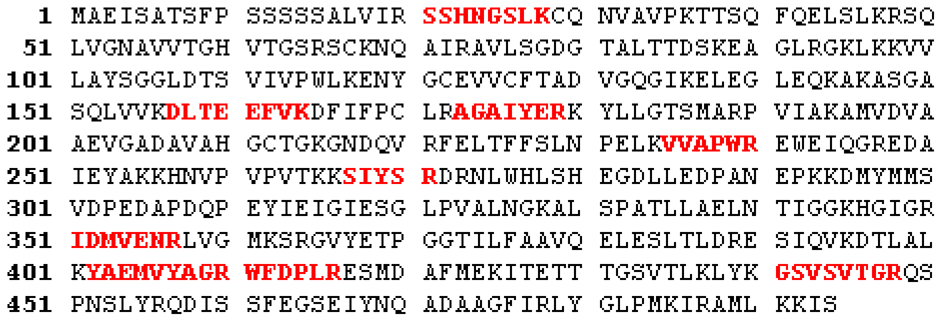


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

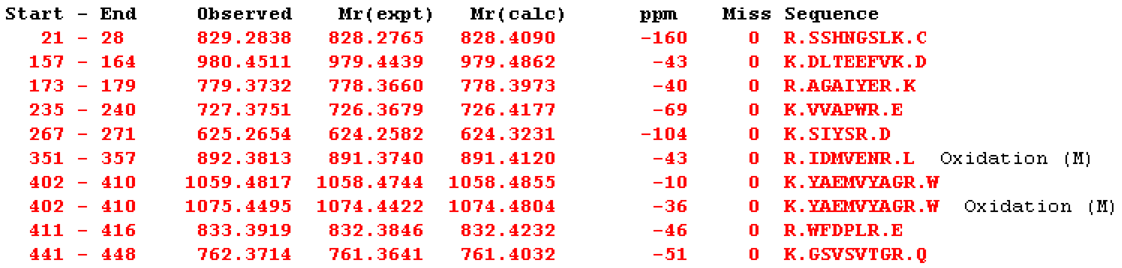


Matched peptide sequences: shown in Bold Red



```
  1 MAEISATSFP SSSSSALVIR SSHNGSLKCQ NVAVPKTTSQ FQELSLKRSQ
 51 LVGNAVVTGH VTGSRSCKNQ AIRAVLSGDG TALTTDSKEA GLRGKLKKVV
101 LAYSGGLDTS VIVPWLKENY GCEVVCFTAD VGQGIKELEG LEQKAKASGA
151 SQLVVKDLTE EFVKDFIFPC LRAGAIYERK YLLGTSMARP VIAKAMVDVA
201 AEVGADAVAH GCTGKGNDQV RFELTFFSLN PELKVVAPWR EWEIQGREDA
251 IEYAKKHNVP VPVTKKSIYS RDRNLWHLSH EGDLLEDPAN EPKKDMYMMS
301 VDPEDAPDQP EYIEIGIESG LPVALNGKAL SPATLLAELN TIGGKHGIGR
351 IDMVENRLVG MKSRGVYETP GGTILFAAVQ ELESLTLDRE SIQVKDTLAL
401 KYAEMVYAGR WFDPLRESMD AFMEKITETT TGSVTLKLYK GSVSVTGRQS
451 PNSLYRQDIS SFEGSEIYNQ ADAAGFIRLY GLPMKIRAML KKIS
```

Matched peptides information:



```
Start - End     Observed    Mr(expt)   Mr(calc)      ppm    Miss Sequence
   21 - 28      829.2838    828.2765   828.4090     -160      0  R.SSHNGSLK.C
  157 - 164     980.4511    979.4439   979.4862      -43      0  K.DLTEEFVK.D
  173 - 179     779.3732    778.3660   778.3973      -40      0  R.AGAIYER.K
  235 - 240     727.3751    726.3679   726.4177      -69      0  K.VVAPWR.E
  267 - 271     625.2654    624.2582   624.3231     -104      0  K.SIYSR.D
  351 - 357     892.3813    891.3740   891.4120      -43      0  R.IDMVENR.L   Oxidation (M)
  402 - 410    1059.4817   1058.4744  1058.4855      -10      0  K.YAEMVYAGR.W
  402 - 410    1075.4495   1074.4422  1074.4804      -36      0  K.YAEMVYAGR.W   Oxidation (M)
  411 - 416     833.3919    832.3846   832.4232      -46      0  R.WFDPLR.E
  441 - 448     762.3714    761.3641   761.4032      -51      0  K.GSVSVTGR.Q
```

Spot No.: **77**

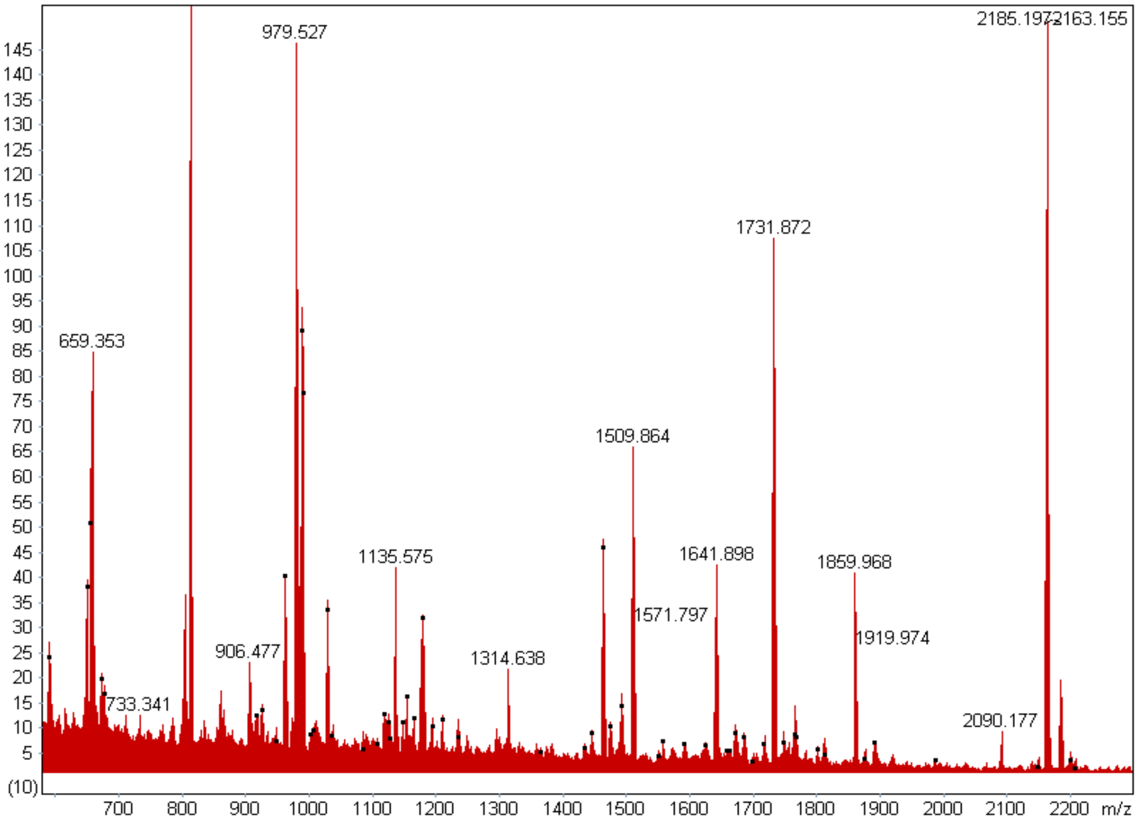
Mascot score: **94**   Sequence coverage %: **21**

NCBI accession No.: **gi| 15218090**

Matched peptides No.: **15**   Total peptides No.: **45**

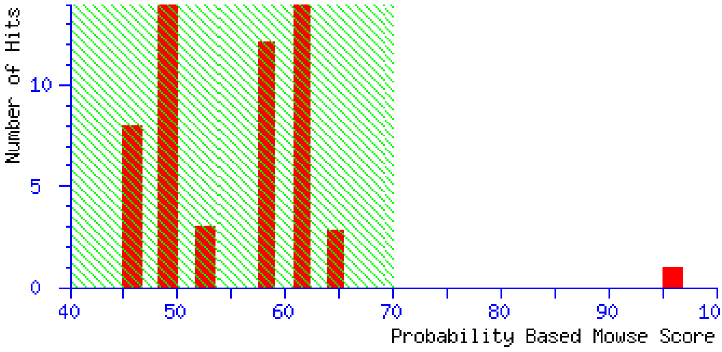
Calculated Mr: **54539**   Calculated *p*I: **5.94**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 MYRTAASRAR ALKGVLTRSL RPARYASSSA VAETSSSTPA YLSWLSGGSR
51 AALTSLDMPL QGVSLPPPLA DKVEPSKLQI TTLPNGLKIA SETTPNPAAS
101 IGLYVDCGSI YEAPYFHGAT HLLERMAFK**S** **TLNR**THFRLV R**EIEAIGGNT**
151 **SASASREQMS** **YTIDALK**TYV PEMVEVLIDS VR**NPAFLDWE** **VNEELRKMKV**
201 **EIAELAK**NPM GFLLEAIHSA GYSGPLASPL YAPESALDRL NGELLEEFMT
251 ENFTAAR**MVL** **AASGVEHEEL** **LK**VAEPLTSD LPNVPPQLAP K**SQYVGGDFR**
301 QHTGGEATHF AVAFEVPGWN NEKEAVTATV LQMLMGGGGS FSAGGPGKGM
351 HSWLYRRVLN EYQEVQSCTA FTSIFNDTGL FGIYGCSSPQ FAAKAIELAA
401 KELKDVAGGK VNQAHLDRAK AATK**SAVLMN** **LESRMIAAED** **IGRQILTYGE**
451 **R**KPVDQFLKS VDQLTLKDIA DFTSKVISKP LTMGSFGDVL AVPSYDTISS
501 KFR

Matched peptides information:

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
130 - 134	590.2720	589.2647	589.3184	-91	0	K.STLNR.T	
142 - 156	1462.7445	1461.7372	1461.7059	21	0	R.EIEAIGGNTSASASR.E	
157 - 167	1314.6385	1313.6312	1313.6173	11	0	R.EQMSYTIDALK.T	Oxidation (M)
183 - 196	1731.8719	1730.8646	1730.8264	22	0	R.NPAFLDWEVNEELR.K	
183 - 197	1859.9684	1858.9611	1858.9213	21	1	R.NPAFLDWEVNEELRK.M	
198 - 207	1147.6213	1146.6140	1146.6318	-16	1	K.MKVEIAELAK.N	Oxidation (M)
258 - 272	1625.8654	1624.8581	1624.8494	5	0	R.MVLAASGVEHEELLK.V	
258 - 272	1641.8976	1640.8903	1640.8443	28	0	R.MVLAASGVEHEELLK.V	Oxidation (M)
292 - 300	1028.5154	1027.5081	1027.4723	35	0	K.SQYVGGDFR.Q	
425 - 434	1119.5605	1118.5532	1118.5754	-20	0	K.SAVLMNLESR.M	
425 - 434	1135.5746	1134.5673	1134.5703	-3	0	K.SAVLMNLESR.M	Oxidation (M)
435 - 443	991.4978	990.4906	990.4804	10	0	R.MIAAEDIGR.Q	Oxidation (M)
444 - 451	979.5271	978.5198	978.5134	7	0	R.QILTYGER.K	

Spot No.: **78**

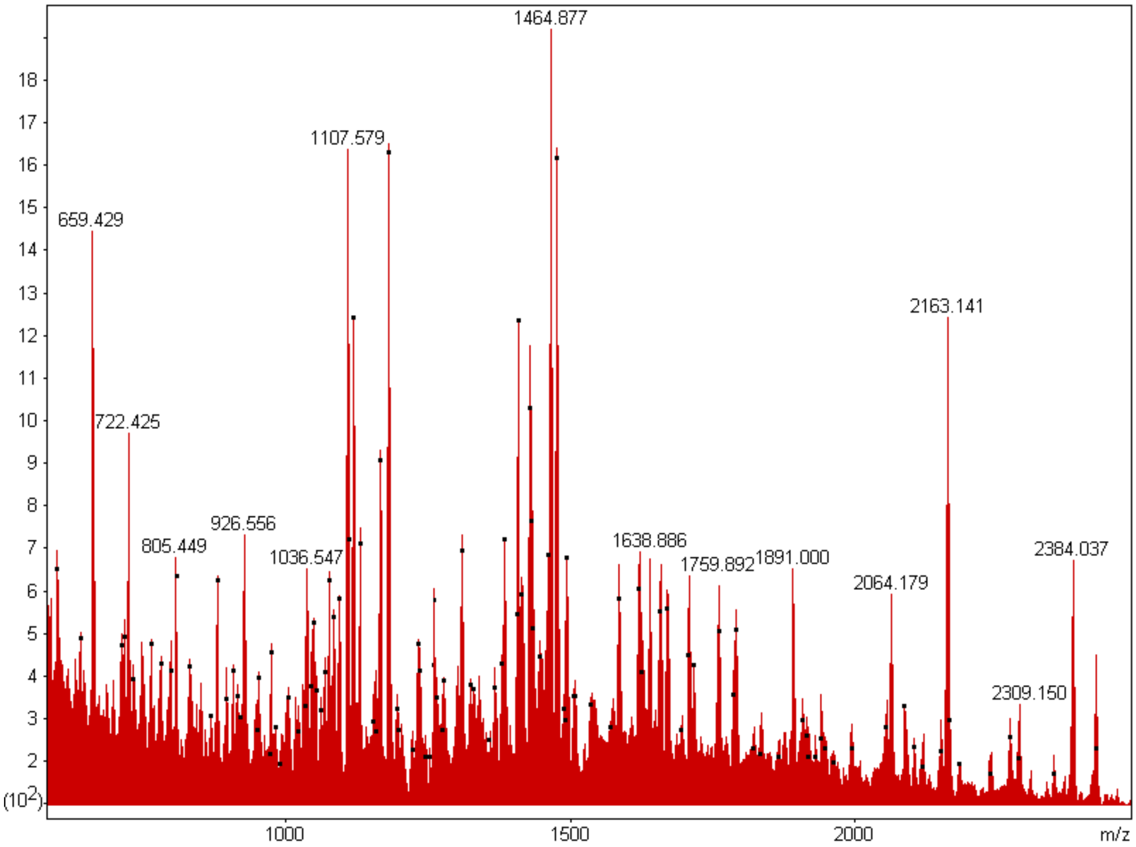
Mascot score: **86**   Sequence coverage %: **54**

NCBI accession No.: **gi| 19769**

Matched peptides No.: **15**   Total peptides No.: **112**

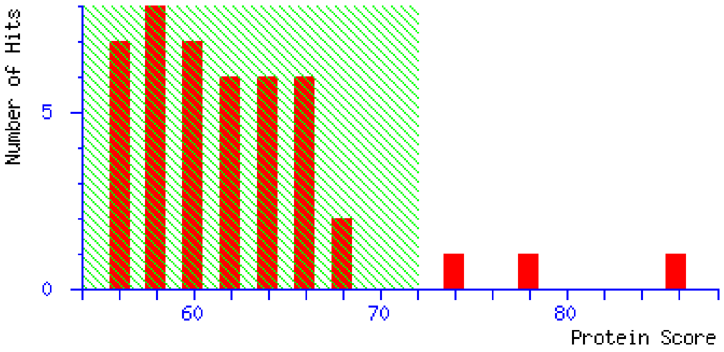
Calculated Mr: **25251**   Calculated *p*I: **9.78**

Annotated PMF **spectra:**

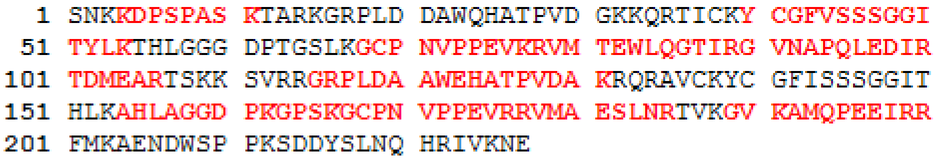


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

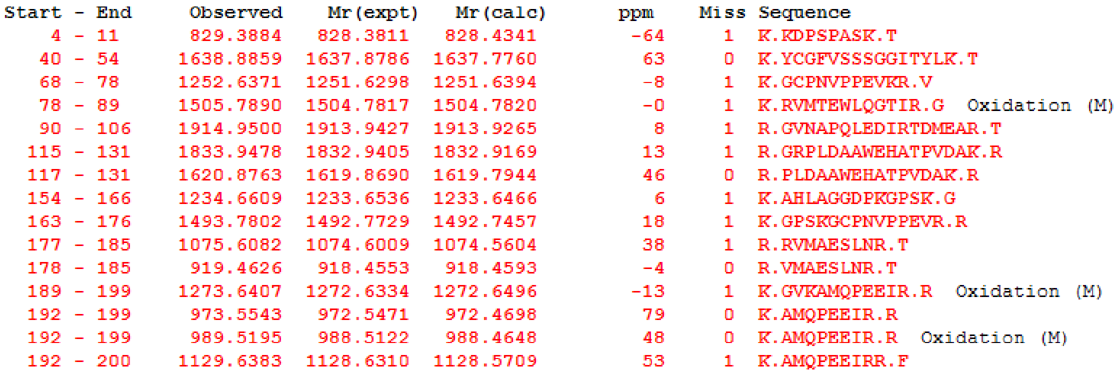


Matched peptide sequences: shown in Bold Red



```
  1 SNKKDPSPAS KTARKGRPLD DAWQHATPVD GKKQRTICKY CGFVSSSGGI
 51 TYLKTHLGGG DPTGSLKGCP NVPPEVKRVM TEWLQGTIRG VNAPQLEDIR
101 TDMEARTSKK SVRRGRPLDA AWEHATPVDA KRQRAVCKYC GFISSSGGIT
151 HLKAHLAGGD PKGPSKGCPN VPPEVRRVMA ESLNRTVKGV KAMQPEEIRR
201 FMKAENDWSP PKSDDYSLNQ HRIVKNE
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    4 - 11      829.3884   828.3811   828.4341      -64     1   K.KDPSPASK.T
   40 - 54     1638.8859  1637.8786  1637.7760       63     0   K.YCGFVSSSGGITYLK.T
   68 - 78     1252.6371  1251.6298  1251.6394       -8     1   K.GCPNVPPEVKR.V
   78 - 89     1505.7890  1504.7817  1504.7820       -0     1   K.RVMTEWLQGTIR.G  Oxidation (M)
   90 - 106    1914.9500  1913.9427  1913.9265        8     1   R.GVNAPQLEDIRTDMEAR.T
  115 - 131    1833.9478  1832.9405  1832.9169       13     1   R.GRPLDAAWEHATPVDAK.R
  117 - 131    1620.8763  1619.8690  1619.7944       46     0   R.PLDAAWEHATPVDAK.R
  154 - 166    1234.6609  1233.6536  1233.6466        6     1   K.AHLAGGDPKGPSK.G
  163 - 176    1493.7802  1492.7729  1492.7457       18     1   K.GPSKGCPNVPPEVR.R
  177 - 185    1075.6082  1074.6009  1074.5604       38     1   R.RVMAESLNR.T
  178 - 185     919.4626   918.4553   918.4593       -4     0   R.VMAESLNR.T
  189 - 199    1273.6407  1272.6334  1272.6496      -13     1   K.GVKAMQPEEIR.R  Oxidation (M)
  192 - 199     973.5543   972.5471   972.4698       79     0   K.AMQPEEIR.R
  192 - 199     989.5195   988.5122   988.4648       48     0   K.AMQPEEIR.R  Oxidation (M)
  192 - 200    1129.6383  1128.6310  1128.5709       53     1   K.AMQPEEIRR.F
```

Spot No.: **79**

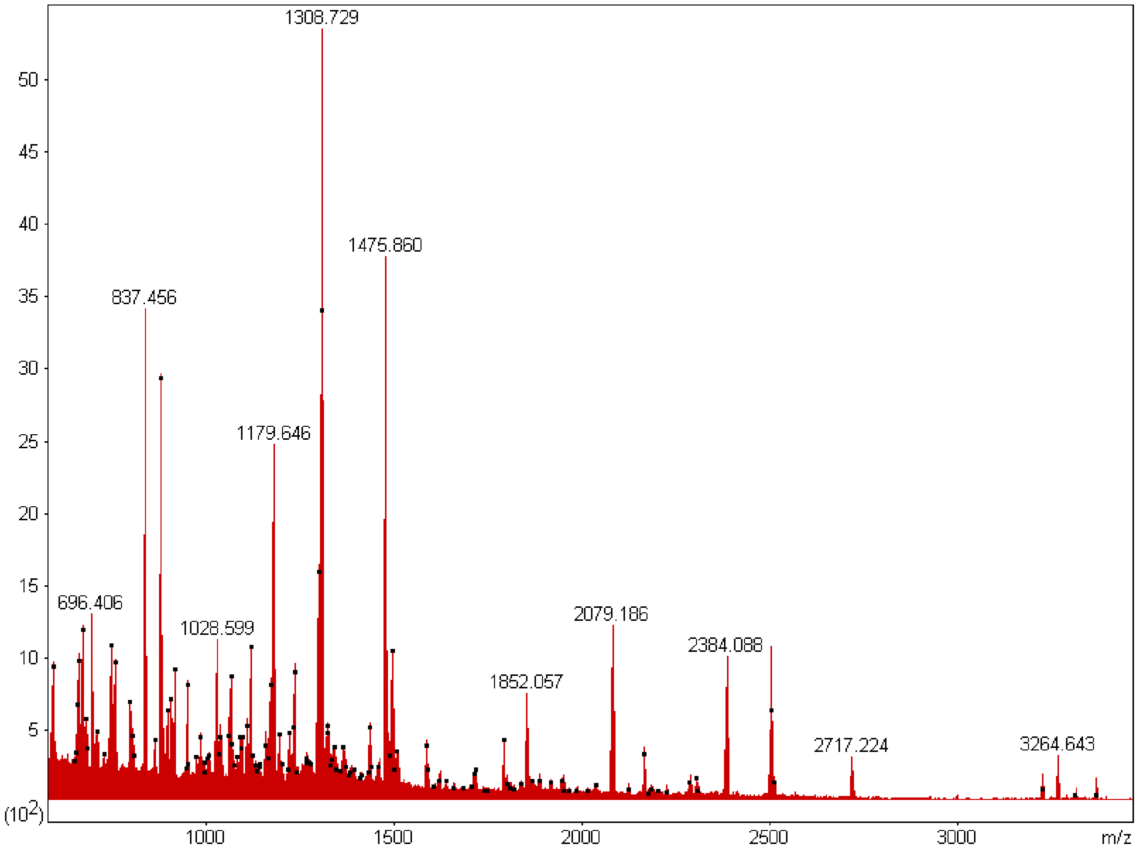
Mascot score: **81**   Sequence coverage %: **32**

NCBI accession No.: **gi| 308799665**

Matched peptides No.: **21**   Total peptides No.: **114**

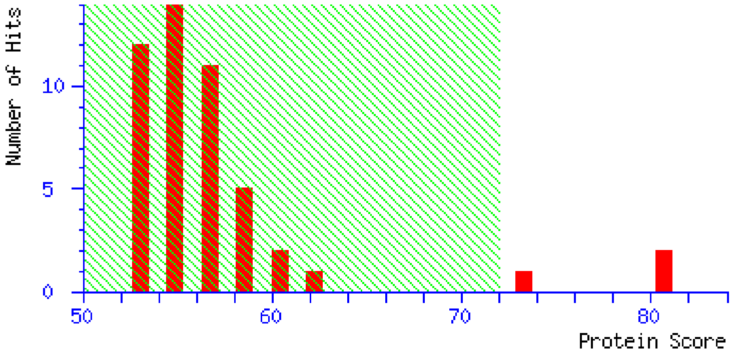
Calculated Mr: **71166**   Calculated p*I*: **10.62**

Annotated PMF **spectra:**

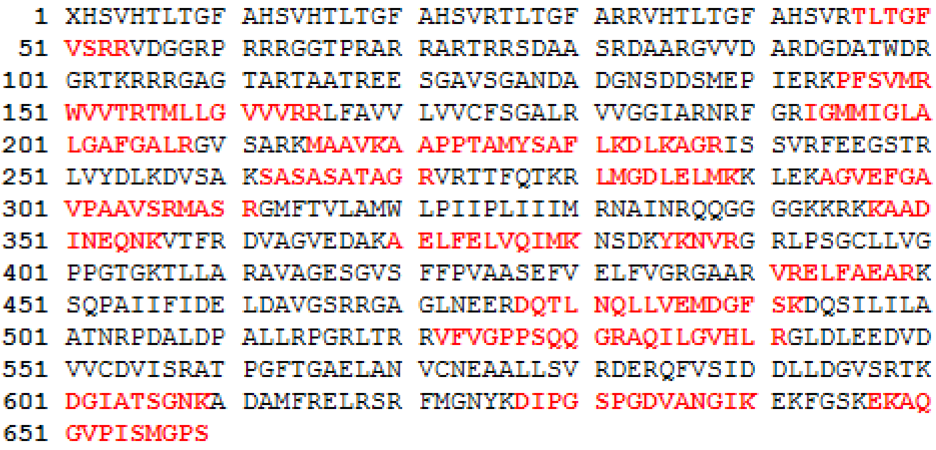


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red



1 XHSVHTLTGF AHSVHTLTGF AHSVRTLTGF ARRVHTLTGF AHSVR**TLTGF**

51 **VSRR**VDGGRP RRRGGTPRAR RARTRRSDAA SRDAARGVVD ARDGDATWDR

101 GRTKRRRGAG TARTAATREE SGAVSGANDA DGNSDDSMEP IERK**PFSVMR**

151 **WVVTRTMLLG** **VVVRR**LFAVV LVVCFSGALR VVGGIARNRF GR**IGMMIGLA**

201 **LGAFGALR**GV SARK**MAAVKA** **APPTAMYSAF** **LKDLKAGR**IS SVRFEEGSTR

251 LVYDLKDVSA K**SASASATAG** **R**VRTTFQTKR **LMGDLELMK**K LEK**AGVEFGA**

301 **VPAAVSRMAS** **R**GMFTVLAMW LPIIPLIIIM RNAINRQQGG GGKKRK**KAAD**

351 **INEQNK**VTFR DVAGVEDAK**A** **ELFELVQIMK** NSDK**YKNVR**G RLPSGCLLVG

401 PPGTGKTLLA RAVAGESGVS FFPVAASEFV ELFVGRGAAR **VRELFAEAR**K

451 SQPAIIFIDE LDAVGSRRGA GLNEER**DQTL** **NQLLVEMDGF** **SK**DQSILILA

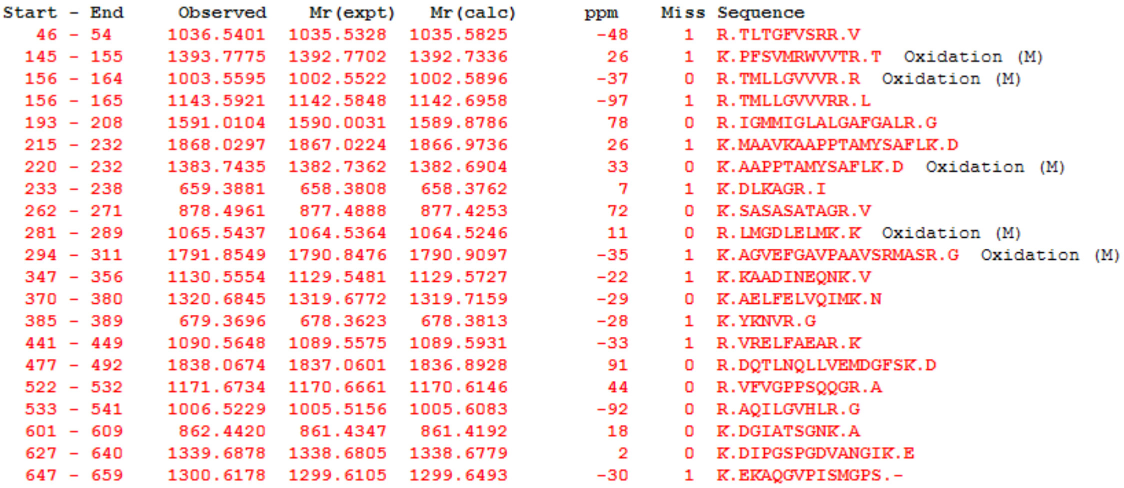
501 ATNRPDALDP ALLRPGRLTR R**VFVGPPSQQ** **GRAQILGVHL** **R**GLDLEEDVD

551 VVCDVISRAT PGFTGAELAN VCNEAALLSV RDERQFVSID DLLDGVSRTK

601 **DGIATSGNK**A DAMFRELRSR FMGNYK**DIPG** **SPGDVANGIK** EKFGSK**EKAQ**

651 **GVPISMGPS**

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
46 - 54	1036.5401	1035.5328	1035.5825	-48	1	R.TLTGFVSRR.V	
145 - 155	1393.7775	1392.7702	1392.7336	26	1	K.PFSVMRWVVTR.T	Oxidation (M)
156 - 164	1003.5595	1002.5522	1002.5896	-37	0	R.TMLLGVVVR.R	Oxidation (M)
156 - 165	1143.5921	1142.5848	1142.6958	-97	1	R.TMLLGVVVRR.L	
193 - 208	1591.0104	1590.0031	1589.8786	78	0	R.IGMMIGLALGAFGALR.G	
215 - 232	1868.0297	1867.0224	1866.9736	26	1	K.MAAVKAAPPTAMYSAFLK.D	
220 - 232	1383.7435	1382.7362	1382.6904	33	0	K.AAPPTAMYSAFLK.D	Oxidation (M)
233 - 238	659.3881	658.3808	658.3762	7	1	K.DLKAGR.I	
262 - 271	878.4961	877.4888	877.4253	72	0	K.SASASATAGR.V	
281 - 289	1065.5437	1064.5364	1064.5246	11	0	R.LMGDLELMK.K	Oxidation (M)
294 - 311	1791.8549	1790.8476	1790.9097	-35	1	K.AGVEFGAVPAAVSRMASR.G	Oxidation (M)
347 - 356	1130.5554	1129.5481	1129.5727	-22	1	K.KAADINEQNK.V	
370 - 380	1320.6845	1319.6772	1319.7159	-29	0	K.AELFELVQIMK.N	
385 - 389	679.3696	678.3623	678.3813	-28	1	K.YKNVR.G	
441 - 449	1090.5648	1089.5575	1089.5931	-33	1	R.VRELFAEAR.K	
477 - 492	1838.0674	1837.0601	1836.8928	91	0	R.DQTLNQLLVEMDGFSK.D	
522 - 532	1171.6734	1170.6661	1170.6146	44	0	R.VFVGPPSQQGR.A	
533 - 541	1006.5229	1005.5156	1005.6083	-92	0	R.AQILGVHLR.G	
601 - 609	862.4420	861.4347	861.4192	18	0	K.DGIATSGNK.A	
627 - 640	1339.6878	1338.6805	1338.6779	2	0	K.DIPGSPGDVANGIK.E	
647 - 659	1300.6178	1299.6105	1299.6493	-30	1	K.EKAQGVPISMGPS.-	

Spot No.: **80**

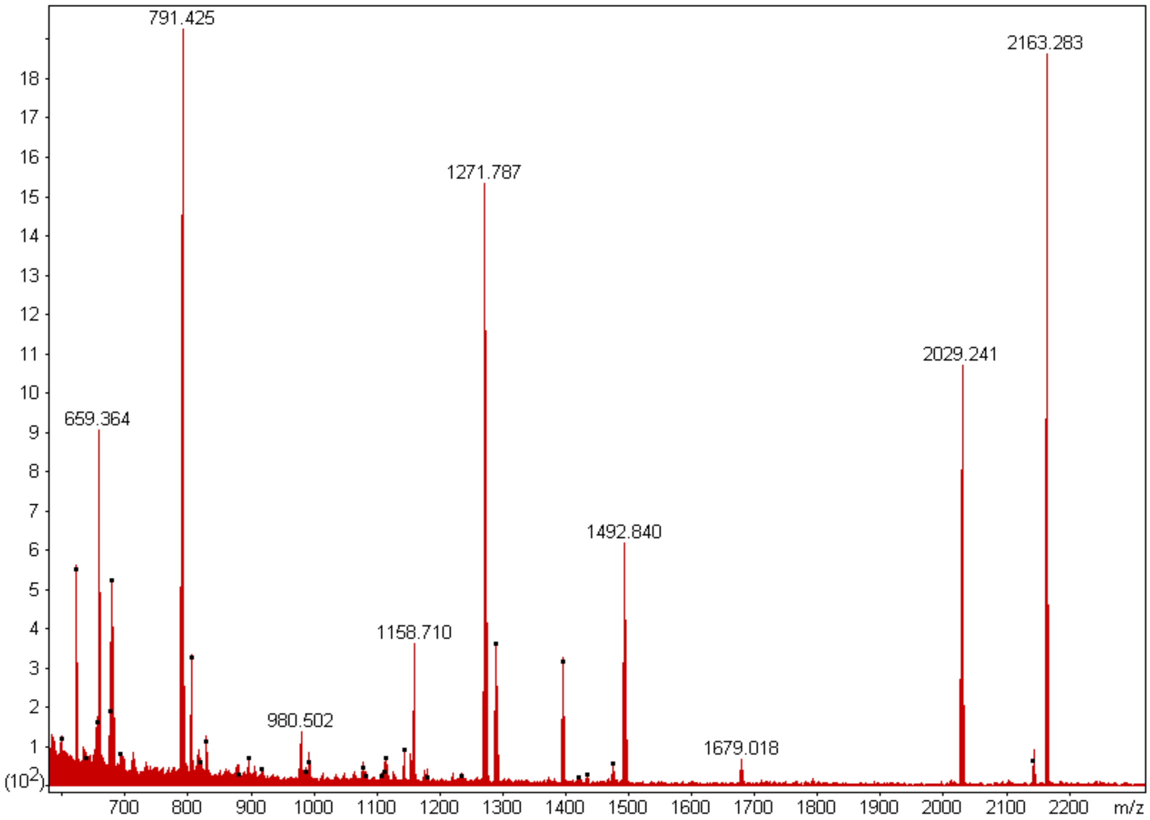
Mascot score: **203** Sequence coverage %: **39**

NCBI accession No.: **gi| 157336951**

Matched peptides No.: **17** Total peptides No.: **31**

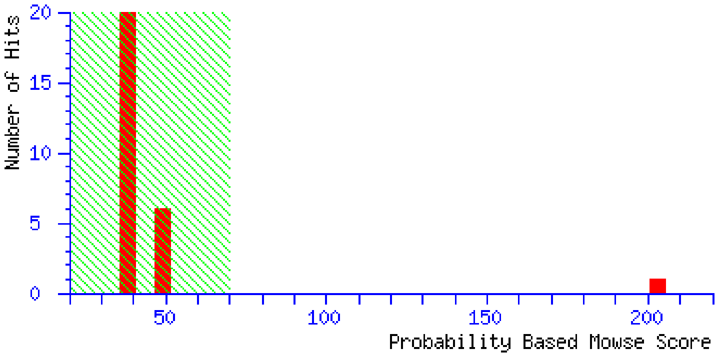
Calculated Mr: **47196** Calculated p*I*: **5.42**

Annotated PMF **spectra:**

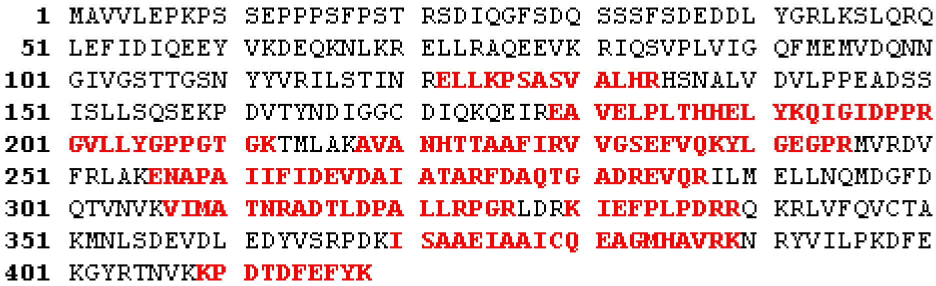


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

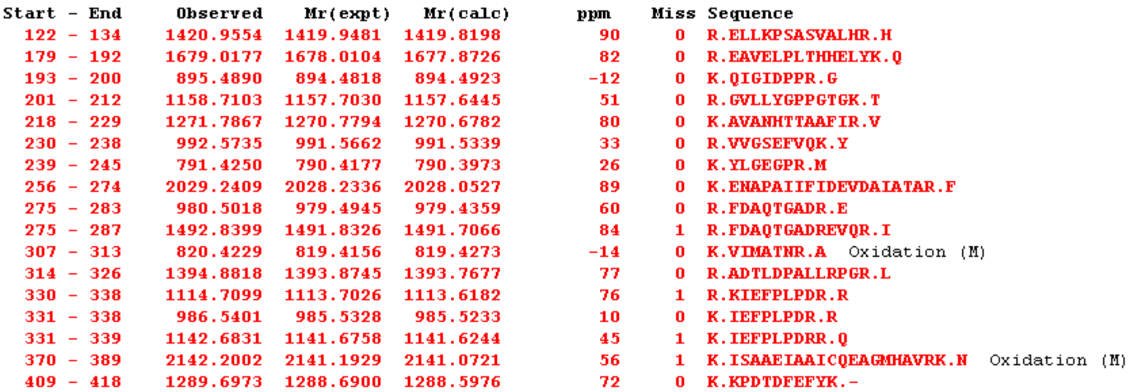


Matched peptide sequences: shown in Bold Red



```
  1 MAVVLEPKPS SEPPPSFPST RSDIQGFSDQ SSSFSDEDDL YGRLKSLQRQ
 51 LEFIDIQEEY VKDEQKNLKR ELLRAQEEVK RIQSVPLVIG QFMEMVDQNN
101 GIVGSTTGSN YYVRILSTIN RELLKPSASV ALHRHSNALV DVLPPEADSS
151 ISLLSQSEKP DVTYNDIGGC DIQKQEIREA VELPLTHHEL YKQIGIDPPR
201 GVLLYGPPGT GKTMLAKAVA NHTTAAFIRV VGSEFVQKYL GEGPRMVRDV
251 FRLAKENAPA IIFIDEVDAI ATARFDAQTG ADREVQRILM ELLNQMDGFD
301 QTVNVKVIMA TNRADTLDPA LLRPGRLDRK IEFPLPDRRQ KRLVFQVCTA
351 KMNLSDEVDL EDYVSRPDKI SAAEIAAICQ EAGMHAVRKN RYVILPKDFE
401 KGYRTNVKKP DTDFEFYK
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)       ppm   Miss Sequence
  122 - 134    1420.9554  1419.9481  1419.8198        90      0 R.ELLKPSASVALHR.H
  179 - 192    1679.0177  1678.0104  1677.8726        82      0 R.EAVELPLTHHELYK.Q
  193 - 200     895.4890   894.4818   894.4923       -12      0 K.QIGIDPPR.G
  201 - 212    1158.7103  1157.7030  1157.6445        51      0 R.GVLLYGPPGTGK.T
  218 - 229    1271.7867  1270.7794  1270.6782        80      0 K.AVANHTTAAFIR.V
  230 - 238     992.5735   991.5662   991.5339        33      0 R.VVGSEFVQK.Y
  239 - 245     791.4250   790.4177   790.3973        26      0 K.YLGEGPR.M
  256 - 274    2029.2409  2028.2336  2028.0527        89      0 K.ENAPAIIFIDEVDAIATAR.F
  275 - 283     980.5018   979.4945   979.4359        60      0 R.FDAQTGADR.E
  275 - 287    1492.8399  1491.8326  1491.7066        84      1 R.FDAQTGADREVQR.I
  307 - 313     820.4229   819.4156   819.4273       -14      0 K.VIMATNR.A  Oxidation (M)
  314 - 326    1394.8818  1393.8745  1393.7677        77      0 R.ADTLDPALLRPGR.L
  330 - 338    1114.7099  1113.7026  1113.6182        76      1 R.KIEFPLPDR.R
  331 - 338     986.5401   985.5328   985.5233        10      0 K.IEFPLPDR.R
  331 - 339    1142.6831  1141.6758  1141.6244        45      1 K.IEFPLPDRR.Q
  370 - 389    2142.2002  2141.1929  2141.0721        56      1 K.ISAAEIAAICQEAGMHAVRK.N  Oxidation (M)
  409 - 418    1289.6973  1288.6900  1288.5976        72      0 K.KPDTDFEFYK.-
```

Spot No.: **81**

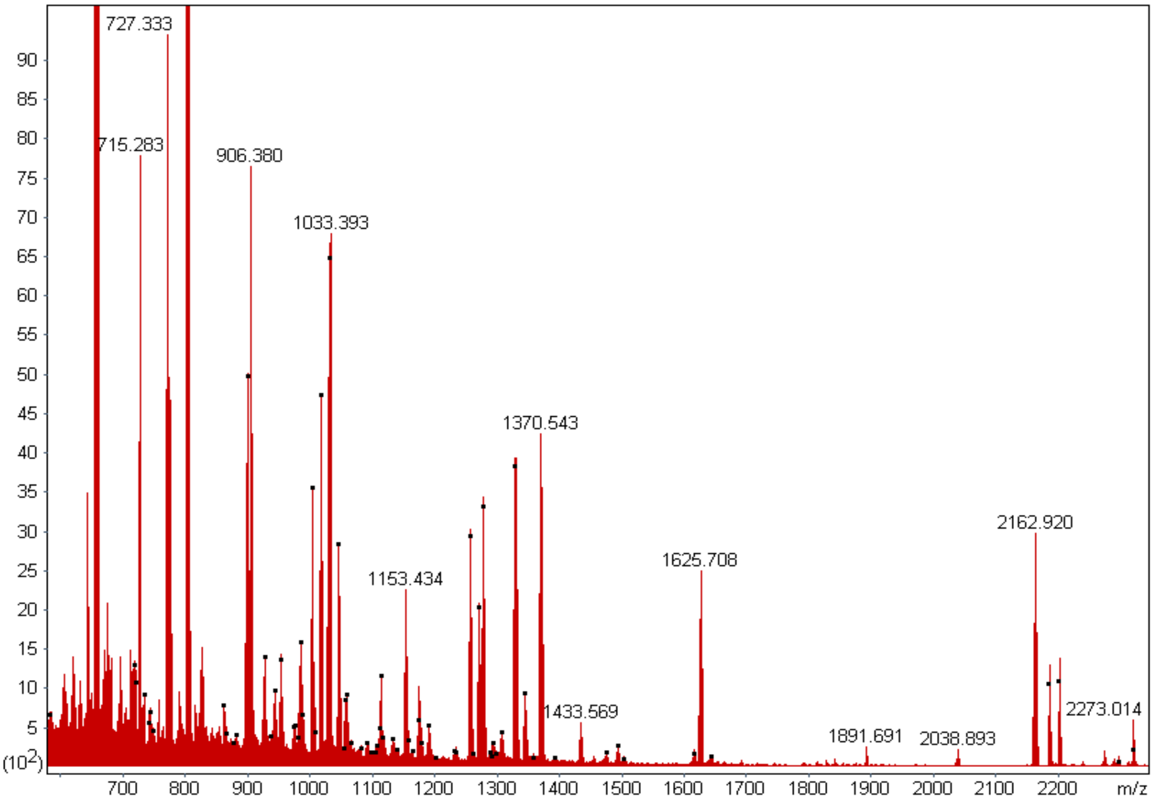
Mascot score: **172**   Sequence coverage %: **43**

NCBI accession No.: **gi| 312281677**

Matched peptides No.: **26**   Total peptides No.: **73**

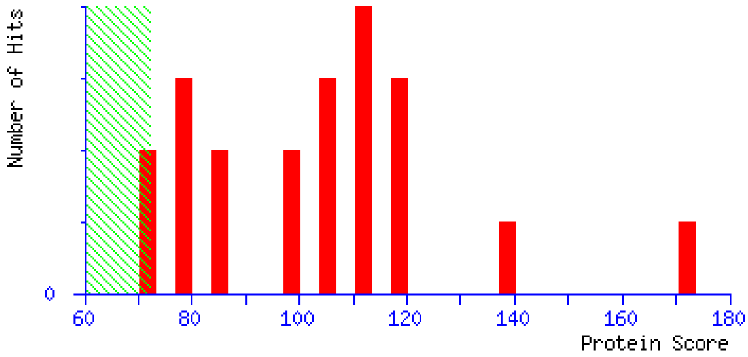
Calculated Mr: **57475**   Calculated p*I*: **6.24**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 MASMAAIGAL KVPAASCSDS TRIVTEAVPA RTLSFSSSVG LSDEKLSLRA
51 TVSRRRESVA RGRVRNPMIV SPKAVSDSQN SQTCLDPDAS R**SVLGIILGG**
101 **GAGTRLYPLT** **KK**R**AKPAVPL** **GANYR**LIDIP VSNCLNSNIN K**IYVLTQFNS**
151 **ASLNR**HLSR**A** **YATNMGGYK**N EGFVEVLAAQ QSPENPNWFQ GTADAVRQYL
201 WLFEEHNVLE YLILAGDHLY RMDYEK**FIQA** **HRETDADITV** **AALPMDEERA**
251 **TAFGLMKIDE** **EGRIVEFAEK** **PK**GEQLKAMK **VDTTILGLDD** **KR**AKEMPYIA
301 SMGIYVVSK**D** **VMLELLRNTF** **PGANDFGSEV** **IPGATSLGLR** VQAYLYDGYW
351 EDIGTIEAFY NANLGITK**KP** **VPDFSFYDRS** **APIYTQPR**YL PPSKMLDADV
401 TDSVIGEGCV IKNCK**IHHSV** **VGLR**SCISEG AIIEDSLLMG ADYYETASEK
451 SLLTAK**GSVP** **IGIGKSSHIK** **RAIIDKNAR**I GDNVK**IINSD** **NVQEAARETE**
501 **GYFIKSGIVT** **VIK**DALIPTG TLI

Matched peptides information:

```
Start - End      Observed   Mr(expt)   Mr(calc)       ppm    Miss Sequence
   92 - 105     1270.6042  1269.5969  1269.7405       -113     0  R.SVLGIILGGGAGTR.L
  106 - 111      734.3071   733.2999   733.4374       -188     0  R.LYPLTK.K
  106 - 112      862.2992   861.2919   861.5324       -279     1  R.LYPLTKK.R
  114 - 125     1256.5662  1255.5589  1255.7037       -115     1  R.AKPAVPLGANYR.L
  116 - 125     1057.4450  1056.4377  1056.5716       -127     0  K.PAVPLGANYR.L
  142 - 155     1625.7078  1624.7005  1624.8573        -96     0  K.IYVLTQFNSASLNR.H
  160 - 169     1091.3732  1090.3659  1090.4753       -100     0  R.AYATNMGGYK.N  Oxidation (M)
  227 - 232      771.3355   770.3282   770.4187       -117     0  K.FIQAHR.E
  233 - 249     1891.6908  1890.6835  1890.8517        -89     0  R.ETDADITVAALPMDEER.A  Oxidation (M)
  250 - 257      854.3034   853.2961   853.4368       -165     0  R.ATAFGLMK.I  Oxidation (M)
  258 - 263      718.2578   717.2505   717.3293       -110     0  K.IDEEGR.I
  264 - 272     1060.4417  1059.4344  1059.5964       -153     1  R.IVEFAEKPK.G
  281 - 292     1345.5819  1344.5746  1344.7249       -112     1  K.VDTTILGLDDKR.A
  310 - 317      988.4052   987.3979   987.5423       -146     0  K.DVMLELLR.N
  310 - 317     1004.4015  1003.3942  1003.5372       -142     0  K.DVMLELLR.N  Oxidation (M)
  318 - 340     2320.0447  2319.0374  2319.1495        -48     0  R.NTFPGANDFGSEVIPGATSLGLR.V
  369 - 379     1370.5429  1369.5356  1369.6667        -96     1  K.KPVPDFSFYDR.S
  380 - 388     1032.4244  1031.4171  1031.5400       -119     0  R.SAPIYTQPR.Y
  416 - 424     1017.4799  1016.4726  1016.5880       -113     0  K.IHHSVVGLR.S
  457 - 465      827.3362   826.3290   826.4913       -196     0  K.GSVPIGIGK.S
  466 - 471      727.3334   726.3262   726.4137       -120     1  K.SSHIKR.A
  471 - 476      715.2835   714.2762   714.4388       -228     1  K.RAIIDK.N
  472 - 479      900.4063   899.3990   899.5188       -133     1  R.AIIDKNAR.I
  486 - 497     1329.5379  1328.5306  1328.6684       -104     0  K.IINSDNVQEAAR.E
  498 - 505      986.3837   985.3764   985.4756       -101     0  R.ETEGYFIK.S
  506 - 513      816.3540   815.3468   815.5117       -202     0  K.SGIVTVIK.D
```

Spot No.: **82**

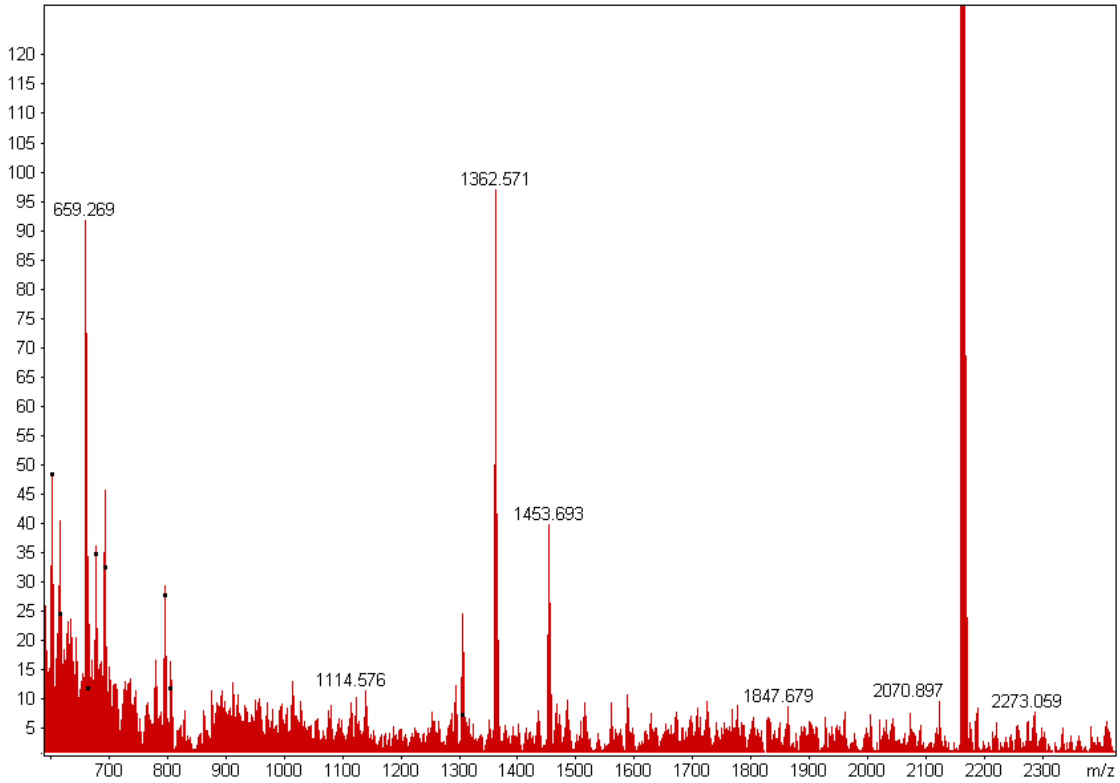
Mascot score: **87** Sequence coverage %: **25**

NCBI accession No.: **gi| 168054422**

Matched peptides No.: **5** Total peptides No.: **17**

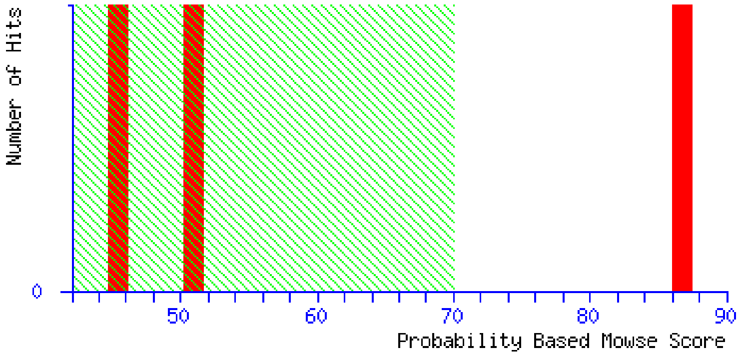
Calculated Mr: **13541** Calculated *p*I: **5.36**

Annotated PMF **spectra:**



Probability Based Mowse Score:

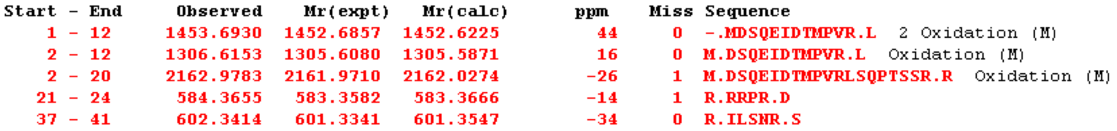
Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 **MDSQEIDTMP VRLSQPTSSR RRPR**DEEPPV PRRRRR**ILSN R**SLVIVFESE
51 PAYDGQLEGI FAGQFHNEDT EVHAWSEVEG VGHYRWLQGP VNYLPREQQL
101 EFIADVMPQI FIFLR

Matched peptides information:



```
Start - End     Observed    Mr(expt)   Mr(calc)      ppm    Miss Sequence
    1 - 12     1453.6930   1452.6857  1452.6225       44      0  -.MDSQEIDTMPVR.L  2 Oxidation (M)
    2 - 12     1306.6153   1305.6080  1305.5871       16      0  M.DSQEIDTMPVR.L  Oxidation (M)
    2 - 20     2162.9783   2161.9710  2162.0274      -26      1  M.DSQEIDTMPVRLSQPTSSR.R  Oxidation (M)
   21 - 24      584.3655    583.3582   583.3666      -14      1  R.RRPR.D
   37 - 41      602.3414    601.3341   601.3547      -34      0  R.ILSNR.S
```

Spot No.: **83**

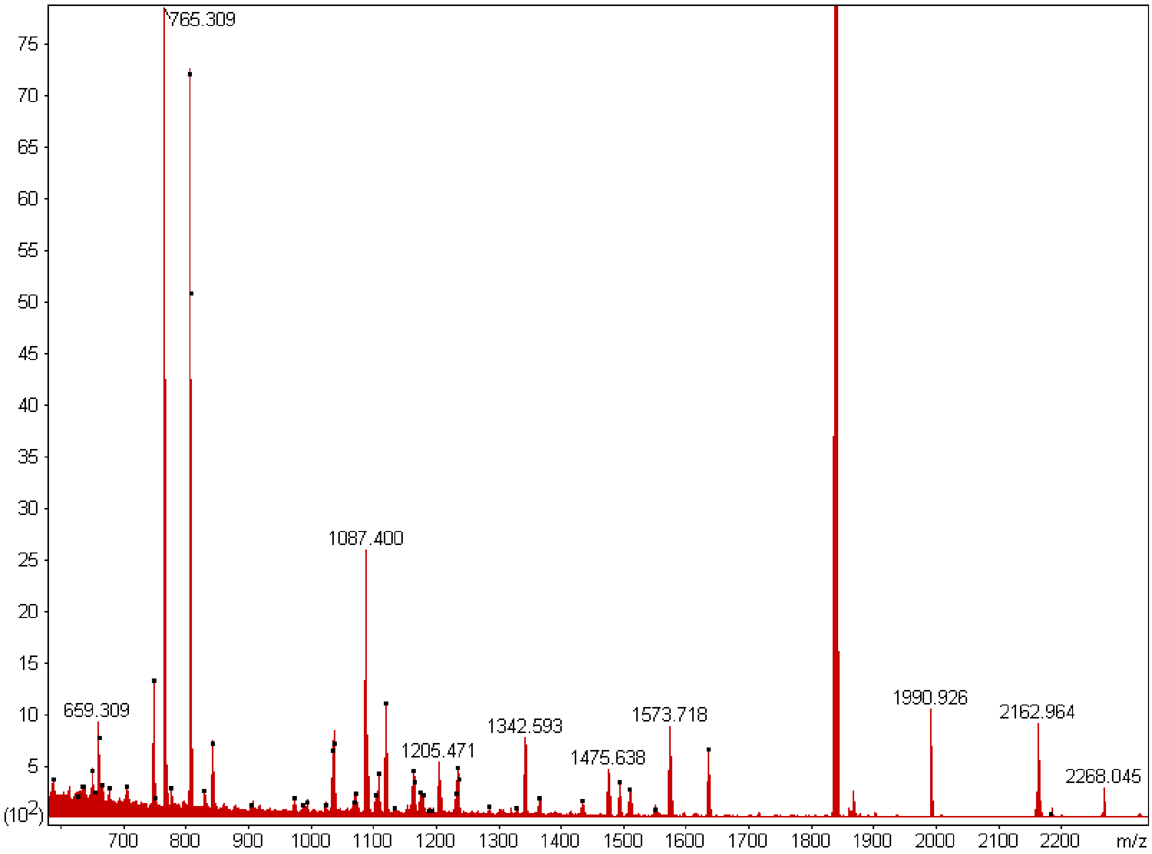
Mascot score: **93** Sequence coverage %: **27**

NCBI accession No.: **gi| 312281815**

Matched peptides No.: **13** Total peptides No.: **29**

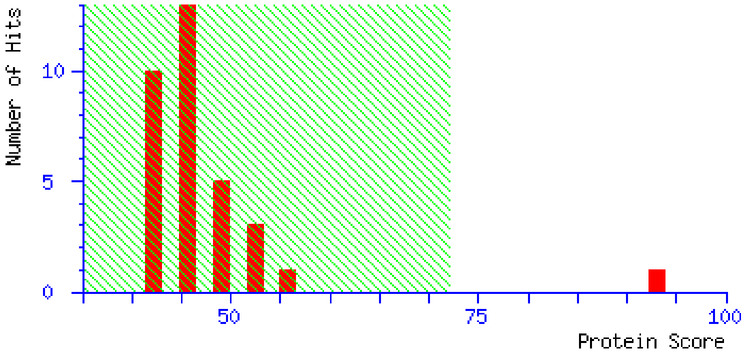
Calculated Mr: **47893** Calculated *p*I: **5.55**

Annotated PMF **spectra:**

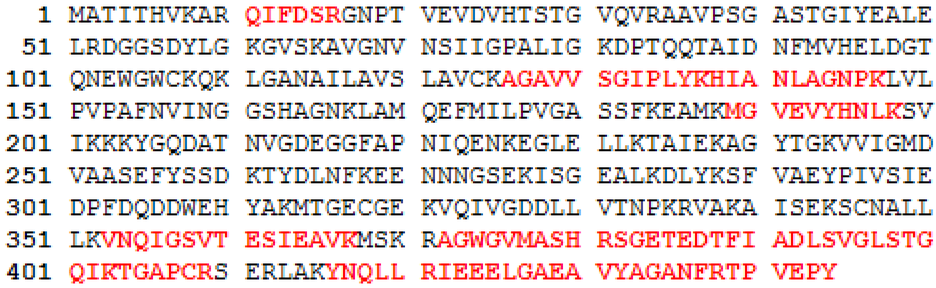


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

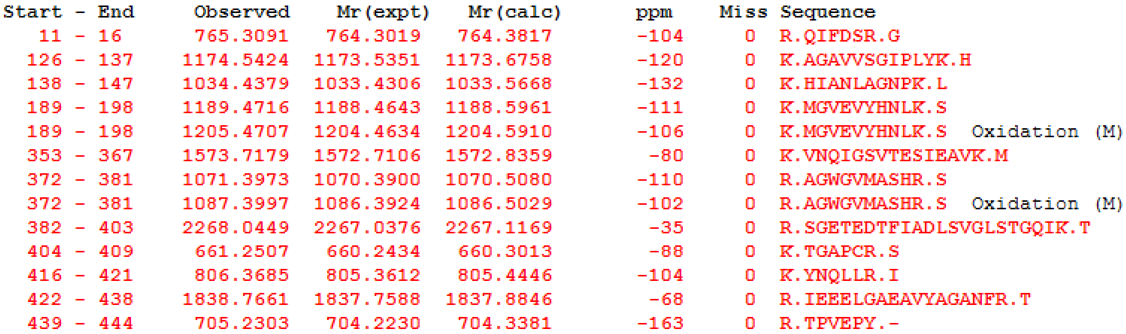


Matched peptide sequences: shown in Bold Red



1 MATITHVKAR **QIFDSR**GNPT VEVDVHTSTG VQVRAAVPSG ASTGIYEALE
51 LRDGGSDYLG KGVSKAVGNV NSIIGPALIG KDPTQQTAID NFMVHELDGT
101 QNEWGWCKQK LGANAILAVS LAVCK**AGAVV SGIPLYKHIA NLAGNPK**LVL
151 PVPAFNVING GSHAGNKLAM QEFMILPVGA SSFKEAMK**MG VEVYHNLK**SV
201 IKKKYGQDAT NVGDEGGFAP NIQENKEGLE LLKTAIEKAG YTGKVVIGMD
251 VAASEFYSSD KTYDLNFKEE NNNGSEKISG EALKDLYKSF VAEYPIVSIE
301 DPFDQDDWEH YAKMTGECGE KVQIVGDDLL VTNPKRVAKA ISEKSCNALL
351 LK**VNQIGSVT ESIEAVK**MSK R**AGWGVMASH RSGETEDTFI ADLSVGLSTG**
401 **QIKTGAPCR**S ERLAK**YNQLL RIEEELGAEA VYAGANFRTP VEPY**

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   11 - 16      765.3091   764.3019   764.3817     -104     0   R.QIFDSR.G
  126 - 137    1174.5424  1173.5351  1173.6758     -120     0   K.AGAVVSGIPLYK.H
  138 - 147    1034.4379  1033.4306  1033.5668     -132     0   K.HIANLAGNPK.L
  189 - 198    1189.4716  1188.4643  1188.5961     -111     0   K.MGVEVYHNLK.S
  189 - 198    1205.4707  1204.4634  1204.5910     -106     0   K.MGVEVYHNLK.S   Oxidation (M)
  353 - 367    1573.7179  1572.7106  1572.8359      -80     0   K.VNQIGSVTESIEAVK.M
  372 - 381    1071.3973  1070.3900  1070.5080     -110     0   R.AGWGVMASHR.S
  372 - 381    1087.3997  1086.3924  1086.5029     -102     0   R.AGWGVMASHR.S   Oxidation (M)
  382 - 403    2268.0449  2267.0376  2267.1169      -35     0   R.SGETEDTFIADLSVGLSTGQIK.T
  404 - 409     661.2507   660.2434   660.3013      -88     0   K.TGAPCR.S
  416 - 421     806.3685   805.3612   805.4446     -104     0   K.YNQLLR.I
  422 - 438    1838.7661  1837.7588  1837.8846      -68     0   R.IEEELGAEAVYAGANFR.T
  439 - 444     705.2303   704.2230   704.3381     -163     0   R.TPVEPY.-
```

Spot No.: **84**

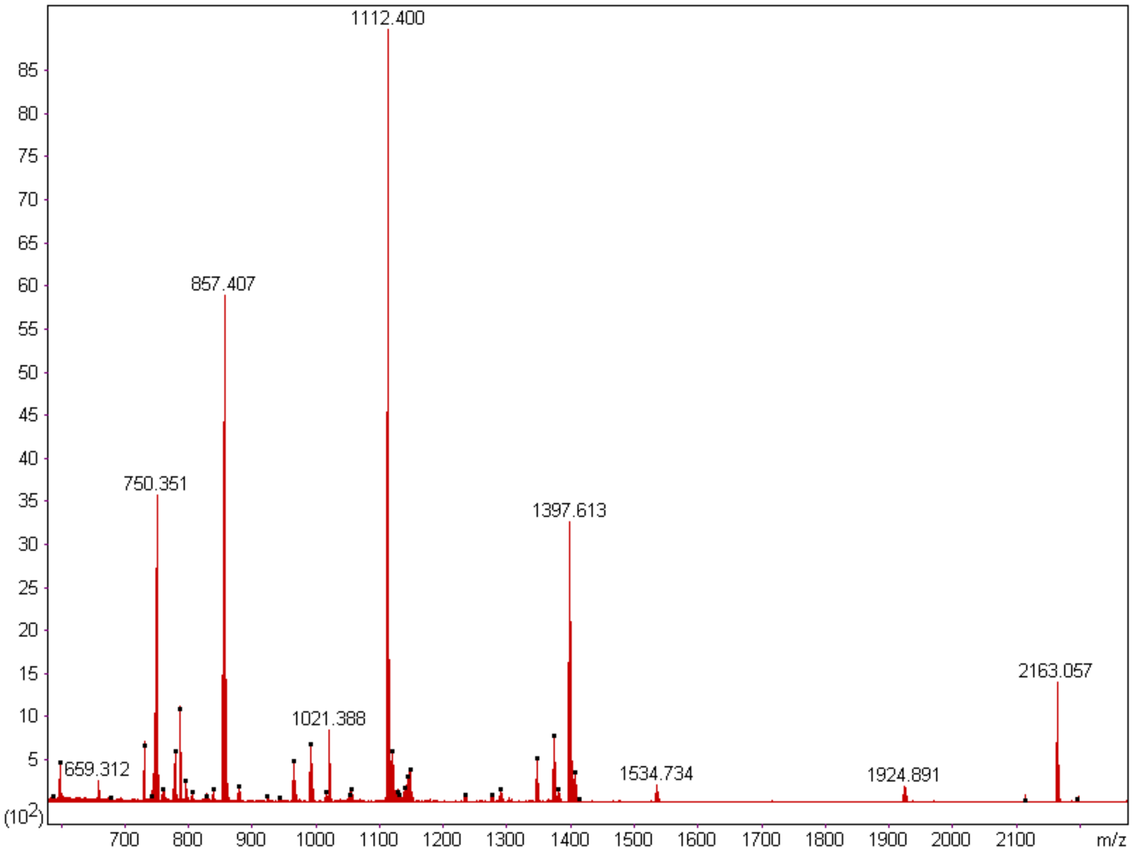
Mascot score: **162** Sequence coverage %: **26**

NCBI accession No.: **gi| 15223186**

Matched peptides No.: **16** Total peptides No.: **34**

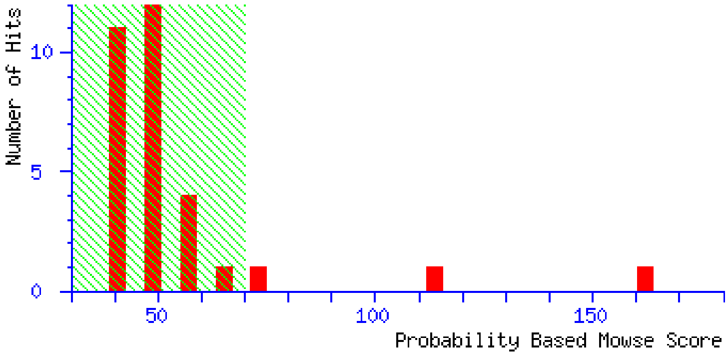
Calculated Mr: **53980** Calculated *p*I: **6.21**

Annotated PMF **spectra:**

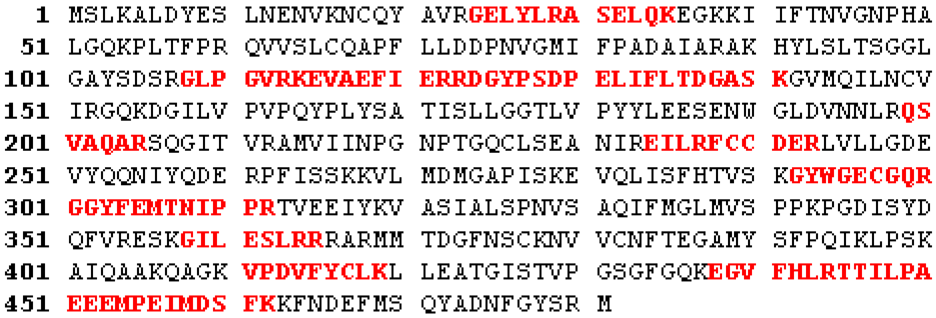


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

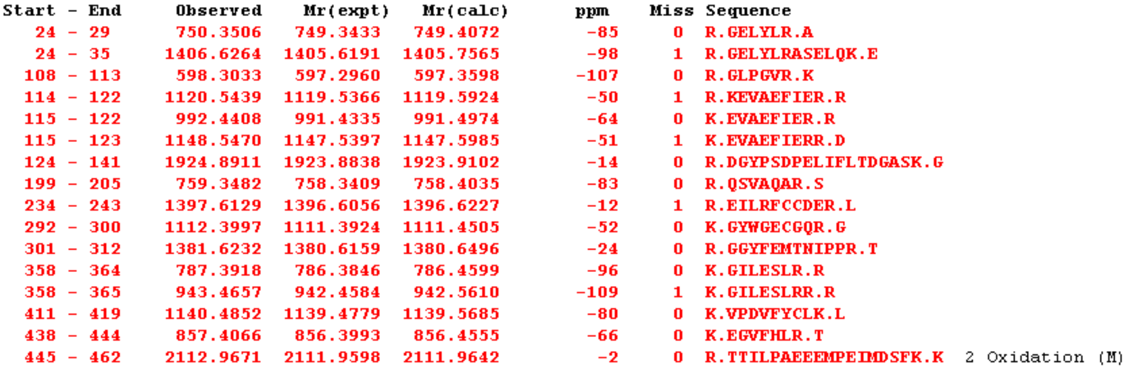


Matched peptide sequences: shown in Bold Red



```
  1 MSLKALDYES LNENVKNCQY AVRGELYLRA SELQKEGKKI IFTNVGNPHA
 51 LGQKPLTFPR QVVSLCQAPF LLDDPNVGMI FPADAIARAK HYLSLTSGGL
101 GAYSDSRGLP GVRKEVAEFI ERRDGYPSDP ELIFLTDGAS KGVMQILNCV
151 IRGQKDGILV PVPQYPLYSA TISLLGGTLV PYYLEESENW GLDVNNLRQS
201 VAQARSQGIT VRAMVIINPG NPTGQCLSEA NIREILRFCC DERLVLLGDE
251 VYQQNIYQDE RPFISSKKVL MDMGAPISKE VQLISFHTVS KGYWGECGQR
301 GGYFEMTNIP PRTVEEIYKV ASIALSPNVS AQIFMGLMVS PPKPGDISYD
351 QFVRESKGIL ESLRRRARMM TDGFNSCKNV VCNFTEGAMY SFPQIKLPSK
401 AIQAAKQAGK VPDVFYCLKL LEATGISTVP GSGFGQKEGV FHLRTTILPA
451 EEEMPEIMDS FKKFNDEFMS QYADNFGYSR M
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss Sequence
   24 - 29      750.3506   749.3433   749.4072      -85     0  R.GELYLR.A
   24 - 35     1406.6264  1405.6191  1405.7565      -98     1  R.GELYLRASELQK.E
  108 - 113     598.3033   597.2960   597.3598     -107     0  R.GLPGVR.K
  114 - 122    1120.5439  1119.5366  1119.5924      -50     1  R.KEVAEFIER.R
  115 - 122     992.4408   991.4335   991.4974      -64     0  K.EVAEFIER.R
  115 - 123    1148.5470  1147.5397  1147.5985      -51     1  K.EVAEFIERR.D
  124 - 141    1924.8911  1923.8838  1923.9102      -14     0  R.DGYPSDPELIFLTDGASK.G
  199 - 205     759.3482   758.3409   758.4035      -83     0  R.QSVAQAR.S
  234 - 243    1397.6129  1396.6056  1396.6227      -12     1  R.EILRFCCDER.L
  292 - 300    1112.3997  1111.3924  1111.4505      -52     0  K.GYWGECGQR.G
  301 - 312    1381.6232  1380.6159  1380.6496      -24     0  R.GGYFEMTNIPPR.T
  358 - 364     787.3918   786.3846   786.4599      -96     0  K.GILESLR.R
  358 - 365     943.4657   942.4584   942.5610     -109     1  K.GILESLRR.R
  411 - 419    1140.4852  1139.4779  1139.5685      -80     0  K.VPDVFYCLK.L
  438 - 444     857.4066   856.3993   856.4555      -66     0  K.EGVFHLR.T
  445 - 462    2112.9671  2111.9598  2111.9642       -2     0  R.TTILPAEEEMPEIMDSFK.K  2 Oxidation (M)
```

Spot No.: **85**

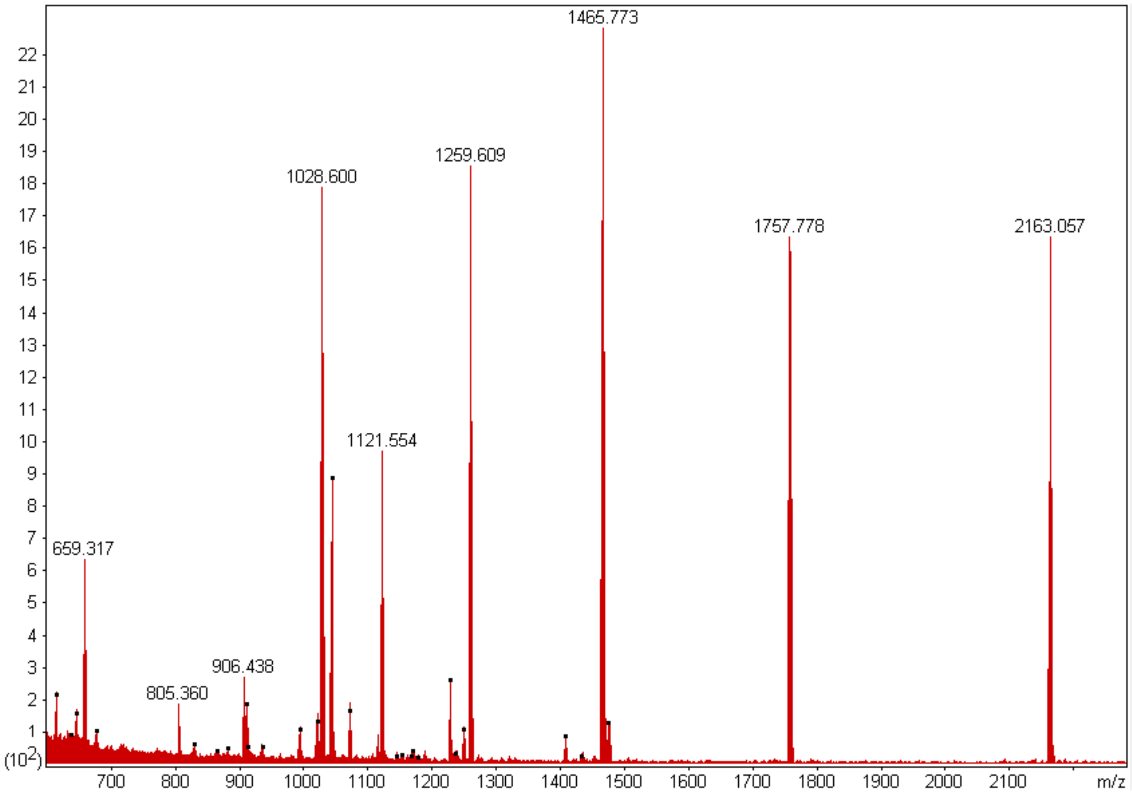
Mascot score: **125** Sequence coverage %: **19**

NCBI accession No.: **gi| 68655456**

Matched peptides No.: **11** Total peptides No.: **21**

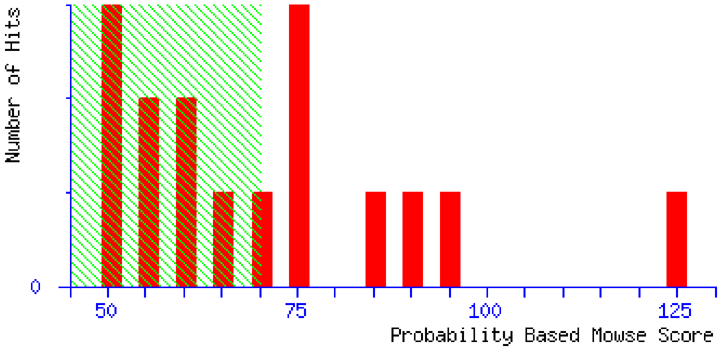
Calculated Mr: **49960** Calculated *p*I: **5.81**

Annotated PMF **spectra:**

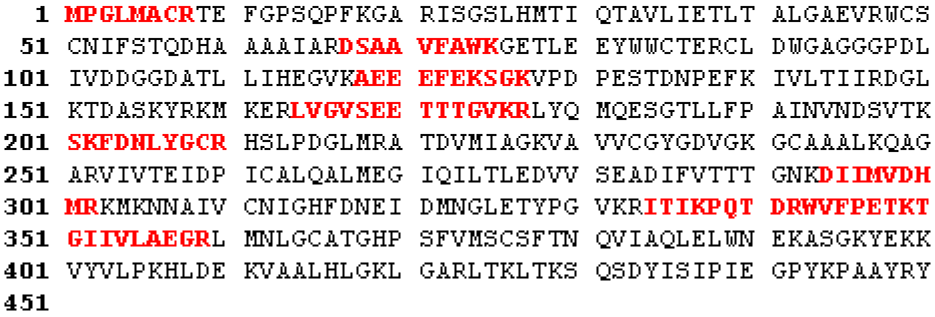


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

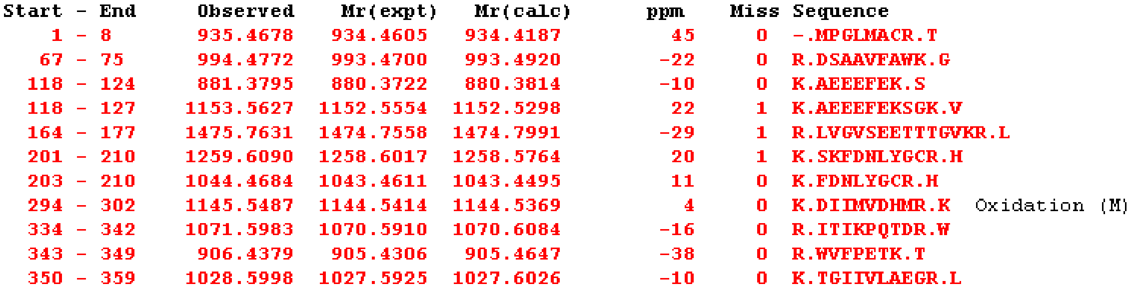


Matched peptide sequences: shown in Bold Red



```
  1 MPGLMACRTE FGPSQPFKGA RISGSLHMTI QTAVLIETLT ALGAEVRWCS
 51 CNIFSTQDHA AAAIARDSAA VFAWKGETLE EYWWCTERCL DWGAGGGPDL
101 IVDDGGDATL LIHEGVKAEE EFEKSGKVPD PESTDNPEFK IVLTIIRDGL
151 KTDASKYRKM KERLVGVSEE TTTGVKRLYQ MQESGTLLFP AINVNDSVTK
201 SKFDNLYGCR HSLPDGLMRA TDVMIAGKVA VVCGYGDVGK GCAAALKQAG
251 ARVIVTEIDP ICALQALMEG IQILTLEDVV SEADIFVTTT GNKDIIMVDH
301 MRKMKNNAIV CNIGHFDNEI DMNGLETYPG VKRITIKPQT DRWVFPETKT
351 GIIVLAEGRL MNLGCATGHP SFVMSCSFTN QVIAQLELWN EKASGKYEKK
401 VYVLPKHLDE KVAALHLGKL GARLTKLTKS QSDYISIPIE GPYKPAAYRY
451
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    1 - 8       935.4678   934.4605   934.4187       45      0  -.MPGLMACR.T
   67 - 75      994.4772   993.4700   993.4920      -22      0  R.DSAAVFAWK.G
  118 - 124     881.3795   880.3722   880.3814      -10      0  K.AEEEFEK.S
  118 - 127    1153.5627  1152.5554  1152.5298       22      1  K.AEEEFEKSGK.V
  164 - 177    1475.7631  1474.7558  1474.7991      -29      1  R.LVGVSEETTTGVKR.L
  201 - 210    1259.6090  1258.6017  1258.5764       20      1  K.SKFDNLYGCR.H
  203 - 210    1044.4684  1043.4611  1043.4495       11      0  K.FDNLYGCR.H
  294 - 302    1145.5487  1144.5414  1144.5369        4      0  K.DIIMVDHMR.K  Oxidation (M)
  334 - 342    1071.5983  1070.5910  1070.6084      -16      0  R.ITIKPQTDR.W
  343 - 349     906.4379   905.4306   905.4647      -38      0  R.WVFPETK.T
  350 - 359    1028.5998  1027.5925  1027.6026      -10      0  K.TGIIVLAEGR.L
```

Spot No.: **86**

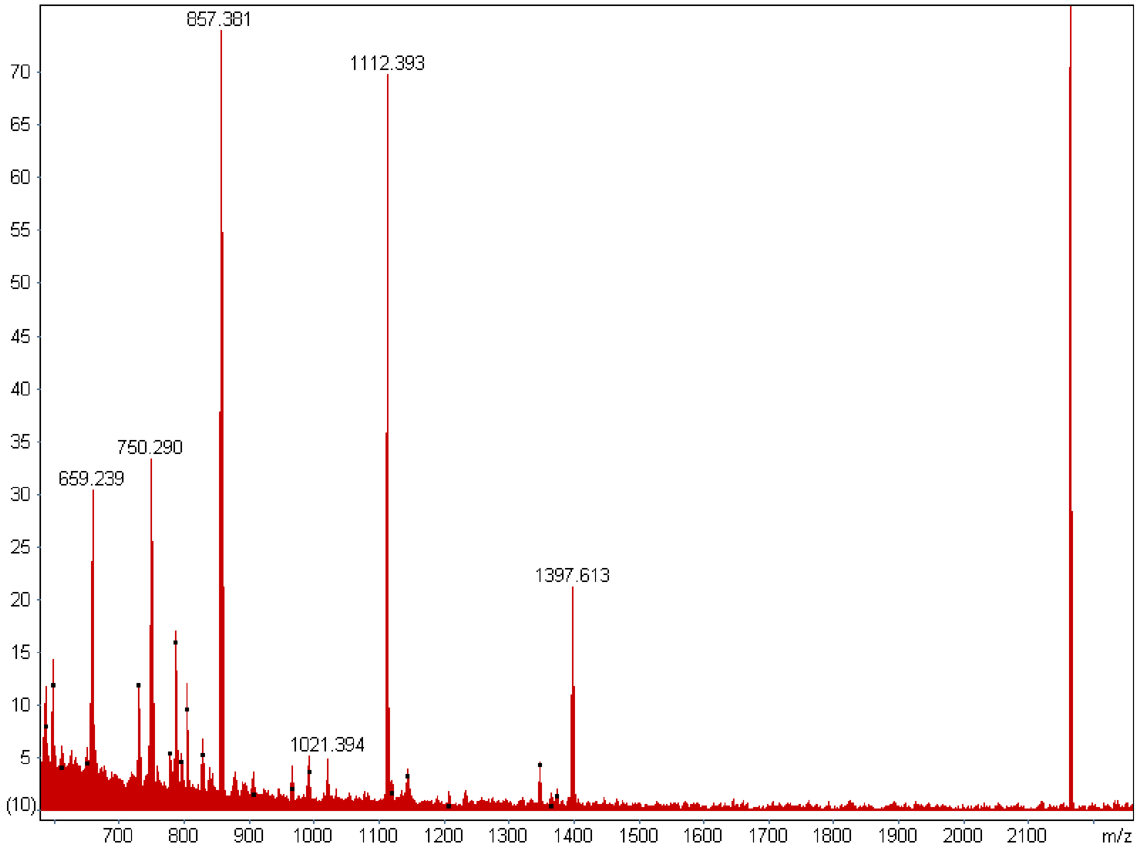
Mascot score: **81** Sequence coverage %: **14**

NCBI accession No.: **gi| 30688330**

Matched peptides No.: **9** Total peptides No.: **15**

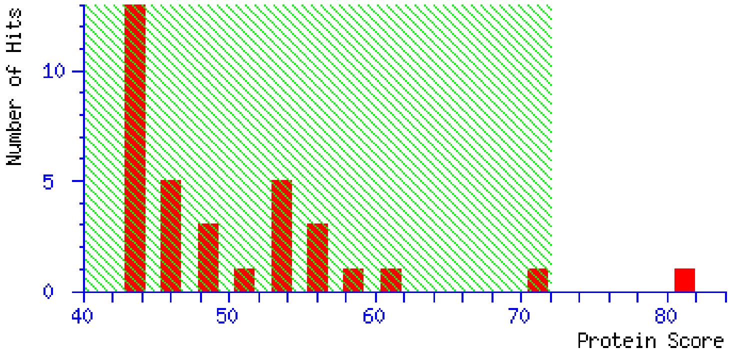
Calculated Mr: **53780** Calculated *p*I: **6.49**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in **Bold Red**

```
  1 MALKALDYDT LNENVKKCQY AVRGELYLRA SELQKEGKKI IFTNVGNPHA
 51 LGQKPLTFPR QVVALCQAPF LLDDPNVGML FPADAIARAK HYLSLTSGGL
101 GAYSDSRGLP GVRKEVAEFI QRRDGYPSDP ELIFLTDGAS KGVMQILNCV
151 IRGNGDGILV PVPQYPLYSA TISLLGGTLV PYYLDESENW GLDVANLRQS
201 VAQARSQGIT VRAMVIINPG NPTGQCLSEA NIREILKFCY NEKLVLLGDE
251 VYQQNIYQDE RPFISSKKVL MEMGSPFSKE VQLVSFHTVS KGYWGECGQR
301 GGYFEMTNLP PRVVEEIYKV ASIALSPNVS AQIFMGLMVN PPKPGDISYD
351 QFARESKGIL ESLRRRARLM TDGFNSCKNV VCNFTEGAMY SFPQIRLPTG
401 ALQAAKQAGK VPDVFYCLKL LEATGISTVP GSGFGQKEGV FHLRTTILPA
451 EDEMPEIMDS FKKFNDEFMT QYDNNFGYSK M
```

Matched peptides information:

```
Start - End     Observed     Mr(expt)    Mr(calc)      ppm    Miss  Sequence
   18 - 23      796.2213     795.2140    795.3698      -196     0   K.CQYAVR.G
   24 - 29      750.2899     749.2826    749.4072      -166     0   R.GELYLR.A
   55 - 60      730.3282     729.3209    729.4174      -132     0   K.PLTFPR.Q
  108 - 113     598.2109     597.2037    597.3598      -261     0   R.GLPGVR.K
  280 - 291    1373.6760    1372.6687   1372.7351       -48     0   K.EVQLVSFHTVSK.G
  292 - 300    1112.3934    1111.3861   1111.4505       -58     0   K.GYWGECGQR.G
  301 - 312    1397.6131    1396.6058   1396.6445       -28     0   R.GGYFEMTNLPPR.V
  358 - 364     787.3150     786.3078    786.4599      -193     0   K.GILESLR.R
  438 - 444     857.3810     856.3737    856.4555       -96     0   K.EGVFHLR.T
```

Spot No.: **87**

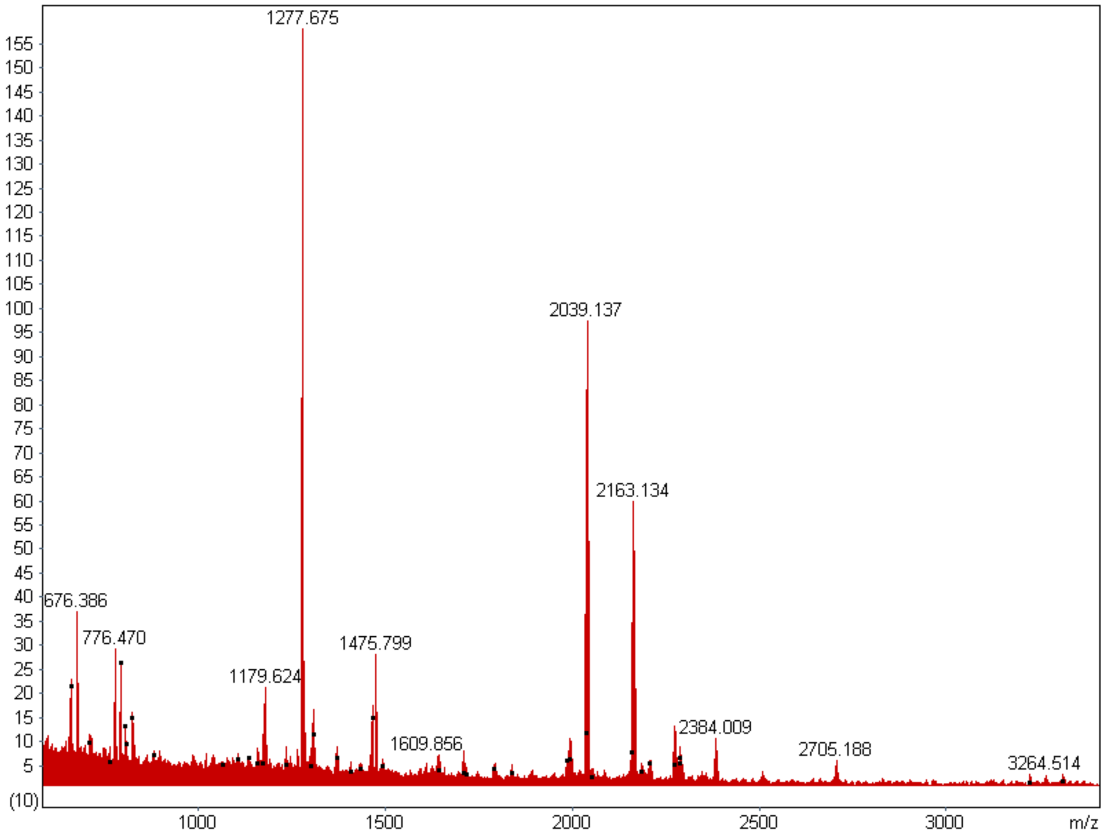
Mascot score: **96**   Sequence coverage %: **26**

NCBI accession No.: **gi| 30688330**

Matched peptides No.: **9**   Total peptides No.: **27**

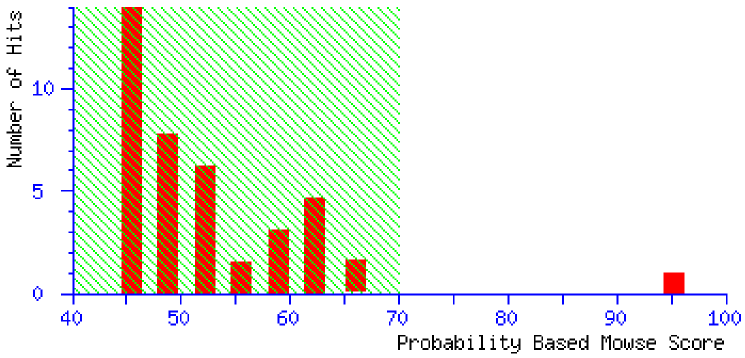
Calculated Mr: **46598**   Calculated *p*I: **5.55**

Annotated PMF **spectra:**

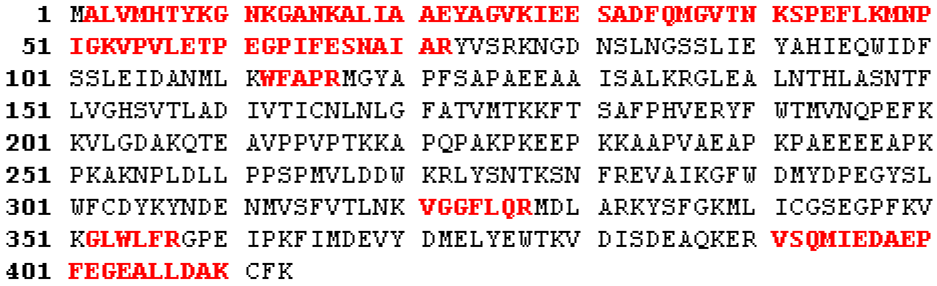


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant ($p<0.05$).

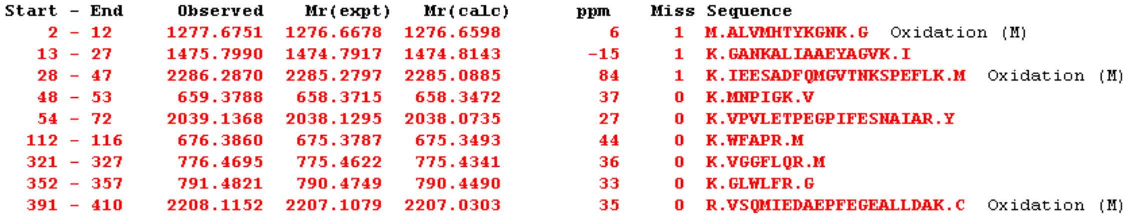


Matched peptide sequences: shown in Bold Red



```
  1 MALVMHTYKG NKGANKALIA AEYAGVKIEE SADFQMGVTN KSPEFLKMNP
 51 IGKVPVLETP EGPIFESNAI ARYVSRKNGD NSLNGSSLIE YAHIEQWIDF
101 SSLEIDANML KWFAPRMGYA PFSAPAEEAA ISALKRGLEA LNTHLASNTF
151 LVGHSVTLAD IVTICNLNLG FATVMTKKFT SAFPHVERYF WTMVNQPEFK
201 KVLGDAKQTE AVPPVPTKKA PQPAKPKEEP KKAAPVAEAP KPAEEEEAPK
251 PKAKNPLDLL PPSPMVLDDW KRLYSNTKSN FREVAIKGFW DMYDPEGYSL
301 WFCDYKYNDE NMVSFVTLNK VGGFLQRMDL ARKYSFGKML ICGSEGPFKV
351 KGLWLFRGPE IPKFIMDEVY DMELYEWTKV DISDEAQKER VSQMIEDAEP
401 FEGEALLDAK CFK
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss Sequence
    2 - 12     1277.6751  1276.6678  1276.6598        6      1 M.ALVMHTYKGNK.G  Oxidation (M)
   13 - 27     1475.7990  1474.7917  1474.8143      -15      1 K.GANKALIAAEYAGVK.I
   28 - 47     2286.2870  2285.2797  2285.0885       84      1 K.IEESADFQMGVTNKSPEFLK.M  Oxidation (M)
   48 - 53      659.3788   658.3715   658.3472       37      0 K.MNPIGK.V
   54 - 72     2039.1368  2038.1295  2038.0735       27      0 K.VPVLETPEGPIFESNAIAR.Y
  112 - 116     676.3860   675.3787   675.3493       44      0 K.WFAPR.M
  321 - 327     776.4695   775.4622   775.4341       36      0 K.VGGFLQR.M
  352 - 357     791.4821   790.4749   790.4490       33      0 K.GLWLFR.G
  391 - 410    2208.1152  2207.1079  2207.0303       35      0 R.VSQMIEDAEPFEGEALLDAK.C  Oxidation (M)
```

Spot No.: **88**

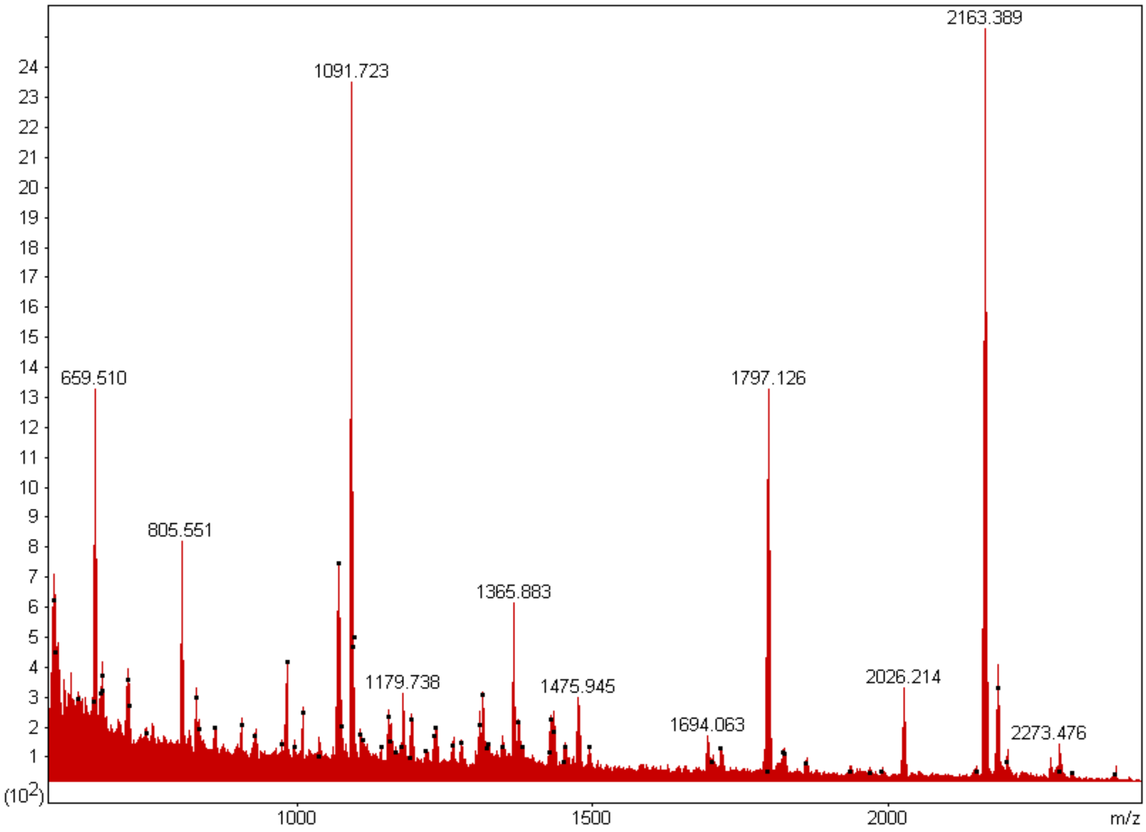
Mascot score: **83** Sequence coverage %: **40**

NCBI accession No.: **gi| 76782076**

Matched peptides No.: **9** Total peptides No.: **61**

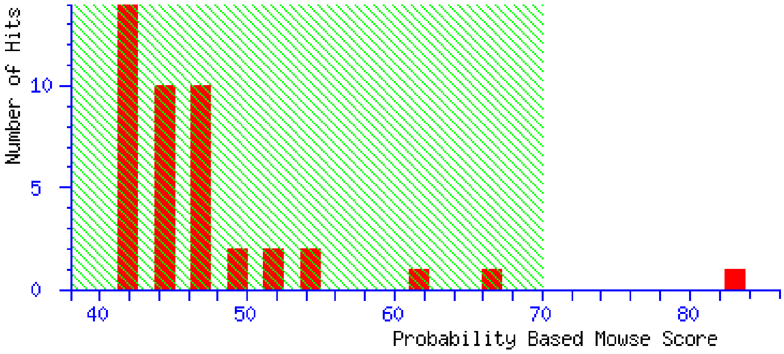
Calculated Mr: **19172** Calculated *p*I: **5.70**

Annotated PMF **spectra:**

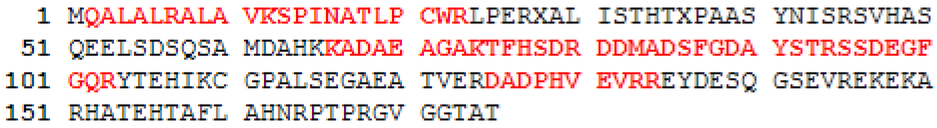


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red



```
  1 MQALALRALA VKSPINATLP CWRLPERXAL ISTHTXPAAS YNISRSVHAS
 51 QEELSDSQSA MDAHKKADAE AGAKTFHSDR DDMADSFGDA YSTRSSDEGF
101 GQRYTEHIKC GPALSEGAEA TVERDADPHV EVRREYDESQ GSEVREKEKA
151 RHATEHTAFL AHNRPTPRGV GGTAT
```

Matched peptides information:

```
Start - End     Observed    Mr(expt)   Mr(calc)      ppm    Miss Sequence
    2 - 7       671.3785    670.3712   670.4126      -62     0   M.QALALR.A
    2 - 12     1153.7147   1152.7074  1152.7342      -23     1   M.QALALRALAVK.S
    8 - 23     1797.1264   1796.1191  1795.9767       79     1   R.ALAVKSPINATLPCWR.L
   13 - 23     1314.8304   1313.8231  1313.6550      128     0   K.SPINATLPCWR.L
   66 - 74      860.5463    859.5390   859.4399      115     1   K.KADAEAGAK.T
   67 - 80     1475.9452   1474.9379  1474.6801      175     1   K.ADAEAGAKTFHSDR.D
   75 - 94     2310.4357   2309.4284  2308.9291      216     1   K.TFHSDRDDMADSFGDAYSTR.S  Oxidation (M)
   95 - 103     982.6394    981.6322   981.4152      221     0   R.SSDEGFGQR.Y
  125 - 134    1193.7383   1192.7310  1192.5949      114     1   R.DADPHVEVRR.E
```

Spot No.: **89**

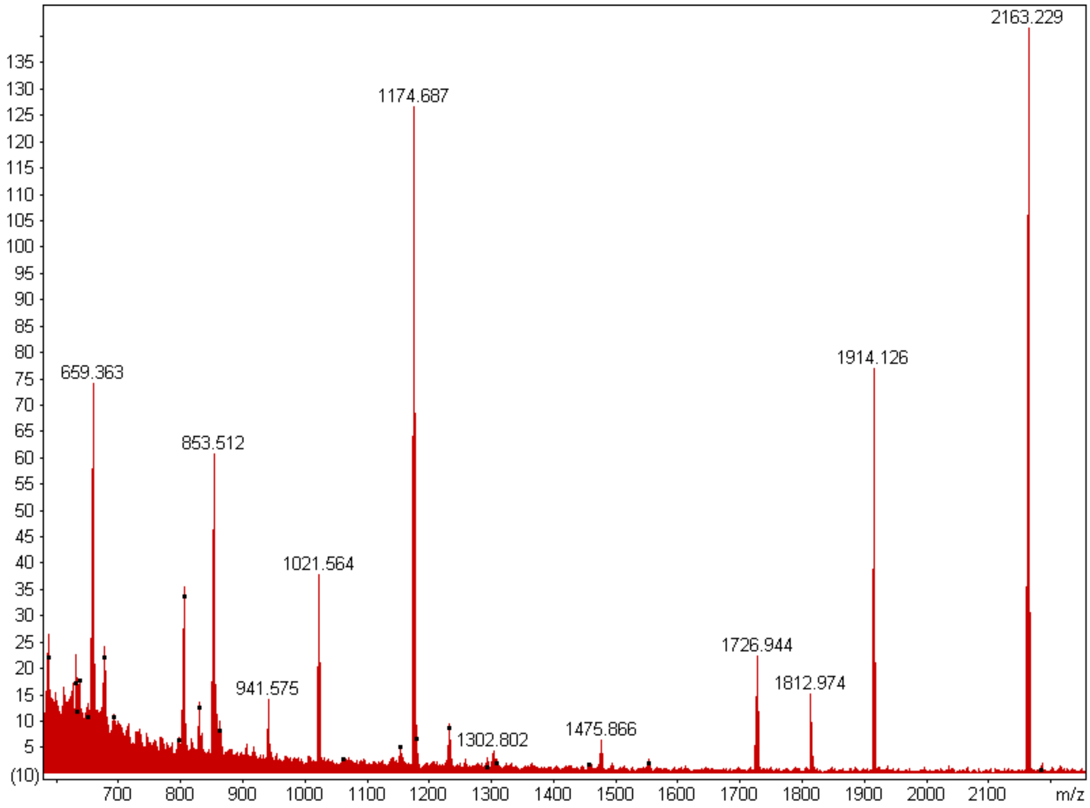
Mascot score: **96**   Sequence coverage %: **20**

NCBI accession No.: **gi| 116787113**

Matched peptides No.: **10**   Total peptides No.: **22**

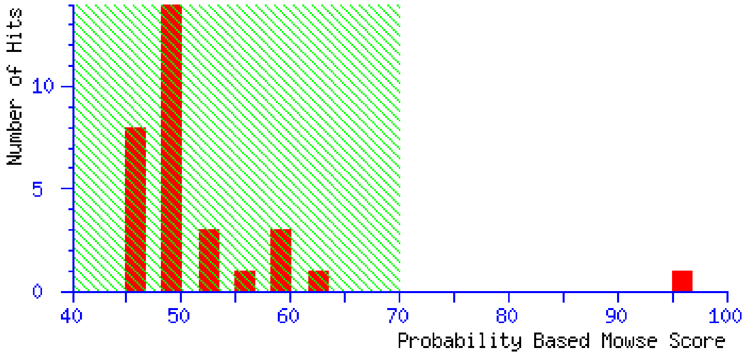
Calculated Mr: **53356**   Calculated *p*I: **5.66**

Annotated PMF **spectra:**

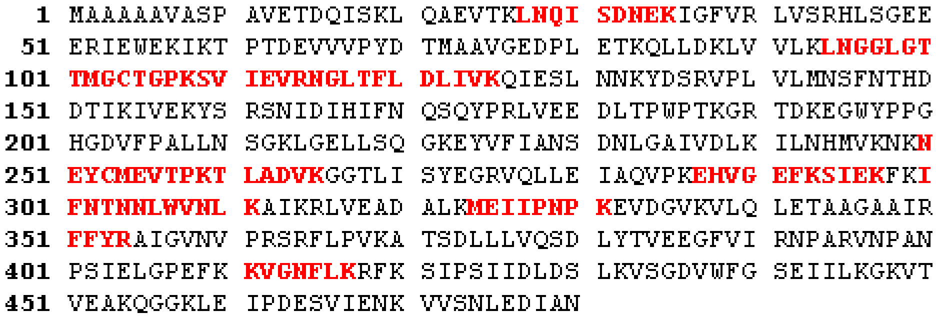


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

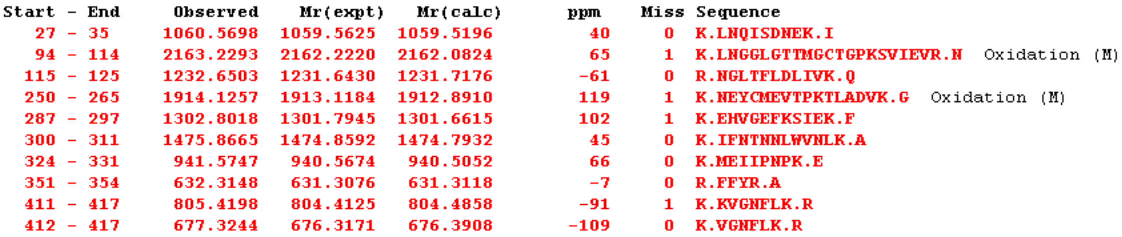


Matched peptide sequences: shown in Bold Red



```
  1 MAAAAAVASP AVETDQISKL QAEVTKLNQI SDNEKIGFVR LVSRHLSGEE
 51 ERIEWEKIKT PTDEVVVPYD TMAAVGEDPL ETKQLLDKLV VLKLNGGLGT
101 TMGCTGPKSV IEVRNGLTFL DLIVKQIESL NNKYDSRVPL VLMNSFNTHD
151 DTIKIVEKYS RSNIDIHIFN QSQYPRLVEE DLTPWPTKGR TDKEGWYPPG
201 HGDVFPALLN SGKLGELLSQ GKEYVFIANS DNLGAIVDLK ILNHMVKNKN
251 EYCMEVTPKT LADVKGGTLI SYEGRVQLLE IAQVPKEHVG EFKSIEKFKI
301 FNTNNLWVNL KAIKRLVEAD ALKMEIIPNP KEVDGVKVLQ LETAAGAAIR
351 FFYRAIGVNV PRSRFLPVKA TSDLLLVQSD LYTVEEGFVI RNPARVNPAN
401 PSIELGPEFK KVGNFLKRFK SIPSIIDLDS LKVSGDVWFG SEIILKGKVT
451 VEAKQGGKLE IPDESVIENK VVSNLEDIAN
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   27 - 35     1060.5698  1059.5625  1059.5196       40      0  K.LNQISDNEK.I
   94 - 114    2163.2293  2162.2220  2162.0824       65      1  K.LNGGLGTTMGCTGPKSVIEVR.N  Oxidation (M)
  115 - 125    1232.6503  1231.6430  1231.7176      -61      0  R.NGLTFLDLIVK.Q
  250 - 265    1914.1257  1913.1184  1912.8910      119      1  K.NEYCMEVTPKTLADVK.G  Oxidation (M)
  287 - 297    1302.8018  1301.7945  1301.6615      102      1  K.EHVGEFKSIEK.F
  300 - 311    1475.8665  1474.8592  1474.7932       45      0  K.IFNTNNLWVNLK.A
  324 - 331     941.5747   940.5674   940.5052       66      0  K.MEIIPNPK.E
  351 - 354     632.3148   631.3076   631.3118       -7      0  R.FFYR.A
  411 - 417     805.4198   804.4125   804.4858      -91      1  K.KVGNFLK.R
  412 - 417     677.3244   676.3171   676.3908     -109      0  K.VGNFLK.R
```

Spot No.: **90**

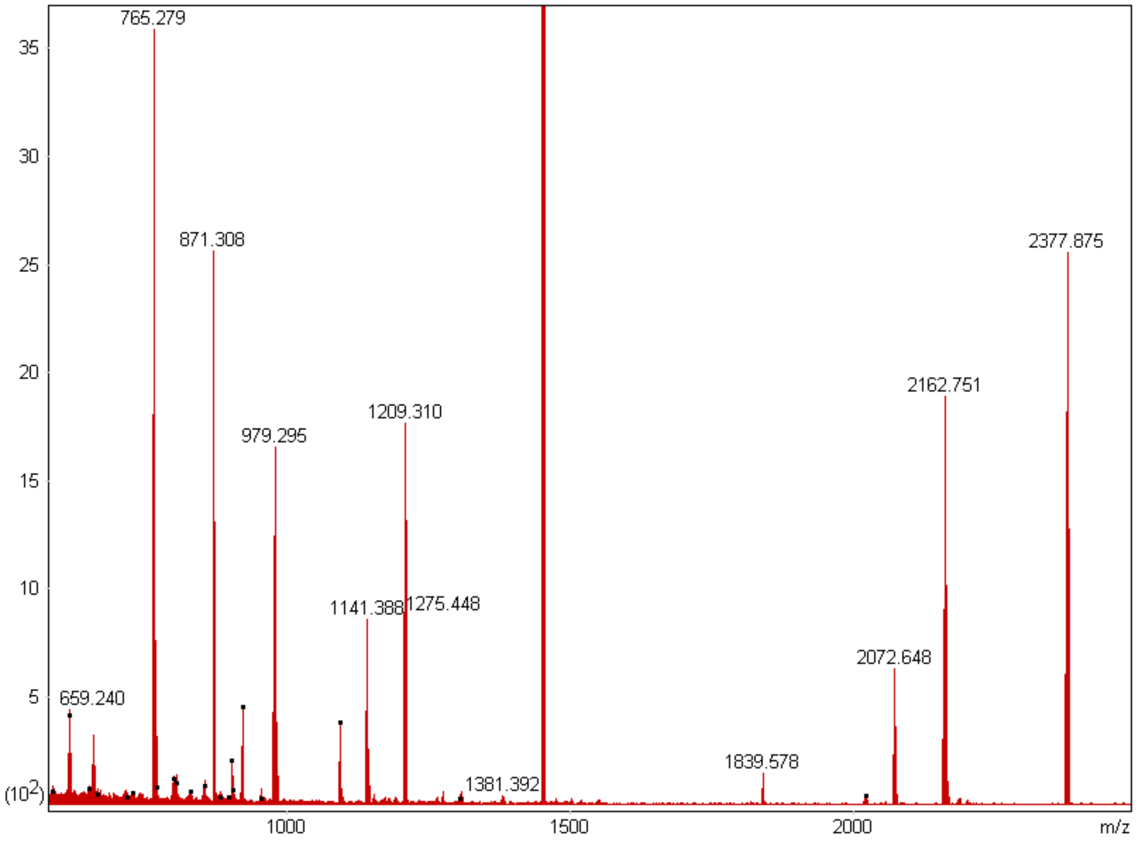
Mascot score: **93** Sequence coverage %: **23**

NCBI accession No.: **gi| 15234354**

Matched peptides No.: **8** Total peptides No.: **19**

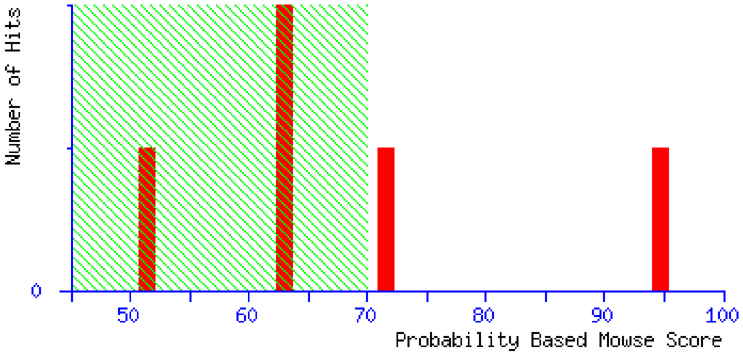
Calculated Mr: **43627** Calculated *p*I: **5.67**

Annotated PMF **spectra:**



Probability Based Mowse Score:

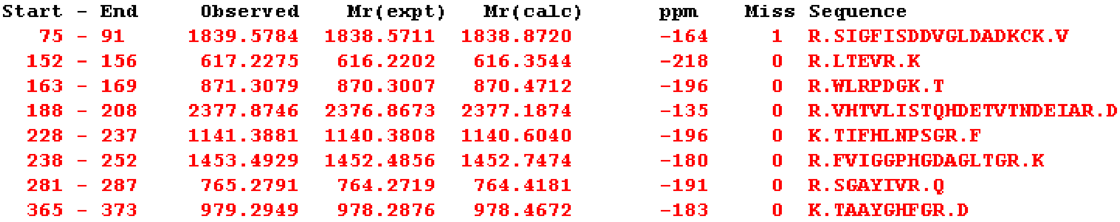
Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 METFLFTSES VNEGHPDKLC DQISDAVLDA CLEQDPDSKV ACETCTKTNM
51 VMVFGEITTK ATIDYEKIVR DTCR**SIGFIS DDVGLDADKC K**VLVNIEQQS
101 PDIAQGVHGH FTKRPEDIGA GDQGHMFGYA TDETPELMPL SHVLATKIGA
151 R**LTEVR**KNGT CR**WLRPDGK**T QVTVEYYNDN GAMVPVR**VHT VLISTQHDET**
201 **VTNDEIAR**DL KEHVIKPIIP EKYLDDK**TIF HLNPSGRFVI GGPHGDAGLT**
251 **GR**KIIIDTYG GWGAHGGGAF SGKDPTKVDR **SGAYIVR**QAA KSVVANGMAR
301 RALVQVSYAI GVPEPLSVFV DTYGTGLIPD KEILKIVKET FDFRPGMMTI
351 NLDLKRGGNG RFQK**TAAYGH FGR**DDPDFTW EVVKPLKWDK PQA

Matched peptides information:



```
Start - End      Observed    Mr(expt)    Mr(calc)       ppm    Miss  Sequence
   75 - 91      1839.5784   1838.5711   1838.8720      -164     1   R.SIGFISDDVGLDADKCK.V
  152 - 156      617.2275    616.2202    616.3544      -218     0   R.LTEVR.K
  163 - 169      871.3079    870.3007    870.4712      -196     0   R.WLRPDGK.T
  188 - 208     2377.8746   2376.8673   2377.1874      -135     0   R.VHTVLISTQHDETVTNDEIAR.D
  228 - 237     1141.3881   1140.3808   1140.6040      -196     0   K.TIFHLNPSGR.F
  238 - 252     1453.4929   1452.4856   1452.7474      -180     0   R.FVIGGPHGDAGLTGR.K
  281 - 287      765.2791    764.2719    764.4181      -191     0   R.SGAYIVR.Q
  365 - 373      979.2949    978.2876    978.4672      -183     0   K.TAAYGHFGR.D
```

Spot No.: **91**

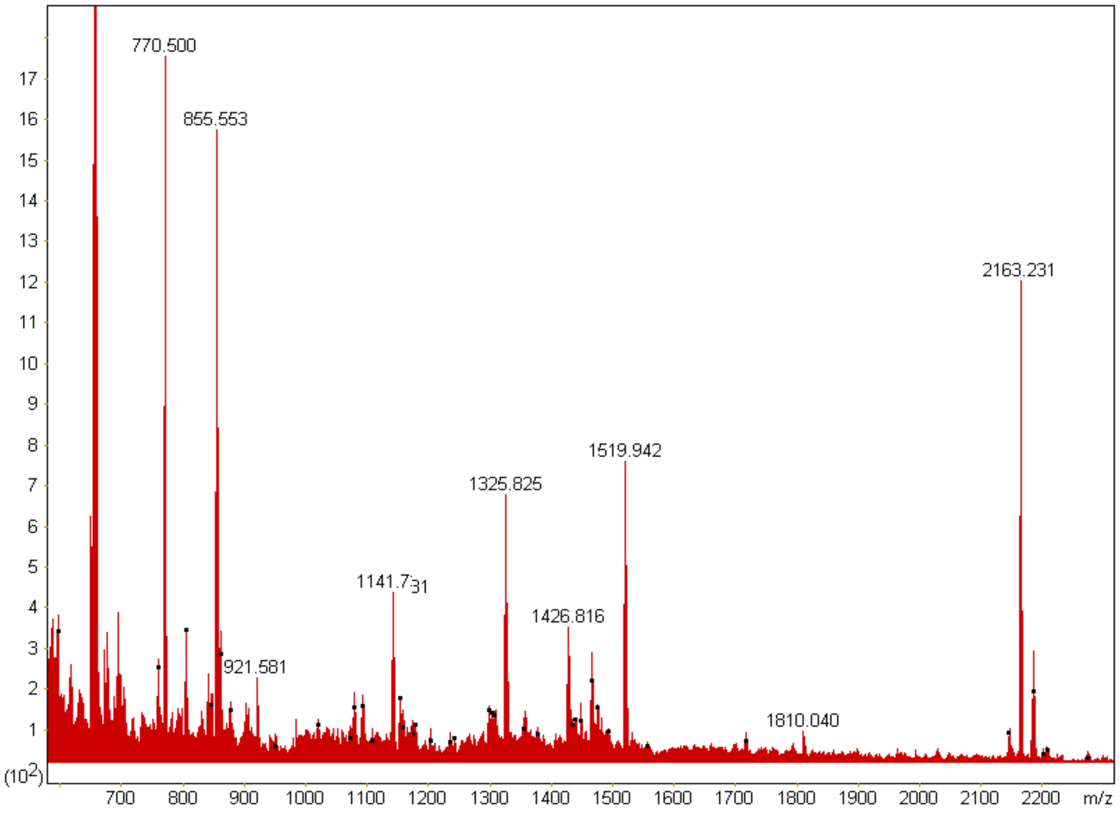
Mascot score: **88** Sequence coverage %: **18**

NCBI accession No.: **gi| 30691729**

Matched peptides No.: **9** Total peptides No.: **30**

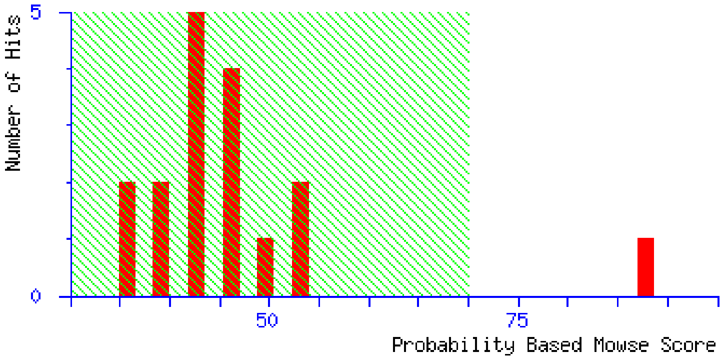
Calculated Mr: **47767** Calculated *p*I: **5.93**

Annotated PMF **spectra:**

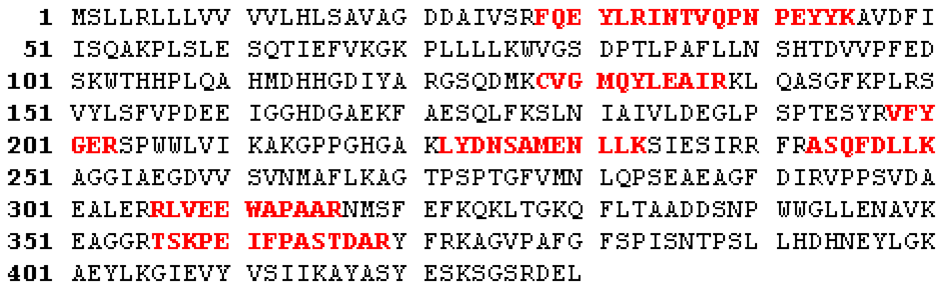


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

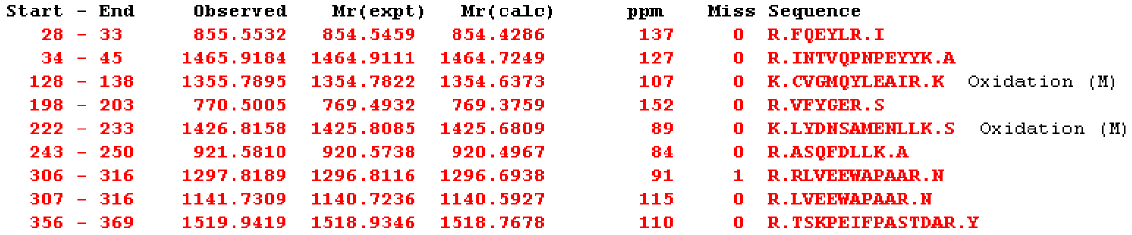


Matched peptide sequences: shown in Bold Red



1 MSLLRLLLVV VVLHLSAVAG DDAIVSR**FQE YLRINTVQPN PEYYK**AVDFI
51 ISQAKPLSLE SQTIEFVKGK PLLLLKWVGS DPTLPAFLLN SHTDVVPFED
101 SKWTHHPLQA HMDHHGDIYA RGSQDMK**CVG MQYLEAIR**KL QASGFKPLRS
151 VYLSFVPDEE IGGHDGAEKF AESQLFKSLN IAIVLDEGLP SPTESYR**VFY**
201 **GER**SPWWLVI KAKGPPGHGA K**LYDNSAMEN LLK**SIESIRR FR**ASQFDLLK**
251 AGGIAEGDVV SVNMAFLKAG TPSPTGFVMN LQPSEAEAGF DIRVPPSVDA
301 EALER**RLVEE WAPAAR**NMSF EFKQKLTGKQ FLTAADDSNP WWGLLENAVK
351 EAGGR**TSKPE IFPASTDAR**Y FRKAGVPAFG FSPISNTPSL LHDHNEYLGK
401 AEYLKGIEVY VSIIKAYASY ESKSGSRDEL

Matched peptides information:



Start	-	End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
28	-	33	855.5532	854.5459	854.4286	137	0	R.FQEYLR.I	
34	-	45	1465.9184	1464.9111	1464.7249	127	0	R.INTVQPNPEYYK.A	
128	-	138	1355.7895	1354.7822	1354.6373	107	0	K.CVGMQYLEAIR.K	Oxidation (M)
198	-	203	770.5005	769.4932	769.3759	152	0	R.VFYGER.S	
222	-	233	1426.8158	1425.8085	1425.6809	89	0	K.LYDNSAMENLLK.S	Oxidation (M)
243	-	250	921.5810	920.5738	920.4967	84	0	R.ASQFDLLK.A	
306	-	316	1297.8189	1296.8116	1296.6938	91	1	R.RLVEEWAPAAR.N	
307	-	316	1141.7309	1140.7236	1140.5927	115	0	R.LVEEWAPAAR.N	
356	-	369	1519.9419	1518.9346	1518.7678	110	0	R.TSKPEIFPASTDAR.Y	

Spot No.: **92**

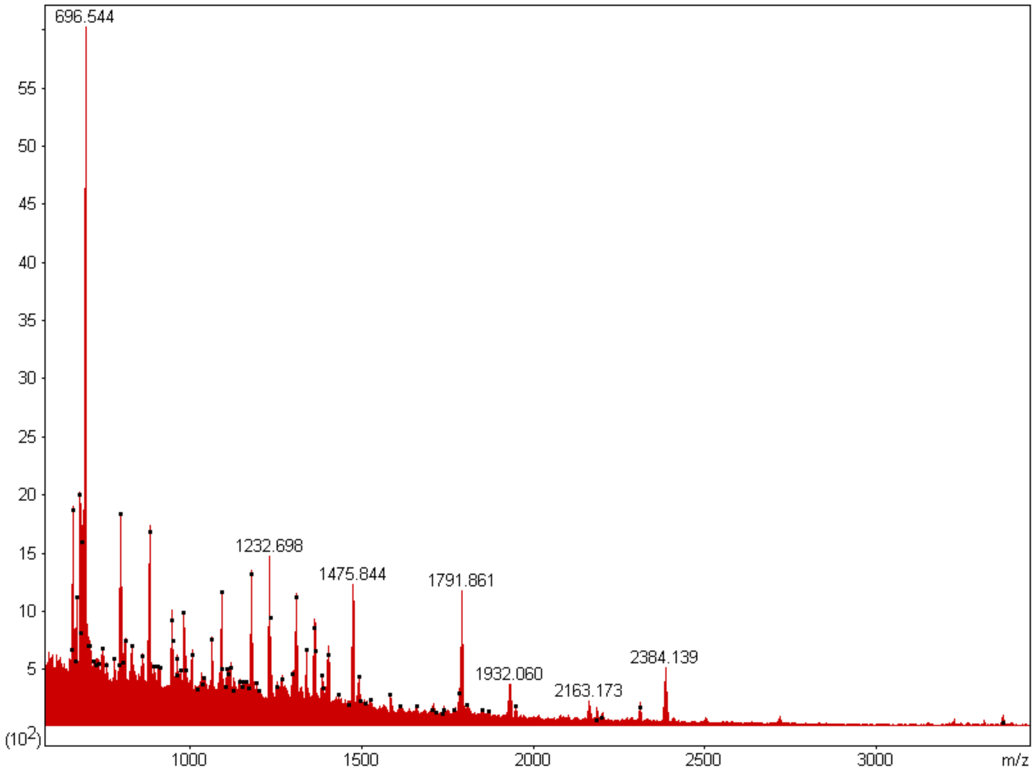
Mascot score: **84**   Sequence coverage %: **23**

NCBI accession No.: **gi| 116057683**

Matched peptides No.: **20**   Total peptides No.: **89**

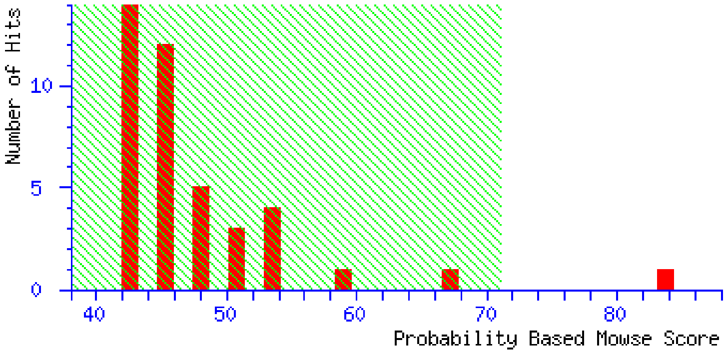
Calculated Mr: **99984**   Calculated *p*I: **6.39**

Annotated PMF **spectra:**

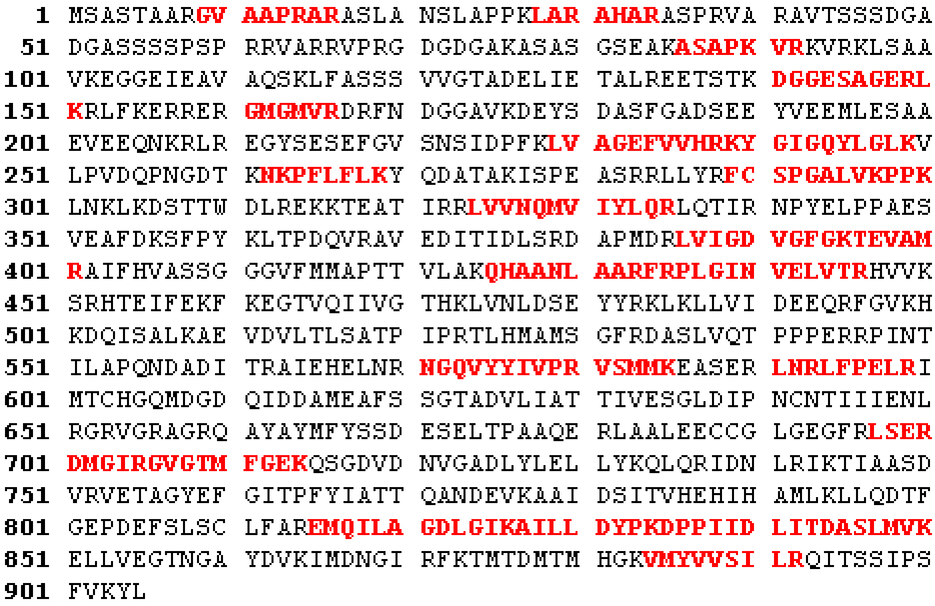


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).

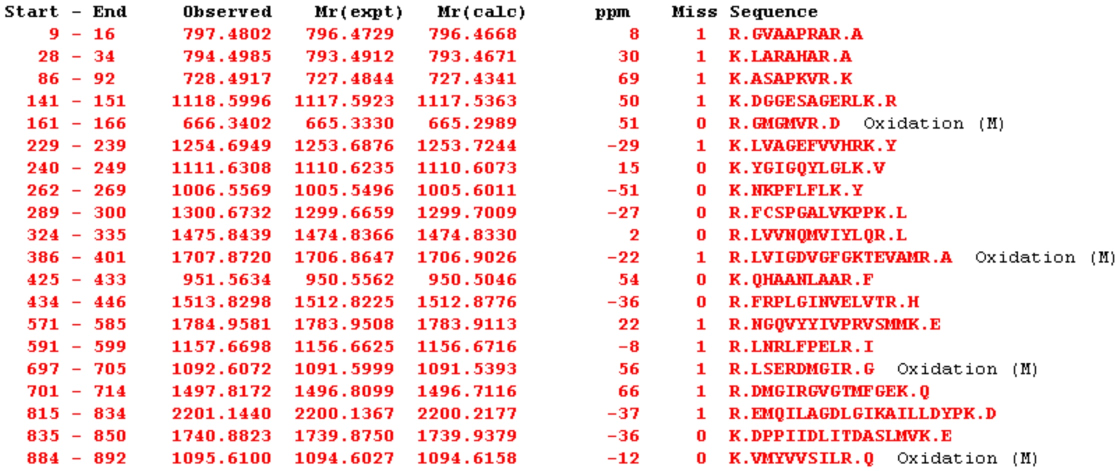


Matched peptide sequences: shown in Bold Red



1 MSASTAAR**GV** **AAPRAR**ASLA NSLAPPK**LAR** **AHAR**ASPRVA RAVTSSSDGA
51 DGASSSSPSP RRVARRVPRG DGDGAKASAS GSEAK**ASAPK** **VR**KVRKLSAA
101 VKEGGEIEAV AQSKLFASSS VVGTADELIE TALREETSTK **DGGESAGERL**
151 **K**RLFKERRER **GMGMVR**DRFN DGGAVKDEYS DASFGADSEE YVEEMLESAA
201 EVEEQNKRLR EGYSESEFGV SNSIDPFK**LV** **AGEFVVHRKY** **GIGQYLGLK**V
251 LPVDQPNGDT K**NKPFLFLK**Y QDATAKISPE ASRRLLYR**FC** **SPGALVKPPK**
301 LNKLKDSTTW DLREKKTEAT IRR**LVVNQMV** **IYLQR**LQTIR NPYELPPAES
351 VEAFDKSFPY KLTPDQVRAV EDITIDLSRD APMDR**LVIGD** **VGFGKTEVAM**
401 **R**AIFHVASSG GGVFMMAPTT VLAK**QHAANL** **AARFRPLGIN** **VELVTR**HVVK
451 SRHTEIFEKF KEGTVQIIVG THKLVNLDSE YYRKLKLLVI DEEQRFGVKH
501 KDQISALKAE VDVLTLSATP IPRTLHMAMS GFRDASLVQT PPPERRPINT
551 ILAPQNDADI TRAIEHELNR **NGQVYYIVPR** **VSMMK**EASER **LNRLFPELR**I
601 MTCHGQMDGD QIDDAMEAFS SGTADVLIAT TIVESGLDIP NCNTIIIENL
651 RGRVGRAGRQ AYAYMFYSSD ESELTPAAQE RLAALEECCG LGEGFR**LSER**
701 **DMGIRGVGTM** **FGEK**QSGDVD NVGADLYLEL LYKQLQRIDN LRIKTIAASD
751 VRVETAGYEF GITPFYIATT QANDEVKAAI DSITVHEHIH AMLKLLQDTF
801 GEPDEFSLSC LFAR**EMQILA** **GDLGIKAILL** **DYPKDPPIID** **LITDASLMVK**
851 ELLVEGTNGA YDVKIMDNGI RFKTMTDMTM HGK**VMYVVSI** **LR**QITSSIPS
901 FVKYL

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
9 - 16	797.4802	796.4729	796.4668	8	1	R.GVAAPRAR.A	
28 - 34	794.4985	793.4912	793.4671	30	1	K.LARAHAR.A	
86 - 92	728.4917	727.4844	727.4341	69	1	K.ASAPKVR.K	
141 - 151	1118.5996	1117.5923	1117.5363	50	1	K.DGGESAGERLK.R	
161 - 166	666.3402	665.3330	665.2989	51	0	R.GMGMVR.D	Oxidation (M)
229 - 239	1254.6949	1253.6876	1253.7244	-29	1	K.LVAGEFVVHRK.Y	
240 - 249	1111.6308	1110.6235	1110.6073	15	0	K.YGIGQYLGLK.V	
262 - 269	1006.5569	1005.5496	1005.6011	-51	0	K.NKPFLFLK.Y	
289 - 300	1300.6732	1299.6659	1299.7009	-27	0	R.FCSPGALVKPPK.L	
324 - 335	1475.8439	1474.8366	1474.8330	2	0	R.LVVNQMVIYLQR.L	
386 - 401	1707.8720	1706.8647	1706.9026	-22	1	R.LVIGDVGFGKTEVAMR.A	Oxidation (M)
425 - 433	951.5634	950.5562	950.5046	54	0	K.QHAANLAAR.F	
434 - 446	1513.8298	1512.8225	1512.8776	-36	0	R.FRPLGINVELVTR.H	
571 - 585	1784.9581	1783.9508	1783.9113	22	1	R.NGQVYYIVPRVSMMK.E	
591 - 599	1157.6698	1156.6625	1156.6716	-8	1	R.LNRLFPELR.I	
697 - 705	1092.6072	1091.5999	1091.5393	56	1	R.LSERDMGIR.G	Oxidation (M)
701 - 714	1497.8172	1496.8099	1496.7116	66	1	R.DMGIRGVGTMFGEK.Q	
815 - 834	2201.1440	2200.1367	2200.2177	-37	1	R.EMQILAGDLGIKAILLDYPK.D	
835 - 850	1740.8823	1739.8750	1739.9379	-36	0	K.DPPIIDLITDASLMVK.E	
884 - 892	1095.6100	1094.6027	1094.6158	-12	0	K.VMYVVSILR.Q	Oxidation (M)

Spot No.: **93**

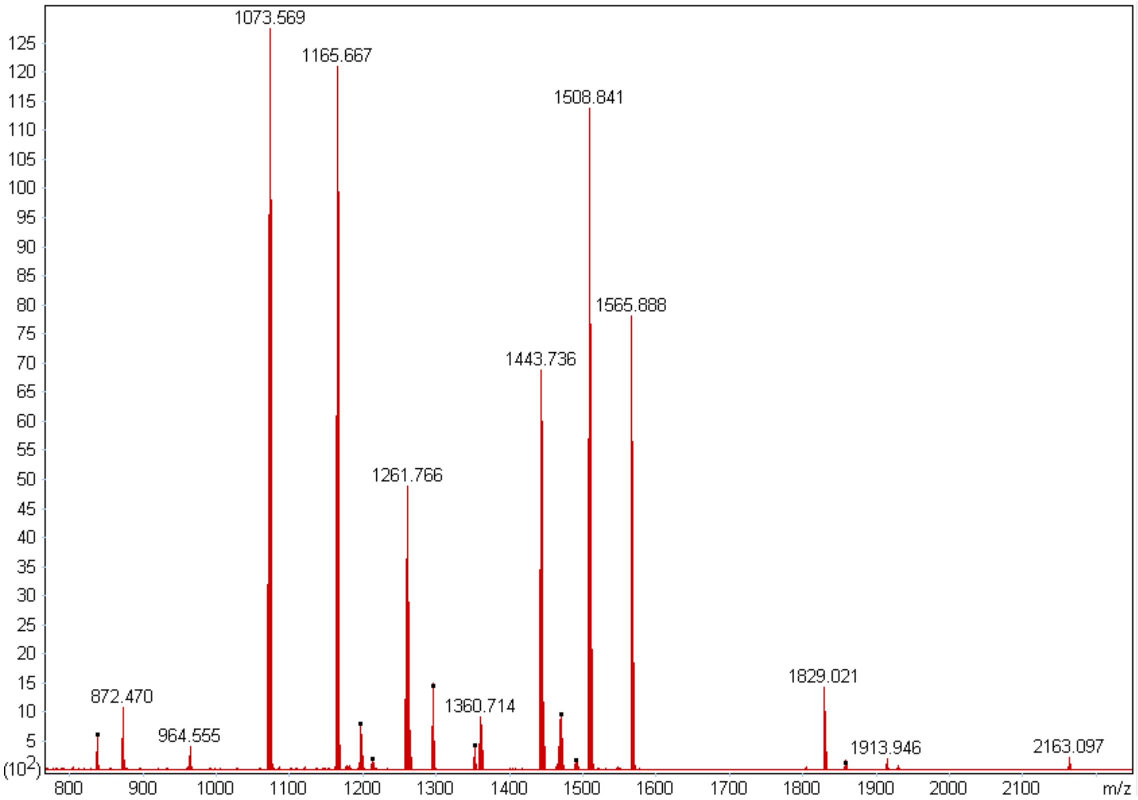
Mascot score: **177** Sequence coverage %: **33**

NCBI accession No.: **gi| 15232704**

Matched peptides No.: **13** Total peptides No.: **20**

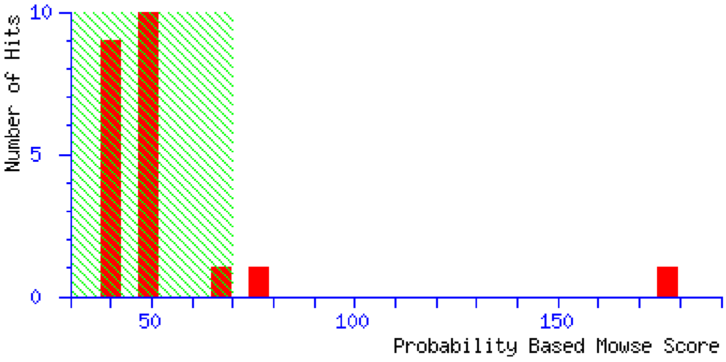
Calculated Mr: **52824** Calculated *p*I: **7.60**

Annotated PMF **spectra:**

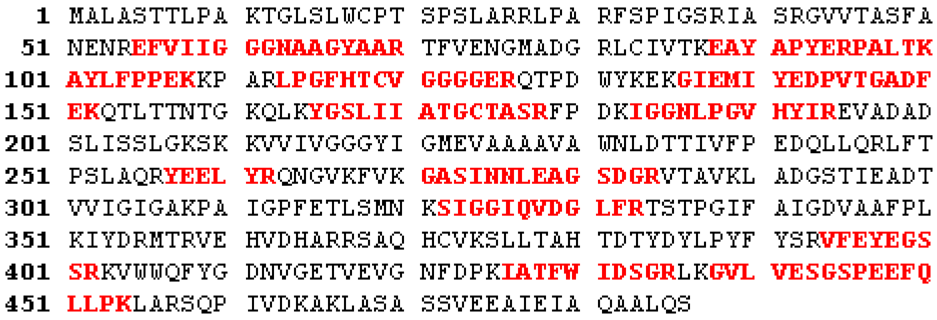


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

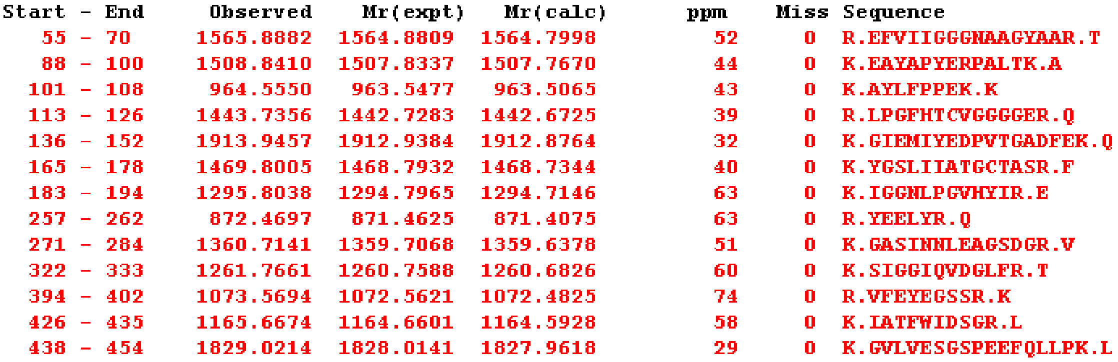


Matched peptide sequences: shown in Bold Red



1 MALASTTLPA KTGLSLWCPT SPSLARRLPA RFSPIGSRIA SRGVVTASFA
51 NENR**EFVIIG** **GGNAAGYAAR** TFVENGMADG RLCIVTK**EAY** **APYERPALTK**
101 **AYLFPPEK**KP AR**LPGFHTCV** **GGGGER**QTPD WYKEK**GIEMI** **YEDPVTGADF**
151 **EK**QTLTTNTG KQLK**YGSLII** **ATGCTASR**FP DK**IGGNLPGV** **HYIR**EVADAD
201 SLISSLGKSK KVVIVGGGYI GMEVAAAAVA WNLDTTIVFP EDQLLQRLFT
251 PSLAQR**YEEL** **YR**QNGVKFVK **GASINNLEAG** **SDGR**VTAVKL ADGSTIEADT
301 VVIGIGAKPA IGPFETLSMN K**SIGGIQVDG** **LFR**TSTPGIF AIGDVAAFPL
351 KIYDRMTRVE HVDHARRSAQ HCVKSLLTAH TDTYDYLPYF YSR**VFEYEGS**
401 **SR**KVWWQFYG DNVGETVEVG NFDPK**IATFW** **IDSGR**LK**GVL** **VESGSPEEFQ**
451 **LLPK**LARSQP IVDKAKLASA SSVEEAIEIA QAALQS

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
55 - 70	1565.8882	1564.8809	1564.7998	52	0	R.EFVIIGGGNAAGYAAR.T
88 - 100	1508.8410	1507.8337	1507.7670	44	0	K.EAYAPYERPALTK.A
101 - 108	964.5550	963.5477	963.5065	43	0	K.AYLFPPEK.K
113 - 126	1443.7356	1442.7283	1442.6725	39	0	R.LPGFHTCVGGGGER.Q
136 - 152	1913.9457	1912.9384	1912.8764	32	0	K.GIEMIYEDPVTGADFEK.Q
165 - 178	1469.8005	1468.7932	1468.7344	40	0	K.YGSLIIATGCTASR.F
183 - 194	1295.8038	1294.7965	1294.7146	63	0	K.IGGNLPGVHYIR.E
257 - 262	872.4697	871.4625	871.4075	63	0	R.YEELYR.Q
271 - 284	1360.7141	1359.7068	1359.6378	51	0	K.GASINNLEAGSDGR.V
322 - 333	1261.7661	1260.7588	1260.6826	60	0	K.SIGGIQVDGLFR.T
394 - 402	1073.5694	1072.5621	1072.4825	74	0	R.VFEYEGSSR.K
426 - 435	1165.6674	1164.6601	1164.5928	58	0	K.IATFWIDSGR.L
438 - 454	1829.0214	1828.0141	1827.9618	29	0	K.GVLVESGSPEEFQLLPK.L

Spot No.: **94**

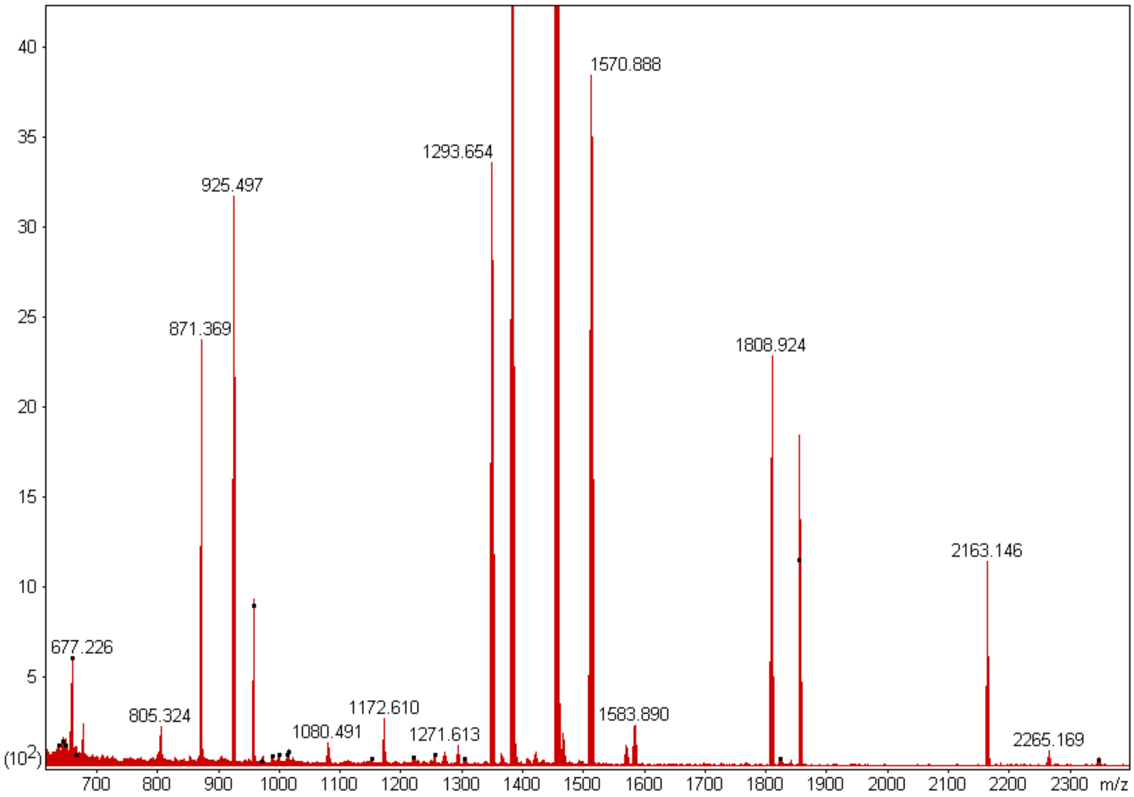
Mascot score: **170**   Sequence coverage %: **24**

NCBI accession No.: **gi| 15383744**

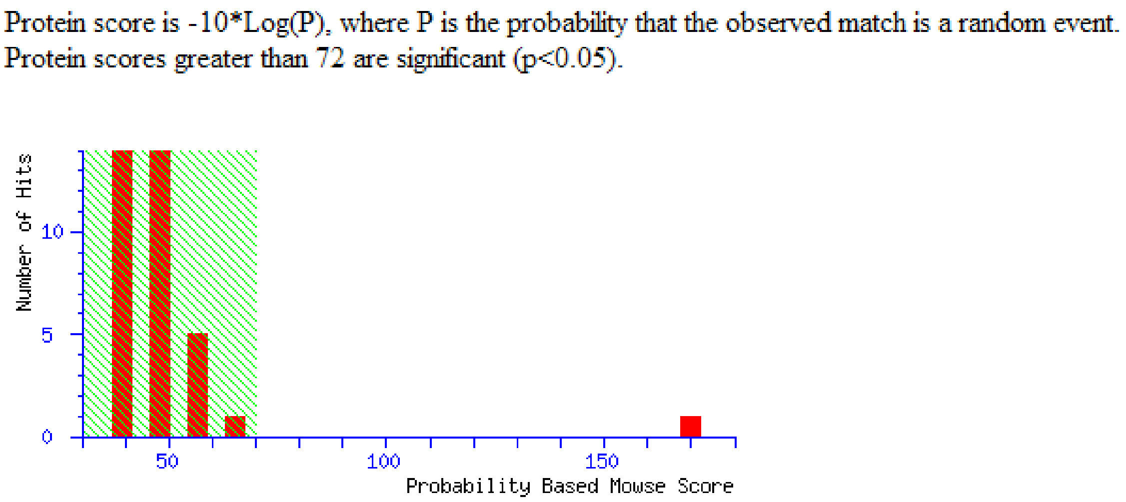
Matched peptides No.: **18**   Total peptides No.: **24**

Calculated Mr: **62192**   Calculated *p*I: **6.26**

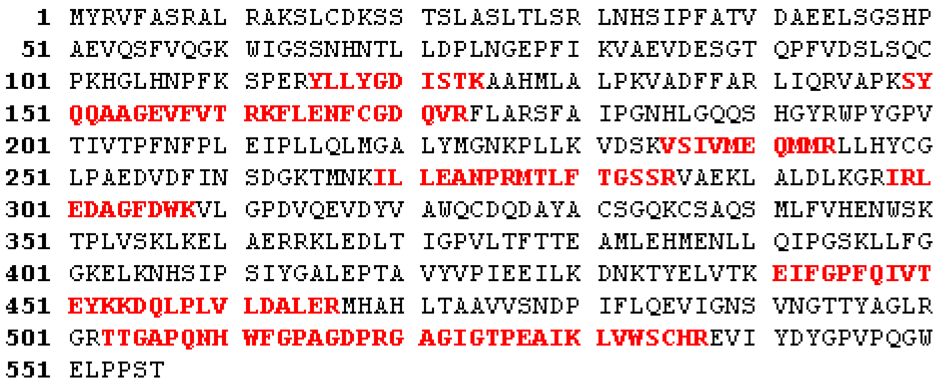
Annotated PMF **spectra:**



Probability Based Mowse Score:

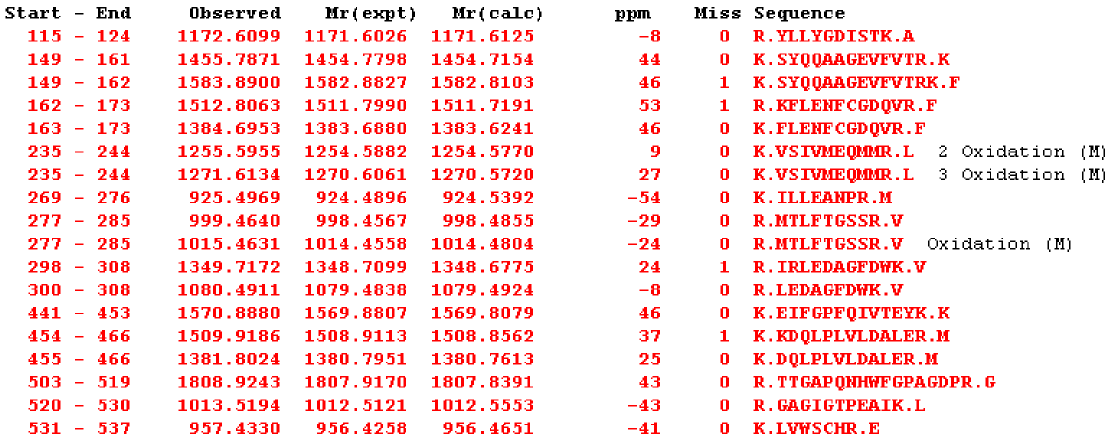

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

Matched peptide sequences: shown in Bold Red



1	MYRVFASRAL	RAKSLCDKSS	TSLASLTLSR	LNHSIPFATV	DAEELSGSHP
51	AEVQSFVQGK	WIGSSNHNTL	LDPLNGEPFI	KVAEVDESGT	QPFVDSLSQC
101	PKHGLHNPFK	SPER**YLLYGD**	**ISTK**AAHMLA	LPKVADFFAR	LIQRVAPK**SY**
151	**QQAAGEVFVT**	**RKFLENFCGD**	**QVR**FLARSFA	IPGNHLGQQS	HGYRWPYGPV
201	TIVTPFNFPL	EIPLLQLMGA	LYMGNKPLLK	VDSK**VSIVME**	**QMMR**LLHYCG
251	LPAEDVDFIN	SDGKTMNK**IL**	**LEANPRMTLF**	**TGSSR**VAEKL	ALDLKGR**IRL**
301	**EDAGFDWK**VL	GPDVQEVDYV	AWQCDQDAYA	CSGQKCSAQS	MLFVHENWSK
351	TPLVSKLKEL	AERRKLEDLT	IGPVLTFTTE	AMLEHMENLL	QIPGSKLLFG
401	GKELKNHSIP	SIYGALEPTA	VYVPIEEILK	DNKTYELVTK	**EIFGPFQIVT**
451	**EYKKDQLPLV**	**LDALER**MHAH	LTAAVVSNDP	IFLQEVIGNS	VNGTTYAGLR
501	GR**TTGAPQNH**	**WFGPAGDPRG**	**AGIGTPEAIK**	**LVWSCHR**EVI	YDYGPVPQGW
551	ELPPST				

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
115 - 124	1172.6099	1171.6026	1171.6125	-8	0	R.YLLYGDISTK.A	
149 - 161	1455.7871	1454.7798	1454.7154	44	0	K.SYQQAAGEVFVTR.K	
149 - 162	1583.8900	1582.8827	1582.8103	46	1	K.SYQQAAGEVFVTRK.F	
162 - 173	1512.8063	1511.7990	1511.7191	53	1	R.KFLENFCGDQVR.F	
163 - 173	1384.6953	1383.6880	1383.6241	46	0	K.FLENFCGDQVR.F	
235 - 244	1255.5955	1254.5882	1254.5770	9	0	K.VSIVMEQMMR.L	2 Oxidation (M)
235 - 244	1271.6134	1270.6061	1270.5720	27	0	K.VSIVMEQMMR.L	3 Oxidation (M)
269 - 276	925.4969	924.4896	924.5392	-54	0	K.ILLEANPR.M	
277 - 285	999.4640	998.4567	998.4855	-29	0	R.MTLFTGSSR.V	
277 - 285	1015.4631	1014.4558	1014.4804	-24	0	R.MTLFTGSSR.V	Oxidation (M)
298 - 308	1349.7172	1348.7099	1348.6775	24	1	R.IRLEDAGFDWK.V	
300 - 308	1080.4911	1079.4838	1079.4924	-8	0	R.LEDAGFDWK.V	
441 - 453	1570.8880	1569.8807	1569.8079	46	0	K.EIFGPFQIVTEYK.K	
454 - 466	1509.9186	1508.9113	1508.8562	37	1	K.KDQLPLVLDALER.M	
455 - 466	1381.8024	1380.7951	1380.7613	25	0	K.DQLPLVLDALER.M	
503 - 519	1808.9243	1807.9170	1807.8391	43	0	R.TTGAPQNHWFGPAGDPR.G	
520 - 530	1013.5194	1012.5121	1012.5553	-43	0	R.GAGIGTPEAIK.L	
531 - 537	957.4330	956.4258	956.4651	-41	0	K.LVWSCHR.E	

Spot No.: **95**

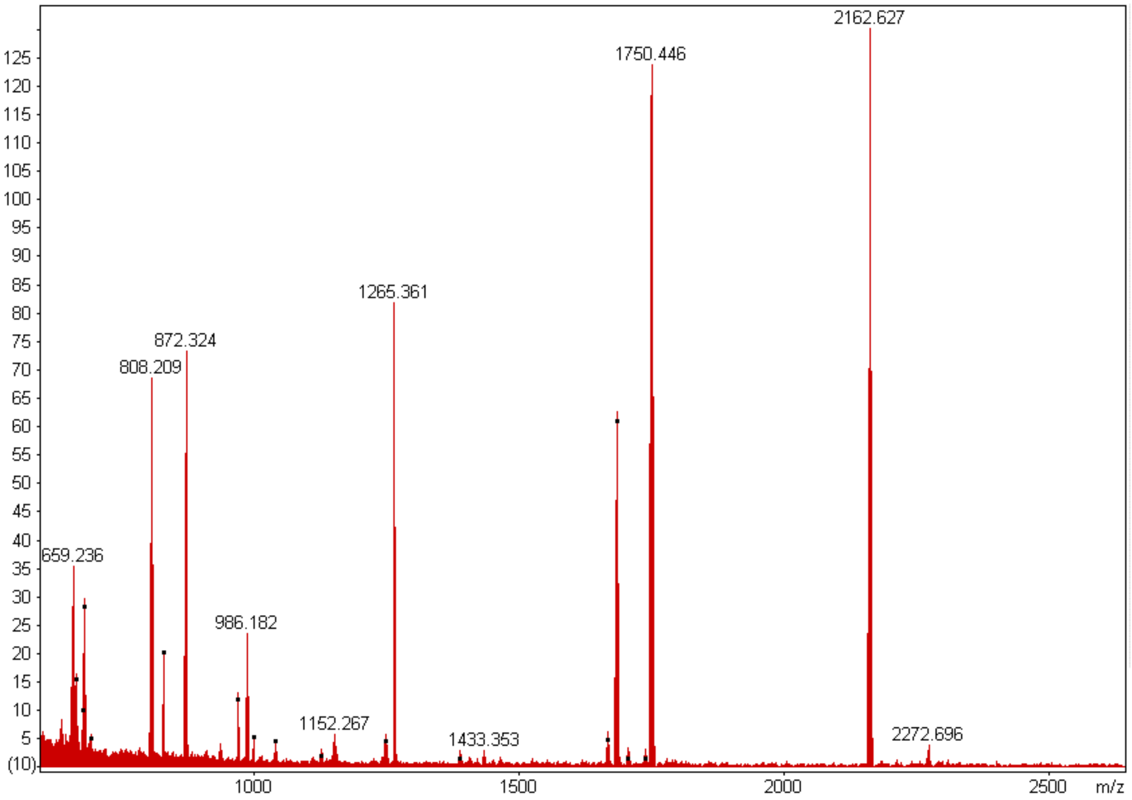
Mascot score: **82** Sequence coverage %: **18**

NCBI accession No.: **gi| 18394801**

Matched peptides No.: **9** Total peptides No.: **14**

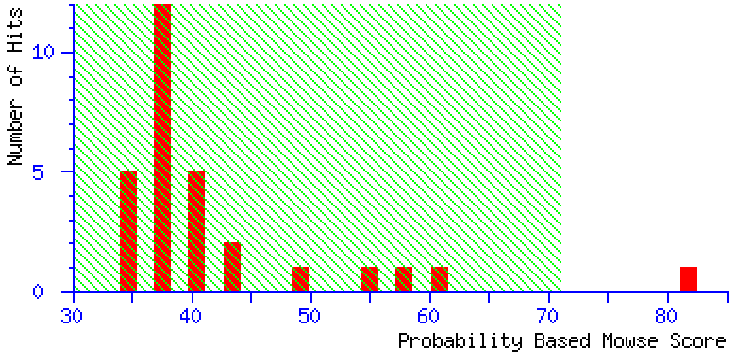
Calculated Mr: **53718** Calculated *p*I: **6.15**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 MSLMIRSSYV SHITLFQPRN SKPSSFTNQI SFLSSSNNNP FLNLVYKRNL
51 TMQSVSKMTV KSSLIDPDGG ELVELIVPET EIGVKKAESE TMPKVKLNQI
101 DLEWVHVISE GWASPLKGFM R**EDEYLQSLH** **FNSLR**LK**NGT** **FVNMSLPIVL**
151 **AIDDDTK**EQI GSSENVALVC PQGDIIGSLR SVEIYKHNKE ERIARTWGTT
201 SPGLPYVEEY ITPSGNWLIG GDLEVFEPIK **YNDGLDHYR**L SPKQLREEFD
251 NR**QADAVFAF** **QLR**NPVHNGH ALLMNDTRKR LLEMGYKNPV LLLHPLGGFT
301 K**ADDVPLDVR** MEQHSKVLED GVLDPKTTIV SIFPSPMHYA GPTEVQWHAK
351 ARINAGANFY IVGRDPAGMG HPTEKRDLYD PDHGKRVLSM APGLEK**LNIL**
401 **PFR**VAAYDTI EKK**MAFFDPS** **R**AK**EFLFISG** **TK**MRTYARTG ENPPDGFMCP
451 SGWNVLVKYY ESLQESEAKQ QAVVSA

Matched peptides information:

```
Start - End     Observed    Mr(expt)    Mr(calc)      ppm    Miss  Sequence
  122 - 135    1750.4456   1749.4383   1749.8322     -225      0   R.EDEYLQSLHFNSLR.L
  138 - 157    2162.6274   2161.6201   2162.0929     -219      0   K.NGTFVNMSLPIVLAIDDDTK.E
  231 - 239    1152.2667   1151.2594   1151.4996     -209      0   K.YNDGLDHYR.L
  253 - 263    1265.3612   1264.3539   1264.6564     -239      0   R.QADAVFAFQLR.N
  302 - 310     999.2843    998.2771    998.5033     -227      0   K.ADDVPLDVR.M
  397 - 403     872.3244    871.3172    871.5280     -242      0   K.LNILPFR.V
  414 - 421     970.1961    969.1888    969.4378     -257      0   K.MAFFDPSR.A
  414 - 421     986.1825    985.1752    985.4328     -261      0   K.MAFFDPSR.A   Oxidation (M)
  424 - 432    1041.2897   1040.2824   1040.5542     -261      0   K.EFLFISGTK.M
```

Spot No.: **96**

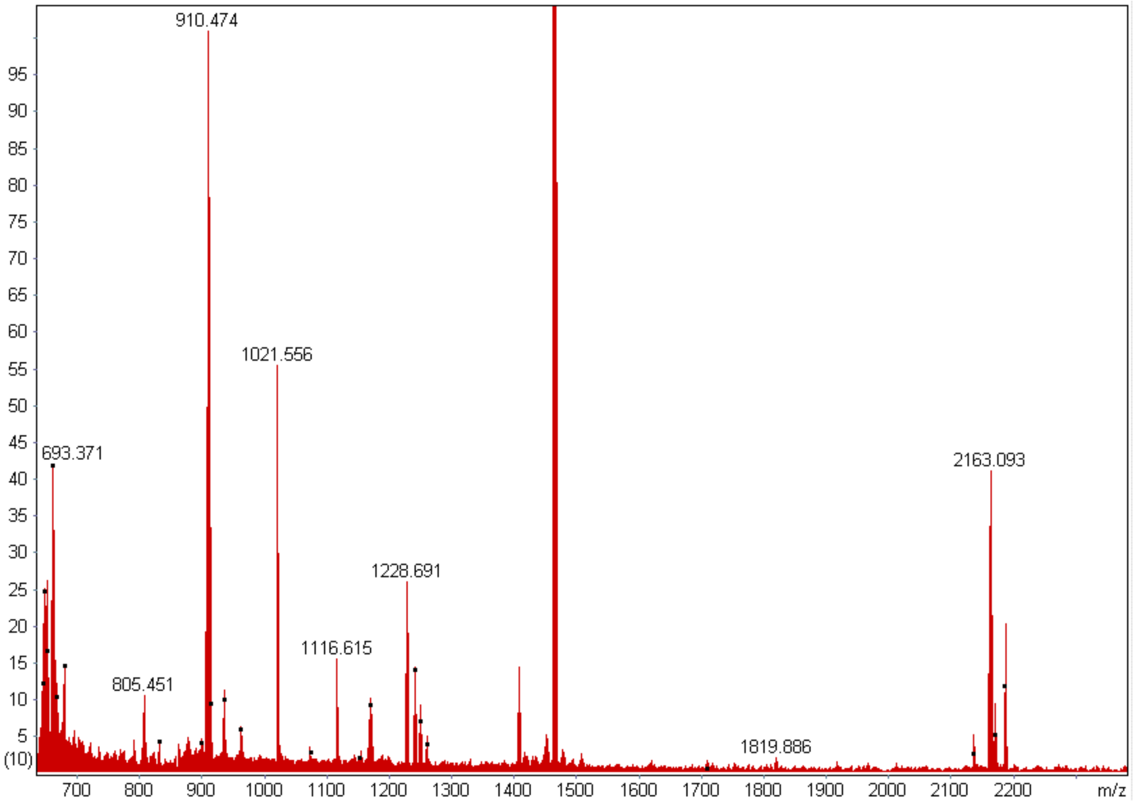
Mascot score: **253**   Sequence coverage %: **33**

NCBI accession No.: **gi| 125857763**

Matched peptides No.: **22**   Total peptides No.: **36**

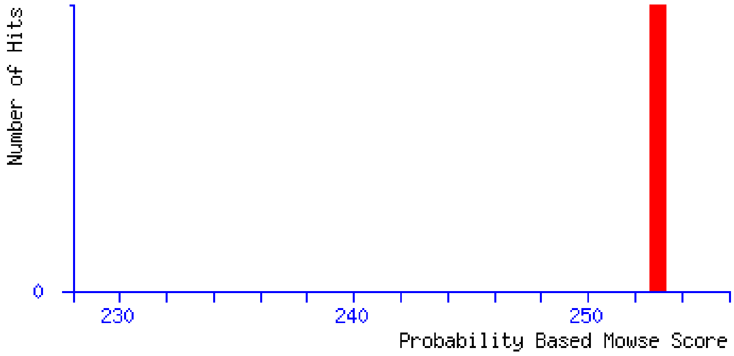
Calculated Mr: **48871**   Calculated *p*I: **6.13**

Annotated PMF **spectra:**

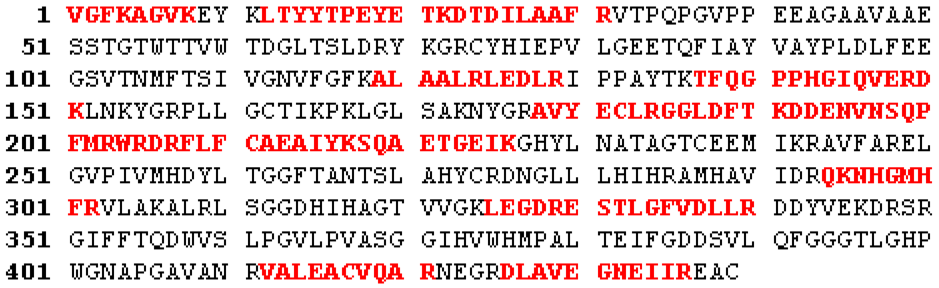


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red



```
  1 VGFKAGVKEY KLTYYTPEYE TKDTDILAAF RVTPQPGVPP EEAGAAVAAE
 51 SSTGTWTTVW TDGLTSLDRY KGRCYHIEPV LGEETQFIAY VAYPLDLFEE
101 GSVTNMFTSI VGNVFGFKAL AALRLEDLRI PPAYTKTFQG PPHGIQVERD
151 KLNKYGRPLL GCTIKPKLGL SAKNYGRAVY ECLRGGLDFT KDDENVNSQP
201 FMRWRDRFLF CAEAIYKSQA ETGEIKGHYL NATAGTCEEM IKRAVFAREL
251 GVPIVMHDYL TGGFTANTSL AHYCRDNGLL LHIHRAMHAV IDRQKNHGMH
301 FRVLAKALRL SGGDHIHAGT VVGKLEGDRE STLGFVDLLR DDYVEKDRSR
351 GIFFTQDWVS LPGVLPVASG GIHVWHMPAL TEIFGDDSVL QFGGGTLGHP
401 WGNAPGAVAN RVALEACVQA RNEGRDLAVE GNEIIREAC
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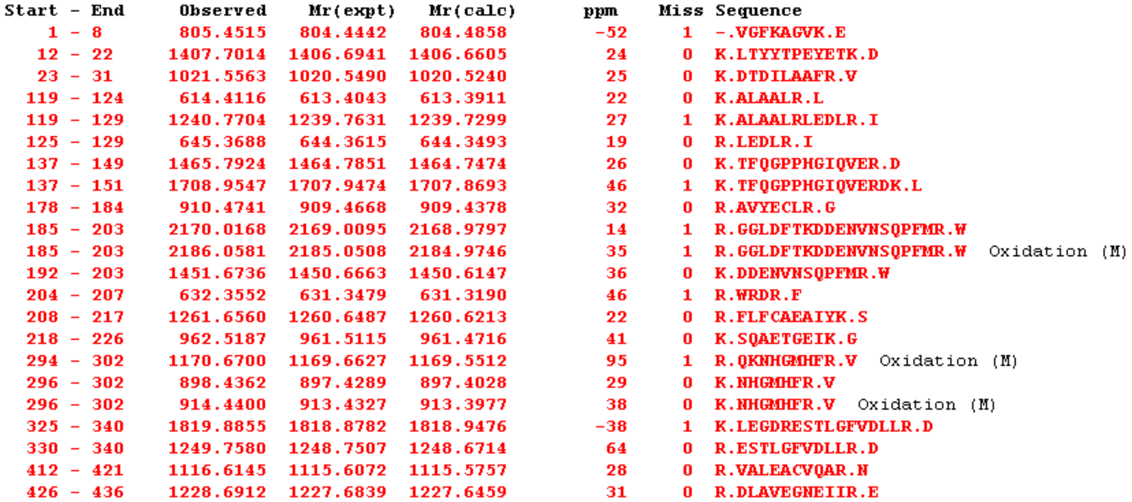
Matched peptides information:



```
Start - End      Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    1 - 8        805.4515   804.4442   804.4858      -52      1  -.VGFKAGVK.E
   12 - 22      1407.7014  1406.6941  1406.6605       24      0  K.LTYYTPEYETK.D
   23 - 31      1021.5563  1020.5490  1020.5240       25      0  K.DTDILAAFR.V
  119 - 124      614.4116   613.4043   613.3911       22      0  K.ALAALR.L
  119 - 129     1240.7704  1239.7631  1239.7299       27      1  K.ALAALRLEDLR.I
  125 - 129      645.3688   644.3615   644.3493       19      0  R.LEDLR.I
  137 - 149     1465.7924  1464.7851  1464.7474       26      0  K.TFQGPPHGIQVER.D
  137 - 151     1708.9547  1707.9474  1707.8693       46      1  K.TFQGPPHGIQVERDK.L
  178 - 184      910.4741   909.4668   909.4378       32      0  R.AVYECLR.G
  185 - 203     2170.0168  2169.0095  2168.9797       14      1  R.GGLDFTKDDENVNSQPFMR.W
  185 - 203     2186.0581  2185.0508  2184.9746       35      1  R.GGLDFTKDDENVNSQPFMR.W  Oxidation (M)
  192 - 203     1451.6736  1450.6663  1450.6147       36      0  K.DDENVNSQPFMR.W
  204 - 207      632.3552   631.3479   631.3190       46      1  R.WRDR.F
  208 - 217     1261.6560  1260.6487  1260.6213       22      0  R.FLFCAEAIYK.S
  218 - 226      962.5187   961.5115   961.4716       41      0  K.SQAETGEIK.G
  294 - 302     1170.6700  1169.6627  1169.5512       95      1  R.QKNHGMHFR.V  Oxidation (M)
  296 - 302      898.4362   897.4289   897.4028       29      0  K.NHGMHFR.V
  296 - 302      914.4400   913.4327   913.3977       38      0  K.NHGMHFR.V  Oxidation (M)
  325 - 340     1819.8855  1818.8782  1818.9476      -38      1  K.LEGDRESTLGFVDLLR.D
  330 - 340     1249.7580  1248.7507  1248.6714       64      0  R.ESTLGFVDLLR.D
  412 - 421     1116.6145  1115.6072  1115.5757       28      0  R.VALEACVQAR.N
  426 - 436     1228.6912  1227.6839  1227.6459       31      0  R.DLAVEGNEIIR.E
```

Spot No.: **97**

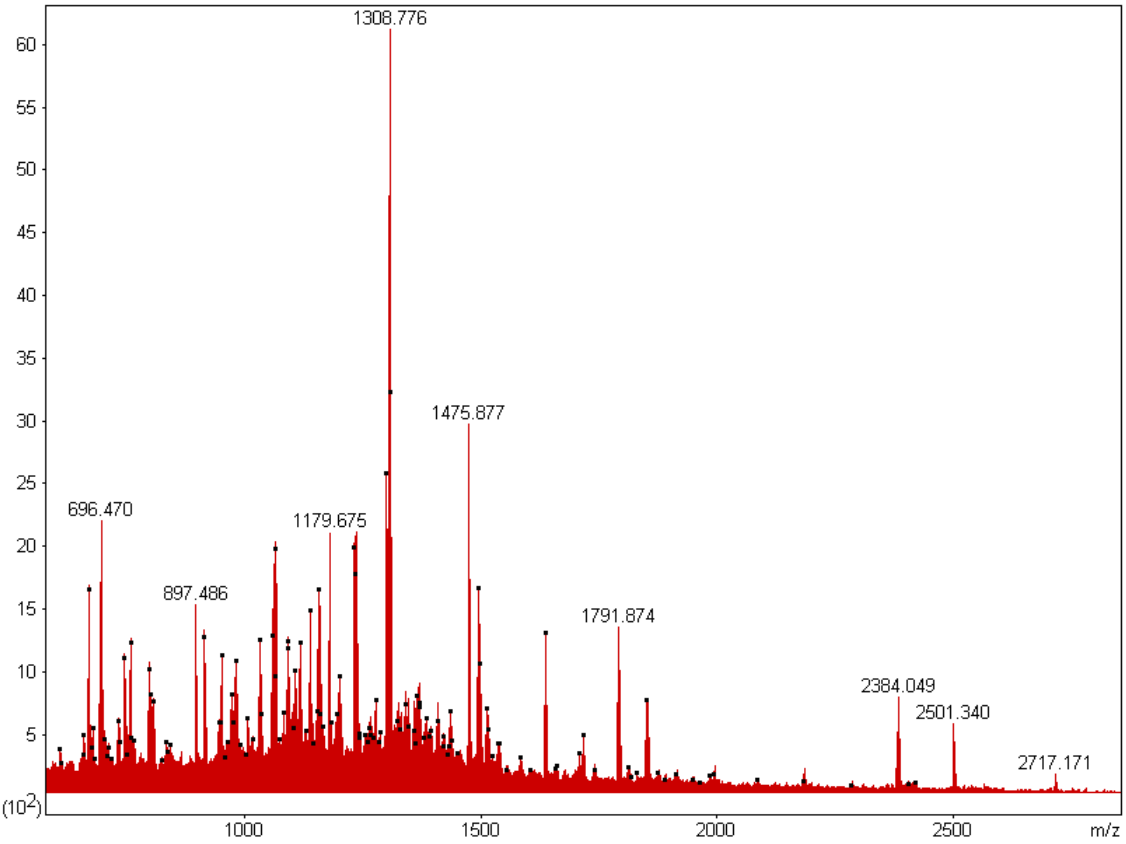
Mascot score: **88** Sequence coverage %: **32**

NCBI accession No.: **gi| 308810769**

Matched peptides No.: **24** Total peptides No.: **130**

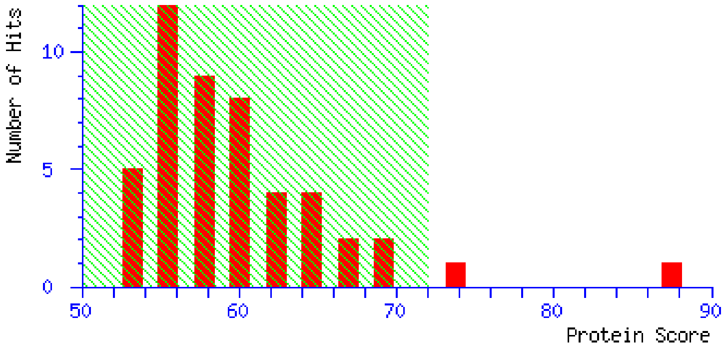
Calculated Mr: **77406** Calculated *p*I: **6.47**

Annotated PMF **spectra:**

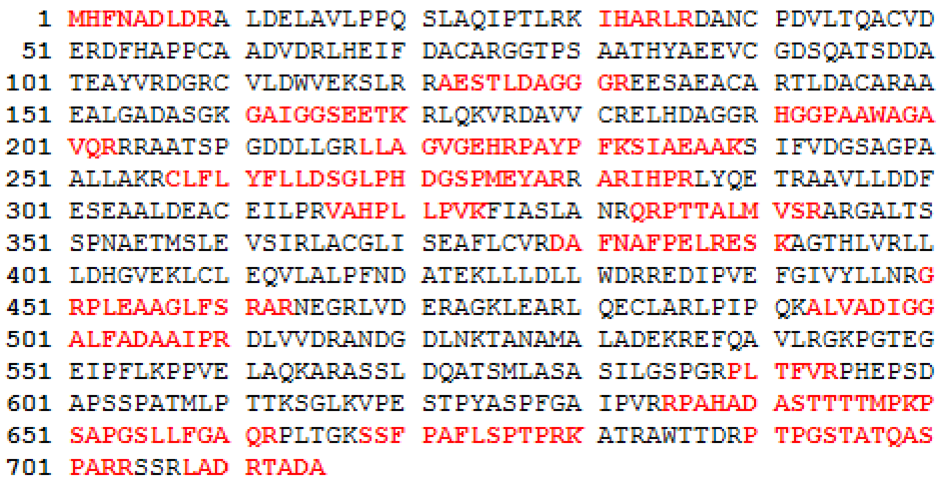


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

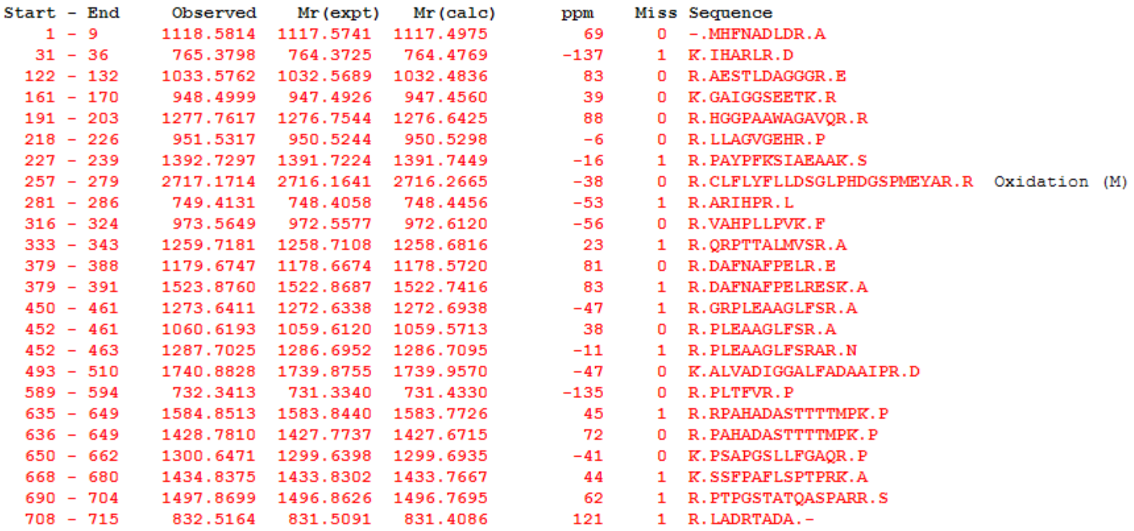


Matched peptide sequences: shown in Bold Red



1 **MHFNADLDR**A LDELAVLPPQ SLAQIPTLRK **IHARLR**DANC PDVLTQACVD
51 ERDFHAPPCA ADVDRLHEIF DACARGGTPS AATHYAEEVC GDSQATSDDA
101 TEAYVRDGRC VLDWVEKSLR R**AESTLDAGG** **GR**EESAEACA RTLDACARAA
151 EALGADASGK **GAIGGSEETK** RLQKVRDAVV CRELHDAGGR **HGGPAAWAGA**
201 **VQR**RRAATSP GDDLLGR**LLA** **GVGEHRPAYP** **FKSIAEAAK**S IFVDGSAGPA
251 ALLAKR**CLFL** **YFLLDSGLPH** **DGSPMEYAR**R **ARIHPR**LYQE TRAAVLLDDF
301 ESEAALDEAC EILPR**VAHPL** **LPVK**FIASLA NR**QRPTTALM** **VSR**ARGALTS
351 SPNAETMSLE VSIRLACGLI SEAFLCVR**DA** **FNAFPELRES** **K**AGTHLVRLL
401 LDHGVEKLCL EQVLALPFND ATEKLLLDLL WDRREDIPVE FGIVYLLNR**G**
451 **RPLEAAGLFS** **RAR**NEGRLVD ERAGKLEARL QECLARLPIP QK**ALVADIGG**
501 **ALFADAAIPR** DLVVDRANDG DLNKTANAMA LADEKREFQA VLRGKPGTEG
551 EIPFLKPPVE LAQKARASSL DQATSMLASA SILGSPGR**PL** **TFVR**PHEPSD
601 APSSPATMLP TTKSGLKVPE STPYASPFGA IPVR**RPAHAD** **ASTTTTMPKP**
651 **SAPGSLLFGA** **QR**PLTGK**SSF** **PAFLSPTPRK** ATRAWTTDR**P** **TPGSTATQAS**
701 **PARR**SSR**LAD** **RTADA**

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
1 - 9	1118.5814	1117.5741	1117.4975	69	0	-.MHFNADLDR.A	
31 - 36	765.3798	764.3725	764.4769	-137	1	K.IHARLR.D	
122 - 132	1033.5762	1032.5689	1032.4836	83	0	R.AESTLDAGGGR.E	
161 - 170	948.4999	947.4926	947.4560	39	0	K.GAIGGSEETK.R	
191 - 203	1277.7617	1276.7544	1276.6425	88	0	R.HGGPAAWAGAVQR.R	
218 - 226	951.5317	950.5244	950.5298	-6	0	R.LLAGVGEHR.P	
227 - 239	1392.7297	1391.7224	1391.7449	-16	1	R.PAYPFKSIAEAAK.S	
257 - 279	2717.1714	2716.1641	2716.2665	-38	0	R.CLFLYFLLDSGLPHDGSPMEYAR.R	Oxidation (M)
281 - 286	749.4131	748.4058	748.4456	-53	1	R.ARIHPR.L	
316 - 324	973.5649	972.5577	972.6120	-56	0	R.VAHPLLPVK.F	
333 - 343	1259.7181	1258.7108	1258.6816	23	1	R.QRPTTALMVSR.A	
379 - 388	1179.6747	1178.6674	1178.5720	81	0	R.DAFNAFPELR.E	
379 - 391	1523.8760	1522.8687	1522.7416	83	1	R.DAFNAFPELRESK.A	
450 - 461	1273.6411	1272.6338	1272.6938	-47	1	R.GRPLEAAGLFSR.A	
452 - 461	1060.6193	1059.6120	1059.5713	38	0	R.PLEAAGLFSR.A	
452 - 463	1287.7025	1286.6952	1286.7095	-11	1	R.PLEAAGLFSRAR.N	
493 - 510	1740.8828	1739.8755	1739.9570	-47	0	K.ALVADIGGALFADAAIPR.D	
589 - 594	732.3413	731.3340	731.4330	-135	0	R.PLTFVR.P	
635 - 649	1584.8513	1583.8440	1583.7726	45	1	R.RPAHADASTTTTMPK.P	
636 - 649	1428.7810	1427.7737	1427.6715	72	0	R.PAHADASTTTTMPK.P	
650 - 662	1300.6471	1299.6398	1299.6935	-41	0	K.PSAPGSLLFGAQR.P	
668 - 680	1434.8375	1433.8302	1433.7667	44	1	K.SSFPAFLSPTPRK.A	
690 - 704	1497.8699	1496.8626	1496.7695	62	1	R.PTPGSTATQASPARR.S	
708 - 715	832.5164	831.5091	831.4086	121	1	R.LADRTADA.-	

Spot No.: **98**

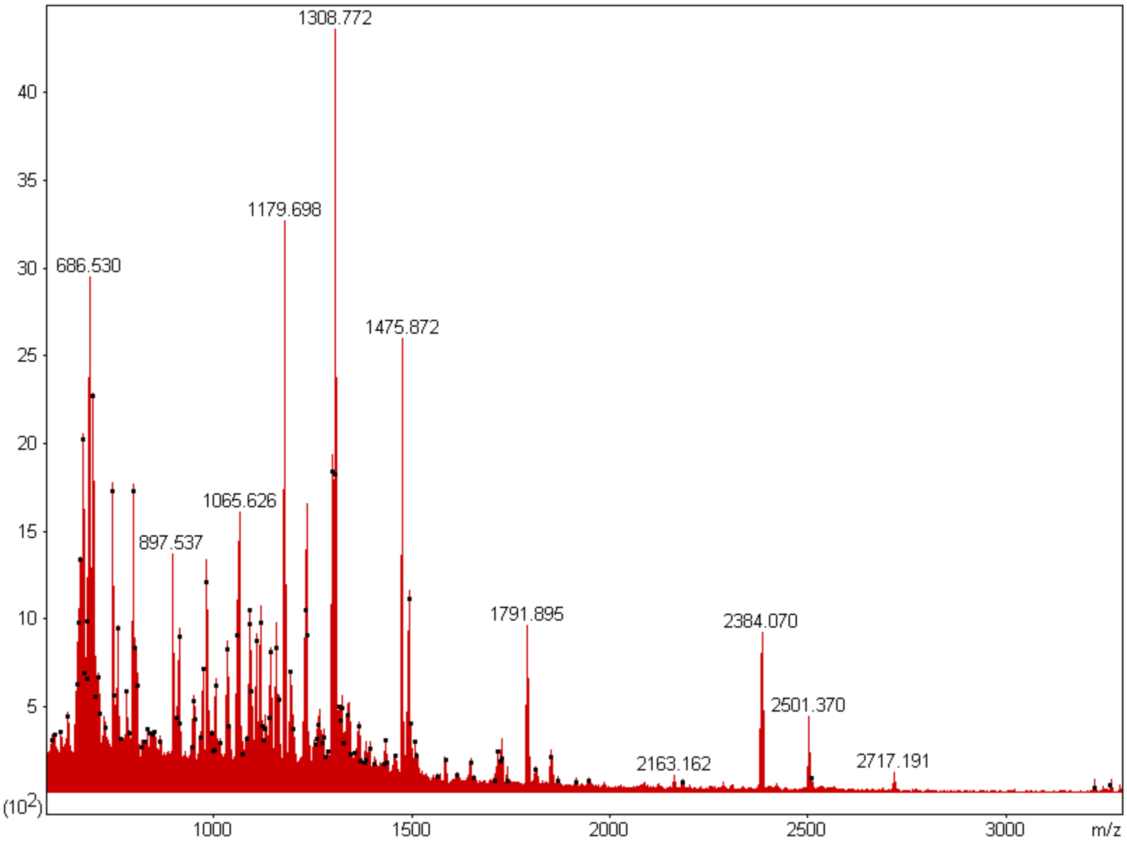
Mascot score: **96** Sequence coverage %: **24**

NCBI accession No.: **gi| 226461739**

Matched peptides No.: **48** Total peptides No.: **111**

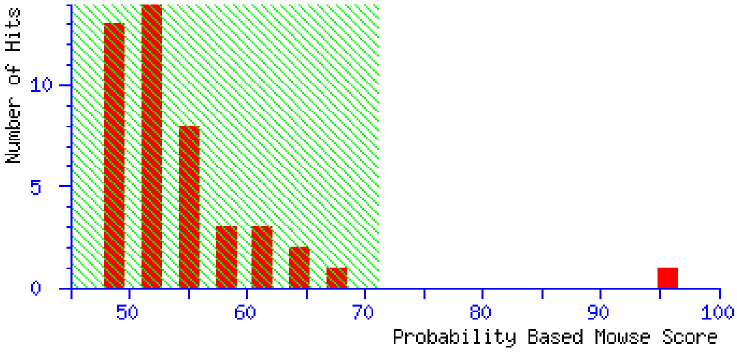
Calculated Mr: **188682** Calculated *p*I: **6.11**

Annotated PMF **spectra:**

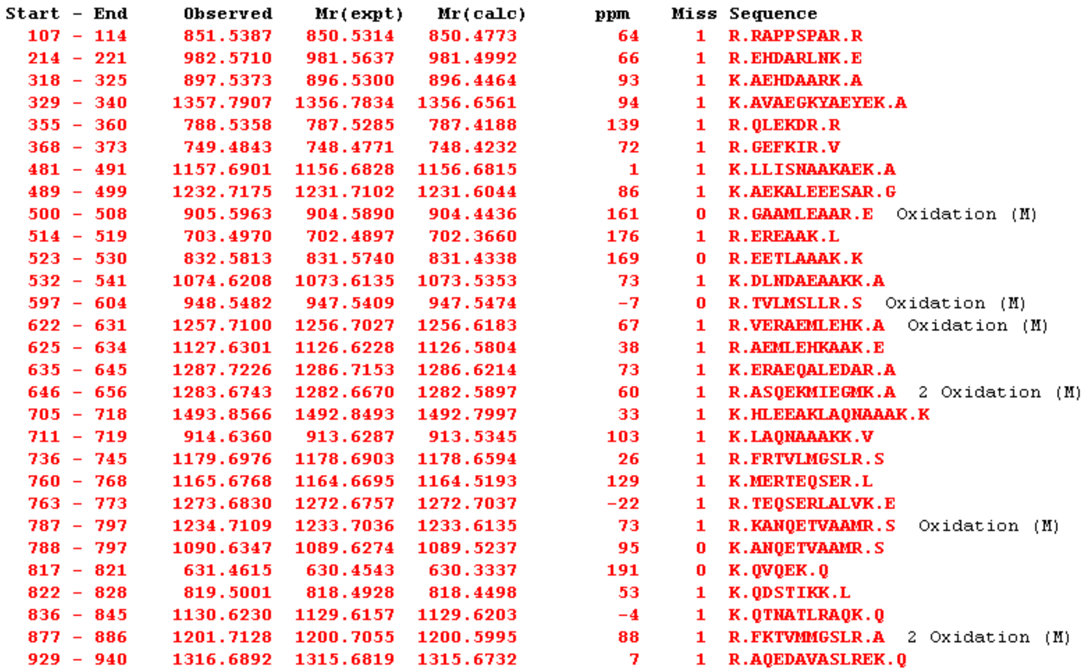


Probability Based Mowse Score:

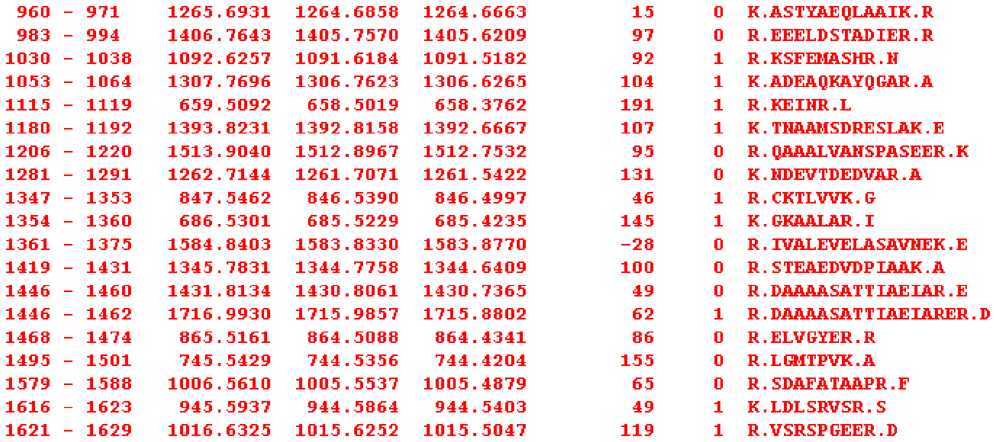
Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
107 - 114	851.5387	850.5314	850.4773	64	1	R.RAPPSPAR.R	
214 - 221	982.5710	981.5637	981.4992	66	1	R.EHDARLNK.E	
318 - 325	897.5373	896.5300	896.4464	93	1	K.AEHDAARK.A	
329 - 340	1357.7907	1356.7834	1356.6561	94	1	K.AVAEGKYAEYEK.A	
355 - 360	788.5358	787.5285	787.4188	139	1	R.QLEKDR.R	
368 - 373	749.4843	748.4771	748.4232	72	1	R.GEFKIR.V	
481 - 491	1157.6901	1156.6828	1156.6815	1	1	K.LLISNAAKAEK.A	
489 - 499	1232.7175	1231.7102	1231.6044	86	1	K.AEKALEEESAR.G	
500 - 508	905.5963	904.5890	904.4436	161	0	R.GAAMLEAAR.E	Oxidation (M)
514 - 519	703.4970	702.4897	702.3660	176	1	R.EREAAK.L	
523 - 530	832.5813	831.5740	831.4338	169	0	R.EETLAAAK.K	
532 - 541	1074.6208	1073.6135	1073.5353	73	1	K.DLNDAEAAKK.A	
597 - 604	948.5482	947.5409	947.5474	-7	0	R.TVLMSLLR.S	Oxidation (M)
622 - 631	1257.7100	1256.7027	1256.6183	67	1	R.VERAEMLEHK.A	Oxidation (M)
625 - 634	1127.6301	1126.6228	1126.5804	38	1	R.AEMLEHKAAK.E	
635 - 645	1287.7226	1286.7153	1286.6214	73	1	K.ERAEQALEDAR.A	
646 - 656	1283.6743	1282.6670	1282.5897	60	1	R.ASQEKMIEGMK.A	2 Oxidation (M)
705 - 718	1493.8566	1492.8493	1492.7997	33	1	K.HLEEAKLAQNAAAK.K	
711 - 719	914.6360	913.6287	913.5345	103	1	K.LAQNAAAKK.V	
736 - 745	1179.6976	1178.6903	1178.6594	26	1	R.FRTVLMGSLR.S	
760 - 768	1165.6768	1164.6695	1164.5193	129	1	K.MERTEQSER.L	
763 - 773	1273.6830	1272.6757	1272.7037	-22	1	R.TEQSERLALVK.E	
787 - 797	1234.7109	1233.7036	1233.6135	73	1	R.KANQETVAAMR.S	Oxidation (M)
788 - 797	1090.6347	1089.6274	1089.5237	95	0	K.ANQETVAAMR.S	
817 - 821	631.4615	630.4543	630.3337	191	0	K.QVQEK.Q	
822 - 828	819.5001	818.4928	818.4498	53	1	K.QDSTIKK.L	
836 - 845	1130.6230	1129.6157	1129.6203	-4	1	K.QTNATLRAQK.Q	
877 - 886	1201.7128	1200.7055	1200.5995	88	1	R.FKTVMMGSLR.A	2 Oxidation (M)
929 - 940	1316.6892	1315.6819	1315.6732	7	1	R.AQEDAVASLREK.Q	



960 - 971	1265.6931	1264.6858	1264.6663	15	0	K.ASTYAEQLAAIK.R
983 - 994	1406.7643	1405.7570	1405.6209	97	0	R.EEELDSTADIER.R
1030 - 1038	1092.6257	1091.6184	1091.5182	92	1	R.KSFEMASHR.N
1053 - 1064	1307.7696	1306.7623	1306.6265	104	1	K.ADEAQKAYQGAR.A
1115 - 1119	659.5092	658.5019	658.3762	191	1	R.KEINR.L
1180 - 1192	1393.8231	1392.8158	1392.6667	107	1	K.TNAAMSDRESLAK.E
1206 - 1220	1513.9040	1512.8967	1512.7532	95	0	R.QAAALVANSPASEER.K
1281 - 1291	1262.7144	1261.7071	1261.5422	131	0	K.NDEVTDEDVAR.A
1347 - 1353	847.5462	846.5390	846.4997	46	1	R.CKTLVVK.G
1354 - 1360	686.5301	685.5229	685.4235	145	1	K.GKAALAR.I
1361 - 1375	1584.8403	1583.8330	1583.8770	-28	0	R.IVALEVELASAVNEK.E
1419 - 1431	1345.7831	1344.7758	1344.6409	100	0	R.STEAEDVDPIAAK.A
1446 - 1460	1431.8134	1430.8061	1430.7365	49	0	R.DAAAASATTIAEIAR.E
1446 - 1462	1716.9930	1715.9857	1715.8802	62	1	R.DAAAASATTIAEIARER.D
1468 - 1474	865.5161	864.5088	864.4341	86	0	R.ELVGYER.R
1495 - 1501	745.5429	744.5356	744.4204	155	0	R.LGMTPVK.A
1579 - 1588	1006.5610	1005.5537	1005.4879	65	0	R.SDAFATAAPR.F
1616 - 1623	945.5937	944.5864	944.5403	49	1	K.LDLSRVSR.S
1621 - 1629	1016.6325	1015.6252	1015.5047	119	1	R.VSRSPGEER.D

Spot No.: **99**

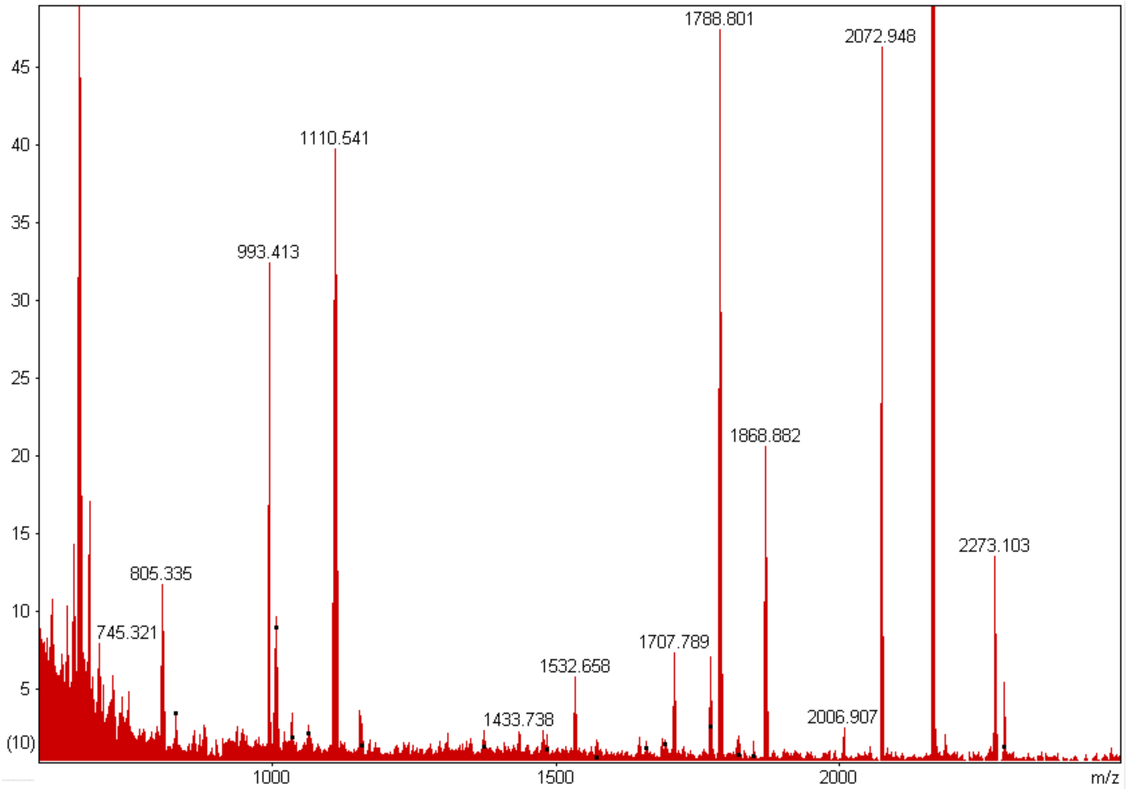
Mascot score: **92** Sequence coverage %: **20**

NCBI accession No.: **gi| 15232704**

Matched peptides No.: **10** Total peptides No.: **22**

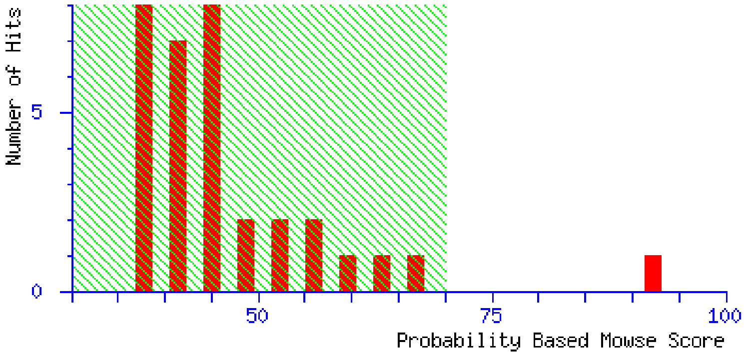
Calculated Mr: **52304** Calculated *p*I: **7.11**

Annotated PMF **spectra:**

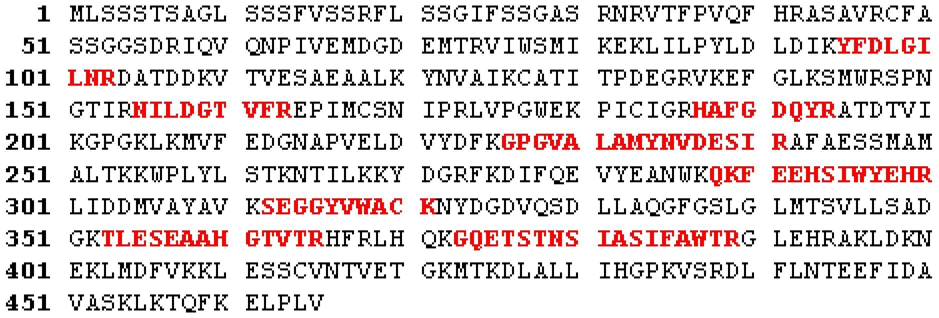


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

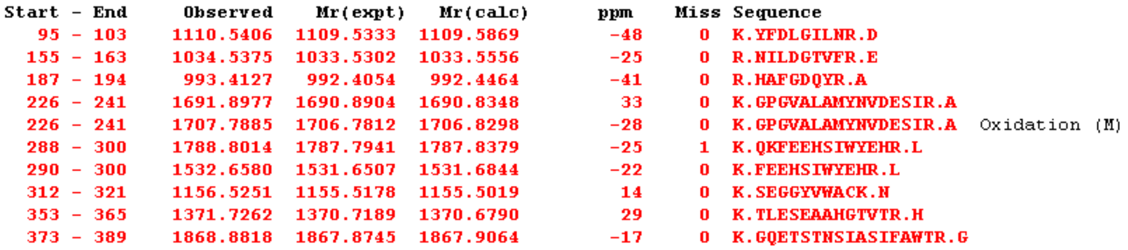


Matched peptide sequences: shown in **Bold Red**



1 MLSSSTSAGL SSSFVSSRFL SSGIFSSGAS RNRVTFPVQF HRASAVRCFA
51 SSGGSDRIQV QNPIVEMDGD EMTRVIWSMI KEKLILPYLD LDIK**YFDLGI**
101 **LNR**DATDDKV TVESAEAALK YNVAIKCATI TPDEGRVKEF GLKSMWRSPN
151 GTIR**NILDGT VFR**EPIMCSN IPRLVPGWEK PICIGR**HAFG DQYR**ATDTVI
201 KGPGKLKMVF EDGNAPVELD VYDFK**GPGVA LAMYNVDESI R**AFAESSMAM
251 ALTKKWPLYL STKNTILKKY DGRFKDIFQE VYEANWK**QKF EEHSIWYEHR**
301 LIDDMVAYAV K**SEGGYVWAC K**NYDGDVQSD LLAQGFGSLG LMTSVLLSAD
351 GK**TLESEAAH GTVTR**HFRLH QK**GQETSTNS IASIFAWTR**G LEHRAKLDKN
401 EKLMDFVKKL ESSCVNTVET GKMTKDLALL IHGPKVSRDL FLNTEEFIDA
451 VASKLKTQFK ELPLV

Matched peptides information:



```
Start - End      Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   95 - 103     1110.5406  1109.5333  1109.5869      -48      0  K.YFDLGILNR.D
  155 - 163     1034.5375  1033.5302  1033.5556      -25      0  R.NILDGTVFR.E
  187 - 194      993.4127   992.4054   992.4464      -41      0  R.HAFGDQYR.A
  226 - 241     1691.8977  1690.8904  1690.8348       33      0  K.GPGVALAMYNVDESIR.A
  226 - 241     1707.7885  1706.7812  1706.8298      -28      0  K.GPGVALAMYNVDESIR.A  Oxidation (M)
  288 - 300     1788.8014  1787.7941  1787.8379      -25      1  K.QKFEEHSIWYEHR.L
  290 - 300     1532.6580  1531.6507  1531.6844      -22      0  K.FEEHSIWYEHR.L
  312 - 321     1156.5251  1155.5178  1155.5019       14      0  K.SEGGYVWACK.N
  353 - 365     1371.7262  1370.7189  1370.6790       29      0  K.TLESEAAHGTVTR.H
  373 - 389     1868.8818  1867.8745  1867.9064      -17      0  K.GQETSTNSIASIFAWTR.G
```

Spot No.: **100**

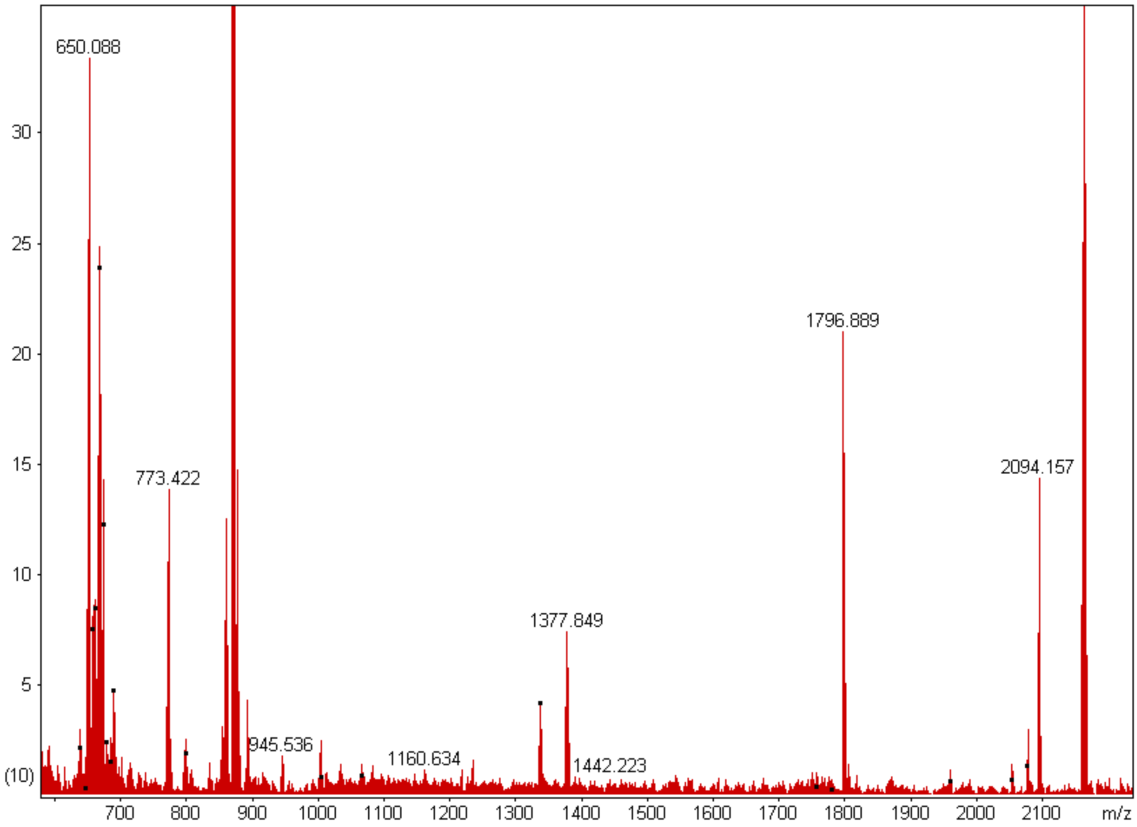
Mascot score: **97**　　Sequence coverage %: **31**

NCBI accession No.: **gi| 312281543**

Matched peptides No.: **11**　　Total peptides No.: **32**

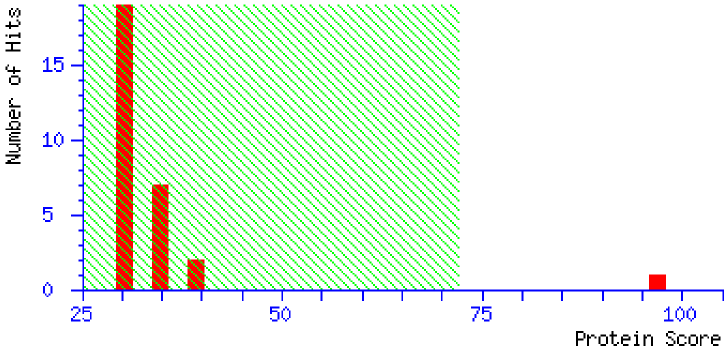
Calculated Mr: **50983**　　Calculated p*I*: **6.67**

Annotated PMF **spectra:**

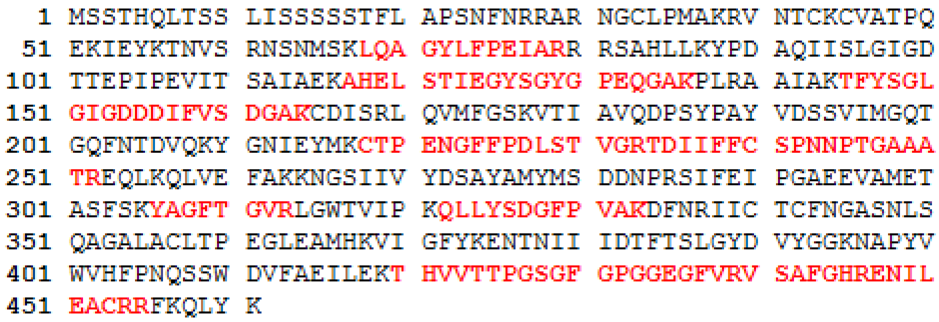


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

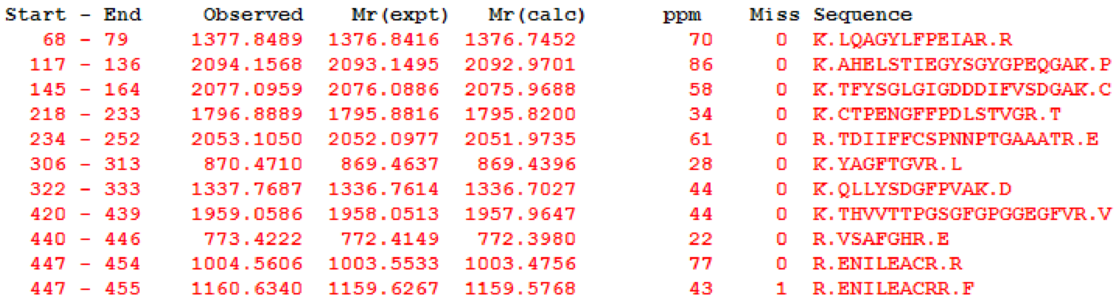


Matched peptide sequences: shown in Bold Red



```
  1 MSSTHQLTSS LISSSSSTFL APSNFNRRAR NGCLPMAKRV NTCKCVATPQ
 51 EKIEYKTNVS RNSNMSKLQA GYLFPEIARR RSAHLLKYPD AQIISLGIGD
101 TTEPIPEVIT SAIAEKAHEL STIEGYSGYG PEQGAKPLRA AIAKTFYSGL
151 GIGDDDIFVS DGAKCDISRL QVMFGSKVTI AVQDPSYPAY VDSSVIMGQT
201 GQFNTDVQKY GNIEYMKCTP ENGFFPDLST VGRTDIIFFC SPNNPTGAAA
251 TREQLKQLVE FAKKNGSIIV YDSAYAMYMS DDNPRSIFEI PGAEEVAMET
301 ASFSKYAGFT GVRLGWTVIP KQLLYSDGFP VAKDFNRIIC TCFNGASNLS
351 QAGALACLTP EGLEAMHKVI GFYKENTNII IDTFTSLGYD VYGGKNAPYV
401 WVHFPNQSSW DVFAEILEKT HVVTTPGSGF GPGGEGFVRV SAFGHRENIL
451 EACRRFKQLY K
```

Matched peptides information:



```
Start - End     Observed    Mr(expt)    Mr(calc)       ppm    Miss  Sequence
   68 - 79     1377.8489   1376.8416   1376.7452        70     0   K.LQAGYLFPEIAR.R
  117 - 136    2094.1568   2093.1495   2092.9701        86     0   K.AHELSTIEGYSGYGPEQGAK.P
  145 - 164    2077.0959   2076.0886   2075.9688        58     0   K.TFYSGLGIGDDDIFVSDGAK.C
  218 - 233    1796.8889   1795.8816   1795.8200        34     0   K.CTPENGFFPDLSTVGR.T
  234 - 252    2053.1050   2052.0977   2051.9735        61     0   R.TDIIFFCSPNNPTGAAATR.E
  306 - 313     870.4710    869.4637    869.4396        28     0   K.YAGFTGVR.L
  322 - 333    1337.7687   1336.7614   1336.7027        44     0   K.QLLYSDGFPVAK.D
  420 - 439    1959.0586   1958.0513   1957.9647        44     0   K.THVVTTPGSGFGPGGEGFVR.V
  440 - 446     773.4222    772.4149    772.3980        22     0   R.VSAFGHR.E
  447 - 454    1004.5606   1003.5533   1003.4756        77     0   R.ENILEACR.R
  447 - 455    1160.6340   1159.6267   1159.5768        43     1   R.ENILEACRR.F
```

Spot No.: **101**

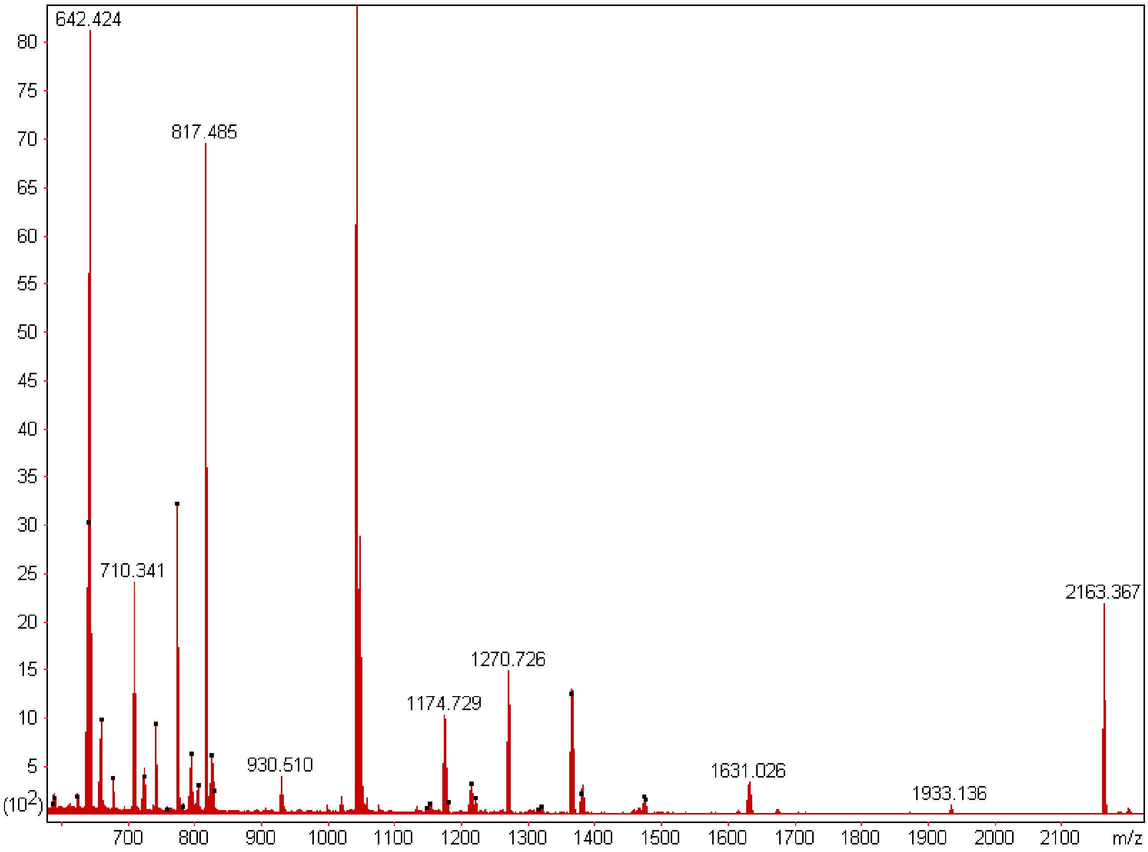
Mascot score: **90**　　Sequence coverage %: **24**

NCBI accession No.: **gi| 297807495**

Matched peptides No.: **13**　　Total peptides No.: **41**

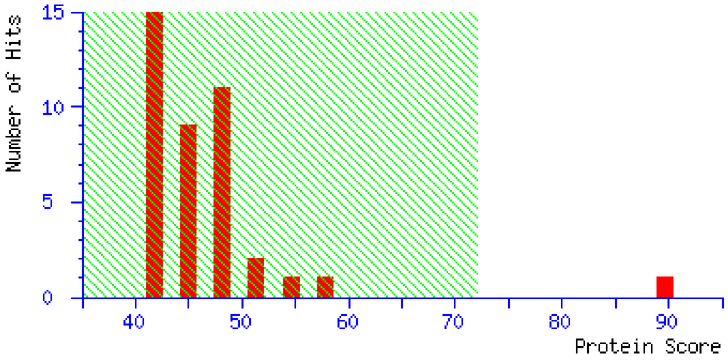
Calculated Mr: **42647**　　Calculated *p*I: **7.64**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 M**AMRQATK**AA IRACVSSSSS GYFARRQFNA SSGDSKK**IVG** **VFYK**ANEYAT
51 KNPNFLGCVE NALGIRDWLE SQGHQYIVTD DK**EGPDCELE** **K**HIPDLHVLI
101 STPFHPAYVT AERIKKAKNL KLLLTAGIGS DHIDLQAAAA AGLTVAEVTG
151 SNVVSVAEDE LMR**ILILMR**N FVPGYNQVVK GEWNVAGIAY R**AYDLEGK**TI
201 GTVGAGRIGK **LLLQR**LKPFG CNLLYHDR**LQ** **MAPELEK**EIG AKFVEDLNEM
251 LPKCDVVVIN MPLTEKTRGM FNKELIGKLK KGVLIVNNAR **GAIMDR**QAVV
301 EAVESGHIGG YSGDVWDPQP APK**DHPWR**YM PNQAMTPHTS GTTIDAQLR**Y**
351 **AAGTKDMLER** YFK**GEDFPAQ** **NYIVKDGELA** **PQYR**

Matched peptides information:

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
2 - 8	805.4180	804.4107	804.4276	-21	1	M.AMRQATK.A	
38 - 44	825.4944	824.4872	824.4796	9	0	K.IVGVFYK.A	
83 - 91	1076.5447	1075.5374	1075.4492	82	0	K.EGPDCELEK.H	
164 - 169	758.4226	757.4153	757.4884	-96	0	R.ILILMR.N	
164 - 169	774.4913	773.4841	773.4833	1	0	R.ILILMR.N	Oxidation (M)
192 - 198	795.3877	794.3804	794.3810	-1	0	R.AYDLEGK.T	
211 - 215	642.4243	641.4170	641.4224	-8	0	K.LLLQR.L	
229 - 237	1058.5791	1057.5718	1057.5477	23	0	R.LQMAPELEK.E	
291 - 296	678.3009	677.2937	677.3166	-34	0	R.GAIMDR.Q	Oxidation (M)
324 - 328	710.3415	709.3342	709.3296	6	0	K.DHPWR.Y	
350 - 360	1270.7262	1269.7189	1269.6023	92	1	R.YAAGTKDMLER.Y	Oxidation (M)
364 - 375	1380.8021	1379.7948	1379.6721	89	0	K.GEDFPAQNYIVK.D	
376 - 384	1048.5862	1047.5789	1047.4985	77	0	K.DGELAPQYR.-	

Spot No.: **102**

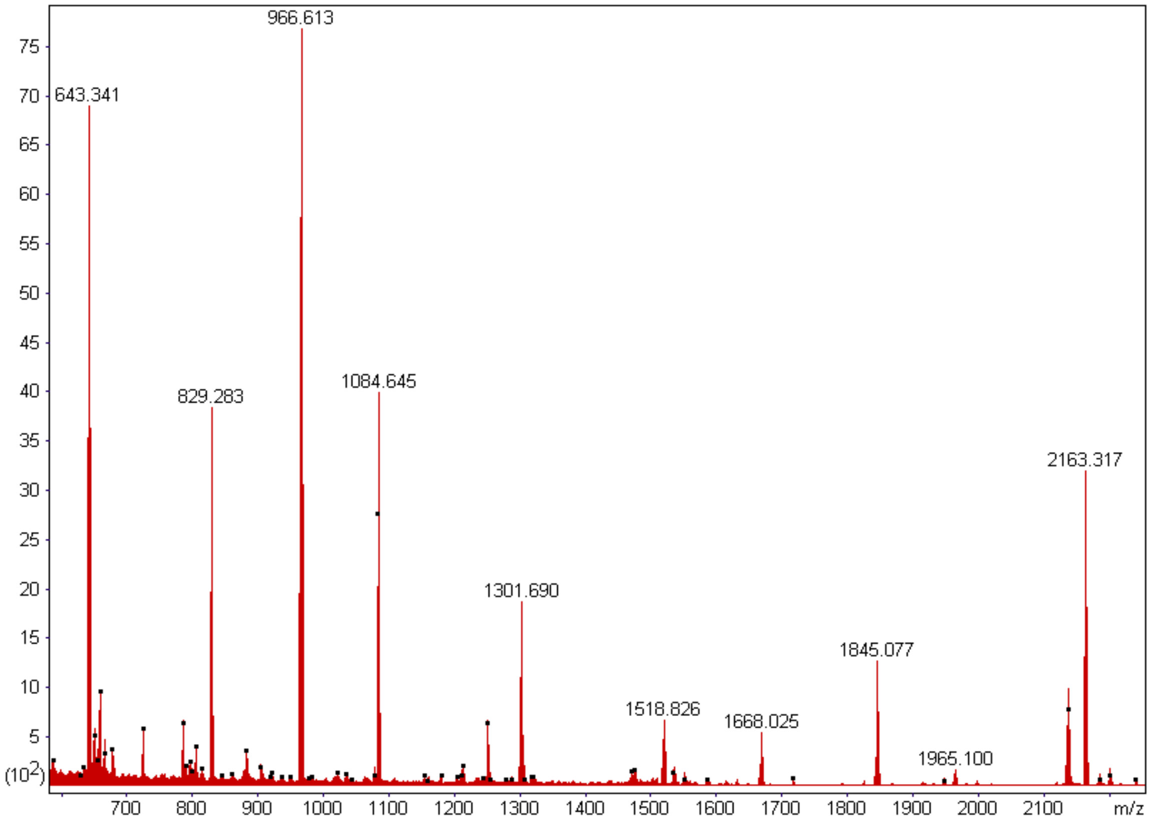
Mascot score: **87** Sequence coverage %: **41**

NCBI accession No.: **gi| 255611315**

Matched peptides No.: **17** Total peptides No.: **82**

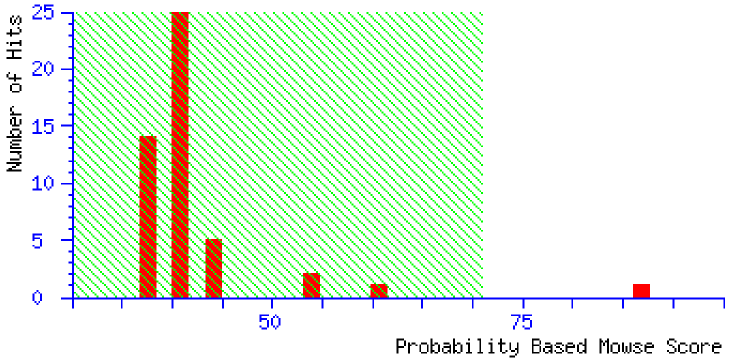
Calculated Mr: **37517** Calculated *p*I: **7.64**

Annotated PMF **spectra:**

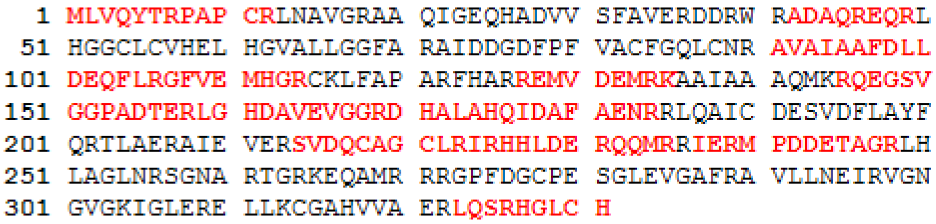


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

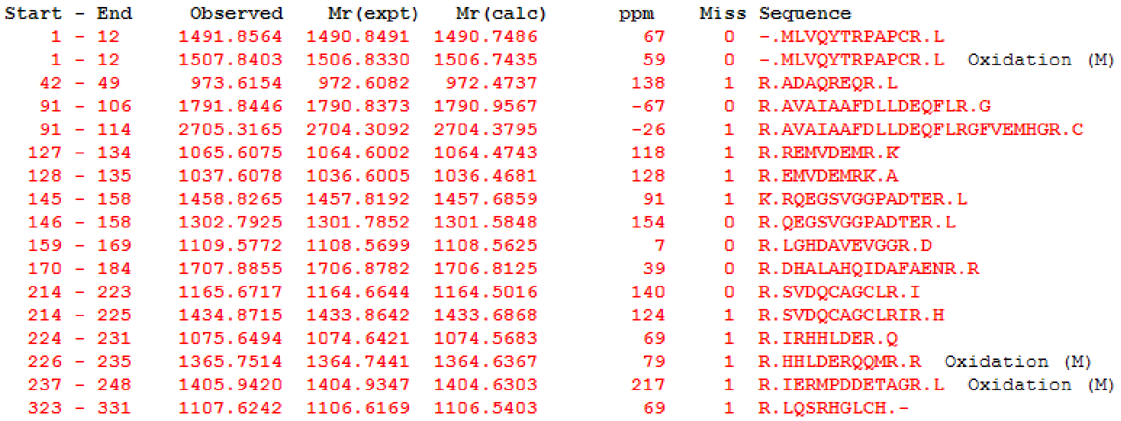


Matched peptide sequences: shown in Bold Red



```
  1 MLVQYTRPAP CRLNAVGRAA QIGEQHADVV SFAVERDDRW RADAQREQRL
 51 HGGCLCVHEL HGVALLGGFA RAIDDGDFPF VACFGQLCNR AVAIAAFDLL
101 DEQFLRGFVE MHGRCKLFAP ARFHARREMV DEMRKAAIAA AQMKRQEGSV
151 GGPADTERLG HDAVEVGGRD HALAHQIDAF AENRRLQAIC DESVDFLAYF
201 QRTLAERAIE VERSVDQCAG CLRIRHHLDE RQQMRRIERM PDDETAGRLH
251 LAGLNRSGNA RTGRKEQAMR RRGPFDGCPE SGLEVGAFRA VLLNEIRVGN
301 GVGKIGLERE LLKCGAHVVA ERLQSRHGLC H
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss  Sequence
    1 - 12     1491.8564  1490.8491  1490.7486       67      0   -.MLVQYTRPAPCR.L
    1 - 12     1507.8403  1506.8330  1506.7435       59      0   -.MLVQYTRPAPCR.L  Oxidation (M)
   42 - 49      973.6154   972.6082   972.4737      138      1   R.ADAQREQR.L
   91 - 106    1791.8446  1790.8373  1790.9567      -67      0   R.AVAIAAFDLLDEQFLR.G
   91 - 114    2705.3165  2704.3092  2704.3795      -26      1   R.AVAIAAFDLLDEQFLRGFVEMHGR.C
  127 - 134    1065.6075  1064.6002  1064.4743      118      1   R.REMVDEMR.K
  128 - 135    1037.6078  1036.6005  1036.4681      128      1   R.EMVDEMRK.A
  145 - 158    1458.8265  1457.8192  1457.6859       91      1   K.RQEGSVGGPADTER.L
  146 - 158    1302.7925  1301.7852  1301.5848      154      0   R.QEGSVGGPADTER.L
  159 - 169    1109.5772  1108.5699  1108.5625        7      0   R.LGHDAVEVGGR.D
  170 - 184    1707.8855  1706.8782  1706.8125       39      0   R.DHALAHQIDAFAENR.R
  214 - 223    1165.6717  1164.6644  1164.5016      140      0   R.SVDQCAGCLR.I
  214 - 225    1434.8715  1433.8642  1433.6868      124      1   R.SVDQCAGCLRIR.H
  224 - 231    1075.6494  1074.6421  1074.5683       69      1   R.IRHHLDER.Q
  226 - 235    1365.7514  1364.7441  1364.6367       79      1   R.HHLDERQQMR.R  Oxidation (M)
  237 - 248    1405.9420  1404.9347  1404.6303      217      1   R.IERMPDDETAGR.L  Oxidation (M)
  323 - 331    1107.6242  1106.6169  1106.5403       69      1   R.LQSRHGLCH.-
```

Spot No.: **103**

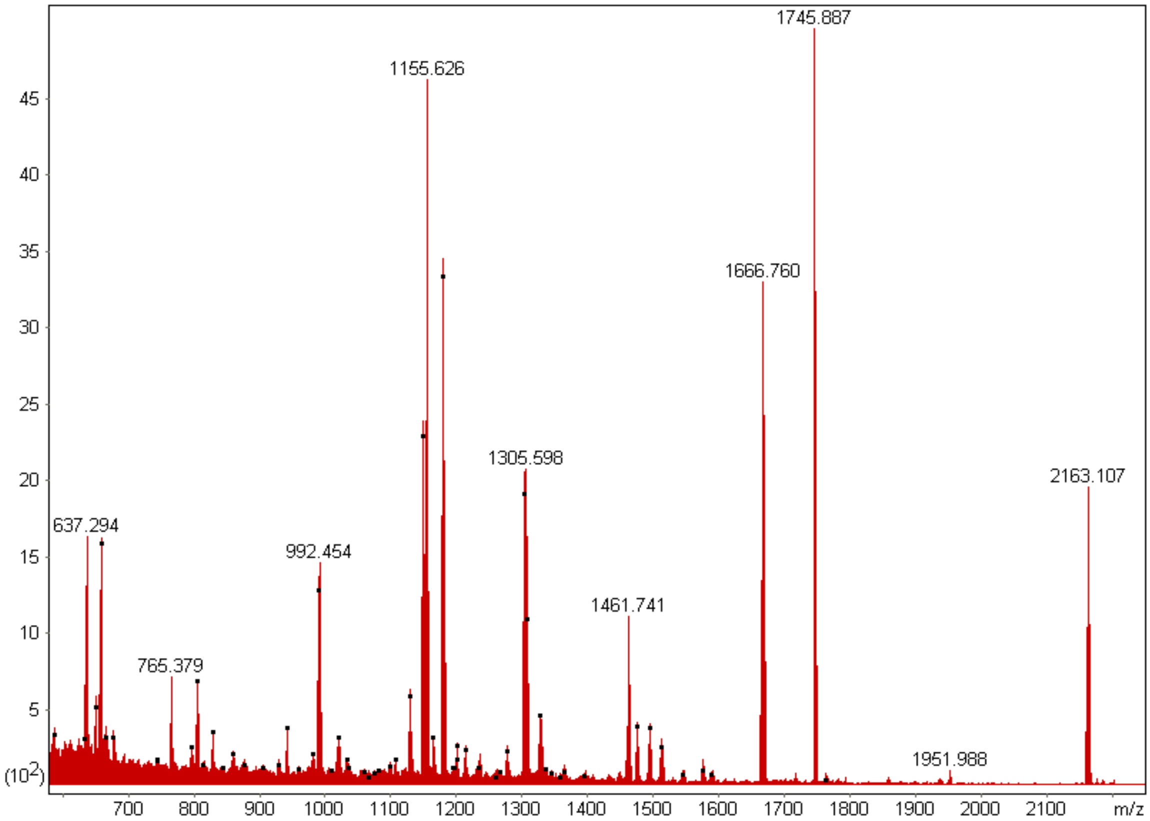
Mascot score: **83**   Sequence coverage %: **28**

NCBI accession No.: **gi| 22326744**

Matched peptides No.: **9**   Total peptides No.: **35**

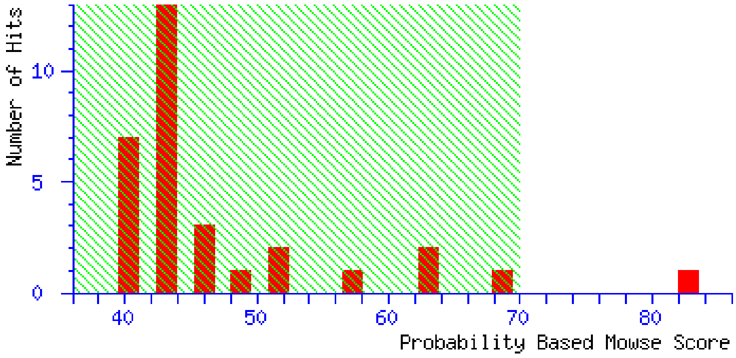
Calculated Mr: **40647**   Calculated *p*I: **8.79**

Annotated PMF **spectra:**

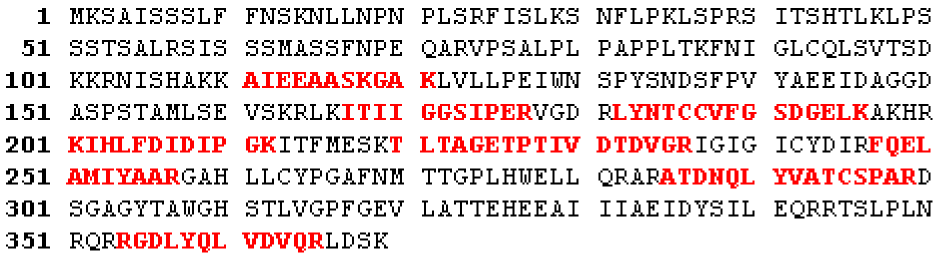


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

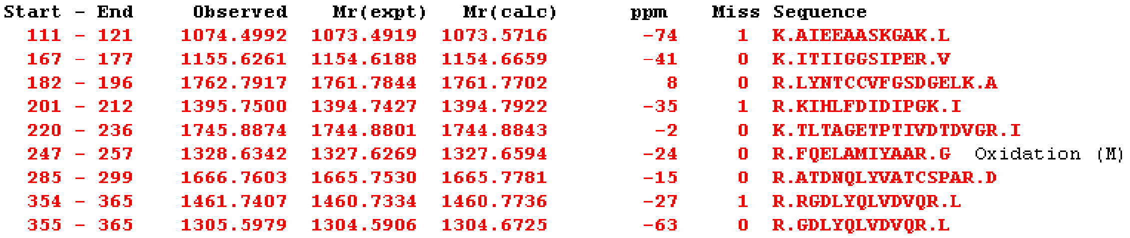


Matched peptide sequences: shown in Bold Red



1 MKSAISSSLF FNSKNLLNPN PLSRFISLKS NFLPKLSPRS ITSHTLKLPS
51 SSTSALRSIS SSMASSFNPE QARVPSALPL PAPPLTKFNI GLCQLSVTSD
101 KKRNISHAKK **AIEEAASKGA** **K**LVLLPEIWN SPYSNDSFPV YAEEIDAGGD
151 ASPSTAMLSE VSKRLK**ITII** **GGSIPER**VGD R**LYNTCCVFG** **SDGELK**AKHR
201 **KIHLFDIDIP** **GK**ITFMESK**T** **LTAGETPTIV** **DTDVGR**IGIG ICYDIR**FQEL**
251 **AMIYAAR**GAH LLCYPGAFNM TTGPLHWELL QRAR**ATDNQL** **YVATCSPAR**D
301 SGAGYTAWGH STLVGPFGEV LATTEHEEAI IIAEIDYSIL EQRRTSLPLN
351 RQR**RGDLYQL** **VDVQR**LDSK

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
111 - 121	1074.4992	1073.4919	1073.5716	-74	1	K.AIEEAASKGAK.L	
167 - 177	1155.6261	1154.6188	1154.6659	-41	0	K.ITIIGGSIPER.V	
182 - 196	1762.7917	1761.7844	1761.7702	8	0	R.LYNTCCVFGSDGELK.A	
201 - 212	1395.7500	1394.7427	1394.7922	-35	1	R.KIHLFDIDIPGK.I	
220 - 236	1745.8874	1744.8801	1744.8843	-2	0	K.TLTAGETPTIVDTDVGR.I	
247 - 257	1328.6342	1327.6269	1327.6594	-24	0	R.FQELAMIYAAR.G	Oxidation (M)
285 - 299	1666.7603	1665.7530	1665.7781	-15	0	R.ATDNQLYVATCSPAR.D	
354 - 365	1461.7407	1460.7334	1460.7736	-27	1	R.RGDLYQLVDVQR.L	
355 - 365	1305.5979	1304.5906	1304.6725	-63	0	R.GDLYQLVDVQR.L	

Spot No.: **104**

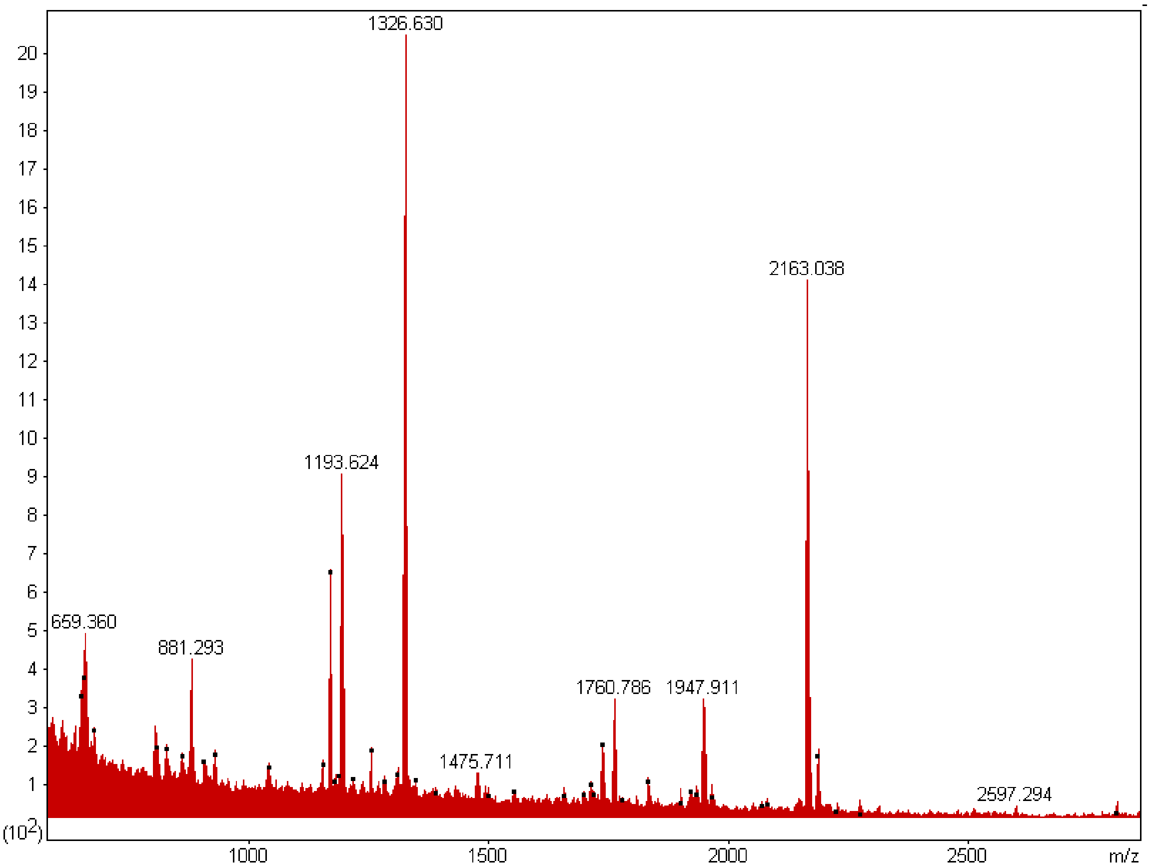
Mascot score: **87** Sequence coverage %: **20**

NCBI accession No.: **gi| 9294283**

Matched peptides No.: **8** Total peptides No.: **23**

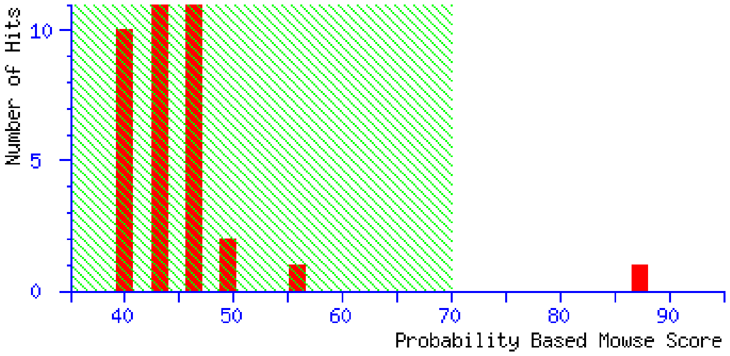
Calculated Mr: **42298** Calculated *p*I: **5.20**

Annotated PMF **spectra:**

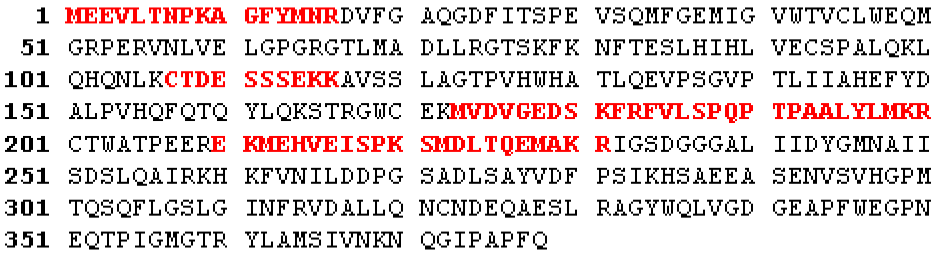


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

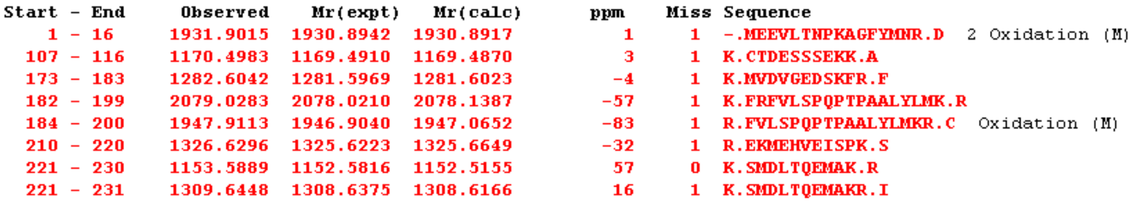


Matched peptide sequences: shown in Bold Red



```
  1 MEEVLTNPKA GFYMNRDVFG AQGDFITSPE VSQMFGEMIG VWTVCLWEQM
 51 GRPERVNLVE LGPGRGTLMA DLLRGTSKFK NFTESLHIHL VECSPALQKL
101 QHQNLKCTDE SSSEKKAVSS LAGTPVHWHA TLQEVPSGVP TLIIAHEFYD
151 ALPVHQFQTQ YLQKSTRGWC EKMVDVGEDS KFRFVLSPQP TPAALYLMKR
201 CTWATPEERE KMEHVEISPK SMDLTQEMAK RIGSDGGGAL IIDYGMNAII
251 SDSLQAIRKH KFVNILDDPG SADLSAYVDF PSIKHSAEEA SENVSVHGPM
301 TQSQFLGSLG INFRVDALLQ NCNDEQAESL RAGYWQLVGD GEAPFWEGPN
351 EQTPIGMGTR YLAMSIVNKN QGIPAPFQ
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    1 - 16     1931.9015  1930.8942  1930.8917        1      1  -.MEEVLTNPKAGFYMNR.D  2 Oxidation (M)
  107 - 116    1170.4983  1169.4910  1169.4870        3      1  K.CTDESSSEKK.A
  173 - 183    1282.6042  1281.5969  1281.6023       -4      1  K.MVDVGEDSKFR.F
  182 - 199    2079.0283  2078.0210  2078.1387      -57      1  K.FRFVLSPQPTPAALYLMK.R
  184 - 200    1947.9113  1946.9040  1947.0652      -83      1  R.FVLSPQPTPAALYLMKR.C  Oxidation (M)
  210 - 220    1326.6296  1325.6223  1325.6649      -32      1  R.EKMEHVEISPK.S
  221 - 230    1153.5889  1152.5816  1152.5155       57      0  K.SMDLTQEMAK.R
  221 - 231    1309.6448  1308.6375  1308.6166       16      1  K.SMDLTQEMAKR.I
```

Spot No.: **105**

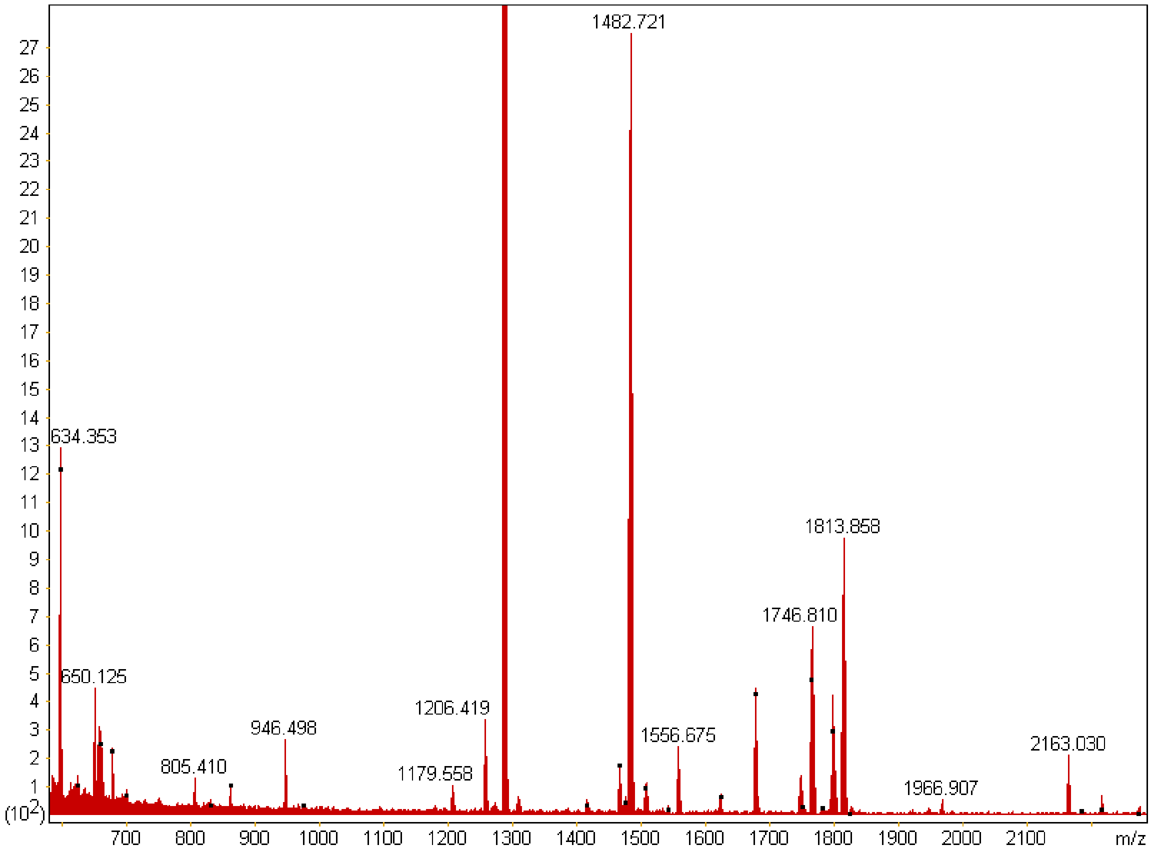
Mascot score: **84**   Sequence coverage %: **25**

NCBI accession No.: **gi| 75149864**

Matched peptides No.: **9**   Total peptides No.: **21**

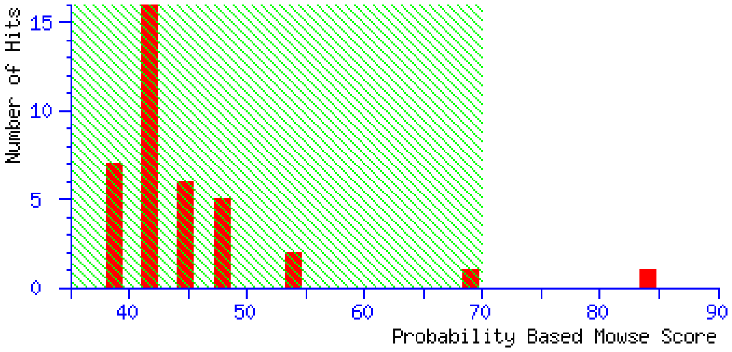
Calculated Mr: **50562**   Calculated *p*I: **6.43**

Annotated PMF **spectra:**

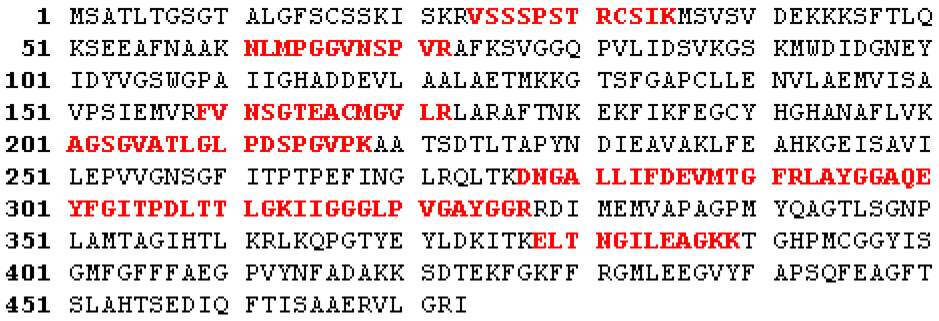


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

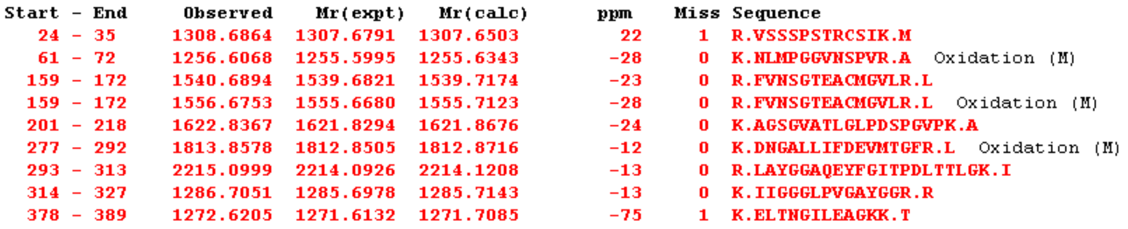


Matched peptide sequences: shown in Bold Red



1 MSATLTGSGT ALGFSCSSKI SKR**VSSSPST** **RCSIK**MSVSV DEKKKSFTLQ
51 KSEEAFNAAK **NLMPGGVNSP** **VR**AFKSVGGQ PVLIDSVKGS KMWDIDGNEY
101 IDYVGSWGPA IIGHADDEVL AALAETMKKG TSFGAPCLLE NVLAEMVISA
151 VPSIEMVR**FV** **NSGTEACMGV** **LR**LARAFTNK EKFIKFEGCY HGHANAFLVK
201 **AGSGVATLGL** **PDSPGVPK**AA TSDTLTAPYN DIEAVAKLFE AHKGEISAVI
251 LEPVVGNSGF ITPTPEFING LRQLTK**DNGA** **LLIFDEVMTG** **FRLAYGGAQE**
301 **YFGITPDLTT** **LGKIIGGGLP** **VGAYGGR**RDI MEMVAPAGPM YQAGTLSGNP
351 LAMTAGIHTL KRLKQPGTYE YLDKITK**ELT** **NGILEAGKK**T GHPMCGGYIS
401 GMFGFFFAEG PVYNFADAKK SDTEKFGKFF RGMLEEGVYF APSQFEAGFT
451 SLAHTSEDIQ FTISAAERVL GRI

Matched peptides information:



Start – End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
24 – 35	1308.6864	1307.6791	1307.6503	22	1	R.VSSSPSTRCSIK.M	
61 – 72	1256.6068	1255.5995	1255.6343	-28	0	K.NLMPGGVNSPVR.A	Oxidation (M)
159 – 172	1540.6894	1539.6821	1539.7174	-23	0	R.FVNSGTEACMGVLR.L	
159 – 172	1556.6753	1555.6680	1555.7123	-28	0	R.FVNSGTEACMGVLR.L	Oxidation (M)
201 – 218	1622.8367	1621.8294	1621.8676	-24	0	K.AGSGVATLGLPDSPGVPK.A	
277 – 292	1813.8578	1812.8505	1812.8716	-12	0	K.DNGALLIFDEVMTGFR.L	Oxidation (M)
293 – 313	2215.0999	2214.0926	2214.1208	-13	0	R.LAYGGAQEYFGITPDLTTLGK.I	
314 – 327	1286.7051	1285.6978	1285.7143	-13	0	K.IIGGGLPVGAYGGR.R	
378 – 389	1272.6205	1271.6132	1271.7085	-75	1	K.ELTNGILEAGKK.T	

Spot No.: **106**

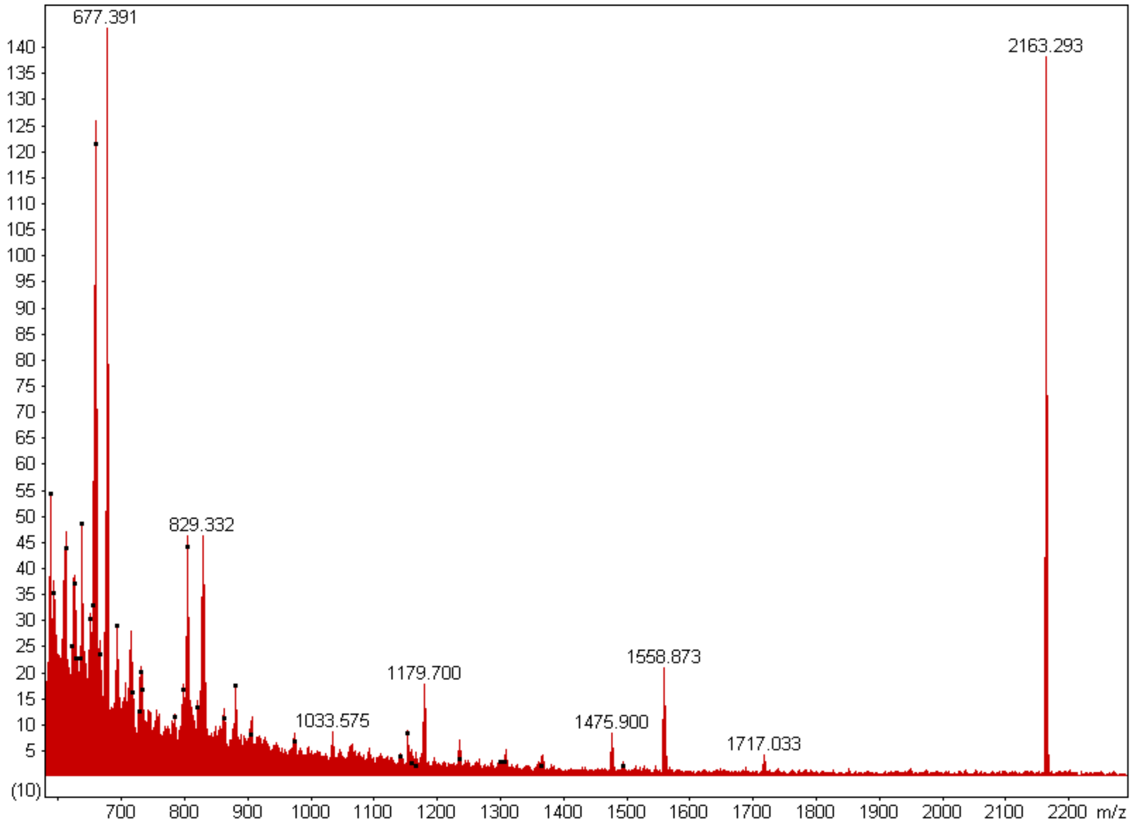
Mascot score: **96** Sequence coverage %: **18**

NCBI accession No.: **gi| 77556926**

Matched peptides No.: **10** Total peptides No.: **23**

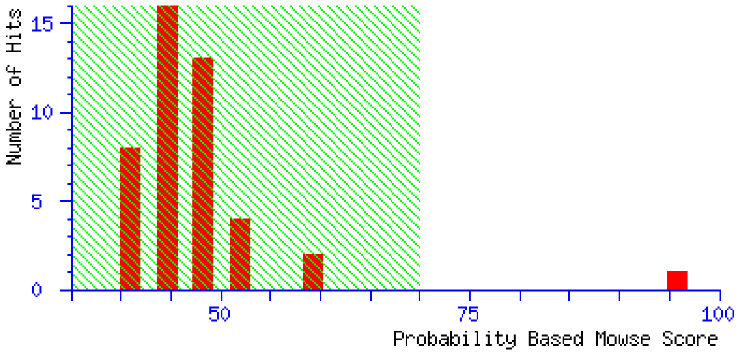
Calculated Mr: **45918** Calculated *p*I: **7.99**

Annotated PMF **spectra:**

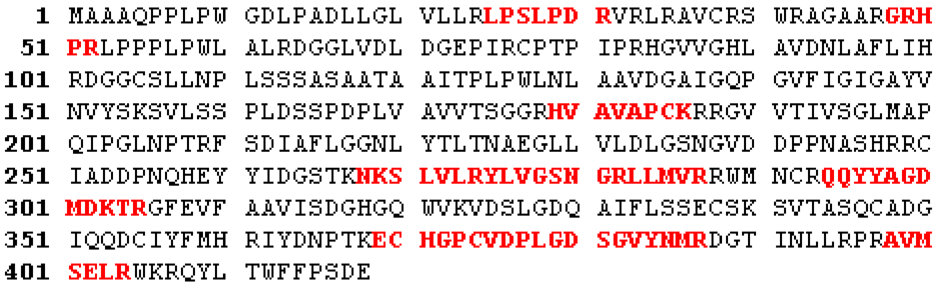


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

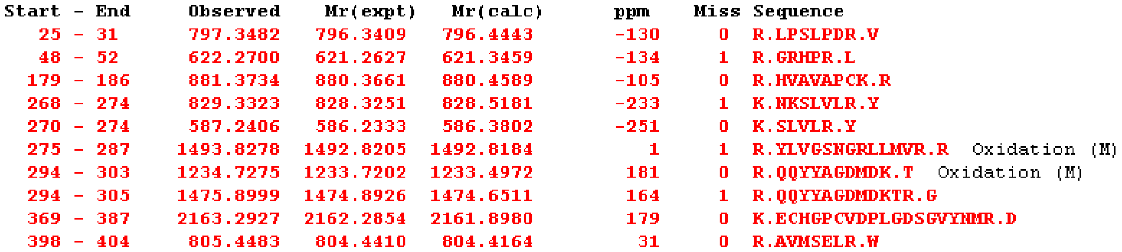


Matched peptide sequences: shown in Bold Red



1 MAAAQPPLPW GDLPADLLGL VLLR**LPSLPD** **R**VRLRAVCRS WRAGAAR**GRH**
51 **PR**LPPPLPWL ALRDGGLVDL DGEPIRCPTP IPRHGVVGHL AVDNLAFLIH
101 RDGGCSLLNP LSSSASAATA AITPLPWLNL AAVDGAIGQP GVFIGIGAYV
151 NVYSKSVLSS PLDSSPDPLV AVVTSGGR**HV** **AVAPCK**RRGV VTIVSGLMAP
201 QIPGLNPTRF SDIAFLGGNL YTLTNAEGLL VLDLGSNGVD DPPNASHRRC
251 IADDPNQHEY YIDGSTK**NKS** **LVLRYLVGSN** **GRLLMVR**RWM NCR**QQYYAGD**
301 **MDKTR**GFEVF AAVISDGHGQ WVKVDSLGDQ AIFLSSECSK SVTASQCADG
351 IQQDCIYFMH RIYDNPTK**EC** **HGPCVDPLGD** **SGVYNMR**DGT INLLRPR**AVM**
401 **SELR**WKRQYL TWFFPSDE

Matched peptides information:



```
Start - End      Observed    Mr(expt)   Mr(calc)       ppm    Miss Sequence
   25 - 31       797.3482    796.3409   796.4443      -130     0   R.LPSLPDR.V
   48 - 52       622.2700    621.2627   621.3459      -134     1   R.GRHPR.L
  179 - 186      881.3734    880.3661   880.4589      -105     0   R.HVAVAPCK.R
  268 - 274      829.3323    828.3251   828.5181      -233     1   K.NKSLVLR.Y
  270 - 274      587.2406    586.2333   586.3802      -251     0   K.SLVLR.Y
  275 - 287     1493.8278   1492.8205  1492.8184         1     1   R.YLVGSNGRLLMVR.R  Oxidation (M)
  294 - 303     1234.7275   1233.7202  1233.4972       181     0   R.QQYYAGDMDK.T  Oxidation (M)
  294 - 305     1475.8999   1474.8926  1474.6511       164     1   R.QQYYAGDMDKTR.G
  369 - 387     2163.2927   2162.2854  2161.8980       179     0   K.ECHGPCVDPLGDSGVYNMR.D
  398 - 404      805.4483    804.4410   804.4164        31     0   R.AVMSELR.W
```

Spot No.: **107**

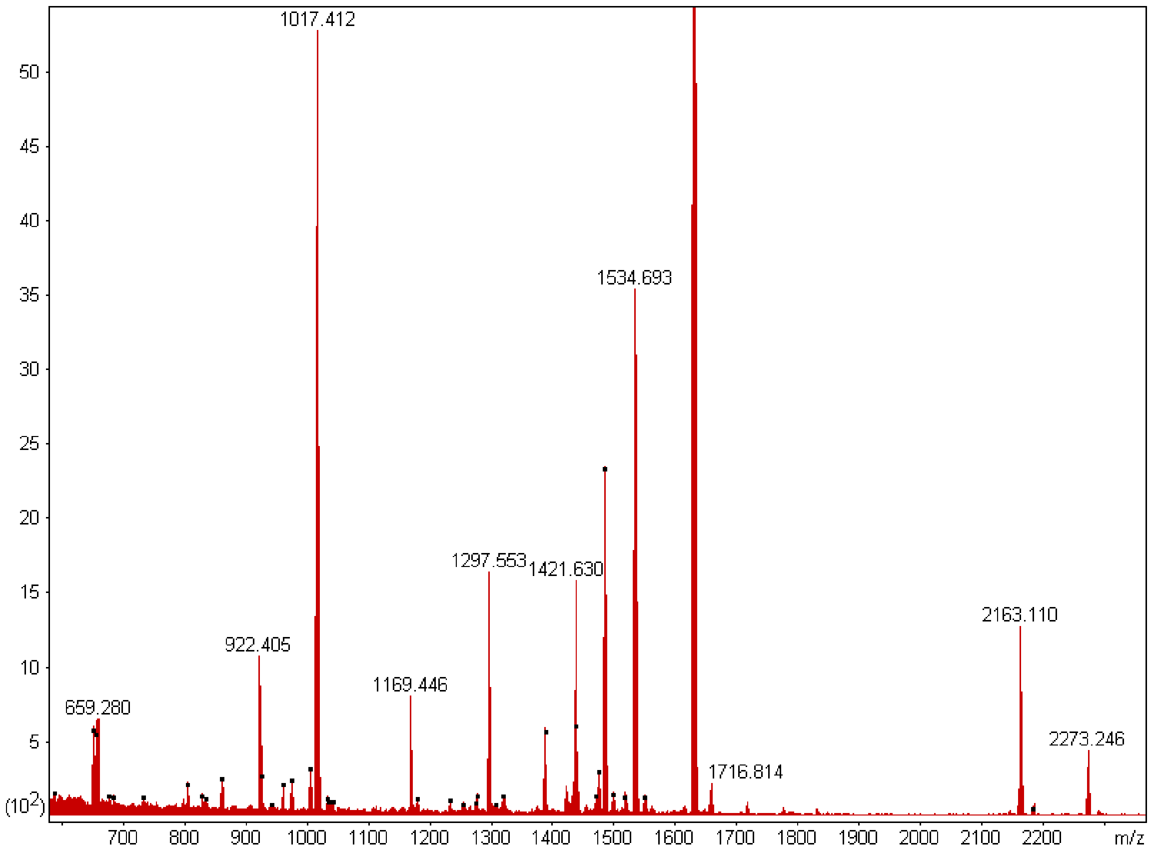
Mascot score: **91** Sequence coverage %: **24**

NCBI accession No.: **gi| 710400**

Matched peptides No.: **13** Total peptides No.: **31**

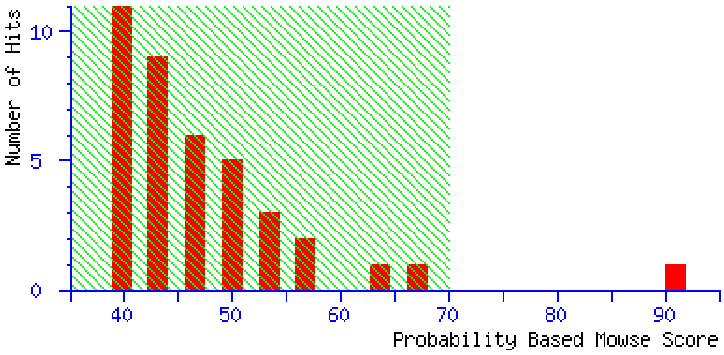
Calculated Mr: **43460** Calculated *p*I: **6.84**

Annotated PMF **spectra:**

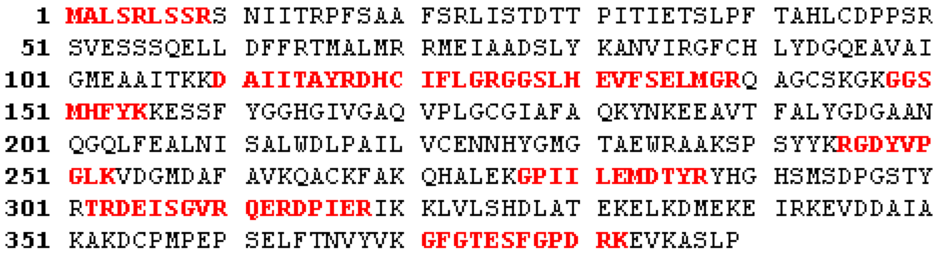


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

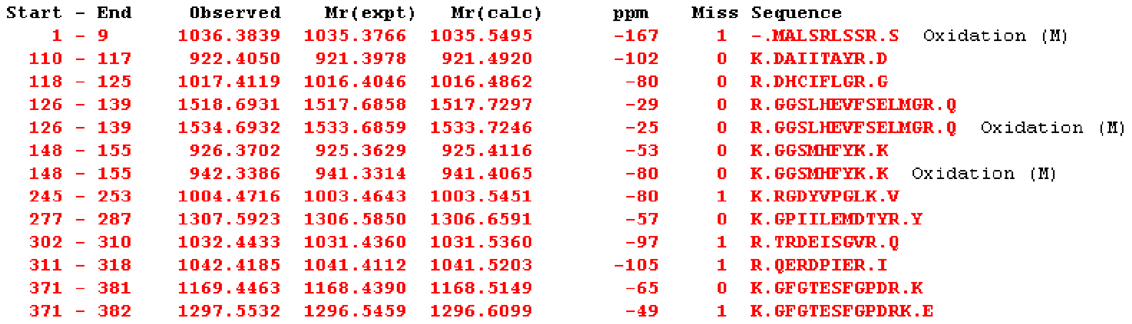


Matched peptide sequences: shown in Bold Red



1 **MALSRLSSR**S NIITRPFSAA FSRLISTDTT PITIETSLPF TAHLCDPPSR
51 SVESSSQELL DFFRTMALMR RMEIAADSLY KANVIRGFCH LYDGQEAVAI
101 GMEAAITKK**D** **AIITAYRDHC** **IFLGRGGSLH** **EVFSELMGR**Q AGCSKGK**GGS**
151 **MHFYK**KESSF YGGHGIVGAQ VPLGCGIAFA QKYNKEEAVT FALYGDGAAN
201 QGQLFEALNI SALWDLPAIL VCENNHYGMG TAEWRAAKSP SYYK**RGDYVP**
251 **GLK**VDGMDAF AVKQACKFAK QHALEK**GPII** **LEMDTYR**YHG HSMSDPGSTY
301 R**TRDEISGVR** **QERDPIER**IK KLVLSHDLAT EKELKDMEKE IRKEVDDAIA
351 KAKDCPMPEP SELFTNVYVK **GFGTESFGPD** **RK**EVKASLP

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)     ppm    Miss Sequence
    1 - 9      1036.3839  1035.3766  1035.5495    -167     1  -.MALSRLSSR.S  Oxidation (M)
  110 - 117     922.4050   921.3978   921.4920    -102     0  K.DAIITAYR.D
  118 - 125    1017.4119  1016.4046  1016.4862     -80     0  R.DHCIFLGR.G
  126 - 139    1518.6931  1517.6858  1517.7297     -29     0  R.GGSLHEVFSELMGR.Q
  126 - 139    1534.6932  1533.6859  1533.7246     -25     0  R.GGSLHEVFSELMGR.Q  Oxidation (M)
  148 - 155     926.3702   925.3629   925.4116     -53     0  K.GGSMHFYK.K
  148 - 155     942.3386   941.3314   941.4065     -80     0  K.GGSMHFYK.K  Oxidation (M)
  245 - 253    1004.4716  1003.4643  1003.5451     -80     1  K.RGDYVPGLK.V
  277 - 287    1307.5923  1306.5850  1306.6591     -57     0  K.GPIILEMDTYR.Y
  302 - 310    1032.4433  1031.4360  1031.5360     -97     1  R.TRDEISGVR.Q
  311 - 318    1042.4185  1041.4112  1041.5203    -105     1  R.QERDPIER.I
  371 - 381    1169.4463  1168.4390  1168.5149     -65     0  K.GFGTESFGPDR.K
  371 - 382    1297.5532  1296.5459  1296.6099     -49     1  K.GFGTESFGPDRK.E
```

Spot No.: **108**

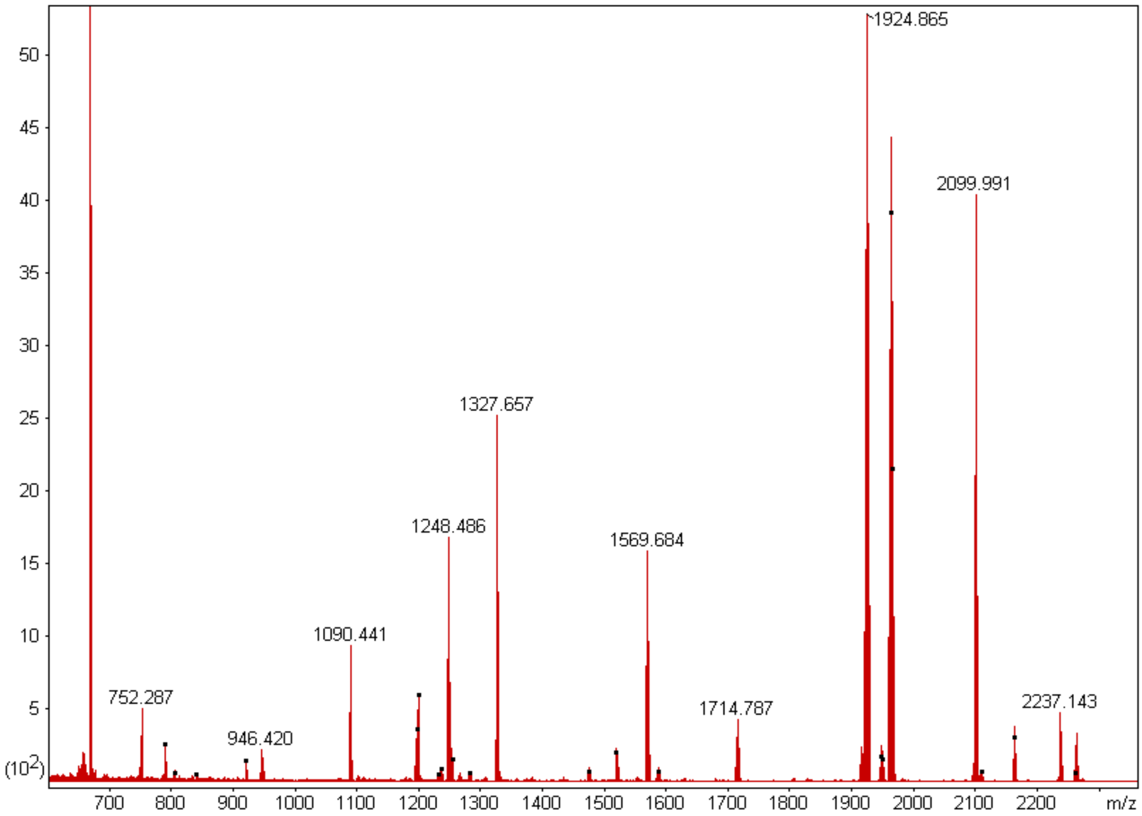
Mascot score: **108** Sequence coverage %: **24**

NCBI accession No.: **gi| 15226690**

Matched peptides No.: **12** Total peptides No.: **29**

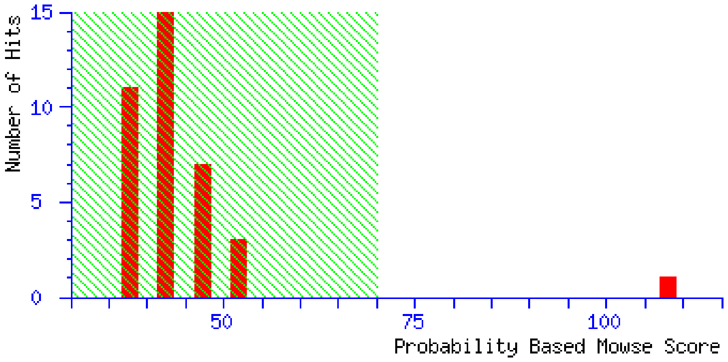
Calculated Mr: **43724** Calculated *p*I: **8.29**

Annotated PMF **spectra:**

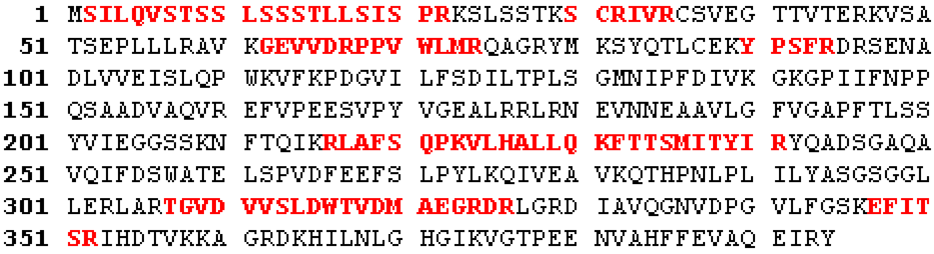


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

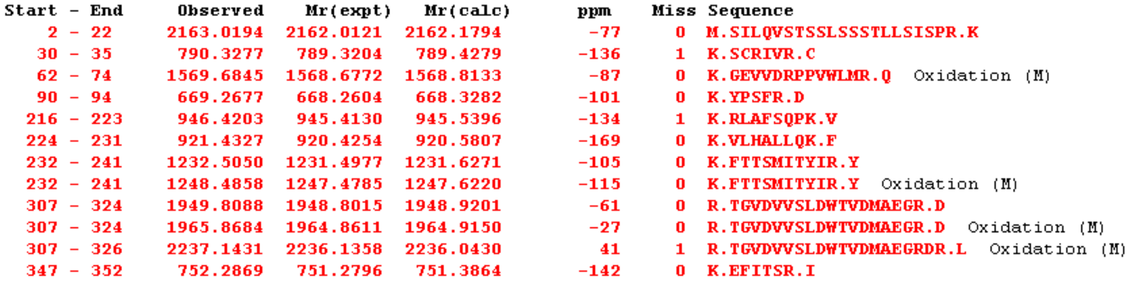


Matched peptide sequences: shown in Bold Red



1 M**SILQVSTSS LSSSTLLSIS PR**KSLSSTK**S CRIVR**CSVEG TTVTERKVSA
51 TSEPLLLRAV K**GEVVDRPPV WLMR**QAGRYM KSYQTLCEK**Y PSFR**DRSENA
101 DLVVEISLQP WKVFKPDGVI LFSDILTPLS GMNIPFDIVK GKGPIIFNPP
151 QSAADVAQVR EFVPEESVPY VGEALRRLRN EVNNEAAVLG FVGAPFTLSS
201 YVIEGGSSKN FTQIK**RLAFS QPKVLHALLQ KFTTSMITYI R**YQADSGAQA
251 VQIFDSWATE LSPVDFEEFS LPYLKQIVEA VKQTHPNLPL ILYASGSGGL
301 LERLAR**TGVD VVSLDWTVDM AEGRDR**LGRD IAVQGNVDPG VLFGSK**EFIT**
351 **SR**IHDTVKKA GRDKHILNLG HGIKVGTPEE NVAHFFEVAQ EIRY

Matched peptides information:



Start – End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
2 – 22	2163.0194	2162.0121	2162.1794	-77	0	M.SILQVSTSSLSSSTLLSISPR.K	
30 – 35	790.3277	789.3204	789.4279	-136	1	K.SCRIVR.C	
62 – 74	1569.6845	1568.6772	1568.8133	-87	0	K.GEVVDRPPVWLMR.Q	Oxidation (M)
90 – 94	669.2677	668.2604	668.3282	-101	0	K.YPSFR.D	
216 – 223	946.4203	945.4130	945.5396	-134	1	K.RLAFSQPK.V	
224 – 231	921.4327	920.4254	920.5807	-169	0	K.VLHALLQK.F	
232 – 241	1232.5050	1231.4977	1231.6271	-105	0	K.FTTSMITYIR.Y	
232 – 241	1248.4858	1247.4785	1247.6220	-115	0	K.FTTSMITYIR.Y	Oxidation (M)
307 – 324	1949.8088	1948.8015	1948.9201	-61	0	R.TGVDVVSLDWTVDMAEGR.D	
307 – 324	1965.8684	1964.8611	1964.9150	-27	0	R.TGVDVVSLDWTVDMAEGR.D	Oxidation (M)
307 – 326	2237.1431	2236.1358	2236.0430	41	1	R.TGVDVVSLDWTVDMAEGRDR.L	Oxidation (M)
347 – 352	752.2869	751.2796	751.3864	-142	0	K.EFITSR.I	

Spot No.: **109**

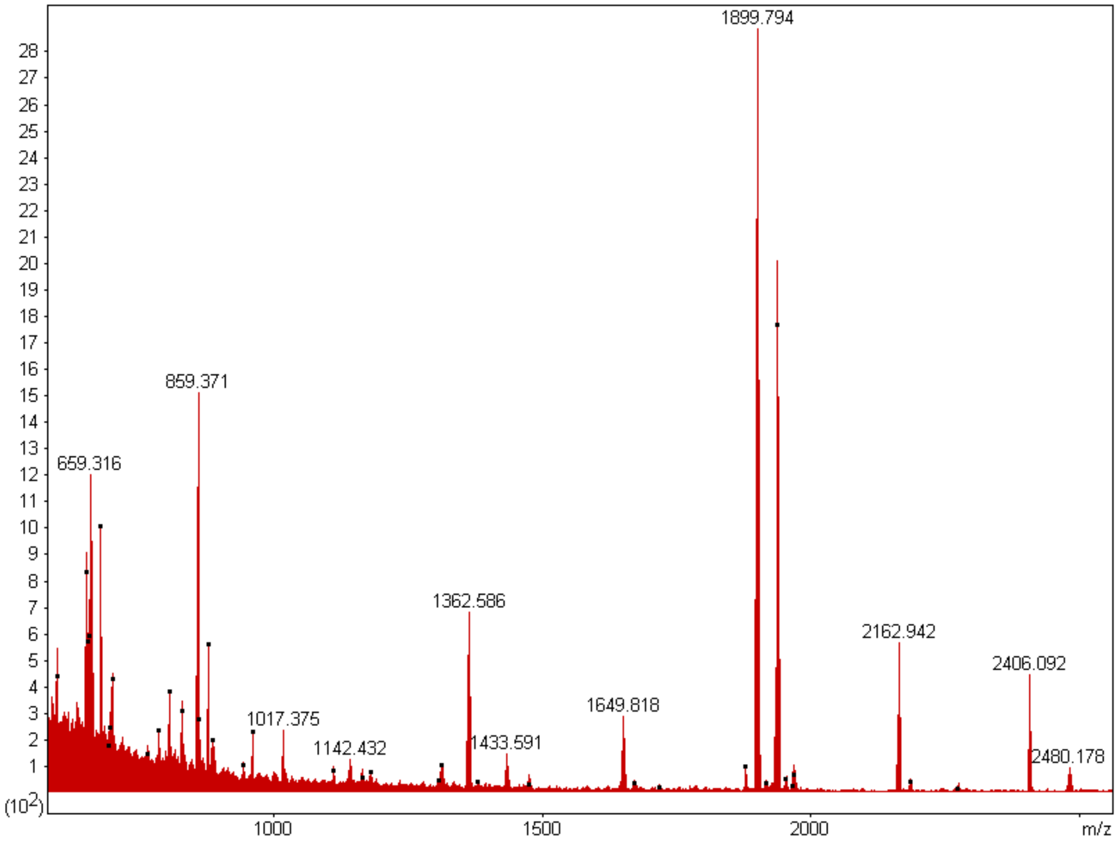
Mascot score: **118** Sequence coverage %: **42**

NCBI accession No.: **gi| 312282695**

Matched peptides No.: **13** Total peptides No.: **30**

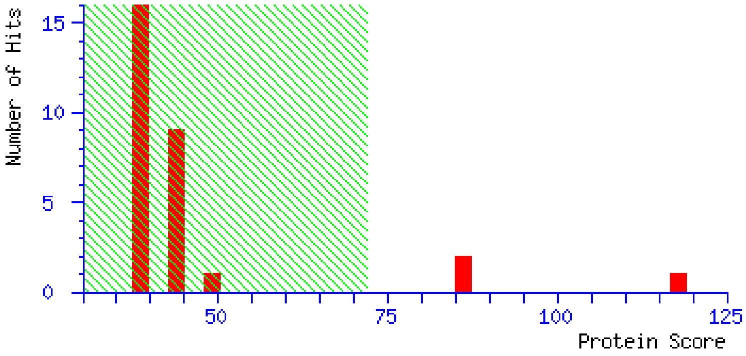
Calculated Mr: **35946** Calculated *p*I: **6.33**

Annotated PMF spectra:

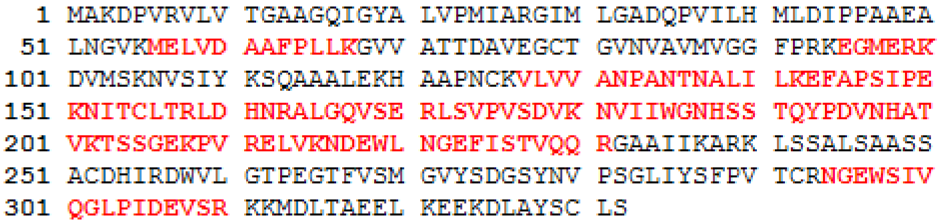


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

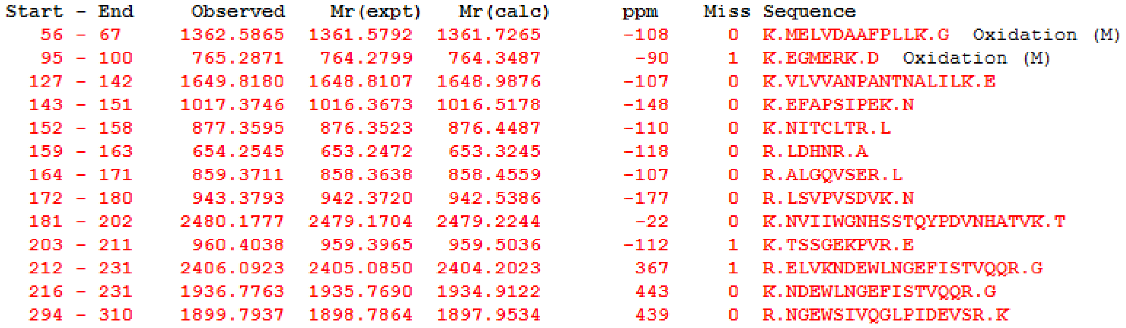


Matched peptide sequences: shown in Bold Red



1 MAKDPVRVLV TGAAGQIGYA LVPMIARGIM LGADQPVILH MLDIPPAAEA
51 LNGVK**MELVD** **AAFPLLK**GVV ATTDAVEGCT GVNVAVMVGG FPRK**EGMERK**
101 DVMSKNVSIY KSQAAALEKH AAPNCK**VLVV** **ANPANTNALI** **LKEFAPSIPE**
151 **KNITCLTRLD** **HNRALGQVSE** **RLSVPVSDVK** **NVIIWGNHSS** **TQYPDVNHAT**
201 **VKTSSGEKPV** **RELVKNDEWL** **NGEFISTVQQ** **R**GAAIIKARK LSSALSAASS
251 ACDHIRDWVL GTPEGTFVSM GVYSDGSYNV PSGLIYSFPV TCR**NGEWSIV**
301 **QGLPIDEVSR** KKMDLTAEEL KEEKDLAYSC LS

Matched peptides information:



```
Start - End      Observed     Mr(expt)   Mr(calc)        ppm    Miss  Sequence
   56 - 67      1362.5865   1361.5792  1361.7265       -108      0   K.MELVDAAFPLLK.G  Oxidation (M)
   95 - 100      765.2871    764.2799   764.3487        -90      1   K.EGMERK.D  Oxidation (M)
  127 - 142     1649.8180   1648.8107  1648.9876       -107      0   K.VLVVANPANTNALILK.E
  143 - 151     1017.3746   1016.3673  1016.5178       -148      0   K.EFAPSIPEK.N
  152 - 158      877.3595    876.3523   876.4487       -110      0   K.NITCLTR.L
  159 - 163      654.2545    653.2472   653.3245       -118      0   R.LDHNR.A
  164 - 171      859.3711    858.3638   858.4559       -107      0   R.ALGQVSER.L
  172 - 180      943.3793    942.3720   942.5386       -177      0   R.LSVPVSDVK.N
  181 - 202     2480.1777   2479.1704  2479.2244        -22      0   K.NVIIWGNHSSTQYPDVNHATVK.T
  203 - 211      960.4038    959.3965   959.5036       -112      1   K.TSSGEKPVR.E
  212 - 231     2406.0923   2405.0850  2404.2023        367      1   R.ELVKNDEWLNGEFISTVQQR.G
  216 - 231     1936.7763   1935.7690  1934.9122        443      0   K.NDEWLNGEFISTVQQR.G
  294 - 310     1899.7937   1898.7864  1897.9534        439      0   R.NGEWSIVQGLPIDEVSR.K
```

Spot No.: **110**

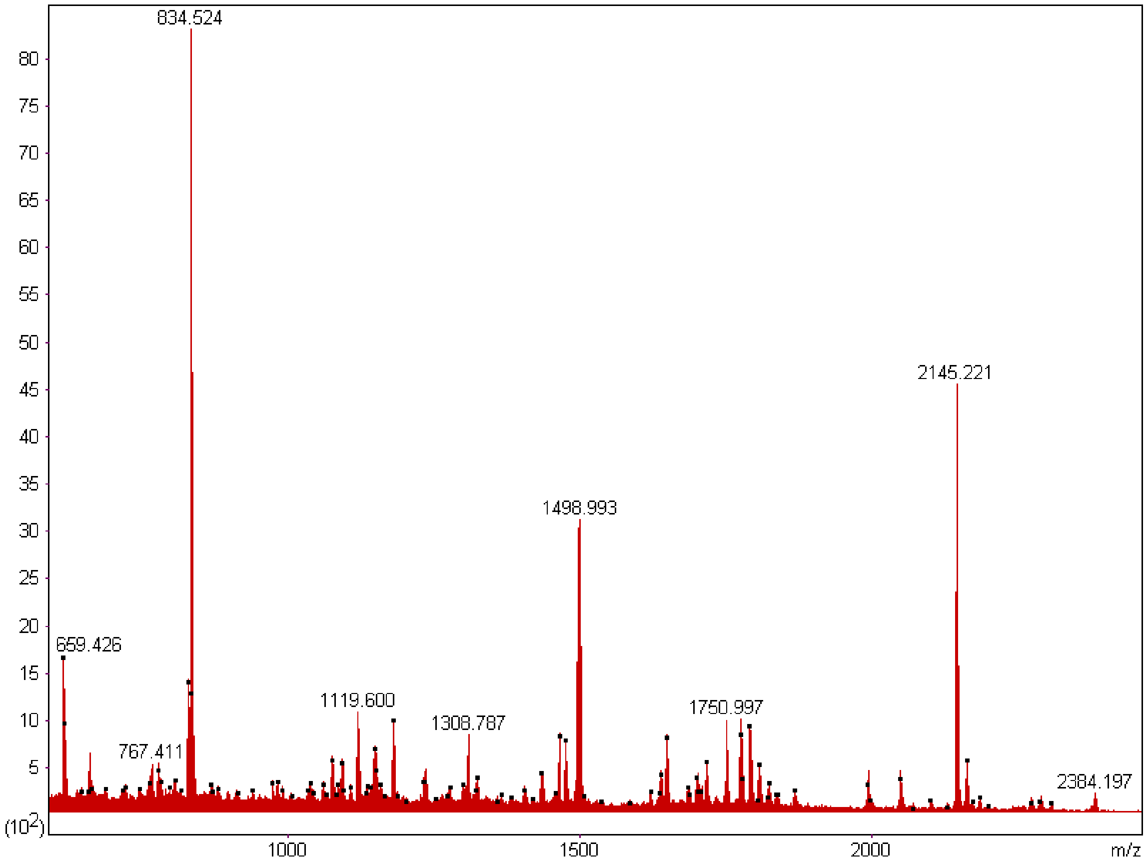
Mascot score: **163** Sequence coverage %: **57**

NCBI accession No.: **gi| 312282121**

Matched peptides No.: **19** Total peptides No.: **50**

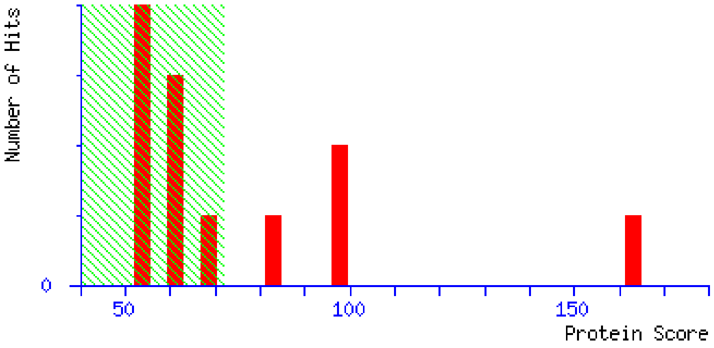
Calculated Mr: **36888** Calculated *p*I: **6.20**

Annotated PMF **spectra:**

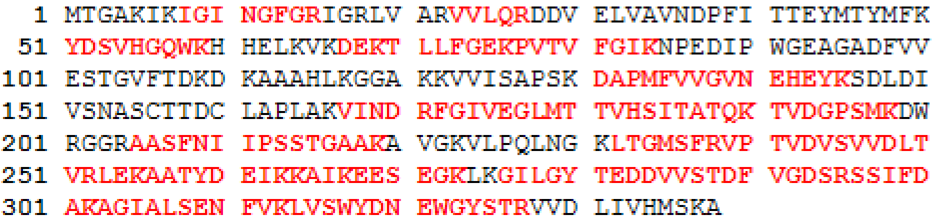


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

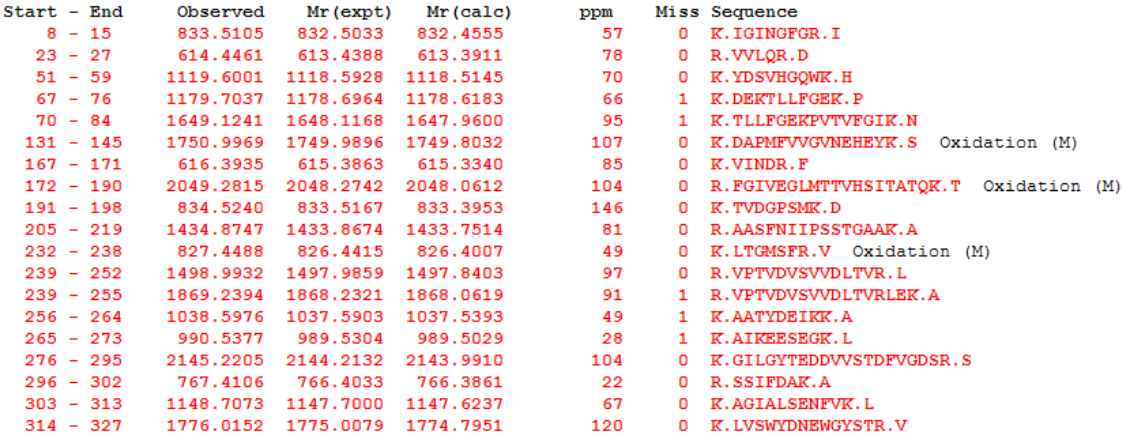


Matched peptide sequences: shown in Bold Red



```
  1 MTGAKIKIGI NGFGRIGRLV ARVVLQRDDV ELVAVNDPFI TTEYMTYMFK
 51 YDSVHGQWKH HELKVKDEKT LLFGEKPVTV FGIKNPEDIP WGEAGADFVV
101 ESTGVFTDKD KAAAHLKGGA KKVVISAPSK DAPMFVVGVN EHEYKSDLDI
151 VSNASCTTDC LAPLAKVIND RFGIVEGLMT TVHSITATQK TVDGPSMKDW
201 RGGRAASFNI IPSSTGAAKA VGKVLPQLNG KLTGMSFRVP TVDVSVVDLT
251 VRLEKAATYD EIKKAIKEES EGKLKGILGY TEDDVVSTDF VGDSRSSIFD
301 AKAGIALSEN FVKLVSWYDN EWGYSTRVVD LIVHMSKA
```

Matched peptides information:



```
Start - End      Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    8 - 15       833.5105   832.5033   832.4555       57      0  K.IGINGFGR.I
   23 - 27       614.4461   613.4388   613.3911       78      0  R.VVLQR.D
   51 - 59      1119.6001  1118.5928  1118.5145       70      0  K.YDSVHGQWK.H
   67 - 76      1179.7037  1178.6964  1178.6183       66      1  K.DEKTLLFGEK.P
   70 - 84      1649.1241  1648.1168  1647.9600       95      1  K.TLLFGEKPVTVFGIK.N
  131 - 145     1750.9969  1749.9896  1749.8032      107      0  K.DAPMFVVGVNEHEYK.S  Oxidation (M)
  167 - 171      616.3935   615.3863   615.3340       85      0  K.VINDR.F
  172 - 190     2049.2815  2048.2742  2048.0612      104      0  R.FGIVEGLMTTVHSITATQK.T  Oxidation (M)
  191 - 198      834.5240   833.5167   833.3953      146      0  K.TVDGPSMK.D
  205 - 219     1434.8747  1433.8674  1433.7514       81      0  R.AASFNIIPSSTGAAK.A
  232 - 238      827.4488   826.4415   826.4007       49      0  K.LTGMSFR.V  Oxidation (M)
  239 - 252     1498.9932  1497.9859  1497.8403       97      0  R.VPTVDVSVVDLTVR.L
  239 - 255     1869.2394  1868.2321  1868.0619       91      1  R.VPTVDVSVVDLTVRLEK.A
  256 - 264     1038.5976  1037.5903  1037.5393       49      1  K.AATYDEIKK.A
  265 - 273      990.5377   989.5304   989.5029       28      1  K.AIKEESEGK.L
  276 - 295     2145.2205  2144.2132  2143.9910      104      0  K.GILGYTEDDVVSTDFVGDSR.S
  296 - 302      767.4106   766.4033   766.3861       22      0  R.SSIFDAK.A
  303 - 313     1148.7073  1147.7000  1147.6237       67      0  K.AGIALSENFVK.L
  314 - 327     1776.0152  1775.0079  1774.7951      120      0  K.LVSWYDNEWGYSTR.V
```

Spot No.: **111**

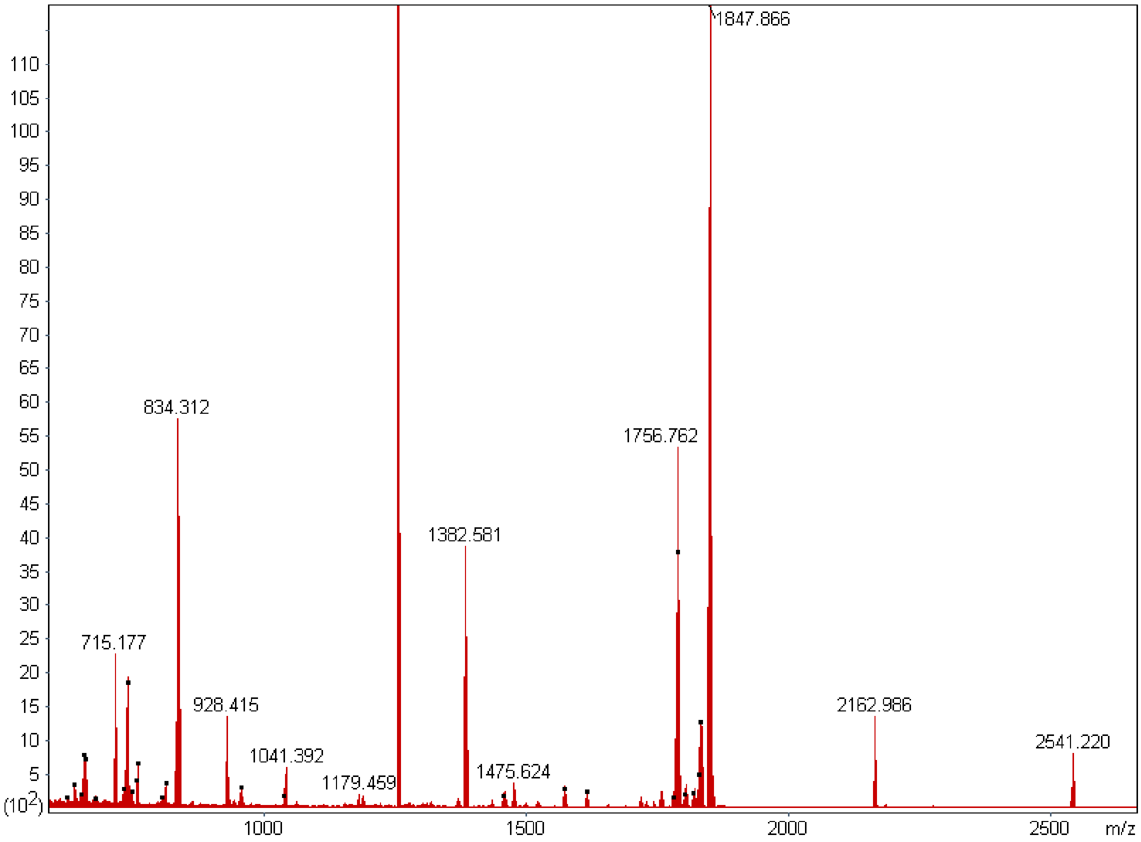
Mascot score: **109**   Sequence coverage %: **35**

NCBI accession No.: **gi| 166702**

Matched peptides No.: **12**   Total peptides No.: **29**

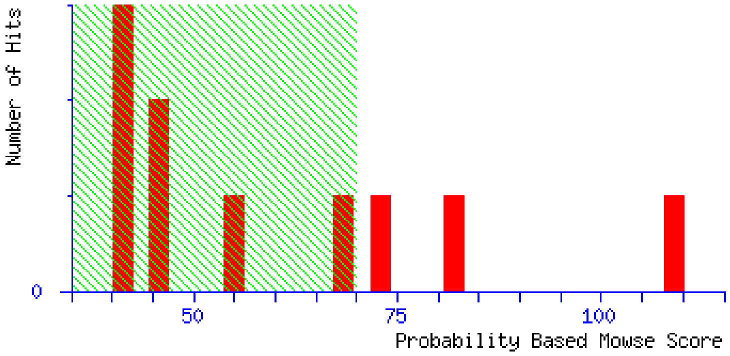
Calculated Mr: **37937**   Calculated *p*I: **7.00**

Annotated PMF **spectra:**

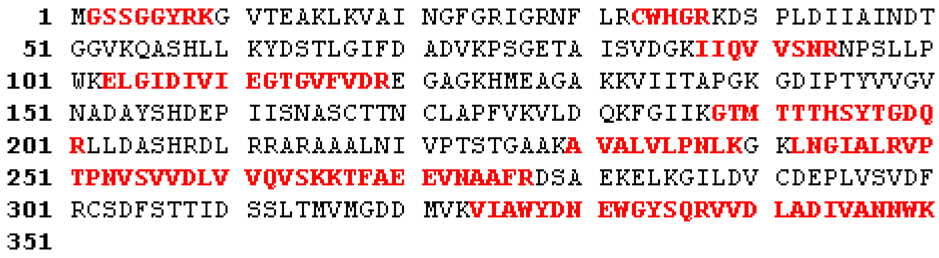


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

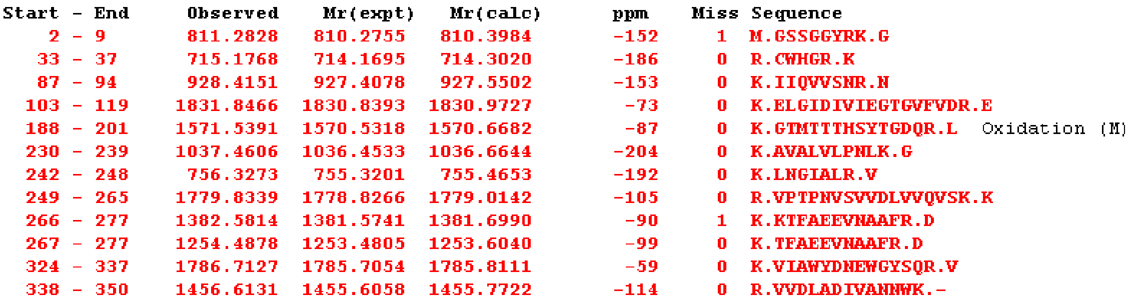


Matched peptide sequences: shown in Bold Red



1 M**GSSGGYRK**G VTEAKLKVAI NGFGRIGRNF LR**CWHGR**KDS PLDIIAINDT
51 GGVKQASHLL KYDSTLGIFD ADVKPSGETA ISVDGK**IIQV** **VSNR**NPSLLP
101 WK**ELGIDIVI** **EGTGVFVDR**E GAGKHMEAGA KKVIITAPGK GDIPTYVVGV
151 NADAYSHDEP IISNASCTTN CLAPFVKVLD QKFGIIK**GTM** **TTTHSYTGDQ**
201 **R**LLDASHRDL RRARAAALNI VPTSTGAAK**A** **VALVLPNLK**G K**LNGIALRVP**
251 **TPNVSVVDLV** **VQVSKKTFAE** **EVNAAFR**DSA EKELKGILDV CDEPLVSVDF
301 RCSDFSTTID SSLTMVMGDD MVK**VIAWYDN** **EWGYSQRVVD** **LADIVANNWK**
351

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    2 - 9       811.2828   810.2755   810.3984     -152      1  M.GSSGGYRK.G
   33 - 37      715.1768   714.1695   714.3020     -186      0  R.CWHGR.K
   87 - 94      928.4151   927.4078   927.5502     -153      0  K.IIQVVSNR.N
  103 - 119    1831.8466  1830.8393  1830.9727      -73      0  K.ELGIDIVIEGTGVFVDR.E
  188 - 201    1571.5391  1570.5318  1570.6682      -87      0  K.GTMTTTHSYTGDQR.L  Oxidation (M)
  230 - 239    1037.4606  1036.4533  1036.6644     -204      0  K.AVALVLPNLK.G
  242 - 248     756.3273   755.3201   755.4653     -192      0  K.LNGIALR.V
  249 - 265    1779.8339  1778.8266  1779.0142     -105      0  R.VPTPNVSVVDLVVQVSK.K
  266 - 277    1382.5814  1381.5741  1381.6990      -90      1  K.KTFAEEVNAAFR.D
  267 - 277    1254.4878  1253.4805  1253.6040      -99      0  K.TFAEEVNAAFR.D
  324 - 337    1786.7127  1785.7054  1785.8111      -59      0  K.VIAWYDNEWGYSQR.V
  338 - 350    1456.6131  1455.6058  1455.7722     -114      0  R.VVDLADIVANNWK.-
```

Spot No.: **112**

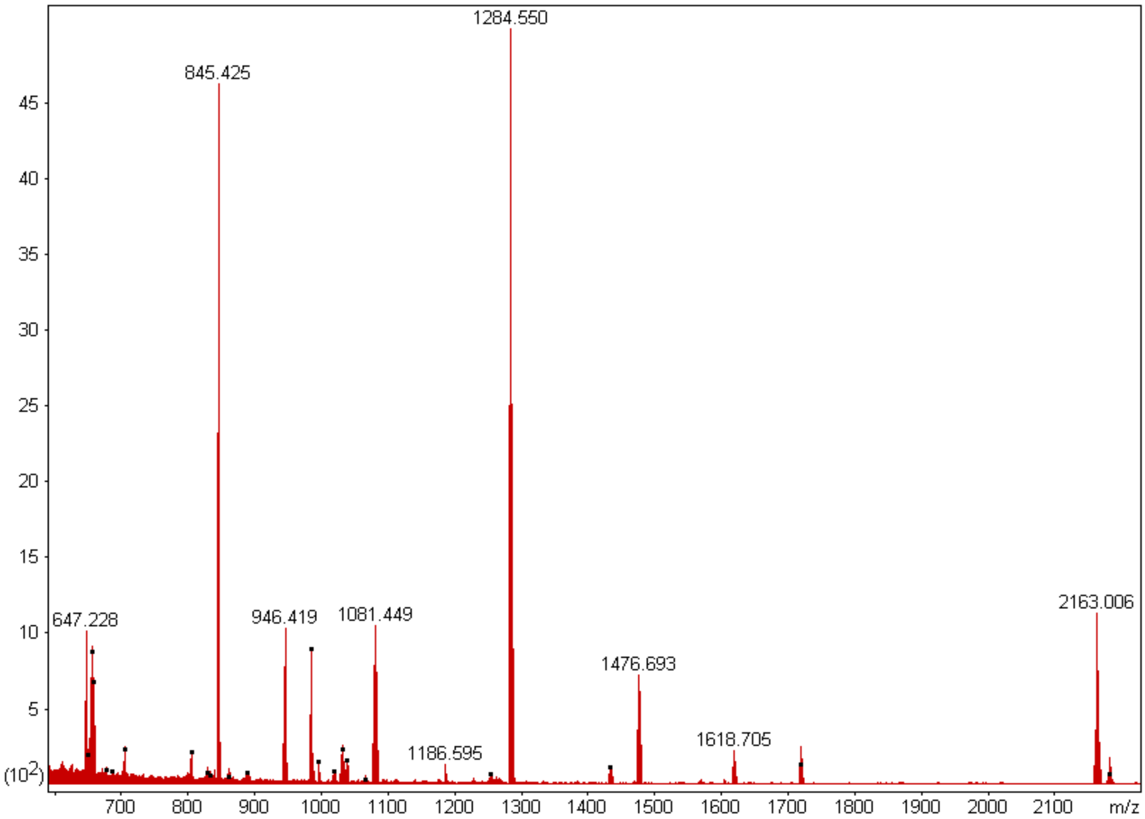
Mascot score: **95** Sequence coverage %: **21**

NCBI accession No.: **gi| 15238762**

Matched peptides No.: **11** Total peptides No.: **21**

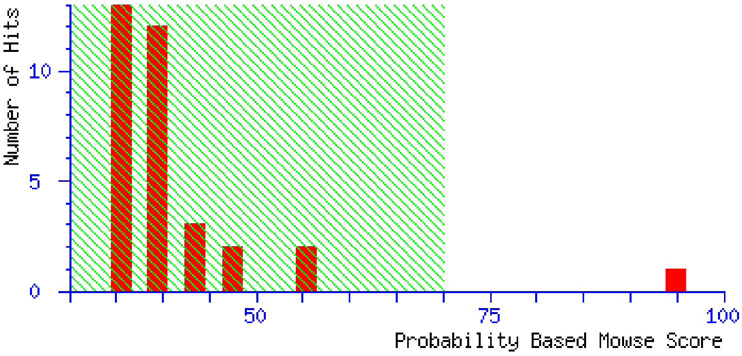
Calculated Mr: **44781** Calculated *p*I: **6.38**

Annotated PMF **spectra:**

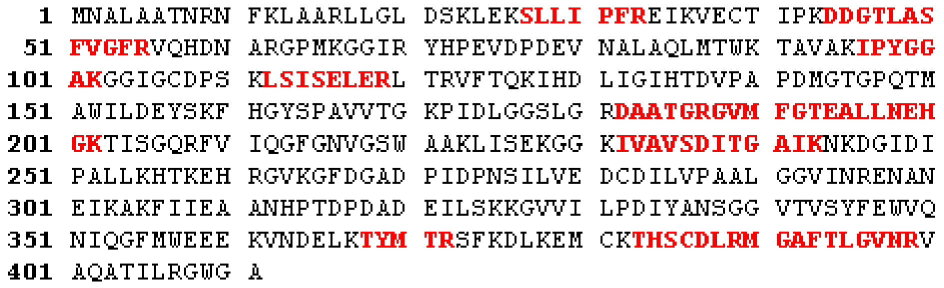


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

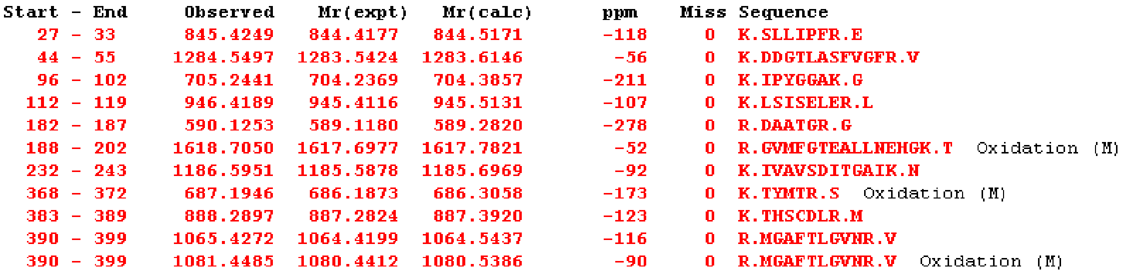


Matched peptide sequences: shown in Bold Red



```
  1 MNALAATNRN FKLAARLLGL DSKLEKSLLI PFREIKVECT IPKDDGTLAS
 51 FVGFRVQHDN ARGPMKGGIR YHPEVDPDEV NALAQLMTWK TAVAKIPYGG
101 AKGGIGCDPS KLSISELERL TRVFTQKIHD LIGIHTDVPA PDMGTGPQTM
151 AWILDEYSKF HGYSPAVVTG KPIDLGGSLG RDAATGRGVM FGTEALLNEH
201 GKTISGQRFV IQGFGNVGSW AAKLISEKGG KIVAVSDITG AIKNKDGIDI
251 PALLKHTKEH RGVKGFDGAD PIDPNSILVE DCDILVPAAL GGVINRENAN
301 EIKAKFIIEA ANHPTDPDAD EILSKKGVVI LPDIYANSGG VTVSYFEWVQ
351 NIQGFMWEEE KVNDELKTYM TRSFKDLKEM CKTHSCDLRM GAFTLGVNRV
401 AQATILRGWG A
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   27 - 33      845.4249   844.4177   844.5171     -118     0   K.SLLIPFR.E
   44 - 55     1284.5497  1283.5424  1283.6146      -56     0   K.DDGTLASFVGFR.V
   96 - 102     705.2441   704.2369   704.3857     -211     0   K.IPYGGAK.G
  112 - 119     946.4189   945.4116   945.5131     -107     0   K.LSISELER.L
  182 - 187     590.1253   589.1180   589.2820     -278     0   R.DAATGR.G
  188 - 202    1618.7050  1617.6977  1617.7821      -52     0   R.GVMFGTEALLNEHGK.T  Oxidation (M)
  232 - 243    1186.5951  1185.5878  1185.6969      -92     0   K.IVAVSDITGAIK.N
  368 - 372     687.1946   686.1873   686.3058     -173     0   K.TYMTR.S  Oxidation (M)
  383 - 389     888.2897   887.2824   887.3920     -123     0   K.THSCDLR.M
  390 - 399    1065.4272  1064.4199  1064.5437     -116     0   R.MGAFTLGVNR.V
  390 - 399    1081.4485  1080.4412  1080.5386      -90     0   R.MGAFTLGVNR.V  Oxidation (M)
```

Spot No.: **113**

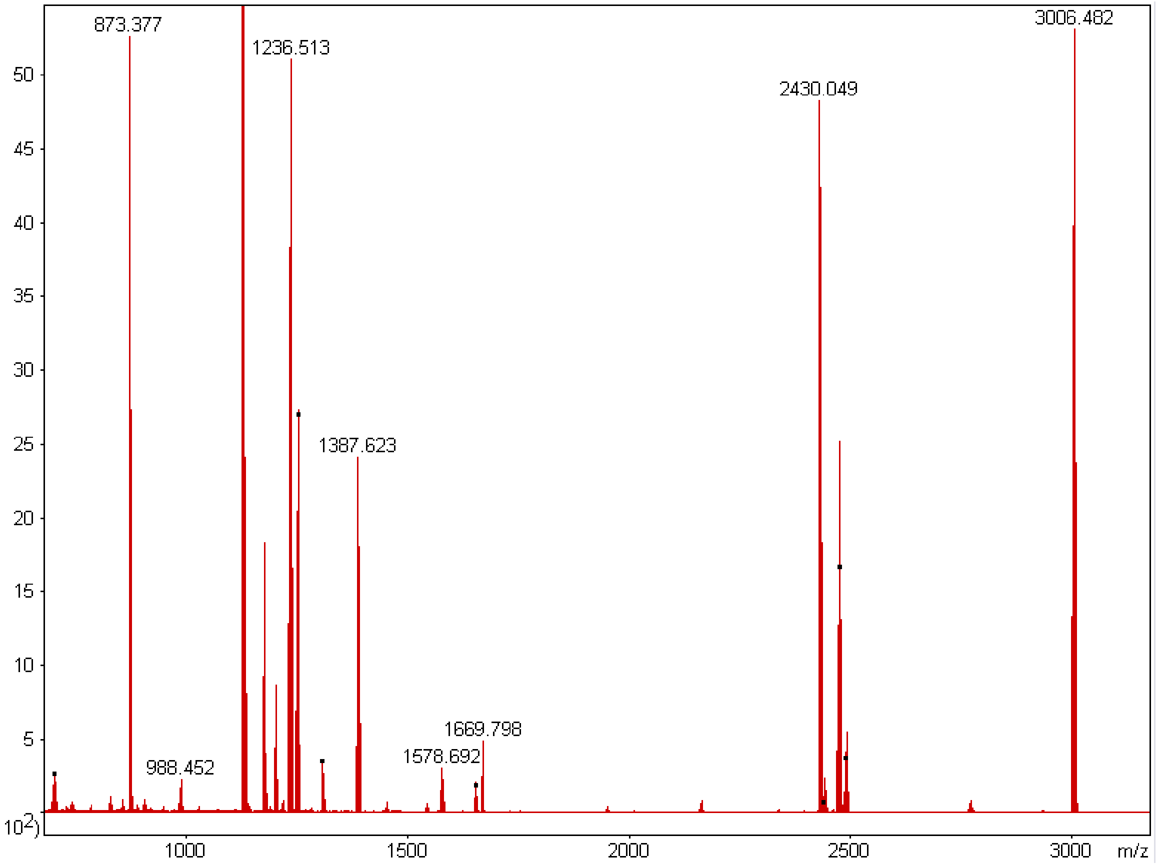
Mascot score: **149** Sequence coverage %: **36**

NCBI accession No.: **gi| 312281829**

Matched peptides No.: **14** Total peptides No.: **24**

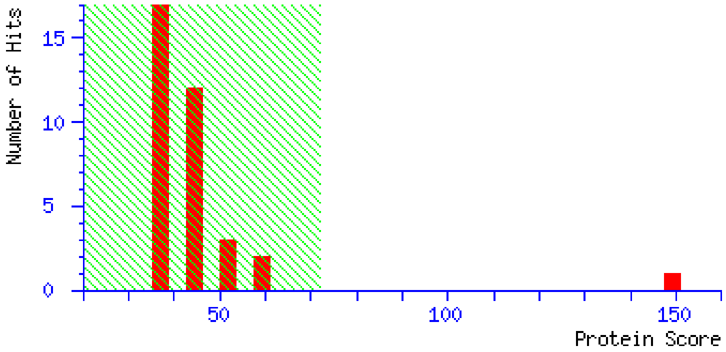
Calculated Mr: **43118** Calculated *p*I: **6.49**

Annotated PMF **spectra:**

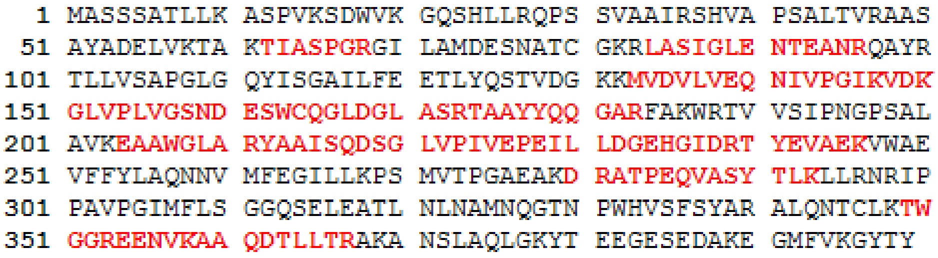


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

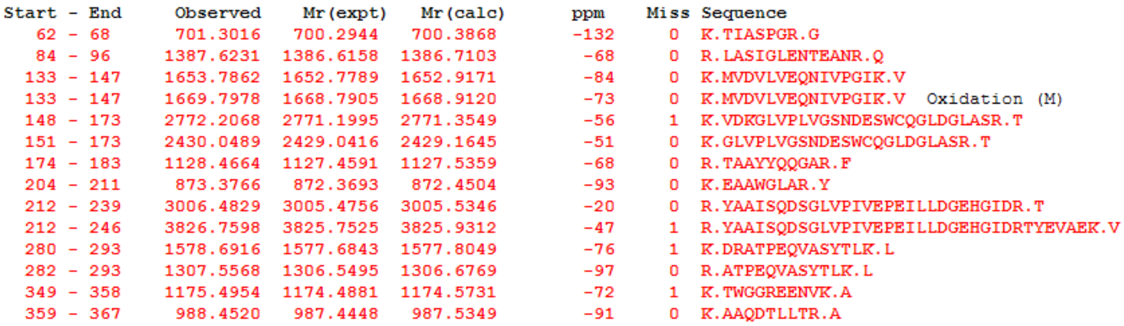


Matched peptide sequences: shown in Bold Red



1 MASSSATLLK ASPVKSDWVK GQSHLLRQPS SVAAIRSHVA PSALTVRAAS
51 AYADELVKTA K**TIASPGR**GI LAMDESNATC GKR**LASIGLE** **NTEANR**QAYR
101 TLLVSAPGLG QYISGAILFE ETLYQSTVDG KK**MVDVLVEQ** **NIVPGIKVDK**
151 **GLVPLVGSND** **ESWCQGLDGL** **ASRTAAYYQQ** **GAR**FAKWRTV VSIPNGPSAL
201 AVK**EAAWGLA** **RYAAISQDSG** **LVPIVEPEIL** **LDGEHGIDRT** **YEVAEK**VWAE
251 VFFYLAQNNV MFEGILLKPS MVTPGAEAK**D** **RATPEQVASY** **TLK**LLRNRIP
301 PAVPGIMFLS GGQSELEATL NLNAMNQGTN PWHVSFSYAR ALQNTCLK**TW**
351 **GGREENVKAA** **QDTLLTR**AKA NSLAQLGKYT EEGESEDAKE GMFVKGYTY

Matched peptides information:



```
Start - End      Observed    Mr(expt)    Mr(calc)       ppm     Miss  Sequence
   62 - 68       701.3016    700.2944    700.3868      -132       0   K.TIASPGR.G
   84 - 96      1387.6231   1386.6158   1386.7103       -68       0   R.LASIGLENTEANR.Q
  133 - 147     1653.7862   1652.7789   1652.9171       -84       0   K.MVDVLVEQNIVPGIK.V
  133 - 147     1669.7978   1668.7905   1668.9120       -73       0   K.MVDVLVEQNIVPGIK.V  Oxidation (M)
  148 - 173     2772.2068   2771.1995   2771.3549       -56       1   K.VDKGLVPLVGSNDESWCQGLDGLASR.T
  151 - 173     2430.0489   2429.0416   2429.1645       -51       0   K.GLVPLVGSNDESWCQGLDGLASR.T
  174 - 183     1128.4664   1127.4591   1127.5359       -68       0   R.TAAYYQQGAR.F
  204 - 211      873.3766    872.3693    872.4504       -93       0   K.EAAWGLAR.Y
  212 - 239     3006.4829   3005.4756   3005.5346       -20       0   R.YAAISQDSGLVPIVEPEILLDGEHGIDR.T
  212 - 246     3826.7598   3825.7525   3825.9312       -47       1   R.YAAISQDSGLVPIVEPEILLDGEHGIDRTYEVAEK.V
  280 - 293     1578.6916   1577.6843   1577.8049       -76       1   K.DRATPEQVASYTLK.L
  282 - 293     1307.5568   1306.5495   1306.6769       -97       0   R.ATPEQVASYTLK.L
  349 - 358     1175.4954   1174.4881   1174.5731       -72       1   K.TWGGREENVK.A
  359 - 367      988.4520    987.4448    987.5349       -91       0   K.AAQDTLLTR.A
```

Spot No.: **114**

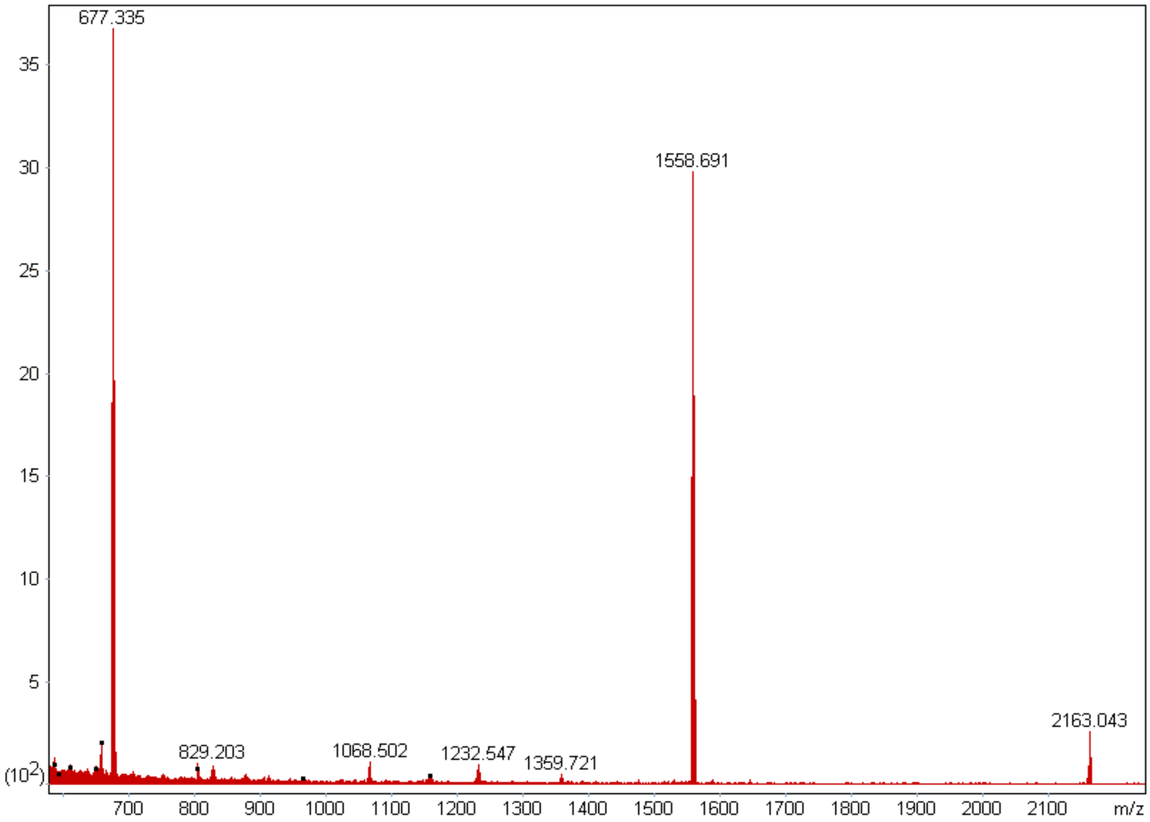
Mascot score: **86** Sequence coverage %: **49**

NCBI accession No.: **gi| 219563256**

Matched peptides No.: **5** Total peptides No.: **17**

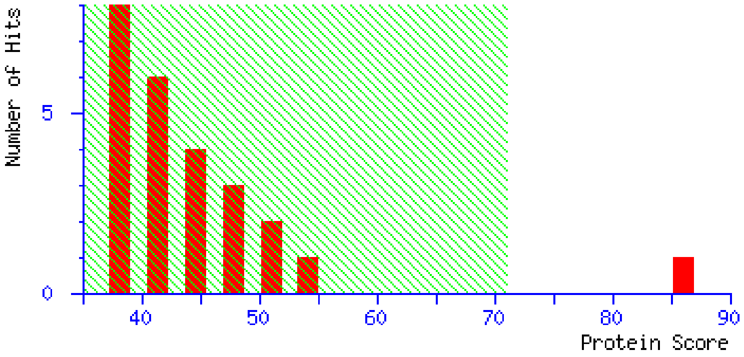
Calculated Mr: **9397** Calculated *p*I: **5.33**

Annotated PMF **spectra:**

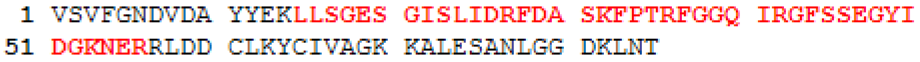


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

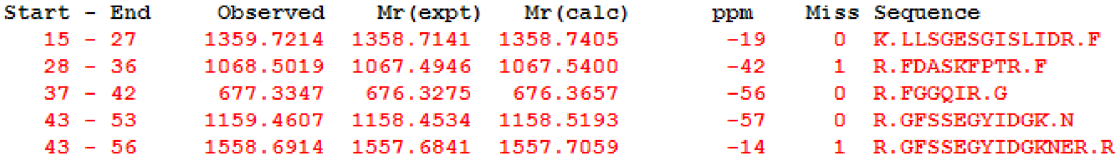


Matched peptide sequences: shown in **Bold Red**



1 VSVFGNDVDA YYEK**LLSGES** **GISLIDRFDA** **SKFPTRFGGQ** **IRGFSSEGYI**
51 **DGKNER**RLDD CLKYCIVAGK KALESANLGG DKLNT

Matched peptides information:



```
Start - End     Observed    Mr(expt)    Mr(calc)       ppm     Miss Sequence
   15 - 27     1359.7214   1358.7141   1358.7405       -19      0   K.LLSGESGISLIDR.F
   28 - 36     1068.5019   1067.4946   1067.5400       -42      1   R.FDASKFPTR.F
   37 - 42      677.3347    676.3275    676.3657       -56      0   R.FGGQIR.G
   43 - 53     1159.4607   1158.4534   1158.5193       -57      0   R.GFSSEGYIDGK.N
   43 - 56     1558.6914   1557.6841   1557.7059       -14      1   R.GFSSEGYIDGKNER.R
```

Spot No.: **115**

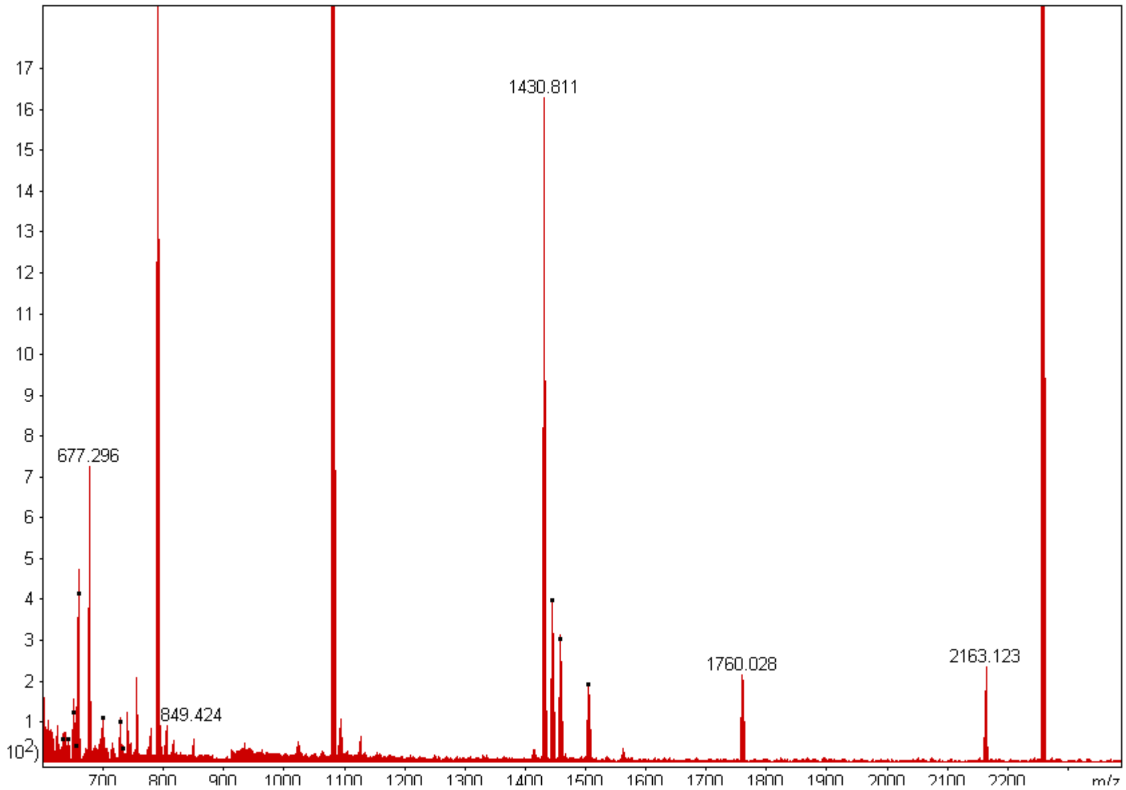
Mascot score: **116** Sequence coverage %: **20**

NCBI accession No.: **gi| 15231702**

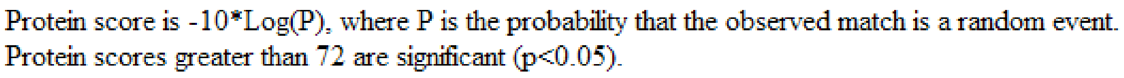
Matched peptides No.: **12** Total peptides No.: **26**

Calculated Mr: **46629** Calculated *p*I: **6.41**

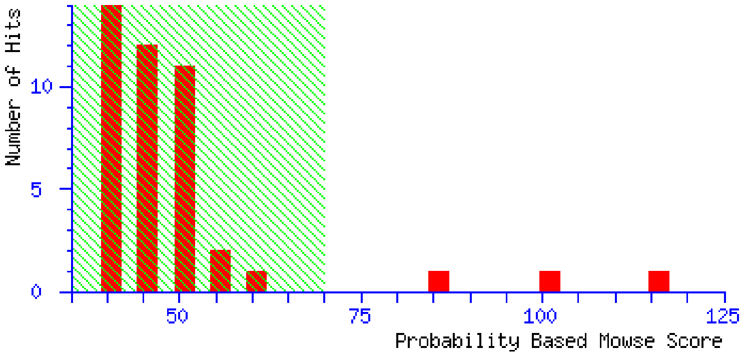
Annotated PMF **spectra:**



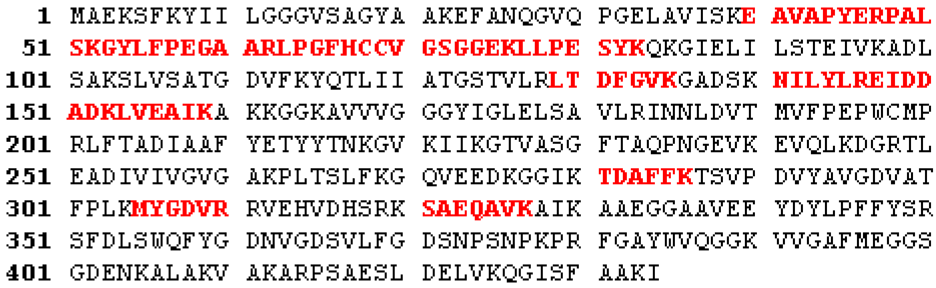
Probability Based Mowse Score:



Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

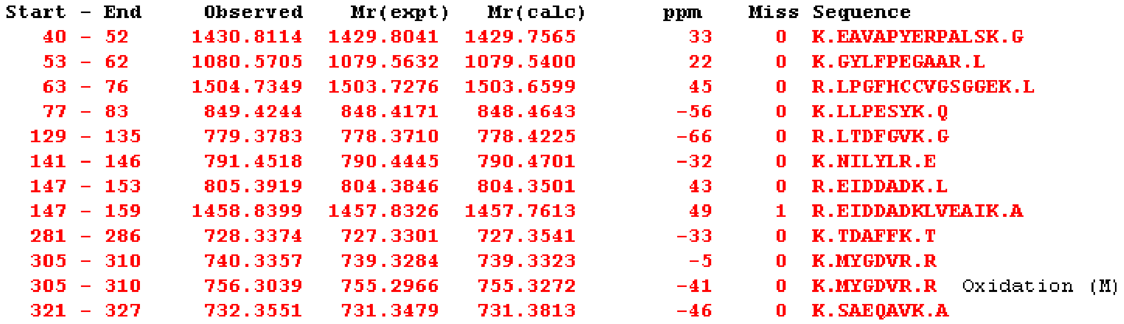


Matched peptide sequences: shown in **Bold Red**



```
  1 MAEKSFKYII LGGGVSAGYA AKEFANQGVQ PGELAVISKE AVAPYERPAL
 51 SKGYLFPEGA ARLPGFHCCV GSGGEKLLPE SYKQKGIELI LSTEIVKADL
101 SAKSLVSATG DVFKYQTLII ATGSTVLRLT DFGVKGADSK NILYLREIDD
151 ADKLVEAIKA KKGGKAVVVG GGYIGLELSA VLRINNLDVT MVFPEPWCMP
201 RLFTADIAAF YETYYTNKGV KIIKGTVASG FTAQPNGEVK EVQLKDGRTL
251 EADIVIVGVG AKPLTSLFKG QVEEDKGGIK TDAFFKTSVP DVYAVGDVAT
301 FPLKMYGDVR RVEHVDHSRK SAEQAVKAIK AAEGGAAVEE YDYLPFFYSR
351 SFDLSWQFYG DNVGDSVLFG DSNPSNPKPR FGAYWVQGGK VVGAFMEGGS
401 GDENKALAKV AKARPSAESL DELVKQGISF AAKI
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)     ppm   Miss Sequence
   40 - 52     1430.8114  1429.8041  1429.7565      33     0  K.EAVAPYERPALSK.G
   53 - 62     1080.5705  1079.5632  1079.5400      22     0  K.GYLFPEGAAR.L
   63 - 76     1504.7349  1503.7276  1503.6599      45     0  R.LPGFHCCVGSGGEK.L
   77 - 83      849.4244   848.4171   848.4643     -56     0  K.LLPESYK.Q
  129 - 135     779.3783   778.3710   778.4225     -66     0  R.LTDFGVK.G
  141 - 146     791.4518   790.4445   790.4701     -32     0  K.NILYLR.E
  147 - 153     805.3919   804.3846   804.3501      43     0  R.EIDDADK.L
  147 - 159    1458.8399  1457.8326  1457.7613      49     1  R.EIDDADKLVEAIK.A
  281 - 286     728.3374   727.3301   727.3541     -33     0  K.TDAFFK.T
  305 - 310     740.3357   739.3284   739.3323      -5     0  K.MYGDVR.R
  305 - 310     756.3039   755.2966   755.3272     -41     0  K.MYGDVR.R  Oxidation (M)
  321 - 327     732.3551   731.3479   731.3813     -46     0  K.SAEQAVK.A
```

Spot No.: **116**

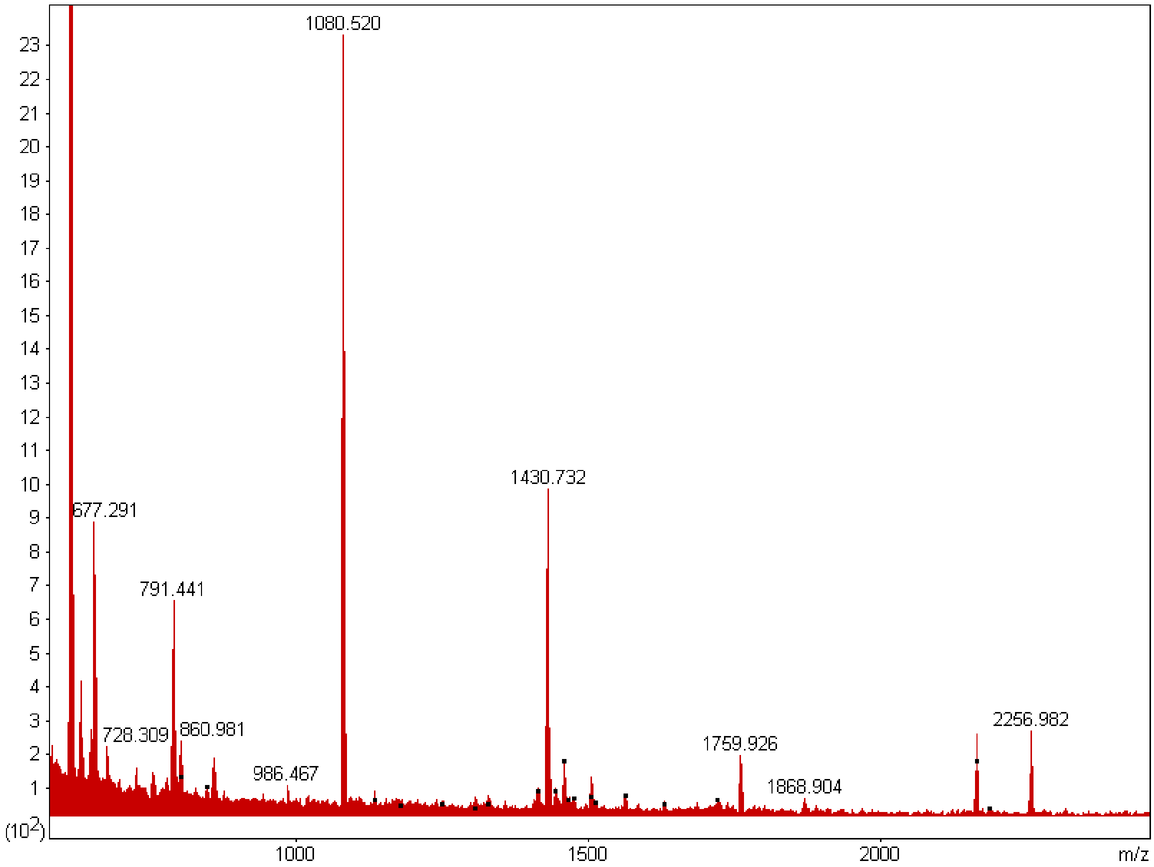
Mascot score: **113** Sequence coverage %: **26**

NCBI accession No.: **gi| 15231702**

Matched peptides No.: **11** Total peptides No.: **25**

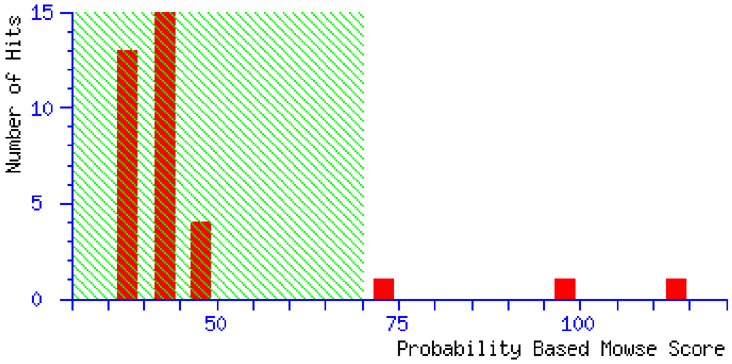
Calculated Mr: **46629** Calculated *p*I: **6.41**

Annotated PMF **spectra:**

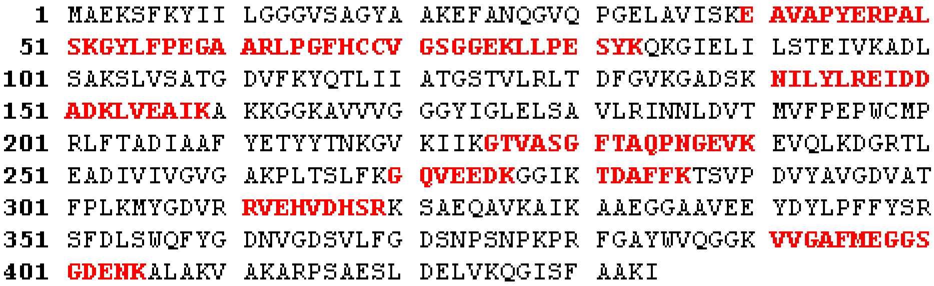


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

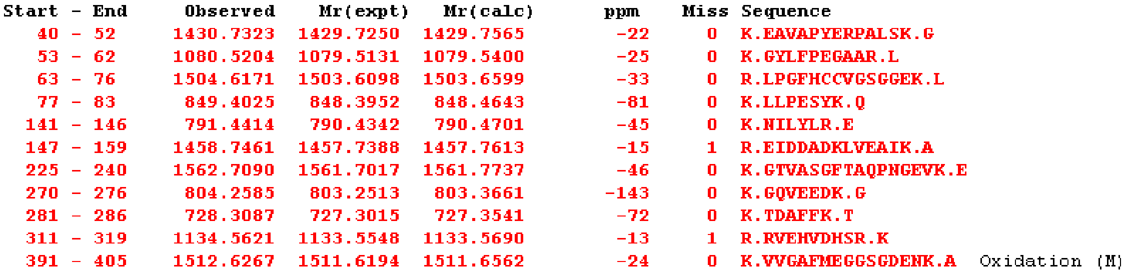


Matched peptide sequences: shown in Bold Red



```
  1 MAEKSFKYII LGGGVSAGYA AKEFANQGVQ PGELAVISKE AVAPYERPAL
 51 SKGYLFPEGA ARLPGFHCCV GSGGEKLLPE SYKQKGIELI LSTEIVKADL
101 SAKSLVSATG DVFKYQTLII ATGSTVLRLT DFGVKGADSK NILYLREIDD
151 ADKLVEAIKA KKGGKAVVVG GGYIGLELSA VLRINNLDVT MVFPEPWCMP
201 RLFTADIAAF YETYYTNKGV KIIKGTVASG FTAQPNGEVK EVQLKDGRTL
251 EADIVIVGVG AKPLTSLFKG QVEEDKGGIK TDAFFKTSVP DVYAVGDVAT
301 FPLKMYGDVR RVEHVDHSRK SAEQAVKAIK AAEGGAAVEE YDYLPFFYSR
351 SFDLSWQFYG DNVGDSVLFG DSNPSNPKPR FGAYWVQGGK VVGAFMEGGS
401 GDENKALAKV AKARPSAESL DELVKQGISF AAKI
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   40 - 52     1430.7323  1429.7250  1429.7565      -22      0  K.EAVAPYERPALSK.G
   53 - 62     1080.5204  1079.5131  1079.5400      -25      0  K.GYLFPEGAAR.L
   63 - 76     1504.6171  1503.6098  1503.6599      -33      0  R.LPGFHCCVGSGGEK.L
   77 - 83      849.4025   848.3952   848.4643      -81      0  K.LLPESYK.Q
  141 - 146     791.4414   790.4342   790.4701      -45      0  K.NILYLR.E
  147 - 159    1458.7461  1457.7388  1457.7613      -15      1  R.EIDDADKLVEAIK.A
  225 - 240    1562.7090  1561.7017  1561.7737      -46      0  K.GTVASGFTAQPNGEVK.E
  270 - 276     804.2585   803.2513   803.3661     -143      0  K.GQVEEDK.G
  281 - 286     728.3087   727.3015   727.3541      -72      0  K.TDAFFK.T
  311 - 319    1134.5621  1133.5548  1133.5690      -13      1  R.RVEHVDHSR.K
  391 - 405    1512.6267  1511.6194  1511.6562      -24      0  K.VVGAFMEGGSGDENK.A  Oxidation (M)
```

Spot No.: **117**

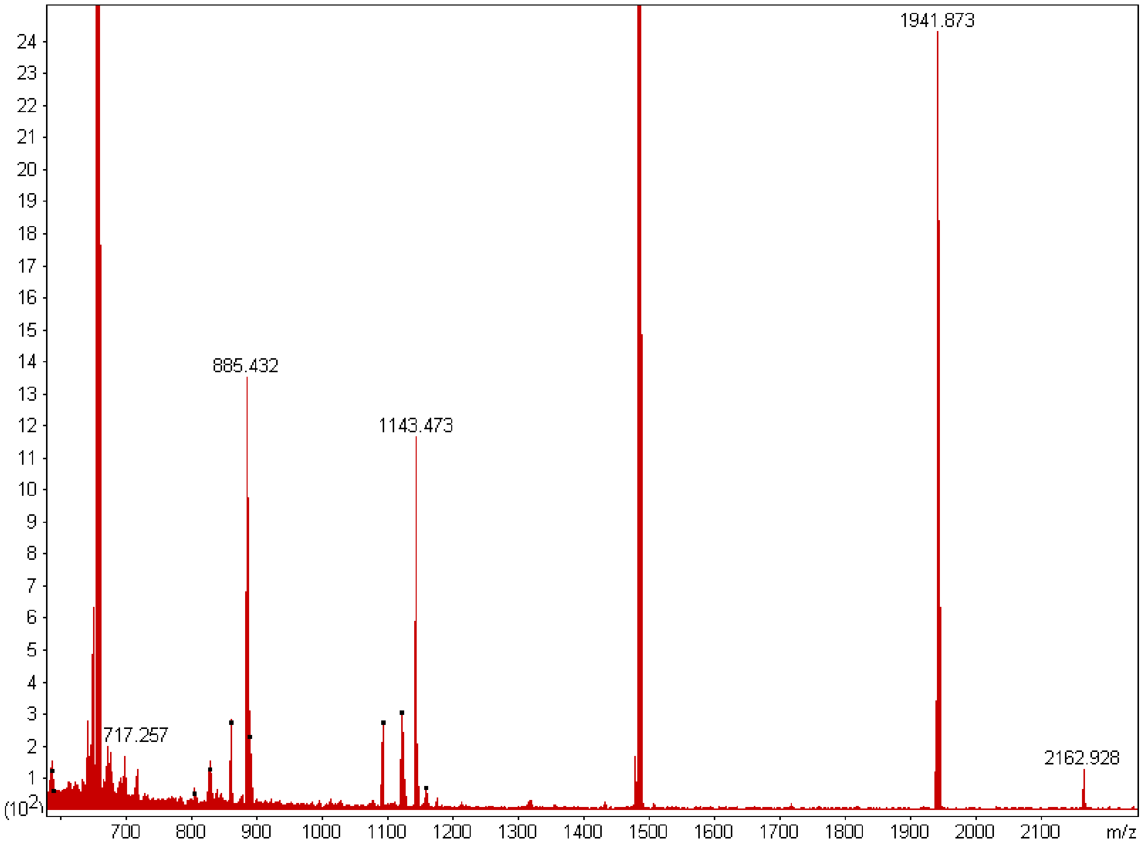
Mascot score: **81**   Sequence coverage %: **17**

NCBI accession No.: **gi| 15226489**

Matched peptides No.: **6**   Total peptides No.: **13**

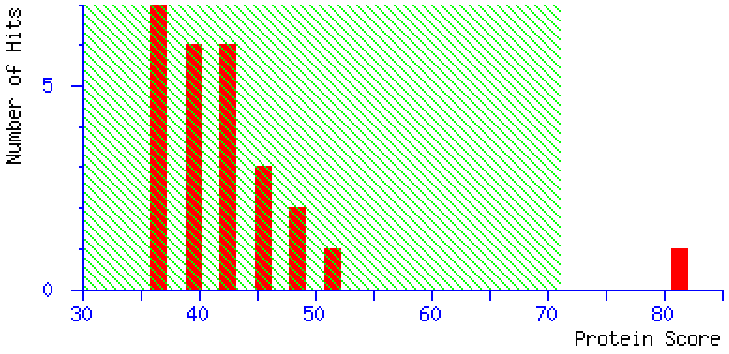
Calculated Mr: **35330**   Calculated *p*I: **6.16**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 MEITLNSGFK **MPIVGLGVWR** MEKEGIRDLI LNAIKIGYRH LDCAADYRNE
51 TEVGDALTEA FKTGLVK**RED** **LFITTK**LWNS DHGHVIEACK DSLKKLQLDY
101 LDLFLVHFPV ATKHTGVGTT DSALGDDGVL DIDTTISLET TWHDMEK**LVS**
151 **MGLVRSIGIS** **NYDVFLTR**DC LAYSKIKPAV NQIETHPYFQ RDSLVKFCQK
201 HGICVTAHTP LGGATANAEW FGTVSCLDDP VLKDVAEKYK K**TVAQVVLRW**
251 **GIQR**KTVVIP KTSKPARLEE NFQVFDFELS KEDMEVIKSM ERKYRTNQPA
301 KFWNIDLYA

Matched peptides information:

```
Start - End     Observed    Mr(expt)   Mr(calc)      ppm    Miss  Sequence
   11 - 20     1143.4733   1142.4660  1142.6270     -141      0   K.MPIVGLGVWR.M   Oxidation (M)
   68 - 76     1122.4540   1121.4467  1121.6081     -144      1   K.REDLFITTK.L
  148 - 155     890.3793    889.3720   889.5055     -150      0   K.LVSMGLVR.S   Oxidation (M)
  156 - 168    1484.6118   1483.6045  1483.7671     -110      0   R.SIGISNYDVFLTR.D
  242 - 249     885.4319    884.4246   884.5444     -135      0   K.TVAQVVLR.W
  250 - 254     659.2794    658.2721   658.3551     -126      0   R.WGIQR.K
```

Spot No.: **118**

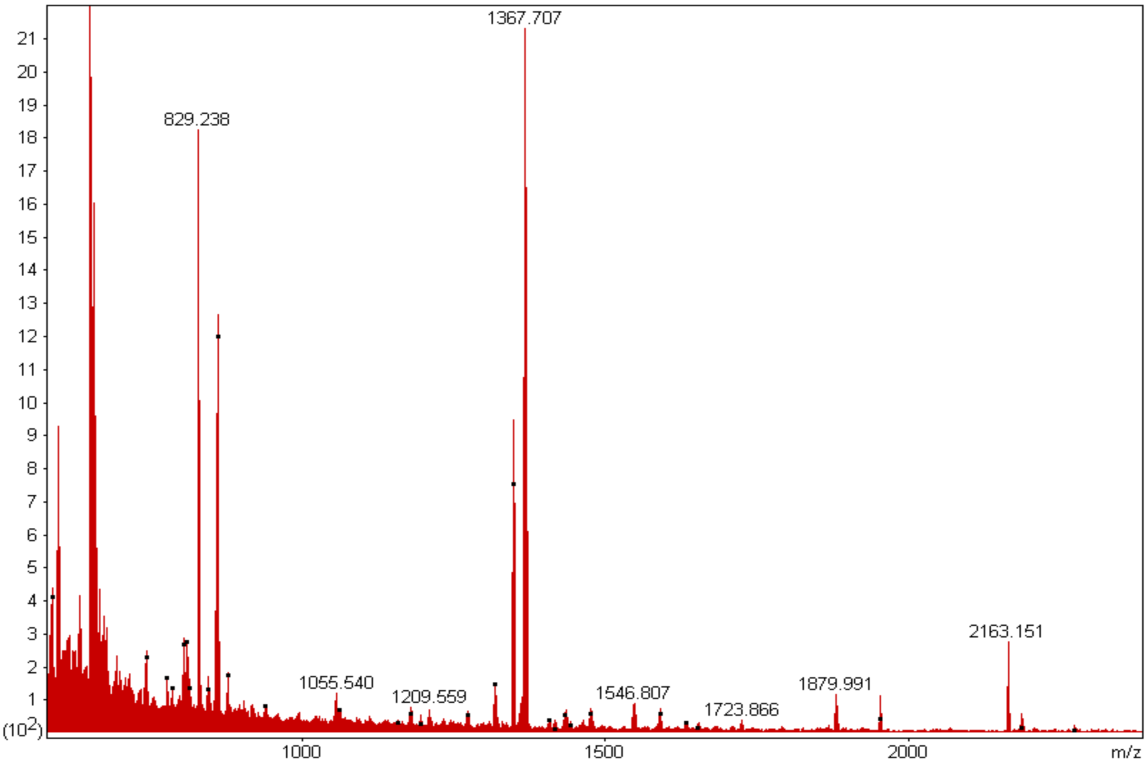
Mascot score: **97**   Sequence coverage %: **38**

NCBI accession No.: **gi| 312281559**

Matched peptides No.: **14**   Total peptides No.: **49**

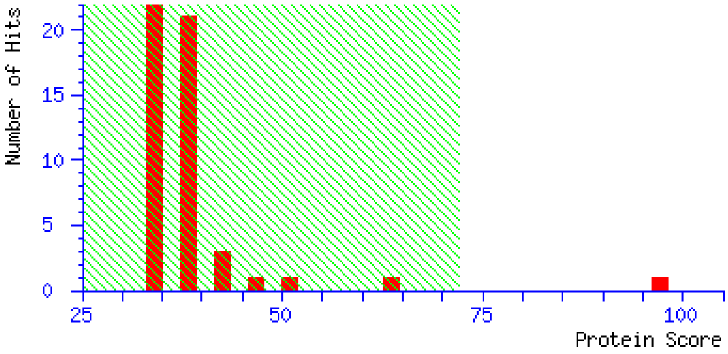
Calculated Mr: **38617**   Calculated *p*I: **5.90**

Annotated PMF **spectra:**

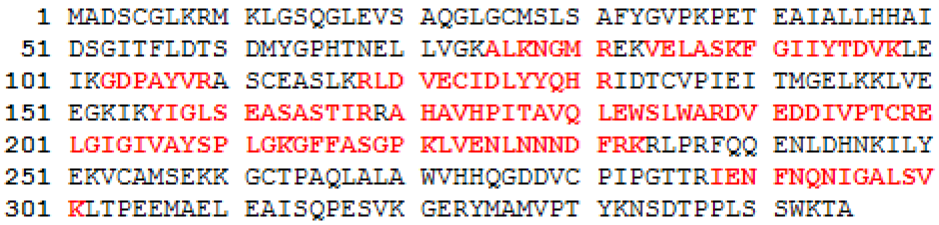


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

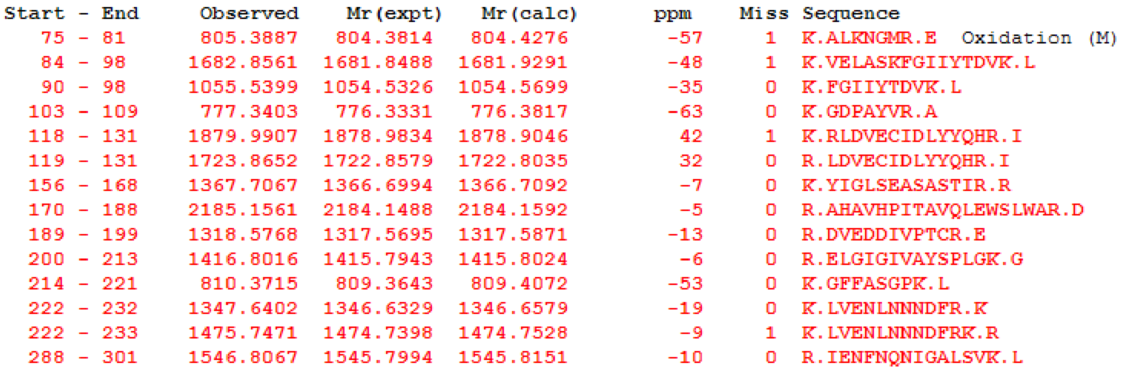


Matched peptide sequences: shown in Bold Red



```
  1 MADSCGLKRM KLGSQGLEVS AQGLGCMSLS AFYGVPKPET EAIALLHHAI
 51 DSGITFLDTS DMYGPHTNEL LVGKALKNGM REKVELASKF GIIYTDVKLE
101 IKGDPAYVRA SCEASLKRLD VECIDLYYQH RIDTCVPIEI TMGELKKLVE
151 EGKIKYIGLS EASASTIRRA HAVHPITAVQ LEWSLWARDV EDDIVPTCRE
201 LGIGIVAYSP LGKGFFASGP KLVENLNNND FRKRLPRFQQ ENLDHNKILY
251 EKVCAMSEKK GCTPAQLALA WVHHQGDDVC PIPGTTRIEN FNQNIGALSV
301 KLTPEEMAEL EAISQPESVK GERYMAMVPT YKNSDTPPLS SWKTA
```

Matched peptides information:



```
Start - End     Observed    Mr(expt)    Mr(calc)      ppm    Miss Sequence
   75 - 81      805.3887    804.3814    804.4276      -57      1  K.ALKNGMR.E   Oxidation (M)
   84 - 98     1682.8561   1681.8488   1681.9291      -48      1  K.VELASKFGIIYTDVK.L
   90 - 98     1055.5399   1054.5326   1054.5699      -35      0  K.FGIIYTDVK.L
  103 - 109     777.3403    776.3331    776.3817      -63      0  K.GDPAYVR.A
  118 - 131    1879.9907   1878.9834   1878.9046       42      1  K.RLDVECIDLYYQHR.I
  119 - 131    1723.8652   1722.8579   1722.8035       32      0  R.LDVECIDLYYQHR.I
  156 - 168    1367.7067   1366.6994   1366.7092       -7      0  K.YIGLSEASASTIR.R
  170 - 188    2185.1561   2184.1488   2184.1592       -5      0  R.AHAVHPITAVQLEWSLWAR.D
  189 - 199    1318.5768   1317.5695   1317.5871      -13      0  R.DVEDDIVPTCR.E
  200 - 213    1416.8016   1415.7943   1415.8024       -6      0  R.ELGIGIVAYSPLGK.G
  214 - 221     810.3715    809.3643    809.4072      -53      0  K.GFFASGPK.L
  222 - 232    1347.6402   1346.6329   1346.6579      -19      0  K.LVENLNNNDFR.K
  222 - 233    1475.7471   1474.7398   1474.7528       -9      1  K.LVENLNNNDFRK.R
  288 - 301    1546.8067   1545.7994   1545.8151      -10      0  R.IENFNQNIGALSVK.L
```

Spot No.: **119**

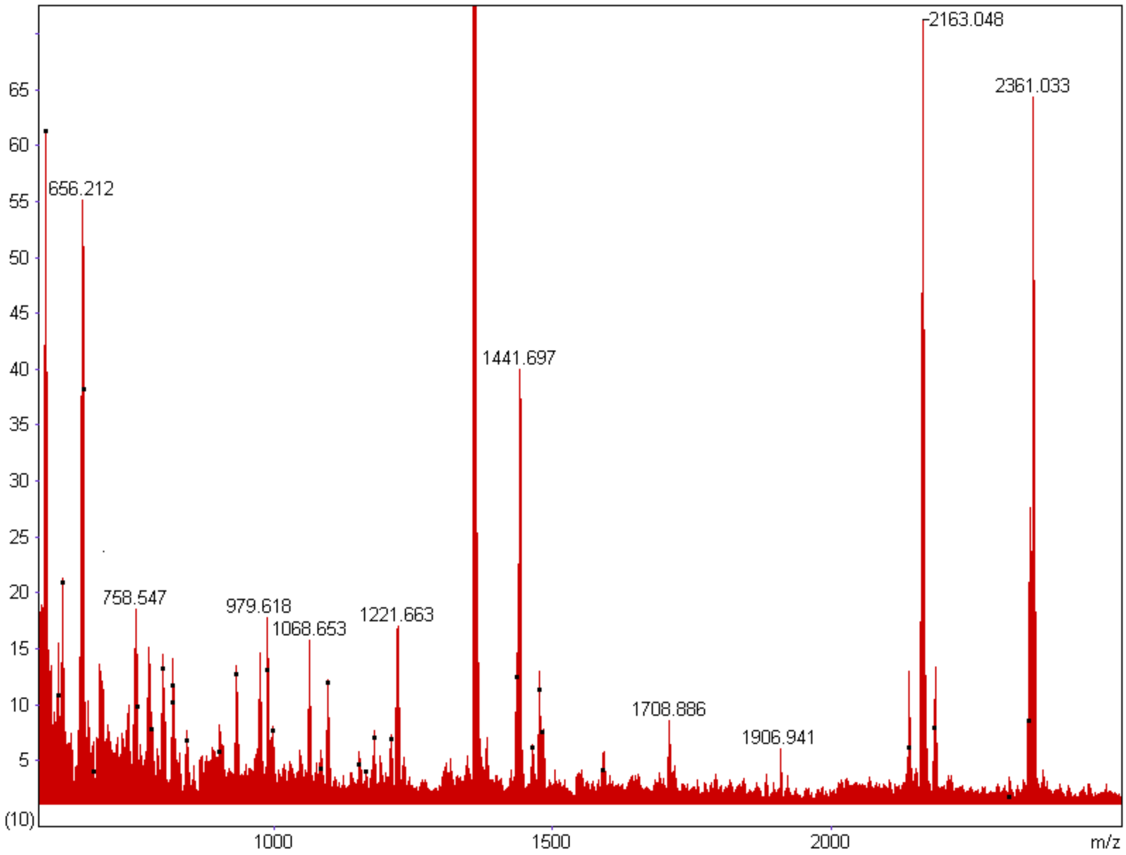
Mascot score: **129** Sequence coverage %: **30**

NCBI accession No.: **gi| 15226610**

Matched peptides No.: **13** Total peptides No.: **33**

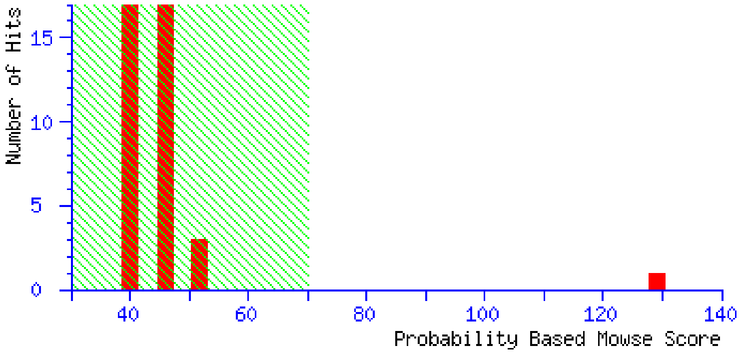
Calculated Mr: **39815** Calculated *p*I: **5.80**

Annotated PMF **spectra:**

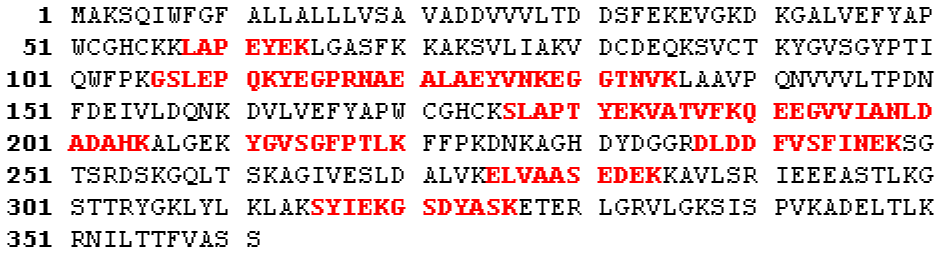


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

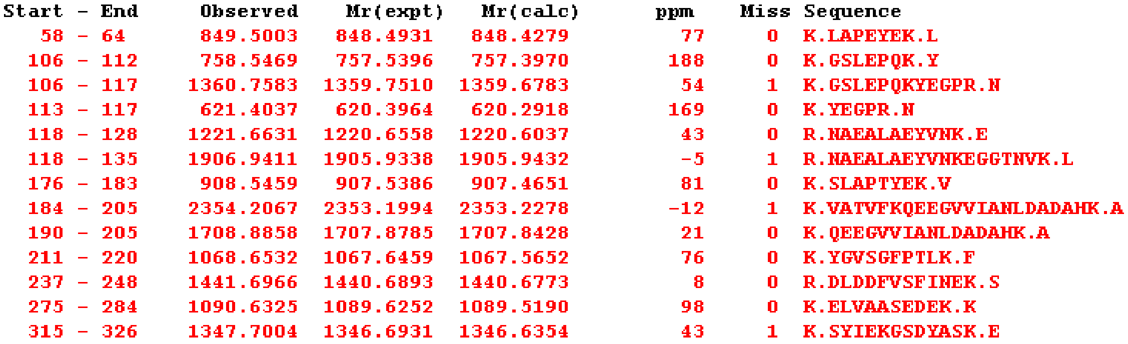


Matched peptide sequences: shown in Bold Red



```
  1 MAKSQIWFGF ALLALLLVSA VADDVVVLTD DSFEKEVGKD KGALVEFYAP
 51 WCGHCKKLAP EYEKLGASFK KAKSVLIAKV DCDEQKSVCT KYGVSGYPTI
101 QWFPKGSLEP QKYEGPRNAE ALAEYVNKEG GTNVKLAAVP QNVVVLTPDN
151 FDEIVLDQNK DVLVEFYAPW CGHCKSLAPT YEKVATVFKQ EEGVVIANLD
201 ADAHKALGEK YGVSGFPTLK FFPKDNKAGH DYDGGRDLDD FVSFINEKSG
251 TSRDSKGQLT SKAGIVESLD ALVKELVAAS EDEKKAVLSR IEEEASTLKG
301 STTRYGKLYL KLAKSYIEKG SDYASKETER LGRVLGKSIS PVKADELTLK
351 RNILTTFVAS S
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   58 - 64      849.5003   848.4931   848.4279       77      0  K.LAPEYEK.L
  106 - 112     758.5469   757.5396   757.3970      188      0  K.GSLEPQK.Y
  106 - 117    1360.7583  1359.7510  1359.6783       54      1  K.GSLEPQKYEGPR.N
  113 - 117     621.4037   620.3964   620.2918      169      0  K.YEGPR.N
  118 - 128    1221.6631  1220.6558  1220.6037       43      0  R.NAEALAEYVNK.E
  118 - 135    1906.9411  1905.9338  1905.9432       -5      1  R.NAEALAEYVNKEGGTNVK.L
  176 - 183     908.5459   907.5386   907.4651       81      0  K.SLAPTYEK.V
  184 - 205    2354.2067  2353.1994  2353.2278      -12      1  K.VATVFKQEEGVVIANLDADAHK.A
  190 - 205    1708.8858  1707.8785  1707.8428       21      0  K.QEEGVVIANLDADAHK.A
  211 - 220    1068.6532  1067.6459  1067.5652       76      0  K.YGVSGFPTLK.F
  237 - 248    1441.6966  1440.6893  1440.6773        8      0  R.DLDDFVSFINEK.S
  275 - 284    1090.6325  1089.6252  1089.5190       98      0  K.ELVAASEDEK.K
  315 - 326    1347.7004  1346.6931  1346.6354       43      1  K.SYIEKGSDYASK.E
```

Spot No.: **120**

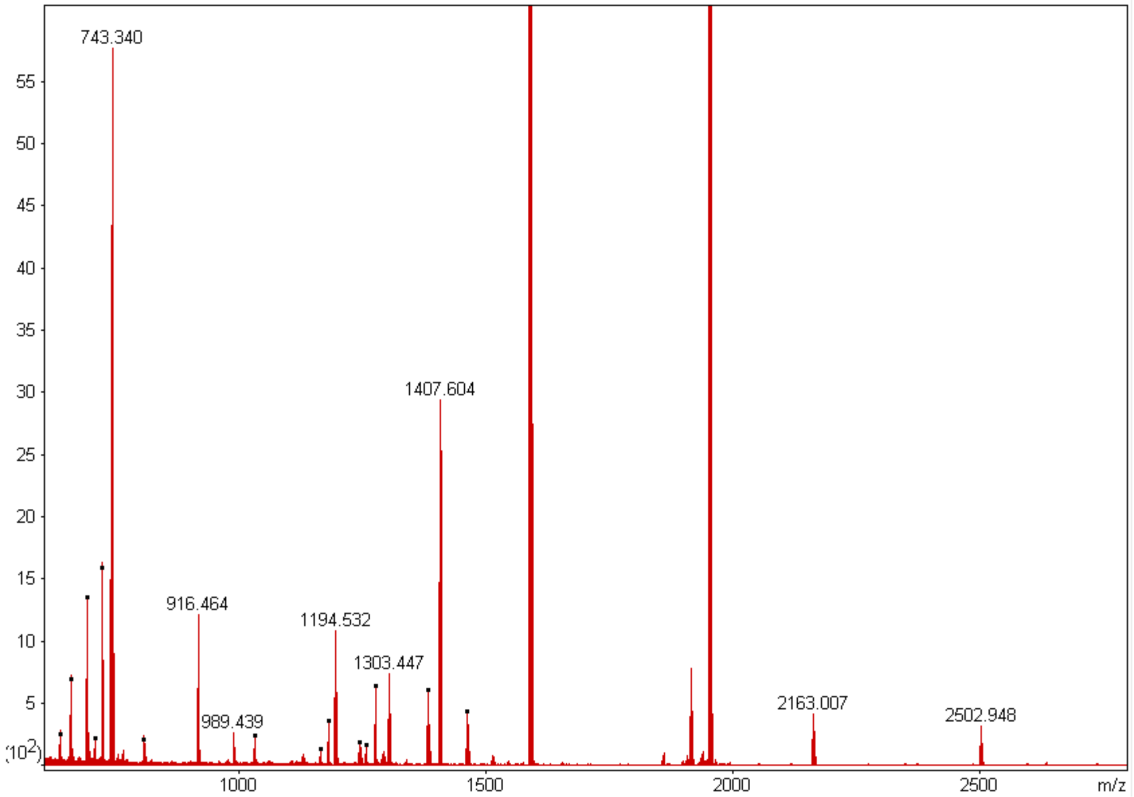
Mascot score: **85**   Sequence coverage %: **14**

NCBI accession No.: **gi| 1145344987**

Matched peptides No.: **11**   Total peptides No.: **17**

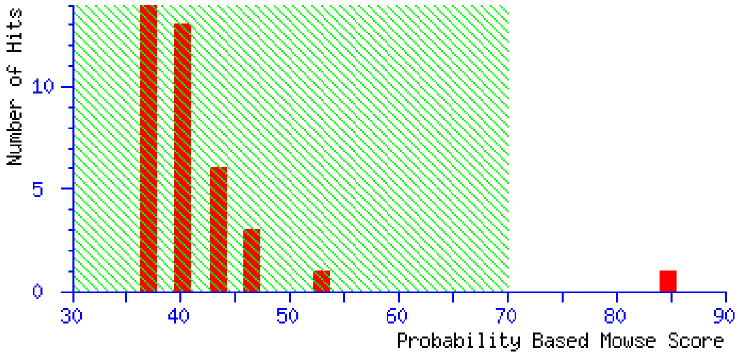
Calculated Mr: **76292**   Calculated *p*I: **5.49**

Annotated PMF **spectra:**

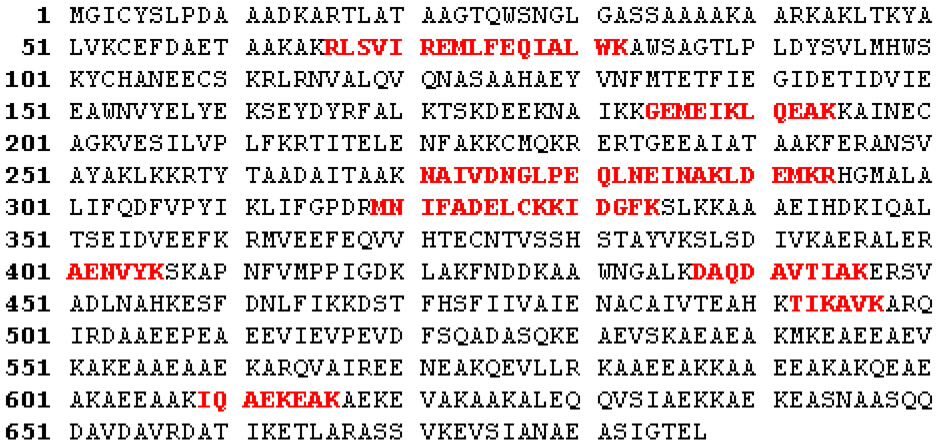


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant ($p<0.05$).

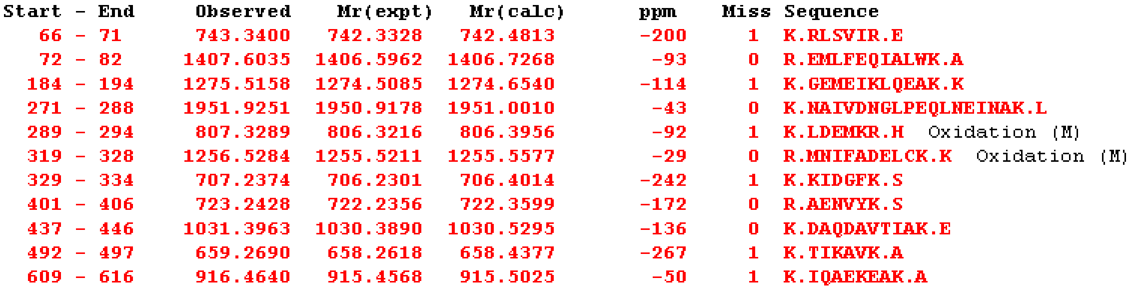


Matched peptide sequences: shown in Bold Red



```
  1 MGICYSLPDA AADKARTLAT AAGTQWSNGL GASSAAAAKA ARKAKLTKYA
 51 LVKCEFDAET AAKAKRLSVI REMLFEQIAL WKAWSAGTLP LDYSVLMHWS
101 KYCHANEECS KRLRNVALQV QNASAAHAEY VNFMTETFIE GIDETIDVIE
151 EAWNVYELYE KSEYDYRFAL KTSKDEEKNA IKKGEMEIKL QEAKKAINEC
201 AGKVESILVP LFKRTITELE NFAKKCMQKR ERTGEEAIAT AAKFERANSV
251 AYAKLKKRTY TAADAITAAK NAIVDNGLPE QLNEINAKLD EMKRHGMALA
301 LIFQDFVPYI KLIFGPDRMN IFADELCKKI DGFKSLKKAA AEIHDKIQAL
351 TSEIDVEEFK RMVEEFEQVV HTECNTVSSH STAYVKSLSD IVKAERALER
401 AENVYKSKAP NFVMPPIGDK LAKFNDDKAA WNGALKDAQD AVTIAKERSV
451 ADLNAHKESF DNLFIKKDST FHSFIIVAIE NACAIVTEAH KTIKAVKARQ
501 IRDAAEEPEA EEVIEVPEVD FSQADASQKE AEVSKAEAEA KMKEAEEAEV
551 KAKEAAEAAE KARQVAIREE NEAKQEVLLR KAAEEAKKAA EEAKAKQEAE
601 AKAEEAAKIQ AEKEAKAEKE VAKAAKALEQ QVSIAEKKAE KEASNAASQQ
651 DAVDAVRDAT IKETLARASS VKEVSIANAE ASIGTEL
```

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
66 - 71	743.3400	742.3328	742.4813	-200	1	K.RLSVIR.E	
72 - 82	1407.6035	1406.5962	1406.7268	-93	0	R.EMLFEQIALWK.A	
184 - 194	1275.5158	1274.5085	1274.6540	-114	1	K.GEMEIKLQEAK.K	
271 - 288	1951.9251	1950.9178	1951.0010	-43	0	K.NAIVDNGLPEQLNEINAK.L	
289 - 294	807.3289	806.3216	806.3956	-92	1	K.LDEMKR.H	Oxidation (M)
319 - 328	1256.5284	1255.5211	1255.5577	-29	0	R.MNIFADELCK.K	Oxidation (M)
329 - 334	707.2374	706.2301	706.4014	-242	1	K.KIDGFK.S	
401 - 406	723.2428	722.2356	722.3599	-172	0	R.AENVYK.S	
437 - 446	1031.3963	1030.3890	1030.5295	-136	0	K.DAQDAVTIAK.E	
492 - 497	659.2690	658.2618	658.4377	-267	1	K.TIKAVK.A	
609 - 616	916.4640	915.4568	915.5025	-50	1	K.IQAEKEAK.A	

Spot No.: **121**

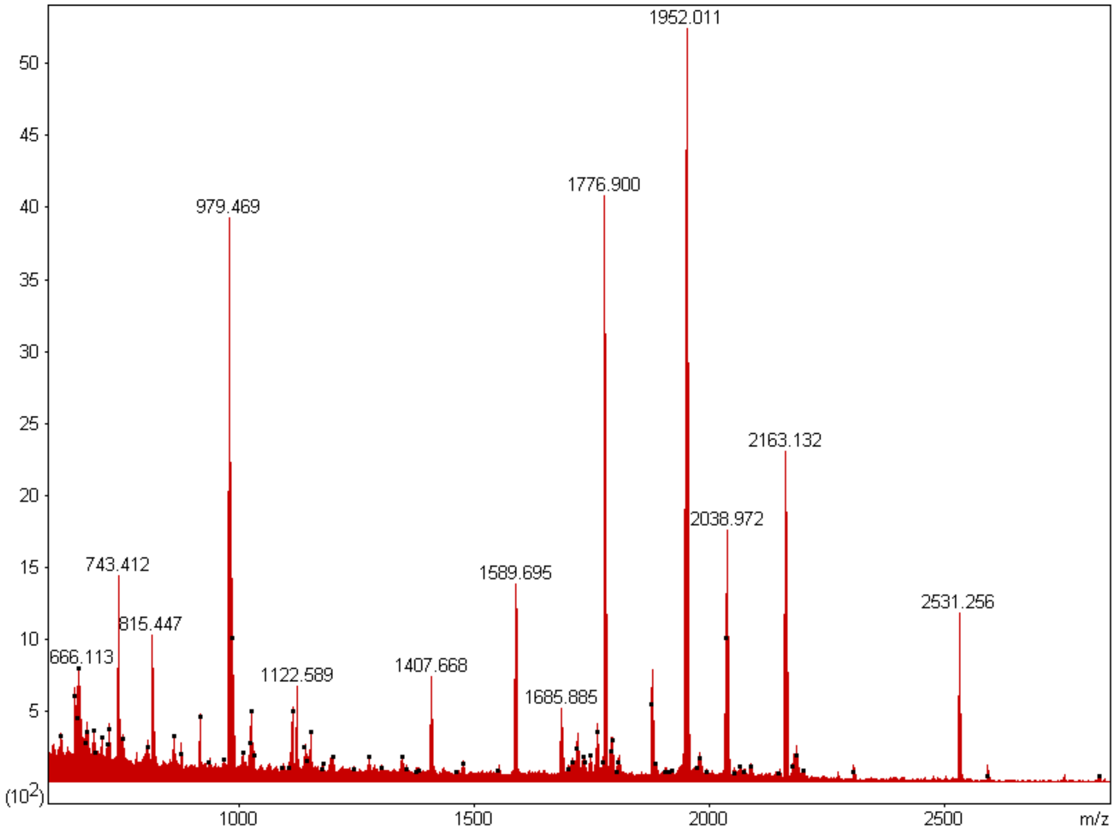
Mascot score: **83** Sequence coverage %: **22**

NCBI accession No.: **gi| 26450910**

Matched peptides No.: **10** Total peptides No.: **48**

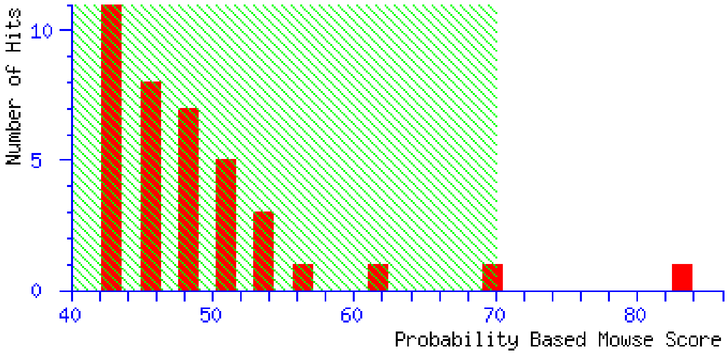
Calculated Mr: **68864** Calculated *p*I: **8.70**

Annotated PMF **spectra:**

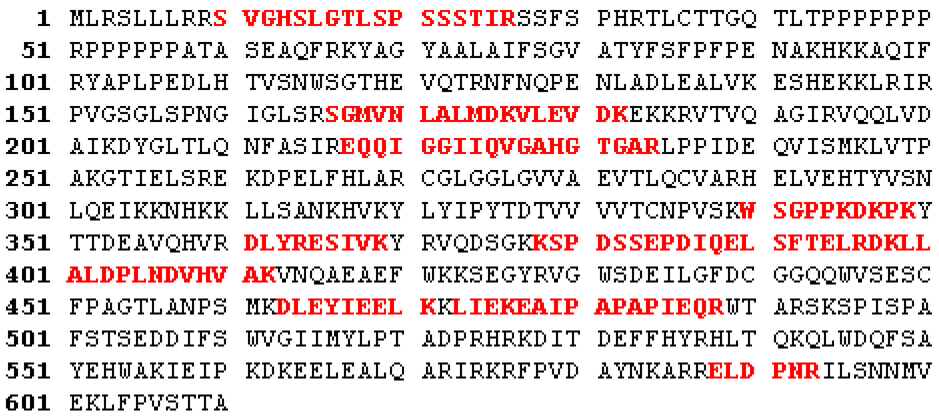


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

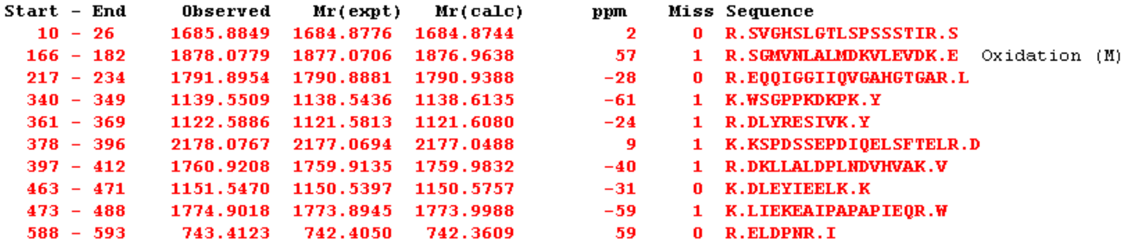


Matched peptide sequences: shown in Bold Red



1 MLRSLLLRR**S** **VGHSLGTLSP** **SSSTIR**SSFS PHRTLCTTGQ TLTPPPPPPP
51 RPPPPPPATA SEAQFRKYAG YAALAIFSGV ATYFSFPFPE NAKHKKAQIF
101 RYAPLPEDLH TVSNWSGTHE VQTRNFNQPE NLADLEALVK ESHEKKLRIR
151 PVGSGLSPNG IGLSR**SGMVN** **LALMDKVLEV** **DK**EKKRVTVQ AGIRVQQLVD
201 AIKDYGLTLQ NFASIR**EQQI** **GGIIQVGAHG** **TGAR**LPPIDE QVISMKLVTP
251 AKGTIELSRE KDPELFHLAR CGLGGLGVVA EVTLQCVARH ELVEHTYVSN
301 LQEIKKNHKK LLSANKHVKY LYIPYTDTVV VVTCNPVSK**W** **SGPPKDKPK**Y
351 TTDEAVQHVR **DLYRESIVK**Y RVQDSGK**KSP** **DSSEPDIQEL** **SFTELRDKLL**
401 **ALDPLNDVHV** **AK**VNQAEAEF WKKSEGYRVG WSDEILGFDC GGQQWVSESC
451 FPAGTLANPS MK**DLEYIEEL** **KKLIEKEAIP** **APAPIEQR**WT ARSKSPISPA
501 FSTSEDDIFS WVGIIMYLPT ADPRHRKDIT DEFFHYRHLT QKQLWDQFSA
551 YEHWAKIEIP KDKEELEALQ ARIRKRFPVD AYNKARR**ELD** **PNR**ILSNNMV
601 EKLFPVSTTA

Matched peptides information:



```
Start - End      Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   10 - 26      1685.8849  1684.8776  1684.8744        2      0  R.SVGHSLGTLSPSSSTIR.S
  166 - 182     1878.0779  1877.0706  1876.9638       57      1  R.SGMVNLALMDKVLEVDK.E  Oxidation (M)
  217 - 234     1791.8954  1790.8881  1790.9388      -28      0  R.EQQIGGIIQVGAHGTGAR.L
  340 - 349     1139.5509  1138.5436  1138.6135      -61      1  K.WSGPPKDKPK.Y
  361 - 369     1122.5886  1121.5813  1121.6080      -24      1  R.DLYRESIVK.Y
  378 - 396     2178.0767  2177.0694  2177.0488        9      1  K.KSPDSSEPDIQELSFTELR.D
  397 - 412     1760.9208  1759.9135  1759.9832      -40      1  R.DKLLALDPLNDVHVAK.V
  463 - 471     1151.5470  1150.5397  1150.5757      -31      0  K.DLEYIEELK.K
  473 - 488     1774.9018  1773.8945  1773.9988      -59      1  K.LIEKEAIPAPAPIEQR.W
  588 - 593      743.4123   742.4050   742.3609       59      0  R.ELDPNR.I
```

Spot No.: **122**

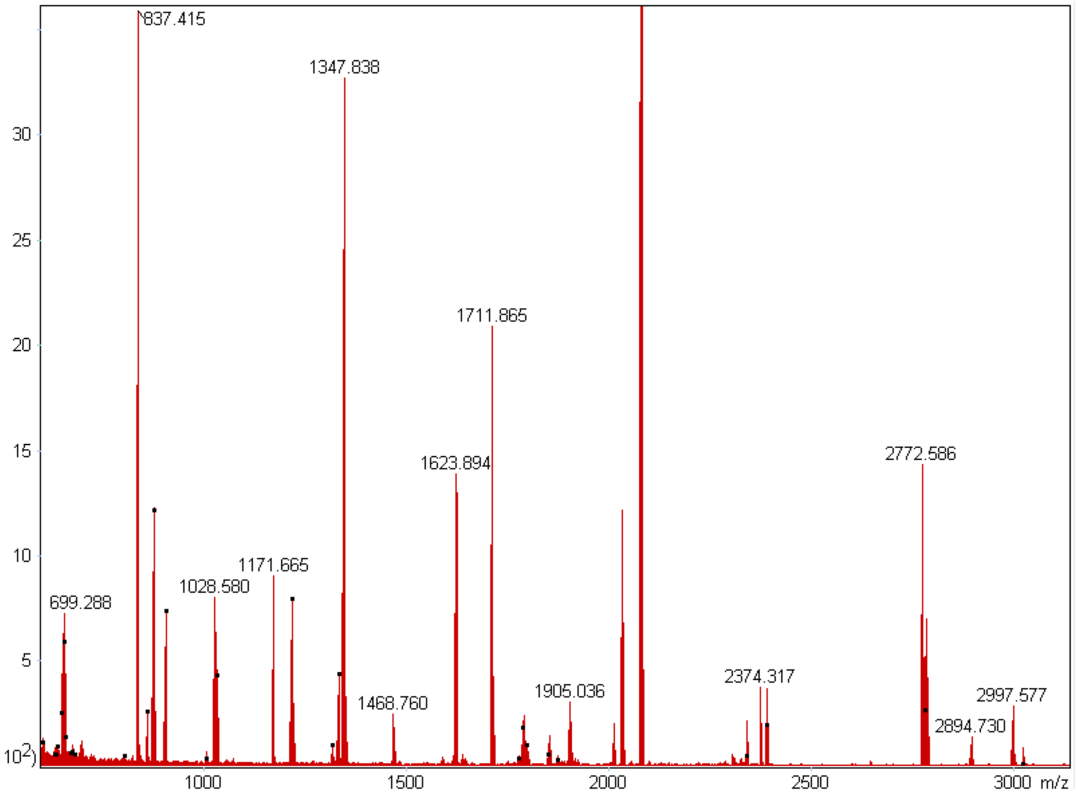
Mascot score: **126** Sequence coverage %: **40**

NCBI accession No.: **gi| 207667274**

Matched peptides No.: **11** Total peptides No.: **26**

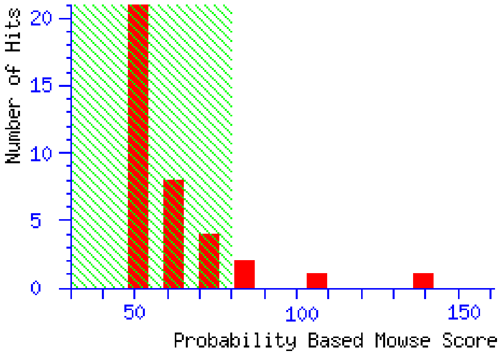
Calculated Mr: **42520** Calculated *p*I: **8.51**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 MAAASSISIG STVPRASSSS SSSSLPQSRA QAVNFNYSLP RFTALRSSTL
51 LSGLDSSSFA KSLRGSVTKP QSTDTKPYGL NINASYK**VAV** **LGAAGGIGQP**
101 **LSLLIK**MSPL VSTLHLYDIA NVK**GVAADLS** **HCNTPSQVR**D FTGPAELADC
151 LK**DVNVVVIP** **AGVPR**KPGMT R**DDLFNINAG** **IVK**TLVEAVA DNCPNAFIHI
201 ISNPVNSTVP IAAEVLRKKG VYDPK**KLFGV** **TTLDVVR**ANT FVSQKKNLK**L**
251 **IDVDVPVIGG** **HAGITILPLL** **SKTKPSVSFT** **DEEIEKLTVR** IQNAGTEVVD
301 AK**AGAGSATL** **SMAYAAARFV** **ESSLRALDGD** **GDVYECSFVD** **STLTDLPFFA**
351 **SR**IKIGRNGV EAVIESDLQG LTEYEHKALE ALKPELKASI EKGVAFANKP
401 AN

Matched peptides information:

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
88 - 106	1777.1096	1776.1023	1776.0873	8	0	K.VAVLGAAGGIGQPLSLLIK.M
124 - 139	1711.8653	1710.8580	1710.8108	28	0	K.GVAADLSHCNTPSQVR.D
153 - 165	1334.7995	1333.7922	1333.7718	15	0	K.DVNVVVIPAGVPR.K
172 - 183	1318.6895	1317.6822	1317.6929	-8	0	R.DDLFNINAGIVK.T
226 - 237	1347.8376	1346.8303	1346.7922	28	1	K.KLFGVTTLDVVR.A
227 - 237	1219.7223	1218.7150	1218.6972	15	0	K.LFGVTTLDVVR.A
250 - 272	2340.4358	2339.4285	2339.3828	20	0	K.LIDVDVPVIGGHAGITILPLLSK.T
273 - 290	2079.1512	2078.1439	2078.0895	26	1	K.TKPSVSFTDEEIEKLTVR.I
303 - 318	1468.7600	1467.7527	1467.7140	26	0	K.AGAGSATLSMAYAAAR.F
319 - 325	837.4154	836.4081	836.4392	-37	0	R.FVESSLR.A
326 - 352	2997.5770	2996.5697	2996.3386	77	0	R.ALDGDGDVYECSFVDSTLTDLPFFASR.I

Spot No.: **123**

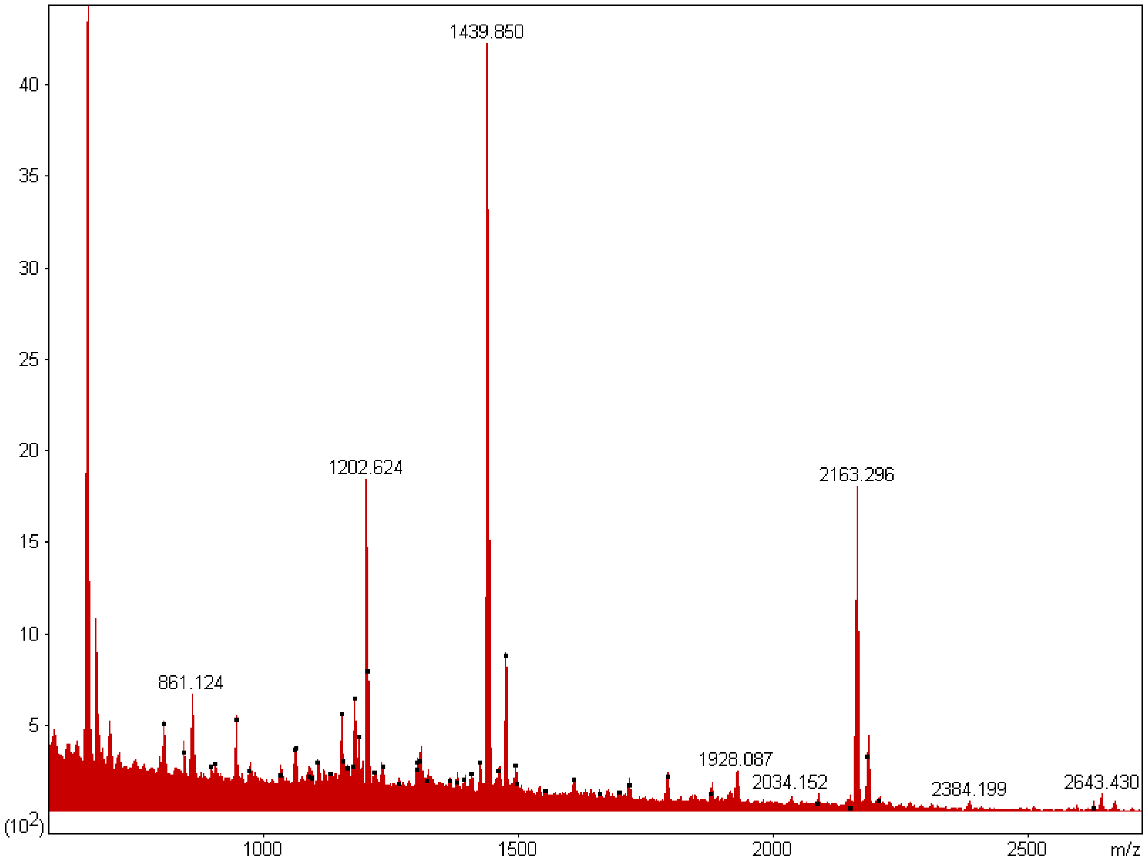
Mascot score: **88**   Sequence coverage %: **30**

NCBI accession No.: **gi| 9454574**

Matched peptides No.: **11**   Total peptides No.: **43**

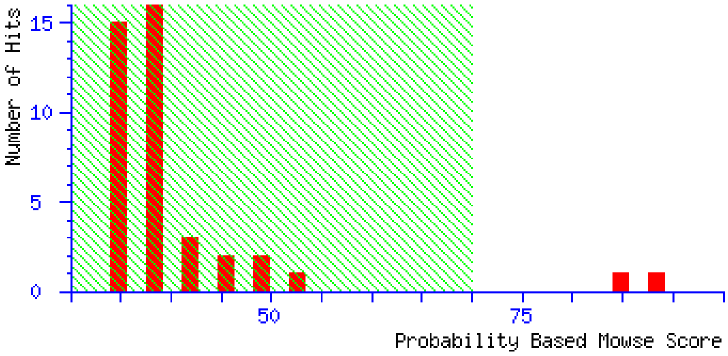
Calculated Mr: **33474**   Calculated *p*I: **7.03**

Annotated PMF **spectra:**

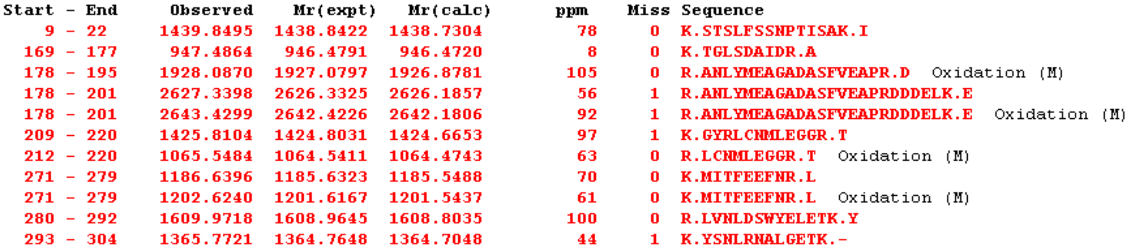


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

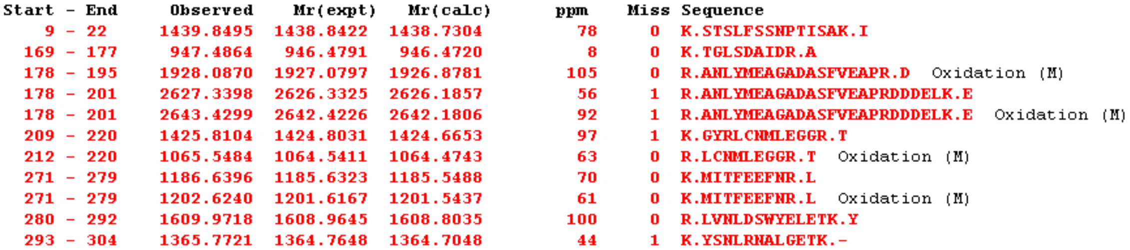


Matched peptide sequences: shown in Bold Red



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    9 - 22     1439.8495  1438.8422  1438.7304       78      0  K.STSLFSSNPTISAK.I
  169 - 177     947.4864   946.4791   946.4720        8      0  K.TGLSDAIDR.A
  178 - 195    1928.0870  1927.0797  1926.8781      105      0  R.ANLYMEAGADASFVEAPR.D  Oxidation (M)
  178 - 201    2627.3398  2626.3325  2626.1857       56      1  R.ANLYMEAGADASFVEAPRDDDELK.E
  178 - 201    2643.4299  2642.4226  2642.1806       92      1  R.ANLYMEAGADASFVEAPRDDDELK.E  Oxidation (M)
  209 - 220    1425.8104  1424.8031  1424.6653       97      1  K.GYRLCNMLEGGR.T
  212 - 220    1065.5484  1064.5411  1064.4743       63      0  R.LCNMLEGGR.T  Oxidation (M)
  271 - 279    1186.6396  1185.6323  1185.5488       70      0  K.MITFEEFNR.L
  271 - 279    1202.6240  1201.6167  1201.5437       61      0  K.MITFEEFNR.L  Oxidation (M)
  280 - 292    1609.9718  1608.9645  1608.8035      100      0  R.LVNLDSWYELETK.Y
  293 - 304    1365.7721  1364.7648  1364.7048       44      1  K.YSNLRNALGETK.-
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    9 - 22     1439.8495  1438.8422  1438.7304       78      0  K.STSLFSSNPTISAK.I
  169 - 177     947.4864   946.4791   946.4720        8      0  K.TGLSDAIDR.A
  178 - 195    1928.0870  1927.0797  1926.8781      105      0  R.ANLYMEAGADASFVEAPR.D  Oxidation (M)
  178 - 201    2627.3398  2626.3325  2626.1857       56      1  R.ANLYMEAGADASFVEAPRDDDELK.E
  178 - 201    2643.4299  2642.4226  2642.1806       92      1  R.ANLYMEAGADASFVEAPRDDDELK.E  Oxidation (M)
  209 - 220    1425.8104  1424.8031  1424.6653       97      1  K.GYRLCNMLEGGR.T
  212 - 220    1065.5484  1064.5411  1064.4743       63      0  R.LCNMLEGGR.T  Oxidation (M)
  271 - 279    1186.6396  1185.6323  1185.5488       70      0  K.MITFEEFNR.L
  271 - 279    1202.6240  1201.6167  1201.5437       61      0  K.MITFEEFNR.L  Oxidation (M)
  280 - 292    1609.9718  1608.9645  1608.8035      100      0  R.LVNLDSWYELETK.Y
  293 - 304    1365.7721  1364.7648  1364.7048       44      1  K.YSNLRNALGETK.-
```

Spot No.: **124**

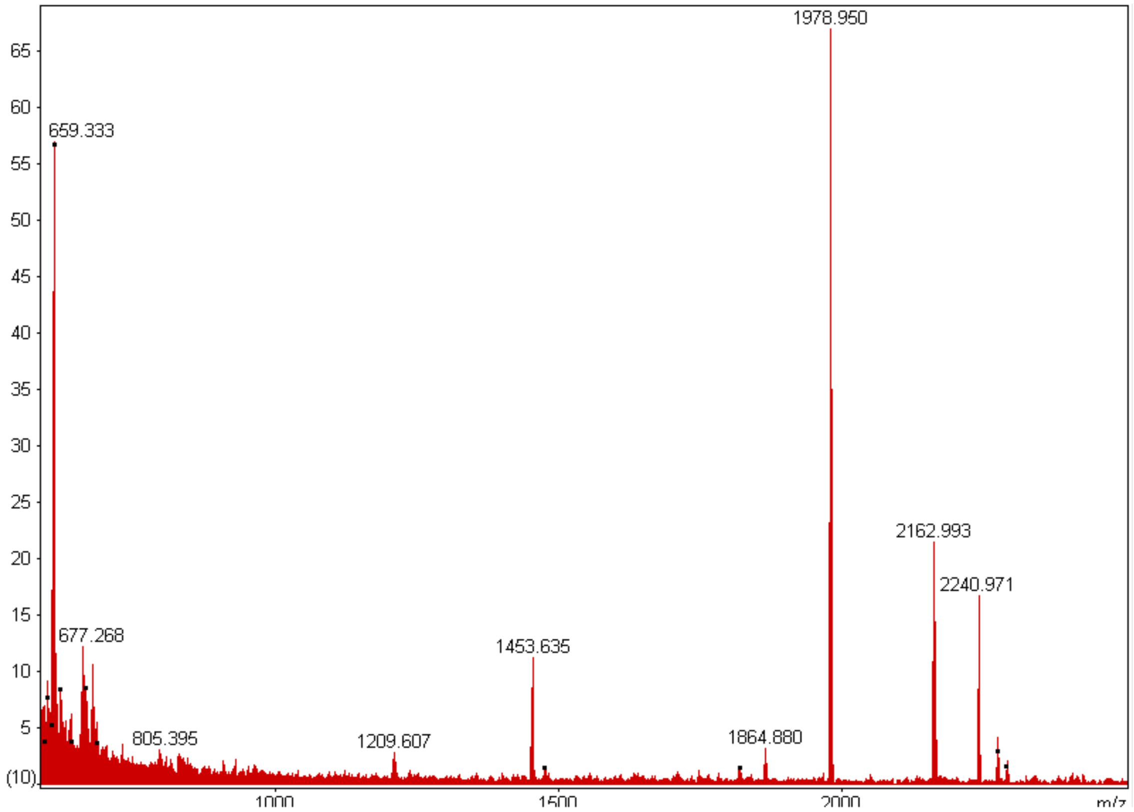
Mascot score: **94** Sequence coverage %: **22**

NCBI accession No.: **gi| 22330196**

Matched peptides No.: **8** Total peptides No.: **12**

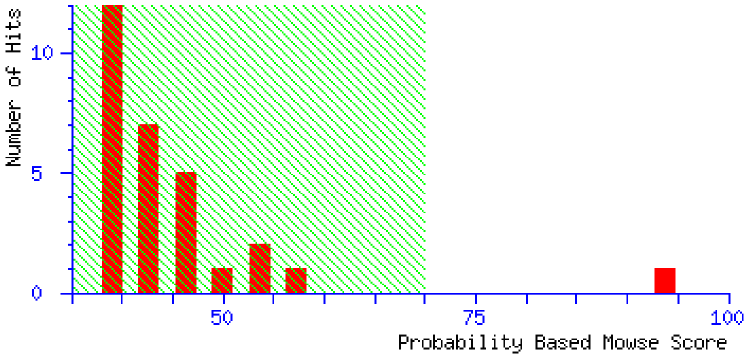
Calculated Mr: **41927** Calculated *p*I: **6.56**

Annotated PMF **spectra:**

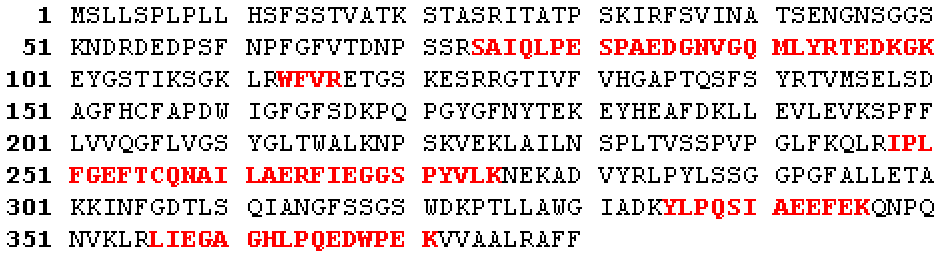


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

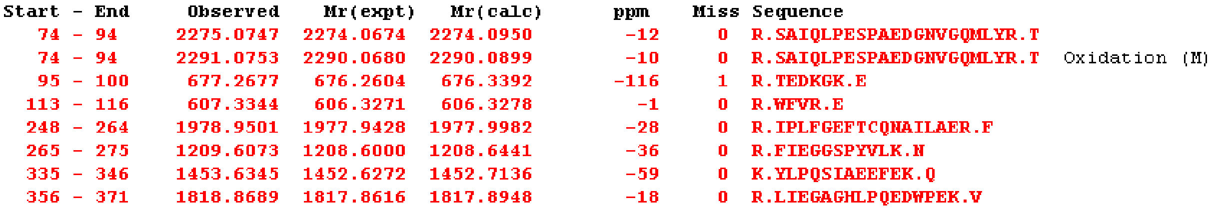


Matched peptide sequences: shown in Bold Red



1 MSLLSPLPLL HSFSSTVATK STASRITATP SKIRFSVINA TSENGNSGGS
51 KNDRDEDPSF NPFGFVTDNP SSR**SAIQLPE** **SPAEDGNVGQ** **MLYRTEDKGK**
101 EYGSTIKSGK LR**WFVR**ETGS KESRRGTIVF VHGAPTQSFS YRTVMSELSD
151 AGFHCFAPDW IGFGFSDKPQ PGYGFNYTEK EYHEAFDKLL EVLEVKSPFF
201 LVVQGFLVGS YGLTWALKNP SKVEKLAILN SPLTVSSPVP GLFKQLR**IPL**
251 **FGEFTCQNAI** **LAERFIEGGS** **PYVLK**NEKAD VYRLPYLSSG GPGFALLETA
301 KKINFGDTLS QIANGFSSGS WDKPTLLAWG IADK**YLPQSI** **AEEFEK**QNPQ
351 NVKLR**LIEGA** **GHLPQEDWPE** **K**VVAALRAFF

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
74 - 94	2275.0747	2274.0674	2274.0950	-12	0	R.SAIQLPESPAEDGNVGQMLYR.T	
74 - 94	2291.0753	2290.0680	2290.0899	-10	0	R.SAIQLPESPAEDGNVGQMLYR.T	Oxidation (M)
95 - 100	677.2677	676.2604	676.3392	-116	1	R.TEDKGK.E	
113 - 116	607.3344	606.3271	606.3278	-1	0	R.WFVR.E	
248 - 264	1978.9501	1977.9428	1977.9982	-28	0	R.IPLFGEFTCQNAILAER.F	
265 - 275	1209.6073	1208.6000	1208.6441	-36	0	R.FIEGGSPYVLK.N	
335 - 346	1453.6345	1452.6272	1452.7136	-59	0	K.YLPQSIAEEFEK.Q	
356 - 371	1818.8689	1817.8616	1817.8948	-18	0	R.LIEGAGHLPQEDWPEK.V	

Spot No.: **125**

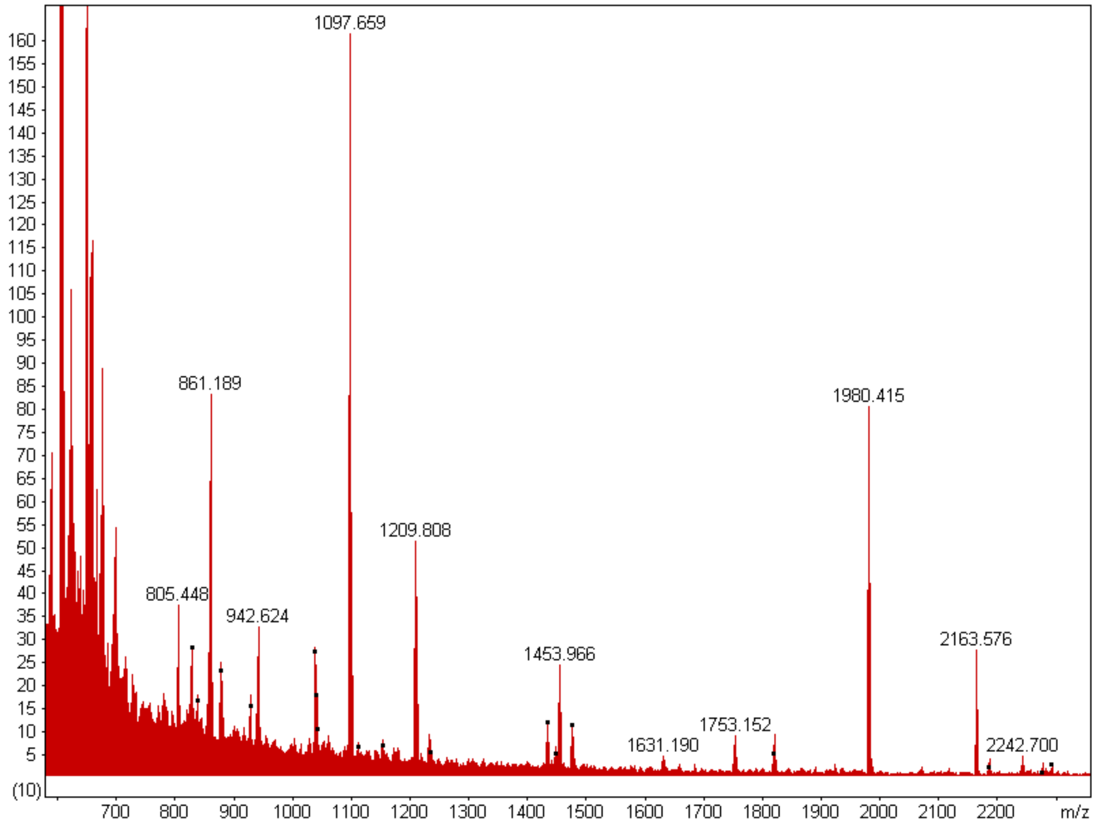
Mascot score: **98** Sequence coverage %: **25**

NCBI accession No.: **gi| 5903052**

Matched peptides No.: **10** Total peptides No.: **28**

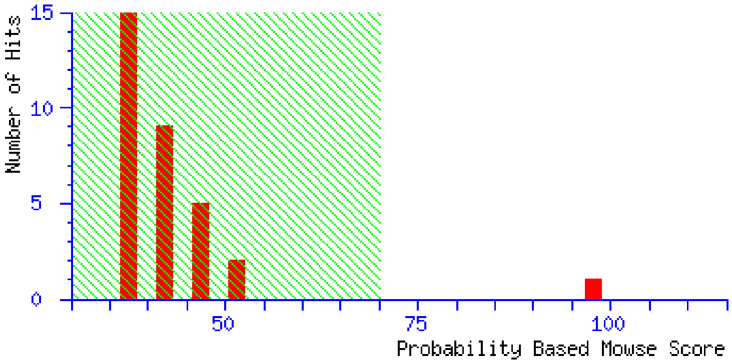
Calculated Mr: **42000** Calculated *p*I: **6.98**

Annotated PMF **spectra:**

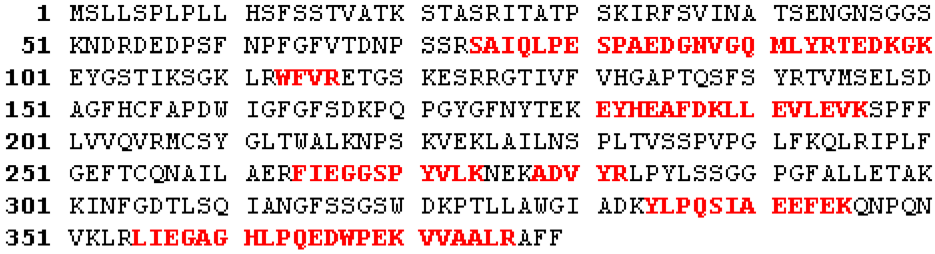


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red



1 MSLLSPLPLL HSFSSTVATK STASRITATP SKIRFSVINA TSENGNSGGS

51 KNDRDEDPSF NPFGFVTDNP SSR**SAIQLPE SPAEDGNVGQ MLYRTEDKGK**

101 EYGSTIKSGK LR**WFVR**ETGS KESRRGTIVF VHGAPTQSFS YRTVMSELSD

151 AGFHCFAPDW IGFGFSDKPQ PGYGFNYTEK **EYHEAFDKLL EVLEVK**SPFF

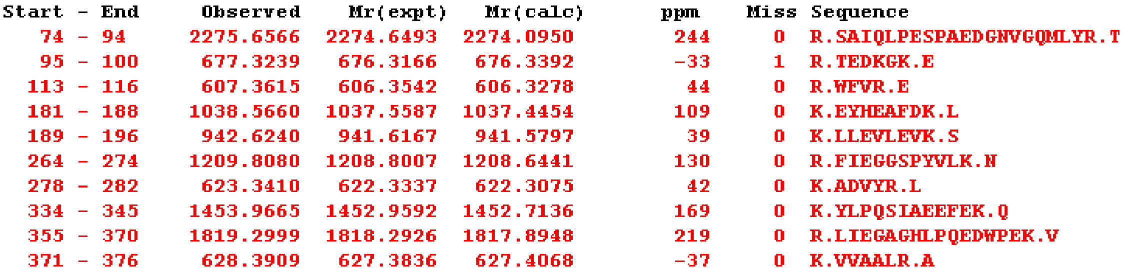
201 LVVQVRMCSY GLTWALKNPS KVEKLAILNS PLTVSSPVPG LFKQLRIPLF

251 GEFTCQNAIL AER**FIEGGSP YVLK**NEK**ADV YR**LPYLSSGG PGFALLETAK

301 KINFGDTLSQ IANGFSSGSW DKPTLLAWGI ADK**YLPQSIA EEFEK**QNPQN

351 VKLR**LIEGAG HLPQEDWPEK VVAALR**AFF

Matched peptides information:



```
Start - End     Observed    Mr(expt)   Mr(calc)      ppm    Miss Sequence
   74 - 94     2275.6566   2274.6493  2274.0950      244      0  R.SAIQLPESPAEDGNVGQMLYR.T
   95 - 100     677.3239    676.3166   676.3392      -33      1  R.TEDKGK.E
  113 - 116     607.3615    606.3542   606.3278       44      0  R.WFVR.E
  181 - 188    1038.5660   1037.5587  1037.4454      109      0  K.EYHEAFDK.L
  189 - 196     942.6240    941.6167   941.5797       39      0  K.LLEVLEVK.S
  264 - 274    1209.8080   1208.8007  1208.6441      130      0  R.FIEGGSPYVLK.N
  278 - 282     623.3410    622.3337   622.3075       42      0  K.ADVYR.L
  334 - 345    1453.9665   1452.9592  1452.7136      169      0  K.YLPQSIAEEFEK.Q
  355 - 370    1819.2999   1818.2926  1817.8948      219      0  R.LIEGAGHLPQEDWPEK.V
  371 - 376     628.3909    627.3836   627.4068      -37      0  K.VVAALR.A
```

Spot No.: **126**

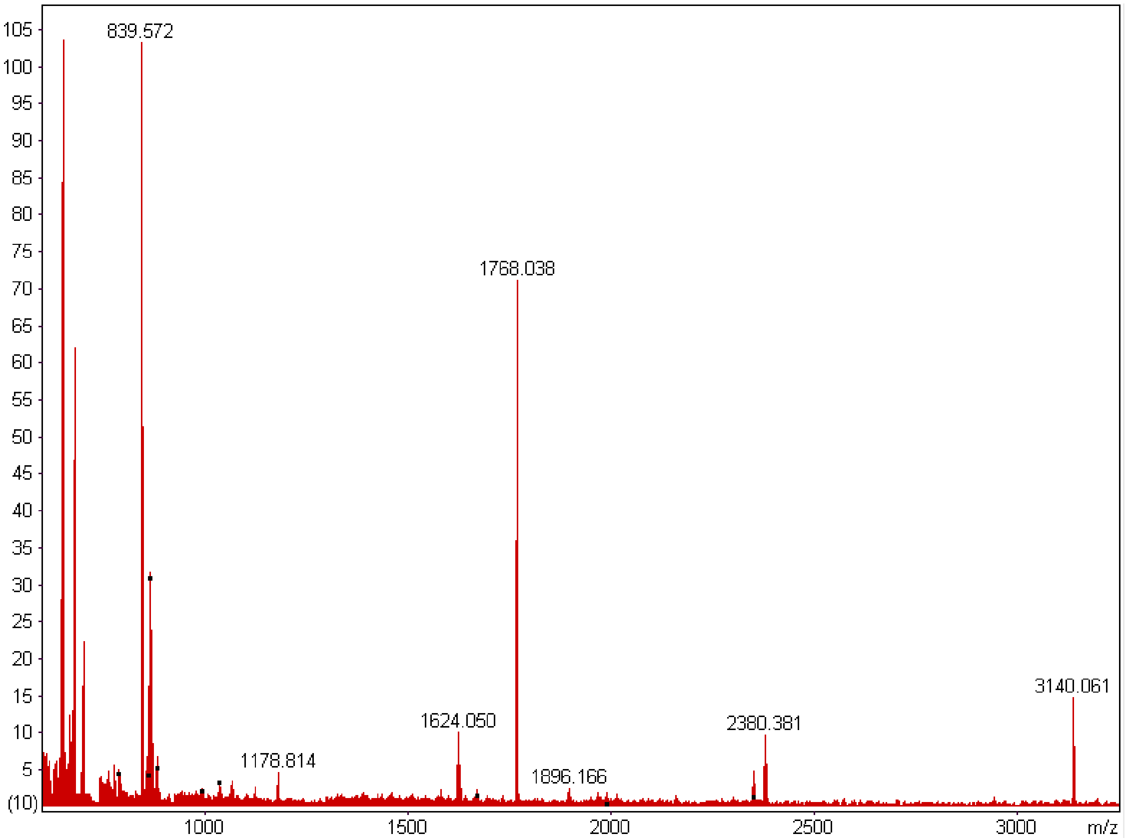
Mascot score: **91** Sequence coverage %: **28**

NCBI accession No.: **gi| 15242351**

Matched peptides No.: **10** Total peptides No.: **18**

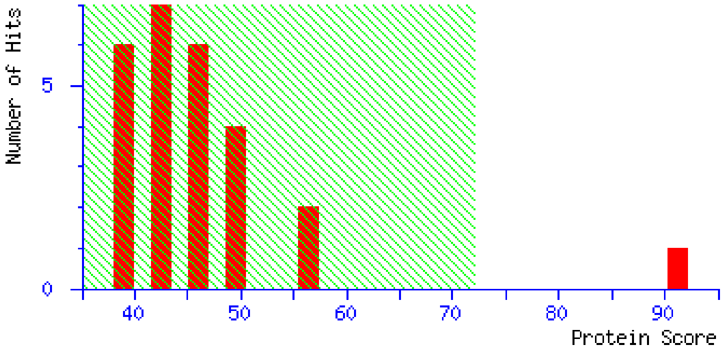
Calculated Mr: **41377** Calculated *p*I: **5.76**

Annotated PMF **spectra:**

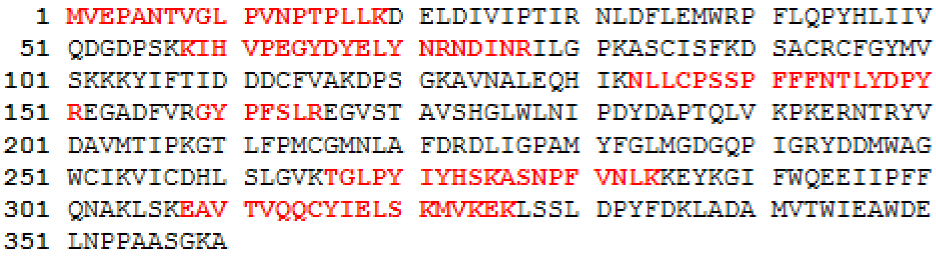


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).

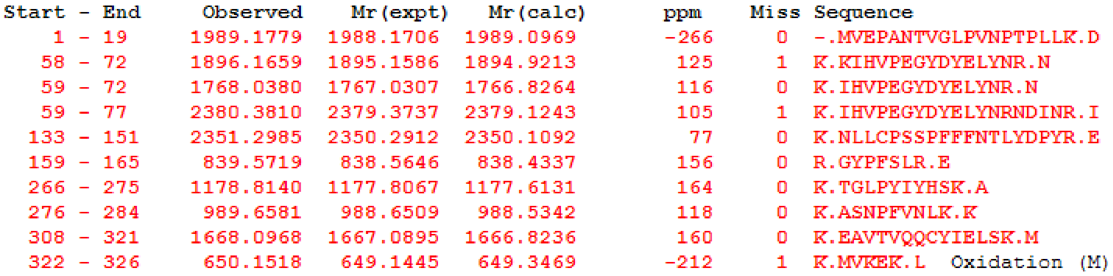


Matched peptide sequences: shown in Bold Red



```
  1 MVEPANTVGL PVNPTPLLKD ELDIVIPTIR NLDFLEMWRP FLQPYHLIIV
 51 QDGDPSKKIH VPEGYDYELY NRNDINRILG PKASCISFKD SACRCFGYMV
101 SKKKYIFTID DDCFVAKDPS GKAVNALEQH IKNLLCPSSP FFFNTLYDPY
151 REGADFVRGY PFSLREGVST AVSHGLWLNI PDYDAPTQLV KPKERNTRYV
201 DAVMTIPKGT LFPMCGMNLA FDRDLIGPAM YFGLMGDGQP IGRYDDMWAG
251 WCIKVICDHL SLGVKTGLPY IYHSKASNPF VNLKKEYKGI FWQEEIIPFF
301 QNAKLSKEAV TVQQCYIELS KMVKEKLSSL DPYFDKLADA MVTWIEAWDE
351 LNPPAASGKA
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    1 - 19     1989.1779  1988.1706  1989.0969     -266      0  -.MVEPANTVGLPVNPTPLLK.D
   58 - 72     1896.1659  1895.1586  1894.9213      125      1  K.KIHVPEGYDYELYNR.N
   59 - 72     1768.0380  1767.0307  1766.8264      116      0  K.IHVPEGYDYELYNR.N
   59 - 77     2380.3810  2379.3737  2379.1243      105      1  K.IHVPEGYDYELYNRNDINR.I
  133 - 151    2351.2985  2350.2912  2350.1092       77      0  K.NLLCPSSPFFFNTLYDPYR.E
  159 - 165     839.5719   838.5646   838.4337      156      0  R.GYPFSLR.E
  266 - 275    1178.8140  1177.8067  1177.6131      164      0  K.TGLPYIYHSK.A
  276 - 284     989.6581   988.6509   988.5342      118      0  K.ASNPFVNLK.K
  308 - 321    1668.0968  1667.0895  1666.8236      160      0  K.EAVTVQQCYIELSK.M
  322 - 326     650.1518   649.1445   649.3469     -212      1  K.MVKEK.L   Oxidation (M)
```

Spot No.: **127**

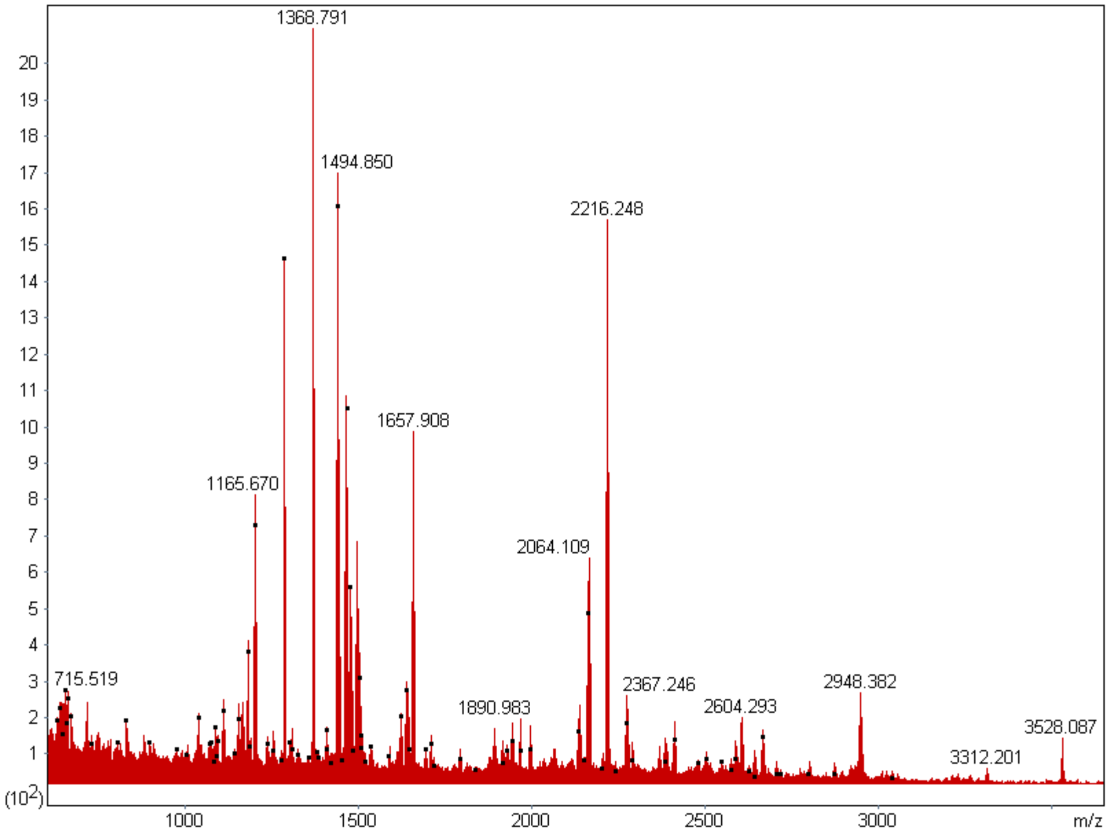
Mascot score: **81**　　Sequence coverage %: **90**

NCBI accession No.: **gi| 115443951**

Matched peptides No.: **12**　　Total peptides No.: **55**

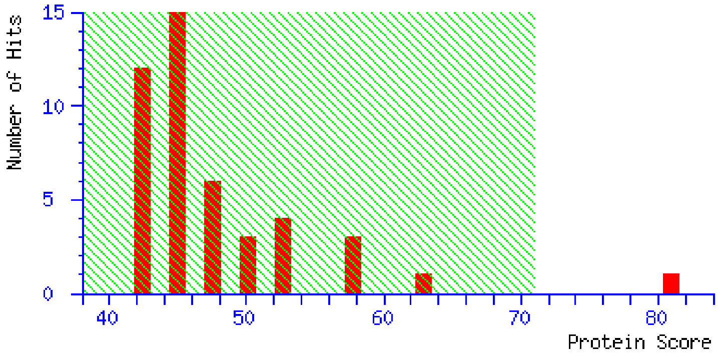
Calculated Mr: **27078**　　Calculated *p*I: **9.30**

Annotated PMF **spectra:**

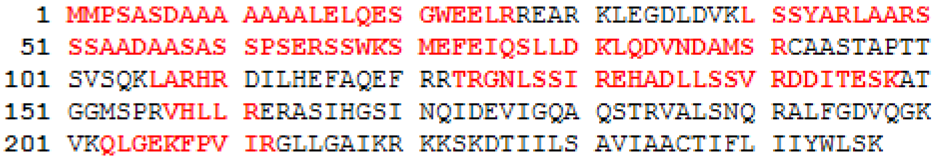


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

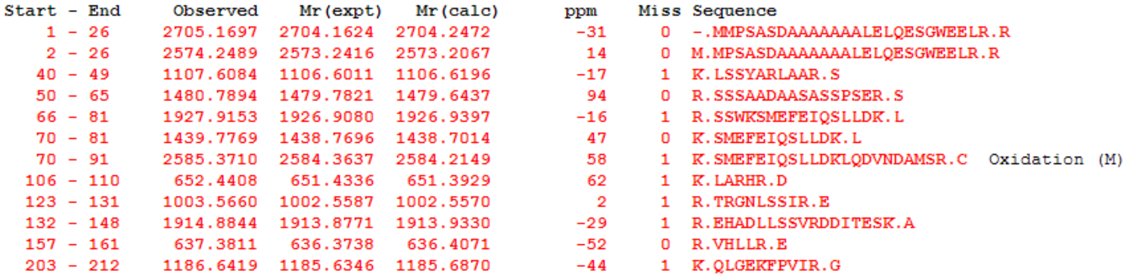


Matched peptide sequences: shown in Bold Red



```
  1 MMPSASDAAA AAAALELQES GWEELRREAR KLEGDLDVKL SSYARLAARS
 51 SSAADAASAS SPSERSSWKS MEFEIQSLLD KLQDVNDAMS RCAASTAPTT
101 SVSQKLARHR DILHEFAQEF RRTRGNLSSI REHADLLSSV RDDITESKAT
151 GGMSPRVHLL RERASIHGSI NQIDEVIGQA QSTRVALSNQ RALFGDVQGK
201 VKQLGEKFPV IRGLLGAIKR KKSKDTIILS AVIAACTIFL IIYWLSK
```

Matched peptides information:



```
Start - End     Observed    Mr(expt)   Mr(calc)      ppm    Miss Sequence
    1 - 26     2705.1697  2704.1624  2704.2472      -31      0  -.MMPSASDAAAAAAALELQESGWEELR.R
    2 - 26     2574.2489  2573.2416  2573.2067       14      0  M.MPSASDAAAAAAALELQESGWEELR.R
   40 - 49     1107.6084  1106.6011  1106.6196      -17      1  K.LSSYARLAAR.S
   50 - 65     1480.7894  1479.7821  1479.6437       94      0  R.SSSAADAASASSPSER.S
   66 - 81     1927.9153  1926.9080  1926.9397      -16      1  R.SSWKSMEFEIQSLLDK.L
   70 - 81     1439.7769  1438.7696  1438.7014       47      0  K.SMEFEIQSLLDK.L
   70 - 91     2585.3710  2584.3637  2584.2149       58      1  K.SMEFEIQSLLDKLQDVNDAMSR.C  Oxidation (M)
  106 - 110     652.4408   651.4336   651.3929       62      1  K.LARHR.D
  123 - 131    1003.5660  1002.5587  1002.5570        2      1  R.TRGNLSSIR.E
  132 - 148    1914.8844  1913.8771  1913.9330      -29      1  R.EHADLLSSVRDDITESK.A
  157 - 161     637.3811   636.3738   636.4071      -52      0  R.VHLLR.E
  203 - 212    1186.6419  1185.6346  1185.6870      -44      1  K.QLGEKFPVIR.G
```

Spot No.: **128**

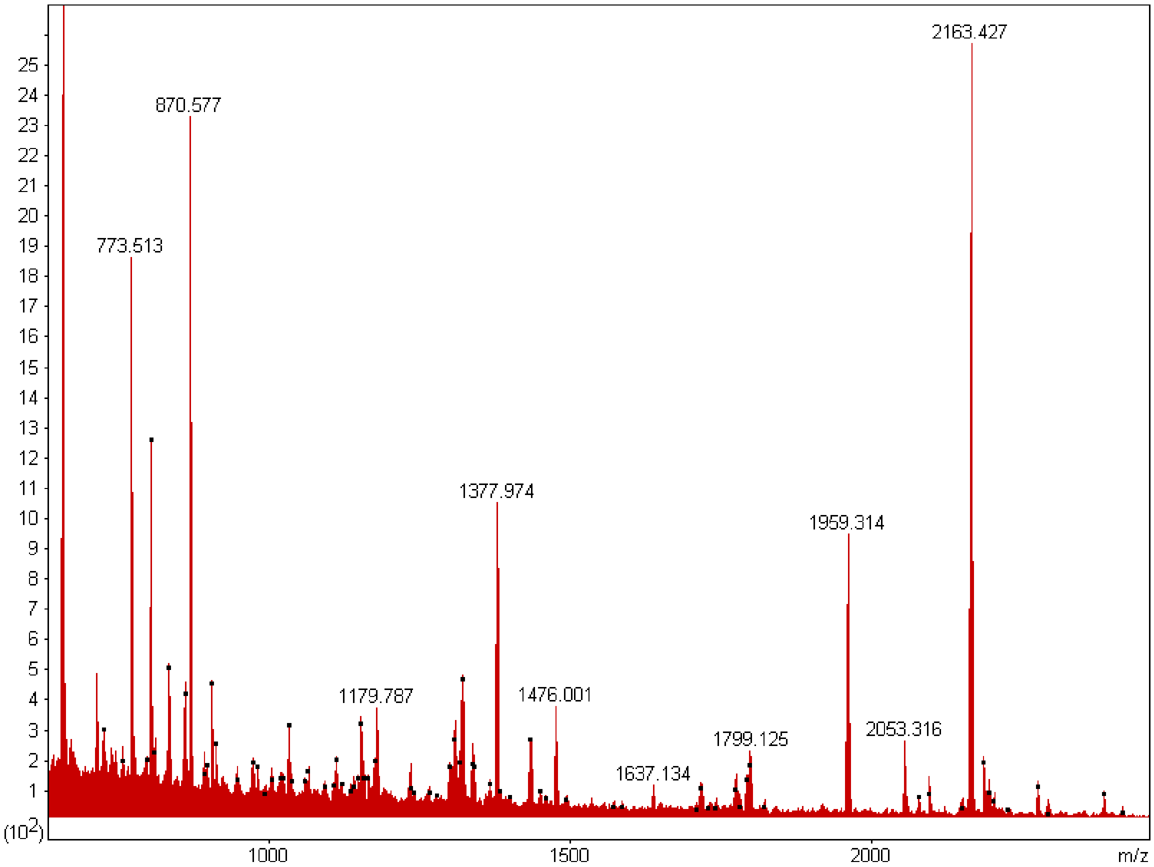
Mascot score: **95** Sequence coverage %: **34**

NCBI accession No.: **gi| 312281543**

Matched peptides No.: **14** Total peptides No.: **49**

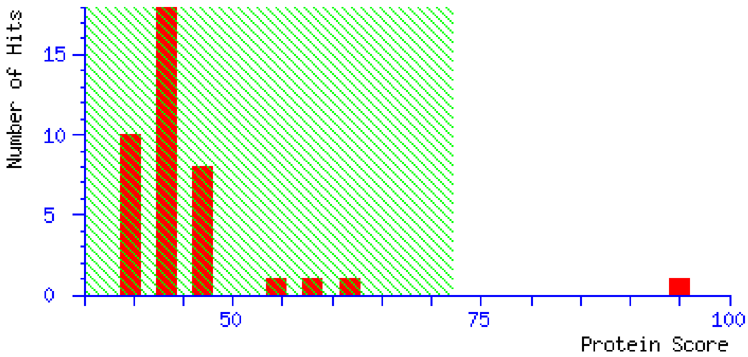
Calculated Mr: **50983** Calculated *p*I: **6.67**

Annotated PMF **spectra:**

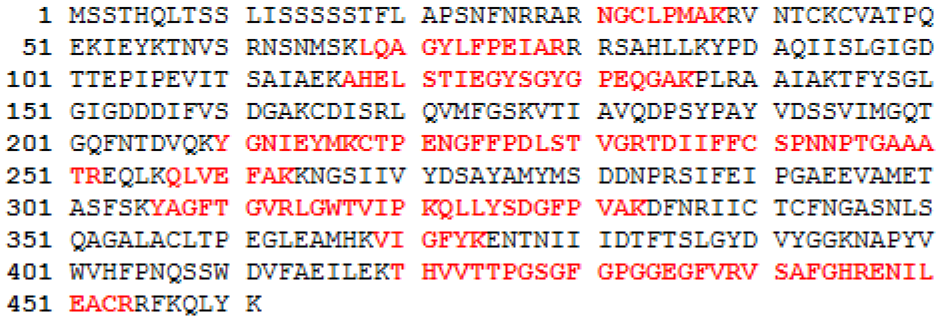


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

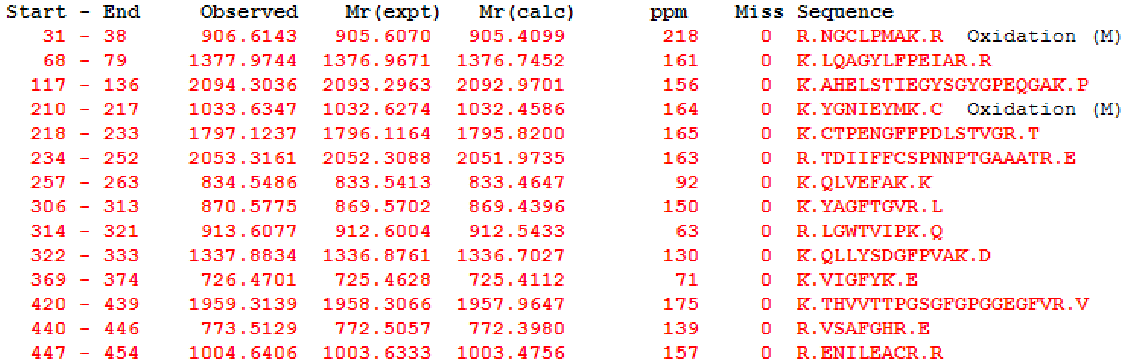


Matched peptide sequences: shown in Bold Red



```
  1 MSSTHQLTSS LISSSSSTFL APSNFNRRAR NGCLPMAKRV NTCKCVATPQ
 51 EKIEYKTNVS RNSNMSKLQA GYLFPEIARR RSAHLLKYPD AQIISLGIGD
101 TTEPIPEVIT SAIAEKAHEL STIEGYSGYG PEQGAKPLRA AIAKTFYSGL
151 GIGDDDIFVS DGAKCDISRL QVMFGSKVTI AVQDPSYPAY VDSSVIMGQT
201 GQFNTDVQKY GNIEYMKCTP ENGFFPDLST VGRTDIIFFC SPNNPTGAAA
251 TREQLKQLVE FAKKNGSIIV YDSAYAMYMS DDNPRSIFEI PGAEEVAMET
301 ASFSKYAGFT GVRLGWTVIP KQLLYSDGFP VAKDFNRIIC TCFNGASNLS
351 QAGALACLTP EGLEAMHKVI GFYKENTNII IDTFTSLGYD VYGGKNAPYV
401 WVHFPNQSSW DVFAEILEKT HVVTTPGSGF GPGGEGFVRV SAFGHRENIL
451 EACRRFKQLY K
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   31 - 38      906.6143   905.6070   905.4099      218      0  R.NGCLPMAK.R  Oxidation (M)
   68 - 79     1377.9744  1376.9671  1376.7452      161      0  K.LQAGYLFPEIAR.R
  117 - 136    2094.3036  2093.2963  2092.9701      156      0  K.AHELSTIEGYSGYGPEQGAK.P
  210 - 217    1033.6347  1032.6274  1032.4586      164      0  K.YGNIEYMK.C  Oxidation (M)
  218 - 233    1797.1237  1796.1164  1795.8200      165      0  K.CTPENGFFPDLSTVGR.T
  234 - 252    2053.3161  2052.3088  2051.9735      163      0  R.TDIIFFCSPNNPTGAAATR.E
  257 - 263     834.5486   833.5413   833.4647       92      0  K.QLVEFAK.K
  306 - 313     870.5775   869.5702   869.4396      150      0  K.YAGFTGVR.L
  314 - 321     913.6077   912.6004   912.5433       63      0  R.LGWTVIPK.Q
  322 - 333    1337.8834  1336.8761  1336.7027      130      0  K.QLLYSDGFPVAK.D
  369 - 374     726.4701   725.4628   725.4112       71      0  K.VIGFYK.E
  420 - 439    1959.3139  1958.3066  1957.9647      175      0  K.THVVTTPGSGFGPGGEGFVR.V
  440 - 446     773.5129   772.5057   772.3980      139      0  R.VSAFGHR.E
  447 - 454    1004.6406  1003.6333  1003.4756      157      0  R.ENILEACR.R
```

Spot No.: **129**

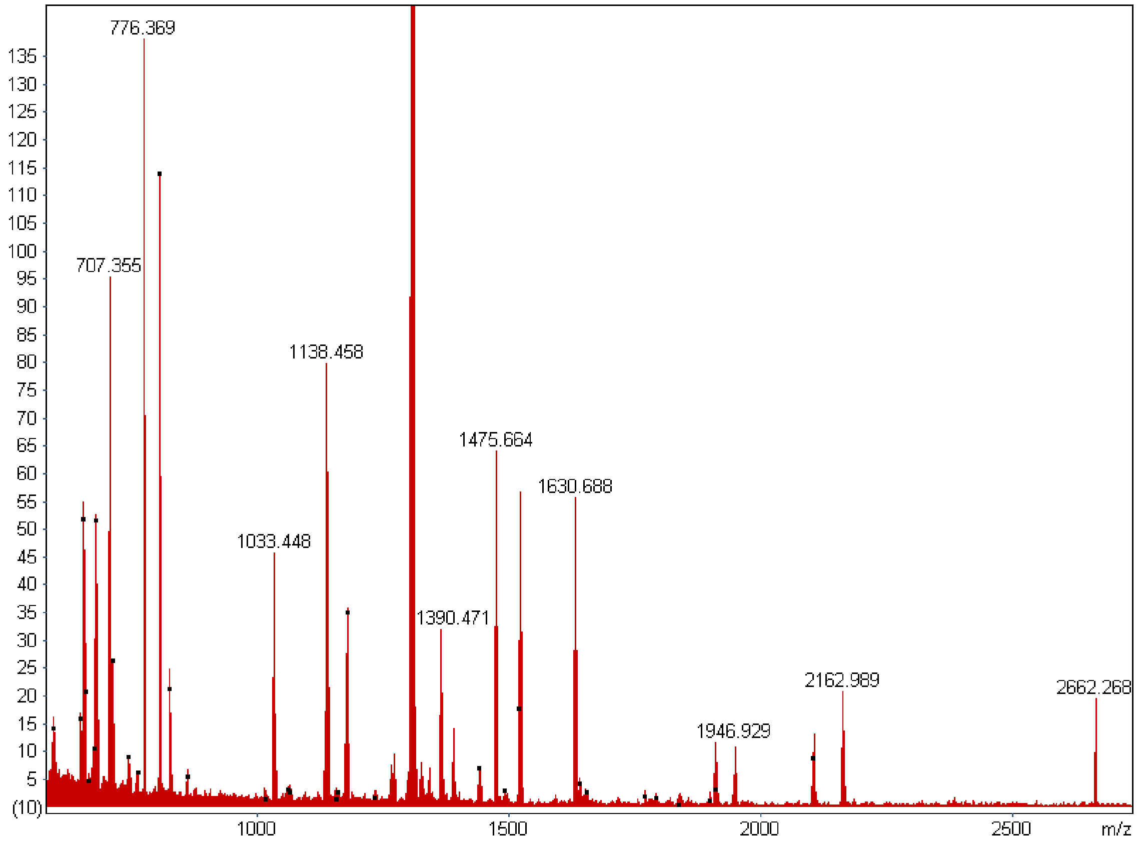
Mascot score: **156**   Sequence coverage %: **40**

NCBI accession No.: **gi| 15239282**

Matched peptides No.: **18**   Total peptides No.: **43**

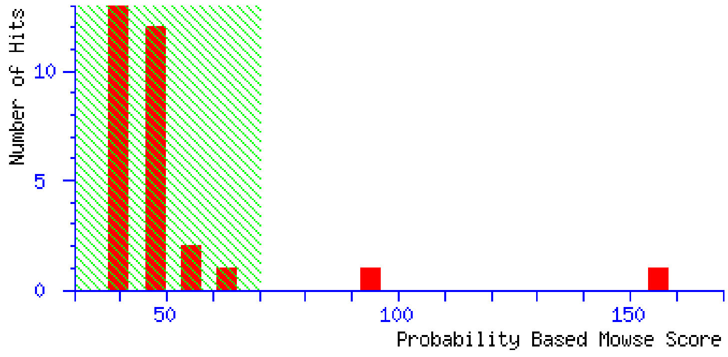
Calculated Mr: **40643**   Calculated *p*I: **8.32**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

```
  1 MAAAISAAVS LPSSKSSSLL TKISSVSPQR IFLKKSTVCY RRVVSVKAQV
 51 TTDTTEAPPV KVVKESKKQE EGIVVNKFKP KNPYTGRCLL NTKITGDDAP
101 GETWHIVFTT EGEVPYREGQ SIGVIPEGID KNGKPHKLRL YSIASSAIGD
151 FGDSKTVSLC VKRLVYTNDG GEIVKGVCSN FLCDLKPGDE AKITGPVGKE
201 MLMPKDPNAT IIMLGTGTGI APFRSFLWKM FFEEHEDYKF NGLAWLFLGV
251 PTSSSLLYKE EFEKMKEKNP DNFRLDFAVS REQTNEKGEK MYIQTRMAEY
301 AEELWELLKK DNTFVYMCGL KGMEKGIDDI MVSLAAKDGI DWLEYKKQLK
351 RSEQWNVEVY
```

Matched peptides information:

```
Start - End      Observed   Mr(expt)   Mr(calc)     ppm   Miss Sequence
   69 - 77      1015.4746  1014.4673  1014.5346     -66     0  K.QEEGIVVNK.F
   82 - 87       707.3550   706.3477   706.3398      11     0  K.NPYTGR.C
  118 - 131     1441.6547  1440.6474  1440.7460     -68     0  R.EGQSIGVIPEGIDK.N
  140 - 155     1630.6885  1629.6812  1629.7886     -66     0  R.LYSIASSAIGDFGDSK.T
  176 - 192     1909.7993  1908.7920  1908.8710     -41     0  K.GVCSNFLCDLKPGDEAK.I
  225 - 229      680.3747   679.3674   679.3693      -3     0  R.SFLWK.M
  230 - 239     1374.4809  1373.4736  1373.5598     -63     0  K.MFFEEHEDYK.F
  230 - 239     1390.4706  1389.4633  1389.5547     -66     0  K.MFFEEHEDYK.F  Oxidation (M)
  275 - 281      807.4221   806.4148   806.4286     -17     0  R.LDFAVSR.E
  291 - 296      827.3824   826.3751   826.4007     -31     0  K.MYIQTR.M  Oxidation (M)
  297 - 309     1640.6884  1639.6811  1639.7803     -60     0  R.MAEYAEELWELLK.K  Oxidation (M)
  297 - 310     1768.7718  1767.7645  1767.8753     -63     1  R.MAEYAEELWELLKK.D  Oxidation (M)
  310 - 321     1475.6642  1474.6569  1474.6949     -26     1  K.KDNTFVYMCGLK.G
  310 - 321     1491.6536  1490.6463  1490.6898     -29     1  K.KDNTFVYMCGLK.G  Oxidation (M)
  326 - 337     1232.5462  1231.5389  1231.6482     -89     0  K.GIDDIMVSLAAK.D
  338 - 346     1138.4575  1137.4502  1137.5342     -74     0  K.DGIDWLEYK.K
  338 - 347     1266.5367  1265.5294  1265.6292     -79     1  K.DGIDWLEYKK.Q
  351 - 360     1309.5316  1308.5243  1308.6098     -65     1  K.RSEQWNVEVY.-
```

Spot No.: **130**

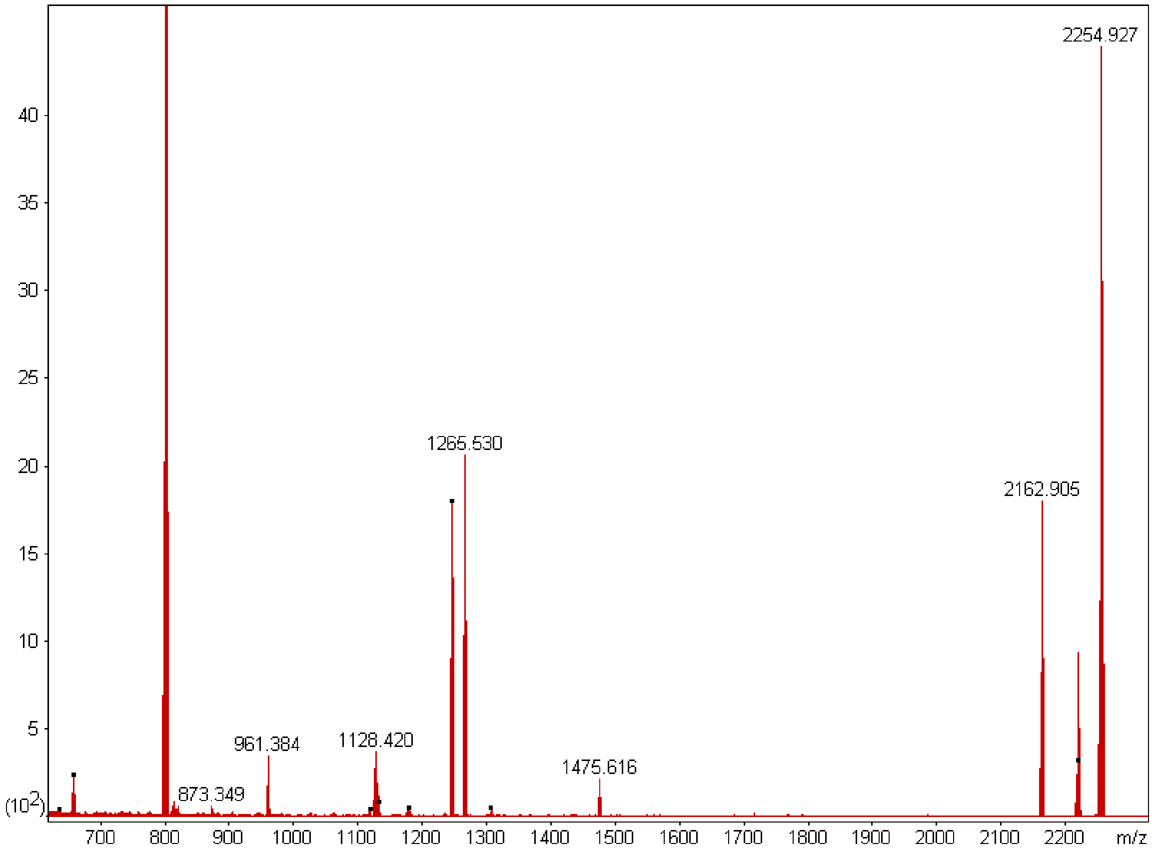
Mascot score: **94**   Sequence coverage %: **21**

NCBI accession No.: **gi| 11228579**

Matched peptides No.: **8**   Total peptides No.: **20**

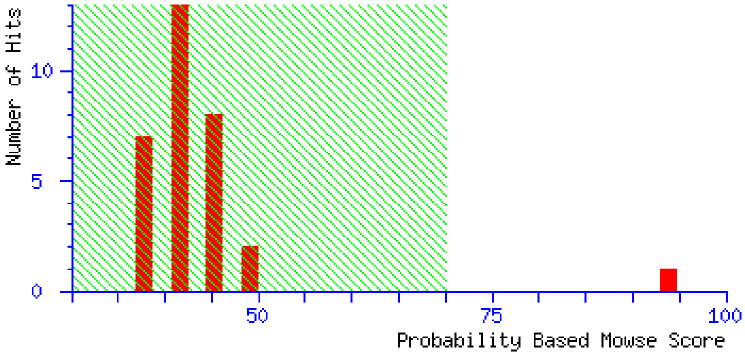
Calculated Mr: **36905**   Calculated *p*I: **5.39**

Annotated PMF **spectra:**

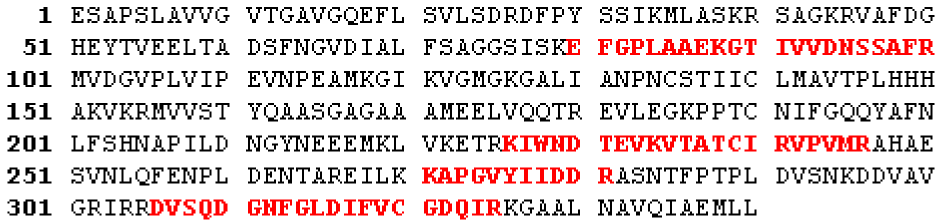


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

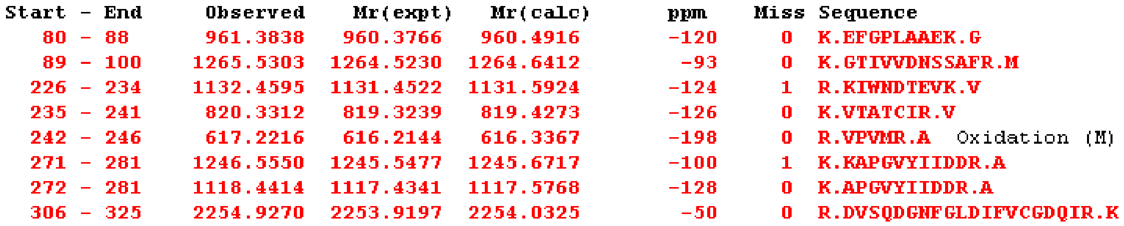


Matched peptide sequences: shown in Bold Red



```
  1 ESAPSLAVVG VTGAVGQEFL SVLSDRDFPY SSIKMLASKR SAGKRVAFDG
 51 HEYTVEELTA DSFNGVDIAL FSAGGSISKE FGPLAAEKGT IVVDNSSAFR
101 MVDGVPLVIP EVNPEAMKGI KVGMGKGALI ANPNCSTIIC LMAVTPLHHH
151 AKVKRMVVST YQAASGAGAA AMEELVQQTR EVLEGKPPTC NIFGQQYAFN
201 LFSHNAPILD NGYNEEEMKL VKETRKIWND TEVKVTATCI RVPVMRAHAE
251 SVNLQFENPL DENTAREILK KAPGVYIIDD RASNTFPTPL DVSNKDDVAV
301 GRIRRDVSQD GNFGLDIFVC GDQIRKGAAL NAVQIAEMLL
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss Sequence
   80 - 88      961.3838   960.3766   960.4916     -120     0  K.EFGPLAAEK.G
   89 - 100    1265.5303  1264.5230  1264.6412      -93     0  K.GTIVVDNSSAFR.M
  226 - 234    1132.4595  1131.4522  1131.5924     -124     1  R.KIWNDTEVK.V
  235 - 241     820.3312   819.3239   819.4273     -126     0  K.VTATCIR.V
  242 - 246     617.2216   616.2144   616.3367     -198     0  R.VPVMR.A  Oxidation (M)
  271 - 281    1246.5550  1245.5477  1245.6717     -100     1  K.KAPGVYIIDDR.A
  272 - 281    1118.4414  1117.4341  1117.5768     -128     0  K.APGVYIIDDR.A
  306 - 325    2254.9270  2253.9197  2254.0325      -50     0  R.DVSQDGNFGLDIFVCGDQIR.K
```

Spot No.: **131**

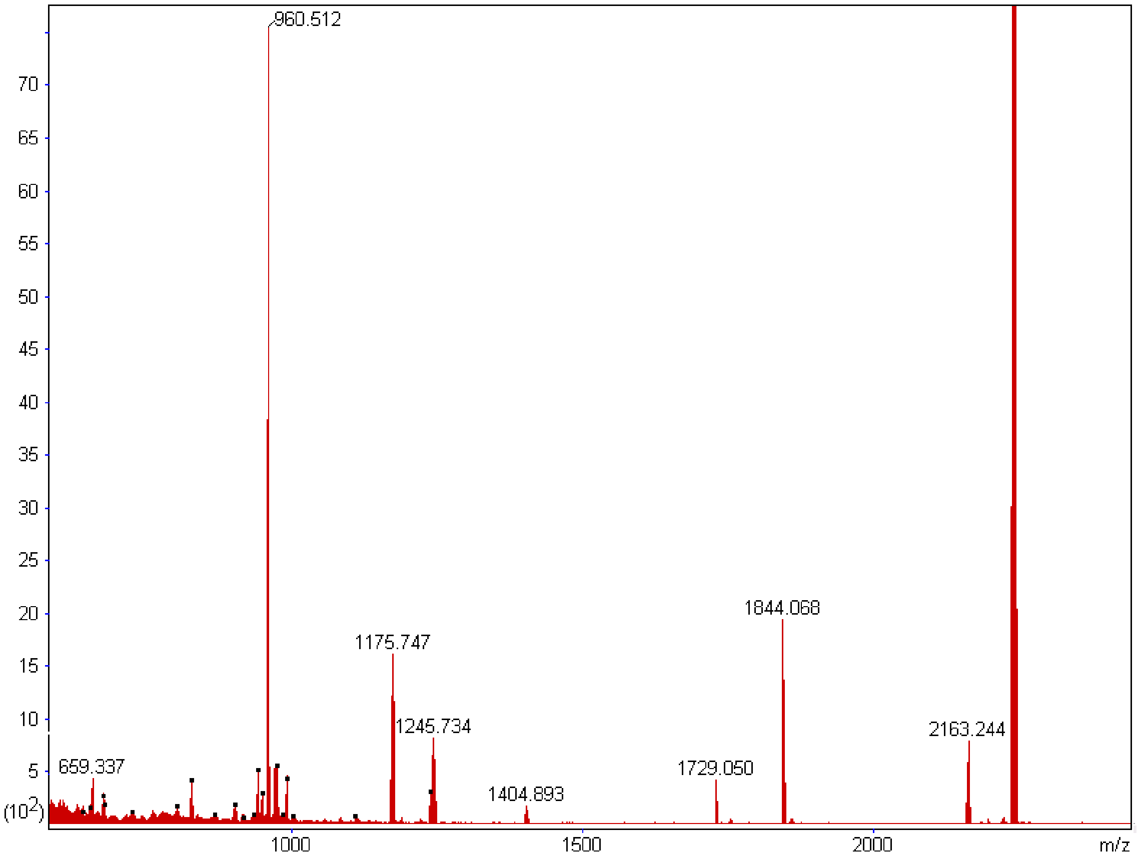
Mascot score: **96** Sequence coverage %: **8**

NCBI accession No.: **gi| 116060520**

Matched peptides No.: **11** Total peptides No.: **17**

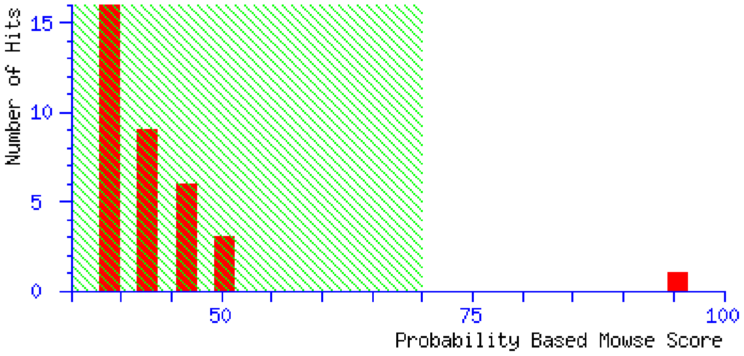
Calculated Mr: **106933** Calculated *p*I: **6.77**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

```
  1 MEPEKRARSS LGVARASRPT IELGKRIDAN VEPPPLTRAE ARDGERFPTE
 51 KLTRALIREG WSENKRRALV MKSTGDDGTM VNPMALRETL LRLANSETLR
101 EIRRRVNETA KEKRRTPEIG ARDRSEYGRG MTEADCKPWS APELVHASAD
151 DVEAFFKDLA SEVELSELEQ FVPHGVRKRK LIENLHAYRV SSHRGVWMVK
201 IVYLAQYKRD VDACRNAWTE DILGHALDSL RDALLTPKSA EDQETELKCV
251 FGLLNHSIQE DLVDTAKIFD EVLRFVHERS LAASKSCSGT AALVLARSMA
301 ATLTALVPHA SQSHEDSIKL AQKVAVCLEG AVSNGSARAD GHLVTRLSEV
351 IASLGSVNAD AFISAPREQG LDVVQKLRTK SKRRQMPLSH RLCQVIDDVE
401 KRVQSLTHAA SPAVIAIKVH NLVKLLNEVL DKSGDEAMMS ELSQKFINAQ
451 EDGEVARKAM VNVACSWAVD ASDDAVNERQ RVTRVFLNEL TQSPRPLILH
501 WIKENSANLR QEDDKIGRIS GLLIQLLQGD VIRMQQLLDF IIAEGILEER
551 ISHDLSMAFH RYLSDIVKDD NAKREILDDS TAQTARQLIG SESEKENTKV
601 VVIPATNVLD FSSDEERLLC TSFAEVSYAN LASKVAELKG ALNASAISHK
651 TLGRVLTVCL MHDATKLGLF AEIVGDMGPE VTKDVLSYVS MDVLSVENLE
701 NTNSIFNCAH WRMCAAFDRW KFARSLVDFQ LCLLHNVPKG KRAVAEGLVE
751 ANTTQLVQLA KSTNIAHKCL HIWTRILVVI PLIGYVLMSA SASNKFSQLI
801 LDVLDSIIGK TVVEESAEDI IAESDMGETL VDRLVALFSV VSVGQIPKWA
851 PVVPKLPFRE LSSVKLALSK SIESKSIAGM VCVRLQRAIS LPLTKLRTRS
901 VNPWKILASG ASSDRSKLSD AEKAEFWLQG TVRRPGGNLA WQNCNAEPTF
951 ITENKILS
```

Matched peptides information:

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
1 - 6	805.4094	804.4021	804.3800	28	1	-.MEPEKR.A	Oxidation (M)
39 - 46	903.4320	902.4247	902.4206	5	1	R.AEARDGER.F	
425 - 432	943.4750	942.4677	942.5386	-75	0	K.LLNEVLDK.S	
480 - 484	659.3374	658.3301	658.3875	-87	1	R.QRVTR.V	
511 - 518	960.5118	959.5045	959.4672	39	1	R.QEDDKIGR.I	
713 - 719	870.4022	869.3949	869.3524	49	0	R.MCAAFDR.W	
856 - 865	1175.7474	1174.7401	1174.6710	59	1	K.LPFRELSSVK.L	
876 - 884	992.5152	991.5080	991.4943	14	0	K.SIAGMVCVR.L	
885 - 895	1239.7298	1238.7225	1238.7710	-39	1	R.LQRAISLPLTK.L	
888 - 897	1111.6574	1110.6501	1110.7124	-56	1	R.AISLPLTKLR.T	
906 - 915	976.5137	975.5065	975.4985	8	0	K.ILASGASSDR.S	

Spot No.: **132**

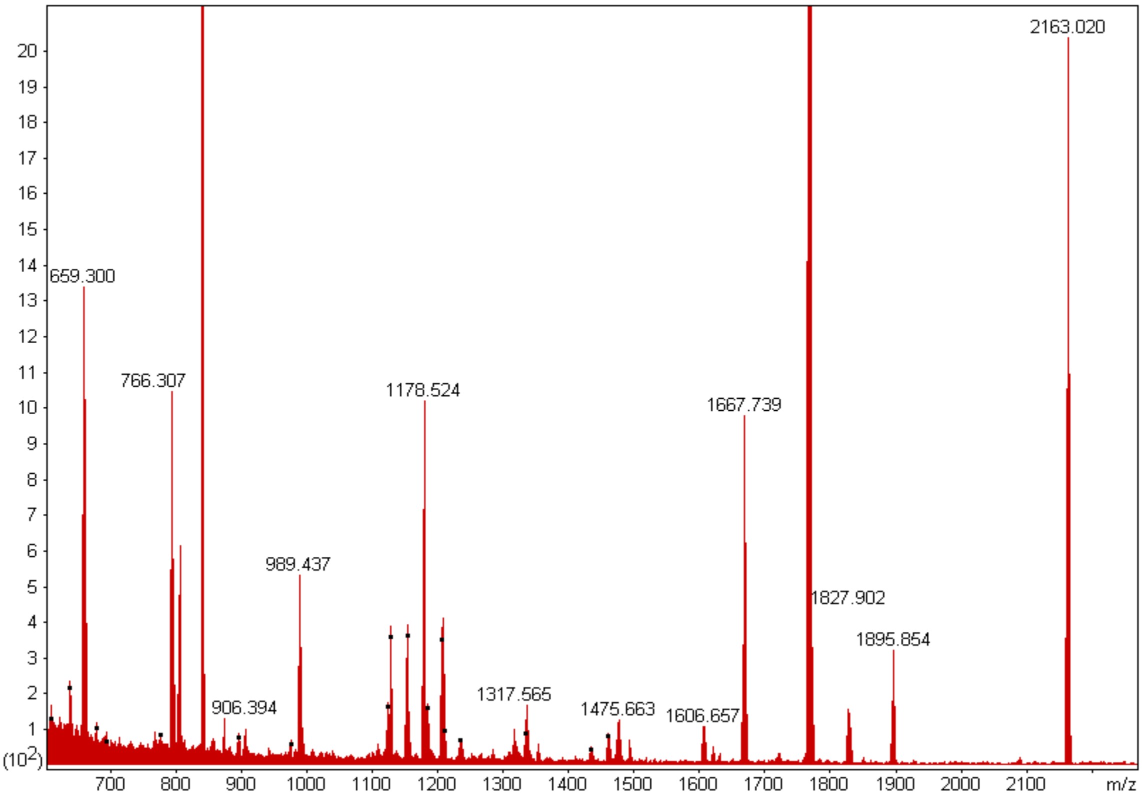
Mascot score: **133**   Sequence coverage %: **32**

NCBI accession No.: **gi| 2317731**

Matched peptides No.: **13**   Total peptides No.: **39**

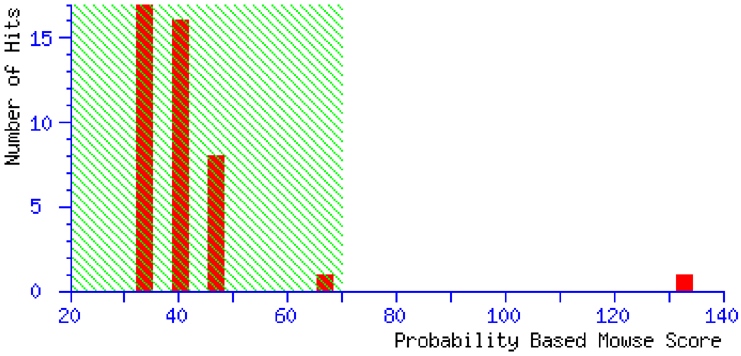
Calculated Mr: **41875**   Calculated p*I*: **5.93**

Annotated PMF **spectra:**

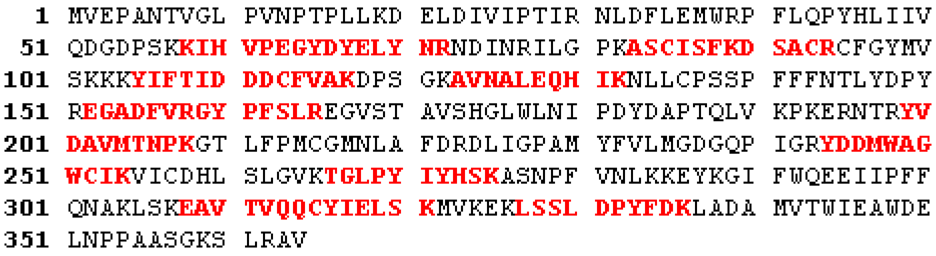


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

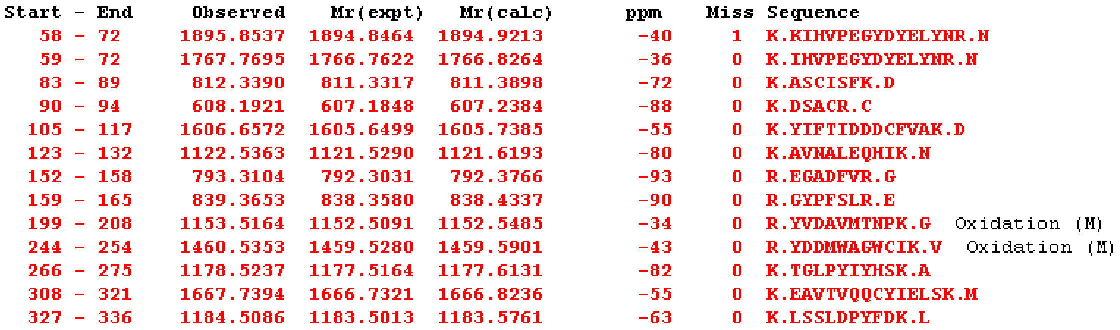


Matched peptide sequences: shown in Bold Red



1 MVEPANTVGL PVNPTPLLKD ELDIVIPTIR NLDFLEMWRP FLQPYHLIIV
51 QDGDPSK**KIH** **VPEGYDYELY** **NR**NDINRILG PK**ASCISFKD** **SACR**CFGYMV
101 SKKK**YIFTID** **DDCFVAK**DPS GK**AVNALEQH** **IK**NLLCPSSP FFFNTLYDPY
151 R**EGADFVRGY** **PFSLR**EGVST AVSHGLWLNI PDYDAPTQLV KPKERNTR**YV**
201 **DAVMTNPK**GT LFPMCGMNLA FDRDLIGPAM YFVLMGDGQP IGR**YDDMWAG**
251 **WCIK**VICDHL SLGVK**TGLPY** **IYHSK**ASNPF VNLKKEYKGI FWQEEIIPFF
301 QNAKLSK**EAV** **TVQQCYIELS** **K**MVKEK**LSSL** **DPYFDK**LADA MVTWIEAWDE
351 LNPPAASGKS LRAV

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
58 - 72	1895.8537	1894.8464	1894.9213	-40	1	K.KIHVPEGYDYELYNR.N
59 - 72	1767.7695	1766.7622	1766.8264	-36	0	K.IHVPEGYDYELYNR.N
83 - 89	812.3390	811.3317	811.3898	-72	0	K.ASCISFK.D
90 - 94	608.1921	607.1848	607.2384	-88	0	K.DSACR.C
105 - 117	1606.6572	1605.6499	1605.7385	-55	0	K.YIFTIDDDCFVAK.D
123 - 132	1122.5363	1121.5290	1121.6193	-80	0	K.AVNALEQHIK.N
152 - 158	793.3104	792.3031	792.3766	-93	0	R.EGADFVR.G
159 - 165	839.3653	838.3580	838.4337	-90	0	R.GYPFSLR.E
199 - 208	1153.5164	1152.5091	1152.5485	-34	0	R.YVDAVMTNPK.G Oxidation (M)
244 - 254	1460.5353	1459.5280	1459.5901	-43	0	R.YDDMWAGWCIK.V Oxidation (M)
266 - 275	1178.5237	1177.5164	1177.6131	-82	0	K.TGLPYIYHSK.A
308 - 321	1667.7394	1666.7321	1666.8236	-55	0	K.EAVTVQQCYIELSK.M
327 - 336	1184.5086	1183.5013	1183.5761	-63	0	K.LSSLDPYFDK.L

Spot No.: **133**

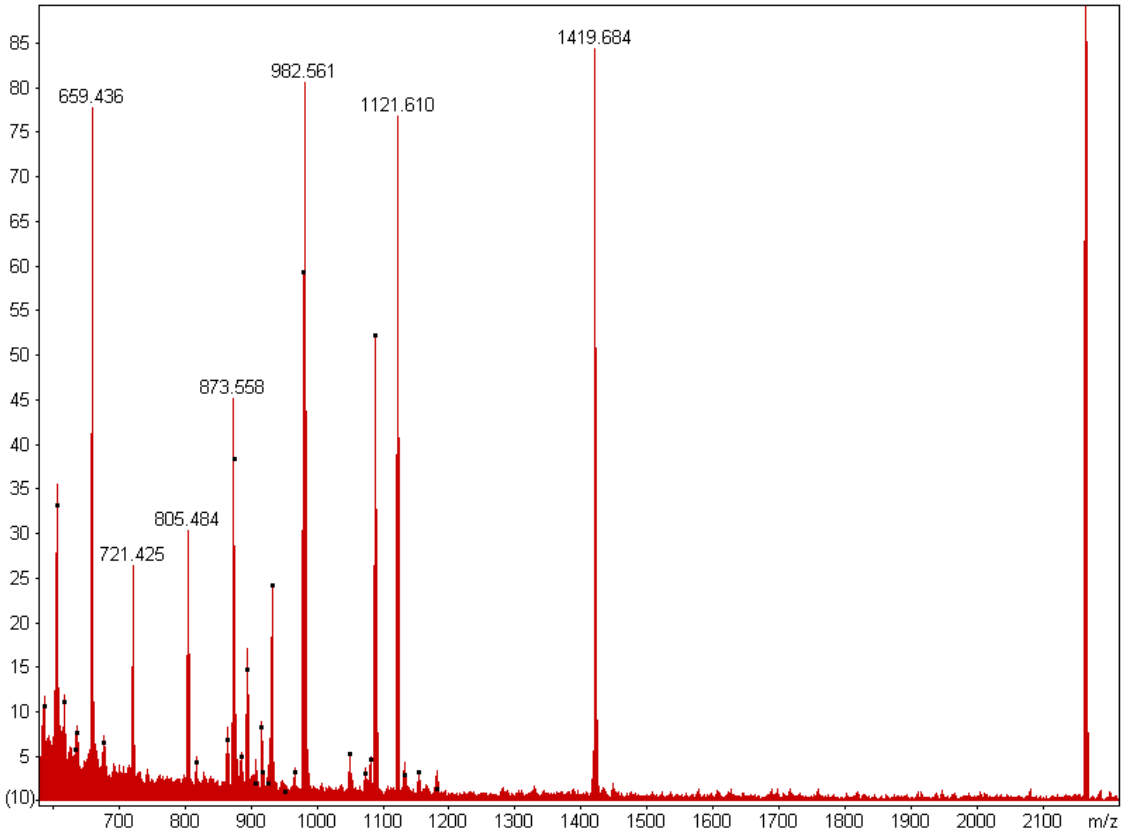
Mascot score: **174**   Sequence coverage %: **26**

NCBI accession No.: **gi| 18391442**

Matched peptides No.: **15**   Total peptides No.: **27**

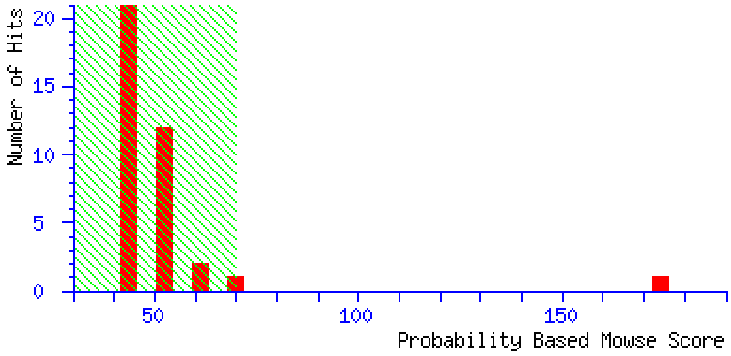
Calculated Mr: **42878**   Calculated *p*I: **5.40**

Annotated PMF **spectra:**

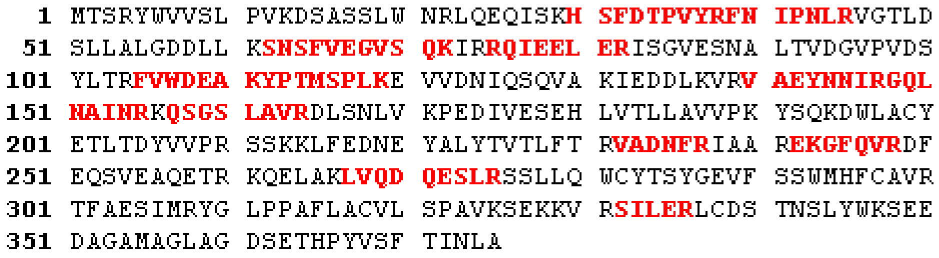


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

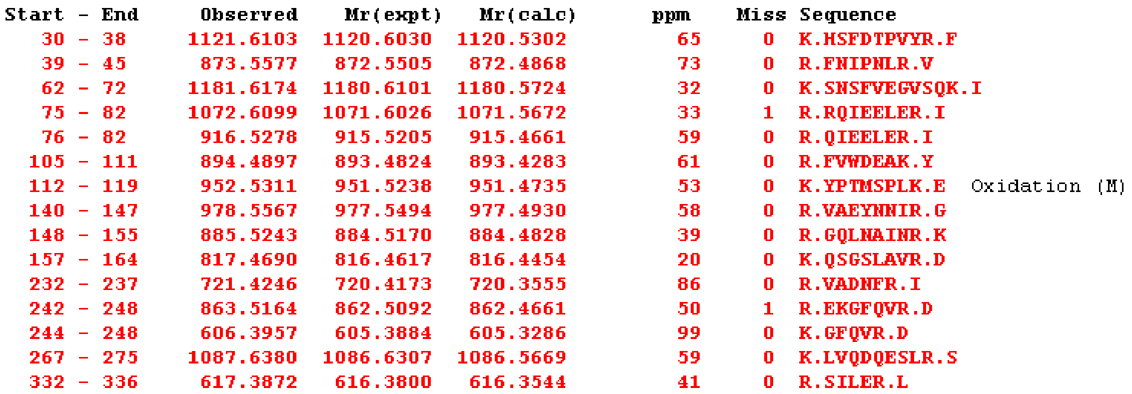


Matched peptide sequences: shown in Bold Red



1 MTSRYWVVSL PVKDSASSLW NRLQEQISK**H** **SFDTPVYRFN** **IPNLR**VGTLD
51 SLLALGDDLL K**SNSFVEGVS** **QK**IR**RQIEEL** **ER**ISGVESNA LTVDGVPVDS
101 YLTR**FVWDEA** **KYPTMSPLK**E VVDNIQSQVA KIEDDLKVR**V** **AEYNNIRGQL**
151 **NAINR**K**QSGS** **LAVR**DLSNLV KPEDIVESEH LVTLLAVVPK YSQKDWLACY
201 ETLTDYVVPR SSKKLFEDNE YALYTVTLFT R**VADNFR**IAA R**EKGFQVR**DF
251 EQSVEAQETR KQELAK**LVQD** **QESLR**SSLLQ WCYTSYGEVF SSWMHFCAVR
301 TFAESIMRYG LPPAFLACVL SPAVKSEKKV R**SILER**LCDS TNSLYWKSEE
351 DAGAMAGLAG DSETHPYVSF TINLA

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
30 - 38	1121.6103	1120.6030	1120.5302	65	0	K.HSFDTPVYR.F	
39 - 45	873.5577	872.5505	872.4868	73	0	R.FNIPNLR.V	
62 - 72	1181.6174	1180.6101	1180.5724	32	0	K.SNSFVEGVSQK.I	
75 - 82	1072.6099	1071.6026	1071.5672	33	1	R.RQIEELER.I	
76 - 82	916.5278	915.5205	915.4661	59	0	R.QIEELER.I	
105 - 111	894.4897	893.4824	893.4283	61	0	R.FVWDEAK.Y	
112 - 119	952.5311	951.5238	951.4735	53	0	K.YPTMSPLK.E	Oxidation (M)
140 - 147	978.5567	977.5494	977.4930	58	0	R.VAEYNNIR.G	
148 - 155	885.5243	884.5170	884.4828	39	0	R.GQLNAINR.K	
157 - 164	817.4690	816.4617	816.4454	20	0	K.QSGSLAVR.D	
232 - 237	721.4246	720.4173	720.3555	86	0	R.VADNFR.I	
242 - 248	863.5164	862.5092	862.4661	50	1	R.EKGFQVR.D	
244 - 248	606.3957	605.3884	605.3286	99	0	K.GFQVR.D	
267 - 275	1087.6380	1086.6307	1086.5669	59	0	K.LVQDQESLR.S	
332 - 336	617.3872	616.3800	616.3544	41	0	R.SILER.L	

Spot No.: **134**

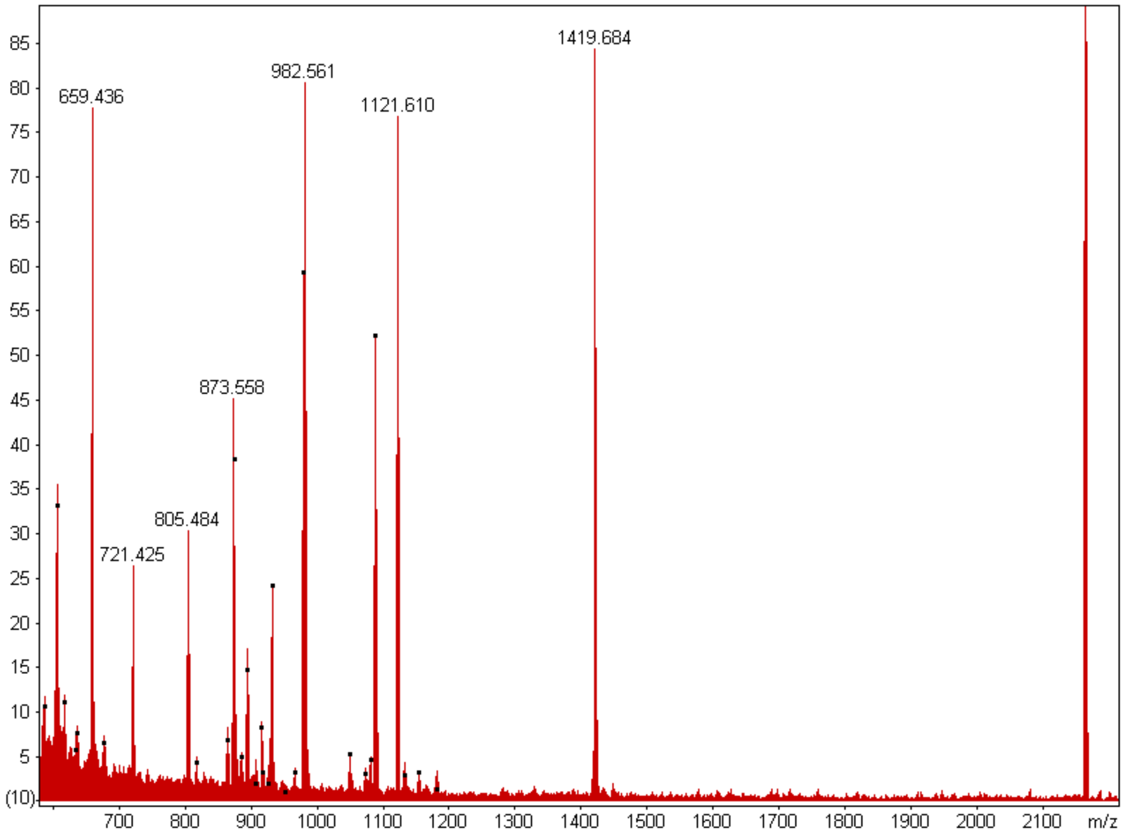
Mascot score: **97** Sequence coverage %: **31**

NCBI accession No.: **gi| 312281543**

Matched peptides No.: **11** Total peptides No.:**32**

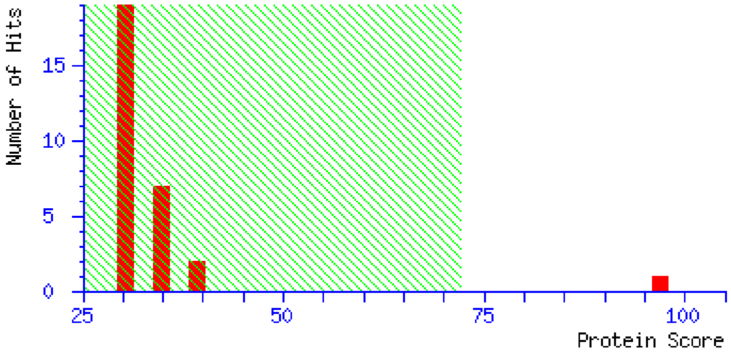
Calculated Mr: **48352** Calculated *p*I: **6.81**

Annotated PMF **spectra:**

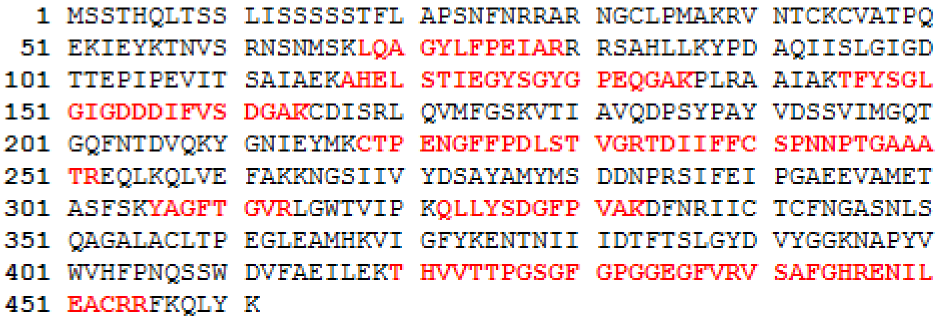


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

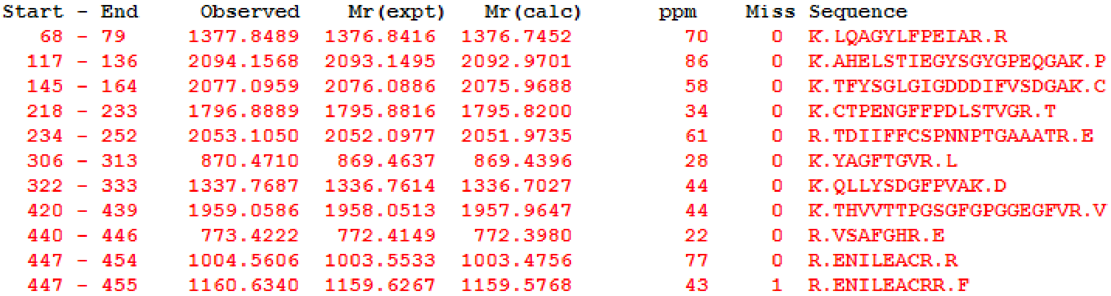


Matched peptide sequences: shown in Bold Red



```
  1 MSSTHQLTSS LISSSSSTFL APSNFNRRAR NGCLPMAKRV NTCKCVATPQ
 51 EKIEYKTNVS RNSNMSKLQA GYLFPEIARR RSAHLLKYPD AQIISLGIGD
101 TTEPIPEVIT SAIAEKAHEL STIEGYSGYG PEQGAKPLRA AIAKTFYSGL
151 GIGDDDIFVS DGAKCDISRL QVMFGSKVTI AVQDPSYPAY VDSSVIMGQT
201 GQFNTDVQKY GNIEYMKCTP ENGFFPDLST VGRTDIIFFC SPNNPTGAAA
251 TREQLKQLVE FAKKNGSIIV YDSAYAMYMS DDNPRSIFEI PGAEEVAMET
301 ASFSKYAGFT GVRLGWTVIP KQLLYSDGFP VAKDFNRIIC TCFNGASNLS
351 QAGALACLTP EGLEAMHKVI GFYKENTNII IDTFTSLGYD VYGGKNAPYV
401 WVHFPNQSSW DVFAEILEKT HVVTTPGSGF GPGGEGFVRV SAFGHRENIL
451 EACRRFKQLY K
```

Matched peptides information:



```
Start - End     Observed    Mr(expt)    Mr(calc)      ppm    Miss  Sequence
  68 - 79      1377.8489   1376.8416   1376.7452      70      0   K.LQAGYLFPEIAR.R
 117 - 136     2094.1568   2093.1495   2092.9701      86      0   K.AHELSTIEGYSGYGPEQGAK.P
 145 - 164     2077.0959   2076.0886   2075.9688      58      0   K.TFYSGLGIGDDDIFVSDGAK.C
 218 - 233     1796.8889   1795.8816   1795.8200      34      0   K.CTPENGFFPDLSTVGR.T
 234 - 252     2053.1050   2052.0977   2051.9735      61      0   R.TDIIFFCSPNNPTGAAATR.E
 306 - 313      870.4710    869.4637    869.4396      28      0   K.YAGFTGVR.L
 322 - 333     1337.7687   1336.7614   1336.7027      44      0   K.QLLYSDGFPVAK.D
 420 - 439     1959.0586   1958.0513   1957.9647      44      0   K.THVVTTPGSGFGPGGEGFVR.V
 440 - 446      773.4222    772.4149    772.3980      22      0   R.VSAFGHR.E
 447 - 454     1004.5606   1003.5533   1003.4756      77      0   R.ENILEACR.R
 447 - 455     1160.6340   1159.6267   1159.5768      43      1   R.ENILEACRR.F
```

Spot No.: **135**

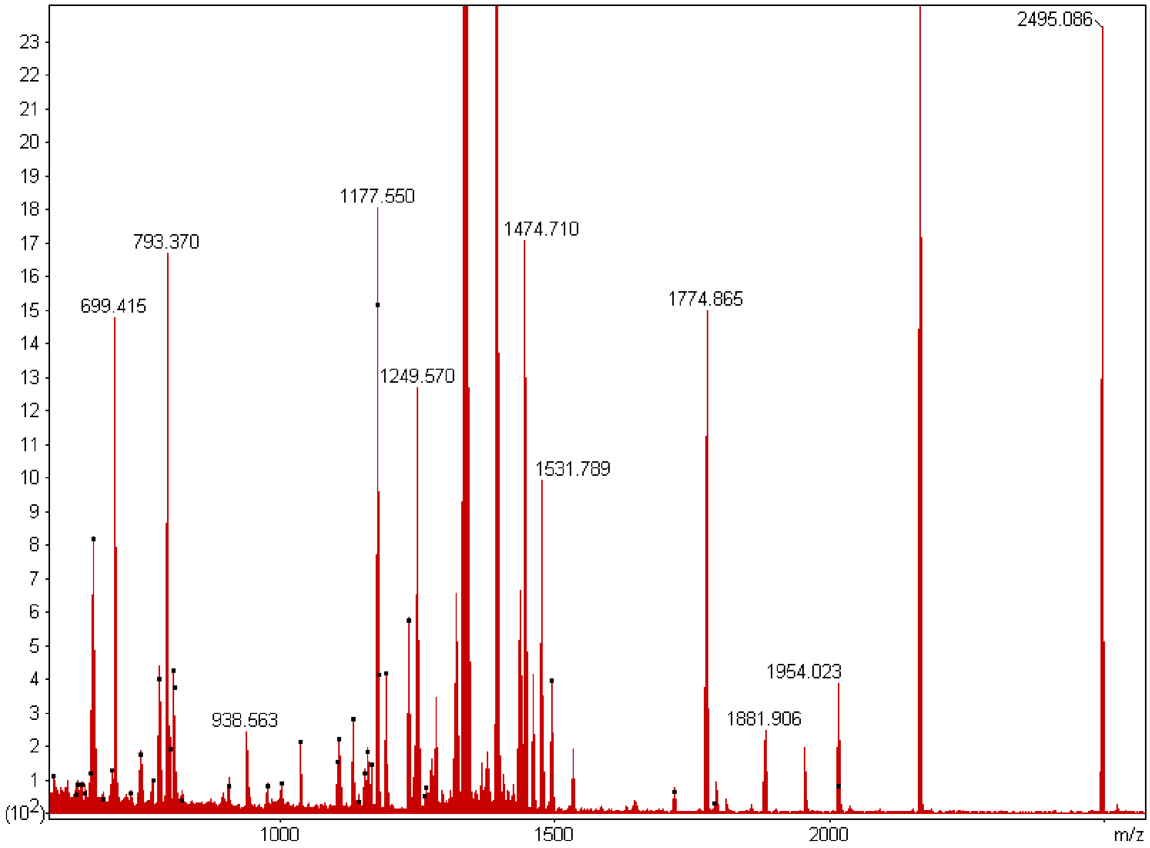
Mascot score: **104** Sequence coverage %: **34**

NCBI accession No.: **gi| 4139264**

Matched peptides No.: **12** Total peptides No.: **42**

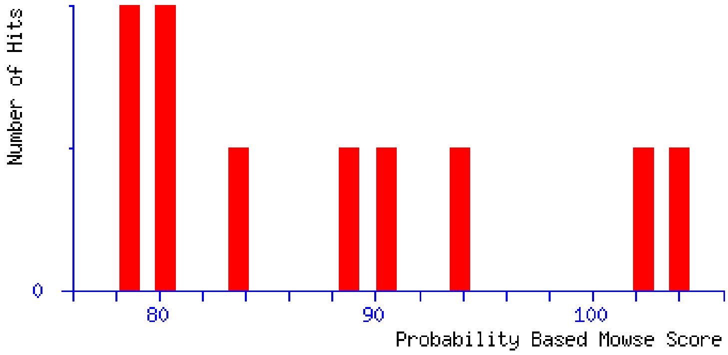
Calculated Mr: **41888** Calculated *p*I: **5.29**

Annotated PMF **spectra:**

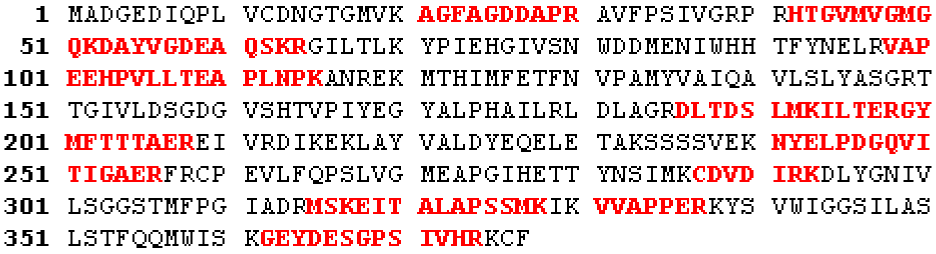


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

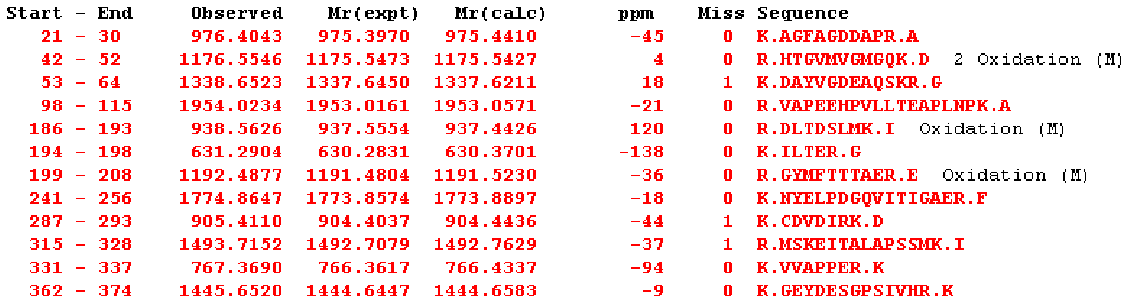


Matched peptide sequences: shown in Bold Red



1 MADGEDIQPL VCDNGTGMVK **AGFAGDDAPR** AVFPSIVGRP R**HTGVMVGMG**
51 **QKDAYVGDEA** **QSKR**GILTLK YPIEHGIVSN WDDMENIWHH TFYNELR**VAP**
101 **EEHPVLLTEA** **PLNPK**ANREK MTHIMFETFN VPAMYVAIQA VLSLYASGRT
151 TGIVLDSGDG VSHTVPIYEG YALPHAILRL DLAGR**DLTDS** **LMKILTERGY**
201 **MFTTTAER**EI VRDIKEKLAY VALDYEQELE TAKSSSSVEK **NYELPDGQVI**
251 **TIGAER**FRCP EVLFQPSLVG MEAPGIHETT YNSIMK**CDVD** **IRK**DLYGNIV
301 LSGGSTMFPG IADR**MSKEIT** **ALAPSSMK**IK **VVAPPER**KYS VWIGGSILAS
351 LSTFQQMWIS K**GEYDESGPS** **IVHR**KCF

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
21 - 30	976.4043	975.3970	975.4410	-45	0	K.AGFAGDDAPR.A
42 - 52	1176.5546	1175.5473	1175.5427	4	0	R.HTGVMVGMGQK.D 2 Oxidation (M)
53 - 64	1338.6523	1337.6450	1337.6211	18	1	K.DAYVGDEAQSKR.G
98 - 115	1954.0234	1953.0161	1953.0571	-21	0	R.VAPEEHPVLLTEAPLNPK.A
186 - 193	938.5626	937.5554	937.4426	120	0	R.DLTDSLMK.I Oxidation (M)
194 - 198	631.2904	630.2831	630.3701	-138	0	K.ILTER.G
199 - 208	1192.4877	1191.4804	1191.5230	-36	0	R.GYMFTTTAER.E Oxidation (M)
241 - 256	1774.8647	1773.8574	1773.8897	-18	0	K.NYELPDGQVITIGAER.F
287 - 293	905.4110	904.4037	904.4436	-44	1	K.CDVDIRK.D
315 - 328	1493.7152	1492.7079	1492.7629	-37	1	R.MSKEITALAPSSMK.I
331 - 337	767.3690	766.3617	766.4337	-94	0	K.VVAPPER.K
362 - 374	1445.6520	1444.6447	1444.6583	-9	0	K.GEYDESGPSIVHR.K

Spot No.: **136**

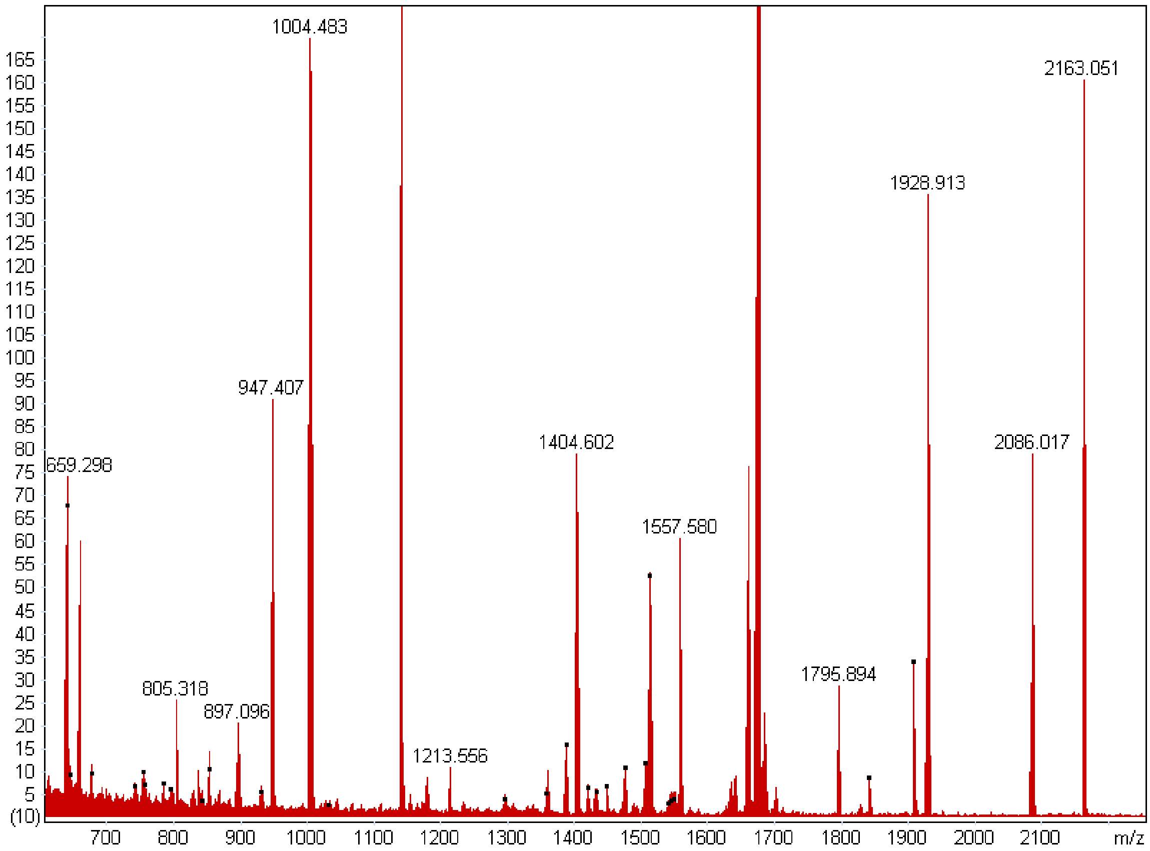
Mascot score: **95** Sequence coverage %: **27**

NCBI accession No.: **gi| 145327759**

Matched peptides No.: **13** Total peptides No.: **47**

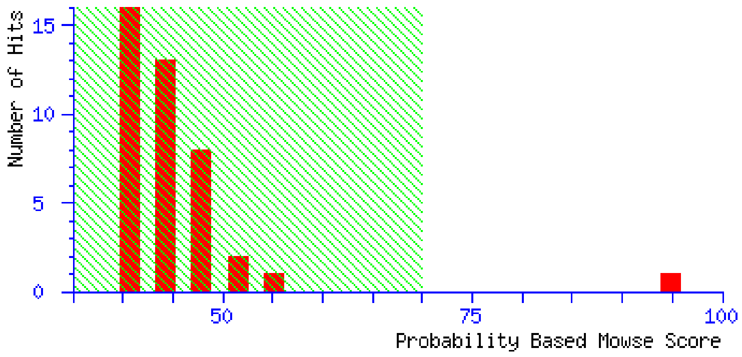
Calculated Mr: **41079** Calculated *p*I: **5.44**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 **MVHDYATTTN GTSKR**CSALP TTNTVDVSSV SDLFEFICSG PLVNK**IGITP**
51 **QR**VGQSIDKW LLYGSQLCR**L FQLNELKLTI PQK**ARLYHYY IPVFIWCEDQ
101 IALHNSKFKD GDDVPPLVIG FSAPQGCGKT TLVFALDYLF KTTKKKSATI
151 SVDDFYLTAE GQAELRKKNP GNALLEYRGN AGSHDLKLSV ETLEALSKLT
201 KEGLK**MKVPR** YNK**SAYSGR**G DRADSSTWPE VEGPLSVILF EGWMLGFKPL
251 PADVVKAVDP QLEVVNK**NLE AYYDAWDK**YI DAWVVIK**IQD PSYVYR**WR**LQ**
301 **AEIAMR**QDGQ AGMSDEEVND FVSR**YLPAYK AYLPTLYAEG PSGSDPDR**VL
351 AIDIDEERNP ILAN

Matched peptides information:

```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    1 - 14     1541.6594  1540.6521  1540.6828      -20     0   -.MVHDYATTTNGTSK.R  Oxidation (M)
    2 - 15     1550.5195  1549.5122  1549.7485     -152     1   M.VHDYATTTNGTSKR.C
   46 - 52      784.3154   783.3081   783.4603     -194     0   K.IGITPQR.V
   70 - 77     1004.4830  1003.4757  1003.5702      -94     0   R.LFQLNELK.L
   70 - 83     1684.8484  1683.8411  1683.9923      -90     1   R.LFQLNELKLTIPQK.A
  206 - 210     646.2557   645.2484   645.3632     -178     1   K.MKVPR.Y  Oxidation (M)
  214 - 219     640.2194   639.2121   639.2976     -134     0   K.SAYSGR.G
  268 - 278    1387.5521  1386.5448  1386.6092      -46     0   K.NLEAYYDAWDK.Y
  288 - 296    1140.5280  1139.5207  1139.5611      -35     0   K.IQDPSYVYR.W
  299 - 306     931.4116   930.4044   930.4957      -98     0   R.LQAEIAMR.Q
  299 - 306     947.4067   946.3994   946.4906      -96     0   R.LQAEIAMR.Q  Oxidation (M)
  325 - 330     754.3030   753.2957   753.4061     -147     0   R.YLPAYK.A
  331 - 348    1908.8467  1907.8394  1907.8901      -27     0   K.AYLPTLYAEGPSGSDPDR.V
```

Spot No.: **137**

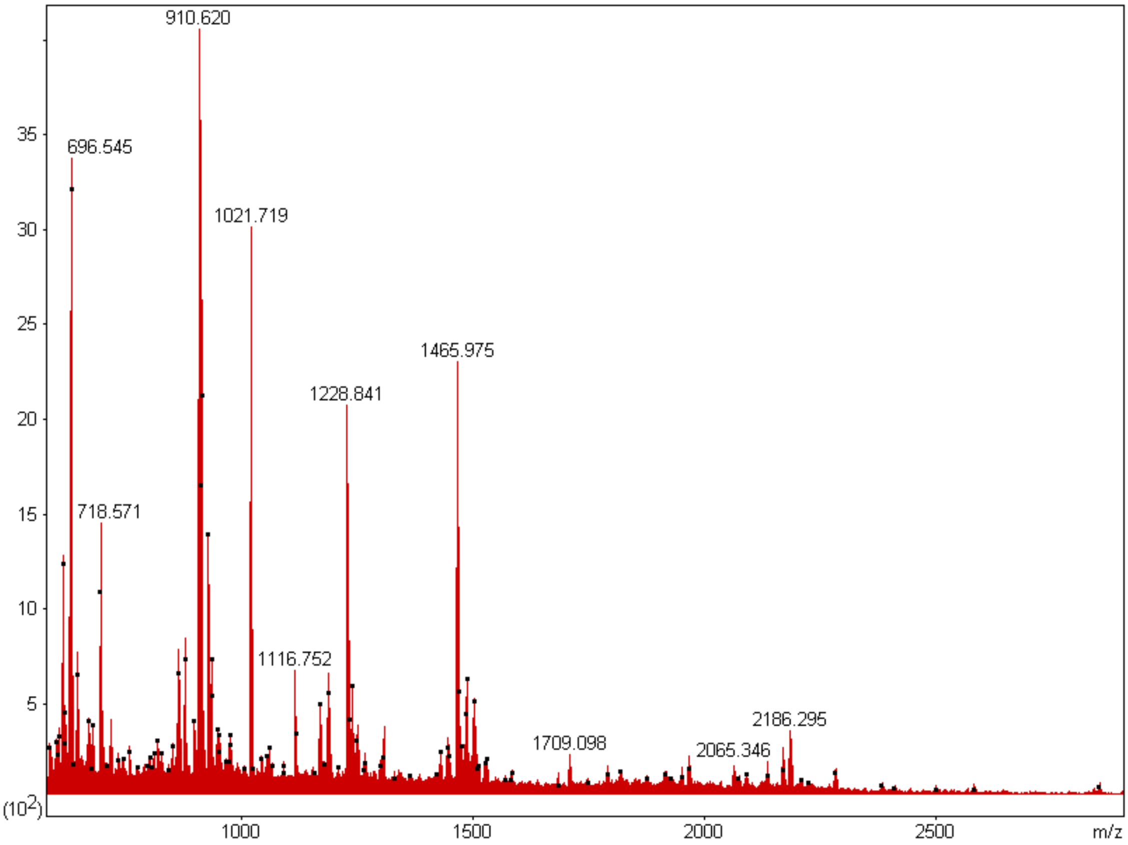
Mascot score: **163**   Sequence coverage %: **37**

NCBI accession No.: **gi| 27752799**

Matched peptides No.: **23**   Total peptides No.: **100**

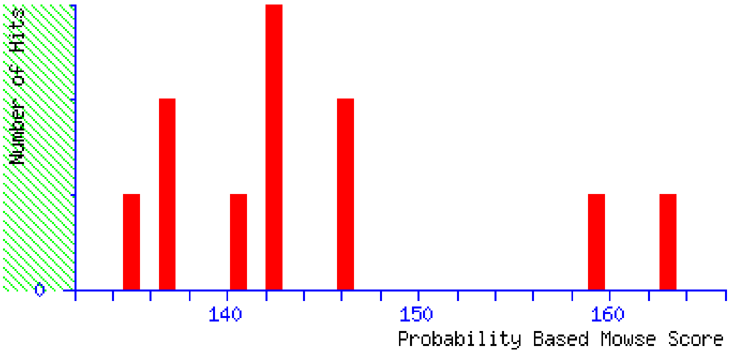
Calculated Mr: **47920**   Calculated *p*I: **6.12**

Annotated PMF **spectra:**

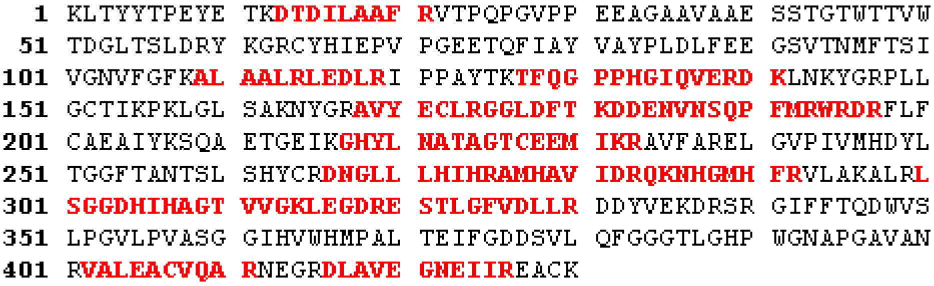


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

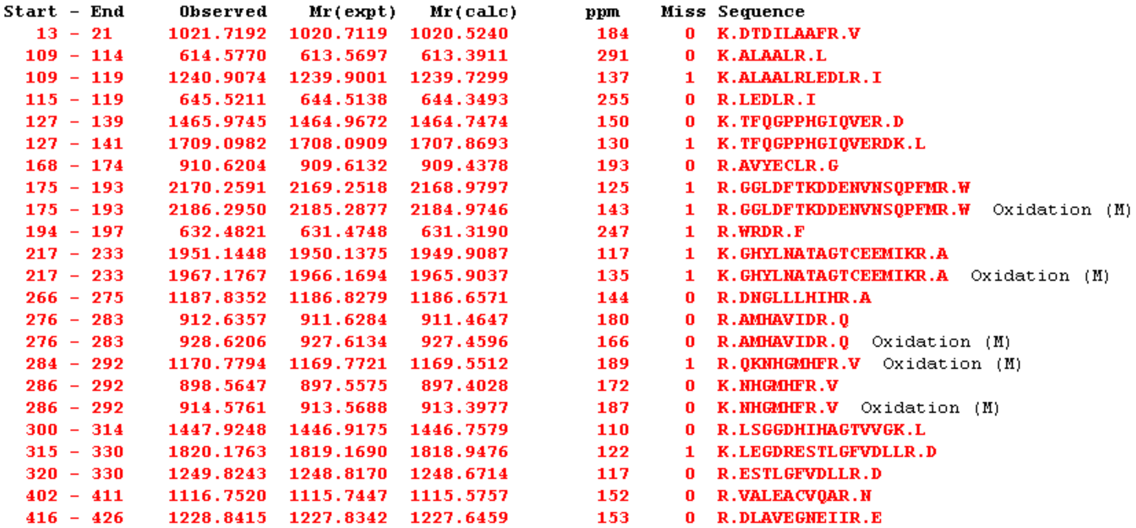


Matched peptide sequences: shown in Bold Red



1 KLTYYTPEYE TK**DTDILAAF** **R**VTPQPGVPP EEAGAAVAAE SSTGTWTTVW
51 TDGLTSLDRY KGRCYHIEPV PGEETQFIAY VAYPLDLFEE GSVTNMFTSI
101 VGNVFGFK**AL** **AALRLEDLR**I PPAYTK**TFQG** **PPHGIQVERD** **K**LNKYGRPLL
151 GCTIKPKLGL SAKNYGR**AVY** **ECLRGGLDFT** **KDDENVNSQP** **FMRWRDR**FLF
201 CAEAIYKSQA ETGEIK**GHYL** **NATAGTCEEM** **IKR**AVFAREL GVPIVMHDYL
251 TGGFTANTSL SHYCR**DNGLL** **LHIHRAMHAV** **IDRQKNHGMH** **FR**VLAKALR**L**
301 **SGGDHIHAGT** **VVGKLEGDRE** **STLGFVDLLR** DDYVEKDRSR GIFFTQDWVS
351 LPGVLPVASG GIHVWHMPAL TEIFGDDSVL QFGGGTLGHP WGNAPGAVAN
401 R**VALEACVQA** **R**NEGR**DLAVE** **GNEIIR**EACK

Matched peptides information:



```
Start - End      Observed   Mr(expt)   Mr(calc)       ppm    Miss Sequence
   13 - 21      1021.7192  1020.7119  1020.5240       184      0  K.DTDILAAFR.V
  109 - 114      614.5770   613.5697   613.3911       291      0  K.ALAALR.L
  109 - 119     1240.9074  1239.9001  1239.7299       137      1  K.ALAALRLEDLR.I
  115 - 119      645.5211   644.5138   644.3493       255      0  R.LEDLR.I
  127 - 139     1465.9745  1464.9672  1464.7474       150      0  K.TFQGPPHGIQVER.D
  127 - 141     1709.0982  1708.0909  1707.8693       130      1  K.TFQGPPHGIQVERDK.L
  168 - 174      910.6204   909.6132   909.4378       193      0  R.AVYECLR.G
  175 - 193     2170.2591  2169.2518  2168.9797       125      1  R.GGLDFTKDDENVNSQPFMR.W
  175 - 193     2186.2950  2185.2877  2184.9746       143      1  R.GGLDFTKDDENVNSQPFMR.W   Oxidation (M)
  194 - 197      632.4821   631.4748   631.3190       247      1  R.WRDR.F
  217 - 233     1951.1448  1950.1375  1949.9087       117      1  K.GHYLNATAGTCEEMIKR.A
  217 - 233     1967.1767  1966.1694  1965.9037       135      1  K.GHYLNATAGTCEEMIKR.A   Oxidation (M)
  266 - 275     1187.8352  1186.8279  1186.6571       144      0  R.DNGLLLHIHR.A
  276 - 283      912.6357   911.6284   911.4647       180      0  R.AMHAVIDR.Q
  276 - 283      928.6206   927.6134   927.4596       166      0  R.AMHAVIDR.Q   Oxidation (M)
  284 - 292     1170.7794  1169.7721  1169.5512       189      1  R.QKNHGMHFR.V   Oxidation (M)
  286 - 292      898.5647   897.5575   897.4028       172      0  K.NHGMHFR.V
  286 - 292      914.5761   913.5688   913.3977       187      0  K.NHGMHFR.V   Oxidation (M)
  300 - 314     1447.9248  1446.9175  1446.7579       110      0  R.LSGGDHIHAGTVVGK.L
  315 - 330     1820.1763  1819.1690  1818.9476       122      1  K.LEGDRESTLGFVDLLR.D
  320 - 330     1249.8243  1248.8170  1248.6714       117      0  R.ESTLGFVDLLR.D
  402 - 411     1116.7520  1115.7447  1115.5757       152      0  R.VALEACVQAR.N
  416 - 426     1228.8415  1227.8342  1227.6459       153      0  R.DLAVEGNEIIR.E
```

Spot No.: **138**

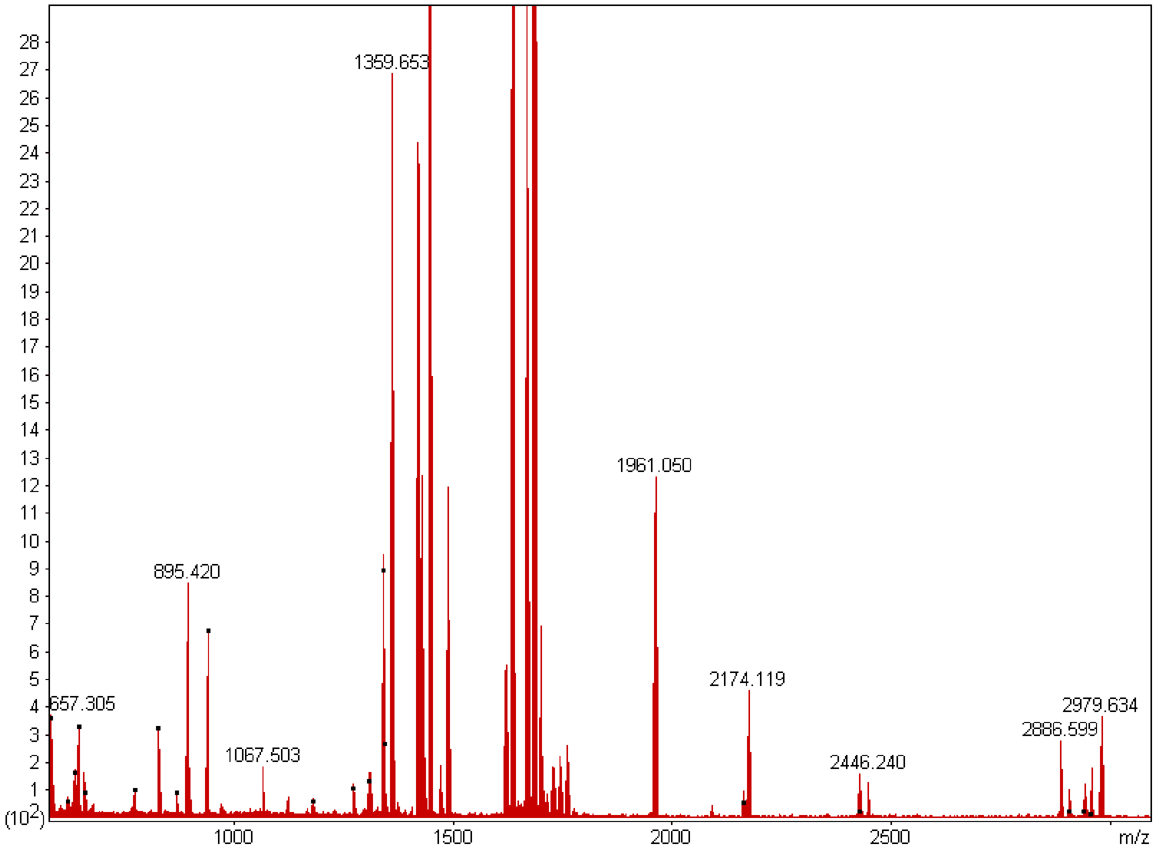
Mascot score: **140** Sequence coverage %: **38**

NCBI accession No.: **gi| 15222551**

Matched peptides No.: **17** Total peptides No.: **31**

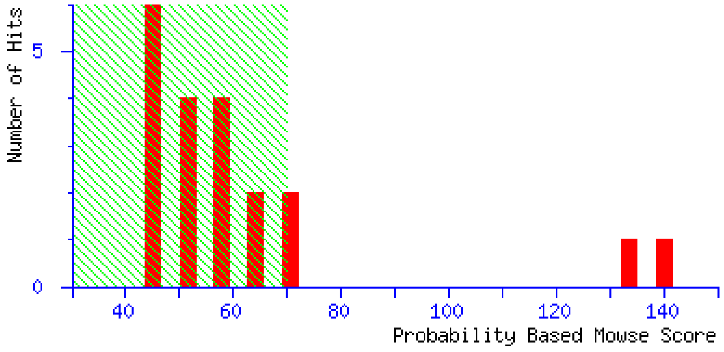
Calculated Mr: **44721** Calculated *p*I: **5.71**

Annotated PMF **spectra:**

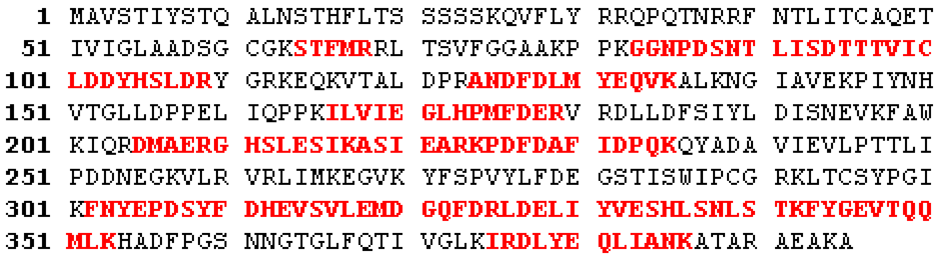


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

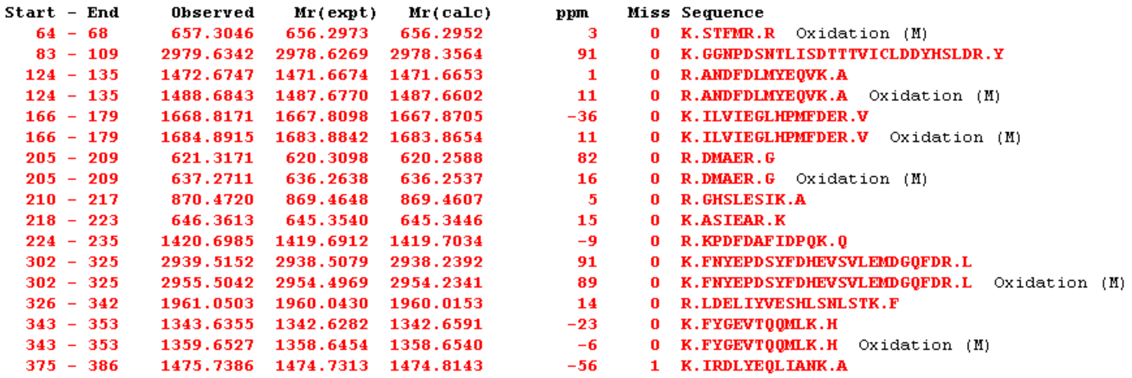


Matched peptide sequences: shown in Bold Red



1 MAVSTIYSTQ ALNSTHFLTS SSSSKQVFLY RRQPQTNRRF NTLITCAQET
51 IVIGLAADSG CGK**STFMR**RL TSVFGGAAKP PK**GGNPDSNT LISDTTTVIC**
101 **LDDYHSLDR**Y GRKEQKVTAL DPR**ANDFDLM YEQVK**ALKNG IAVEKPIYNH
151 VTGLLDPPEL IQPPK**ILVIE GLHPMFDER**V RDLLDFSIYL DISNEVKFAW
201 KIQR**DMAERG HSLESIKASI EARKPDFDAF IDPQK**QYADA VIEVLPTTLI
251 PDDNEGKVLR VRLIMKEGVK YFSPVYLFDE GSTISWIPCG RKLTCSYPGI
301 K**FNYEPDSYF DHEVSVLEMD GQFDRLDELI YVESHLSNLS TKFYGEVTQQ**
351 **MLK**HADFPGS NNGTGLFQTI VGLK**IRDLYE QLIANK**ATAR AEAKA

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
64 - 68	657.3046	656.2973	656.2952	3	0	K.STFMR.R Oxidation (M)
83 - 109	2979.6342	2978.6269	2978.3564	91	0	K.GGNPDSNTLISDTTTVICLDDYHSLDR.Y
124 - 135	1472.6747	1471.6674	1471.6653	1	0	R.ANDFDLMYEQVK.A
124 - 135	1488.6843	1487.6770	1487.6602	11	0	R.ANDFDLMYEQVK.A Oxidation (M)
166 - 179	1668.8171	1667.8098	1667.8705	-36	0	K.ILVIEGLHPMFDER.V
166 - 179	1684.8915	1683.8842	1683.8654	11	0	K.ILVIEGLHPMFDER.V Oxidation (M)
205 - 209	621.3171	620.3098	620.2588	82	0	R.DMAER.G
205 - 209	637.2711	636.2638	636.2537	16	0	R.DMAER.G Oxidation (M)
210 - 217	870.4720	869.4648	869.4607	5	0	R.GHSLESIK.A
218 - 223	646.3613	645.3540	645.3446	15	0	K.ASIEAR.K
224 - 235	1420.6985	1419.6912	1419.7034	-9	0	R.KPDFDAFIDPQK.Q
302 - 325	2939.5152	2938.5079	2938.2392	91	0	K.FNYEPDSYFDHEVSVLEMDGQFDR.L
302 - 325	2955.5042	2954.4969	2954.2341	89	0	K.FNYEPDSYFDHEVSVLEMDGQFDR.L Oxidation (M)
326 - 342	1961.0503	1960.0430	1960.0153	14	0	R.LDELIYVESHLSNLSTK.F
343 - 353	1343.6355	1342.6282	1342.6591	-23	0	K.FYGEVTQQMLK.H
343 - 353	1359.6527	1358.6454	1358.6540	-6	0	K.FYGEVTQQMLK.H Oxidation (M)
375 - 386	1475.7386	1474.7313	1474.8143	-56	1	K.IRDLYEQLIANK.A

Spot No.: **139**

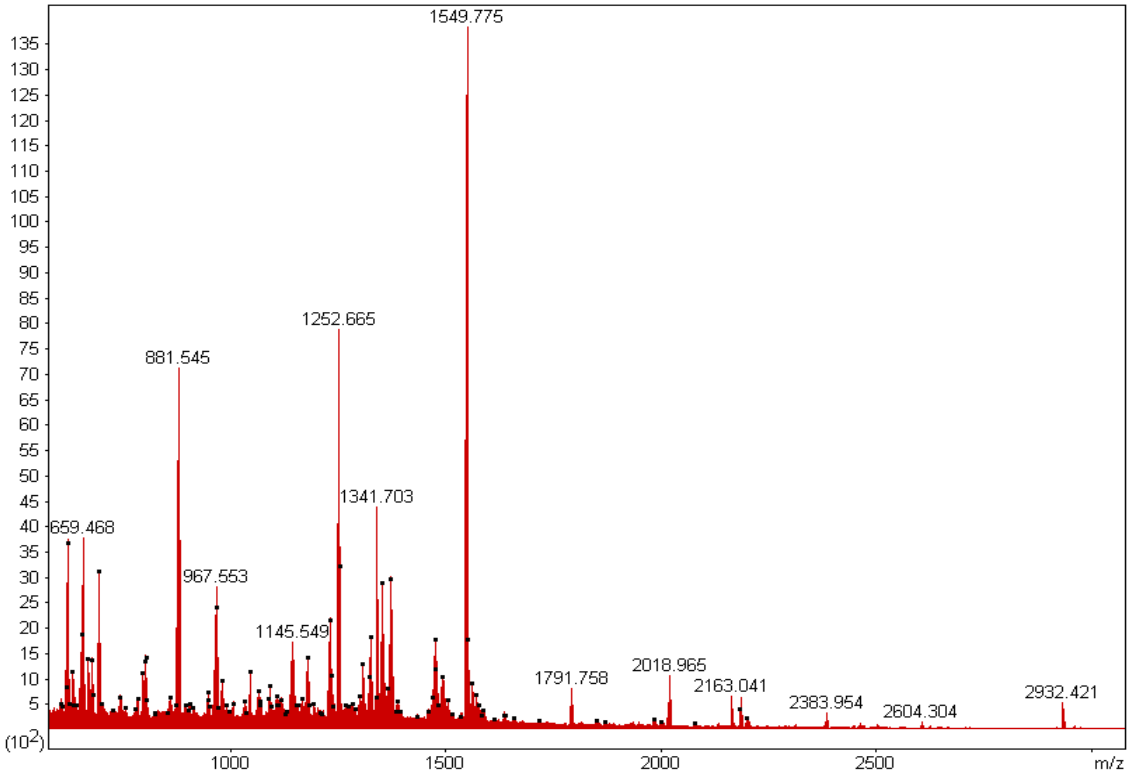
Mascot score: **93**   Sequence coverage %: **48**

NCBI accession No.: **gi| 13926291**

Matched peptides No.: **15**   Total peptides No.: **122**

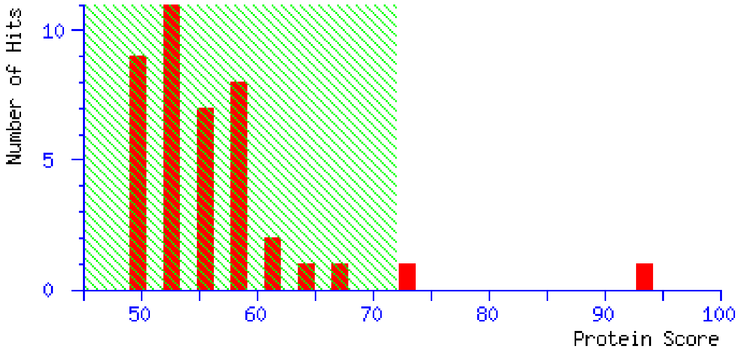
Calculated Mr: **35335**   Calculated *p*I: **5.55**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 MAASLQSTAT FLQSAKIATA PSR**GSSHLRS** **TQAVGK**SFGL ETSSAR**LTCS**
51 **FQSDFK**DFTG KCSDAVKIAG FALATSALVV SGASAEGAPK **RLTYDEIQSK**
101 **TYMEVK**GTGT ANQCPTIDGG SETFSFKPGK YAGKKFCFEP TSFTVK**ADSV**
151 **SKNAPPEFQN** **TK**LMTRLTYT LDEIEGPFEV ASDGSVNFK**E** **EDGIDYAAVT**
201 **VQLPGGERVP** **FLFTVK**QLDA SGK**PDSFTGK** **FLVPSYR**GSS FLDPKGR**GGS**
251 **TGYDNAVALP** **AGGRGDEEEL** **VKENVKNSAA** **SVGEITLK**VT K**SKPETGEVI**
301 **GVFESLQPSD** **TDLGAK**VPKD VKIQGVWYGQ LE

Matched peptides information:

```
Start - End     Observed    Mr(expt)   Mr(calc)      ppm    Miss Sequence
   24 - 36     1327.6472   1326.6399  1326.7004      -46      1  R.GSSHLRSTQAVGK.S
   47 - 56     1232.5979   1231.5906  1231.5543       29      0  R.LTCSFQSDFK.D
   91 - 100    1252.6651   1251.6578  1251.6459       10      1  K.RLTYDEIQSK.T
   92 - 100    1096.5341   1095.5268  1095.5448      -16      0  R.LTYDEIQSK.T
  101 - 106     786.4901    785.4828   785.3629      153      0  K.TYMEVK.G  Oxidation (M)
  147 - 152     606.3794    605.3722   605.3020      116      0  K.ADSVSK.N
  153 - 162    1145.5487   1144.5414  1144.5513       -9      0  K.NAPPEFQNTK.L
  190 - 208    2018.9649   2017.9576  2017.9593       -1      0  K.EEDGIDYAAVTVQLPGGER.V
  209 - 216     950.5348    949.5275   949.5637      -38      0  R.VPFLFTVK.Q
  224 - 237    1613.7542   1612.7469  1612.8250      -48      1  K.PDSFTGKFLVPSYR.G
  231 - 237     881.5445    880.5373   880.4807       64      0  K.FLVPSYR.G
  248 - 264    1562.7964   1561.7891  1561.7485       26      0  R.GGSTGYDNAVALPAGGR.G
  265 - 276    1388.6855   1387.6782  1387.6831       -3      1  R.GDEEELVKENVK.N
  273 - 288    1659.7999   1658.7926  1658.8839      -55      1  K.ENVKNSAASVGEITLK.V
  292 - 316    2604.3037   2603.2964  2603.2966       -0      1  K.SKPETGEVIGVFESLQPSDTDLGAK.V
```

Spot No.: **140**

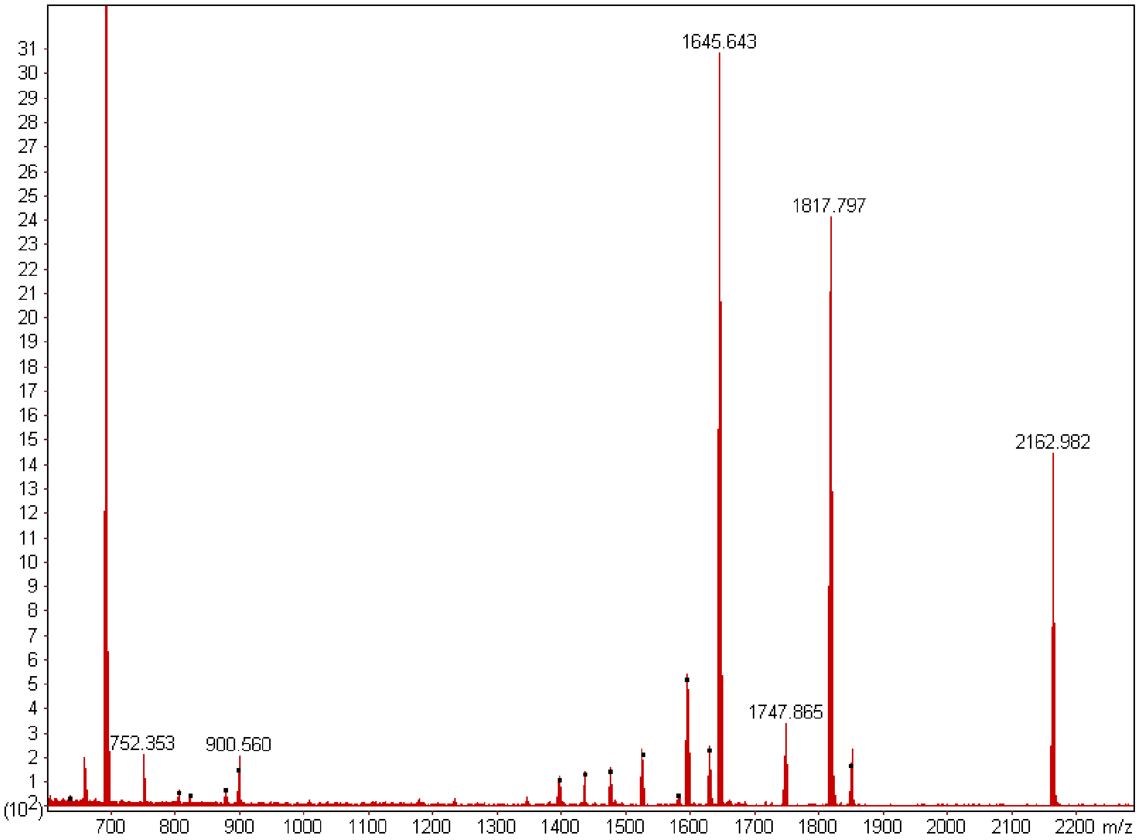
Mascot score: **103** Sequence coverage %: **20**

NCBI accession No.: **gi| 154017627**

Matched peptides No.: **8** Total peptides No.: **23**

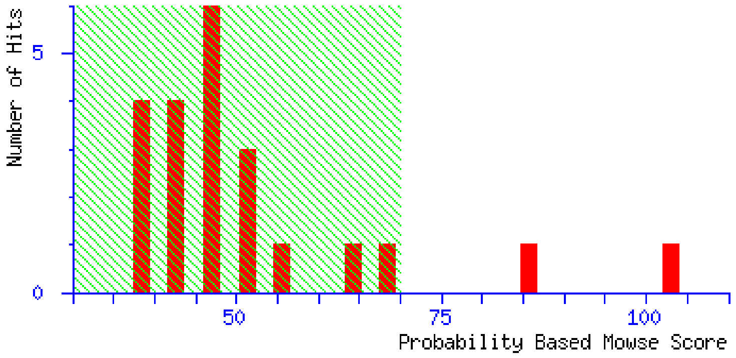
Calculated Mr: **47865** Calculated *p*I: **6.04**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 M**AQILAPSMQ CQMKLSKGLT SSMTPSPWTS ILLK**QGQKGS IKCSTKFRVC
51 ASLQSDHGTV NR**VEQLLNLD VTPYTDK**IIA EYIWIGGTGI DLRSKSRTLS
101 KPVEHPSELP KWNYDGSSTG QAPGQDSEVI LYPQAIFKDP FRGGNNILVI
151 CDAYTPAGEP IPTNKRHKAA EIFNNQKVAS EVPWFGIEQE YTLLQPNVSW
201 PLGWPVGAYP GPQGPYYCGV GADKSFGRDV SDAHYKACLY AGINISGTNG
251 EVMPGQWEFQ VGPSVGIEAG DHVWCAR**YLL ER**ITEQIGVV MTLDPKPIEG
301 DWNGAGCHTN YSTKTMREEG GFEVIKK**AIL NLSLR**HKDHI SAYGEGNERR
351 LTGK**HETADI NTFSWGVANR GCSIR**VGRDT EKEGK**GYLED R**RPASNMDPY
401 VVTGLLAETT ILWEPTLEAE ALAAQKLSLN V

Matched peptides information:

Start – End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
2 – 17	1849.7922	1848.7849	1848.9260	-76	1	M.AQILAPSMQCQMKLSK.G	Oxidation (M)
15 – 34	2162.9815	2161.9742	2162.1657	-89	1	K.LSKGLTSSMTPSPWTSILLK.Q	Oxidation (M)
63 – 77	1747.8653	1746.8580	1746.9040	-26	0	R.VEQLLNLDVTPYTDK.I	
278 – 282	693.3967	692.3894	692.3857	5	0	R.YLLER.I	
328 – 335	899.5485	898.5412	898.5600	-21	0	K.AILNLSLR.H	
355 – 370	1817.7971	1816.7898	1816.8493	-33	0	K.HETADINTFSWGVANR.G	
371 – 375	592.3017	591.2944	591.2799	25	0	R.GCSIR.V	
386 – 391	752.3533	751.3460	751.3501	-5	0	K.GYLEDR.R	

Spot No.: **141**

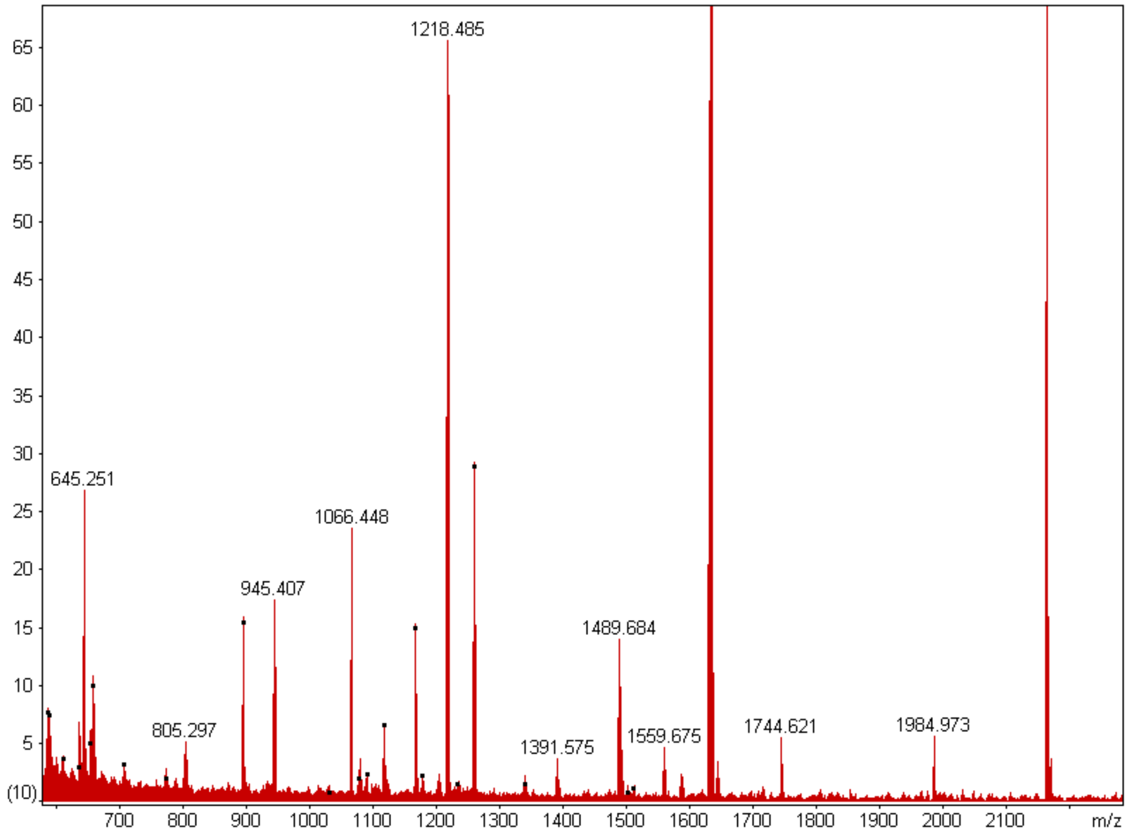
Mascot score: **114**   Sequence coverage %: **28**

NCBI accession No.: **gi| 15233888**

Matched peptides No.: **13**   Total peptides No.: **27**

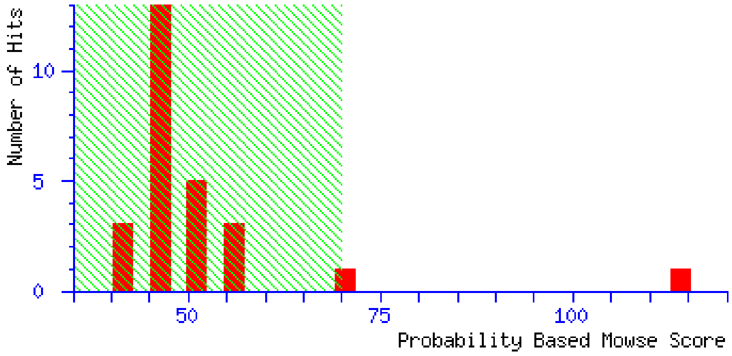
Calculated Mr: **46526**   Calculated *p*I: **6.08**

Annotated PMF **spectra:**

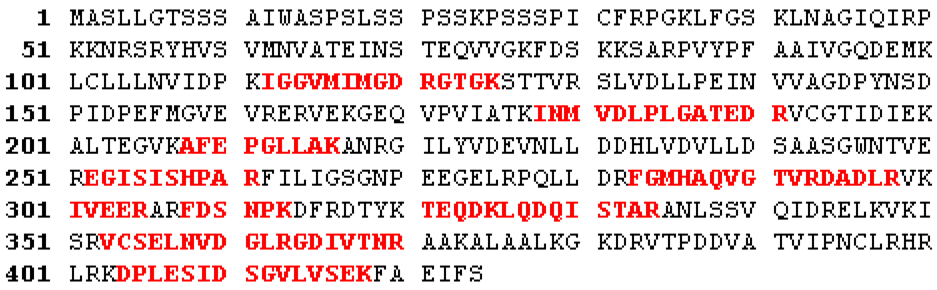


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).

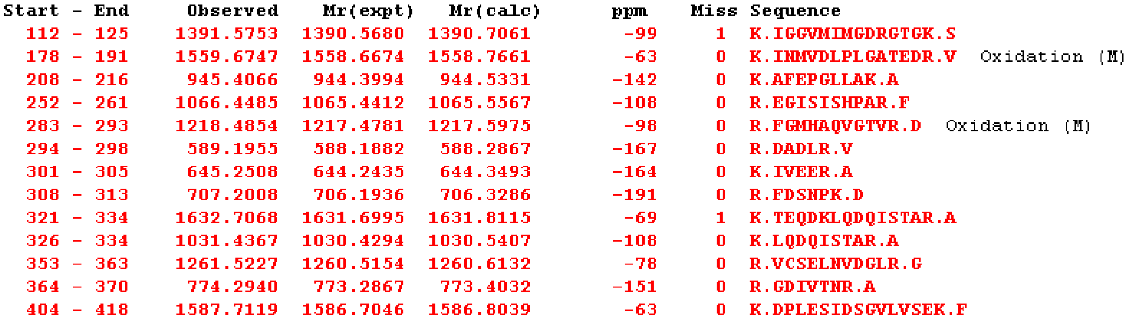


Matched peptide sequences: shown in Bold Red



1 MASLLGTSSS AIWASPSLSS PSSKPSSSPI CFRPGKLFGS KLNAGIQIRP
51 KKNRSRYHVS VMNVATEINS TEQVVGKFDS KKSARPVYPF AAIVGQDEMK
101 LCLLLNVIDP K**IGGVMIMGD RGTGK**STTVR SLVDLLPEIN VVAGDPYNSD
151 PIDPEFMGVE VRERVEKGEQ VPVIATK**INM VDLPLGATED R**VCGTIDIEK
201 ALTEGVK**AFE PGLLAK**ANRG ILYVDEVNLL DDHLVDVLLD SAASGWNTVE
251 R**EGISISHPA R**FILIGSGNP EEGELRPQLL DR**FGMHAQVG TVRDADLR**VK
301 **IVEER**AR**FDS NPK**DFRDTYK **TEQDKLQDQI STAR**ANLSSV QIDRELKVKI
351 SR**VCSELNVD GLRGDIVTNR** AAKALAALKG KDRVTPDDVA TVIPNCLRHR
401 LRK**DPLESID SGVLVSEK**FA EIFS

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
112 - 125	1391.5753	1390.5680	1390.7061	-99	1	K.IGGVMIMGDRGTGK.S	
178 - 191	1559.6747	1558.6674	1558.7661	-63	0	K.INMVDLPLGATEDR.V	Oxidation (M)
208 - 216	945.4066	944.3994	944.5331	-142	0	K.AFEPGLLAK.A	
252 - 261	1066.4485	1065.4412	1065.5567	-108	0	R.EGISISHPAR.F	
283 - 293	1218.4854	1217.4781	1217.5975	-98	0	R.FGMHAQVGTVR.D	Oxidation (M)
294 - 298	589.1955	588.1882	588.2867	-167	0	R.DADLR.V	
301 - 305	645.2508	644.2435	644.3493	-164	0	K.IVEER.A	
308 - 313	707.2008	706.1936	706.3286	-191	0	R.FDSNPK.D	
321 - 334	1632.7068	1631.6995	1631.8115	-69	1	K.TEQDKLQDQISTAR.A	
326 - 334	1031.4367	1030.4294	1030.5407	-108	0	K.LQDQISTAR.A	
353 - 363	1261.5227	1260.5154	1260.6132	-78	0	R.VCSELNVDGLR.G	
364 - 370	774.2940	773.2867	773.4032	-151	0	R.GDIVTNR.A	
404 - 418	1587.7119	1586.7046	1586.8039	-63	0	K.DPLESIDSGVLVSEK.F	

Spot No.: **142**

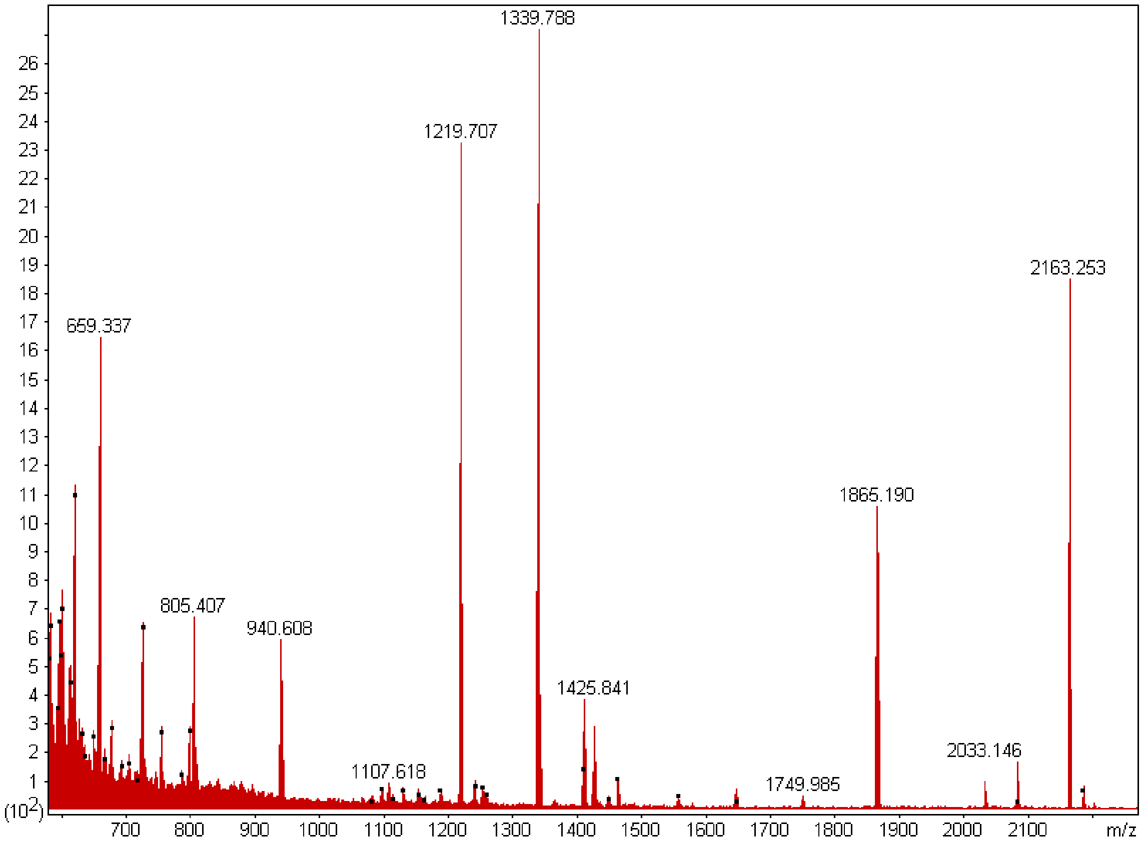
Mascot score: **101**   Sequence coverage %: **34**

NCBI accession No.: **gi| 297841979**

Matched peptides No.: **12**   Total peptides No.: **28**

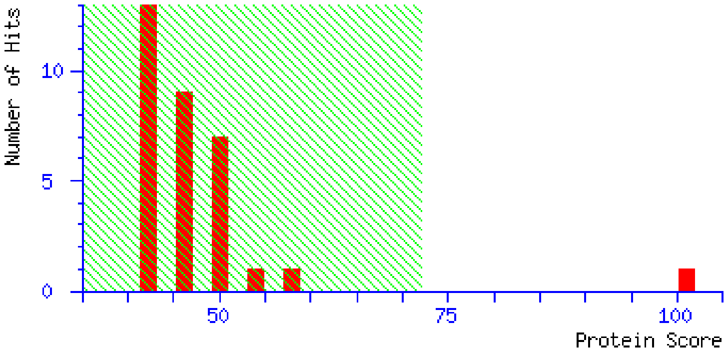
Calculated Mr: **32482**   Calculated *p*I: **5.03**

Annotated PMF **spectra:**

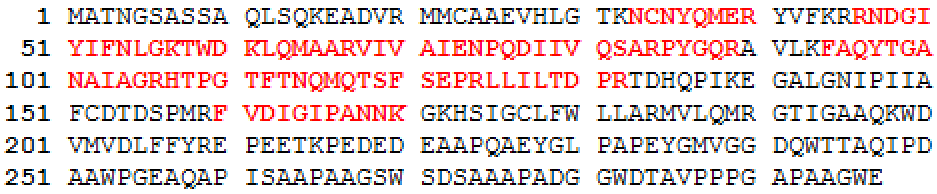


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).

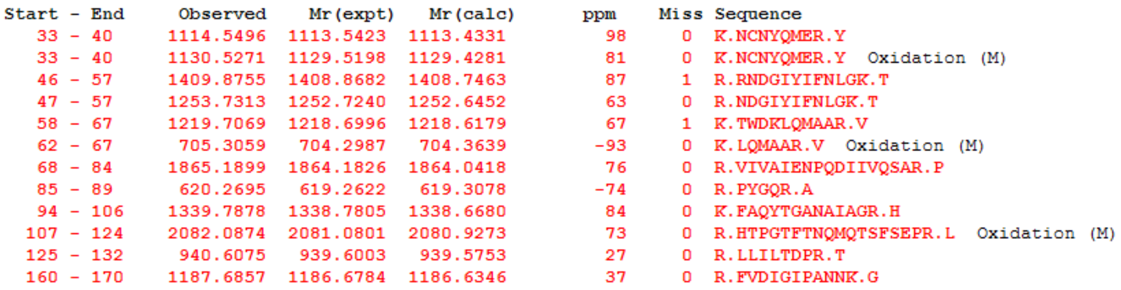


Matched peptide sequences: shown in Bold Red



```
  1 MATNGSASSA QLSQKEADVR MMCAAEVHLG TKNCNYQMER YVFKRRNDGI
 51 YIFNLGKTWD KLQMAARVIV AIENPQDIIV QSARPYGQRA VLKFAQYTGA
101 NAIAGRHTPG TFTNQMQTSF SEPRLLILTD PRTDHQPIKE GALGNIPIIA
151 FCDTDSPMRF VDIGIPANNK GKHSIGCLFW LLARMVLQMR GTIGAAQKWD
201 VMVDLFFYRE PEETKPEDED EAAPQAEYGL PAPEYGMVGG DQWTTAQIPD
251 AAWPGEAQAP ISAAPAAGSW SDSAAAPADG GWDTAVPPPG APAAGWE
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss Sequence
   33 - 40     1114.5496  1113.5423  1113.4331       98     0  K.NCNYQMER.Y
   33 - 40     1130.5271  1129.5198  1129.4281       81     0  K.NCNYQMER.Y  Oxidation (M)
   46 - 57     1409.8755  1408.8682  1408.7463       87     1  R.RNDGIYIFNLGK.T
   47 - 57     1253.7313  1252.7240  1252.6452       63     0  R.NDGIYIFNLGK.T
   58 - 67     1219.7069  1218.6996  1218.6179       67     1  K.TWDKLQMAAR.V
   62 - 67      705.3059   704.2987   704.3639      -93     0  K.LQMAAR.V  Oxidation (M)
   68 - 84     1865.1899  1864.1826  1864.0418       76     0  R.VIVAIENPQDIIVQSAR.P
   85 - 89      620.2695   619.2622   619.3078      -74     0  R.PYGQR.A
   94 - 106    1339.7878  1338.7805  1338.6680       84     0  K.FAQYTGANAIAGR.H
  107 - 124    2082.0874  2081.0801  2080.9273       73     0  R.HTPGTFTNQMQTSFSEPR.L  Oxidation (M)
  125 - 132     940.6075   939.6003   939.5753       27     0  R.LLILTDPR.T
  160 - 170    1187.6857  1186.6784  1186.6346       37     0  R.FVDIGIPANNK.G
```

Spot No.: **143**

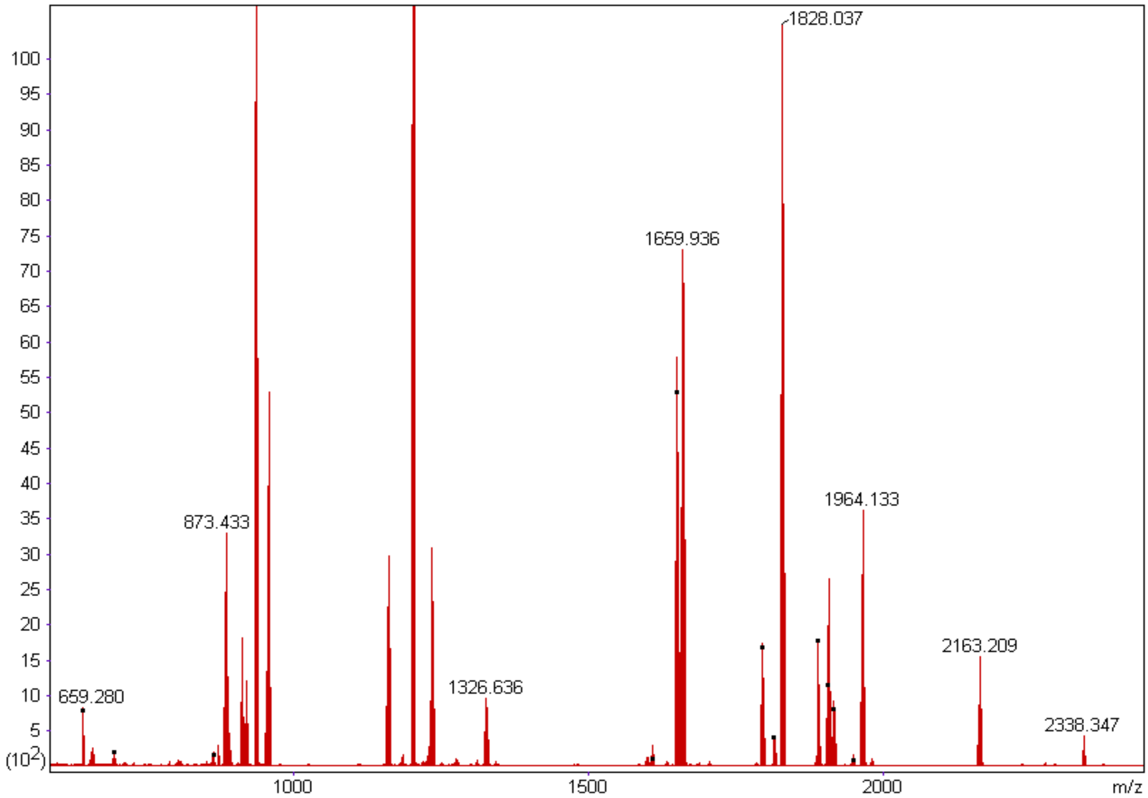
Mascot score: **191** Sequence coverage %: **37**

NCBI accession No.: **gi| 15228149**

Matched peptides No.: **16** Total peptides No.: **23**

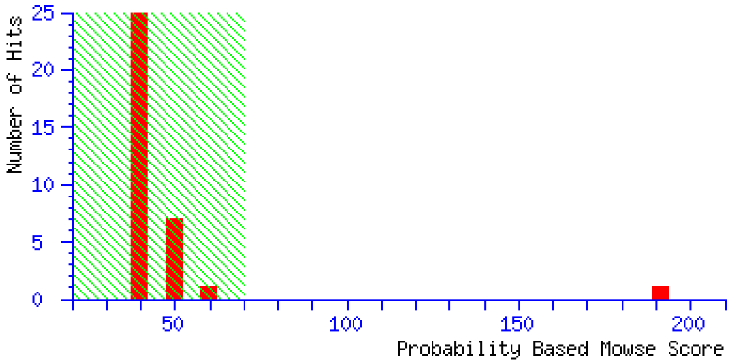
Calculated Mr: **42787** Calculated p*I*: **6.17**

Annotated PMF **spectra:**

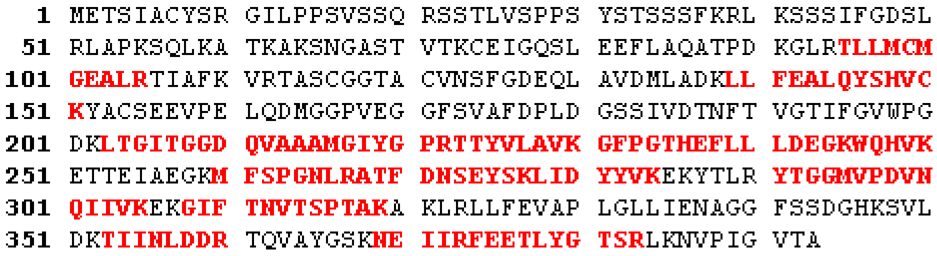


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

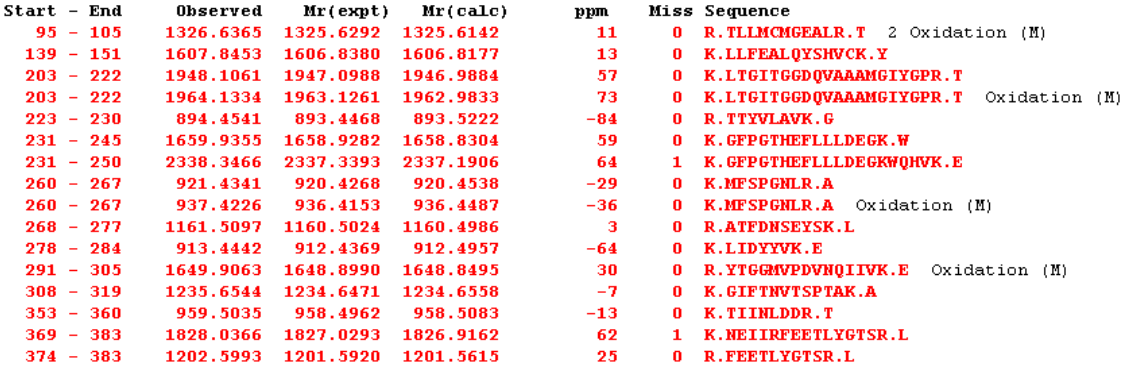


Matched peptide sequences: shown in Bold Red



1 METSIACYSR GILPPSVSSQ RSSTLVSPPS YSTSSSFKRL KSSSIFGDSL
51 RLAPKSQLKA TKAKSNGAST VTKCEIGQSL EEFLAQATPD KGLR**TLLMCM**
101 **GEALR**TIAFK VRTASCGGTA CVNSFGDEQL AVDMLADK**LL FEALQYSHVC**
151 **K**YACSEEVPE LQDMGGPVEG GFSVAFDPLD GSSIVDTNFT VGTIFGVWPG
201 DK**LTGITGGD QVAAAMGIYG PRTTYVLAVK GFPGTHEFLL LDEGKWQHVK**
251 ETTEIAEGK**M FSPGNLRATF DNSEYSKLID YYVK**EKYTLR **YTGGMVPDVN**
301 **QIIVK**EK**GIF TNVTSPTAK**A KLRLLFEVAP LGLLIENAGG FSSDGHKSVL
351 DK**TIINLDDR** TQVAYGSK**NE IIRFEETLYG TSR**LKNVPIG VTA

Matched peptides information:



Start – End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
95 – 105	1326.6365	1325.6292	1325.6142	11	0	R.TLLMCMGEALR.T	2 Oxidation (M)
139 – 151	1607.8453	1606.8380	1606.8177	13	0	K.LLFEALQYSHVCK.Y	
203 – 222	1948.1061	1947.0988	1946.9884	57	0	K.LTGITGGDQVAAAMGIYGPR.T	
203 – 222	1964.1334	1963.1261	1962.9833	73	0	K.LTGITGGDQVAAAMGIYGPR.T	Oxidation (M)
223 – 230	894.4541	893.4468	893.5222	-84	0	R.TTYVLAVK.G	
231 – 245	1659.9355	1658.9282	1658.8304	59	0	K.GFPGTHEFLLLDEGK.W	
231 – 250	2338.3466	2337.3393	2337.1906	64	1	K.GFPGTHEFLLLDEGKWQHVK.E	
260 – 267	921.4341	920.4268	920.4538	-29	0	K.MFSPGNLR.A	
260 – 267	937.4226	936.4153	936.4487	-36	0	K.MFSPGNLR.A	Oxidation (M)
268 – 277	1161.5097	1160.5024	1160.4986	3	0	R.ATFDNSEYSK.L	
278 – 284	913.4442	912.4369	912.4957	-64	0	K.LIDYYVK.E	
291 – 305	1649.9063	1648.8990	1648.8495	30	0	R.YTGGMVPDVNQIIVK.E	Oxidation (M)
308 – 319	1235.6544	1234.6471	1234.6558	-7	0	K.GIFTNVTSPTAK.A	
353 – 360	959.5035	958.4962	958.5083	-13	0	K.TIINLDDR.T	
369 – 383	1828.0366	1827.0293	1826.9162	62	1	K.NEIIRFEETLYGTSR.L	
374 – 383	1202.5993	1201.5920	1201.5615	25	0	R.FEETLYGTSR.L	

Spot No.: **144**

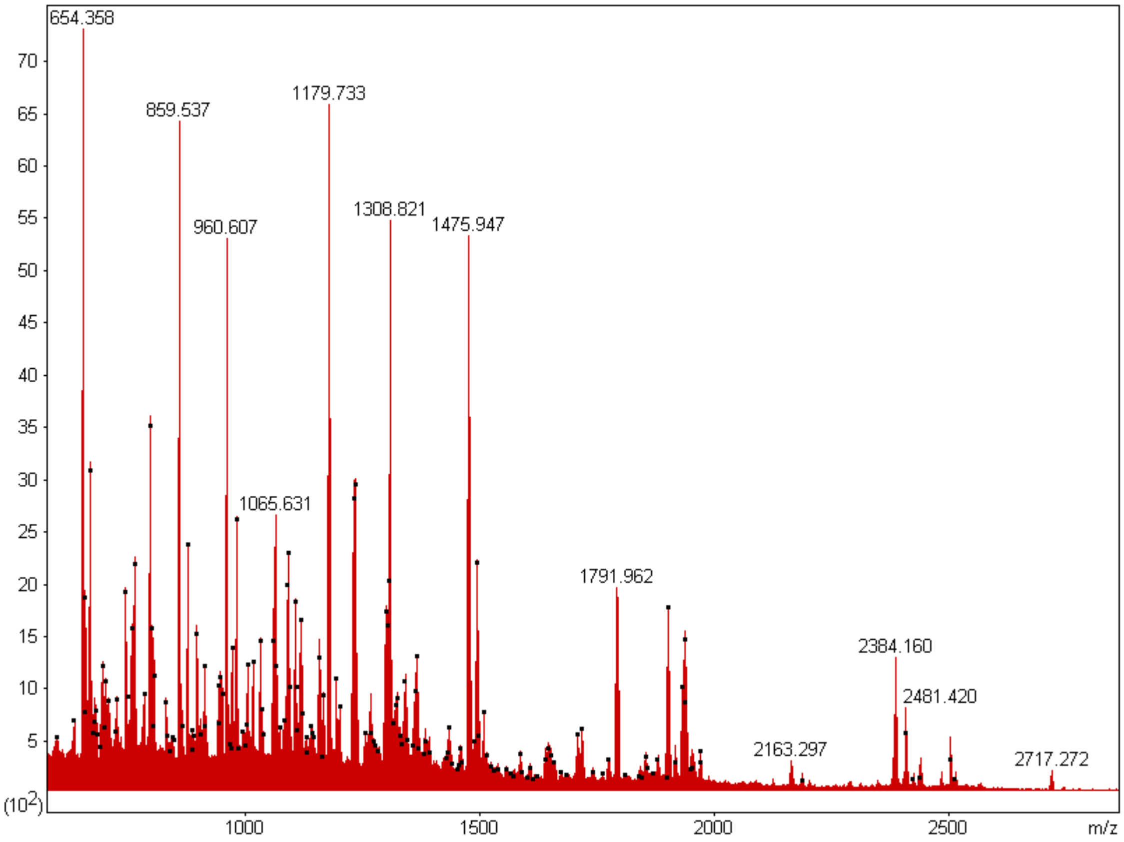
Mascot score: **93** Sequence coverage %: **44**

NCBI accession No.: **gi| 21593565**

Matched peptides No.: **18** Total peptides No.: **70**

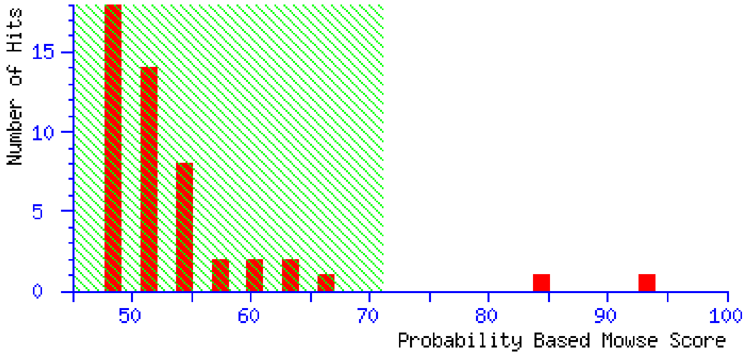
Calculated Mr: **35982** Calculated p*I*: **7.00**

Annotated PMF **spectra:**

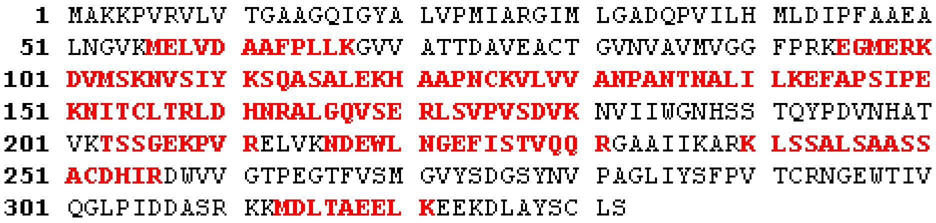


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

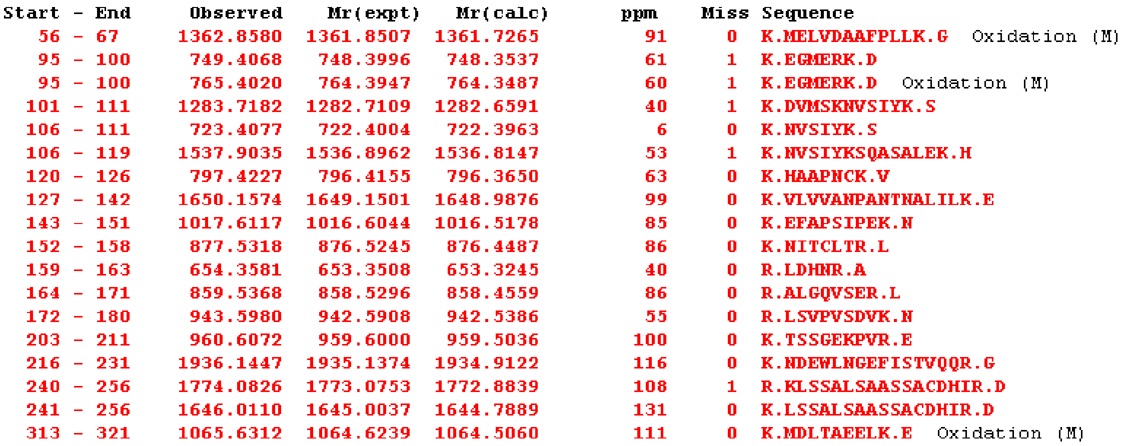


Matched peptide sequences: shown in Bold Red



```
  1 MAKKPVRVLV TGAAGQIGYA LVPMIARGIM LGADQPVILH MLDIPFAAEA
 51 LNGVKMELVD AAFPLLKGVV ATTDAVEACT GVNVAVMVGG FPRKEGMERK
101 DVMSKNVSIY KSQASALEKH AAPNCKVLVV ANPANTNALI LKEFAPSIPE
151 KNITCLTRLD HNRALGQVSE RLSVPVSDVK NVIIWGNHSS TQYPDVNHAT
201 VKTSSGEKPV RELVKNDEWL NGEFISTVQQ RGAAIIKARK LSSALSAASS
251 ACDHIRDWVV GTPEGTFVSM GVYSDGSYNV PAGLIYSFPV TCRNGEWTIV
301 QGLPIDDASR KKMDLTAEEL KEEKDLAYSC LS
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   56 - 67     1362.8580  1361.8507  1361.7265       91      0  K.MELVDAAFPLLK.G   Oxidation (M)
   95 - 100     749.4068   748.3996   748.3537       61      1  K.EGMERK.D   Oxidation (M)
   95 - 100     765.4020   764.3947   764.3487       60      1  K.EGMERK.D   Oxidation (M)
  101 - 111    1283.7182  1282.7109  1282.6591       40      1  K.DVMSKNVSIYK.S
  106 - 111     723.4077   722.4004   722.3963        6      0  K.NVSIYK.S
  106 - 119    1537.9035  1536.8962  1536.8147       53      1  K.NVSIYKSQASALEK.H
  120 - 126     797.4227   796.4155   796.3650       63      0  K.HAAPNCK.V
  127 - 142    1650.1574  1649.1501  1648.9876       99      0  K.VLVVANPANTNALILK.E
  143 - 151    1017.6117  1016.6044  1016.5178       85      0  K.EFAPSIPEK.N
  152 - 158     877.5318   876.5245   876.4487       86      0  K.NITCLTR.L
  159 - 163     654.3581   653.3508   653.3245       40      0  R.LDHNR.A
  164 - 171     859.5368   858.5296   858.4559       86      0  R.ALGQVSER.L
  172 - 180     943.5980   942.5908   942.5386       55      0  R.LSVPVSDVK.N
  203 - 211     960.6072   959.6000   959.5036      100      0  K.TSSGEKPVR.E
  216 - 231    1936.1447  1935.1374  1934.9122      116      0  K.NDEWLNGEFISTVQQR.G
  240 - 256    1774.0826  1773.0753  1772.8839      108      1  R.KLSSALSAASSACDHIR.D
  241 - 256    1646.0110  1645.0037  1644.7889      131      0  K.LSSALSAASSACDHIR.D
  313 - 321    1065.6312  1064.6239  1064.5060      111      0  K.MDLTAEELK.E   Oxidation (M)
```

Spot No.: **145**

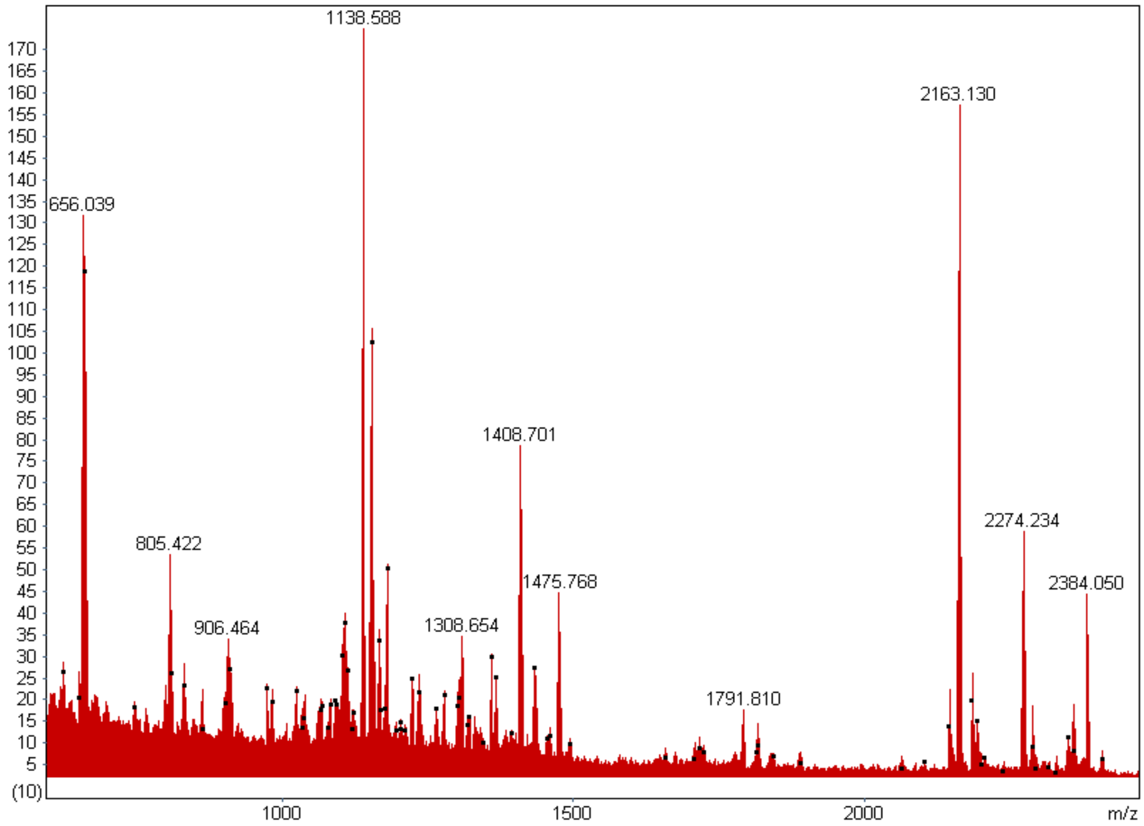
Mascot score: **81** Sequence coverage %: **27**

NCBI accession No.: **gi| 303275508**

Matched peptides No.: **22** Total peptides No.: **87**

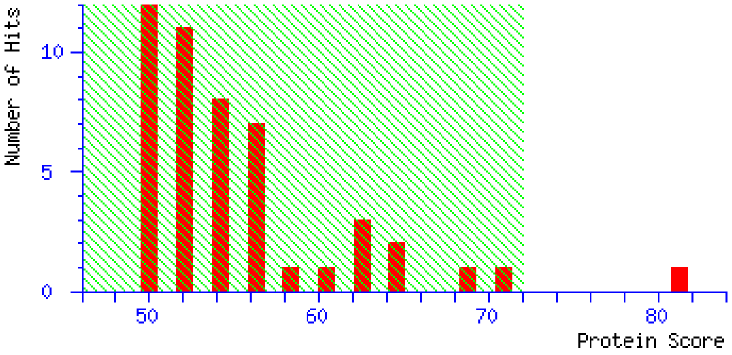
Calculated Mr: **99906** Calculated p*I*: **5.37**

Annotated PMF **spectra:**

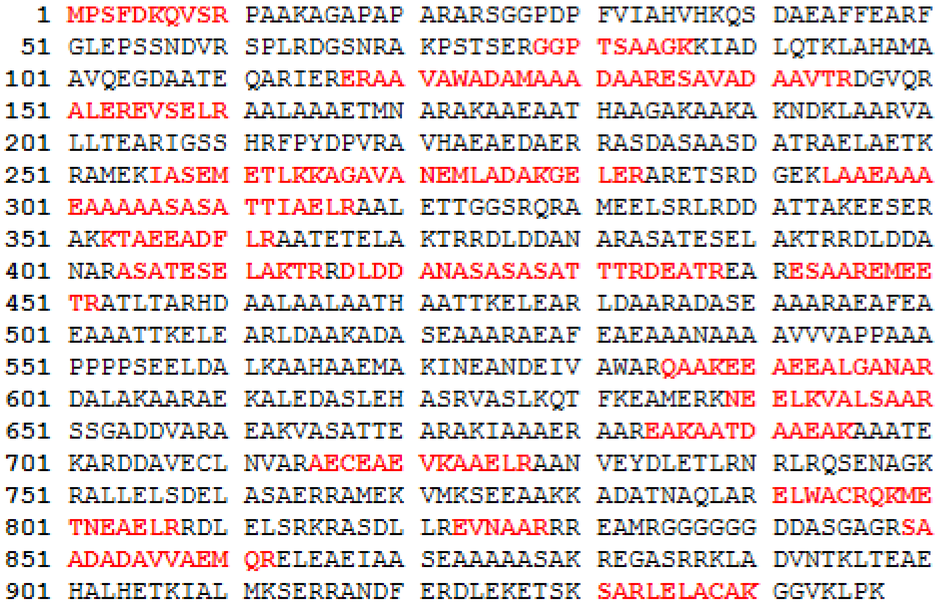


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).

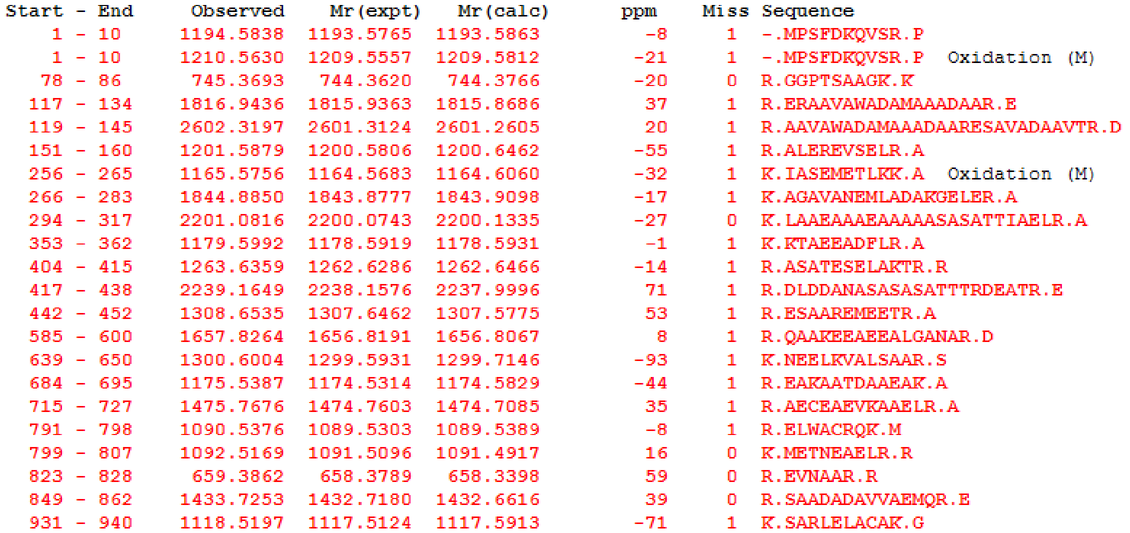


Matched peptide sequences: shown in Bold Red



```
  1 MPSFDKQVSR PAAKAGAPAP ARARSGGPDP FVIAHVHKQS DAEAFFEARF
 51 GLEPSSNDVR SPLRDGSNRA KPSTSERGGP TSAAGKKIAD LQTKLAHAMA
101 AVQEGDAATE QARIERERAA VAWADAMAAA DAARESAVAD AAVTRDGVQR
151 ALEREVSELR AALAAAETMN ARAKAAEAAT HAAGAKAAKA KNDKLAARVA
201 LLTEARIGSS HRFPYDPVRA VHAEAEDAER RASDASAASD ATRAELAETK
251 RAMEKIASEM ETLKKAGAVA NEMLADAKGE LERARETSRD GEKLAAEAAA
301 EAAAAASASA TTIAELRAAL ETTGGSRQRA MEELSRLRDD ATTAKEESER
351 AKKTAEEADF LRAATETELA KTRRDLDDAN ARASATESEL AKTRRDLDDA
401 NARASATESE LAKTRRDLDD ANASASASAT TTRDEATREA RESAAREMEE
451 TRATLTARHD AALAALAATH AATTKELEAR LDAARADASE AAARAEAFEA
501 EAAATTKELE ARLDAAKADA SEAAARAEAF EAEAAANAAA AVVVAPPAAA
551 PPPPSEELDA LKAAHAAEMA KINEANDEIV AWARQAAKEE AEEALGANAR
601 DALAKAARAE KALEDASLEH ASRVASLKQT FKEAMERKNE ELKVALSAAR
651 SSGADDVARA EAKVASATTE ARAKIAAAER AAREAKAATD AAEAKAAATE
701 KARDDAVECL NVARAECEAE VKAAELRAAN VEYDLETLRN RLRQSENAGK
751 RALLELSDEL ASAERRAMEK VMKSEEAAKK ADATNAQLAR ELWACRQKME
801 TNEAELRRDL ELSRKRASDL LREVNAARRR EAMRGGGGGG DDASGAGRSA
851 ADADAVVAEM QRELEAEIAA SEAAAAASAK REGASRRKLA DVNTKLTEAE
901 HALHETKIAL MKSERRANDF ERDLEKETSK SARLELACAK GGVKLPK
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    1 - 10     1194.5838  1193.5765  1193.5863       -8     1   -.MPSFDKQVSR.P
    1 - 10     1210.5630  1209.5557  1209.5812      -21     1   -.MPSFDKQVSR.P  Oxidation (M)
   78 - 86      745.3693   744.3620   744.3766      -20     0   R.GGPTSAAGK.K
  117 - 134    1816.9436  1815.9363  1815.8686       37     1   R.ERAAVAWADAMAAADAAR.E
  119 - 145    2602.3197  2601.3124  2601.2605       20     1   R.AAVAWADAMAAADAARESAVADAAVTR.D
  151 - 160    1201.5879  1200.5806  1200.6462      -55     1   R.ALEREVSELR.A
  256 - 265    1165.5756  1164.5683  1164.6060      -32     1   K.IASEMETLKK.A  Oxidation (M)
  266 - 283    1844.8850  1843.8777  1843.9098      -17     1   K.AGAVANEMLADAKGELER.A
  294 - 317    2201.0816  2200.0743  2200.1335      -27     0   K.LAAEAAAEAAAAASASATTIAELR.A
  353 - 362    1179.5992  1178.5919  1178.5931       -1     1   K.KTAEEADFLR.A
  404 - 415    1263.6359  1262.6286  1262.6466      -14     1   R.ASATESELAKTR.R
  417 - 438    2239.1649  2238.1576  2237.9996       71     1   R.DLDDANASASASATTTRDEATR.E
  442 - 452    1308.6535  1307.6462  1307.5775       53     1   R.ESAAREMEETR.A
  585 - 600    1657.8264  1656.8191  1656.8067        8     1   R.QAAKEEAEEALGANAR.D
  639 - 650    1300.6004  1299.5931  1299.7146      -93     1   K.NEELKVALSAAR.S
  684 - 695    1175.5387  1174.5314  1174.5829      -44     1   R.EAKAATDAAEAK.A
  715 - 727    1475.7676  1474.7603  1474.7085       35     1   R.AECEAEVKAAELR.A
  791 - 798    1090.5376  1089.5303  1089.5389       -8     1   R.ELWACRQK.M
  799 - 807    1092.5169  1091.5096  1091.4917       16     0   K.METNEAELR.R
  823 - 828     659.3862   658.3789   658.3398       59     0   R.EVNAAR.R
  849 - 862    1433.7253  1432.7180  1432.6616       39     0   R.SAADADAVVAEMQR.E
  931 - 940    1118.5197  1117.5124  1117.5913      -71     1   K.SARLELACAK.G
```

Spot No.: **146**

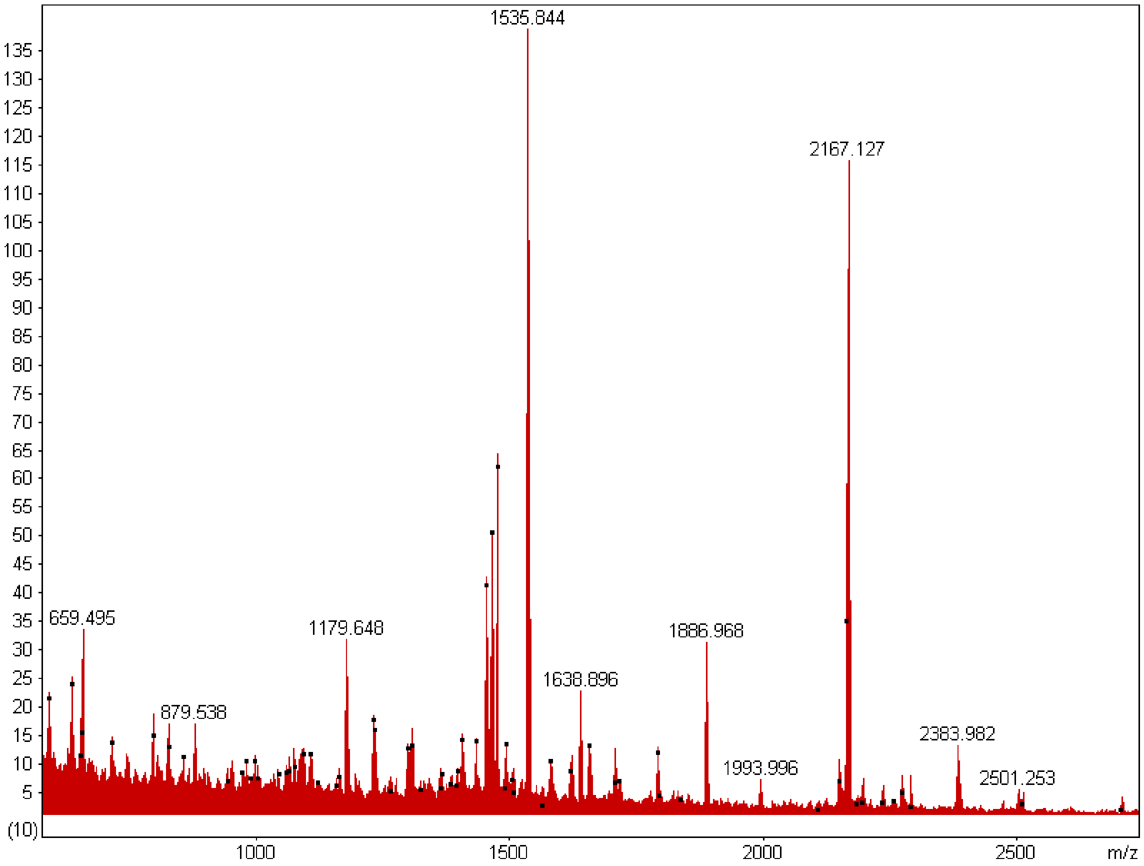
Mascot score: **85** Sequence coverage %: **22**

NCBI accession No.: **gi| 168030082**

Matched peptides No.: **12** Total peptides No.: **26**

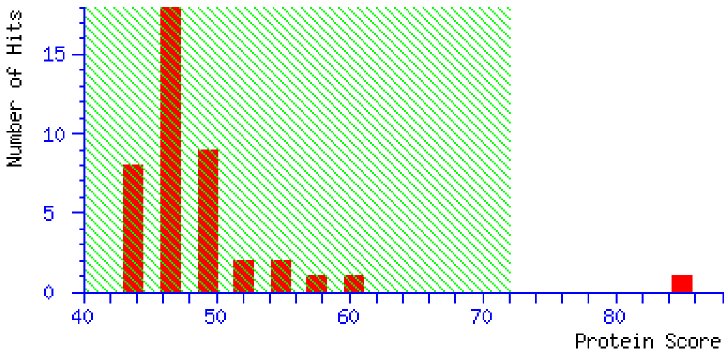
Calculated Mr: **43708** Calculated *p*I: **9.82**

Annotated PMF **spectra:**

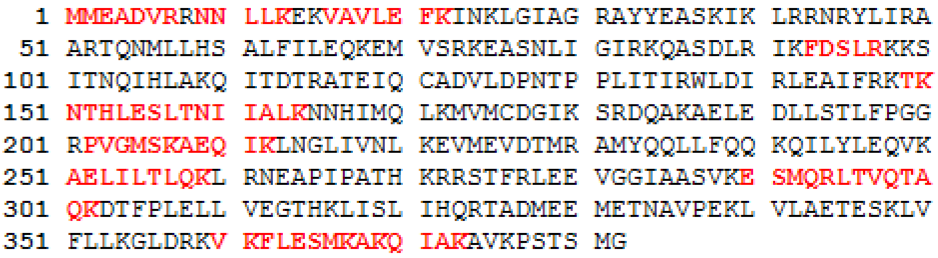


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

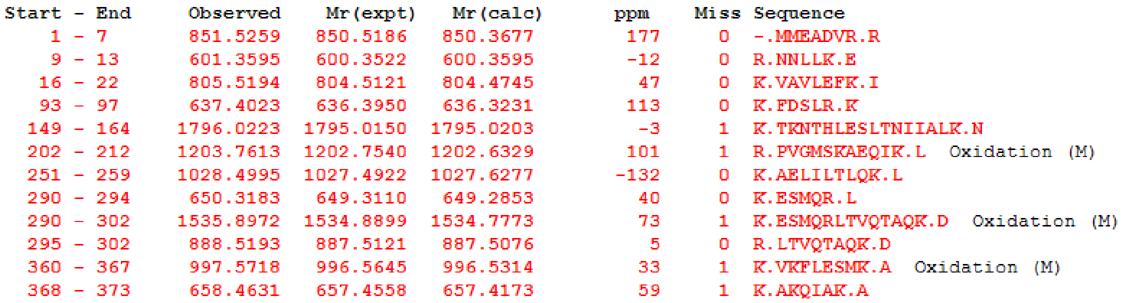


Matched peptide sequences: shown in Bold Red



```
  1 MMEADVRRNN LLKEKVAVLE FKINKLGIAG RAYYEASKIK LRRNRYLIRA
 51 ARTQNMLLHS ALFILEQKEM VSRKEASNLI GIRKQASDLR IKFDSLRKKS
101 ITNQIHLAKQ ITDTRATEIQ CADVLDPNTP PLITIRWLDI RLEAIFRKTK
151 NTHLESLTNI IALKNNHIMQ LKMVMCDGIK SRDQAKAELE DLLSTLFPGG
201 RPVGMSKAEQ IKLNGLIVNL KEVMEVDTMR AMYQQLLFQQ KQILYLEQVK
251 AELILTLQKL RNEAPIPATH KRRSTFRLEE VGGIAASVKE SMQRLTVQTA
301 QKDTFPLELL VEGTHKLISL IHQRTADMEE METNAVPEKL VLAETESKLV
351 FLLKGLDRKV KFLESMKAKQ IAKAVKPSTS MG
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    1 - 7       851.5259   850.5186   850.3677      177     0   -.MMEADVR.R
    9 - 13      601.3595   600.3522   600.3595      -12     0   R.NNLLK.E
   16 - 22      805.5194   804.5121   804.4745       47     0   K.VAVLEFK.I
   93 - 97      637.4023   636.3950   636.3231      113     0   K.FDSLR.K
  149 - 164    1796.0223  1795.0150  1795.0203       -3     1   K.TKNTHLESLTNIIALK.N
  202 - 212    1203.7613  1202.7540  1202.6329      101     1   R.PVGMSKAEQIK.L  Oxidation (M)
  251 - 259    1028.4995  1027.4922  1027.6277     -132     0   K.AELILTLQK.L
  290 - 294     650.3183   649.3110   649.2853       40     0   K.ESMQR.L
  290 - 302    1535.8972  1534.8899  1534.7773       73     1   K.ESMQRLTVQTAQK.D  Oxidation (M)
  295 - 302     888.5193   887.5121   887.5076        5     0   R.LTVQTAQK.D
  360 - 367     997.5718   996.5645   996.5314       33     1   K.VKFLESMK.A  Oxidation (M)
  368 - 373     658.4631   657.4558   657.4173       59     1   K.AKQIAK.A
```

Spot No.: **147**

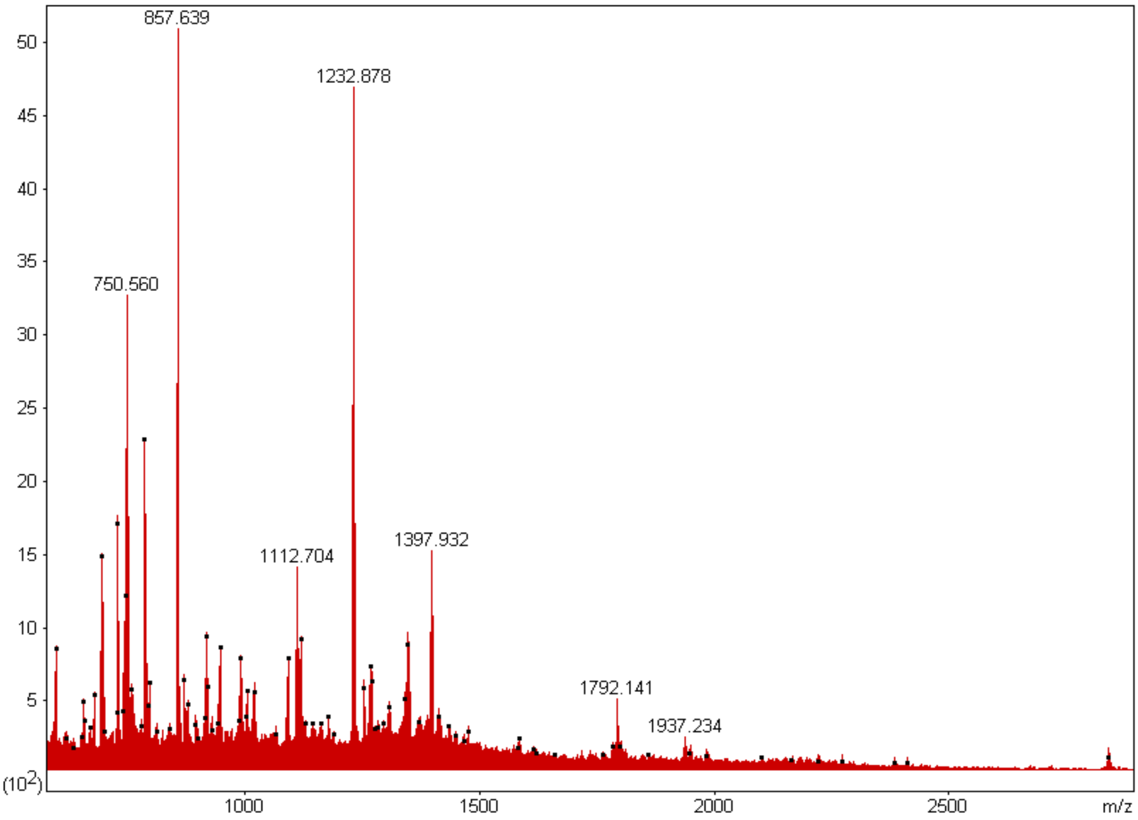
Mascot score: **89** Sequence coverage %: **25**

NCBI accession No.: **gi| 15223186**

Matched peptides No.: **14** Total peptides No.: **58**

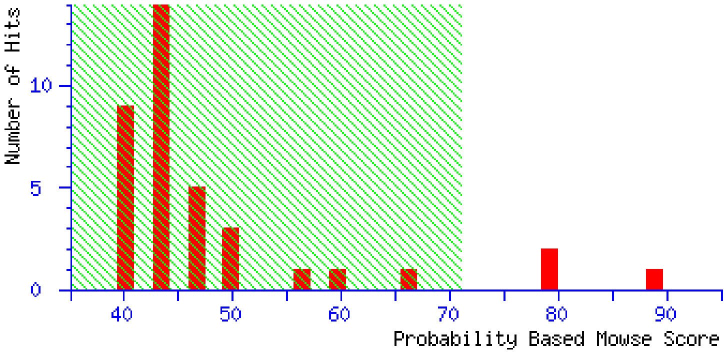
Calculated Mr: **53980** Calculated p*I*: **6.21**

Annotated PMF **spectra:**

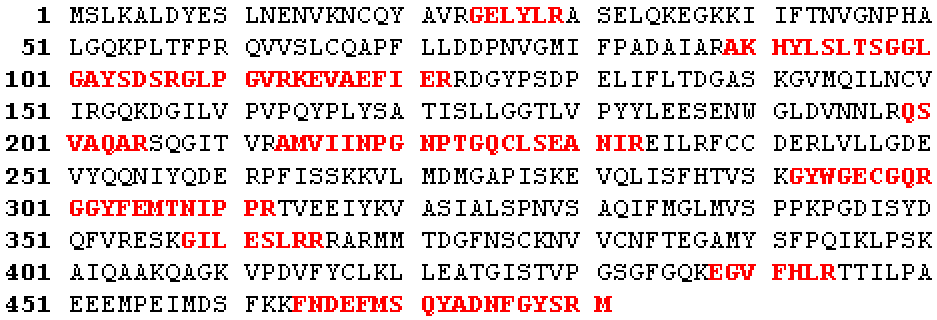


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

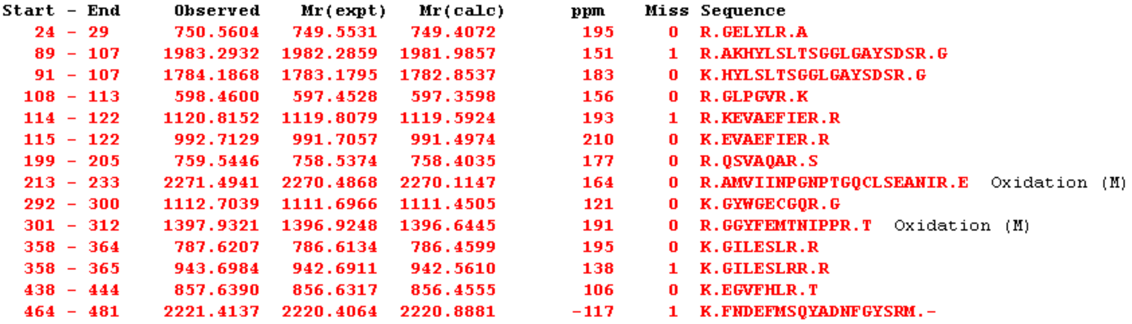


Matched peptide sequences: shown in Bold Red



```
  1 MSLKALDYES LNENVKNCQY AVRGELYLRA SELQKEGKKI IFTNVGNPHA
 51 LGQKPLTFPR QVVSLCQAPF LLDDPNVGMI FPADAIARAK HYLSLTSGGL
101 GAYSDSRGLP GVRKEVAEFI ERRDGYPSDP ELIFLTDGAS KGVMQILNCV
151 IRGQKDGILV PVPQYPLYSA TISLLGGTLV PYYLEESENW GLDVNNLRQS
201 VAQARSQGIT VRAMVIINPG NPTGQCLSEA NIREILRFCC DERLVLLGDE
251 VYQQNIYQDE RPFISSKKVL MDMGAPISKE VQLISFHTVS KGYWGECGQR
301 GGYFEMTNIP PRTVEEIYKV ASIALSPNVS AQIFMGLMVS PPKPGDISYD
351 QFVRESKGIL ESLRRRARMM TDGFNSCKNV VCNFTEGAMY SFPQIKLPSK
401 AIQAAKQAGK VPDVFYCLKL LEATGISTVP GSGFGQKEGV FHLRTTILPA
451 EEEMPEIMDS FKKFNDEFMS QYADNFGYSR M
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   24 - 29      750.5604   749.5531   749.4072      195      0  R.GELYLR.A
   89 - 107    1983.2932  1982.2859  1981.9857      151      1  R.AKHYLSLTSGGLGAYSDSR.G
   91 - 107    1784.1868  1783.1795  1782.8537      183      0  K.HYLSLTSGGLGAYSDSR.G
  108 - 113     598.4600   597.4528   597.3598      156      0  R.GLPGVR.K
  114 - 122    1120.8152  1119.8079  1119.5924      193      1  R.KEVAEFIER.R
  115 - 122     992.7129   991.7057   991.4974      210      0  K.EVAEFIER.R
  199 - 205     759.5446   758.5374   758.4035      177      0  R.QSVAQAR.S
  213 - 233    2271.4941  2270.4868  2270.1147      164      0  R.AMVIINPGNPTGQCLSEANIR.E  Oxidation (M)
  292 - 300    1112.7039  1111.6966  1111.4505      121      0  K.GYWGECGQR.G
  301 - 312    1397.9321  1396.9248  1396.6445      191      0  R.GGYFEMTNIPPR.T  Oxidation (M)
  358 - 364     787.6207   786.6134   786.4599      195      0  K.GILESLR.R
  358 - 365     943.6984   942.6911   942.5610      138      1  K.GILESLRR.R
  438 - 444     857.6390   856.6317   856.4555      106      0  K.EGVFHLR.T
  464 - 481    2221.4137  2220.4064  2220.8881     -117      1  K.FNDEFMSQYADNFGYSRM.-
```

Spot No.: **148**

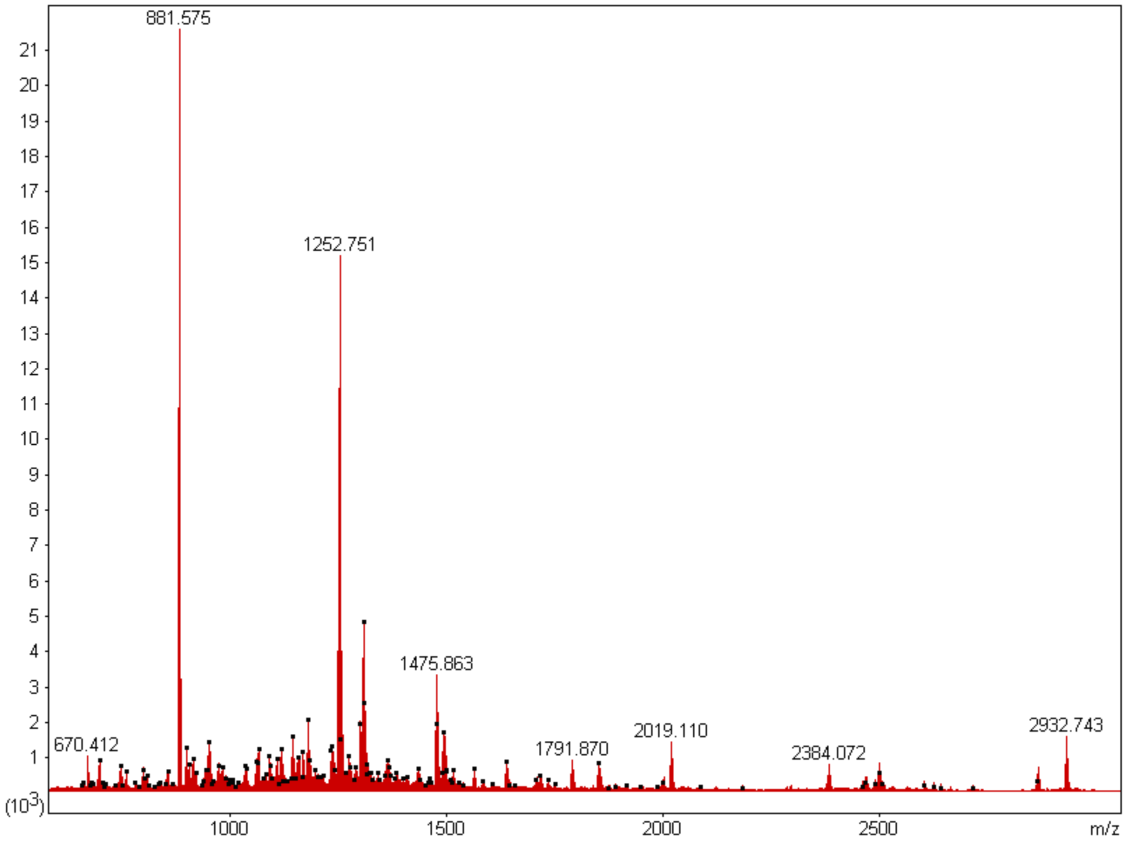
Mascot score: **85**   Sequence coverage %: **38**

NCBI accession No.: **gi| 15240013**

Matched peptides No.: **12**   Total peptides No.: **106**

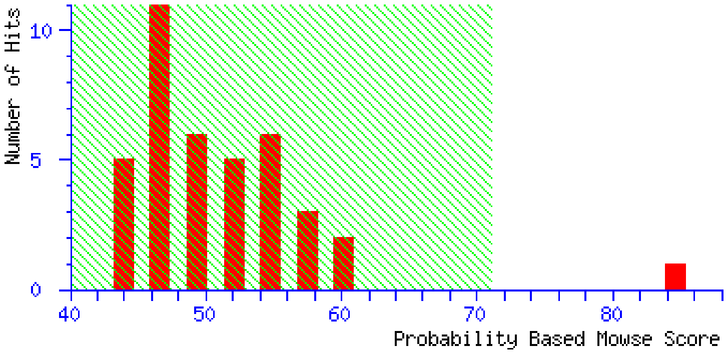
Calculated Mr: **35349**   Calculated *p*I: **5.55**

Annotated PMF **spectra:**

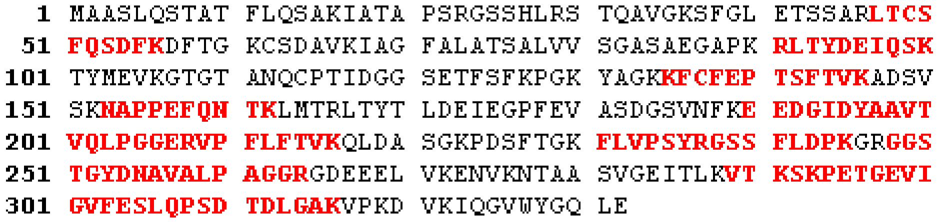


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

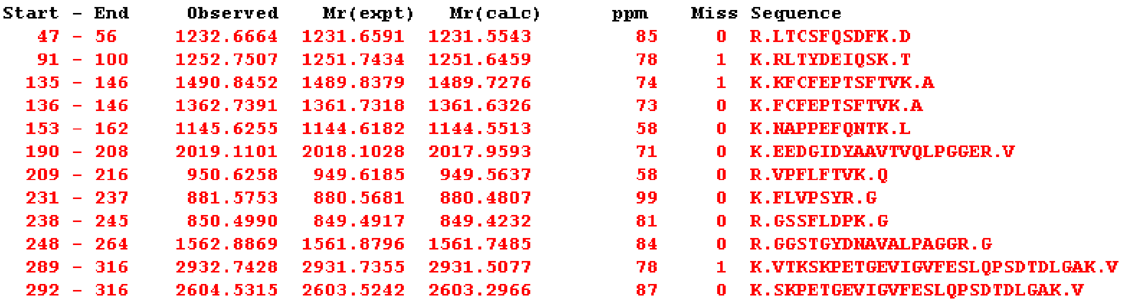


Matched peptide sequences: shown in Bold Red



1 MAASLQSTAT FLQSAKIATA PSRGSSHLRS TQAVGKSFGL ETSSAR**LTCS**
51 **FQSDFK**DFTG KCSDAVKIAG FALATSALVV SGASAEGAPK **RLTYDEIQSK**
101 TYMEVKGTGT ANQCPTIDGG SETFSFKPGK YAGK**KFCFEP** **TSFTVK**ADSV
151 SK**NAPPEFQN** **TK**LMTRLTYT LDEIEGPFEV ASDGSVNFK**E** **EDGIDYAAVT**
201 **VQLPGGERVP** **FLFTVK**QLDA SGKPDSFTGK **FLVPSYRGSS** **FLDPK**GR**GGS**
251 **TGYDNAVALP** **AGGR**GDEEEL VKENVKNTAA SVGEITLK**VT** **KSKPETGEVI**
301 **GVFESLQPSD** **TDLGAK**VPKD VKIQGVWYGQ LE

Matched peptides information:



```
Start - End     Observed    Mr(expt)   Mr(calc)      ppm    Miss Sequence
   47 - 56     1232.6664  1231.6591  1231.5543       85      0  R.LTCSFQSDFK.D
   91 - 100    1252.7507  1251.7434  1251.6459       78      1  K.RLTYDEIQSK.T
  135 - 146    1490.8452  1489.8379  1489.7276       74      1  K.KFCFEPTSFTVK.A
  136 - 146    1362.7391  1361.7318  1361.6326       73      0  K.FCFEPTSFTVK.A
  153 - 162    1145.6255  1144.6182  1144.5513       58      0  K.NAPPEFQNTK.L
  190 - 208    2019.1101  2018.1028  2017.9593       71      0  K.EEDGIDYAAVTVQLPGGER.V
  209 - 216     950.6258   949.6185   949.5637       58      0  R.VPFLFTVK.Q
  231 - 237     881.5753   880.5681   880.4807       99      0  K.FLVPSYR.G
  238 - 245     850.4990   849.4917   849.4232       81      0  R.GSSFLDPK.G
  248 - 264    1562.8869  1561.8796  1561.7485       84      0  R.GGSTGYDNAVALPAGGR.G
  289 - 316    2932.7428  2931.7355  2931.5077       78      1  K.VTKSKPETGEVIGVFESLQPSDTDLGAK.V
  292 - 316    2604.5315  2603.5242  2603.2966       87      0  K.SKPETGEVIGVFESLQPSDTDLGAK.V
```

Spot No.: **149**

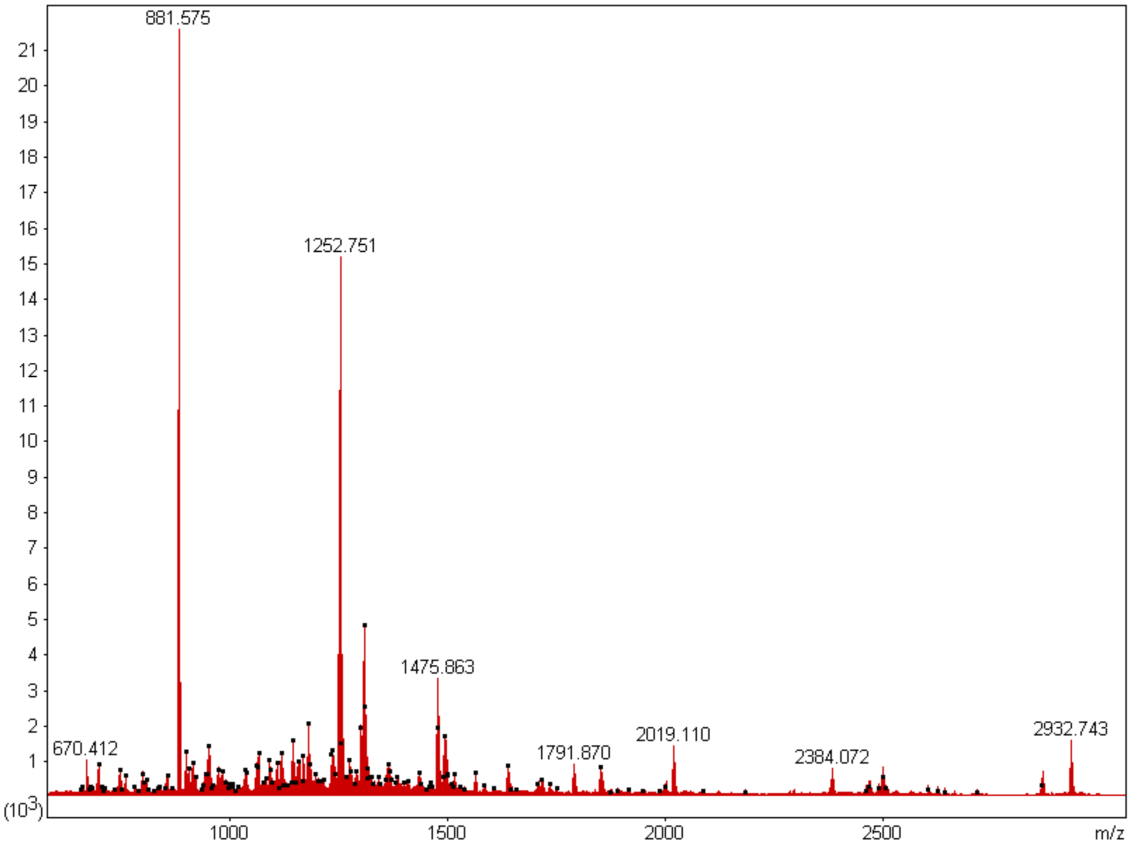
Mascot score: **96** Sequence coverage %: **58**

NCBI accession No.: **gi| 312282325**

Matched peptides No.: **15** Total peptides No.: **78**

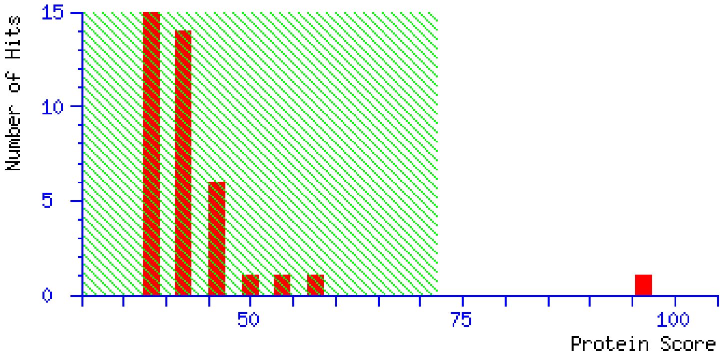
Calculated Mr: **35258** Calculated *p*I: **5.92**

Annotated PMF **spectra:**

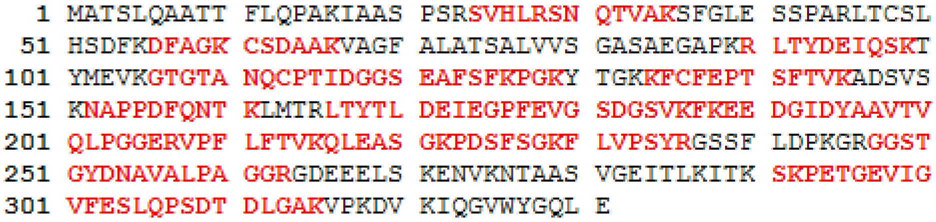


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant ($p<0.05$).

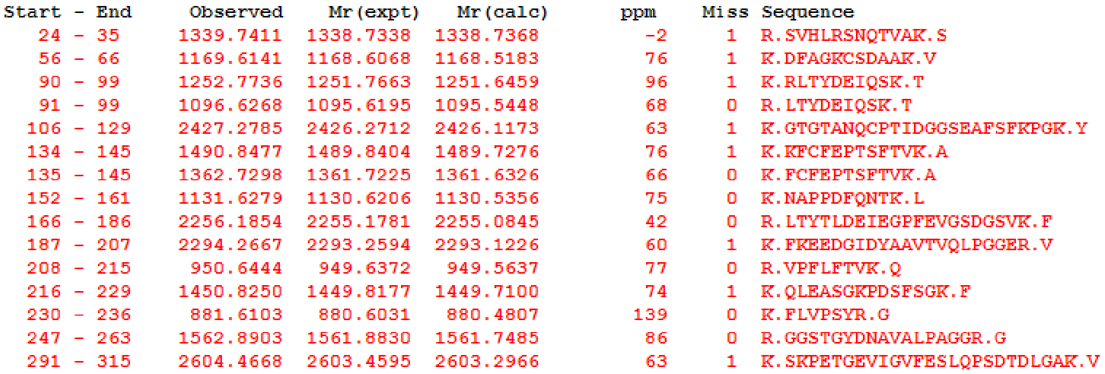


Matched peptide sequences: shown in Bold Red



1 MATSLQAATT FLQPAKIAAS PSR**SVHLRSN** **QTVAK**SFGLE SSPARLTCSL
51 HSDFK**DFAGK** **CSDAAK**VAGF ALATSALVVS GASAEGAPK**R** **LTYDEIQSK**T
101 YMEVK**GTGTA** **NQCPTIDGGS** **EAFSFKPGK**Y TGK**KFCFEPT** **SFTVK**ADSVS
151 K**NAPPDFQNT** **K**LMTR**LTYTL** **DEIEGPFEVG** **SDGSVKFKEE** **DGIDYAAVTV**
201 **QLPGGERVPF** **LFTVKQLEAS** **GKPDSFSGKF** **LVPSYR**GSSF LDPKGR**GGST**
251 **GYDNAVALPA** **GGR**GDEEELS KENVKNTAAS VGEITLKITK **SKPETGEVIG**
301 **VFESLQPSDT** **DLGAK**VPKDV KIQGVWYGQL E

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
24 - 35	1339.7411	1338.7338	1338.7368	-2	1	R.SVHLRSNQTVAK.S
56 - 66	1169.6141	1168.6068	1168.5183	76	1	K.DFAGKCSDAAK.V
90 - 99	1252.7736	1251.7663	1251.6459	96	1	K.RLTYDEIQSK.T
91 - 99	1096.6268	1095.6195	1095.5448	68	0	R.LTYDEIQSK.T
106 - 129	2427.2785	2426.2712	2426.1173	63	1	K.GTGTANQCPTIDGGSEAFSFKPGK.Y
134 - 145	1490.8477	1489.8404	1489.7276	76	1	K.KFCFEPTSFTVK.A
135 - 145	1362.7298	1361.7225	1361.6326	66	0	K.FCFEPTSFTVK.A
152 - 161	1131.6279	1130.6206	1130.5356	75	0	K.NAPPDFQNTK.L
166 - 186	2256.1854	2255.1781	2255.0845	42	0	R.LTYTLDEIEGPFEVGSDGSVK.F
187 - 207	2294.2667	2293.2594	2293.1226	60	1	K.FKEEDGIDYAAVTVQLPGGER.V
208 - 215	950.6444	949.6372	949.5637	77	0	R.VPFLFTVK.Q
216 - 229	1450.8250	1449.8177	1449.7100	74	1	K.QLEASGKPDSFSGK.F
230 - 236	881.6103	880.6031	880.4807	139	0	K.FLVPSYR.G
247 - 263	1562.8903	1561.8830	1561.7485	86	0	R.GGSTGYDNAVALPAGGR.G
291 - 315	2604.4668	2603.4595	2603.2966	63	1	K.SKPETGEVIGVFESLQPSDTDLGAK.V

Spot No.: **150**

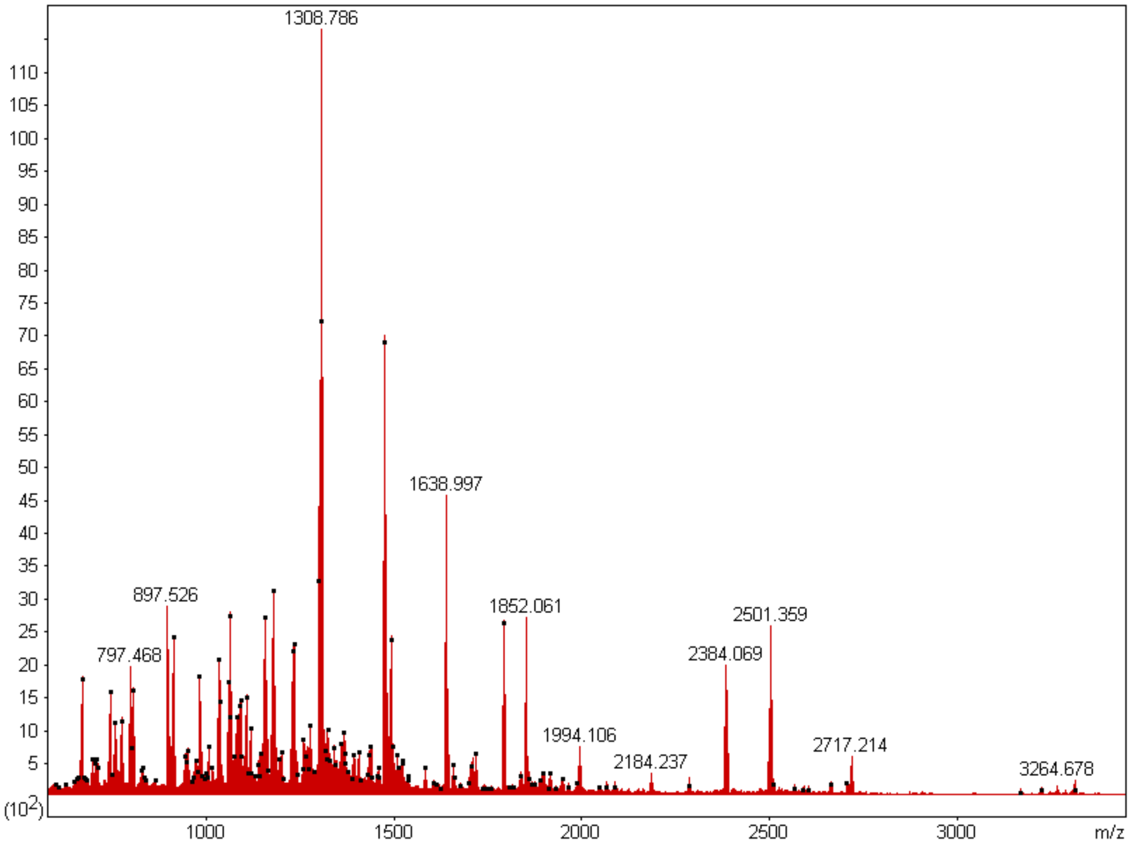
Mascot score: **99** Sequence coverage %: **47**

NCBI accession No.: **gi| 30690323**

Matched peptides No.: **21** Total peptides No.: **129**

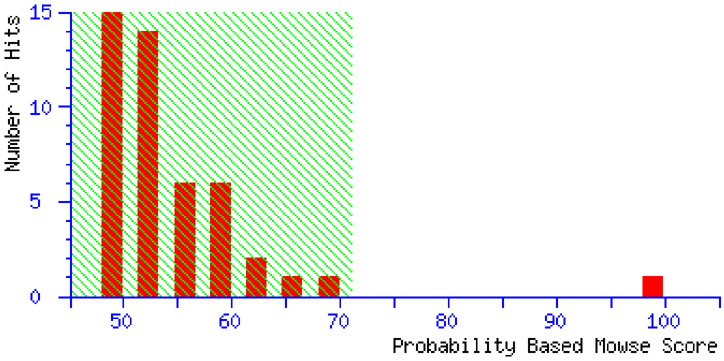
Calculated Mr: **39646** Calculated *p*I: **9.44**

Annotated PMF **spectra:**

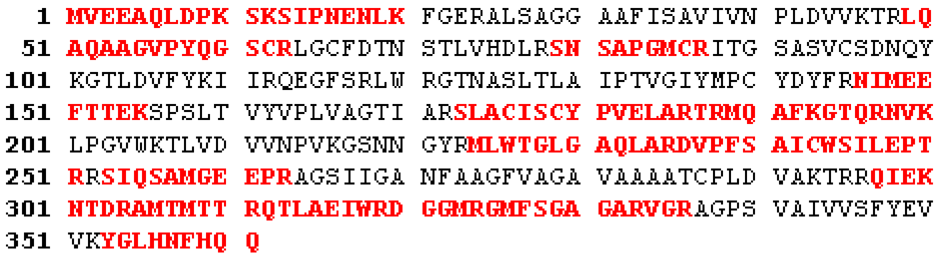


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

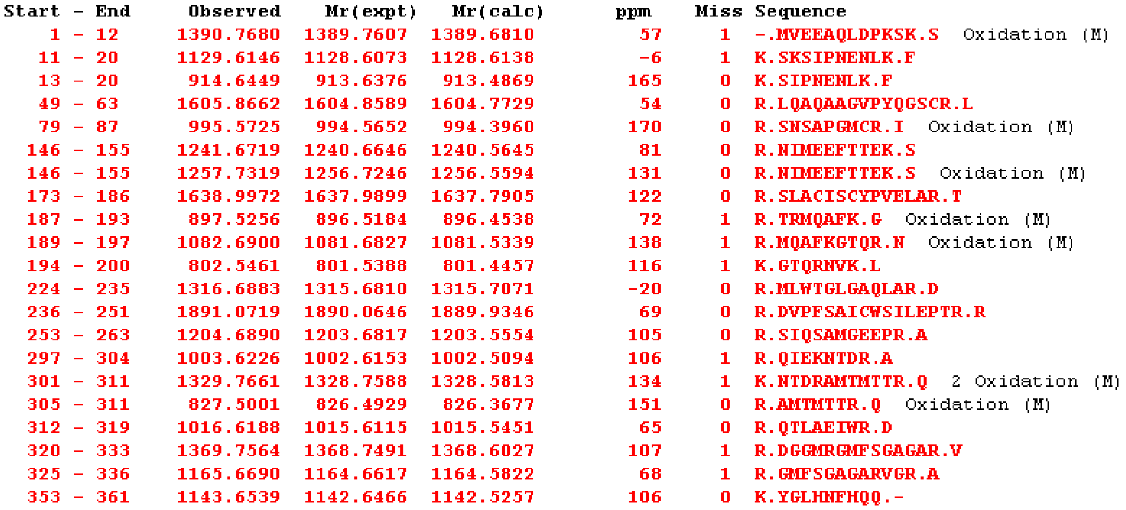


Matched peptide sequences: shown in Bold Red



1 **MVEEAQLDPK SKSIPNENLK** FGERALSAGG AAFISAVIVN PLDVVKTR**LQ**
51 **AQAAGVPYQG SCR**LGCFDTN STLVHDLR**SN SAPGMCR**ITG SASVCSDNQY
101 KGTLDVFYKI IRQEGFSRLW RGTNASLTLA IPTVGIYMPC YDYFR**NIMEE**
151 **FTTEK**SPSLT VYVPLVAGTI AR**SLACISCY PVELARTRMQ AFKGTQRNVK**
201 LPGVWKTLVD VVNPVKGSNN GYR**MLWTGLG AQLARDVPFS AICWSILEPT**
251 **R**R**SIQSAMGE EPR**AGSIIGA NFAAGFVAGA VAAAATCPLD VAKTRR**QIEK**
301 **NTDRAMTMTT RQTLAEIWRD GGMRGMFSGA GARVGR**AGPS VAIVVSFYEV
351 VK**YGLHNFHQ Q**

Matched peptides information:



```
Start - End      Observed    Mr(expt)   Mr(calc)       ppm     Miss Sequence
    1 - 12      1390.7680  1389.7607  1389.6810        57      1   -.MVEEAQLDPKSK.S  Oxidation (M)
   11 - 20      1129.6146  1128.6073  1128.6138        -6      1   K.SKSIPNENLK.F
   13 - 20       914.6449   913.6376   913.4869       165      0   K.SIPNENLK.F
   49 - 63      1605.8662  1604.8589  1604.7729        54      0   R.LQAQAAGVPYQGSCR.L
   79 - 87       995.5725   994.5652   994.3960       170      0   R.SNSAPGMCR.I  Oxidation (M)
  146 - 155     1241.6719  1240.6646  1240.5645        81      0   R.NIMEEFTTEK.S
  146 - 155     1257.7319  1256.7246  1256.5594       131      0   R.NIMEEFTTEK.S  Oxidation (M)
  173 - 186     1638.9972  1637.9899  1637.7905       122      0   R.SLACISCYPVELAR.T
  187 - 193      897.5256   896.5184   896.4538        72      1   R.TRMQAFK.G  Oxidation (M)
  189 - 197     1082.6900  1081.6827  1081.5339       138      1   R.MQAFKGTQR.N  Oxidation (M)
  194 - 200      802.5461   801.5388   801.4457       116      1   K.GTQRNVK.L
  224 - 235     1316.6883  1315.6810  1315.7071       -20      0   R.MLWTGLGAQLAR.D
  236 - 251     1891.0719  1890.0646  1889.9346        69      0   R.DVPFSAICWSILEPTR.R
  253 - 263     1204.6890  1203.6817  1203.5554       105      0   R.SIQSAMGEEPR.A
  297 - 304     1003.6226  1002.6153  1002.5094       106      1   R.QIEKNTDR.A
  301 - 311     1329.7661  1328.7588  1328.5813       134      1   K.NTDRAMTMTTR.Q  2 Oxidation (M)
  305 - 311      827.5001   826.4929   826.3677       151      0   R.AMTMTTR.Q  Oxidation (M)
  312 - 319     1016.6188  1015.6115  1015.5451        65      0   R.QTLAEIWR.D
  320 - 333     1369.7564  1368.7491  1368.6027       107      1   R.DGGMRGMFSGAGAR.V
  325 - 336     1165.6690  1164.6617  1164.5822        68      1   R.GMFSGAGARVGR.A
  353 - 361     1143.6539  1142.6466  1142.5257       106      0   K.YGLHNFHQQ.-
```

Spot No.: **151**

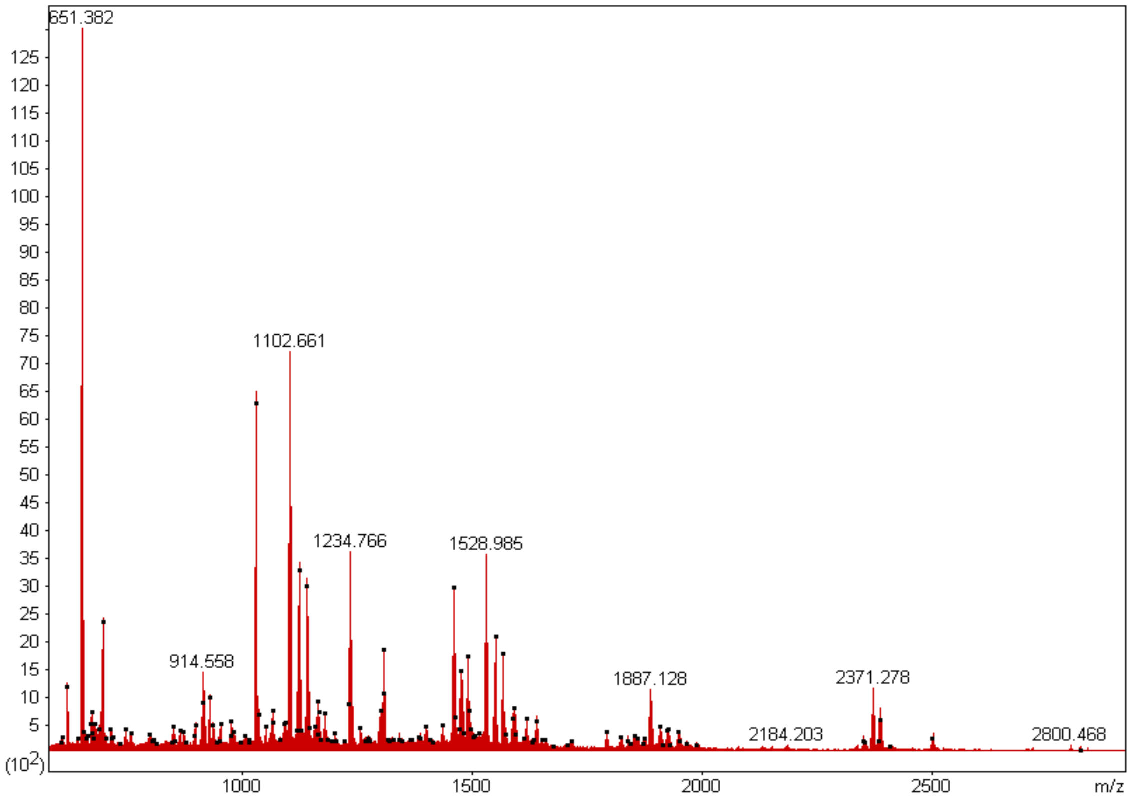
Mascot score: **146**   Sequence coverage %: **54**

NCBI accession No.: **gi| 166359602**

Matched peptides No.: **20**   Total peptides No.: **132**

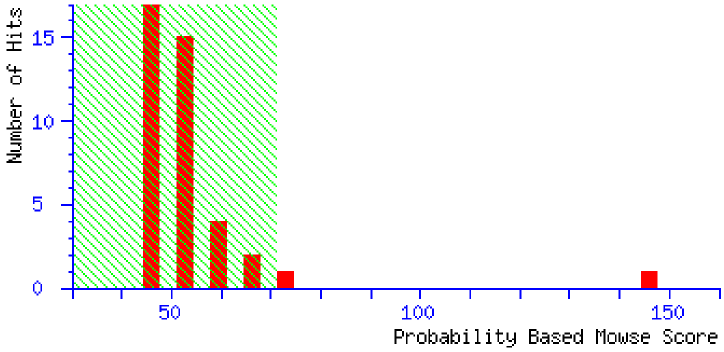
Calculated Mr: **24136**   Calculated *p*I: **6.17**

Annotated PMF **spectra:**

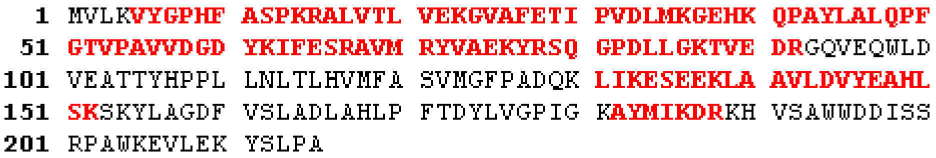


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

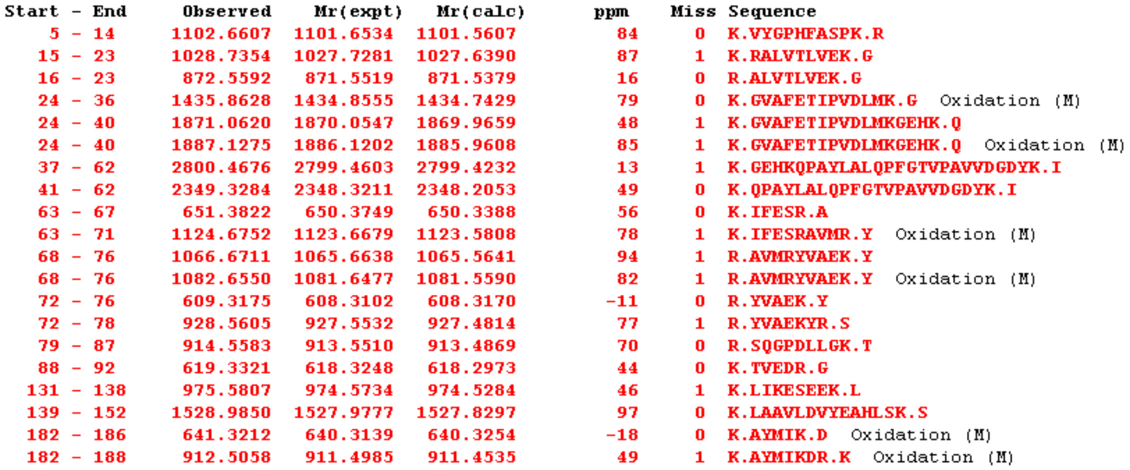


Matched peptide sequences: shown in Bold Red



1 MVLK**VYGPHF ASPKRALVTL VEKGVAFETI PVDLMKGEHK QPAYLALQPF**
51 **GTVPAVVDGD YKIFESRAVM RYVAEKYRSQ GPDLLGKTVE DR**GQVEQWLD
101 VEATTYHPPL LNLTLHVMFA SVMGFPADQK **LIKESEEKLA AVLDVYEAHL**
151 **SK**SKYLAGDF VSLADLAHLP FTDYLVGPIG K**AYMIKDR**KH VSAWWDDISS
201 RPAWKEVLEK YSLPA

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    5 - 14     1102.6607  1101.6534  1101.5607       84     0  K.VYGPHFASPK.R
   15 - 23     1028.7354  1027.7281  1027.6390       87     1  K.RALVTLVEK.G
   16 - 23      872.5592   871.5519   871.5379       16     0  R.ALVTLVEK.G
   24 - 36     1435.8628  1434.8555  1434.7429       79     0  K.GVAFETIPVDLMK.G  Oxidation (M)
   24 - 40     1871.0620  1870.0547  1869.9659       48     1  K.GVAFETIPVDLMKGEHK.Q
   24 - 40     1887.1275  1886.1202  1885.9608       85     1  K.GVAFETIPVDLMKGEHK.Q  Oxidation (M)
   37 - 62     2800.4676  2799.4603  2799.4232       13     1  K.GEHKQPAYLALQPFGTVPAVVDGDYK.I
   41 - 62     2349.3284  2348.3211  2348.2053       49     0  K.QPAYLALQPFGTVPAVVDGDYK.I
   63 - 67      651.3822   650.3749   650.3388       56     0  K.IFESR.A
   63 - 71     1124.6752  1123.6679  1123.5808       78     1  K.IFESRAVMR.Y  Oxidation (M)
   68 - 76     1066.6711  1065.6638  1065.5641       94     1  R.AVMRYVAEK.Y
   68 - 76     1082.6550  1081.6477  1081.5590       82     1  R.AVMRYVAEK.Y  Oxidation (M)
   72 - 76      609.3175   608.3102   608.3170      -11     0  R.YVAEK.Y
   72 - 78      928.5605   927.5532   927.4814       77     1  R.YVAEKYR.S
   79 - 87      914.5583   913.5510   913.4869       70     0  R.SQGPDLLGK.T
   88 - 92      619.3321   618.3248   618.2973       44     0  K.TVEDR.G
  131 - 138     975.5807   974.5734   974.5284       46     1  K.LIKESEEK.L
  139 - 152    1528.9850  1527.9777  1527.8297       97     0  K.LAAVLDVYEAHLSK.S
  182 - 186     641.3212   640.3139   640.3254      -18     0  K.AYMIK.D  Oxidation (M)
  182 - 188     912.5058   911.4985   911.4535       49     1  K.AYMIKDR.K  Oxidation (M)
```

Spot No.: **152**

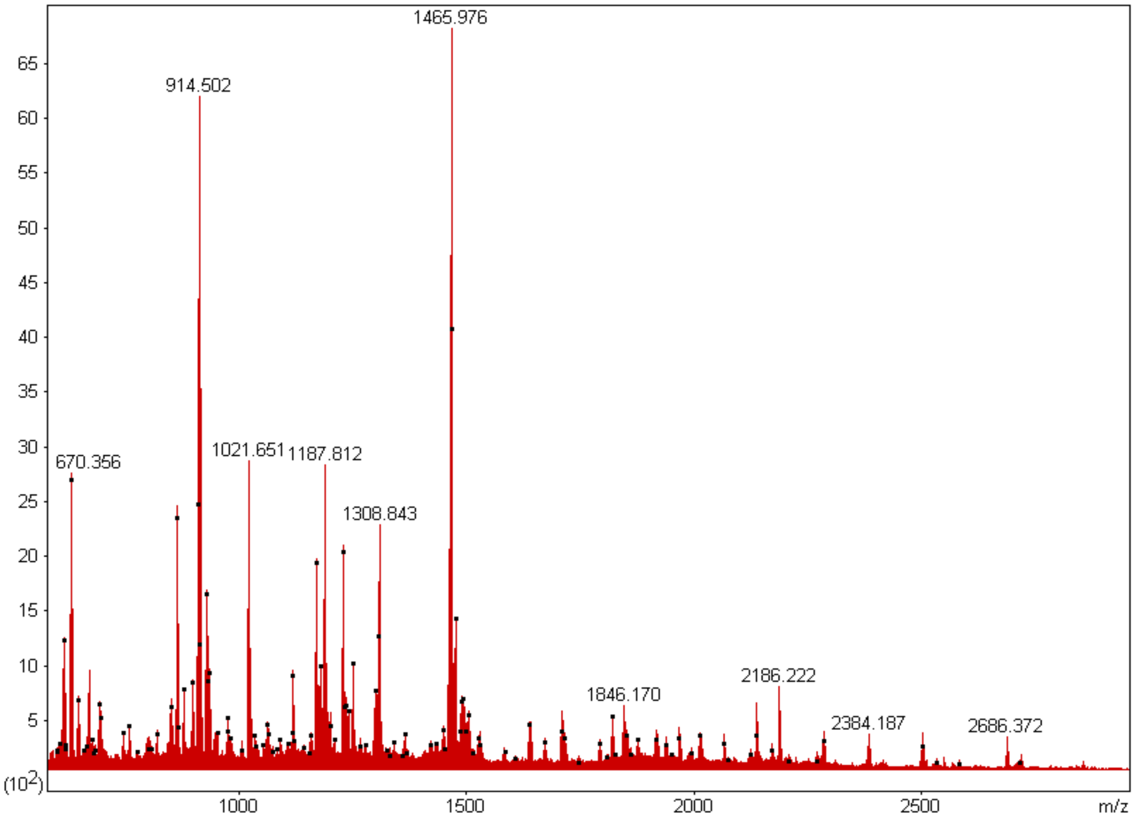
Mascot score: **171** Sequence coverage %: **39**

NCBI accession No.: **gi| 30959098**

Matched peptides No.: **25** Total peptides No.: **108**

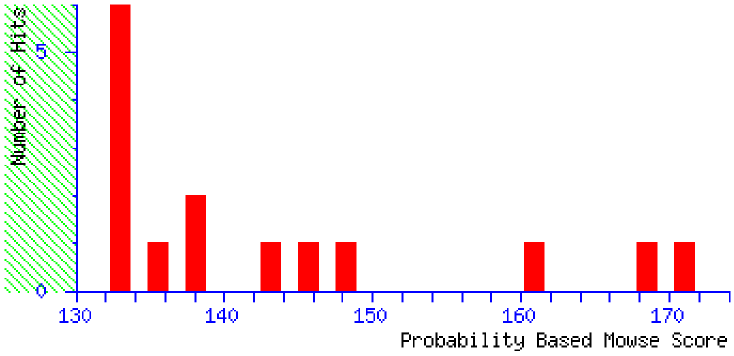
Calculated Mr: **49918** Calculated p*I*: **6.12**

Annotated PMF **spectra:**

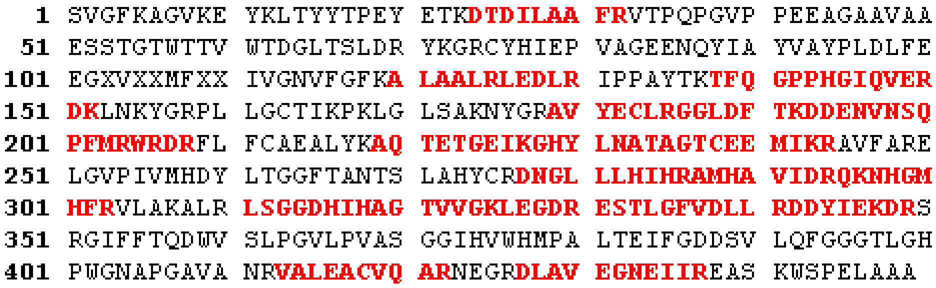


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red



1 SVGFKAGVKE YKLTYYTPEY ETK**DTDILAA** **FR**VTPQPGVP PEEAGAAVAA

51 ESSTGTWTTV WTDGLTSLDR YKGRCYHIEP VAGEENQYIA YVAYPLDLFE

101 EGXVXXMFXX IVGNVFGFK**A** **LAALRLEDLR** IPPAYTK**TFQ** **GPPHGIQVER**

151 **DK**LNKYGRPL LGCTIKPKLG LSAKNYGR**AV** **YECLRGGLDF** **TKDDENVNSQ**

201 **PFMRWRDR**FL FCAEALYK**AQ** **TETGEIKGHY** **LNATAGTCEE** **MIKR**AVFARE

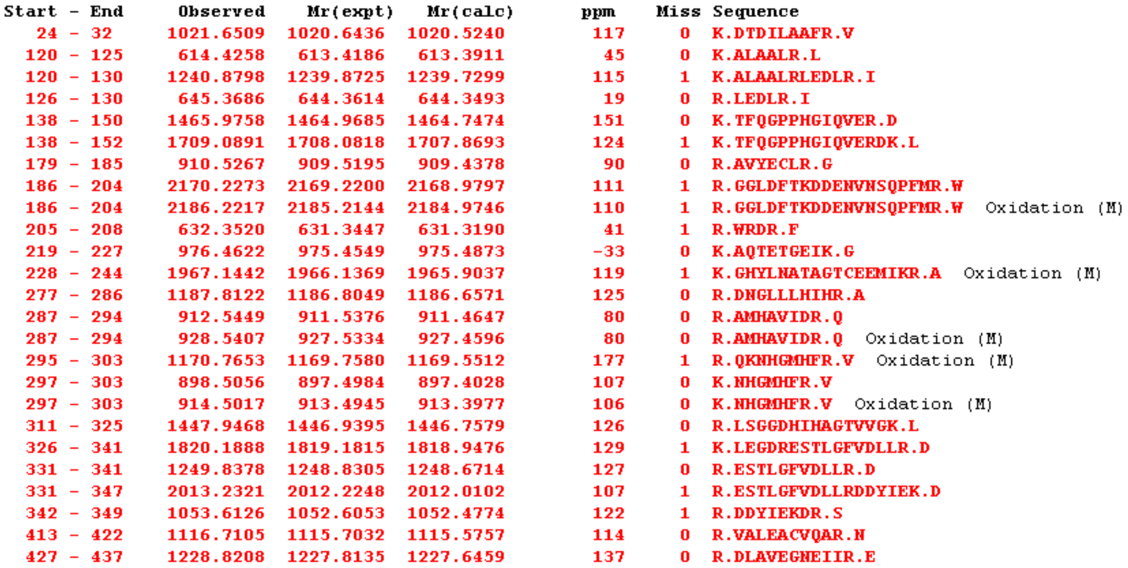
251 LGVPIVMHDY LTGGFTANTS LAHYCR**DNGL** **LLHIHRAMHA** **VIDRQKNHGM**

301 **HFR**VLAKALR **LSGGDHIHAG** **TVVGKLEGDR** **ESTLGFVDLL** **RDDYIEKDR**S

351 RGIFFTQDWV SLPGVLPVAS GGIHVWHMPA LTEIFGDDSV LQFGGGTLGH

401 PWGNAPGAVA NR**VALEACVQ** **AR**NEGR**DLAV** **EGNEIIR**EAS KWSPELAAA

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
24 - 32	1021.6509	1020.6436	1020.5240	117	0	K.DTDILAAFR.V	
120 - 125	614.4258	613.4186	613.3911	45	0	K.ALAALR.L	
120 - 130	1240.8798	1239.8725	1239.7299	115	1	K.ALAALRLEDLR.I	
126 - 130	645.3686	644.3614	644.3493	19	0	R.LEDLR.I	
138 - 150	1465.9758	1464.9685	1464.7474	151	0	K.TFQGPPHGIQVER.D	
138 - 152	1709.0891	1708.0818	1707.8693	124	1	K.TFQGPPHGIQVERDK.L	
179 - 185	910.5267	909.5195	909.4378	90	0	R.AVYECLR.G	
186 - 204	2170.2273	2169.2200	2168.9797	111	1	R.GGLDFTKDDENVNSQPFMR.W	
186 - 204	2186.2217	2185.2144	2184.9746	110	1	R.GGLDFTKDDENVNSQPFMR.W	Oxidation (M)
205 - 208	632.3520	631.3447	631.3190	41	1	R.WRDR.F	
219 - 227	976.4622	975.4549	975.4873	-33	0	K.AQTETGEIK.G	
228 - 244	1967.1442	1966.1369	1965.9037	119	1	K.GHYLNATAGTCEEMIKR.A	Oxidation (M)
277 - 286	1187.8122	1186.8049	1186.6571	125	0	R.DNGLLLHIHR.A	
287 - 294	912.5449	911.5376	911.4647	80	0	R.AMHAVIDR.Q	
287 - 294	928.5407	927.5334	927.4596	80	0	R.AMHAVIDR.Q	Oxidation (M)
295 - 303	1170.7653	1169.7580	1169.5512	177	1	R.QKNHGMHFR.V	Oxidation (M)
297 - 303	898.5056	897.4984	897.4028	107	0	K.NHGMHFR.V	
297 - 303	914.5017	913.4945	913.3977	106	0	K.NHGMHFR.V	Oxidation (M)
311 - 325	1447.9468	1446.9395	1446.7579	126	0	R.LSGGDHIHAGTVVGK.L	
326 - 341	1820.1888	1819.1815	1818.9476	129	1	K.LEGDRESTLGFVDLLR.D	
331 - 341	1249.8378	1248.8305	1248.6714	127	0	R.ESTLGFVDLLR.D	
331 - 347	2013.2321	2012.2248	2012.0102	107	1	R.ESTLGFVDLLRDDYIEK.D	
342 - 349	1053.6126	1052.6053	1052.4774	122	1	R.DDYIEKDR.S	
413 - 422	1116.7105	1115.7032	1115.5757	114	0	R.VALEACVQAR.N	
427 - 437	1228.8208	1227.8135	1227.6459	137	0	R.DLAVEGNEIIR.E	

Spot No.: **153**

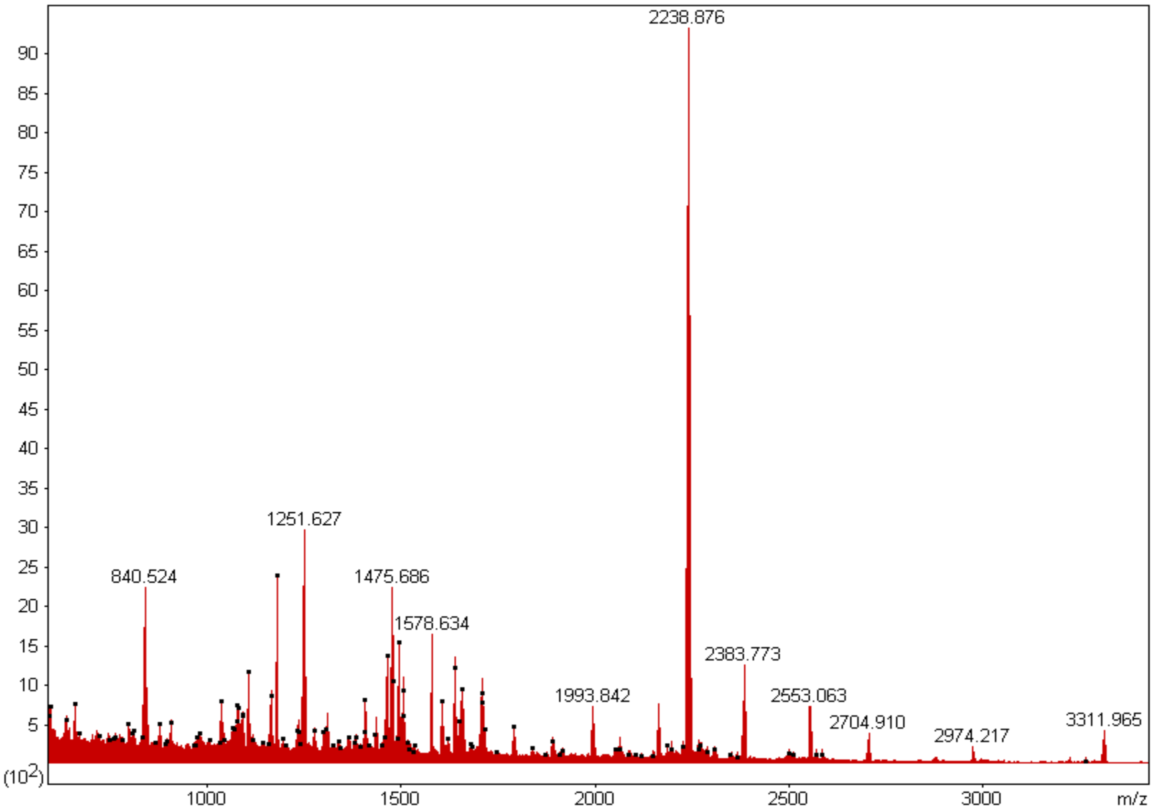
Mascot score: **101** Sequence coverage %: **45**

NCBI accession No.: **gi| 15240599**

Matched peptides No.: **13** Total peptides No.: **57**

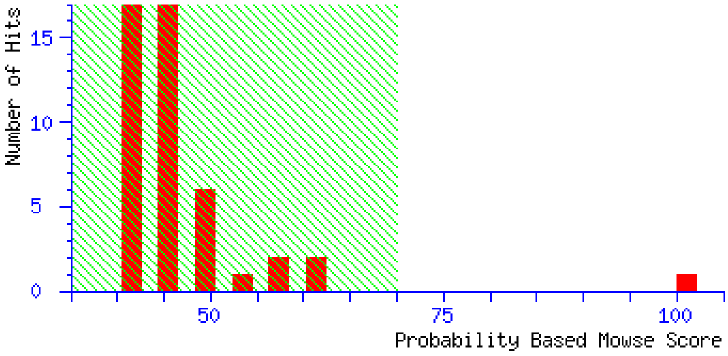
Calculated Mr: **35262** Calculated *p*I: **5.08**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 M**GQDRGFGFP TQRLCSLSSL ALSHLGKQDL NLVSKTCGDT TDMFSTR**GSY
51 QVSTQVSQSY FDGYCGWVHG SSHLQQQFLP PQNQCMKQVP LQVDGVISKA
101 EEQCSQKR**FL VFDQSGDQTT LLLASDIRKS FETLKQHACP DMKEELQR**SN
151 KDLFVCHGMQ GNSEPDLKED SEELNALLYS EDESGYCSEE DEVTSADHSP
201 SIVVSGREDQ KTFLGSYGQP LNAKKR**KILE TSNESMRDAE SSCGSCDNTR**
251 ISFLKRSKLS SNKIGEEK**IF ETVSLLRSVV PGEELVDPIL VIDRAIDYLK**
301 SLKMEAKNRE A

Matched peptides information:

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
2 - 13	1365.5944	1364.5871	1364.6586	-52	1	M.GQDRGFGFPTQR.L	
14 - 35	2383.7732	2382.7659	2382.2941	198	1	R.LCSLSSLALSHLGKQDLNLVSK.T	
36 - 47	1407.6909	1406.6836	1406.5443	99	0	K.TCGDTTDMFSTR.G	Oxidation (M)
109 - 128	2238.8762	2237.8689	2238.1532	-127	0	R.FLVFDQSGDQTTLLLASDIR.K	
109 - 129	2366.9865	2365.9792	2366.2482	-114	1	R.FLVFDQSGDQTTLLLASDIRK.S	
130 - 143	1707.7195	1706.7122	1706.7756	-37	1	K.SFETLKQHACPDMK.E	Oxidation (M)
136 - 148	1657.7221	1656.7148	1656.7348	-12	1	K.QHACPDMKEELQR.S	Oxidation (M)
227 - 237	1307.6347	1306.6274	1306.6551	-21	1	R.KILETSNESMR.D	
227 - 237	1323.6453	1322.6380	1322.6500	-9	1	R.KILETSNESMR.D	Oxidation (M)
228 - 237	1179.5737	1178.5664	1178.5601	5	0	K.ILETSNESMR.D	
238 - 250	1458.6735	1457.6662	1457.5147	104	0	R.DAESSCGSCDNTR.I	
269 - 277	1077.5523	1076.5450	1076.6230	-72	0	K.IFETVSLLR.S	
278 - 300	2553.0626	2552.0553	2552.4101	-139	1	R.SVVPGEELVDPILVIDRAIDYLK.S	

Spot No.: **154**

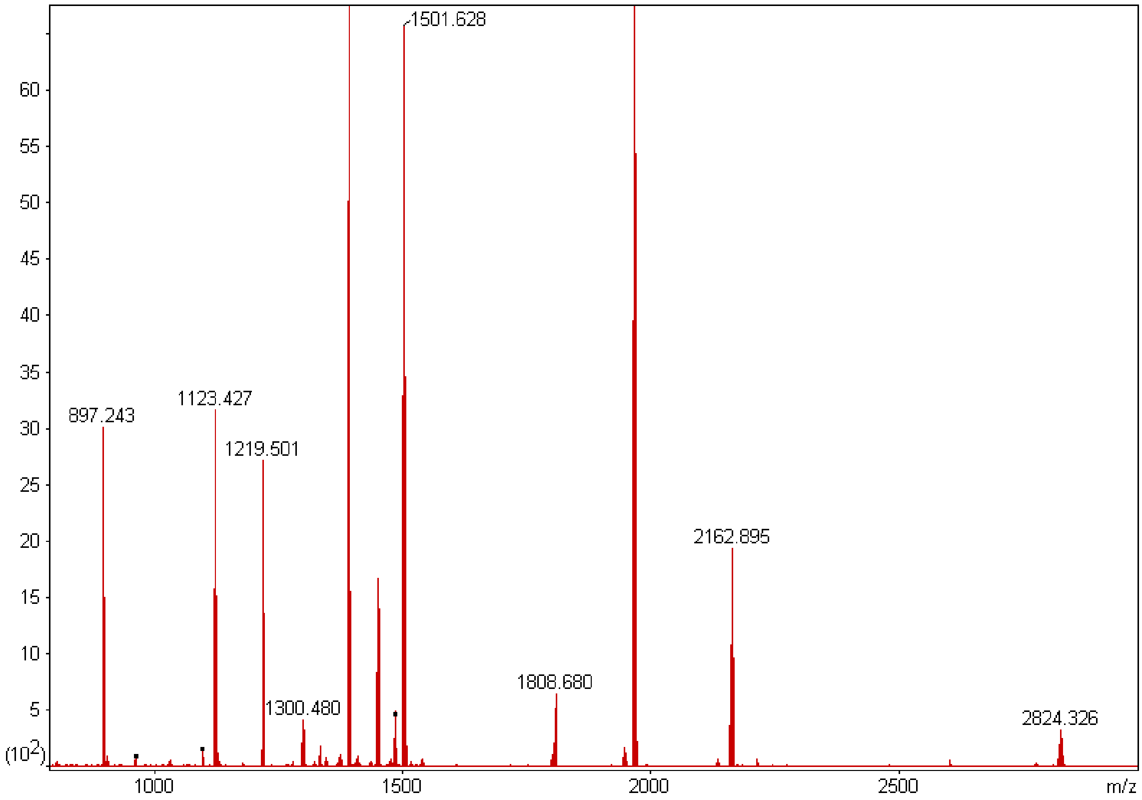
Mascot score: **127** Sequence coverage %: **33**

NCBI accession No.: **gi| 26450878**

Matched peptides No.: **10** Total peptides No.: **14**

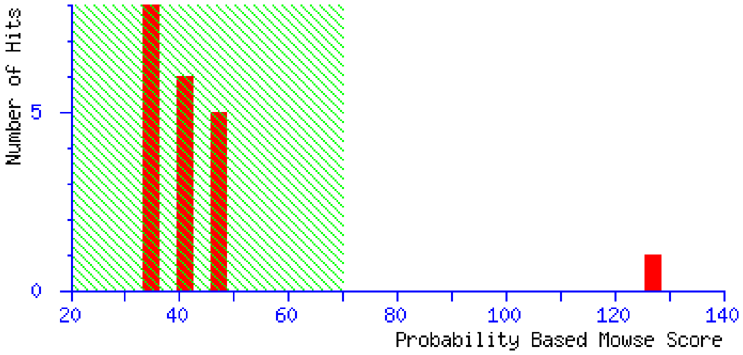
Calculated Mr: **34325** Calculated *p*I: **5.09**

Annotated PMF **spectra:**

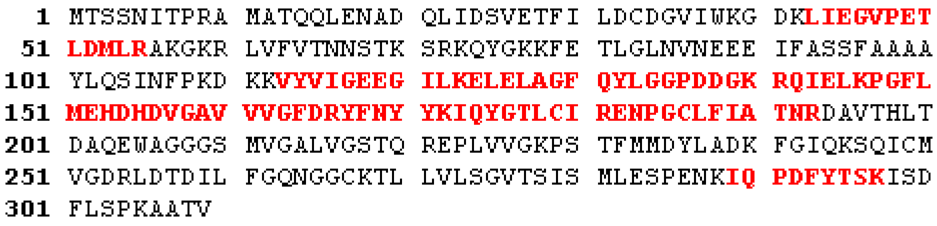


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

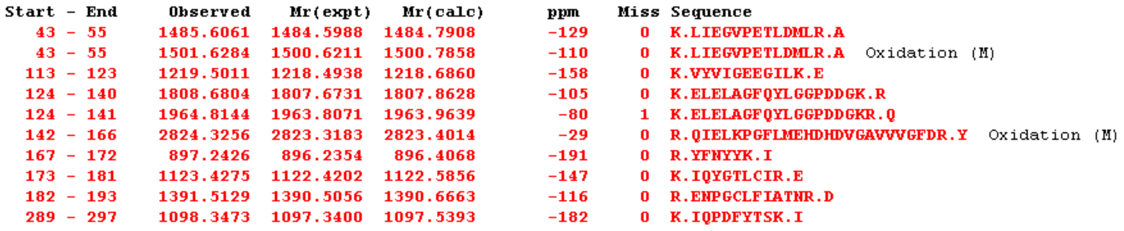


Matched peptide sequences: shown in Bold Red



1 MTSSNITPRA MATQQLENAD QLIDSVETFI LDCDGVIWKG DK**LIEGVPET**
51 **LDMLR**AKGKR LVFVTNNSTK SRKQYGKKFE TLGLNVNEEE IFASSFAAAA
101 YLQSINFPKD KK**VYVIGEEG** **ILKELELAGF** **QYLGGPDDGK** **RQIELKPGFL**
151 **MEHDHDVGAV** **VVGFDRYFNY** **YKIQYGTLCI** **RENPGCLFIA** **TNR**DAVTHLT
201 DAQEWAGGGS MVGALVGSTQ REPLVVGKPS TFMMDYLADK FGIQKSQICM
251 VGDRLDTDIL FGQNGGCKTL LVLSGVTSIS MLESPENK**IQ** **PDFYTSK**ISD
301 FLSPKAATV

Matched peptides information:



```
Start - End     Observed    Mr(expt)    Mr(calc)       ppm    Miss Sequence
   43 - 55     1485.6061   1484.5988   1484.7908      -129      0  K.LIEGVPETLDMLR.A
   43 - 55     1501.6284   1500.6211   1500.7858      -110      0  K.LIEGVPETLDMLR.A   Oxidation (M)
  113 - 123    1219.5011   1218.4938   1218.6860      -158      0  K.VYVIGEEGILK.E
  124 - 140    1808.6804   1807.6731   1807.8628      -105      0  K.ELELAGFQYLGGPDDGK.R
  124 - 141    1964.8144   1963.8071   1963.9639       -80      1  K.ELELAGFQYLGGPDDGKR.Q
  142 - 166    2824.3256   2823.3183   2823.4014       -29      0  R.QIELKPGFLMEHDHDVGAVVVGFDR.Y   Oxidation (M)
  167 - 172     897.2426    896.2354    896.4068      -191      0  R.YFNYYK.I
  173 - 181    1123.4275   1122.4202   1122.5856      -147      0  K.IQYGTLCIR.E
  182 - 193    1391.5129   1390.5056   1390.6663      -116      0  R.ENPGCLFIATNR.D
  289 - 297    1098.3473   1097.3400   1097.5393      -182      0  K.IQPDFYTSK.I
```

Spot No.: **155**

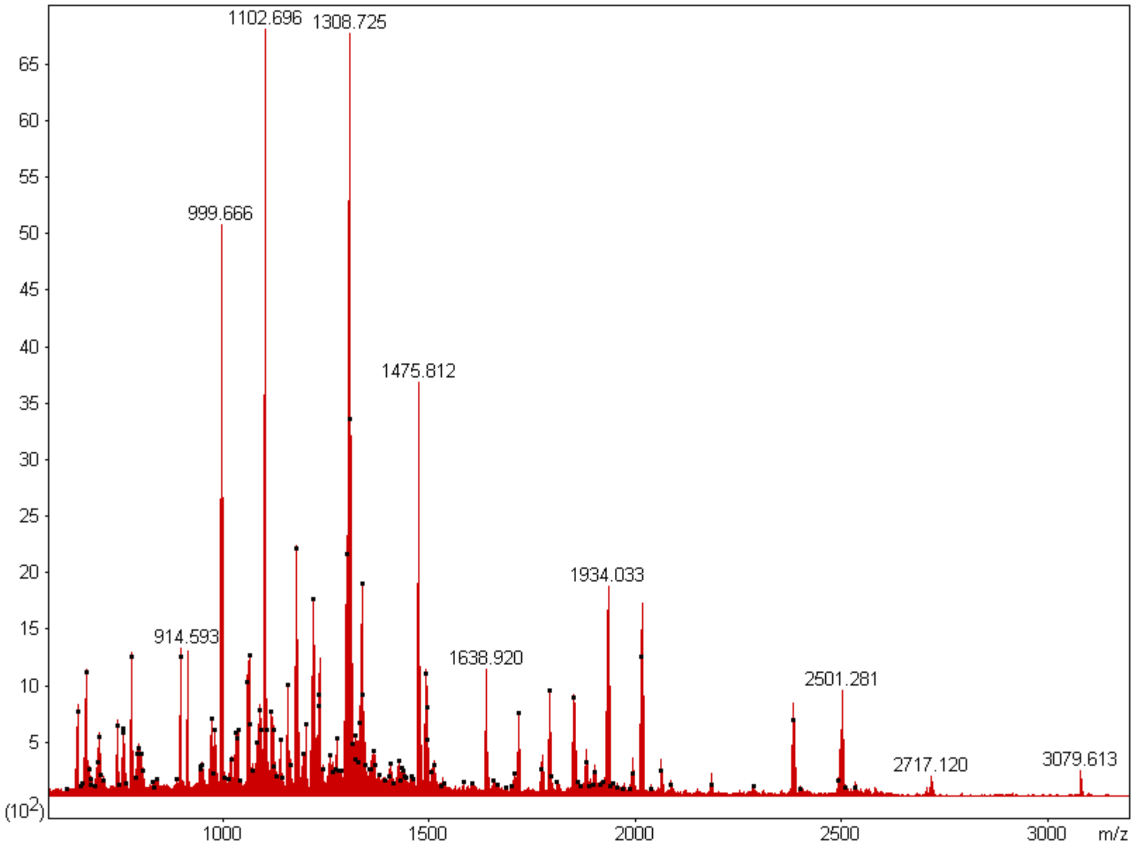
Mascot score: **90** Sequence coverage %: **35**

NCBI accession No.: **gi| 225437683**

Matched peptides No.: **20** Total peptides No.: **109**

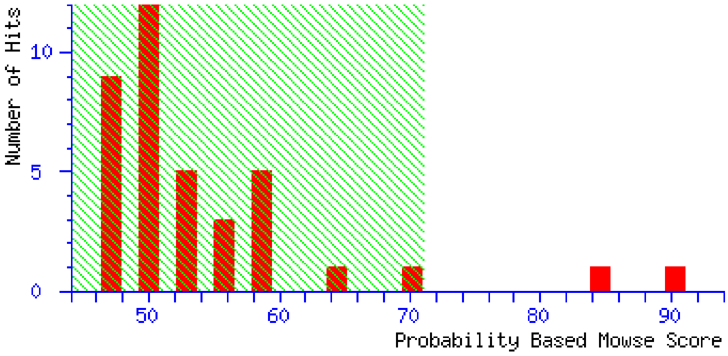
Calculated Mr: **46872** Calculated p*I*: **8.44**

Annotated PMF **spectra:**

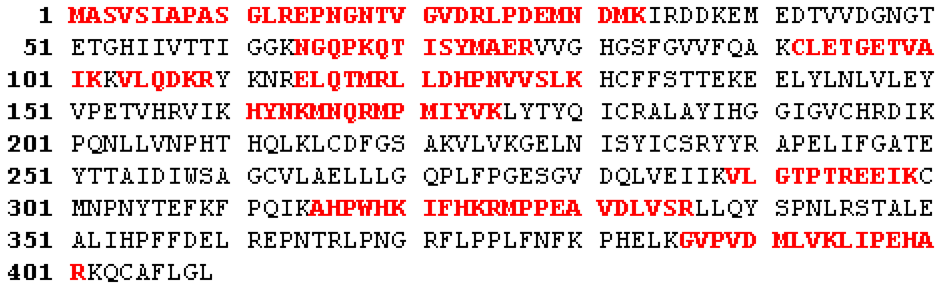


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).

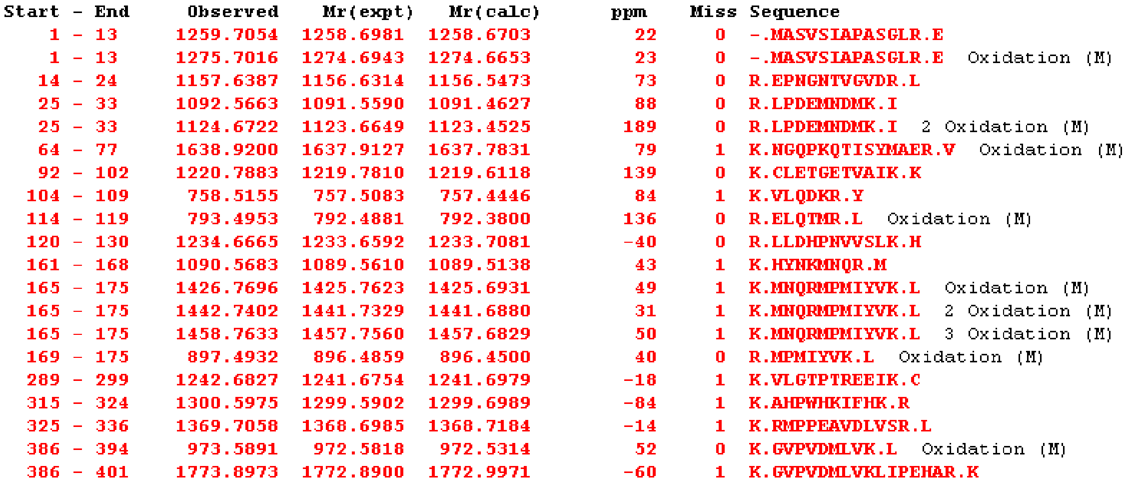


Matched peptide sequences: shown in Bold Red



1 **MASVSIAPAS GLREPNGNTV GVDRLPDEMN DMK**IRDDKEM EDTVVDGNGT
51 ETGHIIVTTI GGK**NGQPKQT ISYMAER**VVG HGSFGVVFQA K**CLETGETVA**
101 **IK**K**VLQDKR**Y KNR**ELQTMRL LDHPNVVSLK** HCFFSTTEKE ELYLNLVLEY
151 VPETVHRVIK **HYNKMNQRMP MIYVK**LYTYQ ICRALAYIHG GIGVCHRDIK
201 PQNLLVNPHT HQLKLCDFGS AKVLVKGELN ISYICSRYYR APELIFGATE
251 YTTAIDIWSA GCVLAELLLG QPLFPGESGV DQLVEIIK**VL GTPTREEIK**C
301 MNPNYTEFKF PQIK**AHPWHK IFHKRMPPEA VDLVSR**LLQY SPNLRSTALE
351 ALIHPFFDEL REPNTRLPNG RFLPPLFNFK PHELK**GVPVD MLVKLIPEHA**
401 **R**KQCAFLGL

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
1 - 13	1259.7054	1258.6981	1258.6703	22	0	-.MASVSIAPASGLR.E	
1 - 13	1275.7016	1274.6943	1274.6653	23	0	-.MASVSIAPASGLR.E	Oxidation (M)
14 - 24	1157.6387	1156.6314	1156.5473	73	0	R.EPNGNTVGVDR.L	
25 - 33	1092.5663	1091.5590	1091.4627	88	0	R.LPDEMNDMK.I	
25 - 33	1124.6722	1123.6649	1123.4525	189	0	R.LPDEMNDMK.I	2 Oxidation (M)
64 - 77	1638.9200	1637.9127	1637.7831	79	1	K.NGQPKQTISYMAER.V	Oxidation (M)
92 - 102	1220.7883	1219.7810	1219.6118	139	0	K.CLETGETVAIK.K	
104 - 109	758.5155	757.5083	757.4446	84	1	K.VLQDKR.Y	
114 - 119	793.4953	792.4881	792.3800	136	0	R.ELQTMR.L	Oxidation (M)
120 - 130	1234.6665	1233.6592	1233.7081	-40	0	R.LLDHPNVVSLK.H	
161 - 168	1090.5683	1089.5610	1089.5138	43	1	K.HYNKMNQR.M	
165 - 175	1426.7696	1425.7623	1425.6931	49	1	K.MNQRMPMIYVK.L	Oxidation (M)
165 - 175	1442.7402	1441.7329	1441.6880	31	1	K.MNQRMPMIYVK.L	2 Oxidation (M)
165 - 175	1458.7633	1457.7560	1457.6829	50	1	K.MNQRMPMIYVK.L	3 Oxidation (M)
169 - 175	897.4932	896.4859	896.4500	40	0	R.MPMIYVK.L	Oxidation (M)
289 - 299	1242.6827	1241.6754	1241.6979	-18	1	K.VLGTPTREEIK.C	
315 - 324	1300.5975	1299.5902	1299.6989	-84	1	K.AHPWHKIFHK.R	
325 - 336	1369.7058	1368.6985	1368.7184	-14	1	K.RMPPEAVDLVSR.L	
386 - 394	973.5891	972.5818	972.5314	52	0	K.GVPVDMLVK.L	Oxidation (M)
386 - 401	1773.8973	1772.8900	1772.9971	-60	1	K.GVPVDMLVKLIPEHAR.K	

Spot No.: **156**

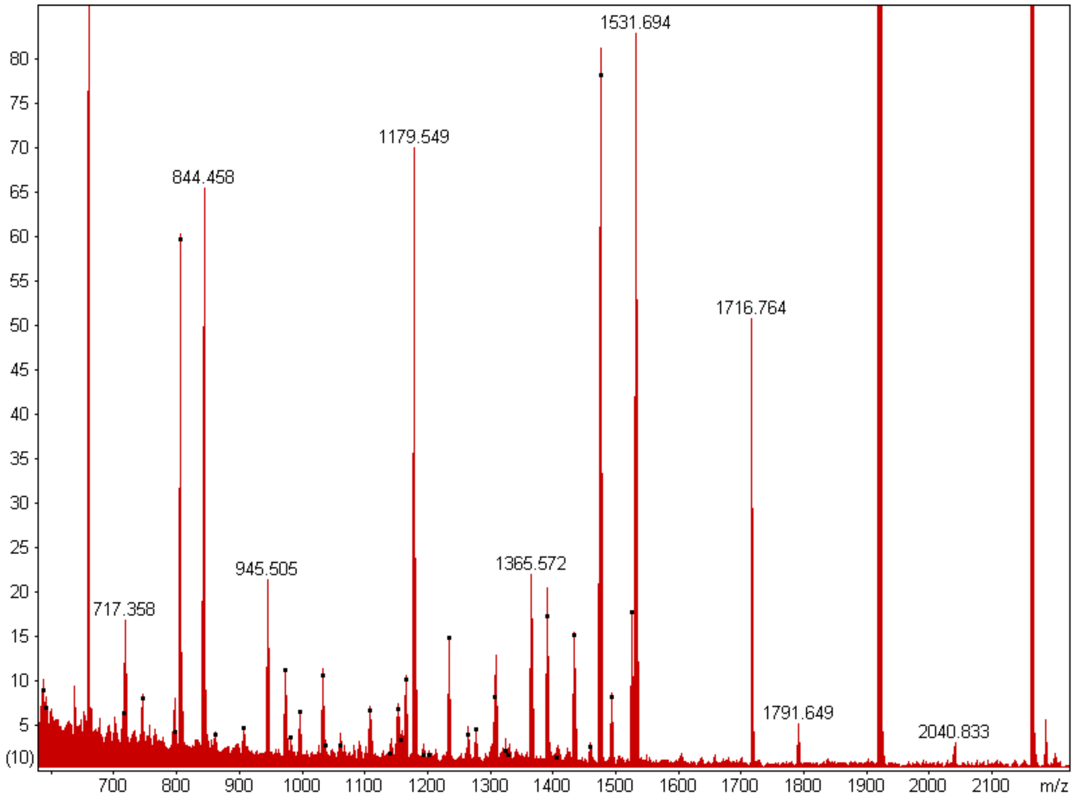
Mascot score: **94** Sequence coverage %: **17**

NCBI accession No.: **gi| 159485986**

Matched peptides No.: **10** Total peptides No.: **38**

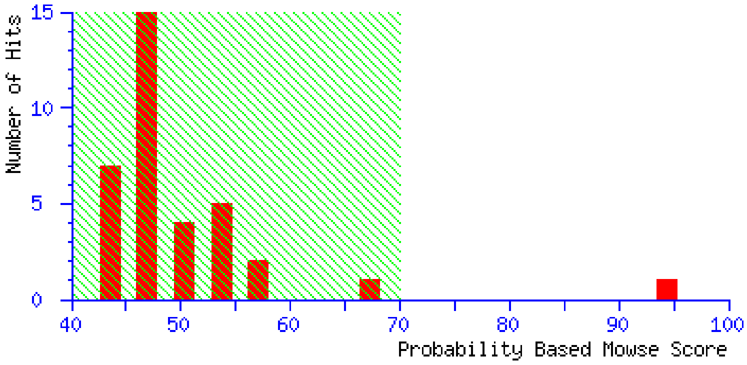
Calculated Mr: **48240** Calculated *p*I: **9.58**

Annotated PMF **spectra:**

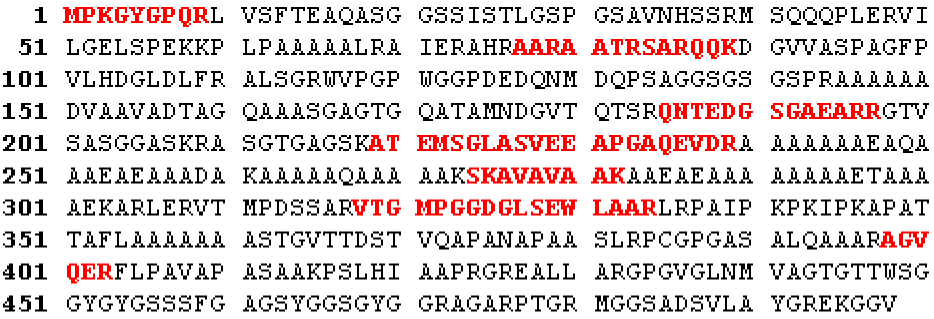


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).

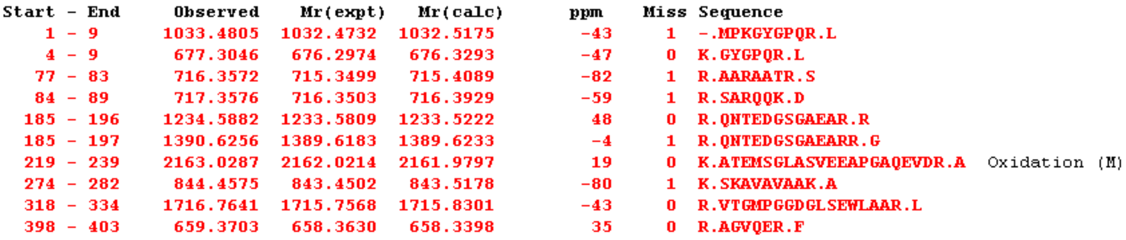


Matched peptide sequences: shown in Bold Red



1 **MPKGYGPQR**L VSFTEAQASG GSSISTLGSP GSAVNHSSRM SQQQPLERVI
51 LGELSPEKKP LPAAAAALRA IERAHR**AARA** **ATRSARQQK**D GVVASPAGFP
101 VLHDGLDLFR ALSGRWVPGP WGGPDEDQNM DQPSAGGSGS GSPRAAAAAA
151 DVAAVADTAG QAAASGAGTG QATAMNDGVT QTSR**QNTEDG** **SGAEARR**GTV
201 SASGGASKRA SGTGAGSK**AT** **EMSGLASVEE** **APGAQEVDR**A AAAAAAEAQA
251 AAEAEAAADA KAAAAAQAAA AAK**SKAVAVA** **AK**AAEAEAAA AAAAAETAAA
301 AEKARLERVT MPDSSAR**VTG** **MPGGDGLSEW** **LAAR**LRPAIP KPKIPKAPAT
351 TAFLAAAAAA ASTGVTTDST VQAPANAPAA SLRPCGPGAS ALQAAAR**AGV**
401 **QER**FLPAVAP ASAAKPSLHI AAPRGREALL ARGPGVGLNM VAGTGTTWSG
451 GYGYGSSSFG AGSYGGSGYG GRAGARPTGR MGGSADSVLA YGREKGGV

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
1 - 9	1033.4805	1032.4732	1032.5175	-43	1	-.MPKGYGPQR.L	
4 - 9	677.3046	676.2974	676.3293	-47	0	K.GYGPQR.L	
77 - 83	716.3572	715.3499	715.4089	-82	1	R.AARAATR.S	
84 - 89	717.3576	716.3503	716.3929	-59	1	R.SARQQK.D	
185 - 196	1234.5882	1233.5809	1233.5222	48	0	R.QNTEDGSGAEAR.R	
185 - 197	1390.6256	1389.6183	1389.6233	-4	1	R.QNTEDGSGAEARR.G	
219 - 239	2163.0287	2162.0214	2161.9797	19	0	K.ATEMSGLASVEEAPGAQEVDR.A	Oxidation (M)
274 - 282	844.4575	843.4502	843.5178	-80	1	K.SKAVAVAAK.A	
318 - 334	1716.7641	1715.7568	1715.8301	-43	0	R.VTGMPGGDGLSEWLAAR.L	
398 - 403	659.3703	658.3630	658.3398	35	0	R.AGVQER.F	

Spot No.: **157**

Mascot score: **98**

Sequence coverage %: **49**

NCBI accession No.: **gi| 312281705**

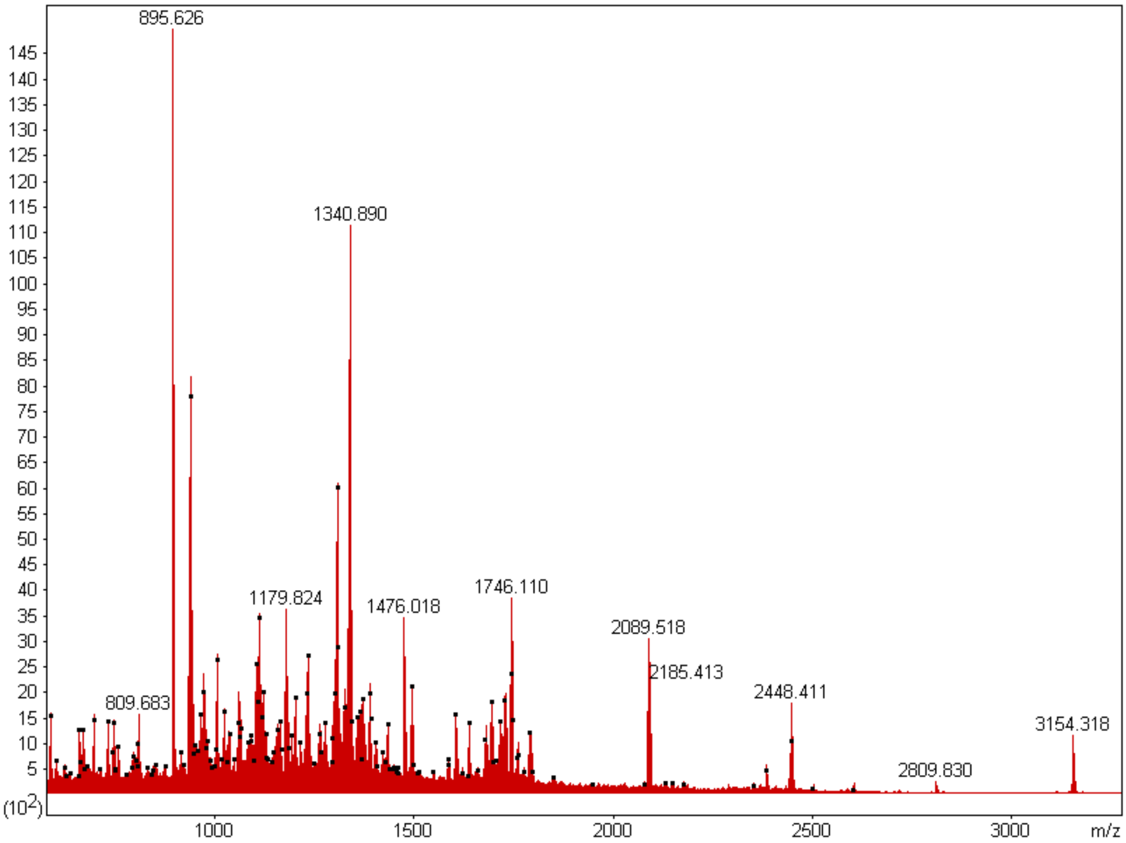
Matched peptides No.: **25**

Total peptides No.: **150**

Calculated Mr: **48202**

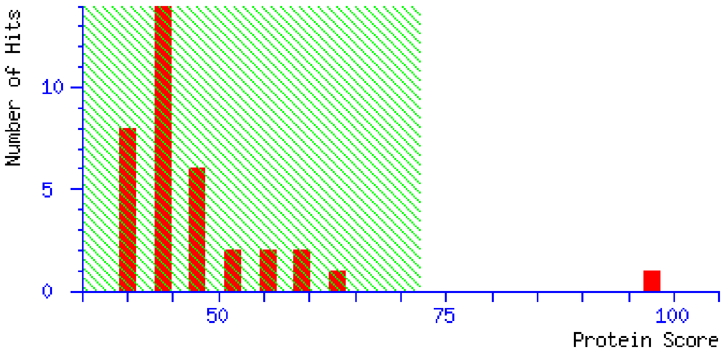
Calculated p*I*: **6.08**

Annotated PMF **spectra:**

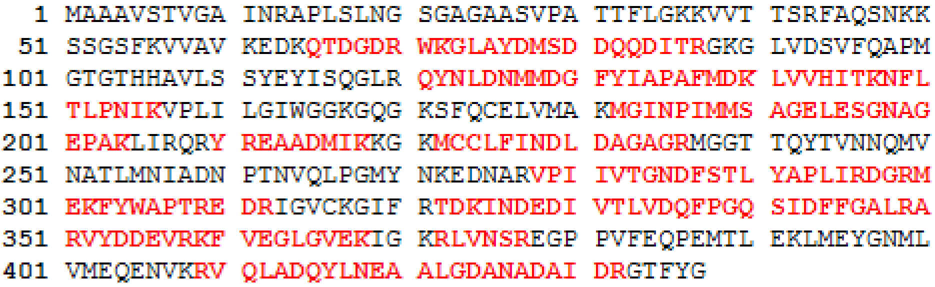


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red



```
  1 MAAAVSTVGA INRAPLSLNG SGAGAASVPA TTFLGKKVVT TSRFAQSNKK
 51 SSGSFKVVAV KEDKQTDGDR WKGLAYDMSD DQQDITRGKG LVDSVFQAPM
101 GTGTHHAVLS SYEYISQGLR QYNLDNMMDG FYIAPAFMDK LVVHITKNFL
151 TLPNIKVPLI LGIWGGKGQG KSFQCELVMA KMGINPIMMS AGELESGNAG
201 EPAKLIRQRY REAADMIKKG KMCCLFINDL DAGAGRMGGT TQYTVNNQMV
251 NATLMNIADN PTNVQLPGMY NKEDNARVPI IVTGNDFSTL YAPLIRDGRM
301 EKFYWAPTRE DRIGVCKGIF RTDKINDEDI VTLVDQFPGQ SIDFFGALRA
351 RVYDDEVRKF VEGLGVEKIG KRLVNSREGP PVFEQPEMTL EKLMEYGNML
401 VMEQENVKRV QLADQYLNEA ALGDANADAI DRGTFYG
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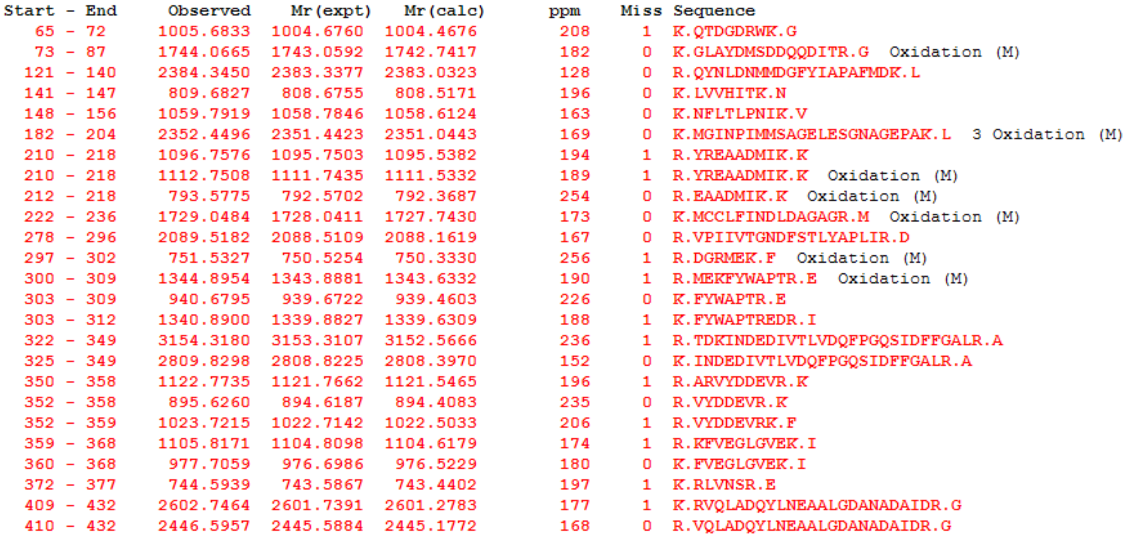
Matched peptides information:



```
Start - End      Observed    Mr(expt)    Mr(calc)       ppm    Miss  Sequence
   65 - 72      1005.6833   1004.6760   1004.4676       208      1   K.QTDGDRWK.G
   73 - 87      1744.0665   1743.0592   1742.7417       182      0   K.GLAYDMSDDQQDITR.G   Oxidation (M)
  121 - 140     2384.3450   2383.3377   2383.0323       128      0   R.QYNLDNMMDGFYIAPAFMDK.L
  141 - 147      809.6827    808.6755    808.5171       196      0   K.LVVHITK.N
  148 - 156     1059.7919   1058.7846   1058.6124       163      0   K.NFLTLPNIK.V
  182 - 204     2352.4496   2351.4423   2351.0443       169      0   K.MGINPIMMSAGELESGNAGEPAK.L   3 Oxidation (M)
  210 - 218     1096.7576   1095.7503   1095.5382       194      1   R.YREAADMIK.K
  210 - 218     1112.7508   1111.7435   1111.5332       189      1   R.YREAADMIK.K   Oxidation (M)
  212 - 218      793.5775    792.5702    792.3687       254      0   R.EAADMIK.K   Oxidation (M)
  222 - 236     1729.0484   1728.0411   1727.7430       173      0   K.MCCLFINDLDAGAGR.M   Oxidation (M)
  278 - 296     2089.5182   2088.5109   2088.1619       167      0   R.VPIIVTGNDFSTLYAPLIR.D
  297 - 302      751.5327    750.5254    750.3330       256      1   R.DGRMEK.F   Oxidation (M)
  300 - 309     1344.8954   1343.8881   1343.6332       190      1   R.MEKFYWAPTR.E   Oxidation (M)
  303 - 309      940.6795    939.6722    939.4603       226      0   K.FYWAPTR.E
  303 - 312     1340.8900   1339.8827   1339.6309       188      1   K.FYWAPTREDR.I
  322 - 349     3154.3180   3153.3107   3152.5666       236      1   R.TDKINDEDIVTLVDQFPGQSIDFFGALR.A
  325 - 349     2809.8298   2808.8225   2808.3970       152      0   K.INDEDIVTLVDQFPGQSIDFFGALR.A
  350 - 358     1122.7735   1121.7662   1121.5465       196      1   R.ARVYDDEVR.K
  352 - 358      895.6260    894.6187    894.4083       235      0   R.VYDDEVR.K
  352 - 359     1023.7215   1022.7142   1022.5033       206      1   R.VYDDEVRK.F
  359 - 368     1105.8171   1104.8098   1104.6179       174      1   R.KFVEGLGVEK.I
  360 - 368      977.7059    976.6986    976.5229       180      0   K.FVEGLGVEK.I
  372 - 377      744.5939    743.5867    743.4402       197      1   K.RLVNSR.E
  409 - 432     2602.7464   2601.7391   2601.2783       177      1   K.RVQLADQYLNEAALGDANADAIDR.G
  410 - 432     2446.5957   2445.5884   2445.1772       168      0   R.VQLADQYLNEAALGDANADAIDR.G
```

Spot No.: **158**

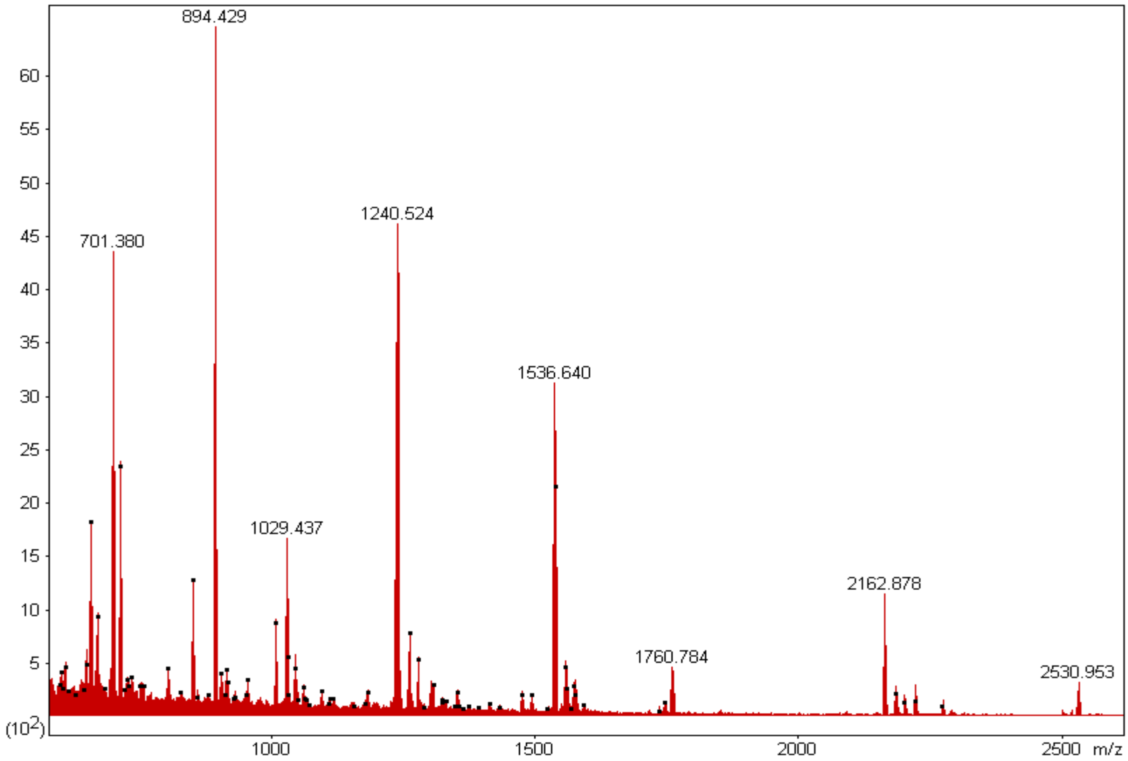
Mascot score: **82** Sequence coverage %: **54**

NCBI accession No.: **gi| 223515525**

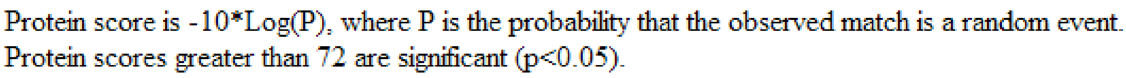
Matched peptides No.: **9** Total peptides No.: **55**

Calculated Mr: **17518** Calculated *p*I: **10.83**

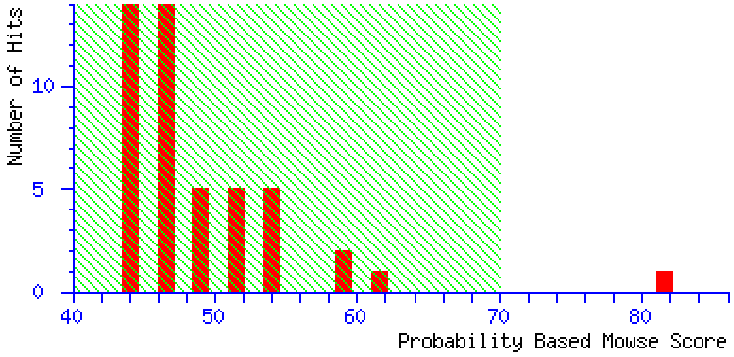
Annotated PMF **spectra:**



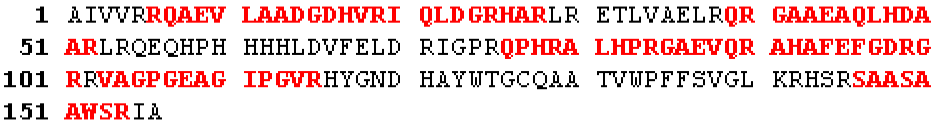
Probability Based Mowse Score:



Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

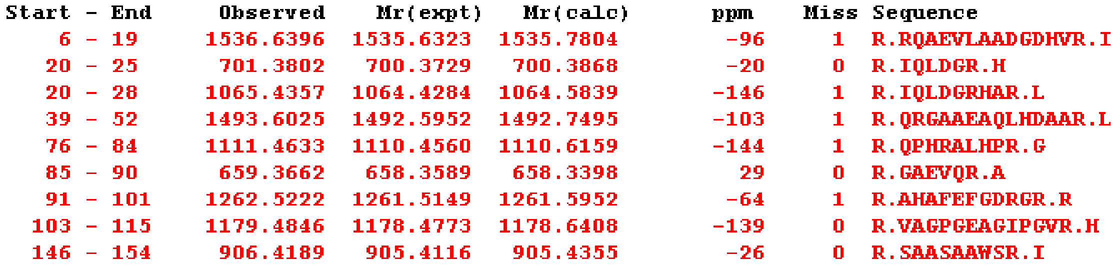


Matched peptide sequences: shown in Bold Red



1 AIVVR**RQAEV LAADGDHVRI QLDGRHAR**LR ETLVAELR**QR GAAEAQLHDA**
51 **AR**LRQEQHPH HHHLDVFELD RIGPR**QPHRA LHPRGAEVQR AHAFEFGDRG**
101 **R**R**VAGPGEAG IPGVR**HYGND HAYWTGCQAA TVWPFFSVGL KRHSR**SAASA**
151 **AWSR**IA

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
6 - 19	1536.6396	1535.6323	1535.7804	-96	1	R.RQAEVLAADGDHVR.I
20 - 25	701.3802	700.3729	700.3868	-20	0	R.IQLDGR.H
20 - 28	1065.4357	1064.4284	1064.5839	-146	1	R.IQLDGRHAR.L
39 - 52	1493.6025	1492.5952	1492.7495	-103	1	R.QRGAAEAQLHDAAR.L
76 - 84	1111.4633	1110.4560	1110.6159	-144	1	R.QPHRALHPR.G
85 - 90	659.3662	658.3589	658.3398	29	0	R.GAEVQR.A
91 - 101	1262.5222	1261.5149	1261.5952	-64	1	R.AHAFEFGDRGR.R
103 - 115	1179.4846	1178.4773	1178.6408	-139	0	R.VAGPGEAGIPGVR.H
146 - 154	906.4189	905.4116	905.4355	-26	0	R.SAASAAWSR.I

Spot No.: **159**

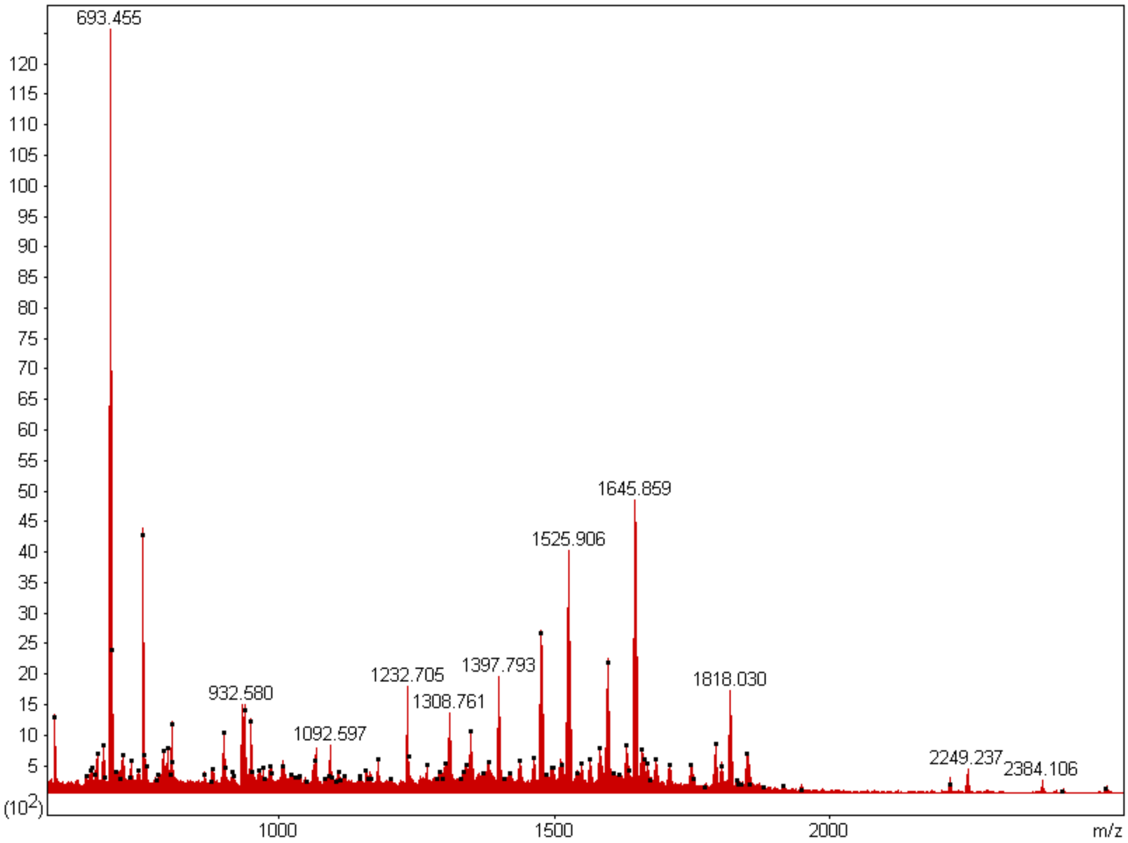
Mascot score: **96** Sequence coverage %: **27**

NCBI accession No.: **gi| 166406194**

Matched peptides No.: **15** Total peptides No.: **119**

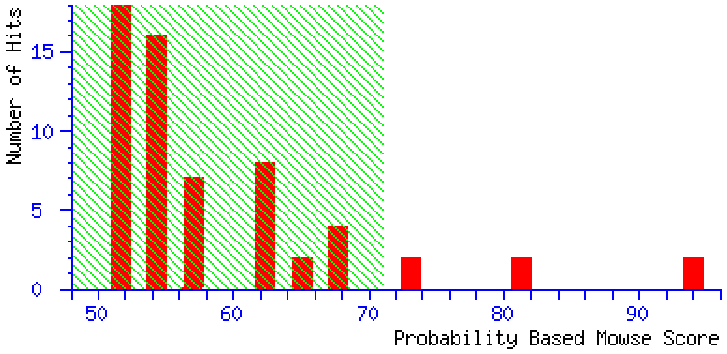
Calculated Mr: **47715** Calculated *p*I: **5.84**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 MAQILAASPT CQMR**LTKPSS** **IASSK**LWNSV VLKQKEQSSS KVRSFKVMAL
51 QSDNSTINR**V** **ESLLNLDTKP** **FTDR**IIAEYI WIGGSGIDLR SKSR**TLEKPV**
101 **EDPSELPK**WN YDGSSTGQAP GEDSEVILYP QAIFRDPFRG GNNILVICDT
151 YTPAGEPIPT NKRAR**AAEIF** **SNK**KVNEEIP WFGIEQEYTL LQPNVNWPLG
201 WPVGAYPGPQ GPYYCGVGAE KSWGR**DISDA** **HYK**ACLYAGI NISGTNGEVM
251 PGQWEFQVGP SVGIEAGDHV WCAR**YLLER**I TEQAGVVLTL DPKPIEGDWN
301 GAGCHTNYST KSMREDGGFE VIKK**AILNLS** **LRHMEHISAY** **GEGNERRLTG**
351 **KHETASIDQF** **SWGVANR**GCS IR**VGRDTEK**K **GKGYLEDR**RP ASNMDPYIVT
401 SLLAETTLLW EPTLEAEALA AQKLSLKV

Matched peptides information:

```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   15 - 25     1118.6023  1117.5950  1117.6343      -35      0  R.LTKPSSIASSK.L
   60 - 74     1748.0518  1747.0445  1746.9152       74      0  R.VESLLNLDTKPFTDR.I
   95 - 108    1581.8891  1580.8818  1580.8297       33      0  R.TLEKPVEDPSELPK.W
  166 - 173     879.4962   878.4889   878.4498       45      0  R.AAEIFSNK.K
  226 - 233     948.5132   947.5059   947.4348       75      0  R.DISDAHYK.A
  275 - 279     693.4549   692.4477   692.3857       89      0  R.YLLER.I
  325 - 332     899.6318   898.6245   898.5600       72      0  K.AILNLSLR.H
  333 - 346    1629.8539  1628.8466  1628.7001       90      0  R.HMEHISAYGEGNER.R
  333 - 346    1645.8592  1644.8519  1644.6950       95      0  R.HMEHISAYGEGNER.R  Oxidation (M)
  333 - 347    1801.9793  1800.9720  1800.7961       98      1  R.HMEHISAYGEGNERR.L  Oxidation (M)
  348 - 367    2217.2330  2216.2257  2216.0974       58      1  R.LTGKHETASIDQFSWGVANR.G
  352 - 367    1818.0300  1817.0227  1816.8493       95      0  K.HETASIDQFSWGVANR.G
  373 - 379     804.4766   803.4693   803.4137       69      1  R.VGRDTEK.K
  381 - 388     937.5547   936.5474   936.4665       86      1  K.GKGYLEDR.R
  383 - 388     752.4234   751.4162   751.3501       88      0  K.GYLEDR.R
```

Spot No.: **160**

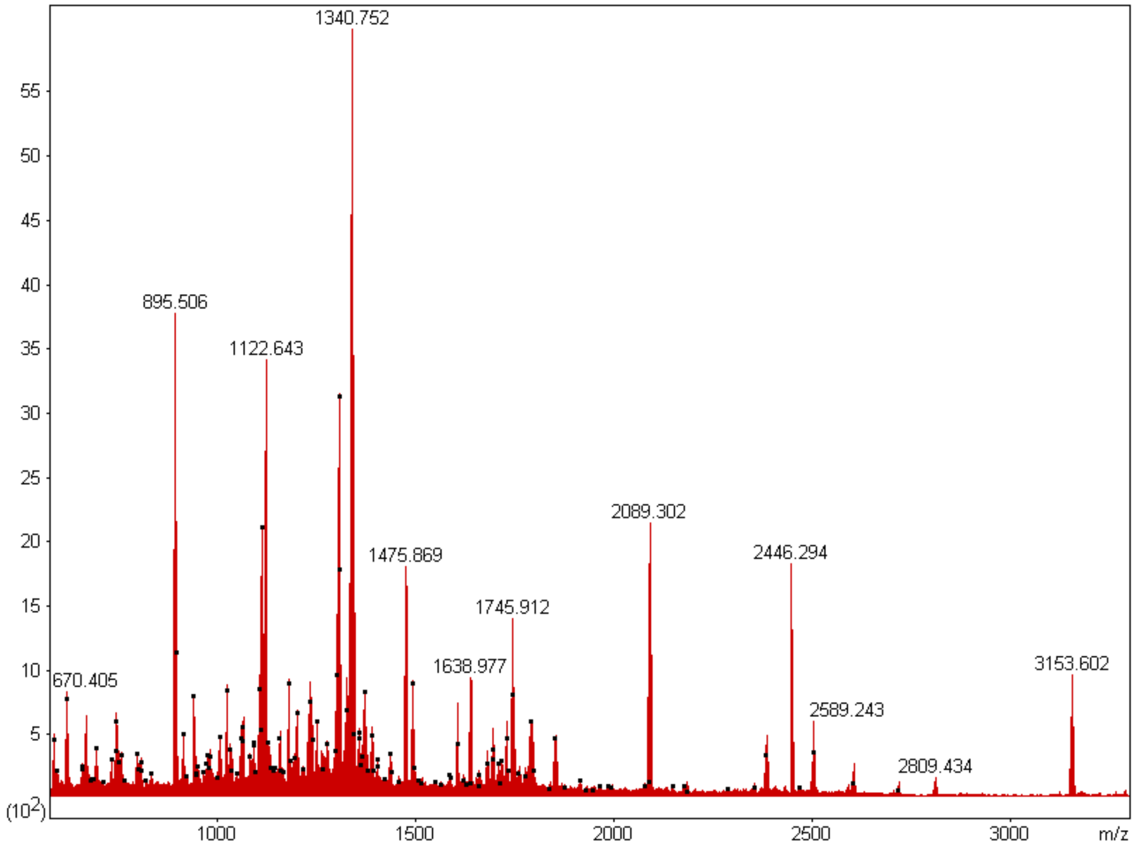
Mascot score: **120** Sequence coverage %: **50**

NCBI accession No.: **gi| 312281705**

Matched peptides No.: **27** Total peptides No.: **147**

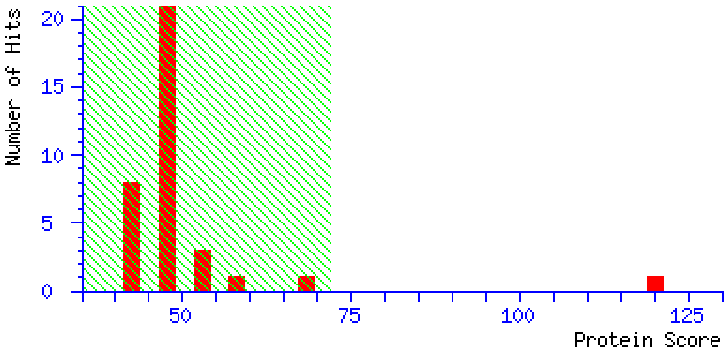
Calculated Mr: **48202** Calculated *p*I: **6.08**

Annotated PMF **spectra:**

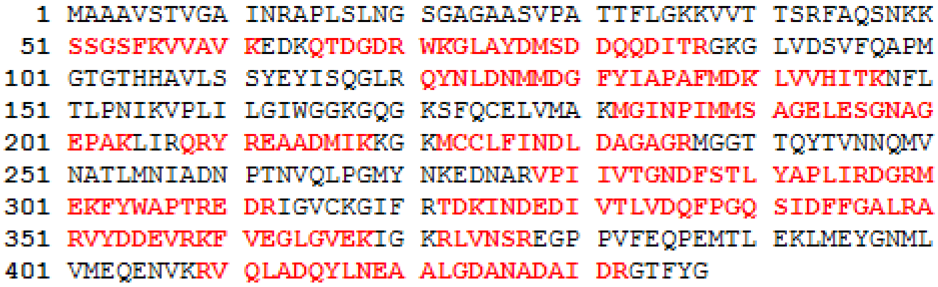


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

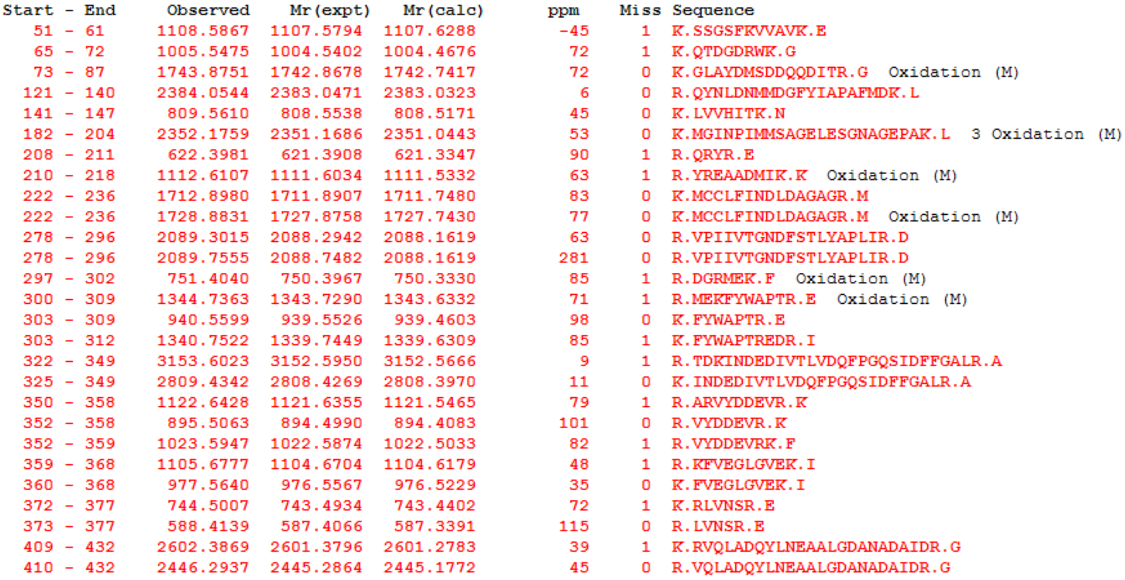


Matched peptide sequences: shown in Bold Red



```
  1 MAAAVSTVGA INRAPLSLNG SGAGAASVPA TTFLGKKVVT TSRFAQSNKK
 51 SSGSFKVVAV KEDKQTDGDR WKGLAYDMSD DQQDITRGKG LVDSVFQAPM
101 GTGTHHAVLS SYEYISQGLR QYNLDNMMDG FYIAPAFMDK LVVHITKNFL
151 TLPNIKVPLI LGIWGGKGQG KSFQCELVMA KMGINPIMMS AGELESGNAG
201 EPAKLIRQRY REAADMIKKG KMCCLFINDL DAGAGRMGGT TQYTVNNQMV
251 NATLMNIADN PTNVQLPGMY NKEDNARVPI IVTGNDFSTL YAPLIRDGRM
301 EKFYWAPTRE DRIGVCKGIF RTDKINDEDI VTLVDQFPGQ SIDFFGALRA
351 RVYDDEVRKF VEGLGVEKIG KRLVNSREGP PVFEQPEMTL EKLMEYGNML
401 VMEQENVKRV QLADQYLNEA ALGDANADAI DRGTFYG
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss Sequence
   51 - 61     1108.5867  1107.5794  1107.6288      -45     1  K.SSGSFKVVAVK.E
   65 - 72     1005.5475  1004.5402  1004.4676       72     1  K.QTDGDRWK.G
   73 - 87     1743.8751  1742.8678  1742.7417       72     0  K.GLAYDMSDDQQDITR.G  Oxidation (M)
  121 - 140    2384.0544  2383.0471  2383.0323        6     0  R.QYNLDNMMDGFYIAPAFMDK.L
  141 - 147     809.5610   808.5538   808.5171       45     0  K.LVVHITK.N
  182 - 204    2352.1759  2351.1686  2351.0443       53     0  K.MGINPIMMSAGELESGNAGEPAK.L  3 Oxidation (M)
  208 - 211     622.3981   621.3908   621.3347       90     1  R.QRYR.E
  210 - 218    1112.6107  1111.6034  1111.5332       63     1  R.YREAADMIK.K  Oxidation (M)
  222 - 236    1712.8980  1711.8907  1711.7480       83     0  K.MCCLFINDLDAGAGR.M
  222 - 236    1728.8831  1727.8758  1727.7430       77     0  K.MCCLFINDLDAGAGR.M  Oxidation (M)
  278 - 296    2089.3015  2088.2942  2088.1619       63     0  R.VPIIVTGNDFSTLYAPLIR.D
  278 - 296    2089.7555  2088.7482  2088.1619      281     0  R.VPIIVTGNDFSTLYAPLIR.D
  297 - 302     751.4040   750.3967   750.3330       85     1  R.DGRMEK.F  Oxidation (M)
  300 - 309    1344.7363  1343.7290  1343.6332       71     1  R.MEKFYWAPTR.E  Oxidation (M)
  303 - 309     940.5599   939.5526   939.4603       98     0  K.FYWAPTR.E
  303 - 312    1340.7522  1339.7449  1339.6309       85     1  K.FYWAPTREDR.I
  322 - 349    3153.6023  3152.5950  3152.5666        9     1  R.TDKINDEDIVTLVDQFPGQSIDFFGALR.A
  325 - 349    2809.4342  2808.4269  2808.3970       11     0  K.INDEDIVTLVDQFPGQSIDFFGALR.A
  350 - 358    1122.6428  1121.6355  1121.5465       79     1  R.ARVYDDEVR.K
  352 - 358     895.5063   894.4990   894.4083      101     0  R.VYDDEVR.K
  352 - 359    1023.5947  1022.5874  1022.5033       82     1  R.VYDDEVRK.F
  359 - 368    1105.6777  1104.6704  1104.6179       48     1  R.KFVEGLGVEK.I
  360 - 368     977.5640   976.5567   976.5229       35     0  K.FVEGLGVEK.I
  372 - 377     744.5007   743.4934   743.4402       72     1  K.RLVNSR.E
  373 - 377     588.4139   587.4066   587.3391      115     0  R.LVNSR.E
  409 - 432    2602.3869  2601.3796  2601.2783       39     1  K.RVQLADQYLNEAALGDANADAIDR.G
  410 - 432    2446.2937  2445.2864  2445.1772       45     0  R.VQLADQYLNEAALGDANADAIDR.G
```

Spot No.: **161**

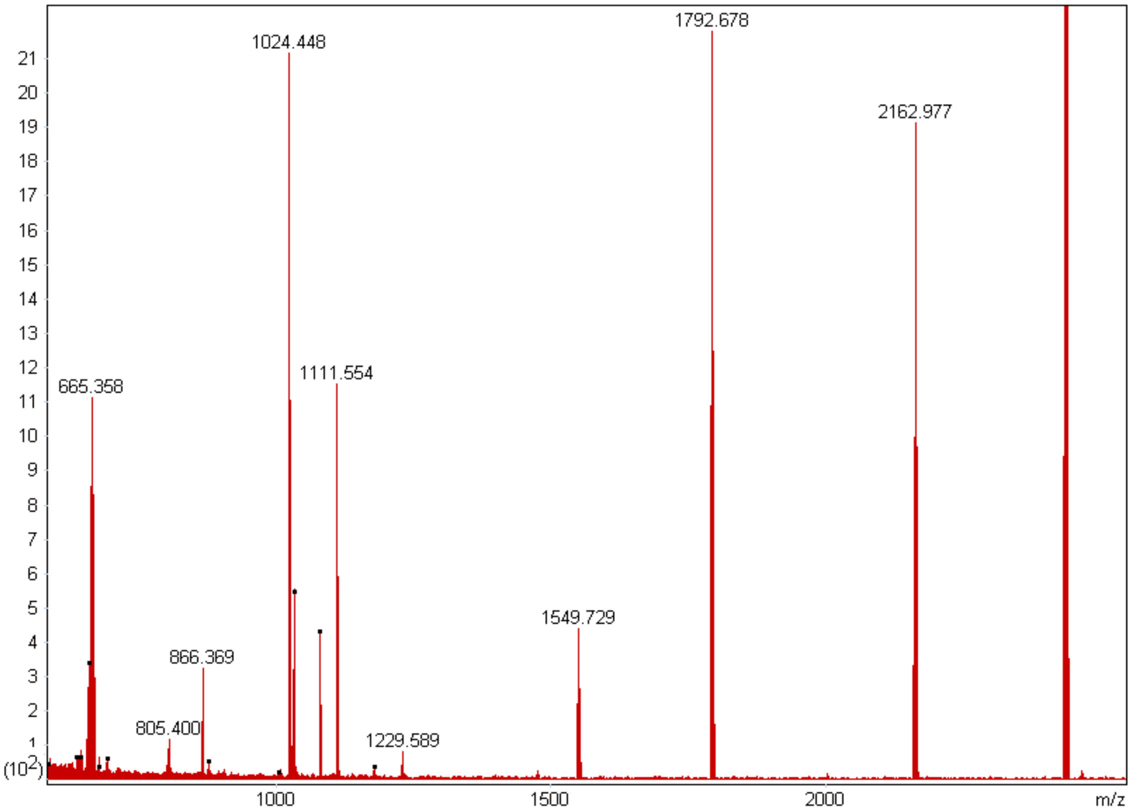
Mascot score: **84**   Sequence coverage %: **15**

NCBI accession No.: **gi| 116060520**

Matched peptides No.: **7**   Total peptides No.: **21**

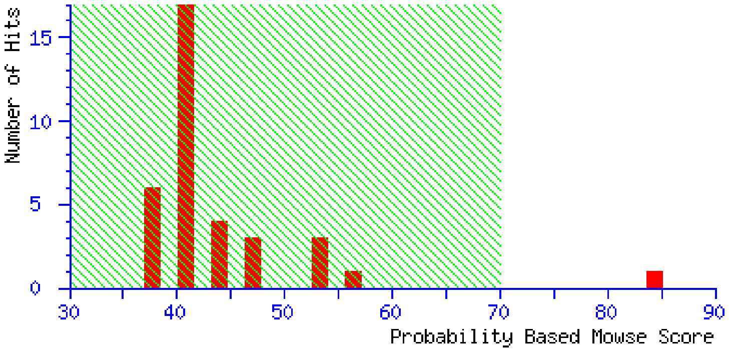
Calculated Mr: **30727**   Calculated *p*I: **5.06**

Annotated PMF **spectra:**

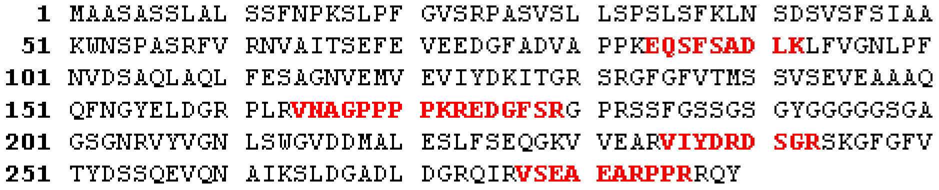


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

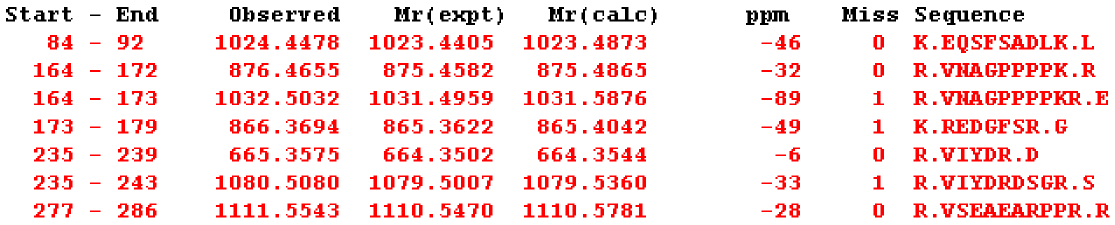


Matched peptide sequences: shown in Bold Red



1 MAASASSLAL SSFNPKSLPF GVSRPASVSL LSPSLSFKLN SDSVSFSIAA
51 KWNSPASRFV RNVAITSEFE VEEDGFADVA PPK**EQSFSAD** **LK**LFVGNLPF
101 NVDSAQLAQL FESAGNVEMV EVIYDKITGR SRGFGFVTMS SVSEVEAAAQ
151 QFNGYELDGR PLR**VNAGPPP** **PKREDGFSR**G PRSSFGSSGS GYGGGGGSGA
201 GSGNRVYVGN LSWGVDDMAL ESLFSEQGKV VEAR**VIYDRD** **SGR**SKGFGFV
251 TYDSSQEVQN AIKSLDGADL DGRQIR**VSEA** **EARPPR**RQY

Matched peptides information:



```
Start - End      Observed   Mr(expt)   Mr(calc)      ppm    Miss  Sequence
   84 - 92      1024.4478  1023.4405  1023.4873      -46      0   K.EQSFSADLK.L
  164 - 172      876.4655   875.4582   875.4865      -32      0   R.VNAGPPPPK.R
  164 - 173     1032.5032  1031.4959  1031.5876      -89      1   R.VNAGPPPPKR.E
  173 - 179      866.3694   865.3622   865.4042      -49      1   K.REDGFSR.G
  235 - 239      665.3575   664.3502   664.3544       -6      0   R.VIYDR.D
  235 - 243     1080.5080  1079.5007  1079.5360      -33      1   R.VIYDRDSGR.S
  277 - 286     1111.5543  1110.5470  1110.5781      -28      0   R.VSEAEARPPR.R
```

Spot No.: **162**

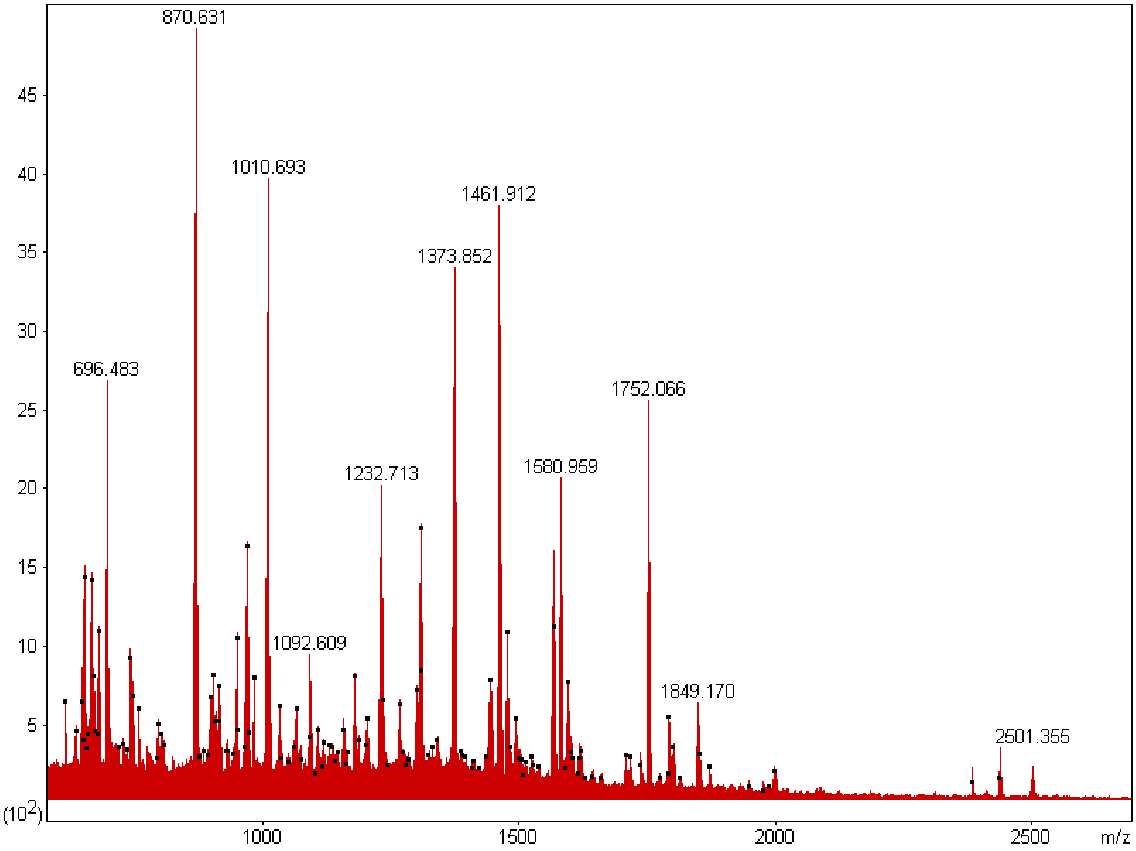
Mascot score: **93**   Sequence coverage %: **33**

NCBI accession No.: **gi| 15240578**

Matched peptides No.: **26**   Total peptides No.: **129**

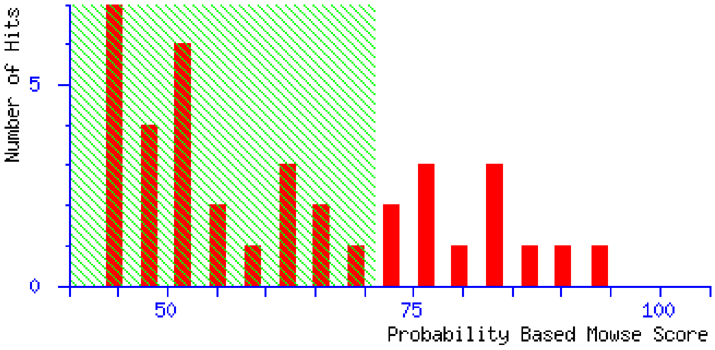
Calculated Mr: **77064**   Calculated p*I*: **5.17**

Annotated PMF **spectra:**

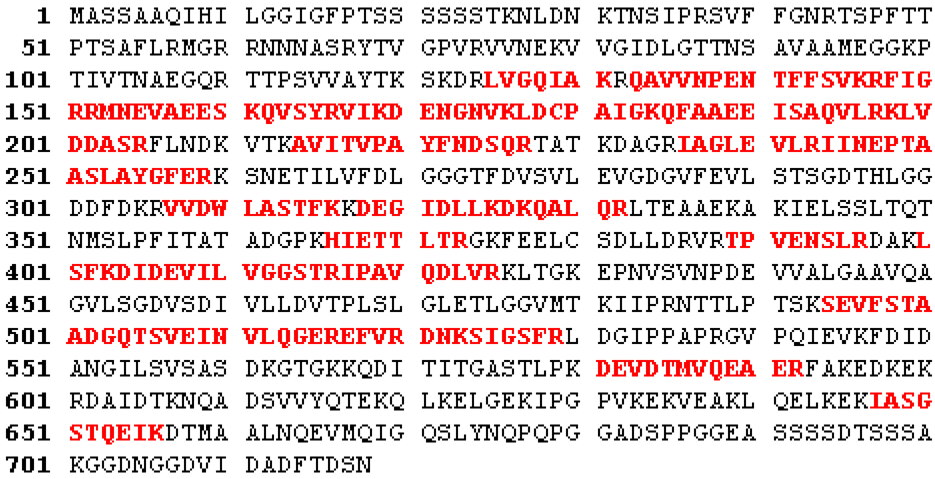


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

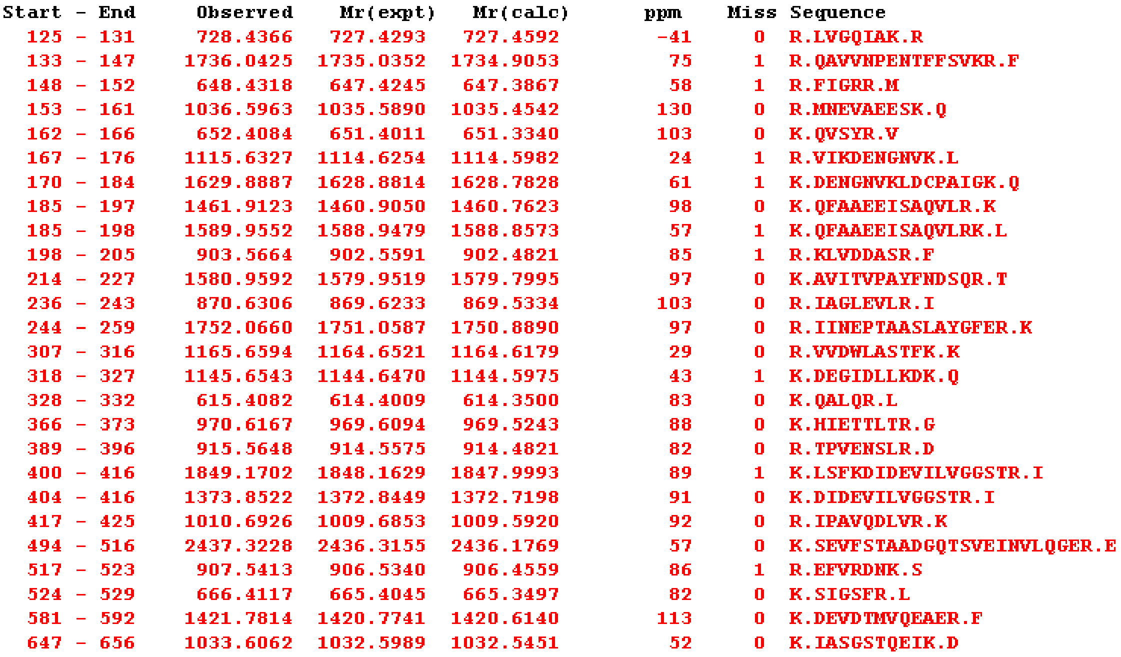


Matched peptide sequences: shown in Bold Red



1 MASSAAQIHI LGGIGFPTSS SSSSTKNLDN KTNSIPRSVF FGNRTSPFTT
51 PTSAFLRMGR RNNNASRYTV GPVRVVNEKV VGIDLGTTNS AVAAMEGGKP
101 TIVTNAEGQR TTPSVVAYTK SKDR**LVGQIA** **K**R**QAVVNPEN** **TFFSVKRFIG**
151 **RRMNEVAEES** **KQVSYRVIKD** **ENGNVKLDCP** **AIGKQFAAEE** **ISAQVLRKLV**
201 **DDASR**FLNDK VTK**AVITVPA** **YFNDSQR**TAT KDAGR**IAGLE** **VLRIINEPTA**
251 **ASLAYGFER**K SNETILVFDL GGGTFDVSVL EVGDGVFEVL STSGDTHLGG
301 DDFDKR**VVDW** **LASTFK**K**DEG** **IDLLKDKQAL** **QR**LTEAAEKA KIELSSLTQT
351 NMSLPFITAT ADGPK**HIETT** **LTR**GKFEELC SDLLDRVR**TP** **VENSLR**DAK**L**
401 **SFKDIDEVIL** **VGGSTRIPAV** **QDLVR**KLTGK EPNVSVNPDE VVALGAAVQA
451 GVLSGDVSDI VLLDVTPLSL GLETLGGVMT KIIPRNTTLP TSK**SEVFSTA**
501 **ADGQTSVEIN** **VLQGEREFVR** **DNKSIGSFR**L DGIPPAPRGV PQIEVKFDID
551 ANGILSVSAS DKGTGKKQDI TITGASTLPK **DEVDTMVQEA** **ER**FAKEDKEK
601 RDAIDTKNQA DSVVYQTEKQ LKELGEKIPG PVKEKVEAKL QELKEK**IASG**
651 **STQEIK**DTMA ALNQEVMQIG QSLYNQPQPG GADSPPGGEA SSSSDTSSSA
701 KGGDNGGDVI DADFTDSN

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
125 - 131	728.4366	727.4293	727.4592	-41	0	R.LVGQIAK.R
133 - 147	1736.0425	1735.0352	1734.9053	75	1	R.QAVVNPENTFFSVKR.F
148 - 152	648.4318	647.4245	647.3867	58	1	R.FIGRR.M
153 - 161	1036.5963	1035.5890	1035.4542	130	0	R.MNEVAEESK.Q
162 - 166	652.4084	651.4011	651.3340	103	0	K.QVSYR.V
167 - 176	1115.6327	1114.6254	1114.5982	24	1	R.VIKDENGNVK.L
170 - 184	1629.8887	1628.8814	1628.7828	61	1	K.DENGNVKLDCPAIGK.Q
185 - 197	1461.9123	1460.9050	1460.7623	98	0	K.QFAAEEISAQVLR.K
185 - 198	1589.9552	1588.9479	1588.8573	57	1	K.QFAAEEISAQVLRK.L
198 - 205	903.5664	902.5591	902.4821	85	1	R.KLVDDASR.F
214 - 227	1580.9592	1579.9519	1579.7995	97	0	K.AVITVPAYFNDSQR.T
236 - 243	870.6306	869.6233	869.5334	103	0	R.IAGLEVLR.I
244 - 259	1752.0660	1751.0587	1750.8890	97	0	R.IINEPTAASLAYGFER.K
307 - 316	1165.6594	1164.6521	1164.6179	29	0	R.VVDWLASTFK.K
318 - 327	1145.6543	1144.6470	1144.5975	43	1	K.DEGIDLLKDK.Q
328 - 332	615.4082	614.4009	614.3500	83	0	K.QALQR.L
366 - 373	970.6167	969.6094	969.5243	88	0	K.HIETTLTR.G
389 - 396	915.5648	914.5575	914.4821	82	0	R.TPVENSLR.D
400 - 416	1849.1702	1848.1629	1847.9993	89	1	K.LSFKDIDEVILVGGSTR.I
404 - 416	1373.8522	1372.8449	1372.7198	91	0	K.DIDEVILVGGSTR.I
417 - 425	1010.6926	1009.6853	1009.5920	92	0	R.IPAVQDLVR.K
494 - 516	2437.3228	2436.3155	2436.1769	57	0	K.SEVFSTAADGQTSVEINVLQGER.E
517 - 523	907.5413	906.5340	906.4559	86	1	R.EFVRDNK.S
524 - 529	666.4117	665.4045	665.3497	82	0	K.SIGSFR.L
581 - 592	1421.7814	1420.7741	1420.6140	113	0	K.DEVDTMVQEAER.F
647 - 656	1033.6062	1032.5989	1032.5451	52	0	K.IASGSTQEIK.D

Spot No.: **163**

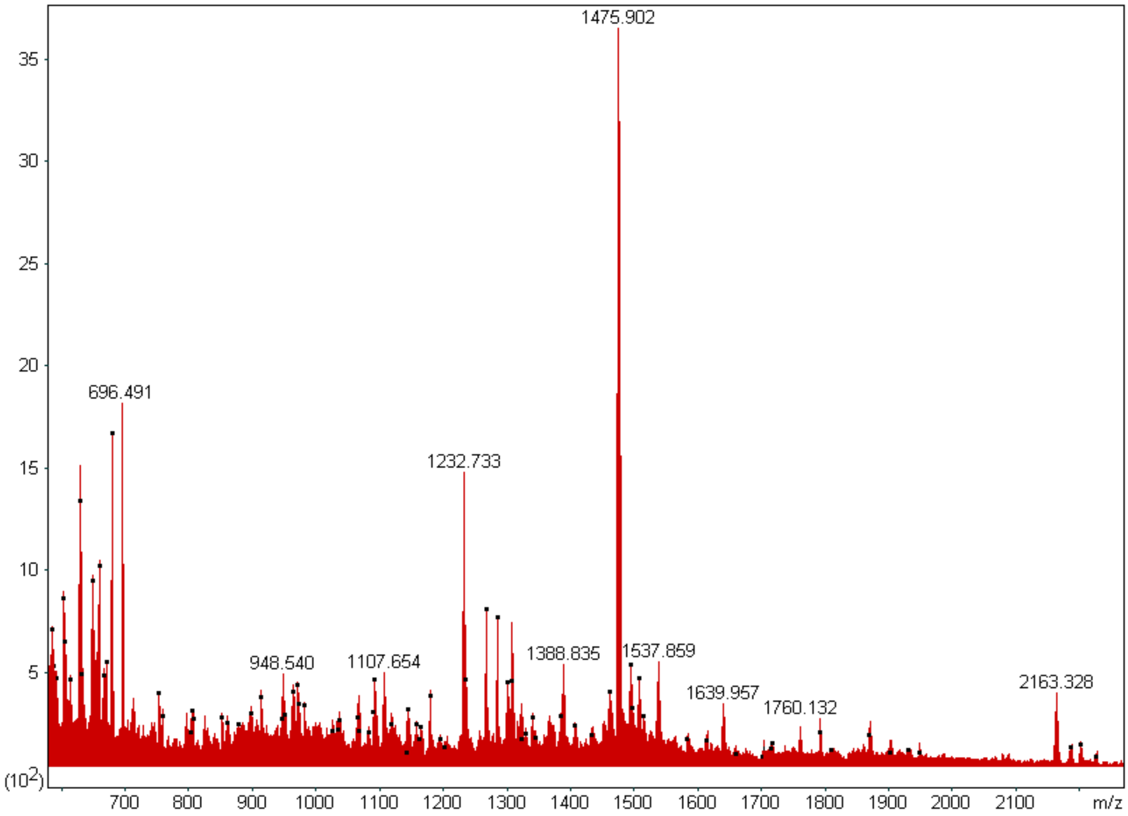
Mascot score: **110**   Sequence coverage %: **31**

NCBI accession No.: **gi| 116059538**

Matched peptides No.: **23**   Total peptides No.: **87**

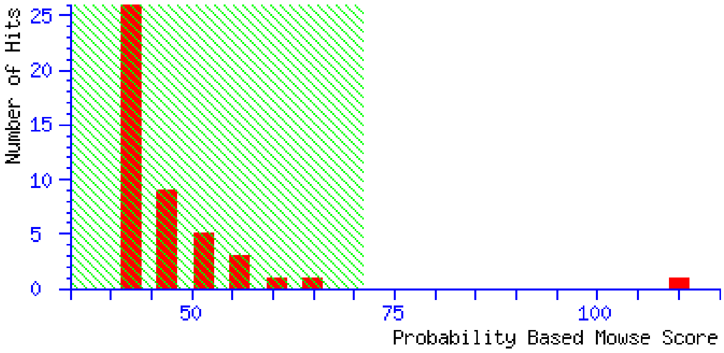
Calculated Mr: **62851**   Calculated p*I*: **6.32**

Annotated PMF **spectra:**

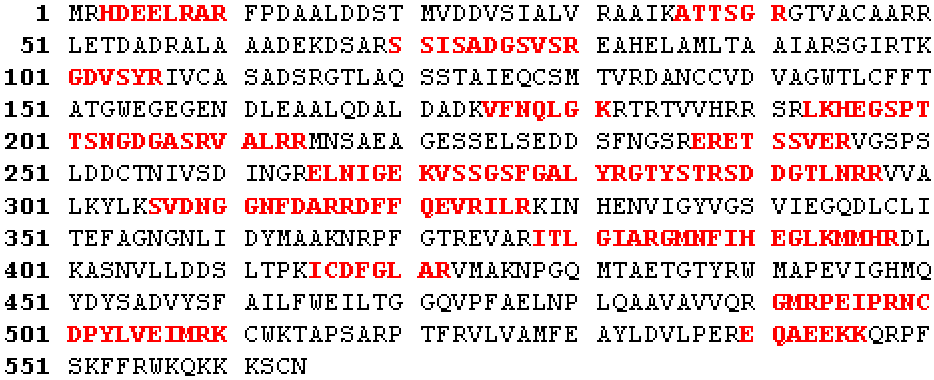


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

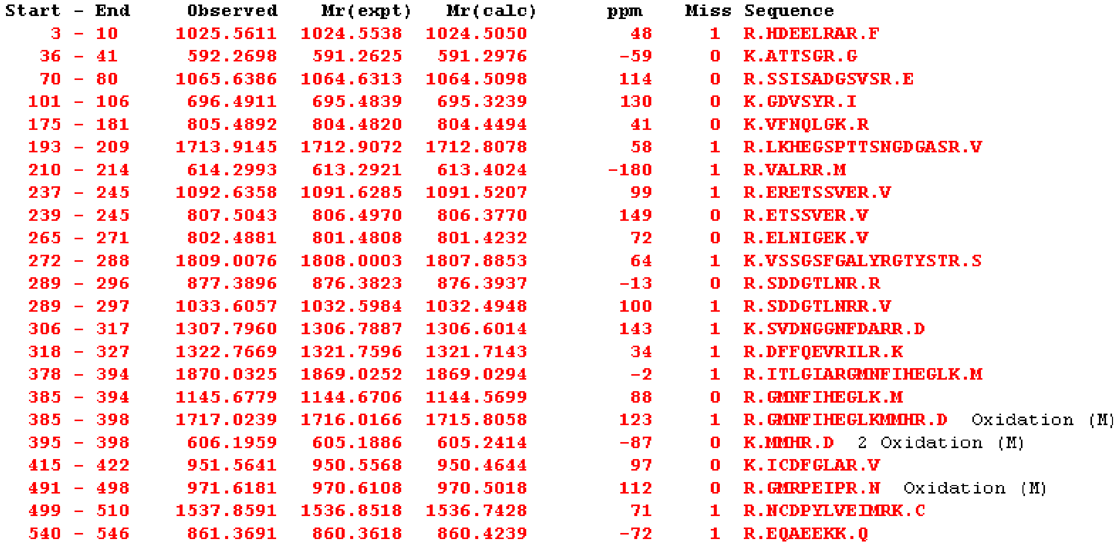


Matched peptide sequences: shown in Bold Red



1 MR**HDEELRAR** FPDAALDDST MVDDVSIALV RAAIK**ATTSG** **R**GTVACAARR
51 LETDADRALA AADEKDSAR**S** **SISADGSVSR** EAHELAMLTA AIARSGIRTK
101 **GDVSYR**IVCA SADSRGTLAQ SSTAIEQCSM TVRDANCCVD VAGWTLCFFT
151 ATGWEGEGEN DLEAALQDAL DADK**VFNQLG** **K**RTRTVVHRR SR**LKHEGSPT**
201 **TSNGDGASRV** **ALRR**MNSAEA GESSELSEDD SFNGSR**ERET** **SSVER**VGSPS
251 LDDCTNIVSD INGR**ELNIGE** **KVSSGSFGAL** **YRGTYSTRSD** **DGTLNRR**VVA
301 LKYLK**SVDNG** **GNFDARRDFF** **QEVRILR**KIN HENVIGYVGS VIEGQDLCLI
351 TEFAGNGNLI DYMAAKNRPF GTREVAR**ITL** **GIARGMNFIH** **EGLKMMHR**DL
401 KASNVLLDDS LTPK**ICDFGL** **AR**VMAKNPGQ MTAETGTYRW MAPEVIGHMQ
451 YDYSADVYSF AILFWEILTG GQVPFAELNP LQAAVAVVQR **GMRPEIPRNC**
501 **DPYLVEIMRK** CWKTAPSARP TFRVLVAMFE AYLDVLPER**E** **QAEEKK**QRPF
551 SKFFRWKQKK KSCN

Matched peptides information:



```
Start - End      Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    3 - 10      1025.5611  1024.5538  1024.5050       48      1  R.HDEELRAR.F
   36 - 41       592.2698   591.2625   591.2976      -59      0  K.ATTSGR.G
   70 - 80      1065.6386  1064.6313  1064.5098      114      0  R.SSISADGSVSR.E
  101 - 106      696.4911   695.4839   695.3239      130      0  K.GDVSYR.I
  175 - 181      805.4892   804.4820   804.4494       41      0  K.VFNQLGK.R
  193 - 209     1713.9145  1712.9072  1712.8078       58      1  R.LKHEGSPTTSNGDGASR.V
  210 - 214      614.2993   613.2921   613.4024     -180      1  R.VALRR.M
  237 - 245     1092.6358  1091.6285  1091.5207       99      1  R.ERETSSVER.V
  239 - 245      807.5043   806.4970   806.3770      149      0  R.ETSSVER.V
  265 - 271      802.4881   801.4808   801.4232       72      0  R.ELNIGEK.V
  272 - 288     1809.0076  1808.0003  1807.8853       64      1  K.VSSGSFGALYRGTYSTR.S
  289 - 296      877.3896   876.3823   876.3937      -13      0  R.SDDGTLNR.R
  289 - 297     1033.6057  1032.5984  1032.4948      100      1  R.SDDGTLNRR.V
  306 - 317     1307.7960  1306.7887  1306.6014      143      1  K.SVDNGGNFDARR.D
  318 - 327     1322.7669  1321.7596  1321.7143       34      1  R.DFFQEVRILR.K
  378 - 394     1870.0325  1869.0252  1869.0294       -2      1  R.ITLGIARGMNFIHEGLK.M
  385 - 394     1145.6779  1144.6706  1144.5699       88      0  R.GMNFIHEGLK.M
  385 - 398     1717.0239  1716.0166  1715.8058      123      1  R.GMNFIHEGLKMMHR.D   Oxidation (M)
  395 - 398      606.1959   605.1886   605.2414      -87      0  K.MMHR.D   2 Oxidation (M)
  415 - 422      951.5641   950.5568   950.4644       97      0  K.ICDFGLAR.V
  491 - 498      971.6181   970.6108   970.5018      112      0  R.GMRPEIPR.N   Oxidation (M)
  499 - 510     1537.8591  1536.8518  1536.7428       71      1  R.NCDPYLVEIMRK.C
  540 - 546      861.3691   860.3618   860.4239      -72      1  R.EQAEEKK.Q
```

Spot No.: **164**

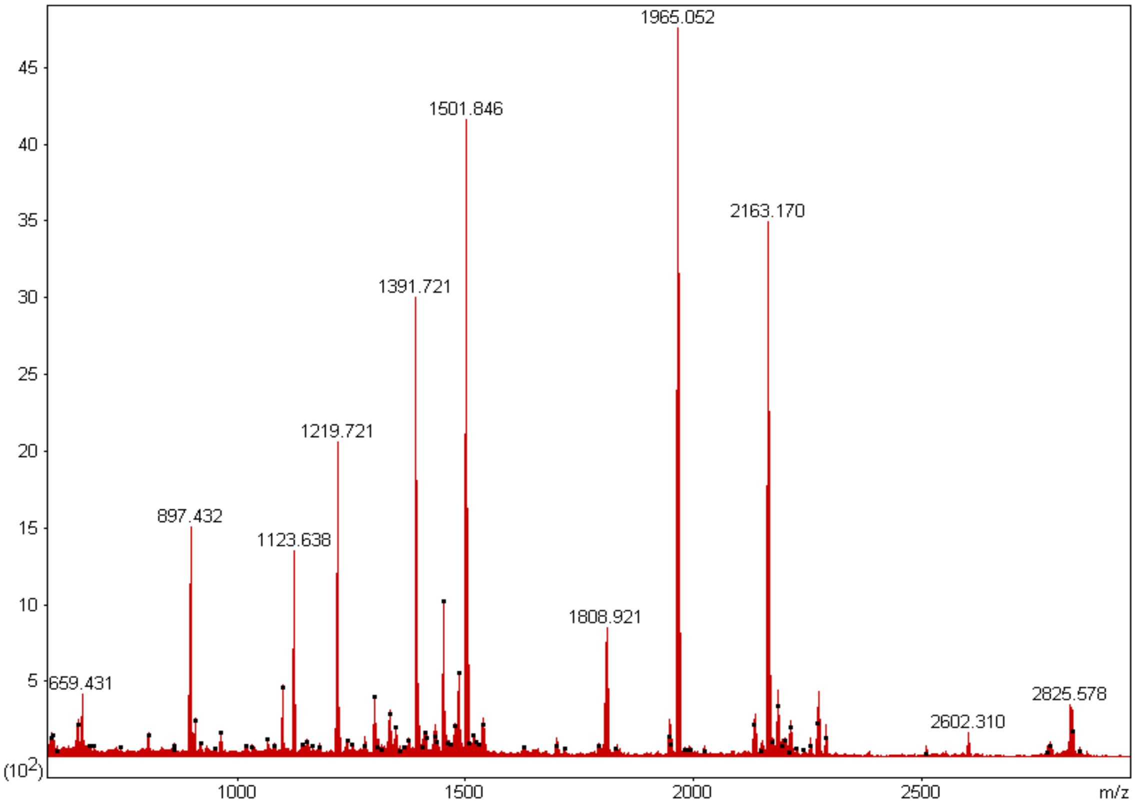
Mascot score: **181** Sequence coverage %: **58**

NCBI accession No.: **gi| 26450878**

Matched peptides No.: **18** Total peptides No.: **62**

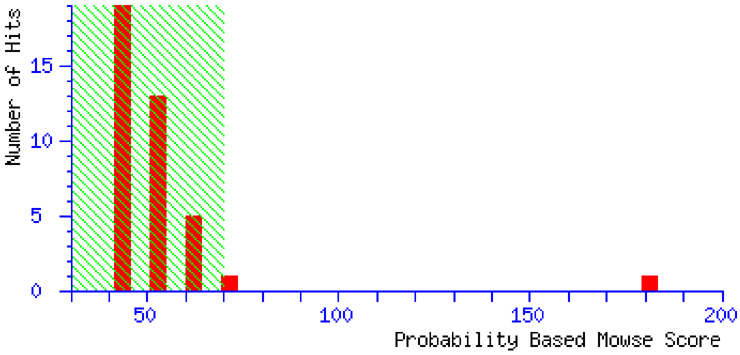
Calculated Mr: **34325** Calculated p*I*: **5.09**

Annotated PMF **spectra:**

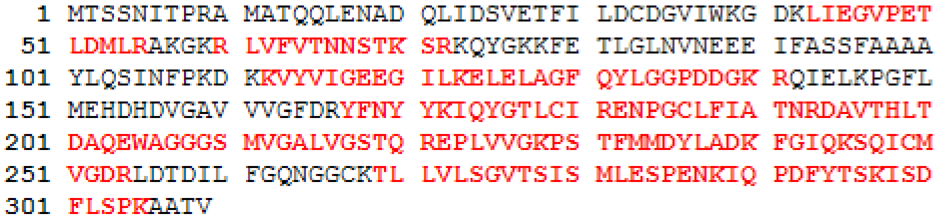


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

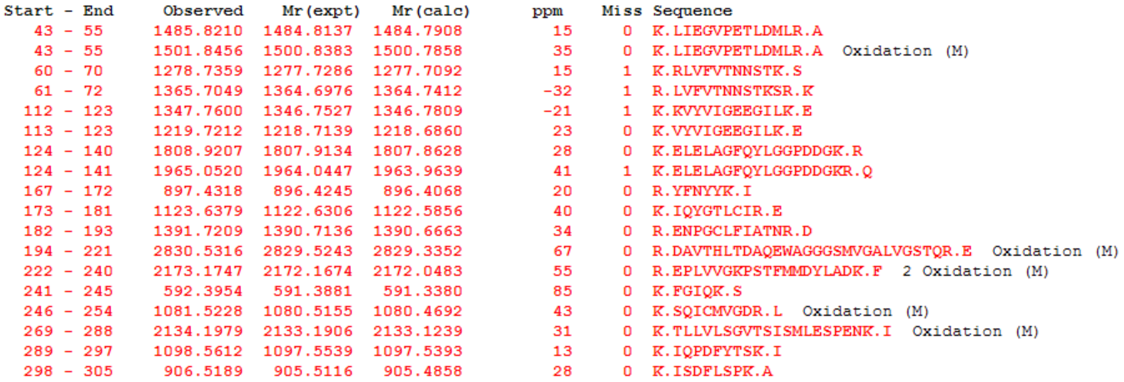


Matched peptide sequences: shown in Bold Red



```
  1 MTSSNITPRA MATQQLENAD QLIDSVETFI LDCDGVIWKG DKLIEGVPET
 51 LDMLRAKGKR LVFVTNNSTK SRKQYGKKFE TLGLNVNEEE IFASSFAAAA
101 YLQSINFPKD KKVYVIGEEG ILKELELAGF QYLGGPDDGK RQIELKPGFL
151 MEHDHDVGAV VVGFDRYFNY YKIQYGTLCI RENPGCLFIA TNRDAVTHLT
201 DAQEWAGGGS MVGALVGSTQ REPLVVGKPS TFMMDYLADK FGIQKSQICM
251 VGDRLDTDIL FGQNGGCKTL LVLSGVTSIS MLESPENKIQ PDFYTSKISD
301 FLSPKAATV
```

Matched peptides information:



```
Start - End      Observed    Mr(expt)   Mr(calc)       ppm    Miss  Sequence
   43 - 55      1485.8210   1484.8137  1484.7908        15      0   K.LIEGVPETLDMLR.A
   43 - 55      1501.8456   1500.8383  1500.7858        35      0   K.LIEGVPETLDMLR.A  Oxidation (M)
   60 - 70      1278.7359   1277.7286  1277.7092        15      1   K.RLVFVTNNSTK.S
   61 - 72      1365.7049   1364.6976  1364.7412       -32      1   R.LVFVTNNSTKSR.K
  112 - 123     1347.7600   1346.7527  1346.7809       -21      1   K.KVYVIGEEGILK.E
  113 - 123     1219.7212   1218.7139  1218.6860        23      0   K.VYVIGEEGILK.E
  124 - 140     1808.9207   1807.9134  1807.8628        28      0   K.ELELAGFQYLGGPDDGK.R
  124 - 141     1965.0520   1964.0447  1963.9639        41      1   K.ELELAGFQYLGGPDDGKR.Q
  167 - 172      897.4318    896.4245   896.4068        20      0   R.YFNYYK.I
  173 - 181     1123.6379   1122.6306  1122.5856        40      0   K.IQYGTLCIR.E
  182 - 193     1391.7209   1390.7136  1390.6663        34      0   R.ENPGCLFIATNR.D
  194 - 221     2830.5316   2829.5243  2829.3352        67      0   R.DAVTHLTDAQEWAGGGSMVGALVGSTQR.E  Oxidation (M)
  222 - 240     2173.1747   2172.1674  2172.0483        55      0   R.EPLVVGKPSTFMMDYLADK.F  2 Oxidation (M)
  241 - 245      592.3954    591.3881   591.3380        85      0   K.FGIQK.S
  246 - 254     1081.5228   1080.5155  1080.4692        43      0   K.SQICMVGDR.L  Oxidation (M)
  269 - 288     2134.1979   2133.1906  2133.1239        31      0   K.TLLVLSGVTSISMLESPENK.I  Oxidation (M)
  289 - 297     1098.5612   1097.5539  1097.5393        13      0   K.IQPDFYTSK.I
  298 - 305      906.5189    905.5116   905.4858        28      0   K.ISDFLSPK.A
```

Spot No.: **165**

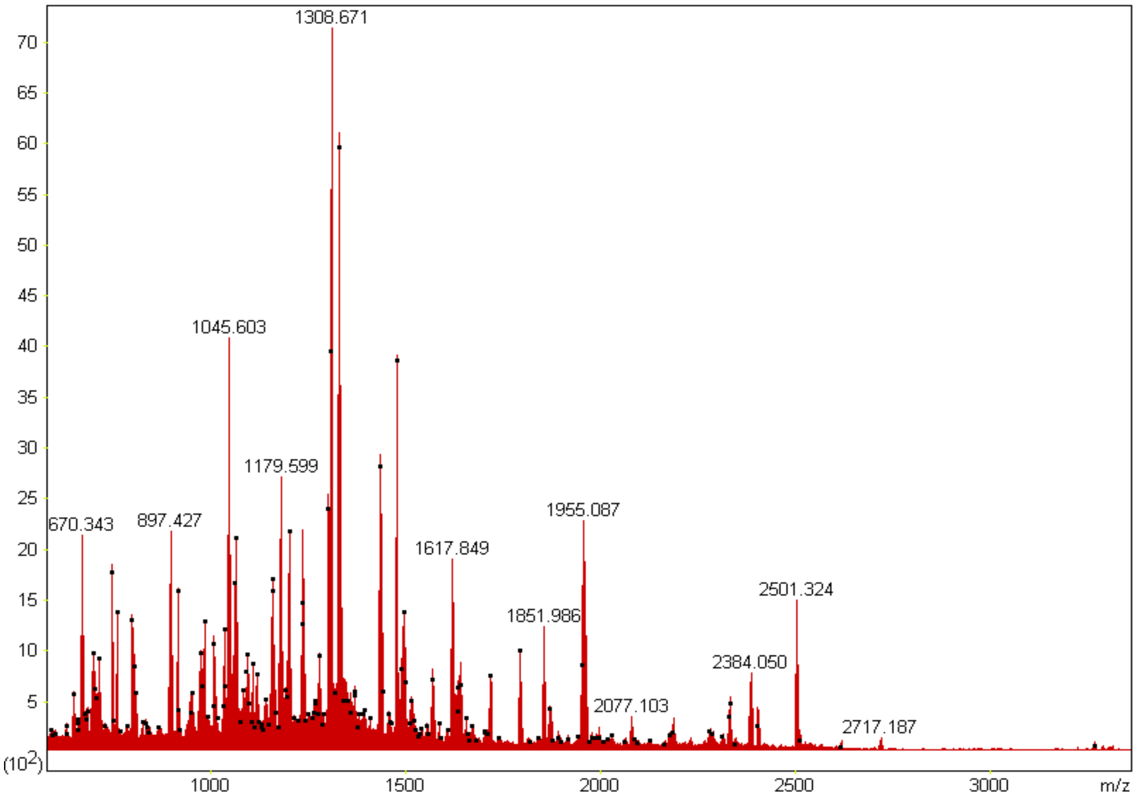
Mascot score: **109** Sequence coverage %: **58**

NCBI accession No.: **gi| 7525040**

Matched peptides No.: **26** Total peptides No.: **178**

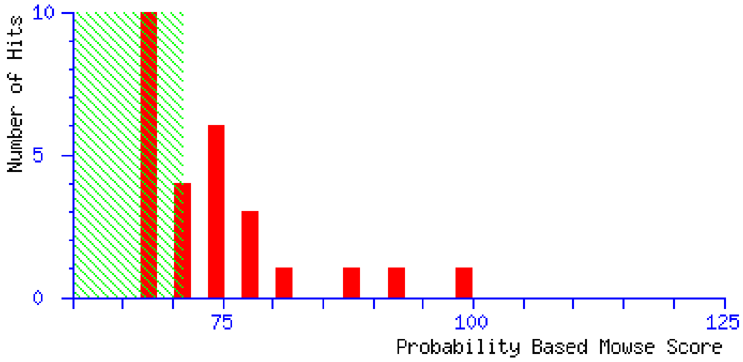
Calculated Mr: **53957** Calculated *p*I: **5.38**

Annotated PMF **spectra:**

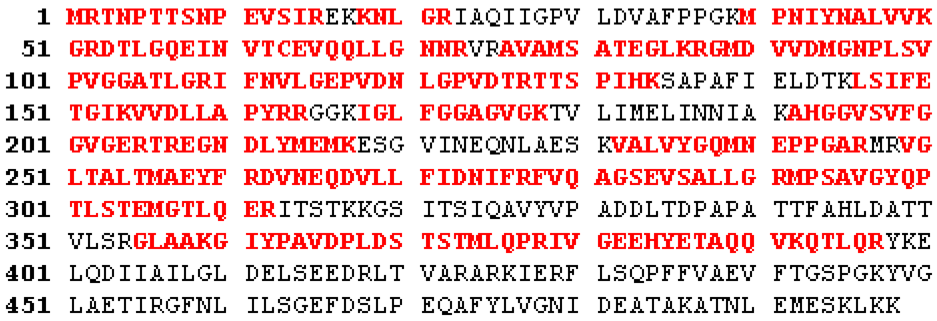


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

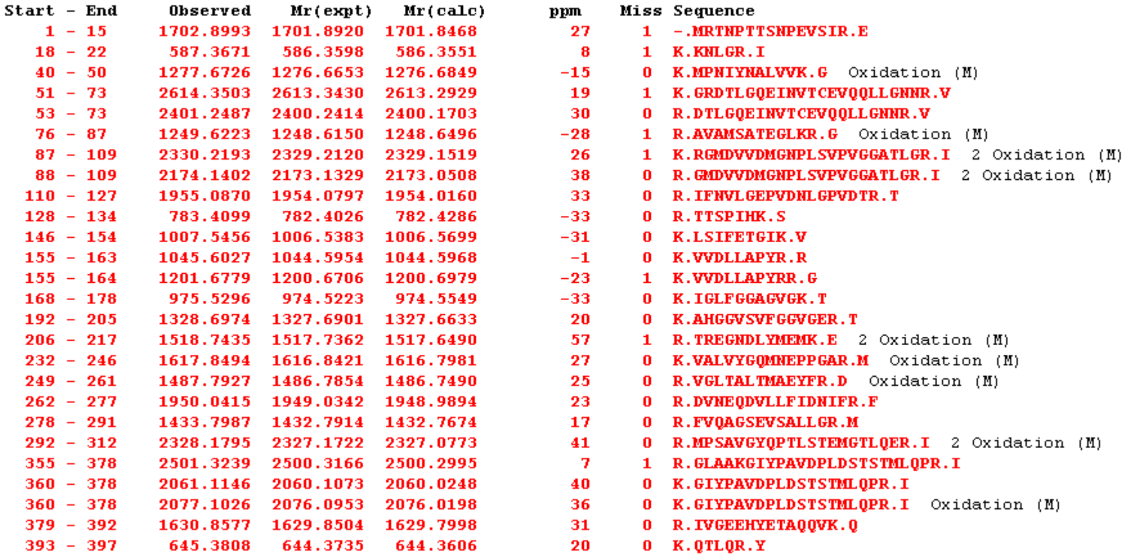


Matched peptide sequences: shown in Bold Red



1 **MRTNPTTSNP** **EVSIR**EK**KNL** **GR**IAQIIGPV LDVAFPPGK**M** **PNIYNALVVK**
51 **GRDTLGQEIN** **VTCEVQQLLG** **NNR**VR**AVAMS** **ATEGLKRGMD** **VVDMGNPLSV**
101 **PVGGATLGRI** **FNVLGEPVDN** **LGPVDTRTTS** **PIHK**SAPAFI ELDTK**LSIFE**
151 **TGIKVVDLLA** **PYRR**GGK**IGL** **FGGAGVGK**TV LIMELINNIA K**AHGGVSVFG**
201 **GVGERTREGN** **DLYMEMK**ESG VINEQNLAES K**VALVYGQMN** **EPPGAR**MR**VG**
251 **LTALTMAEYF** **RDVNEQDVLL** **FIDNIFRFVQ** **AGSEVSALLG** **RMPSAVGYQP**
301 **TLSTEMGTLQ** **ER**ITSTKKGS ITSIQAVYVP ADDLTDPAPA TTFAHLDATT
351 VLSR**GLAAKG** **IYPAVDPLDS** **TSTMLQPRIV** **GEEHYETAQQ** **VKQTLQR**YKE
401 LQDIIAILGL DELSEEDRLT VARARKIERF LSQPFFVAEV FTGSPGKYVG
451 LAETIRGFNL ILSGEFDSLP EQAFYLVGNI DEATAKATNL EMESKLKK

Matched peptides information:



```
Start - End      Observed    Mr(expt)   Mr(calc)        ppm    Miss Sequence
    1 - 15      1702.8993   1701.8920  1701.8468         27      1  -.MRTNPTTSNPEVSIR.E
   18 - 22       587.3671    586.3598   586.3551          8      1  K.KNLGR.I
   40 - 50      1277.6726   1276.6653  1276.6849        -15      0  K.MPNIYNALVVK.G  Oxidation (M)
   51 - 73      2614.3503   2613.3430  2613.2929         19      1  K.GRDTLGQEINVTCEVQQLLGNNR.V
   53 - 73      2401.2487   2400.2414  2400.1703         30      0  R.DTLGQEINVTCEVQQLLGNNR.V
   76 - 87      1249.6223   1248.6150  1248.6496        -28      1  R.AVAMSATEGLKR.G  Oxidation (M)
   87 - 109     2330.2193   2329.2120  2329.1519         26      1  K.RGMDVVDMGNPLSVPVGGATLGR.I  2 Oxidation (M)
   88 - 109     2174.1402   2173.1329  2173.0508         38      0  R.GMDVVDMGNPLSVPVGGATLGR.I  2 Oxidation (M)
  110 - 127     1955.0870   1954.0797  1954.0160         33      0  R.IFNVLGEPVDNLGPVDTR.T
  128 - 134      783.4099    782.4026   782.4286        -33      0  R.TTSPIHK.S
  146 - 154     1007.5456   1006.5383  1006.5699        -31      0  K.LSIFETGIK.V
  155 - 163     1045.6027   1044.5954  1044.5968         -1      0  K.VVDLLAPYR.R
  155 - 164     1201.6779   1200.6706  1200.6979        -23      1  K.VVDLLAPYRR.G
  168 - 178      975.5296    974.5223   974.5549        -33      0  K.IGLFGGAGVGK.T
  192 - 205     1328.6974   1327.6901  1327.6633         20      0  K.AHGGVSVFGGVGER.T
  206 - 217     1518.7435   1517.7362  1517.6490         57      1  R.TREGNDLYMEMK.E  2 Oxidation (M)
  232 - 246     1617.8494   1616.8421  1616.7981         27      0  K.VALVYGQMNEPPGAR.M  Oxidation (M)
  249 - 261     1487.7927   1486.7854  1486.7490         25      0  R.VGLTALTMAEYFR.D  Oxidation (M)
  262 - 277     1950.0415   1949.0342  1948.9894         23      0  R.DVNEQDVLLFIDNIFR.F
  278 - 291     1433.7987   1432.7914  1432.7674         17      0  R.FVQAGSEVSALLGR.M
  292 - 312     2328.1795   2327.1722  2327.0773         41      0  R.MPSAVGYQPTLSTEMGTLQER.I  2 Oxidation (M)
  355 - 378     2501.3239   2500.3166  2500.2995          7      1  R.GLAAKGIYPAVDPLDSTSTMLQPR.I
  360 - 378     2061.1146   2060.1073  2060.0248         40      0  K.GIYPAVDPLDSTSTMLQPR.I
  360 - 378     2077.1026   2076.0953  2076.0198         36      0  K.GIYPAVDPLDSTSTMLQPR.I  Oxidation (M)
  379 - 392     1630.8577   1629.8504  1629.7998         31      0  R.IVGEEHYETAQQVK.Q
  393 - 397      645.3808    644.3735   644.3606         20      0  K.QTLQR.Y
```

Spot No.: **166**

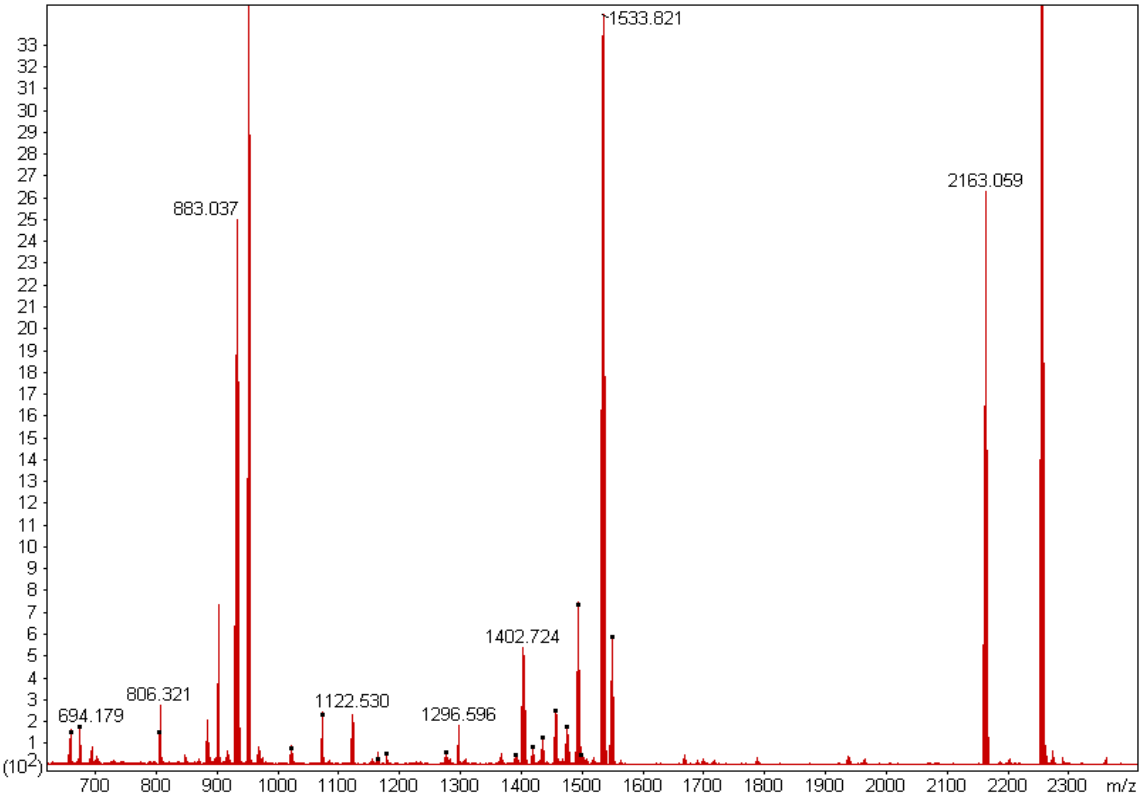
Mascot score: **128**   Sequence coverage %: **32**

NCBI accession No.: **gi| 21537360**

Matched peptides No.: **14**   Total peptides No.: **27**

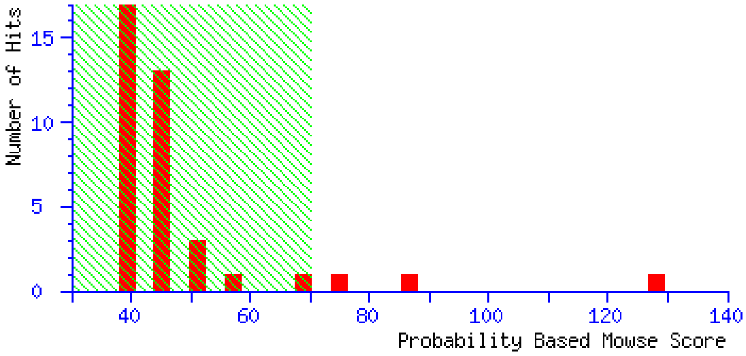
Calculated Mr: **39459**   Calculated *p*I: **6.97**

Annotated PMF **spectra:**

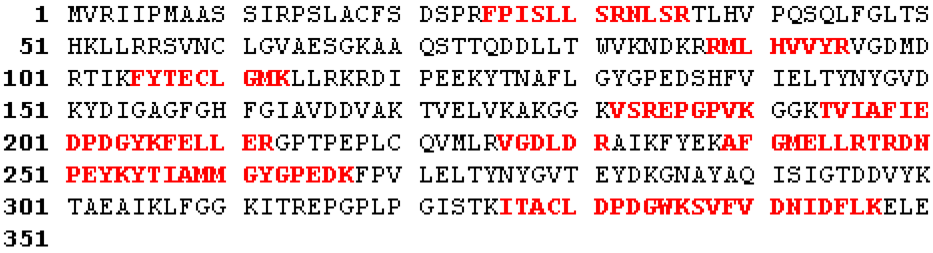


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red



```
  1 MVRIIPMAAS SIRPSLACFS DSPRFPISLL SRNLSRTLHV PQSQLFGLTS
 51 HKLLRRSVNC LGVAESGKAA QSTTQDDLLT WVKNDKRRML HVVYRVGDMD
101 RTIKFYTECL GMKLLRKRDI PEEKYTNAFL GYGPEDSHFV IELTYNYGVD
151 KYDIGAGFGH FGIAVDDVAK TVELVKAKGG KVSREPGPVK GGKTVIAFIE
201 DPDGYKFELL ERGPTPEPLC QVMLRVGDLD RAIKFYEKAF GMELLRTRDN
251 PEYKYTIAMM GYGPEDKFPV LELTYNYGVT EYDKGNAYAQ ISIGTDDVYK
301 TAEAIKLFGG KITREPGPLP GISTKITACL DPDGWKSVFV DNIDFLKELE
351
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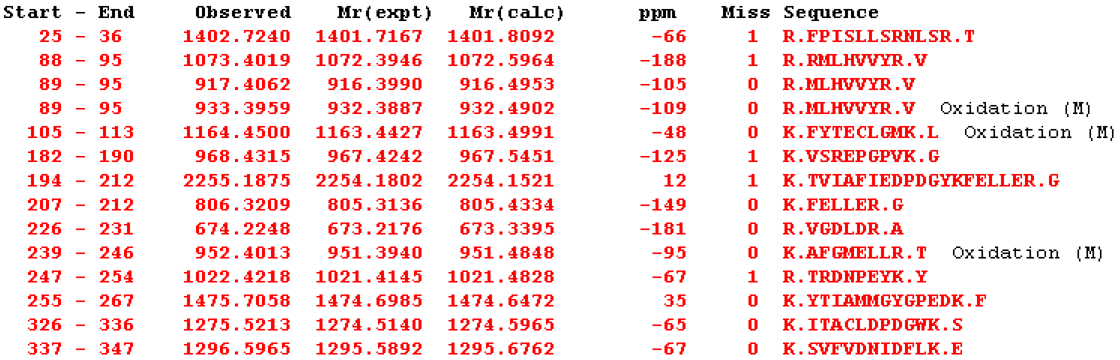
Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   25 - 36     1402.7240  1401.7167  1401.8092      -66      1  R.FPISLLSRNLSR.T
   88 - 95     1073.4019  1072.3946  1072.5964     -188      1  R.RMLHVVYR.V
   89 - 95      917.4062   916.3990   916.4953     -105      0  R.MLHVVYR.V
   89 - 95      933.3959   932.3887   932.4902     -109      0  R.MLHVVYR.V  Oxidation (M)
  105 - 113    1164.4500  1163.4427  1163.4991      -48      0  K.FYTECLGMK.L  Oxidation (M)
  182 - 190     968.4315   967.4242   967.5451     -125      1  K.VSREPGPVK.G
  194 - 212    2255.1875  2254.1802  2254.1521       12      1  K.TVIAFIEDPDGYKFELLER.G
  207 - 212     806.3209   805.3136   805.4334     -149      0  K.FELLER.G
  226 - 231     674.2248   673.2176   673.3395     -181      0  R.VGDLDR.A
  239 - 246     952.4013   951.3940   951.4848      -95      0  K.AFGMELLR.T  Oxidation (M)
  247 - 254    1022.4218  1021.4145  1021.4828      -67      1  R.TRDNPEYK.Y
  255 - 267    1475.7058  1474.6985  1474.6472       35      0  K.YTIAMMGYGPEDK.F
  326 - 336    1275.5213  1274.5140  1274.5965      -65      0  K.ITACLDPDGWK.S
  337 - 347    1296.5965  1295.5892  1295.6762      -67      0  K.SVFVDNIDFLK.E
```

Spot No.: **167**

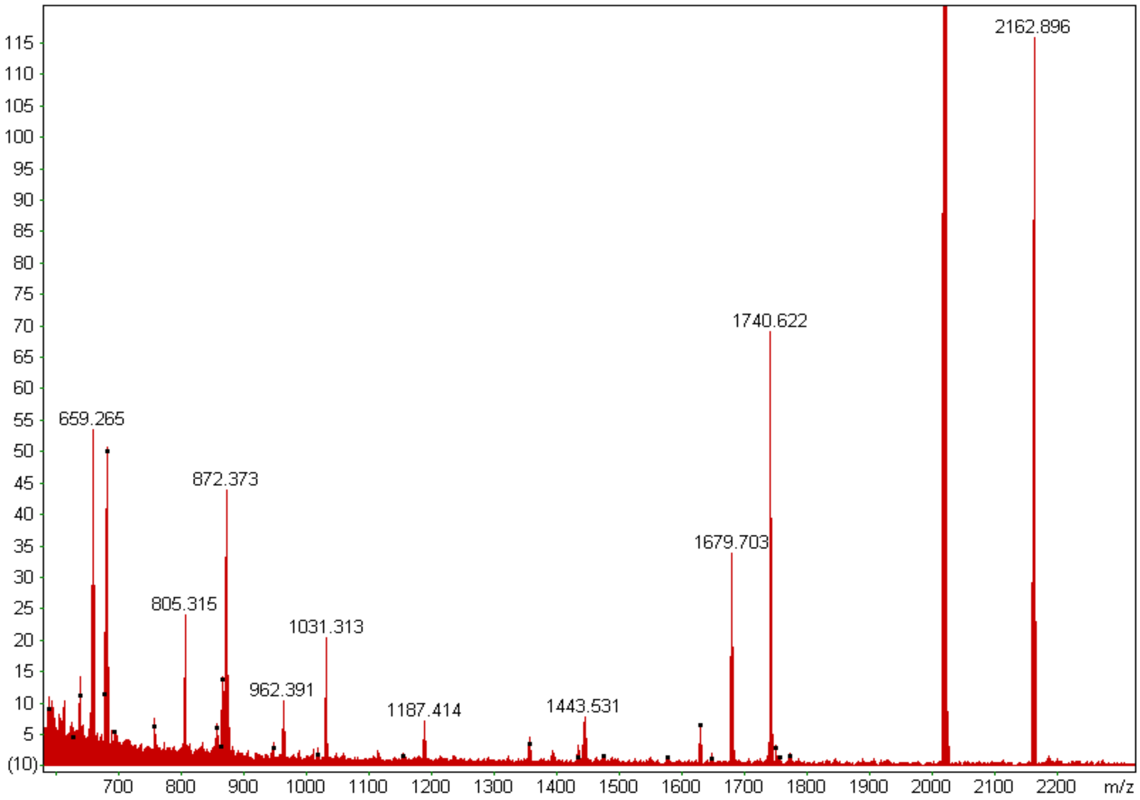
Mascot score: **168** Sequence coverage %: **46**

NCBI accession No.: **gi| 15239061**

Matched peptides No.: **15** Total peptides No.: **33**

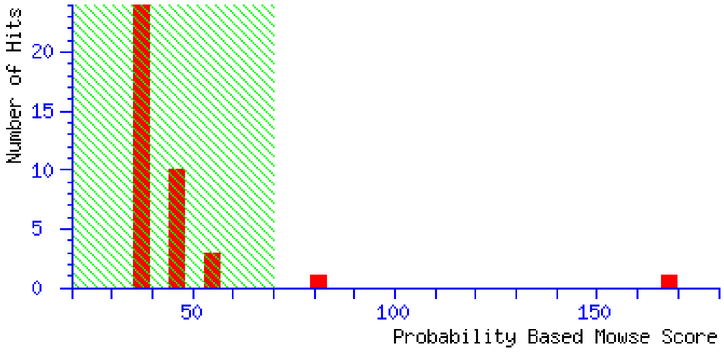
Calculated Mr: **30685** Calculated *p*I: **4.99**

Annotated PMF **spectra:**

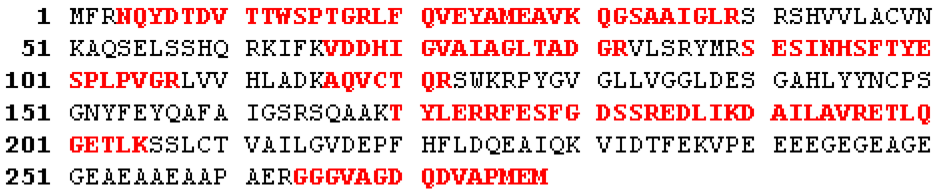


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

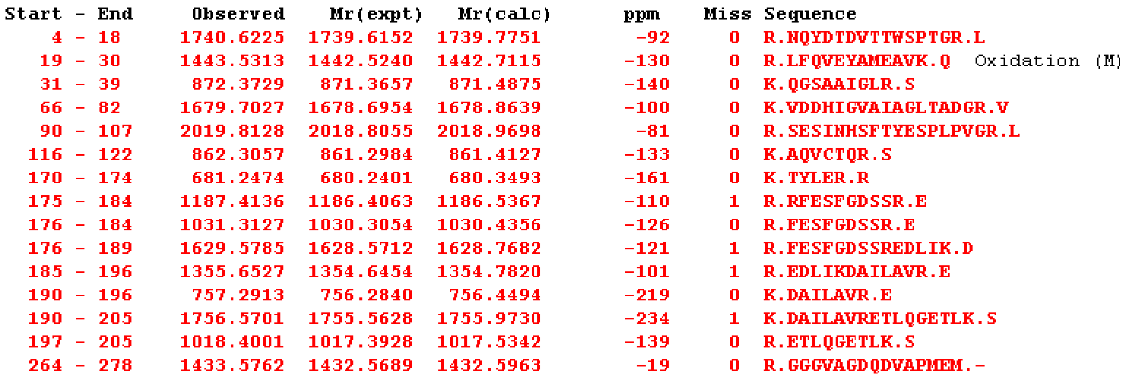


Matched peptide sequences: shown in Bold Red



1 MFR**NQYDTDV TTWSPTGRLF QVEYAMEAVK QGSAAIGLR**S RSHVVLACVN
51 KAQSELSSHQ RKIFK**VDDHI GVAIAGLTAD GR**VLSRYMR**S ESINHSFTYE**
101 **SPLPVGR**LVV HLADK**AQVCT QR**SWKRPYGV GLLVGGLDES GAHLYYNCPS
151 GNYFEYQAFA IGSRSQAAK**T YLERRFESFG DSSREDLIKD AILAVRETLQ**
201 **GETLK**SSLCT VAILGVDEPF HFLDQEAIQK VIDTFEKVPE EEEGEGEAGE
251 GEAEAAEAAP AER**GGGVAGD QDVAPMEM**

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
4 - 18	1740.6225	1739.6152	1739.7751	-92	0	R.NQYDTDVTTWSPTGR.L
19 - 30	1443.5313	1442.5240	1442.7115	-130	0	R.LFQVEYAMEAVK.Q Oxidation (M)
31 - 39	872.3729	871.3657	871.4875	-140	0	K.QGSAAIGLR.S
66 - 82	1679.7027	1678.6954	1678.8639	-100	0	K.VDDHIGVAIAGLTADGR.V
90 - 107	2019.8128	2018.8055	2018.9698	-81	0	R.SESINHSFTYESPLPVGR.L
116 - 122	862.3057	861.2984	861.4127	-133	0	K.AQVCTQR.S
170 - 174	681.2474	680.2401	680.3493	-161	0	K.TYLER.R
175 - 184	1187.4136	1186.4063	1186.5367	-110	1	R.RFESFGDSSR.E
176 - 184	1031.3127	1030.3054	1030.4356	-126	0	R.FESFGDSSR.E
176 - 189	1629.5785	1628.5712	1628.7682	-121	1	R.FESFGDSSREDLIK.D
185 - 196	1355.6527	1354.6454	1354.7820	-101	1	R.EDLIKDAILAVR.E
190 - 196	757.2913	756.2840	756.4494	-219	0	K.DAILAVR.E
190 - 205	1756.5701	1755.5628	1755.9730	-234	1	K.DAILAVRETLQGETLK.S
197 - 205	1018.4001	1017.3928	1017.5342	-139	0	R.ETLQGETLK.S
264 - 278	1433.5762	1432.5689	1432.5963	-19	0	R.GGGVAGDQDVAPMEM.-

Spot No.: **168**

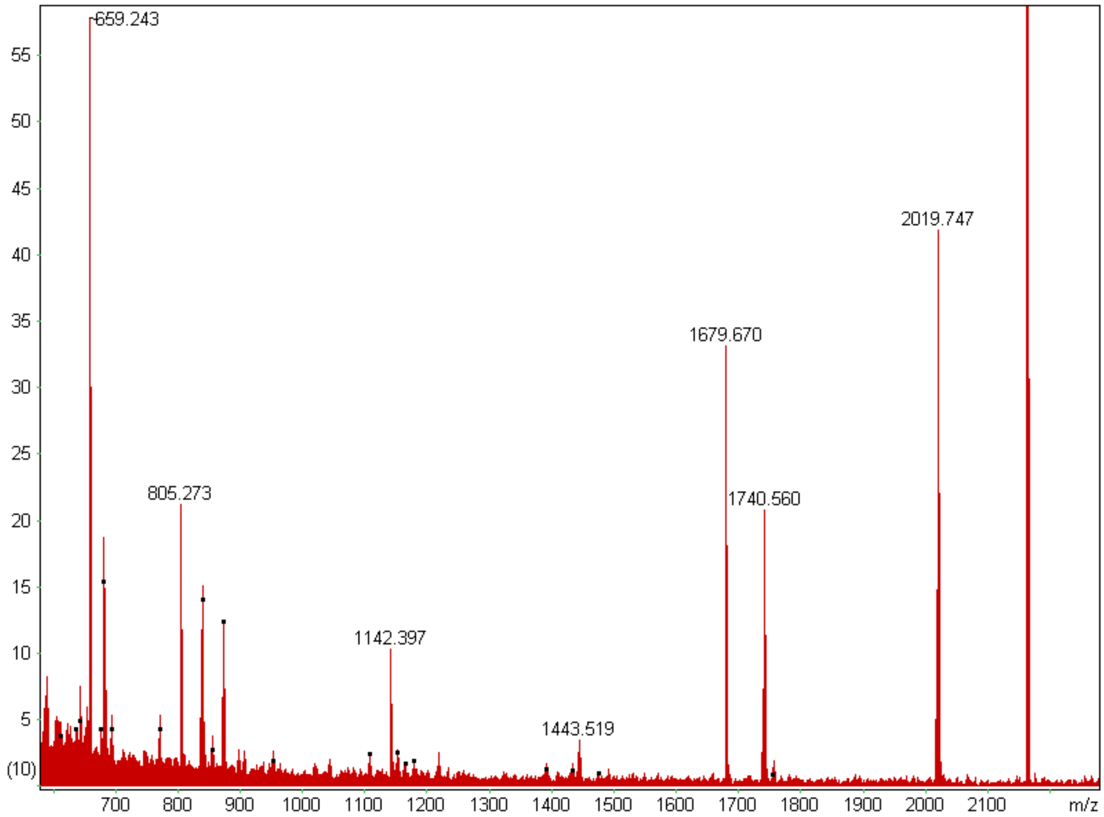
Mascot score: **96** Sequence coverage %: **33**

NCBI accession No.: **gi| 15220151**

Matched peptides No.: **8** Total peptides No.: **29**

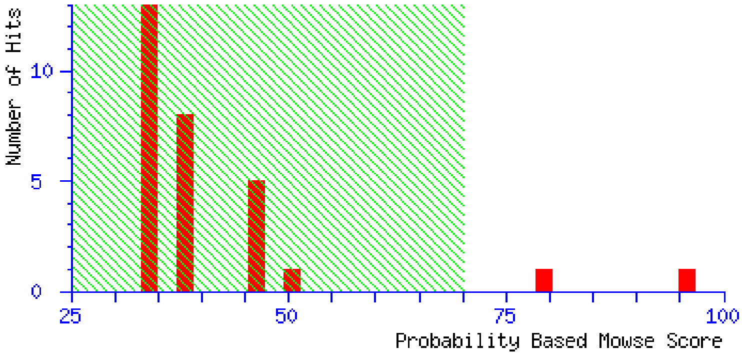
Calculated Mr: **30619** Calculated *p*I: **4.97**

Annotated PMF **spectra:**

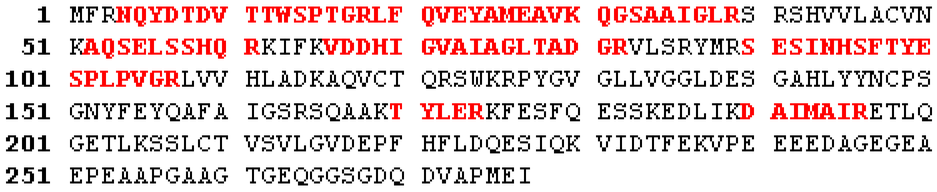


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

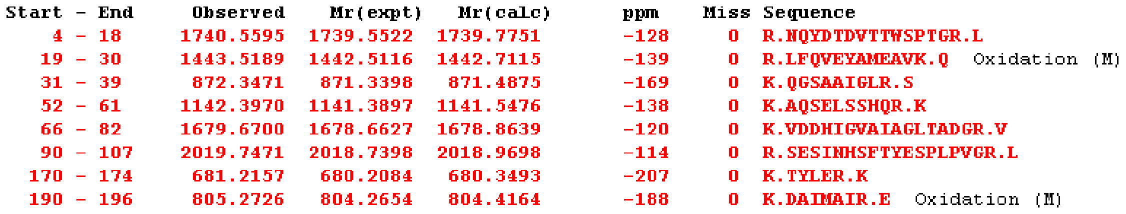


Matched peptide sequences: shown in Bold Red



```
  1 MFRNQYDTDV TTWSPTGRLF QVEYAMEAVK QGSAAIGLRS RSHVVLACVN
 51 KAQSELSSHQ RKIFKVDDHI GVAIAGLTAD GRVLSRYMRS ESINHSFTYE
101 SPLPVGRLVV HLADKAQVCT QRSWKRPYGV GLLVGGLDES GAHLYYNCPS
151 GNYFEYQAFA IGSRSQAAKT YLERKFESFQ ESSKEDLIKD AIMAIRETLQ
201 GETLKSSLCT VSVLGVDEPF HFLDQESIQK VIDTFEKVPE EEEDAGEGEA
251 EPEAAPGAAG TGEQGGSGDQ DVAPMEI
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    4 - 18     1740.5595  1739.5522  1739.7751     -128      0  R.NQYDTDVTTWSPTGR.L
   19 - 30     1443.5189  1442.5116  1442.7115     -139      0  R.LFQVEYAMEAVK.Q  Oxidation (M)
   31 - 39      872.3471   871.3398   871.4875     -169      0  K.QGSAAIGLR.S
   52 - 61     1142.3970  1141.3897  1141.5476     -138      0  K.AQSELSSHQR.K
   66 - 82     1679.6700  1678.6627  1678.8639     -120      0  K.VDDHIGVAIAGLTADGR.V
   90 - 107    2019.7471  2018.7398  2018.9698     -114      0  R.SESINHSFTYESPLPVGR.L
  170 - 174     681.2157   680.2084   680.3493     -207      0  K.TYLER.K
  190 - 196     805.2726   804.2654   804.4164     -188      0  K.DAIMAIR.E  Oxidation (M)
```

Spot No.: **169**

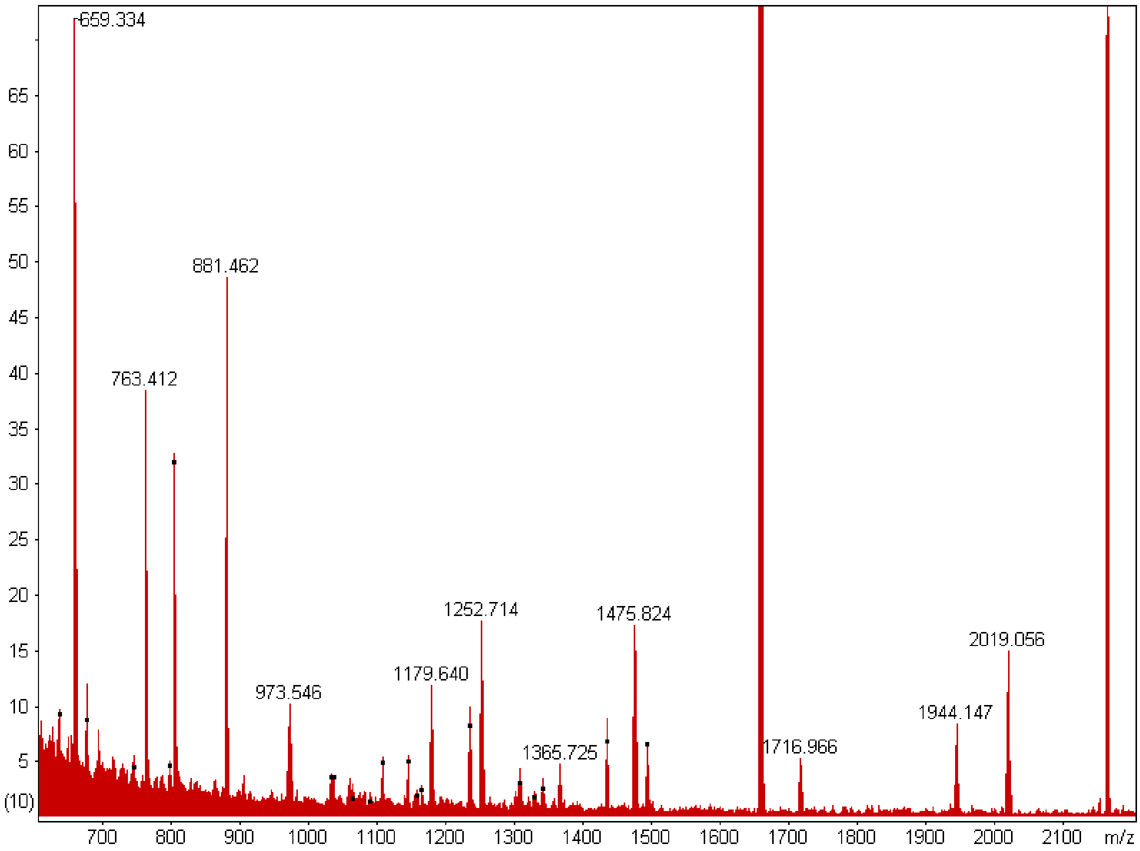
Mascot score: **94** Sequence coverage %: **15**

NCBI accession No.: **gi| 225461150**

Matched peptides No.: **12** Total peptides No.: **33**

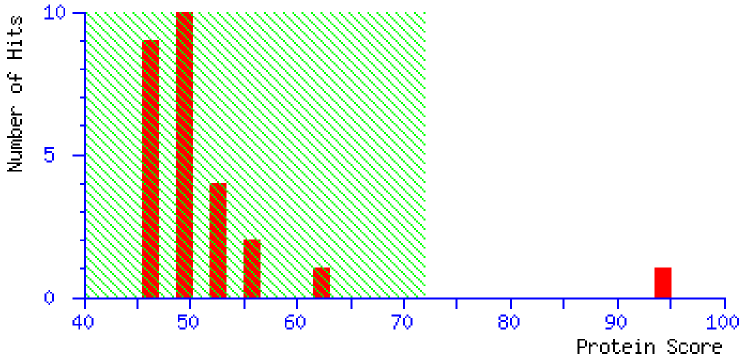
Calculated Mr: **86688** Calculated *p*I: **6.66**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

```
  1 MVGPANSGRT RQAFSVVNGG QENGGPPSSA GSECGGIEFT KEDVEALLNE
 51 KMKGKNKFNL KEKCDQMMDY IRKLRLCIKW FQELEGSYLL EQEKLRNMLD
101 CAERKCNELE VLMKNKEEEL NSIIMELRKN CASLHEKLTK EESEKLAAMD
151 SLTREKEARL AAERLQTSLT DELGKAQREH LSASQKITSL NDMYKRLQEY
201 NTSLQQYNSK LQTELPTVNE ALKRVEKEKA AVVENLSTLR GHYNALQDQF
251 TLTRASQDEA MKQREALVND VVCLRGELQQ ARDDRDRYLS QVEVLTTEVV
301 KYKECTGKSF AELENLSLKS NELEARCLSQ SDQIKALQDK LGAAEKKLQV
351 SDLSAMETRT EYEEQKKLIH DLQNRLADAE IKIIEGEKLR KKLHNTILEL
401 KGNIRVFCRV RPLLADDSAA EAKVISYPTS TEFFGRGIDL MQSGQKHSFT
451 FDKVFMPDAP QQEVFVEISQ LVQSALDGYK VCIFAYGQTG SGKTHTMMGR
501 PGNPEQKGLI PRSLEQIFET RQSLKSQGWK YEMQVSMLEI YNETIRDLLS
551 TNRSCSDVSR TENGVAGKQY AIKHDGNGNT HVSDLTVVDV RSTREVSFLL
601 DQAAQSRSVG KTQMNEQSSR SHFVFTLRIS GVNESTEQQV QGVLNLIDLA
651 GSERLSKSGS TGDRLKETQA INKSLSSLSD VIFALAKKED HVPFRNSKLT
701 YLLQPCLGGD SKTLMFVNIS PDPSSLGESL CSLRFAARVN ACEIGIPRRQ
751 TNMRPSDSRL SYG
```

Matched peptides information:

```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    1 - 11     1145.5746  1144.5673  1144.5771       -9      1  -.MVGPANSGRTR.Q
   42 - 53     1434.8466  1433.8393  1433.7072       92      1  K.EDVEALLNEKMK.G  Oxidation (M)
   56 - 61      763.4122   762.4049   762.4388      -44      1  K.NKFNLK.E
  117 - 128    1475.8236  1474.8163  1474.7337       56      0  K.EEELNSIIMELR.K
  146 - 156    1234.6996  1233.6923  1233.6387       43      1  K.LAAMDSLTREK.E
  255 - 264    1179.6400  1178.6327  1178.5350       83      1  R.ASQDEAMKQR.E  Oxidation (M)
  347 - 359    1493.8309  1492.8236  1492.7555       46      1  K.KLQVSDLSAMETR.T  Oxidation (M)
  348 - 359    1365.7246  1364.7173  1364.6606       42      0  K.LQVSDLSAMETR.T  Oxidation (M)
  447 - 453     881.4618   880.4545   880.4079       53      0  K.HSFTFDK.V
  508 - 521    1658.9956  1657.9883  1657.9151       44      1  K.GLIPRSLEQIFETR.Q
  531 - 546    2019.0557  2018.0484  2017.9489       49      0  K.YEMQVSMLEIYNETIR.D
  749 - 754     805.4046   804.3973   804.4024       -6      1  R.RQTNMR.P
```

Spot No.: **170**

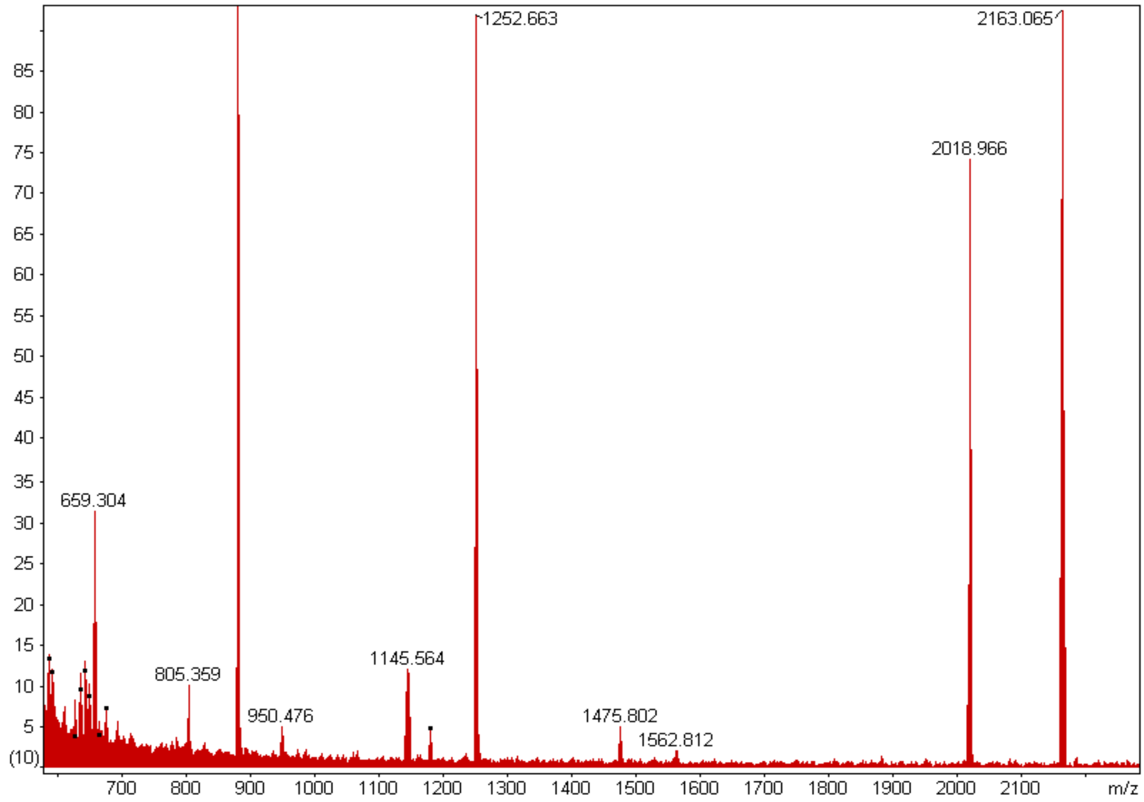
Mascot score: **84** Sequence coverage %: **21**

NCBI accession No.: **gi| 15240013**

Matched peptides No.: **6** Total peptides No.: **10**

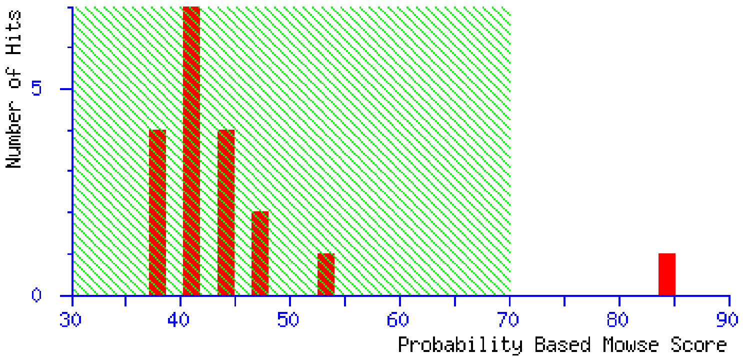
Calculated Mr: **35349** Calculated *p*I: **5.55**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 MAASLQSTAT FLQSAKIATA PSRGSSHLRS TQAVGKSFGL ETSSARLTCS
51 FQSDFKDFTG KCSDAVKIAG FALATSALVV SGASAEGAPK **RLTYDEIQSK**
101 TYMEVKGTGT ANQCPTIDGG SETFSFKPGK YAGKKFCFEP TSFTVKADSV
151 SK**NAPPEFQN** **TK**LMTRLTYT LDEIEGPFEV ASDGSVNFK**E** **EDGIDYAAVT**
201 **VQLPGGERVP** **FLFTVK**QLDA SGKPDSFTGK **FLVPSYR**GSS FLDPKGR**GGS**
251 **TGYDNAVALP** **AGGR**GDEEEL VKENVKNTAA SVGEITLKVT KSKPETGEVI
301 GVFESLQPSD TDLGAKVPKD VKIQGVWYGQ LE

Matched peptides information:

```
Start - End     Observed   Mr(expt)   Mr(calc)     ppm    Miss  Sequence
   91 - 100    1252.6627  1251.6554  1251.6459       8     1   K.RLTYDEIQSK.T
  153 - 162    1145.5645  1144.5572  1144.5513       5     0   K.NAPPEFQNTK.L
  190 - 208    2018.9656  2017.9583  2017.9593      -0     0   K.EEDGIDYAAVTVQLPGGER.V
  209 - 216     950.4765   949.4692   949.5637     -99     0   R.VPFLFTVK.Q
  231 - 237     881.4463   880.4390   880.4807     -47     0   K.FLVPSYR.G
  248 - 264    1562.8119  1561.8046  1561.7485      36     0   R.GGSTGYDNAVALPAGGR.G
```

Spot No.: **171**

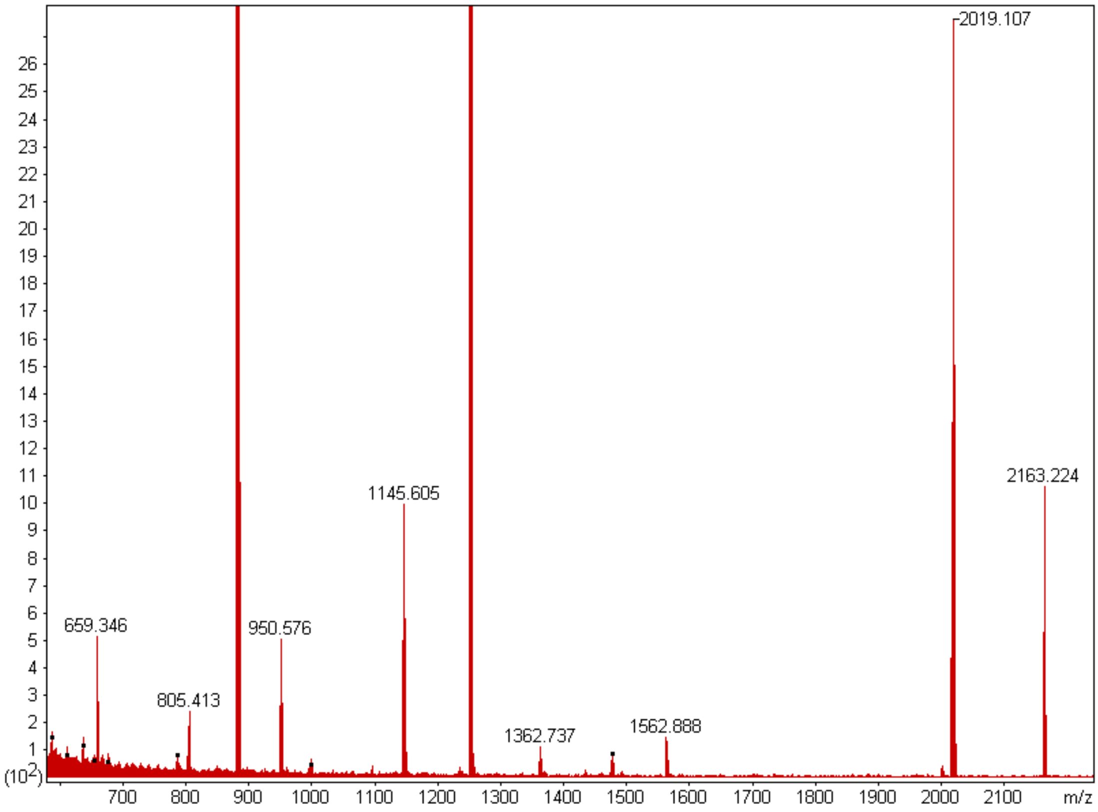
Mascot score: **119**   Sequence coverage %: **29**

NCBI accession No.: **gi| 49359169**

Matched peptides No.: **9**   Total peptides No.: **18**

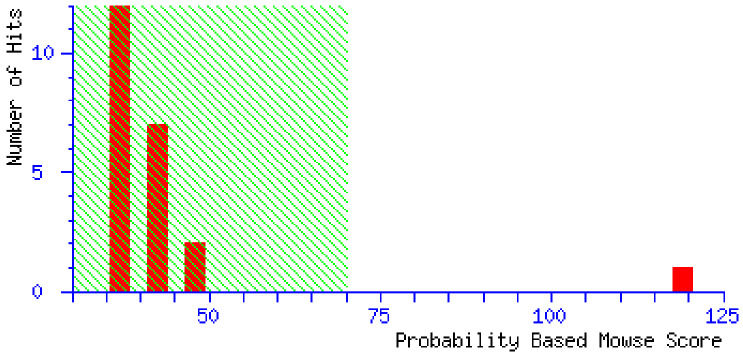
Calculated Mr: **37078**   Calculated *p*I: **6.78**

Annotated PMF **spectra:**

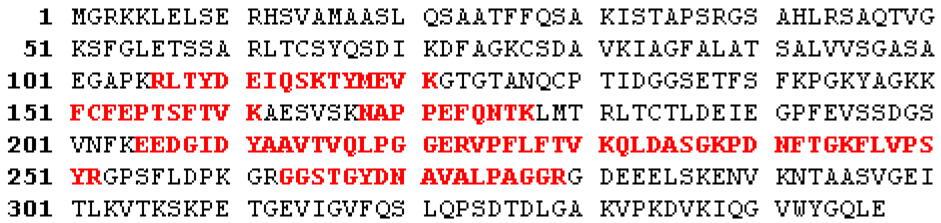


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

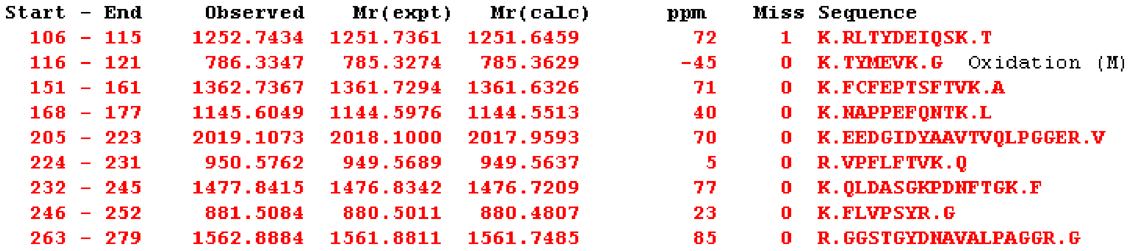


Matched peptide sequences: shown in Bold Red



1 MGRKKLELSE RHSVAMAASL QSAATFFQSA KISTAPSRGS AHLRSAQTVG
51 KSFGLETSSA RLTCSYQSDI KDFAGKCSDA VKIAGFALAT SALVVSGASA
101 EGAPK**RLTYD** **EIQSKTYMEV** **K**GTGTANQCP TIDGGSETFS FKPGKYAGKK
151 **FCFEPTSFTV** **K**AESVSK**NAP** **PEFQNTK**LMT RLTCTLDEIE GPFEVSSDGS
201 VNFK**EEDGID** **YAAVTVQLPG** **GERVPFLFTV** **KQLDASGKPD** **NFTGKFLVPS**
251 **YR**GPSFLDPK GR**GGSTGYDN** **AVALPAGGR**G DEEELSKENV KNTAASVGEI
301 TLKVTKSKPE TGEVIGVFQS LQPSDTDLGA KVPKDVKIQG VWYGQLE

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
106 - 115	**1252.7434**	**1251.7361**	**1251.6459**	**72**	**1**	**K.RLTYDEIQSK.T**	
116 - 121	**786.3347**	**785.3274**	**785.3629**	**-45**	**0**	**K.TYMEVK.G**	Oxidation (M)
151 - 161	**1362.7367**	**1361.7294**	**1361.6326**	**71**	**0**	**K.FCFEPTSFTVK.A**	
168 - 177	**1145.6049**	**1144.5976**	**1144.5513**	**40**	**0**	**K.NAPPEFQNTK.L**	
205 - 223	**2019.1073**	**2018.1000**	**2017.9593**	**70**	**0**	**K.EEDGIDYAAVTVQLPGGER.V**	
224 - 231	**950.5762**	**949.5689**	**949.5637**	**5**	**0**	**R.VPFLFTVK.Q**	
232 - 245	**1477.8415**	**1476.8342**	**1476.7209**	**77**	**0**	**K.QLDASGKPDNFTGK.F**	
246 - 252	**881.5084**	**880.5011**	**880.4807**	**23**	**0**	**K.FLVPSYR.G**	
263 - 279	**1562.8884**	**1561.8811**	**1561.7485**	**85**	**0**	**R.GGSTGYDNAVALPAGGR.G**	

Spot No.: **172**

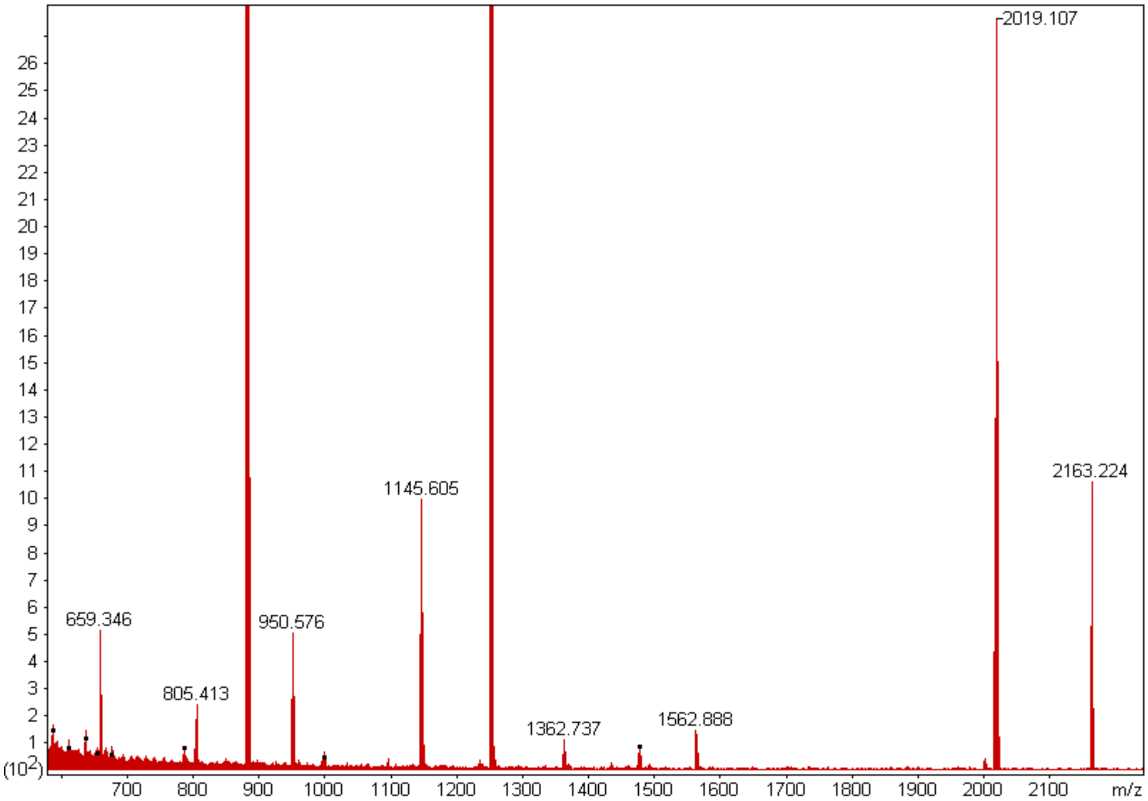
Mascot score: **84** Sequence coverage %: **21**

NCBI accession No.: **gi| 18408627**

Matched peptides No.: **9** Total peptides No.: **22**

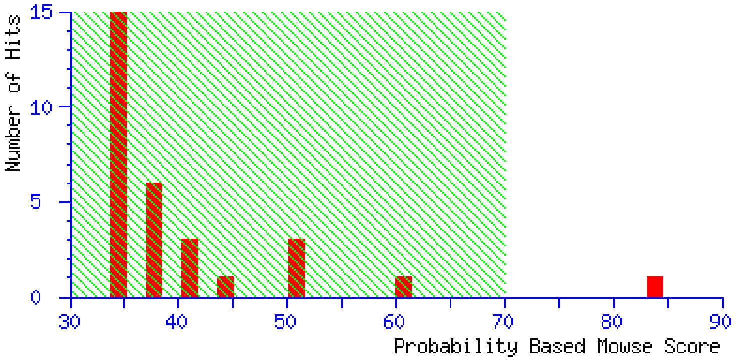
Calculated Mr: **34680** Calculated *p*I: **8.31**

Annotated PMF **spectra:**

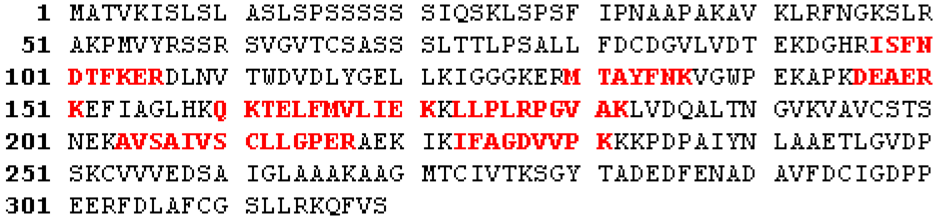


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

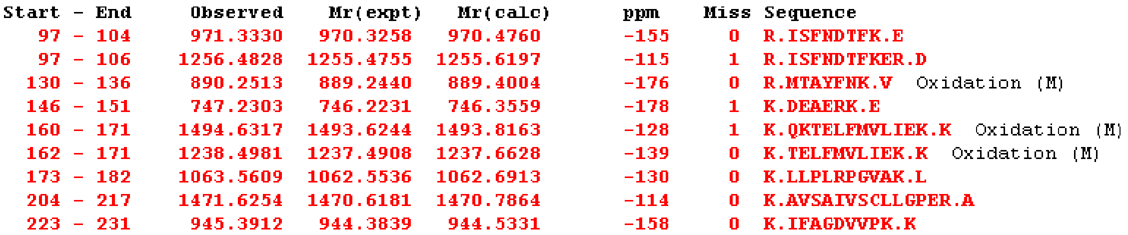


Matched peptide sequences: shown in Bold Red



```
  1 MATVKISLSL ASLSPSSSSS SIQSKLSPSF IPNAAPAKAV KLRFNGKSLR
 51 AKPMVYRSSR SVGVTCSASS SLTTLPSALL FDCDGVLVDT EKDGHRISFN
101 DTFKERDLNV TWDVDLYGEL LKIGGGKERM TAYFNKVGWP EKAPKDEAER
151 KEFIAGLHKQ KTELFMVLIE KKLLPLRPGV AKLVDQALTN GVKVAVCSTS
201 NEKAVSAIVS CLLGPERAEK IKIFAGDVVP KKKPDPAIYN LAAETLGVDP
251 SKCVVVEDSA IGLAAAKAAG MTCIVTKSGY TADEDFENAD AVFDCIGDPP
301 EERFDLAFCG SLLRKQFVS
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss Sequence
   97 - 104     971.3330   970.3258   970.4760     -155      0 R.ISFNDTFK.E
   97 - 106    1256.4828  1255.4755  1255.6197     -115      1 R.ISFNDTFKER.D
  130 - 136     890.2513   889.2440   889.4004     -176      0 R.MTAYFNK.V  Oxidation (M)
  146 - 151     747.2303   746.2231   746.3559     -178      1 K.DEAERK.E
  160 - 171    1494.6317  1493.6244  1493.8163     -128      1 K.QKTELFMVLIEK.K  Oxidation (M)
  162 - 171    1238.4981  1237.4908  1237.6628     -139      0 K.TELFMVLIEK.K  Oxidation (M)
  173 - 182    1063.5609  1062.5536  1062.6913     -130      0 K.LLPLRPGVAK.L
  204 - 217    1471.6254  1470.6181  1470.7864     -114      0 K.AVSAIVSCLLGPER.A
  223 - 231     945.3912   944.3839   944.5331     -158      0 K.IFAGDVVPK.K
```

Spot No.: **173**

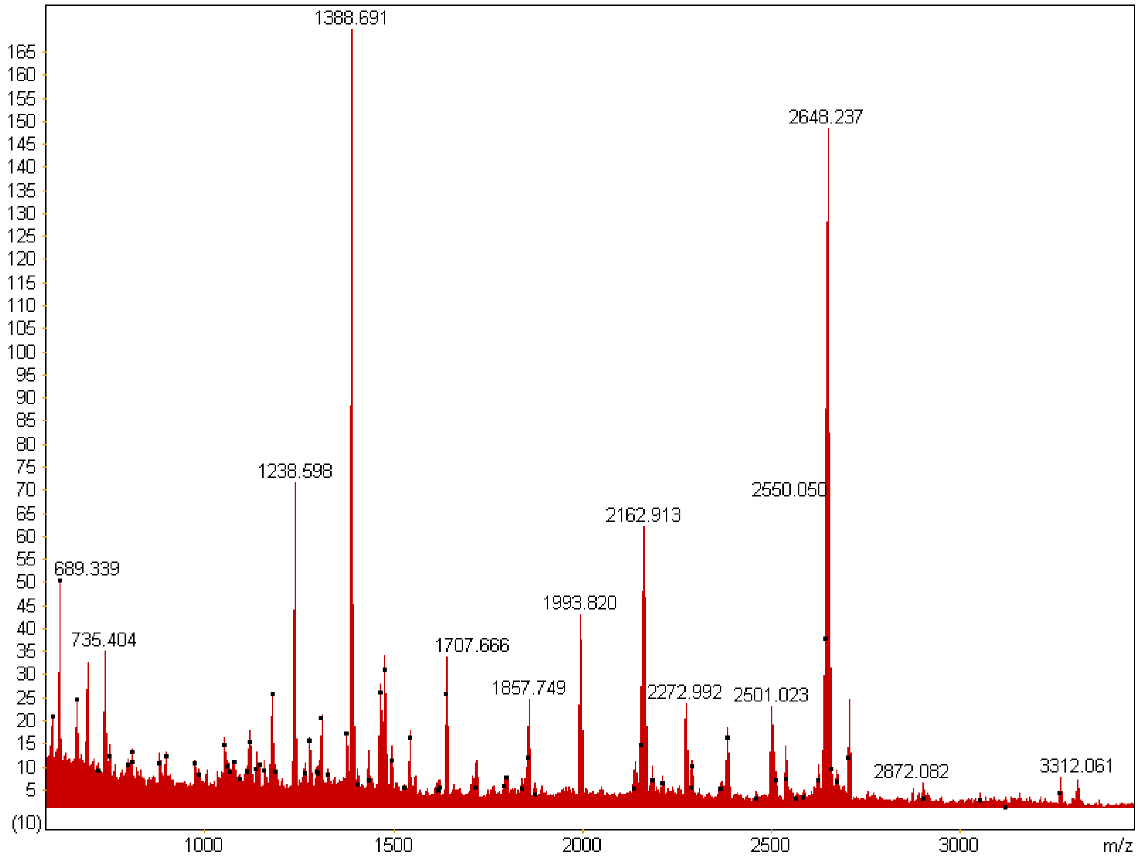
Mascot score: **84** Sequence coverage %: **24**

NCBI accession No.: **gi| 312282781**

Matched peptides No.: **10** Total peptides No.: **23**

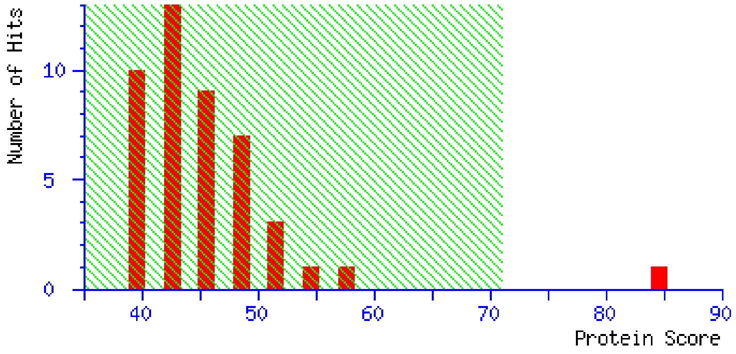
Calculated Mr: **27997** Calculated p*I*: **6.00**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in **Bold Red**

1 MASRALSSFT TKPAPSPKPH GVSSASSPAF SIGFSRKTSG RAMVVAAAPV
51 DTNNMPMTGV VFQPFEEVKK ADLAIPIK**SH** **VSLAR**QGYAD ATEAAINEQI
101 NVEYNVSYVY HSMYAYFDR**D** **NVALK**GLAK**F** **FKESSEEERG** **HAEKFMEYQN**
151 **KR**GGRVK**LHP** **IVSPISEFEH** **AEK**GDALYAM ELALSLEKLT NEKLLNVHSV
201 ATENNDPQLA DFVETEFLGE QIEAIKK**ISD** **FITQLR**MVGK GHGVWHFDQS
251 LLN

Matched peptides information:

```
Start - End     Observed    Mr(expt)    Mr(calc)      ppm    Miss  Sequence
   79 - 85      769.5782    768.5709    768.4242      191     0    K.SHVSLAR.Q
  120 - 125     659.5341    658.5268    658.3650      246     0    R.DNVALK.G
  130 - 139    1287.6679   1286.6606   1286.5779       64     1    K.FFKESSEEER.G
  140 - 151    1497.7578   1496.7505   1496.6718       53     1    R.GHAEKFMEYQNK.R  Oxidation (M)
  145 - 151     959.5492    958.5419    958.4218      125     0    K.FMEYQNK.R
  145 - 151     975.5365    974.5292    974.4167      115     0    K.FMEYQNK.R  Oxidation (M)
  145 - 152    1115.6351   1114.6278   1114.5229       94     1    K.FMEYQNKR.G
  145 - 152    1131.5949   1130.5876   1130.5179       62     1    K.FMEYQNKR.G  Oxidation (M)
  158 - 173    1833.0210   1832.0137   1831.9468       37     0    K.LHPIVSPISEFEHAEK.G
  228 - 236    1092.7344   1091.7271   1091.5975      119     0    K.ISDFITQLR.M
```

Spot No.: **174**

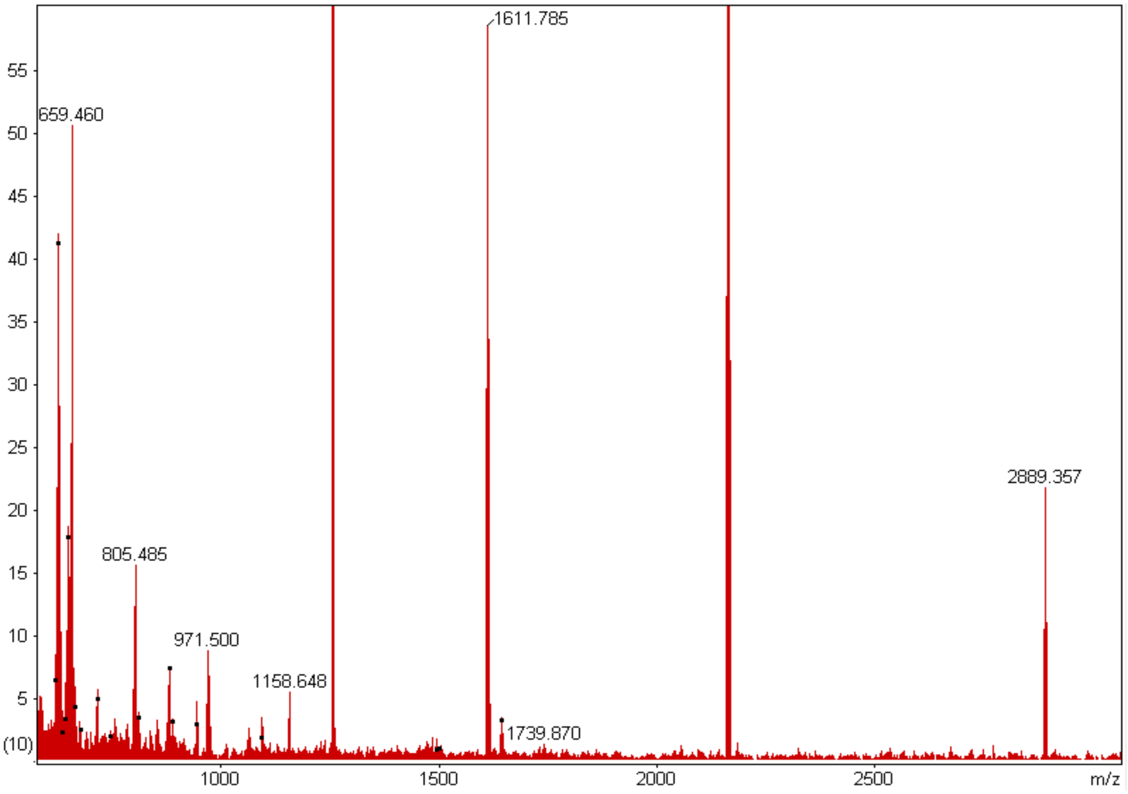
Mascot score: **100**   Sequence coverage %: **21**

NCBI accession No.: **gi| 18408627**

Matched peptides No.: **9**   Total peptides No.: **19**

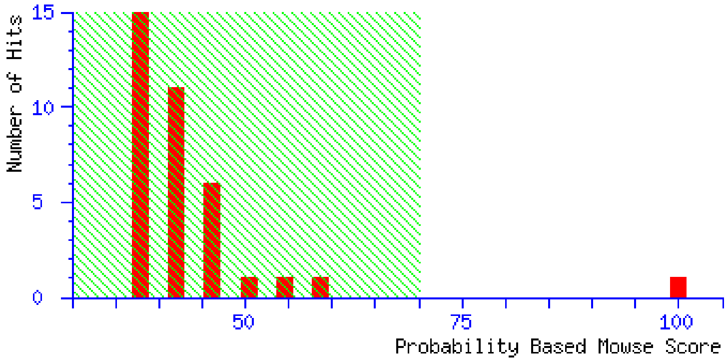
Calculated Mr: **34680**   Calculated *p*I: **8.31**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 MATVKISLSL ASLSPSSSSS SIQSKLSPSF IPNAAPAKAV KLRFNGKSLR
51 AKPMVYRSSR SVGVTCSASS SLTTLPSALL FDCDGVLVDT EKDGHR**ISFN**
101 **DTFKER**DLNV TWDVDLYGEL LK**IGGGKERM** **TAYFNK**VGWP EKAPKDEAER
151 KEFIAGLHK**Q** **KTELFMVLIE** **K**KLLPLRPGV AKLVDQALTN GVK**VAVCSTS**
201 **NEK**AVSAIVS CLLGPERAEK IK**IFAGDVVP** **K**KKPDPAIYN LAAETLGVDP
251 SK**CVVVEDSA** **IGLAAAK**AAG MTCIVTKSGY TADEDFENAD AVFDCIGDPP
301 EERFDLAFCG SLLRKQFVS

Matched peptides information:

Start – End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
97 – 104	971.5005	970.4932	970.4760	18	0	R.ISFNDTFK.E
97 – 106	1256.6203	1255.6130	1255.6197	-5	1	R.ISFNDTFKER.D
123 – 129	716.4403	715.4330	715.3977	49	1	K.IGGGKER.M
130 – 136	890.4219	889.4146	889.4004	16	0	R.MTAYFNK.V Oxidation (M)
160 – 171	1494.8055	1493.7982	1493.8163	-12	1	K.QKTELFMVLIEK.K Oxidation (M)
162 – 171	1238.6130	1237.6057	1237.6628	-46	0	K.TELFMVLIEK.K Oxidation (M)
194 – 203	1094.5573	1093.5500	1093.5074	39	0	K.VAVCSTSNEK.A
223 – 231	945.5579	944.5506	944.5331	18	0	K.IFAGDVVPK.K
253 – 267	1502.7375	1501.7302	1501.7810	-34	0	K.CVVVEDSAIGLAAAK.A

Spot No.: **175**

Mascot score: **85**

Sequence coverage %: **36**

NCBI accession No.: **gi| 15222972**

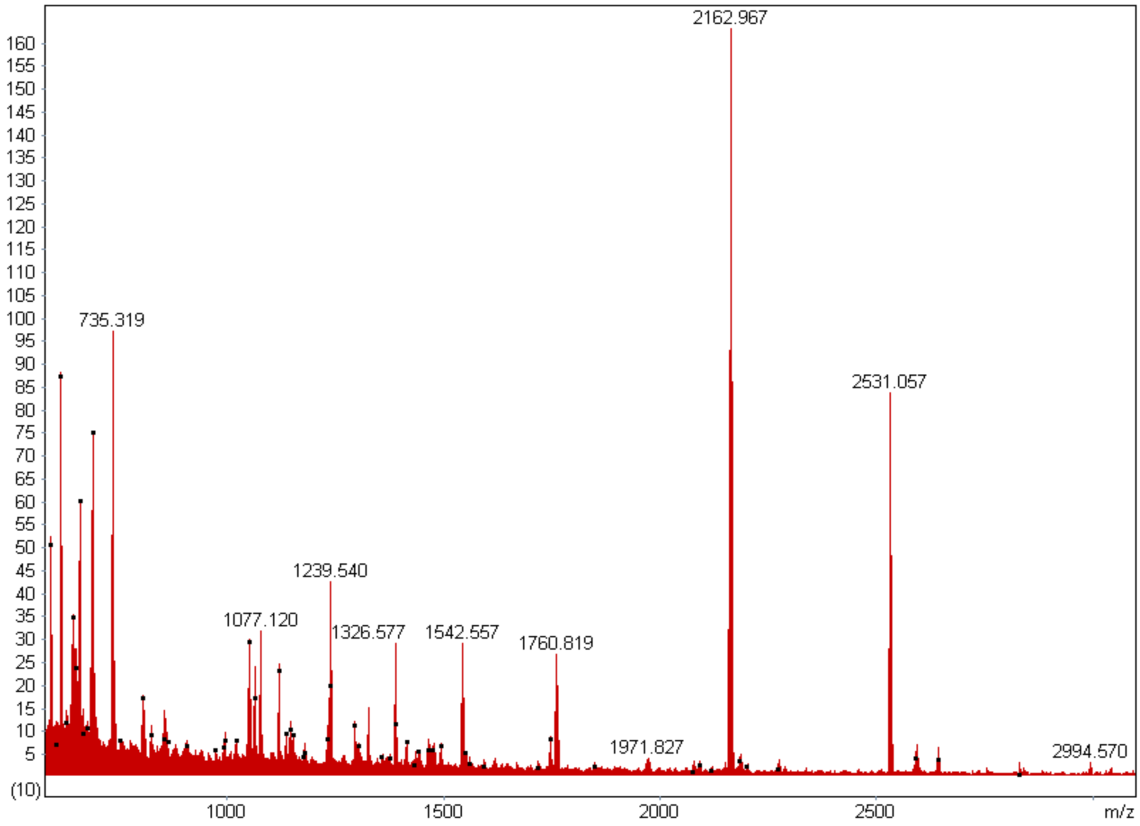
Matched peptides No.: **8**

Total peptides No.: **42**

Calculated Mr: **34442**

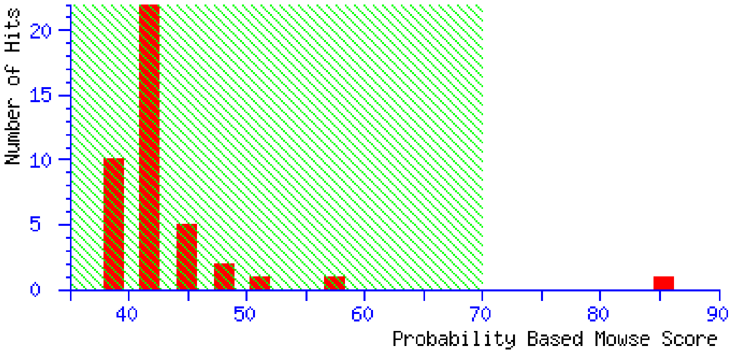
Calculated *p*I: **5.93**

Annotated PMF **spectra:**

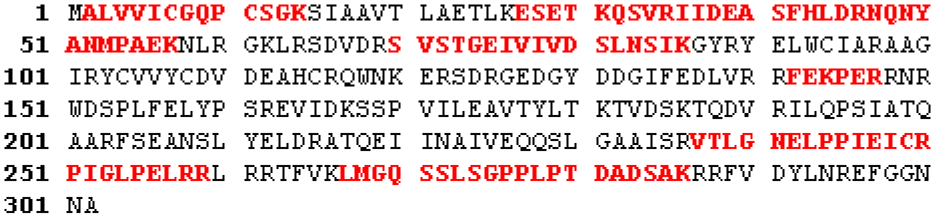


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red



1 M**ALVVICGQP CSGK**SIAAVT LAETLK**ESET KQSVRIIDEA SFHLDRNQNY**

51 **ANMPAEK**NLR GKLRSDVDR**S VSTGEIVIVD SLNSIK**GYRY ELWCIARAAG

101 IRYCVVYCDV DEAHCRQWNK ERSDRGEDGY DDGIFEDLVR R**FEKPER**RNR

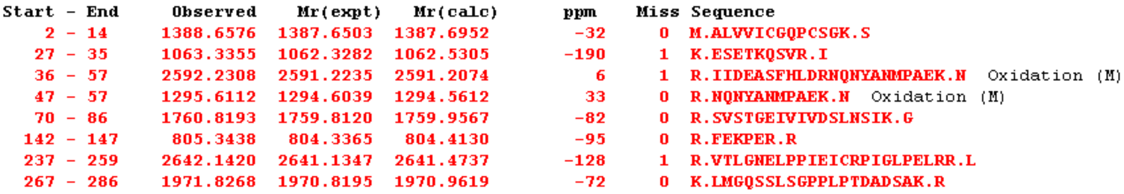
151 WDSPLFELYP SREVIDKSSP VILEAVTYLT KTVDSKTQDV RILQPSIATQ

201 AARFSEANSL YELDRATQEI INAIVEQQSL GAAISR**VTLG NELPPIEICR**

251 **PIGLPELRR**L RRTFVK**LMGQ SSLSGPPLPT DADSAK**RRFV DYLNREFGGN

301 NA

Matched peptides information:



```
Start - End      Observed    Mr(expt)   Mr(calc)       ppm     Miss Sequence
    2 - 14      1388.6576   1387.6503  1387.6952       -32      0   M.ALVVICGQPCSGK.S
   27 - 35      1063.3355   1062.3282  1062.5305      -190      1   K.ESETKQSVR.I
   36 - 57      2592.2308   2591.2235  2591.2074         6      1   R.IIDEASFHLDRNQNYANMPAEK.N  Oxidation (M)
   47 - 57      1295.6112   1294.6039  1294.5612        33      0   R.NQNYANMPAEK.N  Oxidation (M)
   70 - 86      1760.8193   1759.8120  1759.9567       -82      0   R.SVSTGEIVIVDSLNSIK.G
  142 - 147      805.3438    804.3365   804.4130       -95      0   R.FEKPER.R
  237 - 259     2642.1420   2641.1347  2641.4737      -128      1   R.VTLGNELPPIEICRPIGLPELRR.L
  267 - 286     1971.8268   1970.8195  1970.9619       -72      0   K.LMGQSSLSGPPLPTDADSAK.R
```

Spot No.: **176**

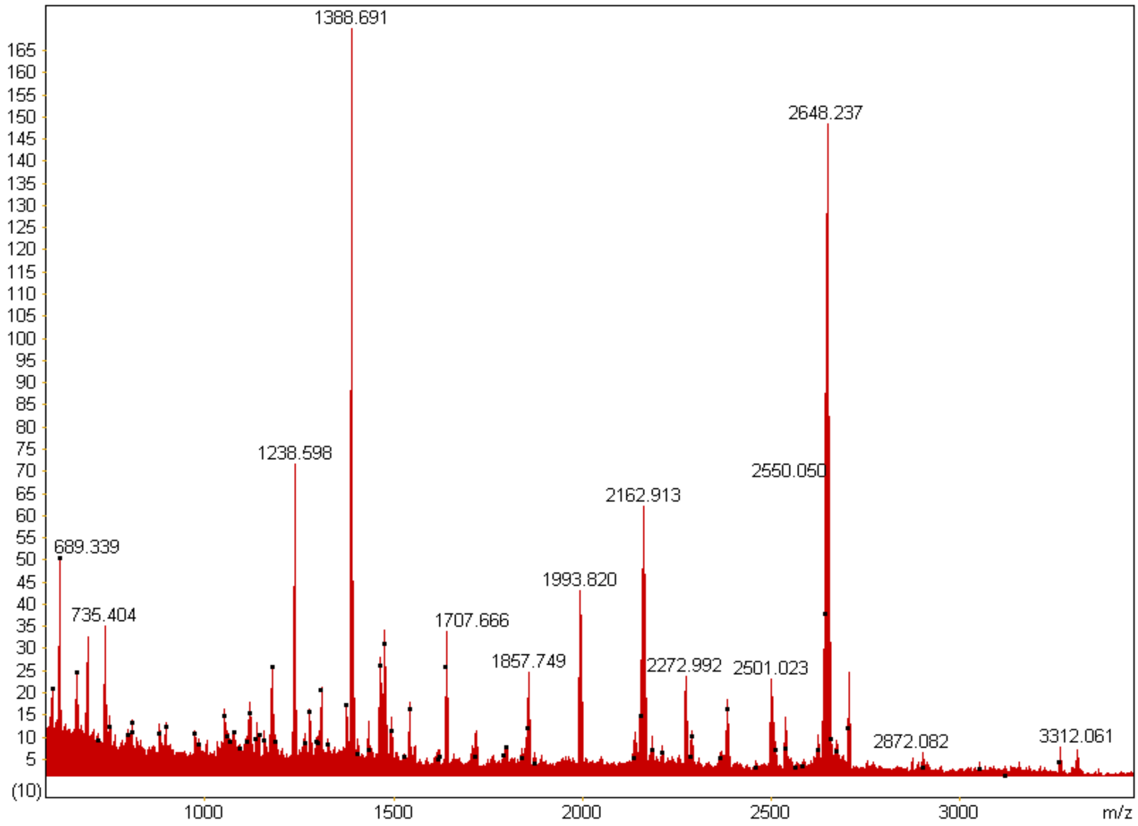
Mascot score: **83** Sequence coverage %: **19**

NCBI accession No.: **gi| 147795173**

Matched peptides No.: **19** Total peptides No.: **61**

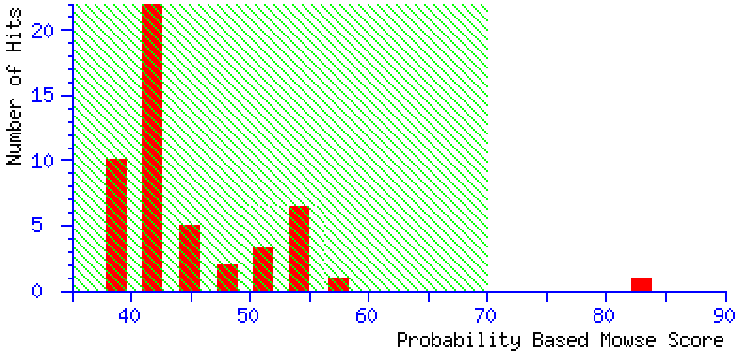
Calculated Mr: **112287** Calculated *p*I: **8.88**

Annotated PMF **spectra:**

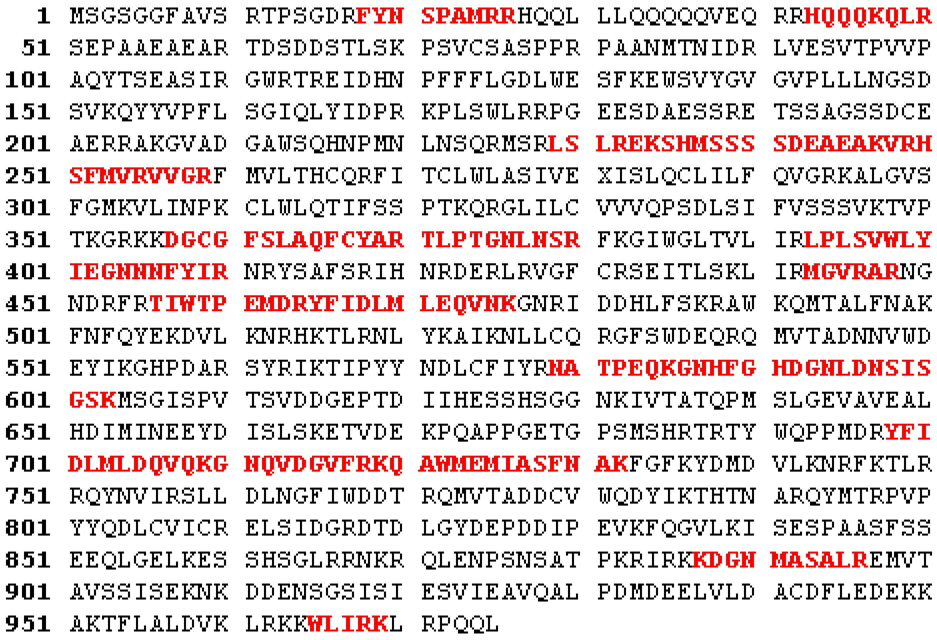


Probability Based Mowse Score:

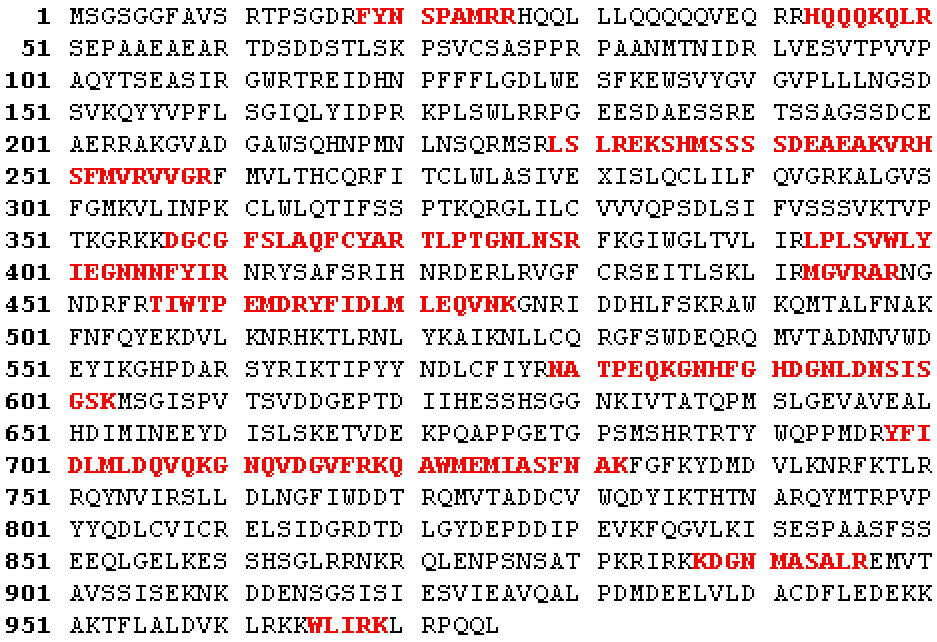
Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red


1 MSGSGGFAVS RTPSGDR**FYN SPAMRR**HQQL LLQQQQQVEQ RR**HQQQKQLR**
51 SEPAAEAEAR TDSDDSTLSK PSVCSASPPR PAANMTNIDR LVESVTPVVP
101 AQYTSEASIR GWRTREIDHN PFFFLGDLWE SFKEWSVYGV GVPLLLNGSD
151 SVKQYYVPFL SGIQLYIDPR KPLSWLRRPG EESDAESSRE TSSAGSSDCE
201 AERRAKGVAD GAWSQHNPMN LNSQRMSR**LS LREKSHMSSS SDEAEAKVRH**
251 **SFMVRVVGR**F MVLTHCQRFI TCLWLASIVE XISLQCLILF QVGRKALGVS
301 FGMKVLINPK CLWLQTIFSS PTKQRGLILC VVVQPSDLSI FVSSSVKTVP
351 TKGRKK**DGCG FSLAQFCYAR TLPTGNLNSR** FKGIWGLTVL IR**LPLSVWLY**
401 **IEGNNNFYIR** NRYSAFSRIH NRDERLRVGF CRSEITLSKL IR**MGVRAR**NG
451 NDRFR**TIWTP EMDRYFIDLM LEQVNK**GNRI DDHLFSKRAW KQMTALFNAK
501 FNFQYEKDVL KNRHKTLRNL YKAIKNLLCQ RGFSWDEQRQ MVTADNNVWD
551 EYIKGHPDAR SYRIKTIPYY NDLCFIYR**NA TPEQKGNHFG HDGNLDNSIS**
601 **GSK**MSGISPV TSVDDGEPTD IIHESSHSGG NKIVTATQPM SLGEVAVEAL
651 HDIMINEEYD ISLSKETVDE KPQAPPGETG PSMSHRTRTY WQPPMDR**YFI**
701 **DLMLDQVQKG NQVDGVFRKQ AWMEMIASFN AK**FGFKYDMD VLKNRFKTLR
751 RQYNVIRSLL DLNGFIWDDT RQMVTADDCV WQDYIKTHTN ARQYMTRPVP
801 YYQDLCVICR ELSIDGRDTD LGYDEPDDIP EVKFQGVLKI SESPAASFSS
851 EEQLGELKES SHSGLRRNKR QLENPSNSAT PKRIRK**KDGN MASALR**EMVT
901 AVSSISEKNK DDENSGSISI ESVIEAVQAL PDMDEELVLD ACDFLEDEKK
951 AKTFLALDVK LRKK**WLIRK**L RPQQL

Matched peptides information:


1 MSGSGGFAVS RTPSGDR**FYN SPAMRR**HQQL LLQQQQQVEQ RR**HQQQKQLR**
51 SEPAAEAEAR TDSDDSTLSK PSVCSASPPR PAANMTNIDR LVESVTPVVP
101 AQYTSEASIR GWRTREIDHN PFFFLGDLWE SFKEWSVYGV GVPLLLNGSD
151 SVKQYYVPFL SGIQLYIDPR KPLSWLRRPG EESDAESSRE TSSAGSSDCE
201 AERRAKGVAD GAWSQHNPMN LNSQRMSR**LS LREKSHMSSS SDEAEAKVRH**
251 **SFMVRVVGR**F MVLTHCQRFI TCLWLASIVE XISLQCLILF QVGRKALGVS
301 FGMKVLINPK CLWLQTIFSS PTKQRGLILC VVVQPSDLSI FVSSSVKTVP
351 TKGRKK**DGCG FSLAQFCYAR TLPTGNLNSR** FKGIWGLTVL IR**LPLSVWLY**
401 **IEGNNNFYIR** NRYSAFSRIH NRDERLRVGF CRSEITLSKL IR**MGVRAR**NG
451 NDRFR**TIWTP EMDRYFIDLM LEQVNK**GNRI DDHLFSKRAW KQMTALFNAK
501 FNFQYEKDVL KNRHKTLRNL YKAIKNLLCQ RGFSWDEQRQ MVTADNNVWD
551 EYIKGHPDAR SYRIKTIPYY NDLCFIYR**NA TPEQKGNHFG HDGNLDNSIS**
601 **GSK**MSGISPV TSVDDGEPTD IIHESSHSGG NKIVTATQPM SLGEVAVEAL
651 HDIMINEEYD ISLSKETVDE KPQAPPGETG PSMSHRTRTY WQPPMDR**YFI**
701 **DLMLDQVQKG NQVDGVFRKQ AWMEMIASFN AK**FGFKYDMD VLKNRFKTLR
751 RQYNVIRSLL DLNGFIWDDT RQMVTADDCV WQDYIKTHTN ARQYMTRPVP
801 YYQDLCVICR ELSIDGRDTD LGYDEPDDIP EVKFQGVLKI SESPAASFSS
851 EEQLGELKES SHSGLRRNKR QLENPSNSAT PKRIRK**KDGN MASALR**EMVT
901 AVSSISEKNK DDENSGSISI ESVIEAVQAL PDMDEELVLD ACDFLEDEKK
951 AKTFLALDVK LRKK**WLIRK**L RPQQL

Spot No.: **177**

Mascot score: **82**

Sequence coverage %: **25**

NCBI accession No.: **gi| 226523893**

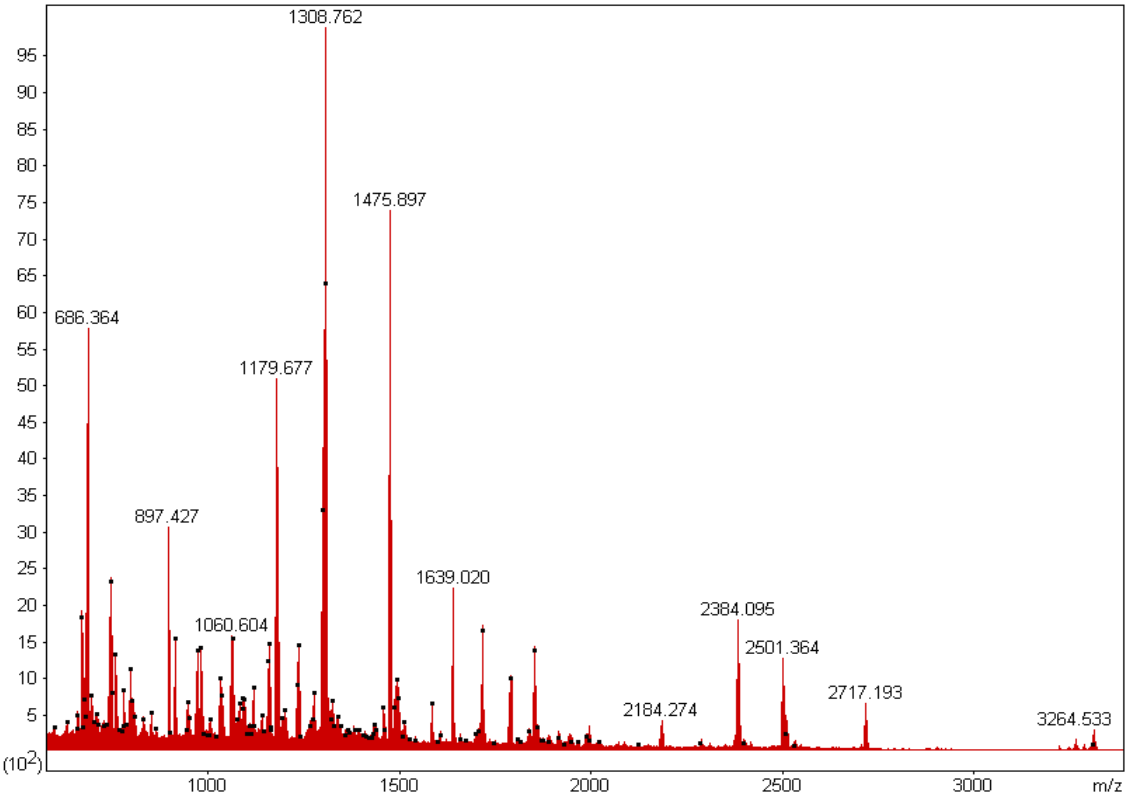
Matched peptides No.: **31**

Total peptides No.: **128**

Calculated Mr: **129198**

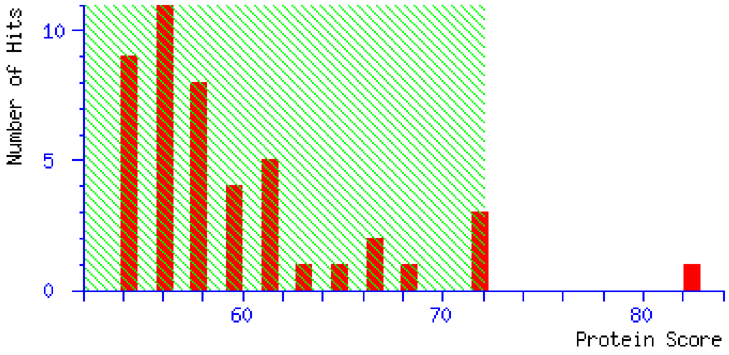
Calculated *p*I: **9.62**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in **Bold Red**

1 MVLTTNNQGV AALASRMTKP AVIVAPRSNT TRLEDFEIQR KLGKGSFGVV

51 YAVTRRR**DPT** **ERKRTYVMKQ** **ISMGPSR**R**DQ** **EEAINECRVL** **AKLNHAHVVR**

101 YHESFVASGN RLCIVMEYAP KGTVHSLVQG AKPK**ALSEDV** **VWR**LTLQSAL

151 GLHHIHGLKI LHRDIK**AENI** **FLDKDGNAK**I GDLGVAK**VMT** **HAVDFAK**TLV

201 GTPYYLSPEL CENKPYNHKS DVWSLGCVVY EMMTGSHPFN AQNQGALFVK

251 ILKGK**YPPVR** DASFSADLK**E** **LMDR**CLTVNQ TR**RPDTAGIL** **RSR**AARAKAN

301 ALGLQLPSDV PPPSNPREAF AAAARPVTDQ PPDKPDQATQ LAARQQRRAA

351 TAVGSSRADR **AAARGGPNGG** **PTETALQAVE** **R**IASARGADR VGRRVGHPGD

401 FVRVRLGEIS GLPVGYGGAG GLAYAAARMA DASAAARRPS TATHDRTAGR

451 SAAVIAGIAA AAAGGGVR**GV** **AAAESELRRI** **RAESAR**TAAR ADDAAR**HRAV**

501 **AVDAAR**DAED EASRRRK**EAG** **DAMR**AARERR REREEEERQK VLAERRRARV

551 EAAAIAAEES RAKLAAAKAE LVNQRRRR**QS** **GRVNTGGYDG** **NGPETAGK**RL

601 ETDR**TPPSFP** **LR**KTALPPSP LQGLAAATGA APAGAAPRRA PSSRKPTAAN

651 PGTVAPARPA SAMPVTAPVT VLVGSRVGEP STSRPKSAAE RREAARVADA

701 DLVAALPESP GADGVRTDRV PPTAIHPFDR PDDFDEAR**AM** **AELAARHVPP**

751 **K**VNFEGKNRS EQPETPKPAR DDGWDEGVSP SPAAPSRR**SR** **PRTAGGVVDV**

801 **AK**ARRDAAEA SR**AAVRAAK**S PKKSPKKSPK ASHPSSRPAS AFIRRTGDIF

851 GGARGRARPV TARDVSDSTS SESSSSK**MPH** **PAVSSYAEAH** **ERR**TRAPHPS

901 PPVQGTAAAA IGVARLAVLA VDHFVASAGE GNDGSLGSLG AGSGSSISSE

951 EISRAAAEAA AAAR**AAASVA** **SEGRAEPASS** **SSGTSSSSSR** DGVEGDKENR

1001 DGGVPAFVFG DATGDASGDD DDDYSPSAAF EDSGNLR**AAA** **GPSPDPAGAV**

1051 **AR**ALRATVRA LESVLGPSHP SINSDAGLKP FYDDEEESSE SGSEPGTNPS

1101 TPRSEYYSDA AR**HSECSDSE** **ER**FVRAHGAS RAERVEELVS EMTATEDAAV

1151 ALVGAESFGL LYDFLAR**RSE** **AAQDGR**LHEK PGTPEKVR**QL** **SERVFDIVPR**

1201 **EKAEAVALAH** **R**YAYLVERLE AV

Matched peptides information:

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
58 - 63	745.3946	744.3873	744.3766	14	1	R.DPTERK.R
64 - 69	797.3515	796.3442	796.4265	-103	1	K.RTYVMK.Q
65 - 69	657.2327	656.2254	656.3203	-145	0	R.TYVMK.Q Oxidation (M)
65 - 77	1497.9091	1496.9018	1496.7479	103	1	R.TYVMKQISMGPSR.R
65 - 77	1513.8842	1512.8769	1512.7429	89	1	R.TYVMKQISMGPSR.R Oxidation (M)
79 - 92	1674.8790	1673.8717	1673.8042	40	1	R.DQEEAINECRVLAK.L
93 - 100	945.5112	944.5039	944.5304	-28	0	K.LNHAHVVR.Y
135 - 143	1074.5824	1073.5751	1073.5506	23	0	K.ALSEDVVWR.L
167 - 179	1434.8666	1433.8593	1433.7150	101	1	K.AENIFLDKDGNAK.I
188 - 197	1118.5784	1117.5711	1117.5590	11	0	K.VMTHAVDFAK.T
256 - 260	631.2763	630.2690	630.3489	-127	0	K.YPPVR.D
270 - 274	679.3334	678.3261	678.3007	38	0	K.ELMDR.C Oxidation (M)
283 - 293	1241.6548	1240.6475	1240.7000	-42	1	R.RPDTAGILRSR.A
361 - 381	2023.0821	2022.0748	2022.0242	25	1	R.AAARGGPNGGPTETALQAVER.I
469 - 479	1158.6695	1157.6622	1157.6153	41	1	R.GVAAAESELRR.I
480 - 486	802.4276	801.4204	801.4457	-32	1	R.IRAESAR.T
497 - 506	1065.5644	1064.5571	1064.5839	-25	1	R.HRAVAVDAAR.D
518 - 524	749.3433	748.3360	748.3174	25	0	K.EAGDAMR.A
579 - 598	1965.0928	1964.0855	1963.8984	95	1	R.QSGRVNTGGYDGNGPETAGK.R
605 - 612	914.5542	913.5469	913.5022	49	0	R.TPPSFPLR.K
739 - 746	832.4666	831.4594	831.4272	39	0	R.AMAELAAR.H
739 - 751	1406.7897	1405.7824	1405.7500	23	1	R.AMAELAARHVPPK.V Oxidation (M)
789 - 802	1412.7661	1411.7588	1411.7896	-22	1	R.SRPRTAGGVVDVAK.A
813 - 819	686.3641	685.3568	685.4235	-97	1	R.AAVRAAK.S
878 - 893	1838.1080	1837.1007	1836.8689	126	1	K.MPHPAVSSYAEAHERR.T
965 - 990	2384.0954	2383.0881	2383.0847	1	1	R.AAASVASEGRAEPASSSSGTSSSSSR.D
1038 - 1052	1307.7834	1306.7761	1306.6629	87	0	R.AAAGPSPDPAGAVAR.A
1113 - 1122	1235.6618	1234.6545	1234.4520	164	0	R.HSECSDSEER.F
1168 - 1176	989.5283	988.5210	988.4686	53	1	R.RSEAAQDGR.L
1189 - 1200	1458.8390	1457.8317	1457.7991	22	1	R.QLSERVFDIVPR.E
1201 - 1211	1194.6639	1193.6566	1193.6516	4	1	R.EKAEAVALAHR.Y

Spot No.: **178**

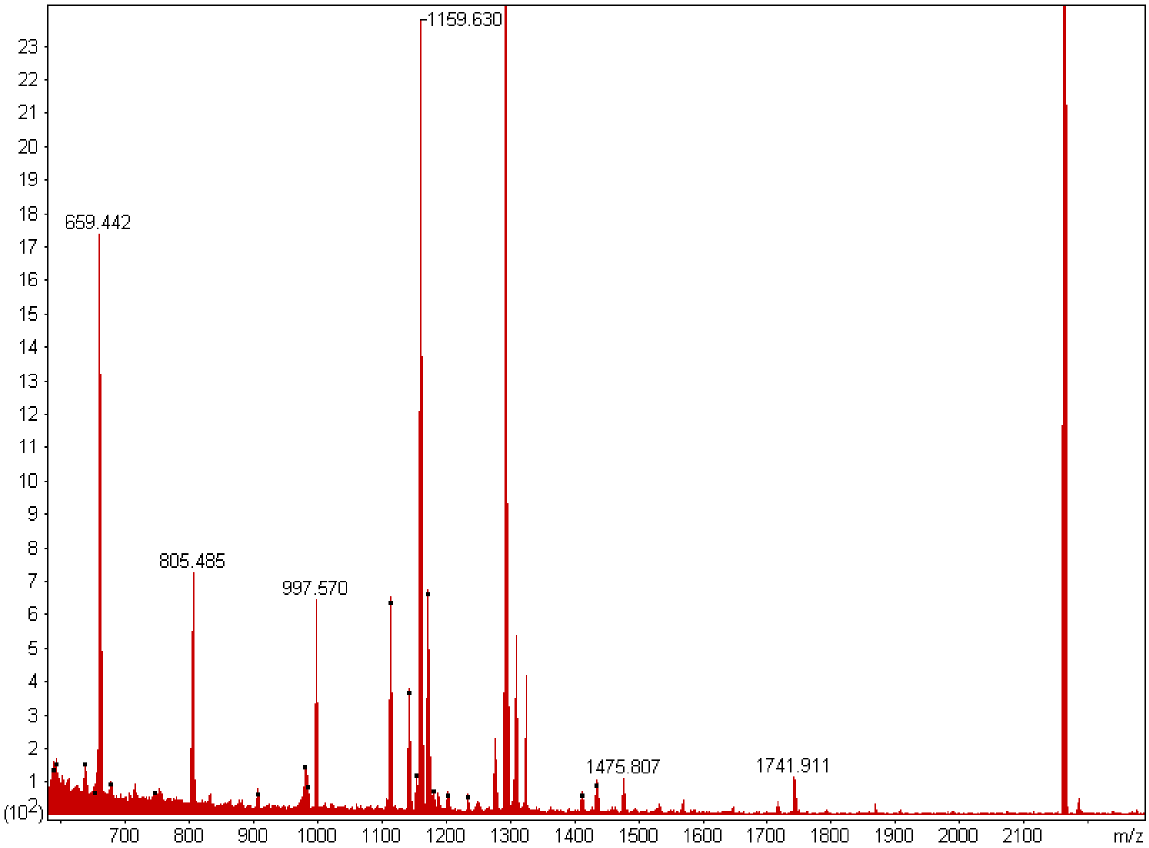
Mascot score: **92** Sequence coverage %: **28**

NCBI accession No.: **gi| 312282781**

Matched peptides No.: **9** Total peptides No.: **28**

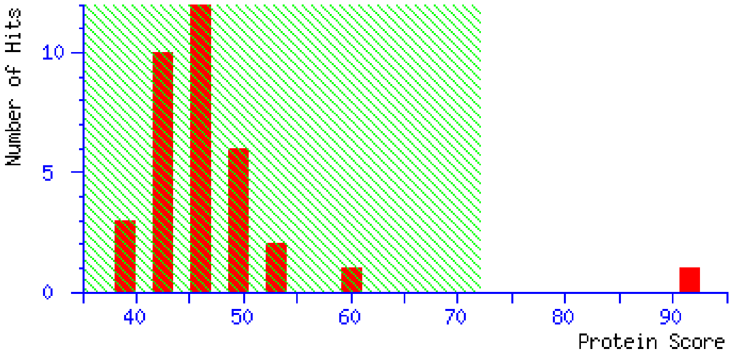
Calculated Mr: **27997** Calculated *p*I: **6.00**

Annotated PMF **spectra:**

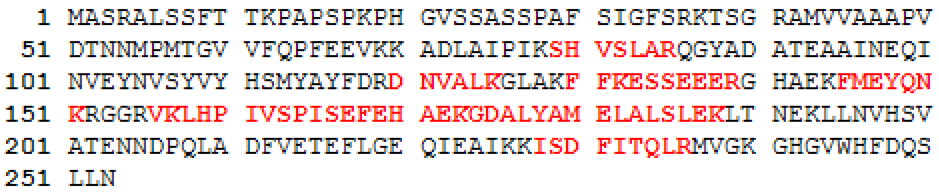


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

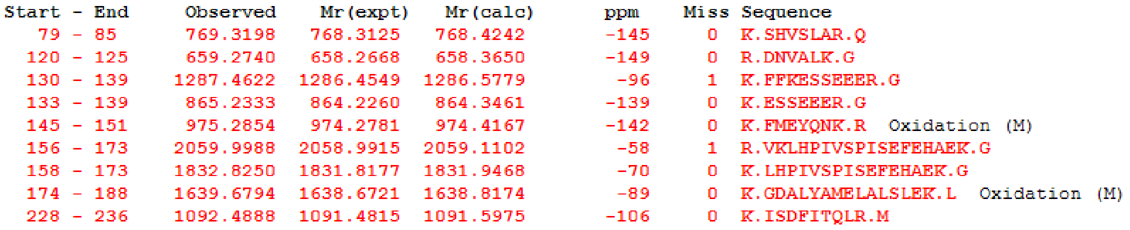


Matched peptide sequences: shown in Bold Red



1 MASRALSSFT TKPAPSPKPH GVSSASSPAF SIGFSRKTSG RAMVVAAAPV
51 DTNNMPMTGV VFQPFEEVKK ADLAIPIK**SH** **VSLAR**QGYAD ATEAAINEQI
101 NVEYNVSYVY HSMYAYFDR**D** **NVALK**GLAK**F** **FKESSEEER**G HAEK**FMEYQN**
151 **K**RGGR**VKLHP** **IVSPISEFEH** **AEKGDALYAM** **ELALSLEK**LT NEKLLNVHSV
201 ATENNDPQLA DFVETEFLGE QIEAIKK**ISD** **FITQLR**MVGK GHGVWHFDQS
251 LLN

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   79 - 85      769.3198   768.3125   768.4242     -145     0   K.SHVSLAR.Q
  120 - 125     659.2740   658.2668   658.3650     -149     0   R.DNVALK.G
  130 - 139    1287.4622  1286.4549  1286.5779      -96     1   K.FFKESSEEER.G
  133 - 139     865.2333   864.2260   864.3461     -139     0   K.ESSEEER.G
  145 - 151     975.2854   974.2781   974.4167     -142     0   K.FMEYQNK.R  Oxidation (M)
  156 - 173    2059.9988  2058.9915  2059.1102      -58     1   R.VKLHPIVSPISEFEHAEK.G
  158 - 173    1832.8250  1831.8177  1831.9468      -70     0   K.LHPIVSPISEFEHAEK.G
  174 - 188    1639.6794  1638.6721  1638.8174      -89     0   K.GDALYAMELALSLEK.L  Oxidation (M)
  228 - 236    1092.4888  1091.4815  1091.5975     -106     0   K.ISDFITQLR.M
```

Spot No.: **179**

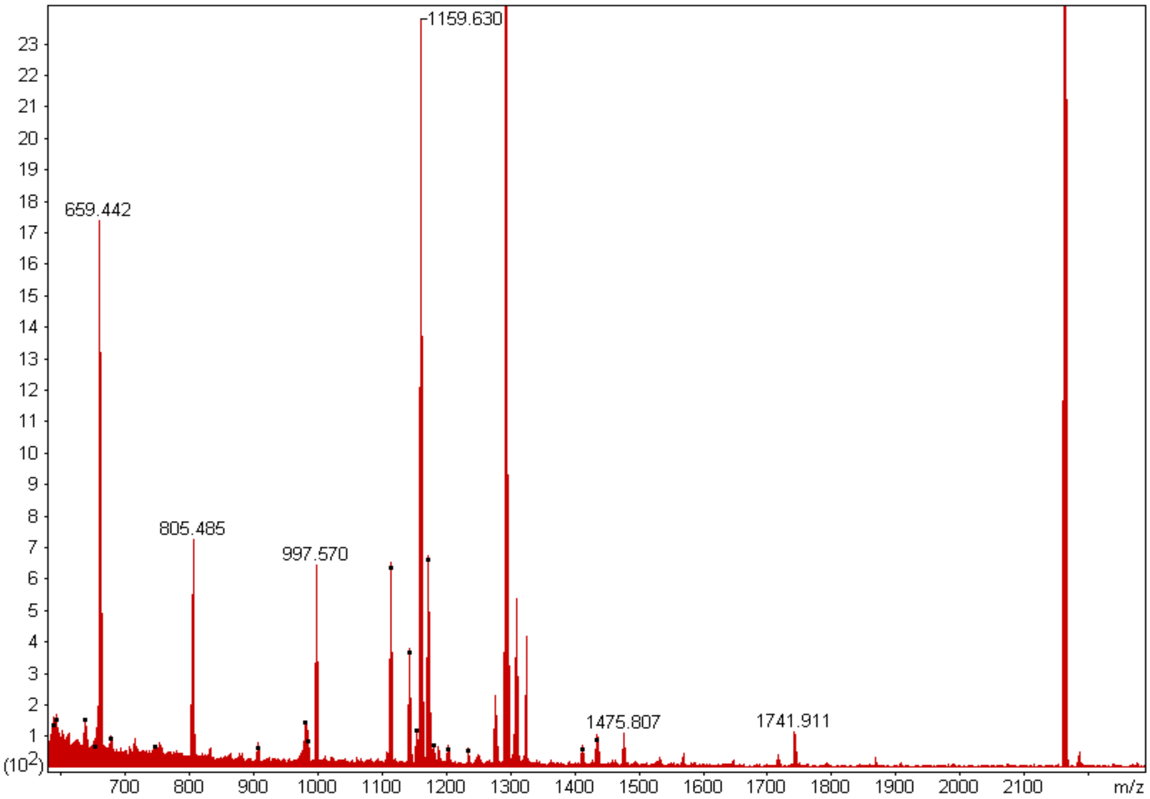
Mascot score: **89** Sequence coverage %: **28**

NCBI accession No.: **gi| 88175069**

Matched peptides No.: **7** Total peptides No.: **18**

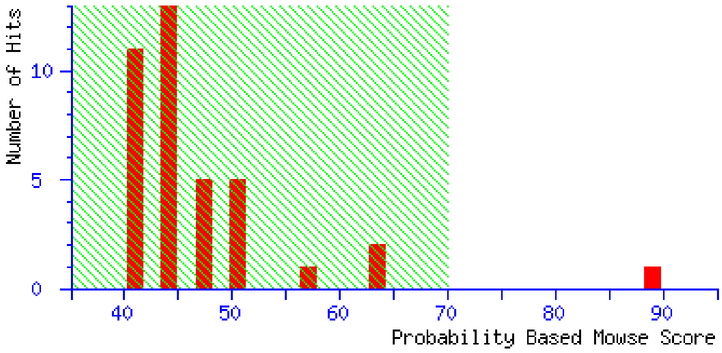
Calculated Mr: **24790** Calculated *p*I: **5.16**

Annotated PMF **spectra:**

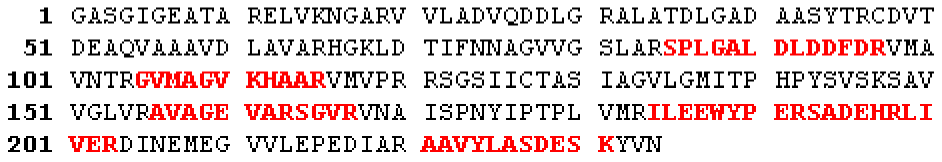


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

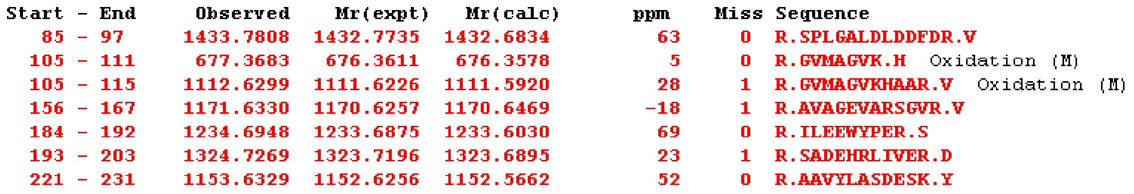


Matched peptide sequences: shown in Bold Red



```
  1 GASGIGEATA RELVKNGARV VLADVQDDLG RALATDLGAD AASYTRCDVT
 51 DEAQVAAAVD LAVARHGKLD TIFNNAGVVG SLARSPLGAL DLDDFDRVMA
101 VNTRGVMAGV KHAARVMVPR RSGSIICTAS IAGVLGMITP HPYSVSKSAV
151 VGLVRAVAGE VARSGVRVNA ISPNYIPTPL VMRILEEWYP ERSADEHRLI
201 VERDINEMEG VVLEPEDIAR AAVYLASDES KYVN
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss  Sequence
   85 - 97     1433.7808  1432.7735  1432.6834       63     0   R.SPLGALDLDDFDR.V
  105 - 111     677.3683   676.3611   676.3578        5     0   R.GVMAGVK.H  Oxidation (M)
  105 - 115    1112.6299  1111.6226  1111.5920       28     1   R.GVMAGVKHAAR.V  Oxidation (M)
  156 - 167    1171.6330  1170.6257  1170.6469      -18     1   R.AVAGEVARSGVR.V
  184 - 192    1234.6948  1233.6875  1233.6030       69     0   R.ILEEWYPER.S
  193 - 203    1324.7269  1323.7196  1323.6895       23     1   R.SADEHRLIVER.D
  221 - 231    1153.6329  1152.6256  1152.5662       52     0   R.AAVYLASDESK.Y
```

Spot No.: **180**

Mascot score: **84**

Sequence coverage %: **29**

NCBI accession No.: **gi| 183206803**

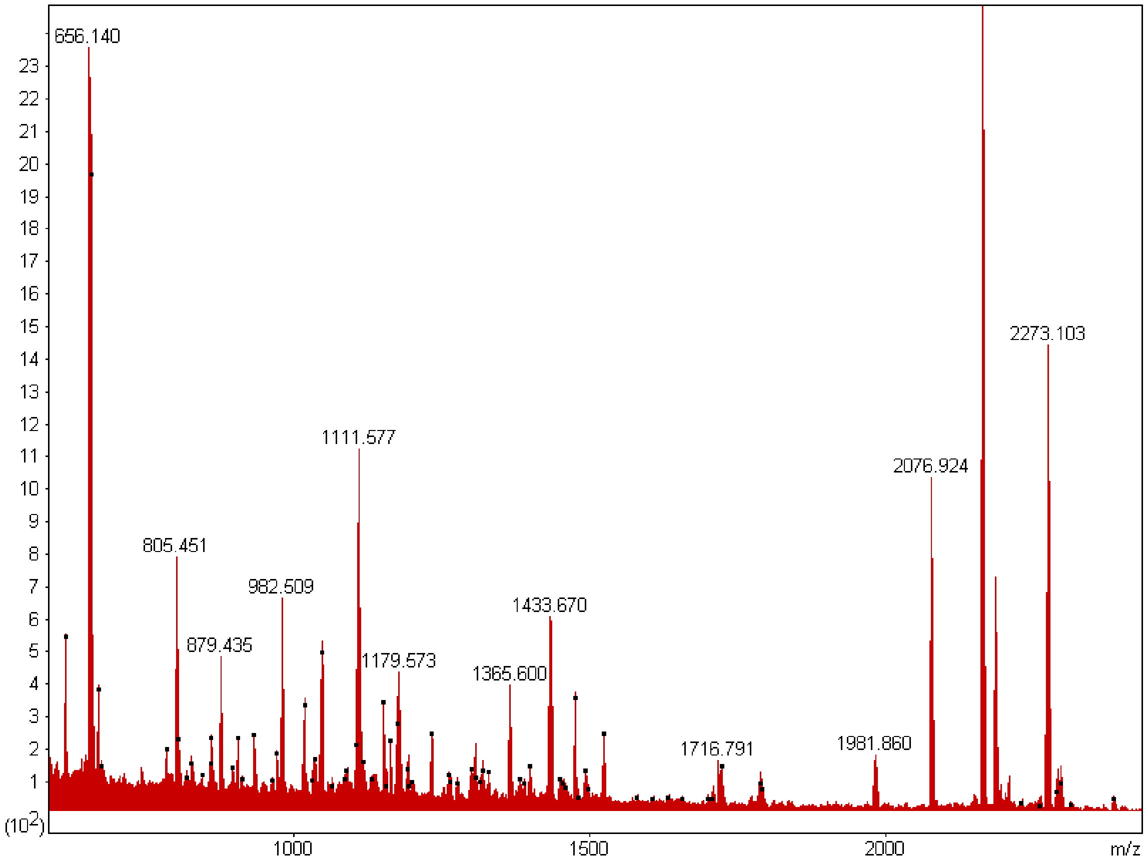
Matched peptides No.: **16**

Total peptides No.: **91**

Calculated Mr: **54896**

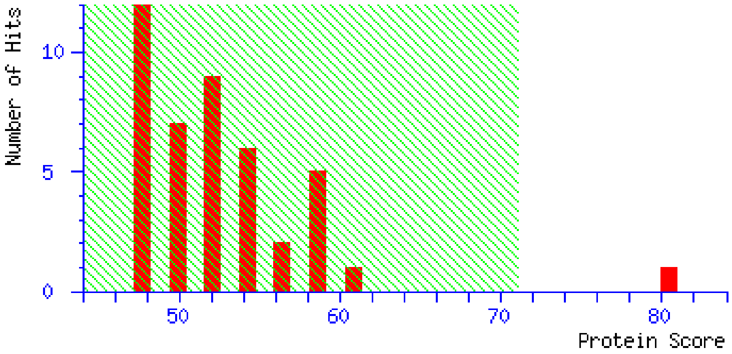
Calculated *p*I: **6.27**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

```
  1 MHSSLSFAAV CRPEAVGPRT LSNGRGSSVI ADSSAILSIR LTRAMQPDVC
 51 RNLKLRRTQV RSDAAPSAVG SHTGEFDTKA FRRTLTRKEN YNRKGFGHKE
101 ETLEAMDKEY TSDIIKTLKE NNNEYTWGNV TVKLAESFGF CWGVERAVQI
151 AYEARKQFPD QKLWITNEIM HNPTVNQRLK EMQIEDIPVM EEGKKFDVVN
201 NDDVVILPAF GAALSEMQIL DEKGVKIADT TCPWVSKVWN TVEKHKKESF
251 TSVIHGKKGH EETVATSSFA GKYIIVKDIK EATYVCDYIL AGKLDGSSST
301 KEEFLKKFEK AISRGFDPDC DLVKVGIANQ TTMLKGETEE IGKLLEKTMM
351 QKYGVEFINE HFMCFNTICD ATQERQDAMY NLVKEKLDLI LVVGGWNSSN
401 TSHLQEIAEQ NGTPTYWIDS EKRIGPGNRI AYKLSHGELV GKENWLPTGP
451 LKIGITSGAS TPDKILEDTL KVVFKMKDEE ALQMV
```

Matched peptides information:

```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   2 - 25      2569.0767  2568.0694  2568.2979      -89      1  M.HSSLSFAAVCRPEAVGPRTLSNGR.G
  26 - 40      1475.7141  1474.7068  1474.7991      -63      0  R.GSSVIADSSAILSIR.L
  57 - 61       659.4546   658.4474   658.3875       91      1  R.RTQVR.S
 100 - 108     1065.5144  1064.5071  1064.4696       35      0  K.EETLEAMDK.E
 147 - 155     1020.4968  1019.4895  1019.5400      -49      0  R.AVQIAYEAR.K
 163 - 178     1981.8603  1980.8530  1980.9840      -66      0  K.LWITNEIMHNPTVNQR.L  Oxidation (M)
 163 - 180     2206.9711  2205.9638  2206.1681      -93      1  K.LWITNEIMHNPTVNQRLK.E
 181 - 195     1791.6926  1790.6853  1790.8430      -88      1  K.EMQIEDIPVMEEGKK.F  Oxidation (M)
 227 - 237     1277.6640  1276.6567  1276.6122       35      0  K.IADTTCPWVSK.V
 315 - 324     1165.5601  1164.5528  1164.5121       35      0  R.GFDPDCDLVK.V
 325 - 335     1175.5333  1174.5260  1174.6380      -95      0  K.VGIANQTTMLK.G
 336 - 343      862.4543   861.4470   861.4080       45      0  K.GETEEIGK.L
 344 - 352     1153.5425  1152.5352  1152.5882      -46      1  K.LLEKTMMQK.Y  2 Oxidation (M)
 476 - 485     1193.5664  1192.5591  1192.5468       10      1  K.MKDEEALQMV.-
 478 - 485      934.5047   933.4975   933.4113       92      0  K.DEEALQMV.-
```

Spot No.: **181**

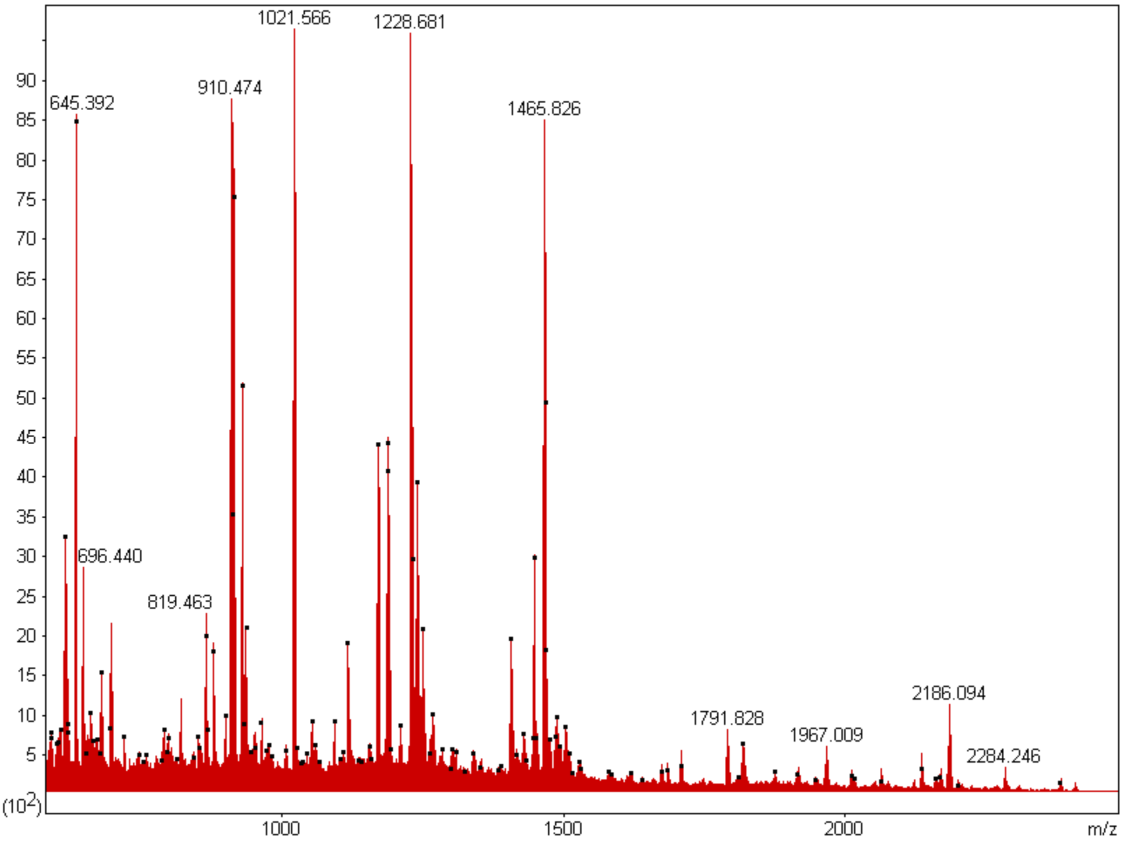
Mascot score: **276** Sequence coverage %: **49**

NCBI accession No.: **gi| 27752799**

Matched peptides No.: **35** Total peptides No.: **127**

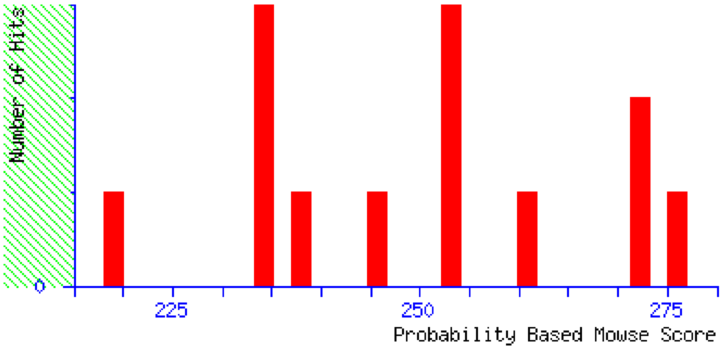
Calculated Mr: **47920** Calculated *p*I: **6.12**

Annotated PMF **spectra:**

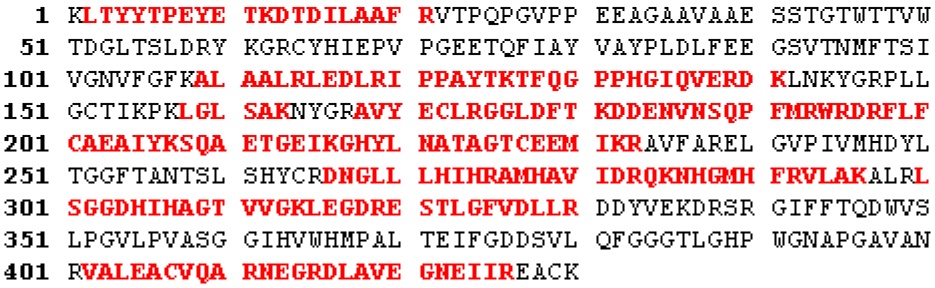


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

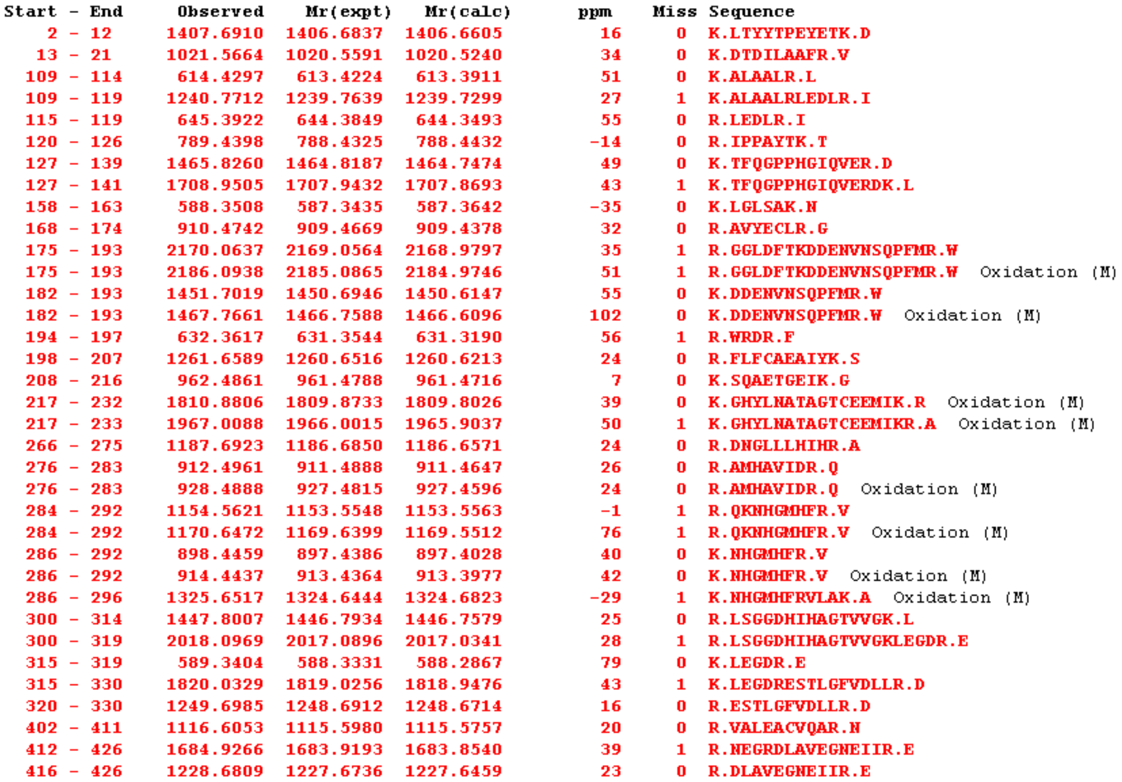


Matched peptide sequences: shown in Bold Red



1 K**LTYYTPEYE** **TKDTDILAAF** **R**VTPQPGVPP EEAGAAVAAE SSTGTWTTVW
51 TDGLTSLDRY KGRCYHIEPV PGEETQFIAY VAYPLDLFEE GSVTNMFTSI
101 VGNVFGFK**AL** **AALRLEDLRI** **PPAYTKTFQG** **PPHGIQVERD** **K**LNKYGRPLL
151 GCTIKPK**LGL** **SAK**NYGR**AVY** **ECLRGGLDFT** **KDDENVNSQP** **FMRWRDRFLF**
201 **CAEAIYKSQA** **ETGEIKGHYL** **NATAGTCEEM** **IKR**AVFAREL GVPIVMHDYL
251 TGGFTANTSL SHYCR**DNGLL** **LHIHRAMHAV** **IDRQKNHGMH** **FRVLAK**ALR**L**
301 **SGGDHIHAGT** **VVGKLEGDRE** **STLGFVDLLR** DDYVEKDRSR GIFFTQDWVS
351 LPGVLPVASG GIHVWHMPAL TEIFGDDSVL QFGGGTLGHP WGNAPGAVAN
401 R**VALEACVQA** **RNEGRDLAVE** **GNEIIR**EACK

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
2 - 12	1407.6910	1406.6837	1406.6605	16	0	K.LTYYTPEYETK.D	
13 - 21	1021.5664	1020.5591	1020.5240	34	0	K.DTDILAAFR.V	
109 - 114	614.4297	613.4224	613.3911	51	0	K.ALAALR.L	
109 - 119	1240.7712	1239.7639	1239.7299	27	1	K.ALAALRLEDLR.I	
115 - 119	645.3922	644.3849	644.3493	55	0	R.LEDLR.I	
120 - 126	789.4398	788.4325	788.4432	-14	0	R.IPPAYTK.T	
127 - 139	1465.8260	1464.8187	1464.7474	49	0	K.TFQGPPHGIQVER.D	
127 - 141	1708.9505	1707.9432	1707.8693	43	1	K.TFQGPPHGIQVERDK.L	
158 - 163	588.3508	587.3435	587.3642	-35	0	K.LGLSAK.N	
168 - 174	910.4742	909.4669	909.4378	32	0	R.AVYECLR.G	
175 - 193	2170.0637	2169.0564	2168.9797	35	1	R.GGLDFTKDDENVNSQPFMR.W	
175 - 193	2186.0938	2185.0865	2184.9746	51	1	R.GGLDFTKDDENVNSQPFMR.W	Oxidation (M)
182 - 193	1451.7019	1450.6946	1450.6147	55	0	K.DDENVNSQPFMR.W	
182 - 193	1467.7661	1466.7588	1466.6096	102	0	K.DDENVNSQPFMR.W	Oxidation (M)
194 - 197	632.3617	631.3544	631.3190	56	1	R.WRDR.F	
198 - 207	1261.6589	1260.6516	1260.6213	24	0	R.FLFCAEAIYK.S	
208 - 216	962.4861	961.4788	961.4716	7	0	K.SQAETGEIK.G	
217 - 232	1810.8806	1809.8733	1809.8026	39	0	K.GHYLNATAGTCEEMIK.R	Oxidation (M)
217 - 233	1967.0088	1966.0015	1965.9037	50	1	K.GHYLNATAGTCEEMIKR.A	Oxidation (M)
266 - 275	1187.6923	1186.6850	1186.6571	24	0	R.DNGLLLHIHR.A	
276 - 283	912.4961	911.4888	911.4647	26	0	R.AMHAVIDR.Q	
276 - 283	928.4888	927.4815	927.4596	24	0	R.AMHAVIDR.Q	Oxidation (M)
284 - 292	1154.5621	1153.5548	1153.5563	-1	1	R.QKNHGMHFR.V	
284 - 292	1170.6472	1169.6399	1169.5512	76	1	R.QKNHGMHFR.V	Oxidation (M)
286 - 292	898.4459	897.4386	897.4028	40	0	K.NHGMHFR.V	
286 - 292	914.4437	913.4364	913.3977	42	0	K.NHGMHFR.V	Oxidation (M)
286 - 296	1325.6517	1324.6444	1324.6823	-29	1	K.NHGMHFRVLAK.A	Oxidation (M)
300 - 314	1447.8007	1446.7934	1446.7579	25	0	R.LSGGDHIHAGTVVGK.L	
300 - 319	2018.0969	2017.0896	2017.0341	28	1	R.LSGGDHIHAGTVVGKLEGDR.E	
315 - 319	589.3404	588.3331	588.2867	79	0	K.LEGDR.E	
315 - 330	1820.0329	1819.0256	1818.9476	43	1	K.LEGDRESTLGFVDLLR.D	
320 - 330	1249.6985	1248.6912	1248.6714	16	0	R.ESTLGFVDLLR.D	
402 - 411	1116.6053	1115.5980	1115.5757	20	0	R.VALEACVQAR.N	
412 - 426	1684.9266	1683.9193	1683.8540	39	1	R.NEGRDLAVEGNEIIR.E	
416 - 426	1228.6809	1227.6736	1227.6459	23	0	R.DLAVEGNEIIR.E	

Spot No.: **182**

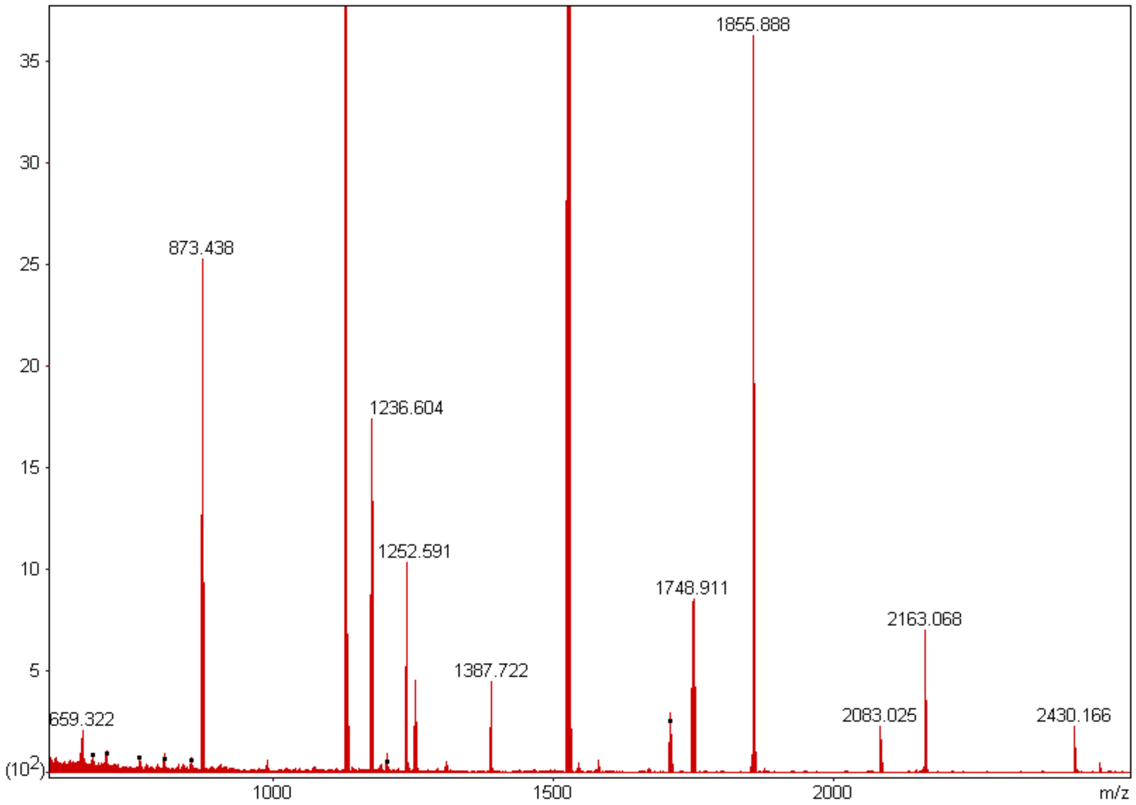
Mascot score: **94** Sequence coverage %: **29**

NCBI accession No.: **gi| 3121825**

Matched peptides No.: **8** Total peptides No.: **15**

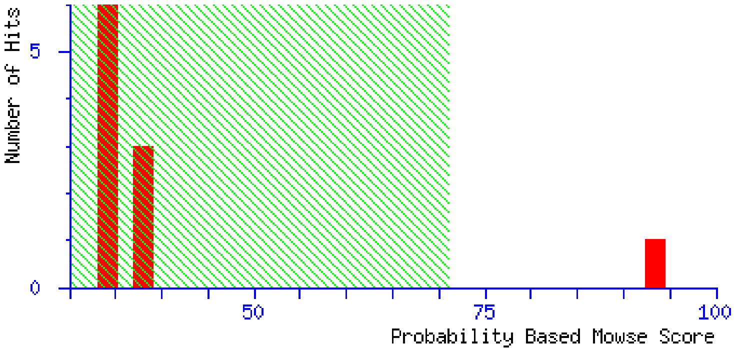
Calculated Mr: **29049** Calculated *p*I: **7.70**

Annotated PMF **spectra:**

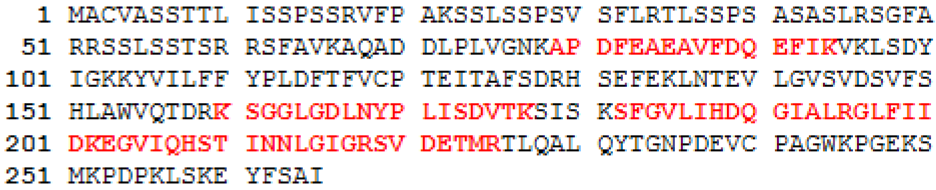


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

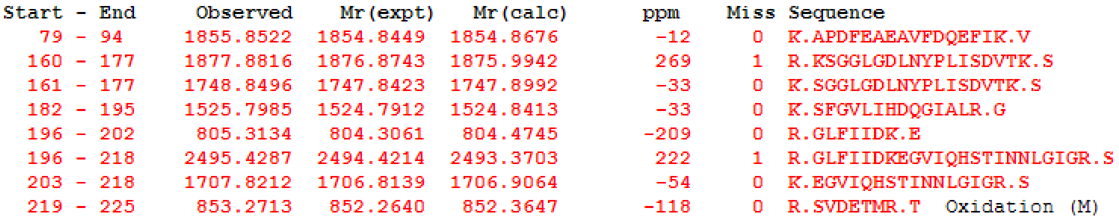


Matched peptide sequences: shown in Bold Red



```
  1 MACVASSTTL ISSPSSRVFP AKSSLSSPSV SFLRTLSSPS ASASLRSGFA
 51 RRSSLSSTSR RSFAVKAQAD DLPLVGNKAP DFEAEAVFDQ EFIKVKLSDY
101 IGKKYVILFF YPLDFTFVCP TEITAFSDRH SEFEKLNTEV LGVSVDSVFS
151 HLAWVQTDRK SGGLGDLNYP LISDVTKSIS KSFGVLIHDQ GIALRGLFII
201 DKEGVIQHST INNLGIGRSV DETMRTLQAL QYTGNPDEVC PAGWKPGEKS
251 MKPDPKLSKE YFSAI
```

Matched peptides information:



```
Start - End     Observed    Mr(expt)   Mr(calc)       ppm    Miss Sequence
   79 - 94     1855.8522  1854.8449  1854.8676       -12      0  K.APDFEAEAVFDQEFIK.V
  160 - 177    1877.8816  1876.8743  1875.9942       269      1  R.KSGGLGDLNYPLISDVTK.S
  161 - 177    1748.8496  1747.8423  1747.8992       -33      0  K.SGGLGDLNYPLISDVTK.S
  182 - 195    1525.7985  1524.7912  1524.8413       -33      0  K.SFGVLIHDQGIALR.G
  196 - 202     805.3134   804.3061   804.4745      -209      0  R.GLFIIDK.E
  196 - 218    2495.4287  2494.4214  2493.3703       222      1  R.GLFIIDKEGVIQHSTINNLGIGR.S
  203 - 218    1707.8212  1706.8139  1706.9064       -54      0  K.EGVIQHSTINNLGIGR.S
  219 - 225     853.2713   852.2640   852.3647      -118      0  R.SVDETMR.T   Oxidation (M)
```

Spot No.: **183**

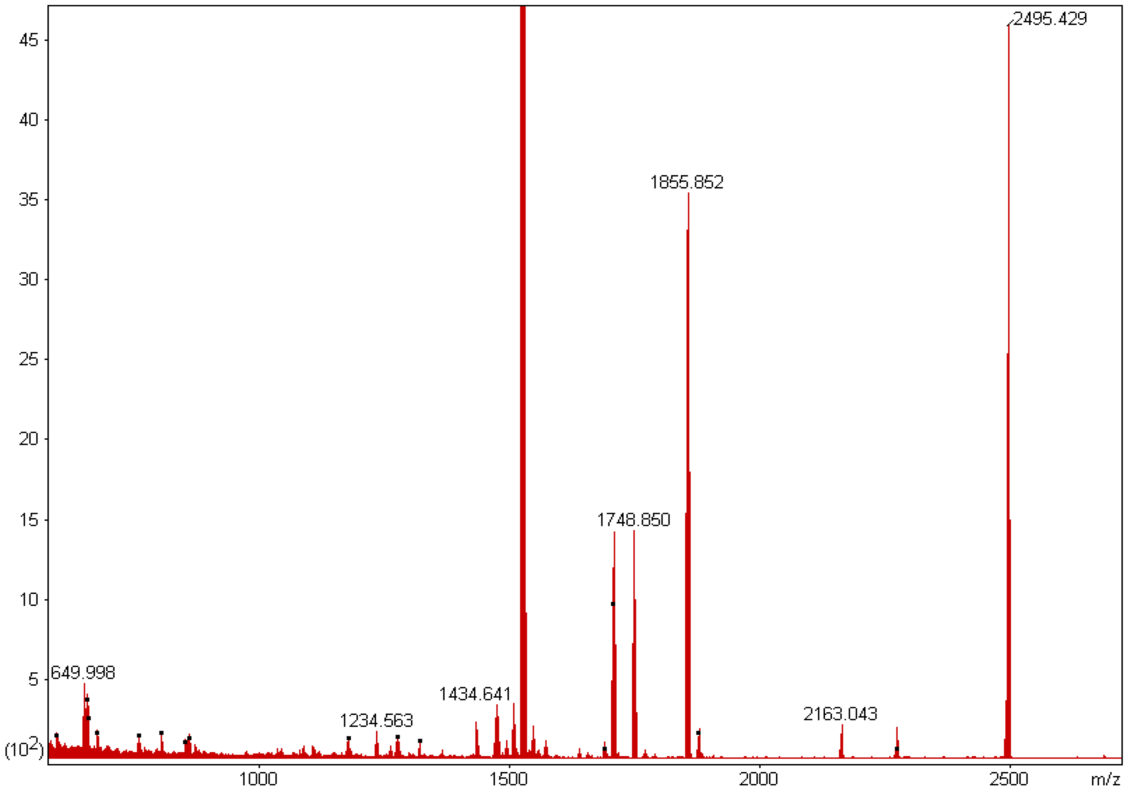
Mascot score: **94** Sequence coverage %: **29**

NCBI accession No.: **gi| 1498198**

Matched peptides No.: **8** Total peptides No.: **12**

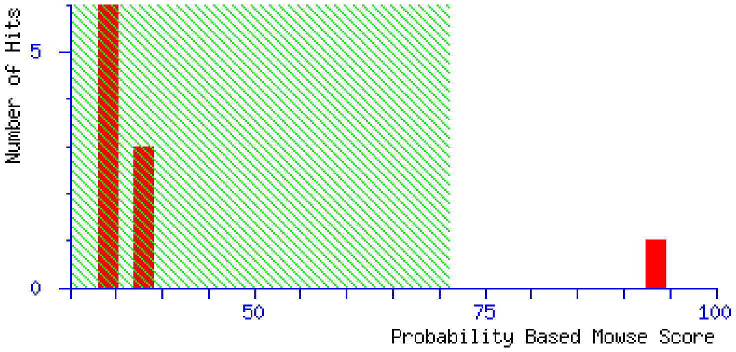
Calculated Mr: **28966** Calculated *p*I: **8.76**

Annotated PMF **spectra:**

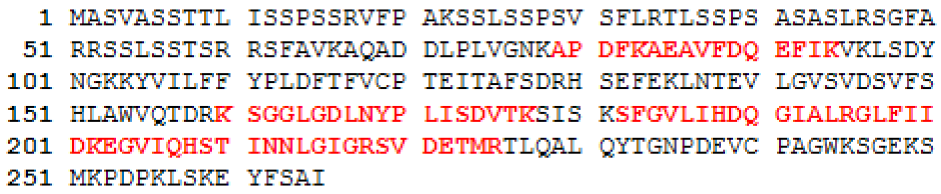


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).

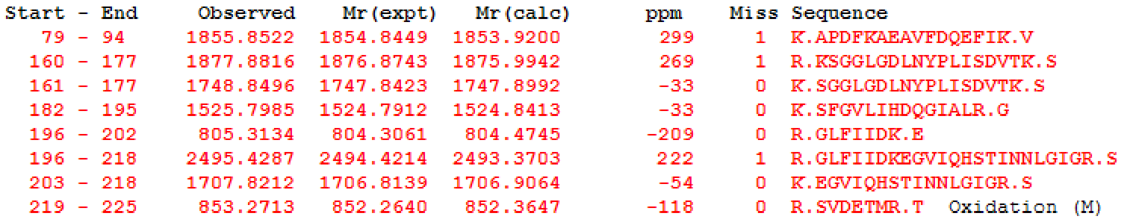


Matched peptide sequences: shown in Bold Red



1 MASVASSTTL ISSPSSRVFP AKSSLSSPSV SFLRTLSSPS ASASLRSGFA
51 RRSSLSSTSR RSFAVKAQAD DLPLVGNK**AP** **DFKAEAVFDQ** **EFIK**VKLSDY
101 NGKKYVILFF YPLDFTFVCP TEITAFSDRH SEFEKLNTEV LGVSVDSVFS
151 HLAWVQTDR**K** **SGGLGDLNYP** **LISDVTK**SIS **KSFGVLIHDQ** **GIALRGLFII**
201 **DKEGVIQHST** **INNLGIGRSV** **DETMR**TLQAL QYTGNPDEVC PAGWKSGEKS
251 MKPDPKLSKE YFSAI

Matched peptides information:



```
Start - End      Observed    Mr(expt)    Mr(calc)       ppm    Miss Sequence
   79 - 94     1855.8522   1854.8449   1853.9200       299      1  K.APDFKAEAVFDQEFIK.V
  160 - 177     1877.8816   1876.8743   1875.9942       269      1  R.KSGGLGDLNYPLISDVTK.S
  161 - 177     1748.8496   1747.8423   1747.8992       -33      0  K.SGGLGDLNYPLISDVTK.S
  182 - 195     1525.7985   1524.7912   1524.8413       -33      0  K.SFGVLIHDQGIALR.G
  196 - 202      805.3134    804.3061    804.4745      -209      0  R.GLFIIDK.E
  196 - 218     2495.4287   2494.4214   2493.3703       222      1  R.GLFIIDKEGVIQHSTINNLGIGR.S
  203 - 218     1707.8212   1706.8139   1706.9064       -54      0  K.EGVIQHSTINNLGIGR.S
  219 - 225      853.2713    852.2640    852.3647      -118      0  R.SVDETMR.T   Oxidation (M)
```

Spot No.: **184**

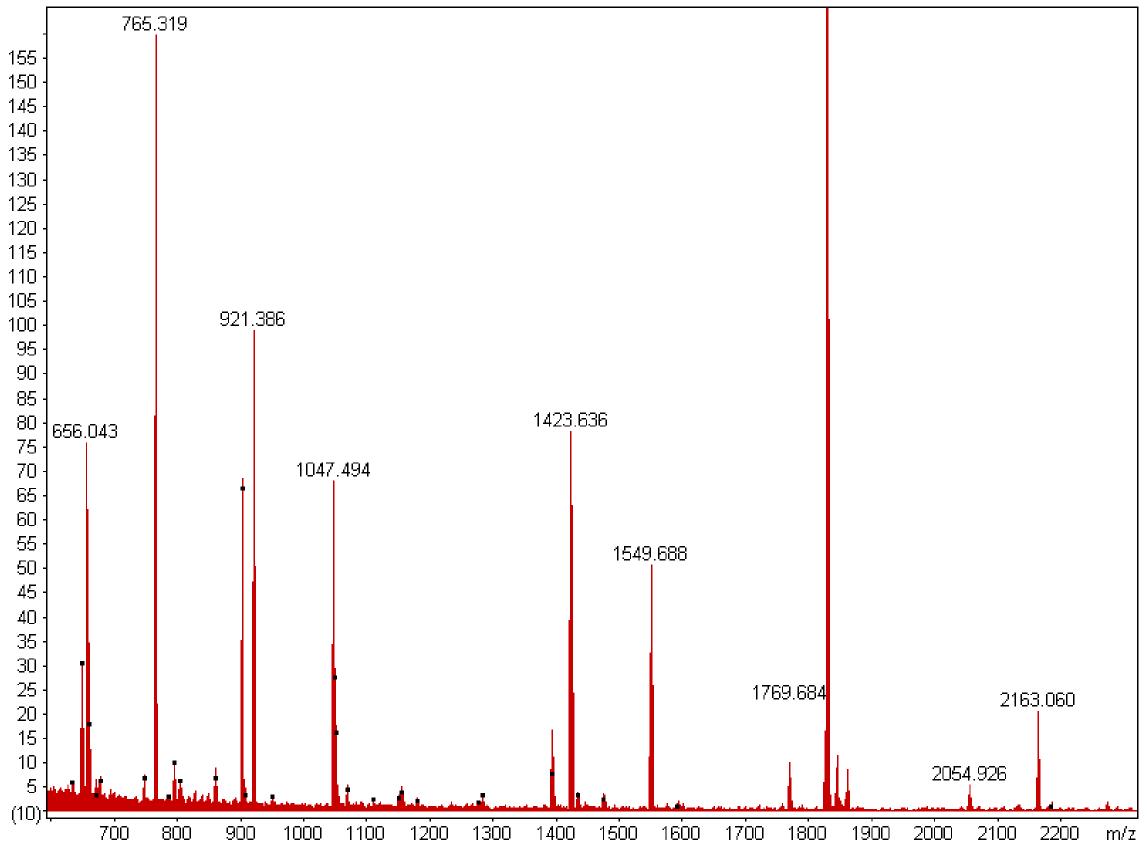
Mascot score: **116** Sequence coverage %: **48**

NCBI accession No.: **gi| 15231176**

Matched peptides No.: **10** Total peptides No.: **30**

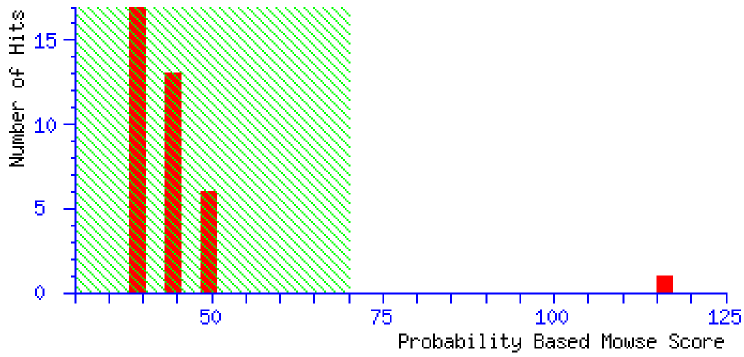
Calculated Mr: **19574** Calculated *p*I: **5.09**

Annotated PMF **spectra:**

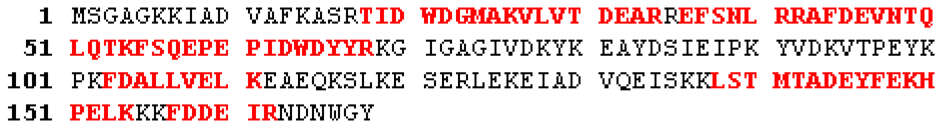


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

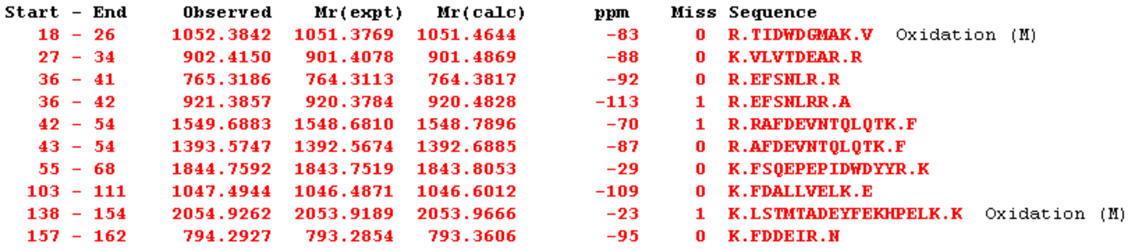


Matched peptide sequences: shown in Bold Red



1 MSGAGKKIAD VAFKASR**TID WDGMAKVLVT DEAR**R**EFSNL RRAFDEVNTQ**
51 **LQTKFSQEPE PIDWDYYR**KG IGAGIVDKYK EAYDSIEIPK YVDKVTPEYK
101 PK**FDALLVEL K**EAEQKSLKE SERLEKEIAD VQEISKK**LST MTADEYFEKH**
151 **PELK**KK**FDDE IR**NDNWGY

Matched peptides information:



```
Start - End      Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
   18 - 26      1052.3842  1051.3769  1051.4644      -83      0  R.TIDWDGMAK.V  Oxidation (M)
   27 - 34       902.4150   901.4078   901.4869      -88      0  K.VLVTDEAR.R
   36 - 41       765.3186   764.3113   764.3817      -92      0  R.EFSNLR.R
   36 - 42       921.3857   920.3784   920.4828     -113      1  R.EFSNLRR.A
   42 - 54      1549.6883  1548.6810  1548.7896      -70      1  R.RAFDEVNTQLQTK.F
   43 - 54      1393.5747  1392.5674  1392.6885      -87      0  R.AFDEVNTQLQTK.F
   55 - 68      1844.7592  1843.7519  1843.8053      -29      0  K.FSQEPEPIDWDYYR.K
  103 - 111     1047.4944  1046.4871  1046.6012     -109      0  K.FDALLVELK.E
  138 - 154     2054.9262  2053.9189  2053.9666      -23      1  K.LSTMTADEYFEKHPELK.K  Oxidation (M)
  157 - 162      794.2927   793.2854   793.3606      -95      0  K.FDDEIR.N
```

Spot No.: **185**

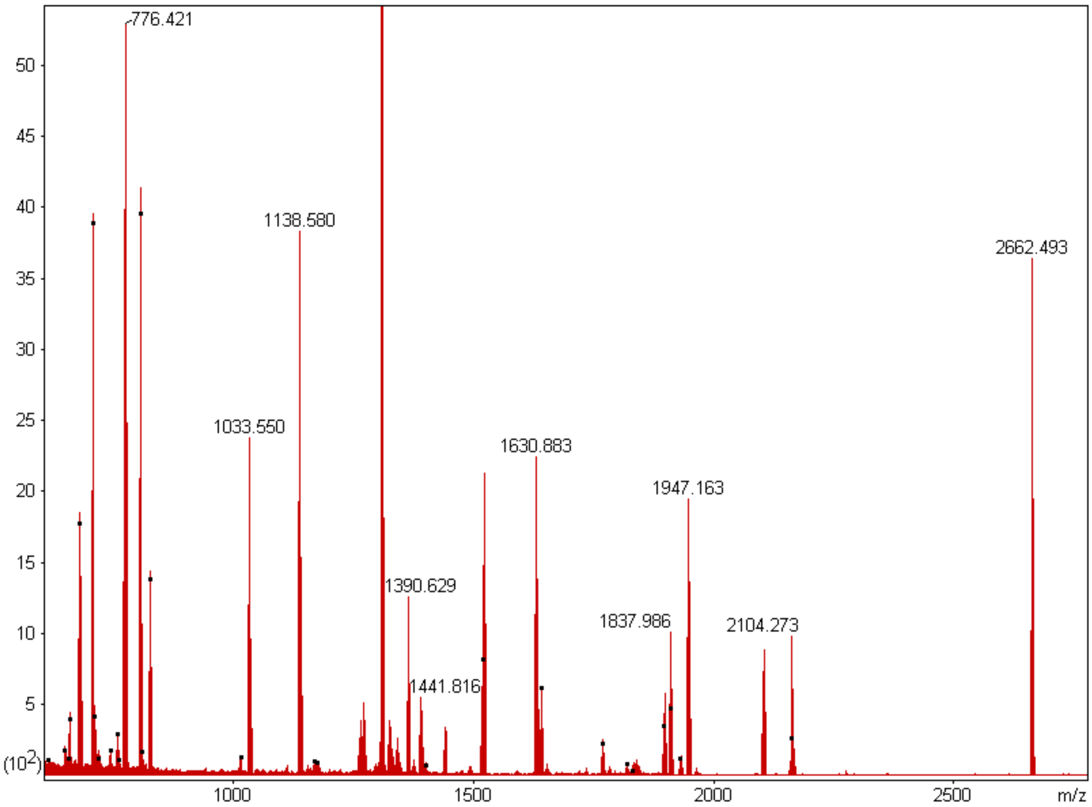
Mascot score: **156** Sequence coverage %: **45**

NCBI accession No.: **gi| 15239282**

Matched peptides No.: **19** Total peptides No.: **49**

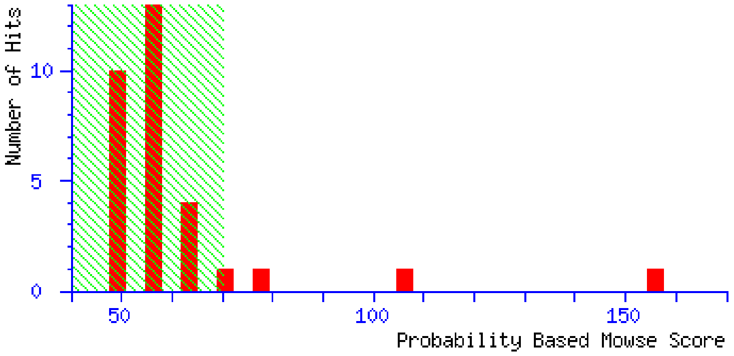
Calculated Mr: **40643** Calculated p*I*: **8.32**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 M**AAAISAAVS LPSSK**SSSLL TKISSVSPQR IFLKKSTVCY RRVVSVKAQV
51 TTDTTEAPPV KVVKESKK**QE EGIVVNK**FKP K**NPYTGR**CLL NTKITGDDAP
101 GETWHIVFTT EGEVPYR**EGQ SIGVIPEGID KNGKPHK**LR**L YSIASSAIGD**
151 **FGDSK**TVSLC VKRLVYTNDG GEIVK**GVCSN FLCDLKPGDE AKITGPVGKE**
201 **MLMPK**DPNAT IIMLGTGTGI APFRSFLWK**M FFEEHEDYK**F NGLAWLFLGV
251 PTSSSLLYKE EFEKMKEKNP DNFR**LDFAVS R**EQTNEKGEK **MYIQTRMAEY**
301 **AEELWELLKK DNTFVYMCGL K**GMEKGIDDI MVSLAAK**DGI DWLEYKK**QLK
351 **RSEQWNVEVY**

Matched peptides information:

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
2 - 15	1272.6370	1271.6297	1271.7085	-62	0	M.AAAISAAVSLPSSK.S	
69 - 77	1015.5140	1014.5067	1014.5346	-27	0	K.QEEGIVVNK.F	
82 - 87	707.3896	706.3823	706.3398	60	0	K.NPYTGR.C	
118 - 131	1441.8165	1440.8092	1440.7460	44	0	R.EGQSIGVIPEGIDK.N	
132 - 137	680.4021	679.3948	679.3765	27	0	K.NGKPHK.L	
140 - 155	1630.8828	1629.8755	1629.7886	53	0	R.LYSIASSAIGDFGDSK.T	
176 - 192	1910.0109	1909.0036	1908.8710	69	0	K.GVCSNFLCDLKPGDEAK.I	
193 - 205	1400.7542	1399.7469	1399.7567	-7	1	K.ITGPVGKEMLMPK.D	
230 - 239	1374.6482	1373.6409	1373.5598	59	0	K.MFFEEHEDYK.F	
230 - 239	1390.6288	1389.6215	1389.5547	48	0	K.MFFEEHEDYK.F	Oxidation (M)
275 - 281	807.4803	806.4730	806.4286	55	0	R.LDFAVSR.E	
291 - 296	811.4411	810.4338	810.4058	35	0	K.MYIQTR.M	
291 - 296	827.4341	826.4268	826.4007	32	0	K.MYIQTR.M	Oxidation (M)
297 - 309	1640.8870	1639.8797	1639.7803	61	0	R.MAEYAEELWELLK.K	Oxidation (M)
297 - 310	1768.9945	1767.9872	1767.8753	63	1	R.MAEYAEELWELLKK.D	Oxidation (M)
311 - 321	1347.6761	1346.6688	1346.5999	51	0	K.DNTFVYMCGLK.G	
338 - 346	1138.5802	1137.5729	1137.5342	34	0	K.DGIDWLEYK.K	
338 - 347	1266.6620	1265.6547	1265.6292	20	1	K.DGIDWLEYKK.Q	
351 - 360	1309.6883	1308.6810	1308.6098	54	1	K.RSEQWNVEVY.-	

Spot No.: **186**

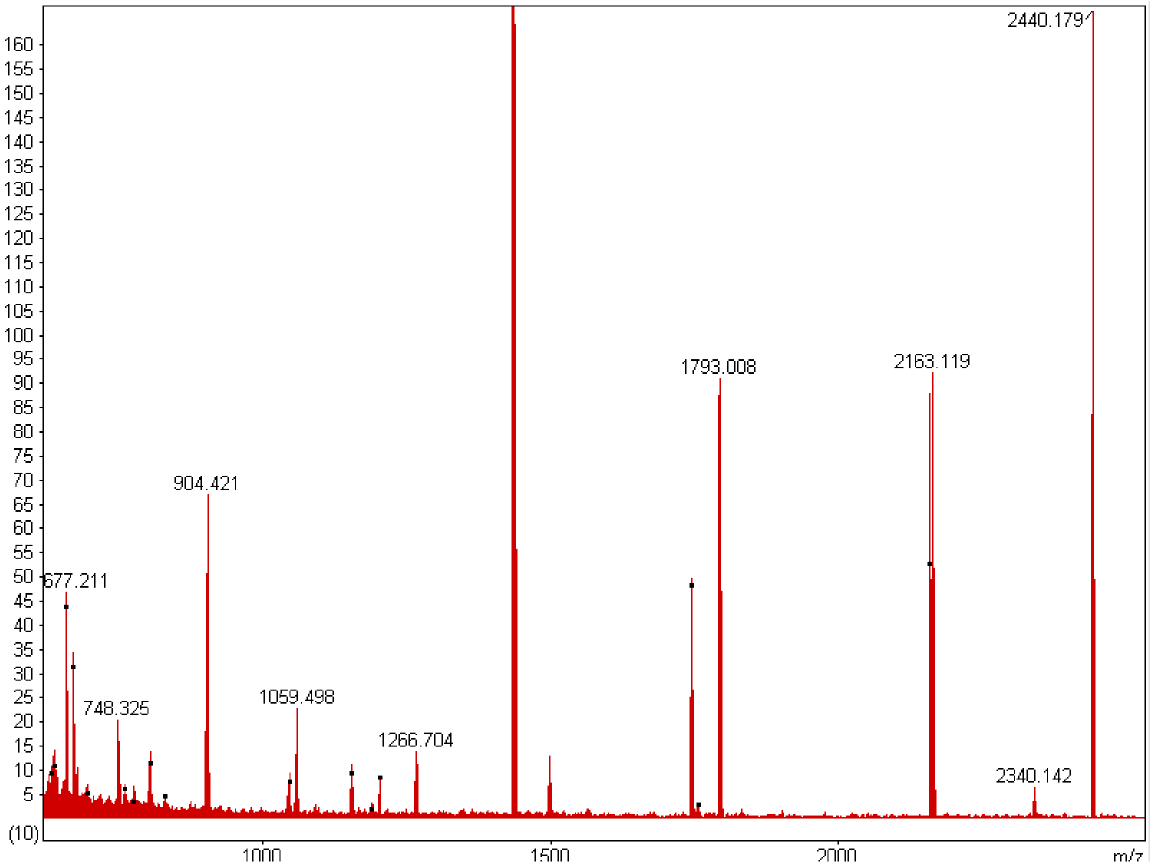
Mascot score: **85**   Sequence coverage %: **25**

NCBI accession No.: **gi| 84468402**

Matched peptides No.: **8**   Total peptides No.: **18**

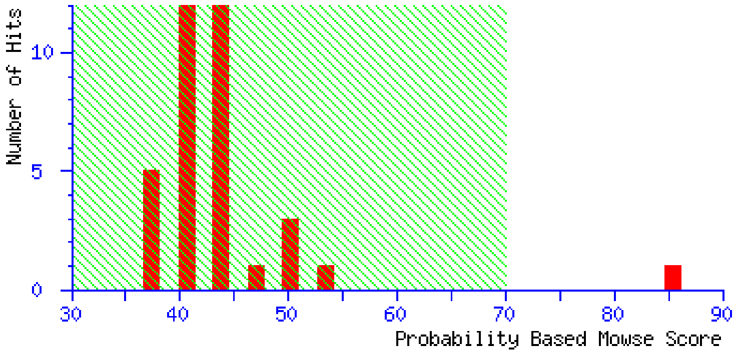
Calculated Mr: **33553**   Calculated *p*I: **4.55**

Annotated PMF **spectra:**

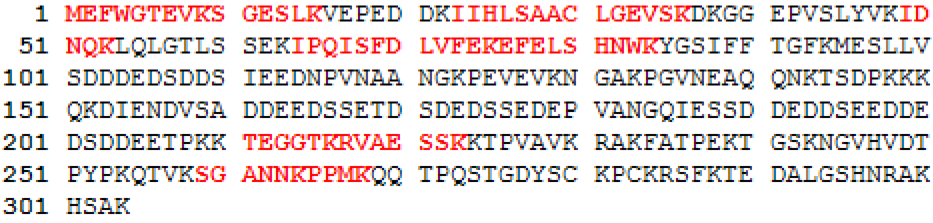


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

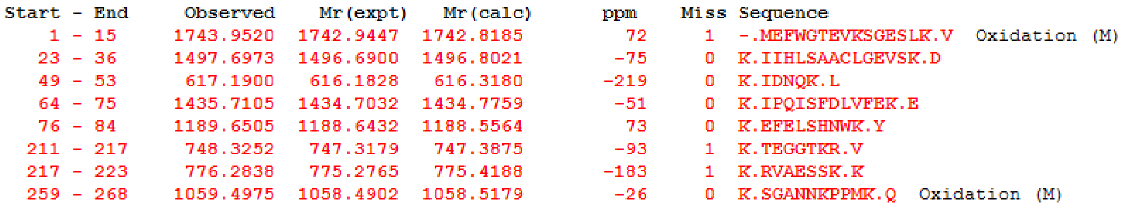


Matched peptide sequences: shown in Bold Red



1 **MEFWGTEVKS** **GESLK**VEPED DK**IIHLSAAC** **LGEVSK**DKGG EPVSLYVK**ID**
51 **NQK**LQLGTLS SEK**IPQISFD** **LVFEKEFELS** **HNWK**YGSIFF TGFKMESLLV
101 SDDDEDSDDS IEEDNPVNAA NGKPEVEVKN GAKPGVNEAQ QNKTSDPKKK
151 QKDIENDVSA DDEEDSSETD SDEDSSEDEP VANGQIESSD DEDDSEEDDE
201 DSDDEETPKK **TEGGTKRVAE** **SSK**KTPVAVK RAKFATPEKT GSKNGVHVDT
251 PYPKQTVK**SG** **ANNKPPMK**QQ TPQSTGDYSC KPCKRSFKTE DALGSHNRAK
301 HSAK

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
1 - 15	1743.9520	1742.9447	1742.8185	72	1	-.MEFWGTEVKSGESLK.V	Oxidation (M)
23 - 36	1497.6973	1496.6900	1496.8021	-75	0	K.IIHLSAACLGEVSK.D	
49 - 53	617.1900	616.1828	616.3180	-219	0	K.IDNQK.L	
64 - 75	1435.7105	1434.7032	1434.7759	-51	0	K.IPQISFDLVFEK.E	
76 - 84	1189.6505	1188.6432	1188.5564	73	0	K.EFELSHNWK.Y	
211 - 217	748.3252	747.3179	747.3875	-93	1	K.TEGGTKR.V	
217 - 223	776.2838	775.2765	775.4188	-183	1	K.RVAESSK.K	
259 - 268	1059.4975	1058.4902	1058.5179	-26	0	K.SGANNKPPMK.Q	Oxidation (M)

Spot No.: **187**

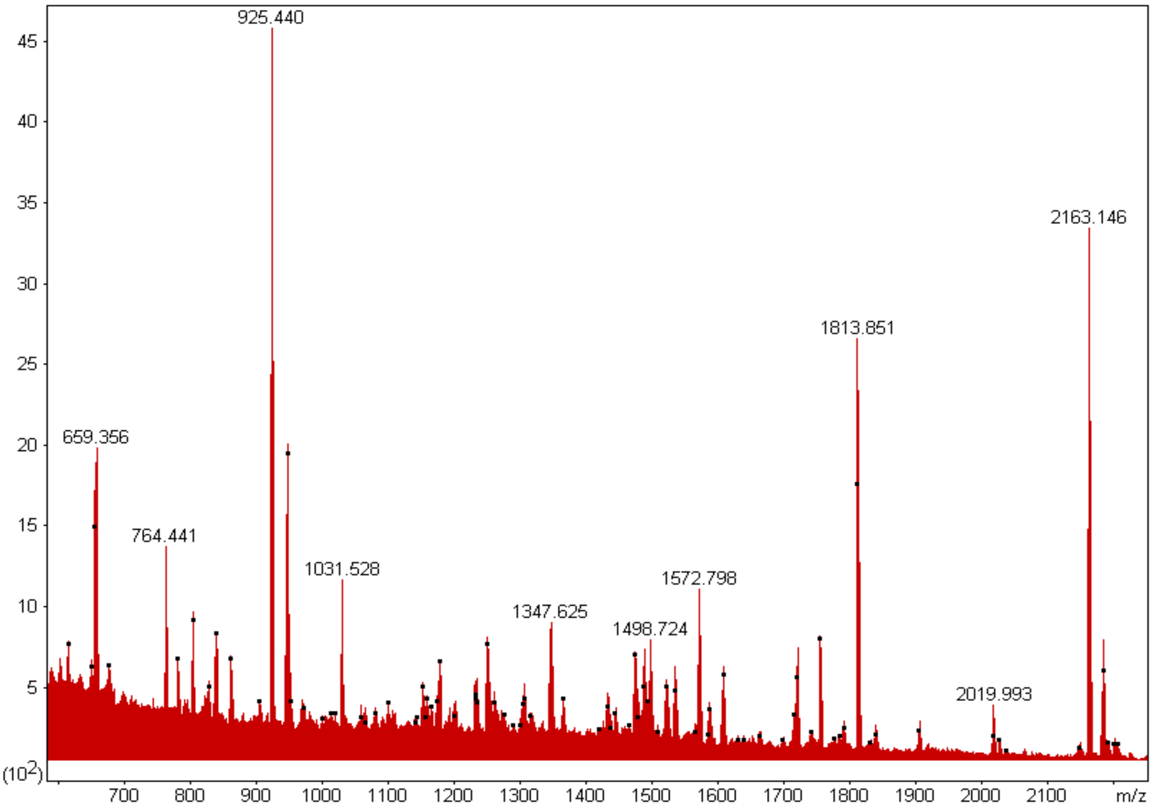
Mascot score: **88** Sequence coverage %: **29**

NCBI accession No.: **gi| 15232645**

Matched peptides No.: **8** Total peptides No.: **25**

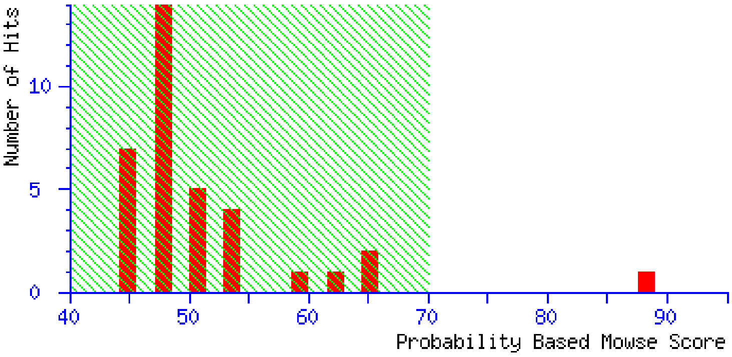
Calculated Mr: **27743** Calculated *p*I: **7.79**

Annotated PMF **spectra:**

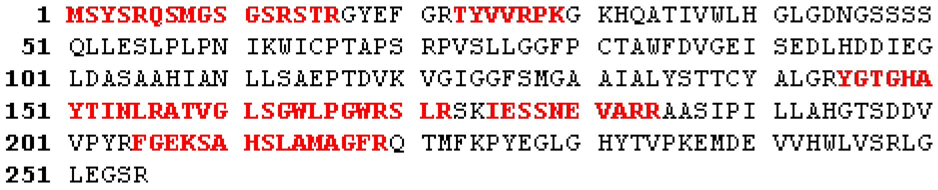


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant ($p<0.05$).

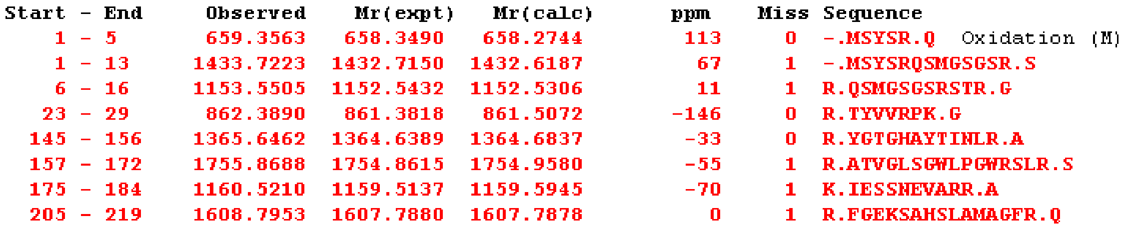


Matched peptide sequences: shown in Bold Red



1 **MSYSRQSMGS GSRSTR**GYEF GR**TYVVRPK**G KHQATIVWLH GLGDNGSSSS
51 QLLESLPLPN IKWICPTAPS RPVSLLGGFP CTAWFDVGEI SEDLHDDIEG
101 LDASAAHIAN LLSAEPTDVK VGIGGFSMGA AIALYSTTCY ALGR**YGTGHA**
151 **YTINLRATVG LSGWLPGWRS LR**SK**IESSNE VARR**AASIPI LLAHGTSDDV
201 VPYR**FGEKSA HSLAMAGFR**Q TMFKPYEGLG HYTVPKEMDE VVHWLVSRLG
251 LEGSR

Matched peptides information:



```
Start - End     Observed    Mr(expt)    Mr(calc)       ppm    Miss  Sequence
    1 - 5       659.3563    658.3490    658.2744       113      0   -.MSYSR.Q  Oxidation (M)
    1 - 13     1433.7223   1432.7150   1432.6187        67      1   -.MSYSRQSMGSGSR.S
    6 - 16     1153.5505   1152.5432   1152.5306        11      1   R.QSMGSGSRSTR.G
   23 - 29      862.3890    861.3818    861.5072      -146      0   R.TYVVRPK.G
  145 - 156    1365.6462   1364.6389   1364.6837       -33      0   R.YGTGHAYTINLR.A
  157 - 172    1755.8688   1754.8615   1754.9580       -55      1   R.ATVGLSGWLPGWRSLR.S
  175 - 184    1160.5210   1159.5137   1159.5945       -70      1   K.IESSNEVARR.A
  205 - 219    1608.7953   1607.7880   1607.7878         0      1   R.FGEKSAHSLAMAGFR.Q
```

Spot No.: **188**

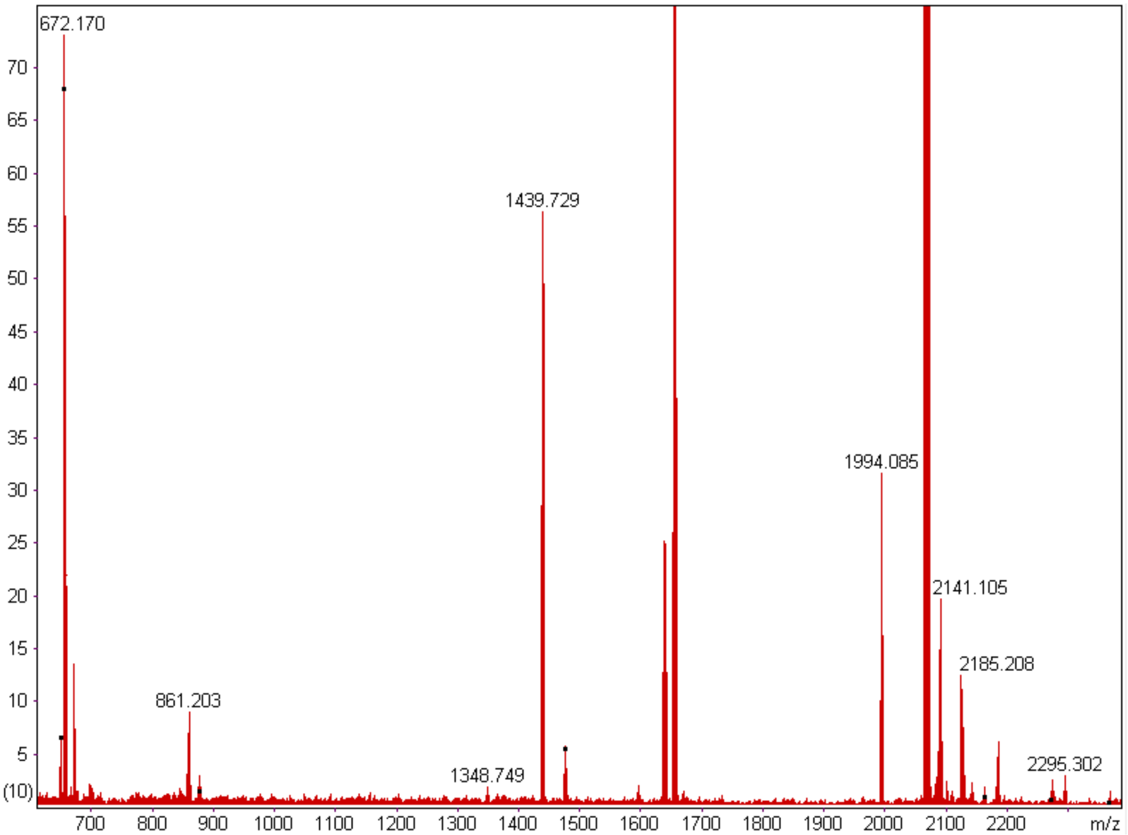
Mascot score: **85** Sequence coverage %: **51**

NCBI accession No.: **gi| 145334185**

Matched peptides No.: **6** Total peptides No.: **12**

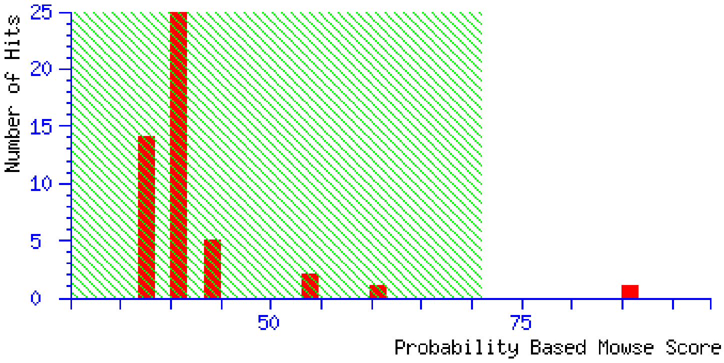
Calculated Mr: **12734** Calculated *p*I: **7.79**

Annotated PMF **spectra:**



Probability Based Mowse Score:

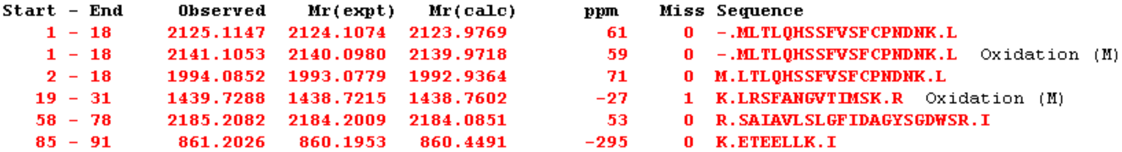
Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 **MLTLQHSSFV SFCPNDNKLR SFANGVTIMS K**RRDFSEKSN EERPILRIKV
51 PNTIVAR**SAI AVLSLGFIDA GYSGDWSR**IG VISK**ETEELL K**IAAFLVVPL
101 CIFLALSFSN DSTD

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
1 - 18	2125.1147	2124.1074	2123.9769	61	0	-.MLTLQHSSFVSFCPNDNK.L
1 - 18	2141.1053	2140.0980	2139.9718	59	0	-.MLTLQHSSFVSFCPNDNK.L Oxidation (M)
2 - 18	1994.0852	1993.0779	1992.9364	71	0	M.LTLQHSSFVSFCPNDNK.L
19 - 31	1439.7288	1438.7215	1438.7602	-27	1	K.LRSFANGVTIMSK.R Oxidation (M)
58 - 78	2185.2082	2184.2009	2184.0851	53	0	R.SAIAVLSLGFIDAGYSGDWSR.I
85 - 91	861.2026	860.1953	860.4491	-295	0	K.ETEELLK.I

Spot No.: **189**

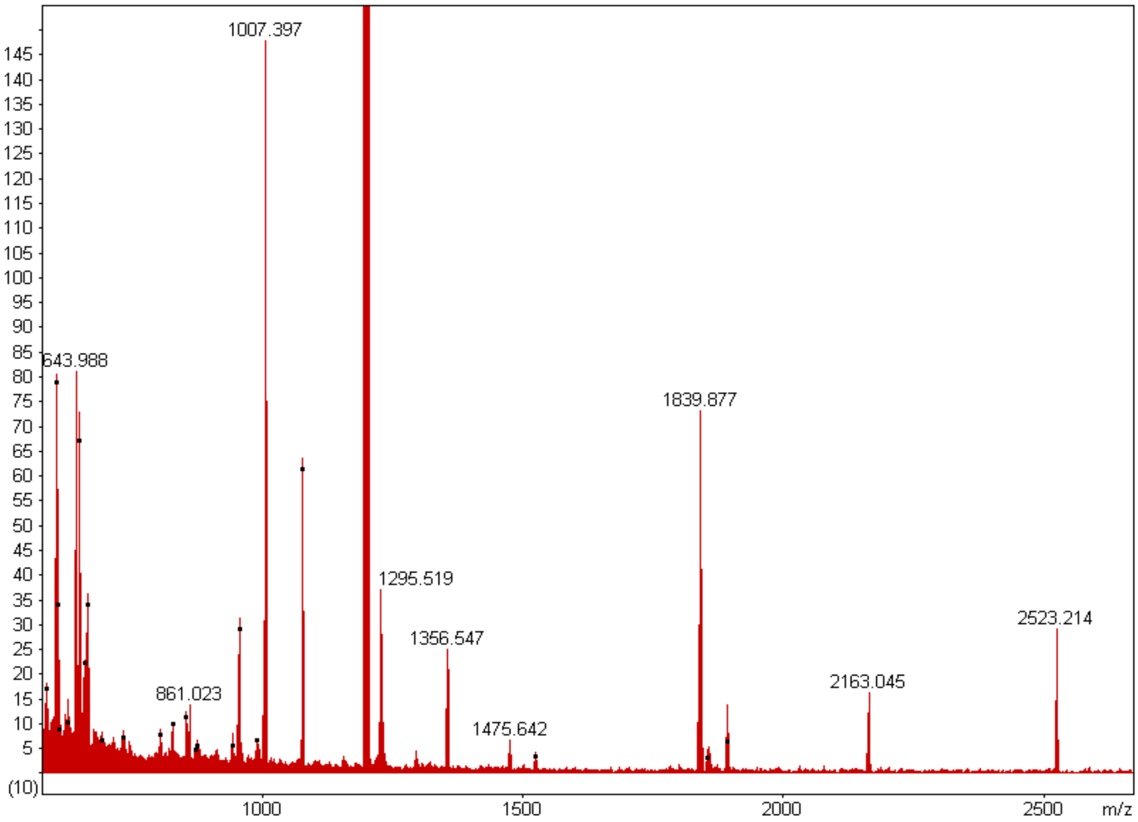
Mascot score: **89**　　Sequence coverage %: **32**

NCBI accession No.: **gi| 15223288**

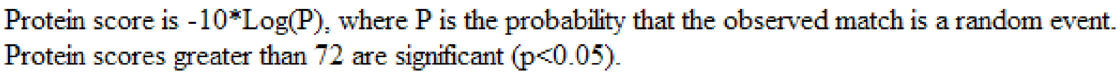
Matched peptides No.: **9**　　Total peptides No.: **27**

Calculated Mr: **24640**　　Calculated *p*I: **5.73**

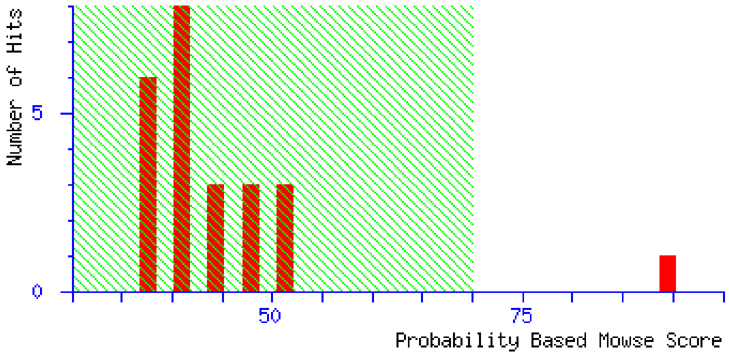
Annotated PMF **spectra:**



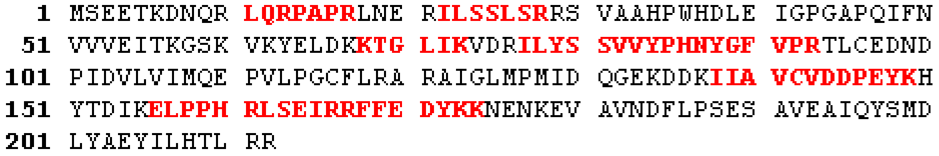
Probability Based Mowse Score:



Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

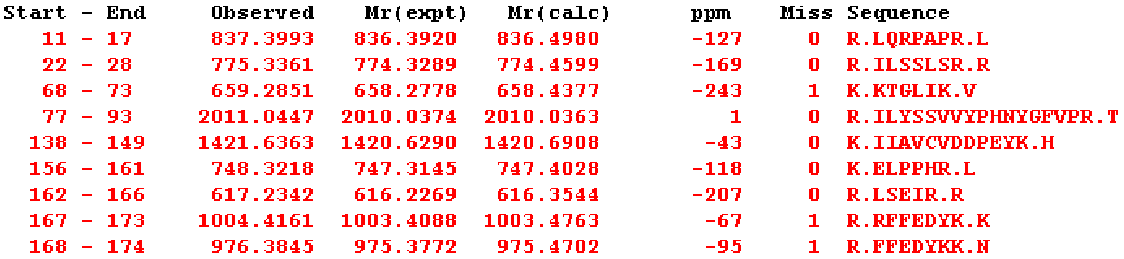


Matched peptide sequences: shown in Bold Red



```
  1 MSEETKDNQR LQRPAPRLNE RILSSLSRRS VAAHPWHDLE IGPGAPQIFN
 51 VVVEITKGSK VKYELDKKTG LIKVDRILYS SVVYPHNYGF VPRTLCEDND
101 PIDVLVIMQE PVLPGCFLRA RAIGLMPMID QGEKDDKIIA VCVDDPEYKH
151 YTDIKELPPH RLSEIRRFFE DYKKNENKEV AVNDFLPSES AVEAIQYSMD
201 LYAEYILHTL RR
```

Matched peptides information:



```
Start - End      Observed    Mr(expt)    Mr(calc)       ppm    Miss Sequence
   11 - 17       837.3993    836.3920    836.4980      -127      0  R.LQRPAPR.L
   22 - 28       775.3361    774.3289    774.4599      -169      0  R.ILSSLSR.R
   68 - 73       659.2851    658.2778    658.4377      -243      1  K.KTGLIK.V
   77 - 93      2011.0447   2010.0374   2010.0363         1      0  R.ILYSSVVYPHNYGFVPR.T
  138 - 149     1421.6363   1420.6290   1420.6908       -43      0  K.IIAVCVDDPEYK.H
  156 - 161      748.3218    747.3145    747.4028      -118      0  K.ELPPHR.L
  162 - 166      617.2342    616.2269    616.3544      -207      0  R.LSEIR.R
  167 - 173     1004.4161   1003.4088   1003.4763       -67      1  R.RFFEDYK.K
  168 - 174      976.3845    975.3772    975.4702       -95      1  R.FFEDYKK.N
```

Spot No.: **190**

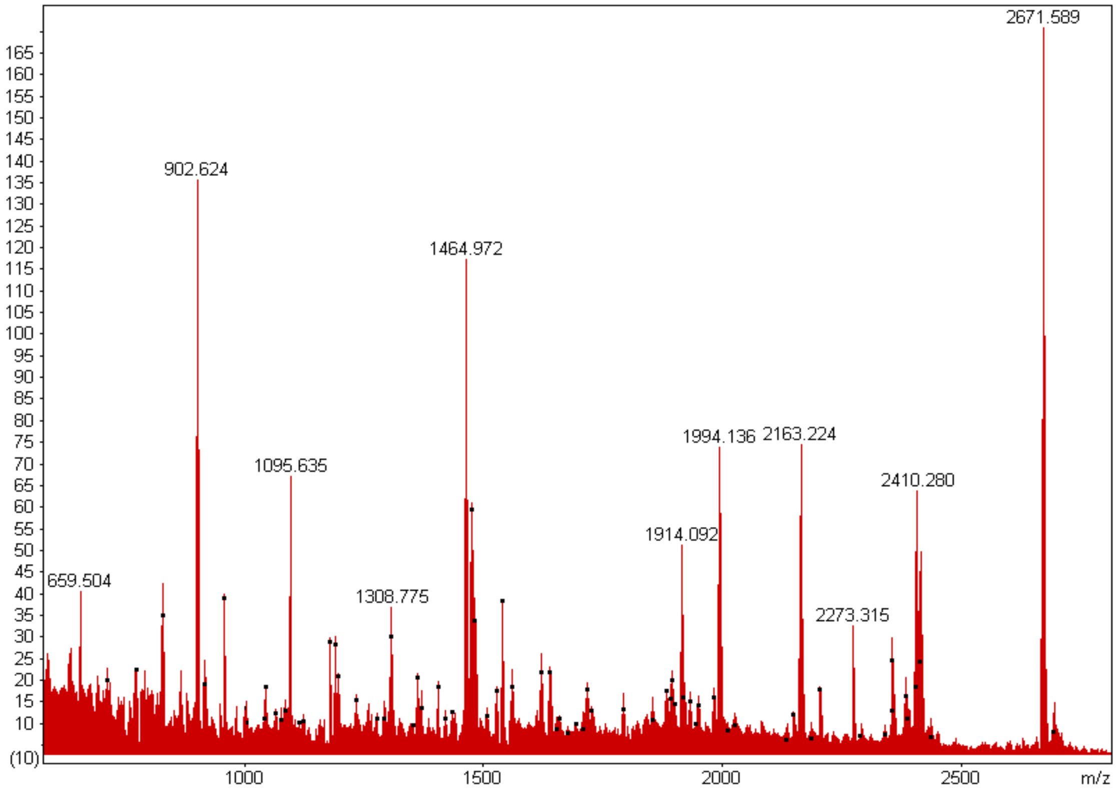
Mascot score: **109**   Sequence coverage %: **50**

NCBI accession No.: **gi| 18391006**

Matched peptides No.: **11**   Total peptides No.: **43**

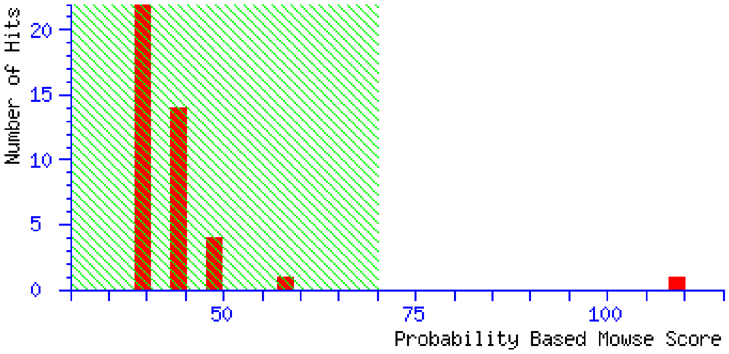
Calculated Mr: **20049**   Calculated *p*I: **5.37**

Annotated PMF **spectra:**

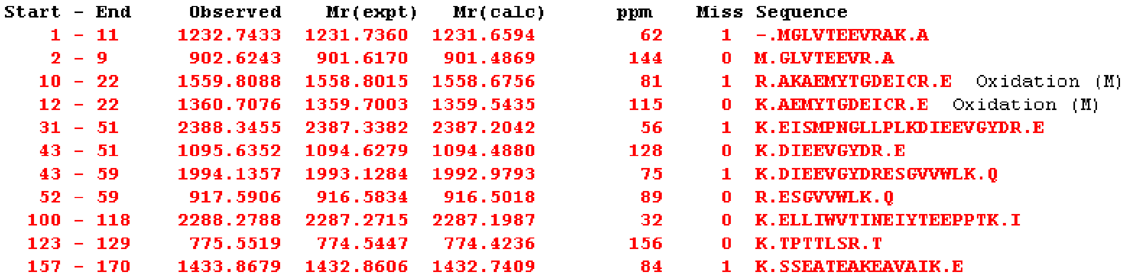


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

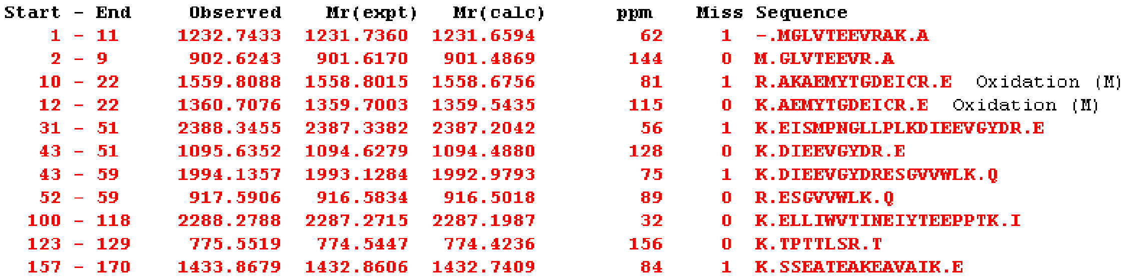


Matched peptide sequences: shown in Bold Red



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss  Sequence
    1 - 11     1232.7433  1231.7360  1231.6594       62     1   -.MGLVTEEVRAK.A
    2 - 9       902.6243   901.6170   901.4869      144     0   M.GLVTEEVR.A
   10 - 22     1559.8088  1558.8015  1558.6756       81     1   R.AKAEMYTGDEICR.E  Oxidation (M)
   12 - 22     1360.7076  1359.7003  1359.5435      115     0   K.AEMYTGDEICR.E  Oxidation (M)
   31 - 51     2388.3455  2387.3382  2387.2042       56     1   K.EISMPNGLLPLKDIEEVGYDR.E
   43 - 51     1095.6352  1094.6279  1094.4880      128     0   K.DIEEVGYDR.E
   43 - 59     1994.1357  1993.1284  1992.9793       75     1   K.DIEEVGYDRESGVVWLK.Q
   52 - 59      917.5906   916.5834   916.5018       89     0   R.ESGVVWLK.Q
  100 - 118    2288.2788  2287.2715  2287.1987       32     0   K.ELLIWVTINEIYTEEPPTK.I
  123 - 129     775.5519   774.5447   774.4236      156     0   K.TPTTLSR.T
  157 - 170    1433.8679  1432.8606  1432.7409       84     1   K.SSEATEAKEAVAIK.E
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss  Sequence
    1 - 11     1232.7433  1231.7360  1231.6594       62     1   -.MGLVTEEVRAK.A
    2 - 9       902.6243   901.6170   901.4869      144     0   M.GLVTEEVR.A
   10 - 22     1559.8088  1558.8015  1558.6756       81     1   R.AKAEMYTGDEICR.E  Oxidation (M)
   12 - 22     1360.7076  1359.7003  1359.5435      115     0   K.AEMYTGDEICR.E  Oxidation (M)
   31 - 51     2388.3455  2387.3382  2387.2042       56     1   K.EISMPNGLLPLKDIEEVGYDR.E
   43 - 51     1095.6352  1094.6279  1094.4880      128     0   K.DIEEVGYDR.E
   43 - 59     1994.1357  1993.1284  1992.9793       75     1   K.DIEEVGYDRESGVVWLK.Q
   52 - 59      917.5906   916.5834   916.5018       89     0   R.ESGVVWLK.Q
  100 - 118    2288.2788  2287.2715  2287.1987       32     0   K.ELLIWVTINEIYTEEPPTK.I
  123 - 129     775.5519   774.5447   774.4236      156     0   K.TPTTLSR.T
  157 - 170    1433.8679  1432.8606  1432.7409       84     1   K.SSEATEAKEAVAIK.E
```

Spot No.: **191**

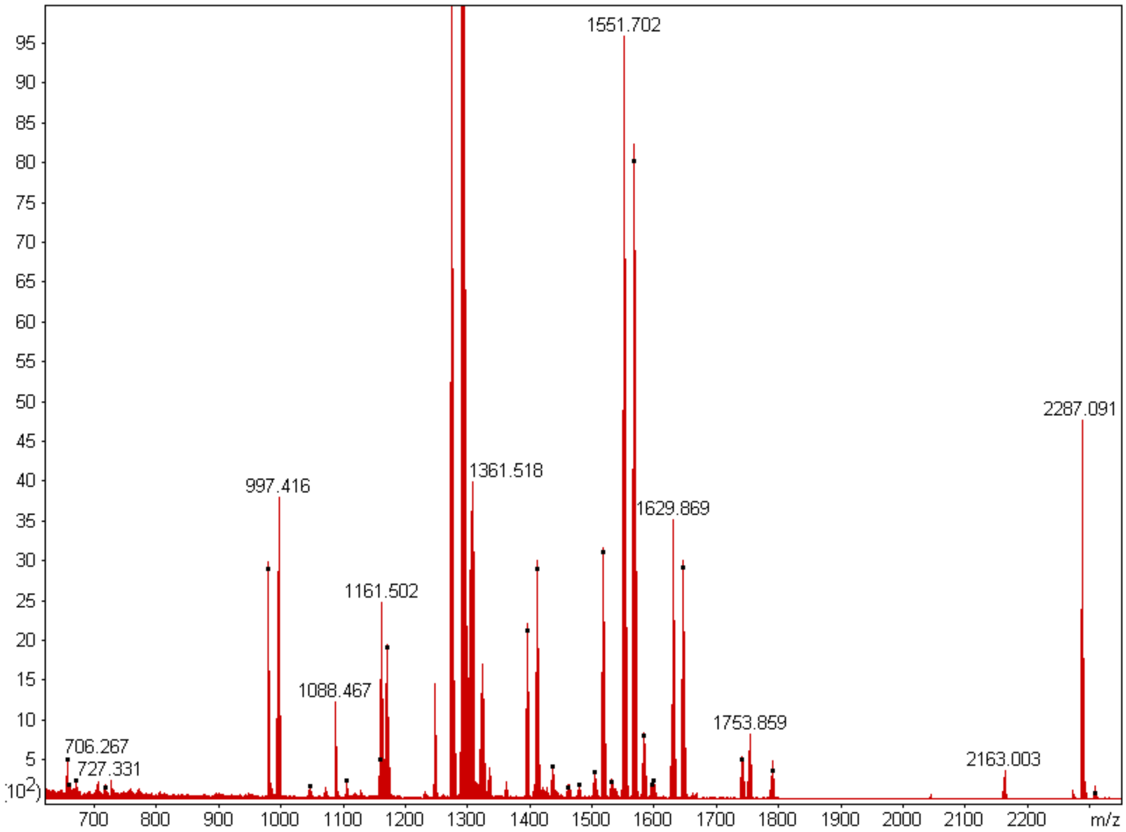
Mascot score: **81** Sequence coverage %: **27**

NCBI accession No.: **gi| 312281797**

Matched peptides No.: **10** Total peptides No.: **29**

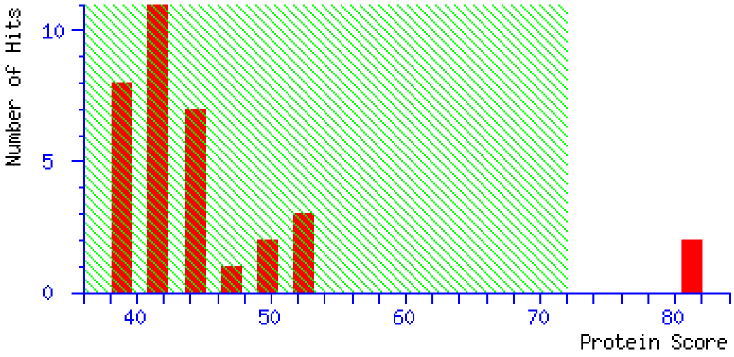
Calculated Mr: **29391** Calculated *p*I: **8.94**

Annotated PMF **spectra:**

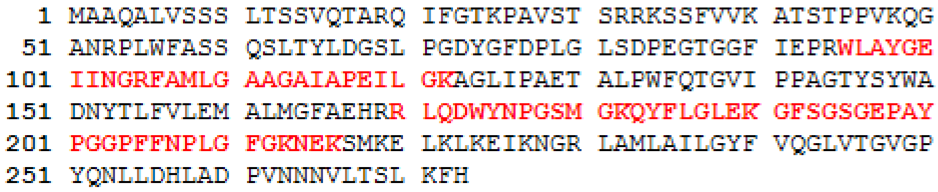


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).

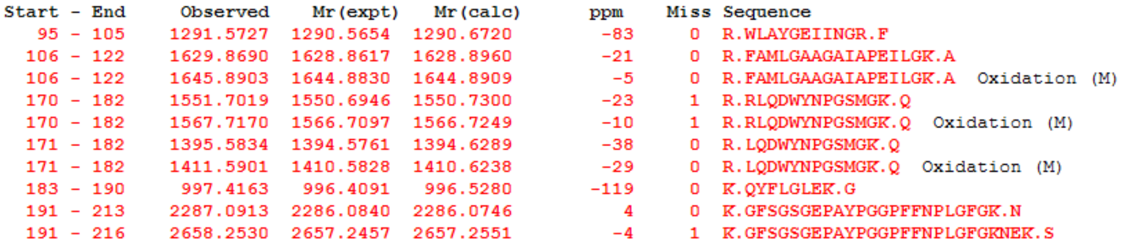


Matched peptide sequences: shown in Bold Red



```
  1 MAAQALVSSS LTSSVQTARQ IFGTKPAVST SRRKSSFVVK ATSTPPVKQG
 51 ANRPLWFASS QSLTYLDGSL PGDYGFDPLG LSDPEGTGGF IEPRWLAYGE
101 IINGRFAMLG AAGAIAPEIL GKAGLIPAET ALPWFQTGVI PPAGTYSYWA
151 DNYTLFVLEM ALMGFAEHRR LQDWYNPGSM GKQYFLGLEK GFSGSGEPAY
201 PGGPFFNPLG FGKNEKSMKE LKLKEIKNGR LAMLAILGYF VQGLVTGVGP
251 YQNLLDHLAD PVNNNVLTSL KFH
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm   Miss Sequence
   95 - 105    1291.5727  1290.5654  1290.6720      -83     0  R.WLAYGEIINGR.F
  106 - 122    1629.8690  1628.8617  1628.8960      -21     0  R.FAMLGAAGAIAPEILGK.A
  106 - 122    1645.8903  1644.8830  1644.8909       -5     0  R.FAMLGAAGAIAPEILGK.A  Oxidation (M)
  170 - 182    1551.7019  1550.6946  1550.7300      -23     1  R.RLQDWYNPGSMGK.Q
  170 - 182    1567.7170  1566.7097  1566.7249      -10     1  R.RLQDWYNPGSMGK.Q  Oxidation (M)
  171 - 182    1395.5834  1394.5761  1394.6289      -38     0  R.LQDWYNPGSMGK.Q
  171 - 182    1411.5901  1410.5828  1410.6238      -29     0  R.LQDWYNPGSMGK.Q  Oxidation (M)
  183 - 190     997.4163   996.4091   996.5280     -119     0  K.QYFLGLEK.G
  191 - 213    2287.0913  2286.0840  2286.0746        4     0  K.GFSGSGEPAYPGGPFFNPLGFGK.N
  191 - 216    2658.2530  2657.2457  2657.2551       -4     1  K.GFSGSGEPAYPGGPFFNPLGFGKNEK.S
```

Spot No.: **192**

Mascot score: **94**

Sequence coverage %: **35**

NCBI accession No.: **gi| 312282625**

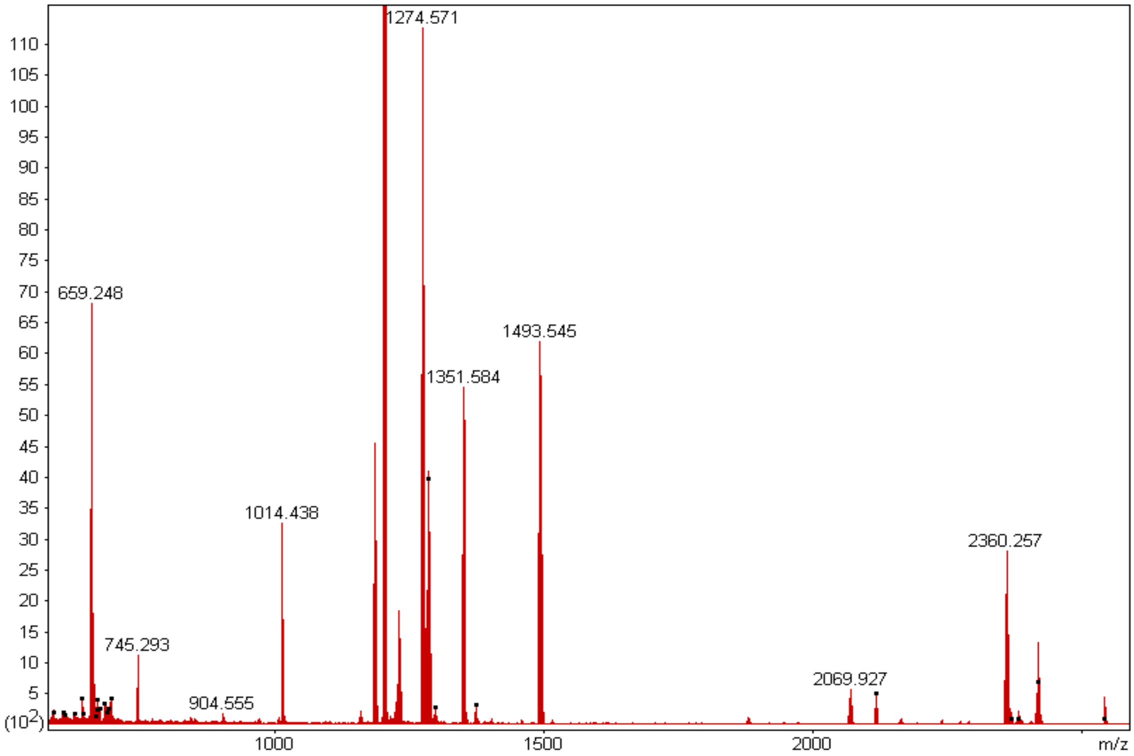
Matched peptides No.: **8**

Total peptides No.: **16**

Calculated Mr: **28229**

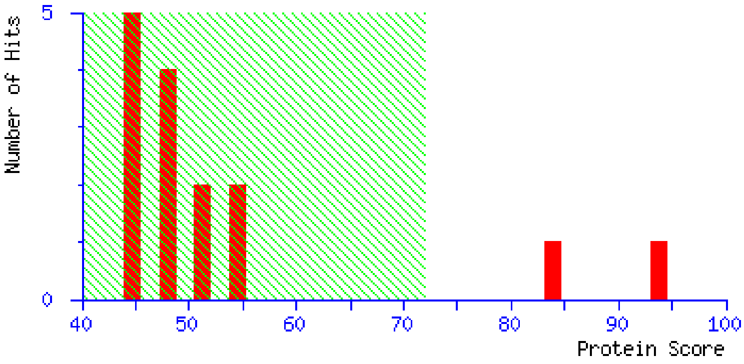
Calculated *p*I: **6.84**

Annotated PMF **spectra:**

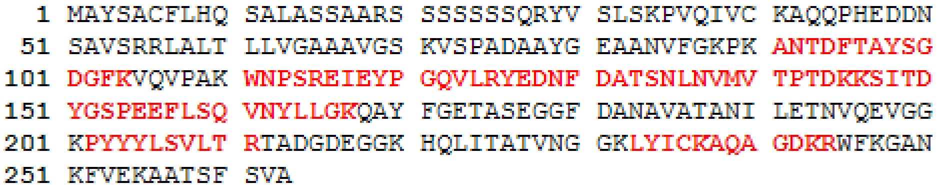


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

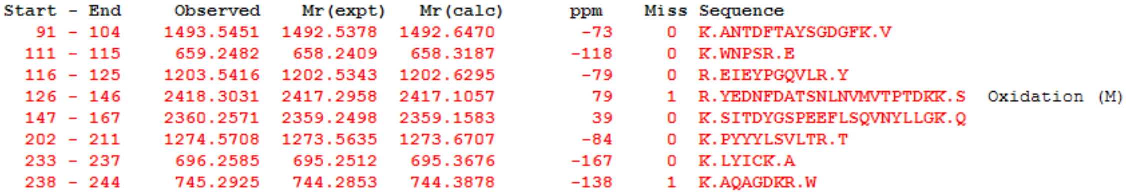


Matched peptide sequences: shown in **Bold Red**



```
  1 MAYSACFLHQ SALASSAARS SSSSSSQRYV SLSKPVQIVC KAQQPHEDDN
 51 SAVSRRLALT LLVGAAAVGS KVSPADAAYG EAANVFGKPK ANTDFTAYSG
101 DGFKVQVPAK WNPSREIEYP GQVLRYEDNF DATSNLNVMV TPTDKKSITD
151 YGSPEEFLSQ VNYLLGKQAY FGETASEGGF DANAVATANI LETNVQEVGG
201 KPYYYLSVLT RTADGDEGGK HQLITATVNG GKLYICKAQA GDKRWFKGAN
251 KFVEKAATSF SVA
```

Matched peptides information:



```
Start - End     Observed    Mr(expt)   Mr(calc)      ppm    Miss Sequence
   91 - 104    1493.5451  1492.5378  1492.6470       -73     0  K.ANTDFTAYSGDGFK.V
  111 - 115     659.2482   658.2409   658.3187      -118     0  K.WNPSR.E
  116 - 125    1203.5416  1202.5343  1202.6295       -79     0  R.EIEYPGQVLR.Y
  126 - 146    2418.3031  2417.2958  2417.1057        79     1  R.YEDNFDATSNLNVMVTPTDKK.S  Oxidation (M)
  147 - 167    2360.2571  2359.2498  2359.1583        39     0  K.SITDYGSPEEFLSQVNYLLGK.Q
  202 - 211    1274.5708  1273.5635  1273.6707       -84     0  K.PYYYLSVLTR.T
  233 - 237     696.2585   695.2512   695.3676      -167     0  K.LYICK.A
  238 - 244     745.2925   744.2853   744.3878      -138     1  K.AQAGDKR.W
```

Spot No.: **193**

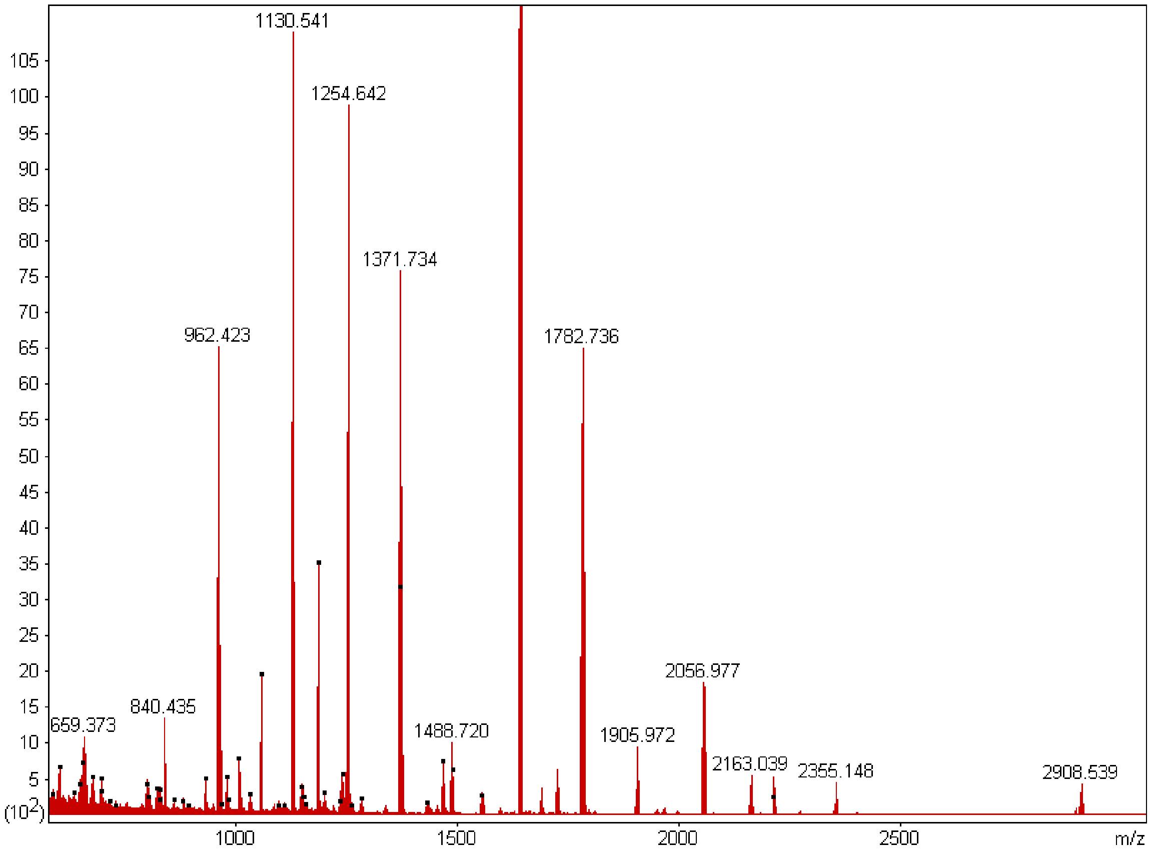
Mascot score: **81** Sequence coverage %: **37**

NCBI accession No.: **gi| 312282463**

Matched peptides No.: **10** Total peptides No.: **37**

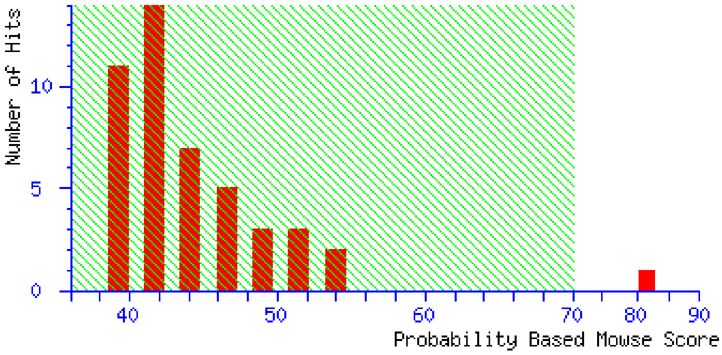
Calculated Mr: **30515** Calculated *p*I: **7.63**

Annotated PMF **spectra:**

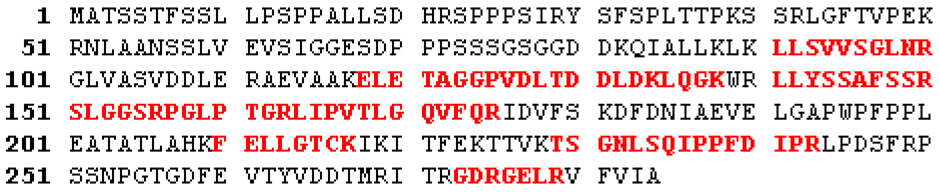


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

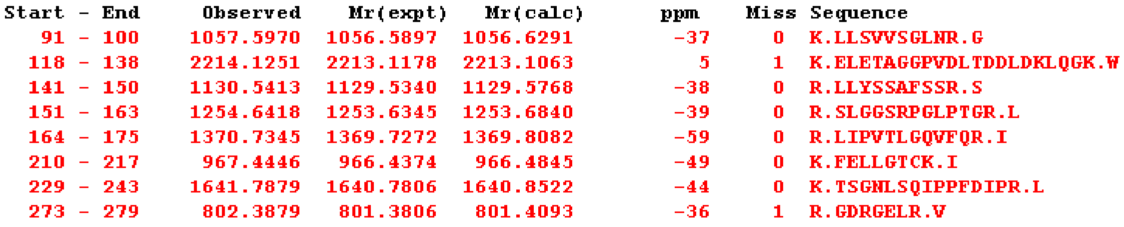


Matched peptide sequences: shown in Bold Red



1 MATSSTFSSL LPSPPALLSD HRSPPPSIRY SFSPLTTPKS SRLGFTVPEK
51 RNLAANSSLV EVSIGGESDP PPSSSGSGGD DKQIALLKLK **LLSVVSGLNR**
101 GLVASVDDLE RAEVAAK**ELE** **TAGGPVDLTD** **DLDKLQGK**WR **LLYSSAFSSR**
151 **SLGGSRPGLP** **TGRLIPVTLG** **QVFQR**IDVFS KDFDNIAEVE LGAPWPFPPL
201 EATATLAHK**F** **ELLGTCK**IKI TFEKTTVK**TS** **GNLSQIPPFD** **IPR**LPDSFRP
251 SSNPGTGDFE VTYVDDTMRI TR**GDRGELR**V FVIA

Matched peptides information:



```
Start - End      Observed    Mr(expt)    Mr(calc)       ppm    Miss  Sequence
   91 - 100     1057.5970   1056.5897   1056.6291       -37      0   K.LLSVVSGLNR.G
  118 - 138     2214.1251   2213.1178   2213.1063         5      1   K.ELETAGGPVDLTDDLDKLQGK.W
  141 - 150     1130.5413   1129.5340   1129.5768       -38      0   R.LLYSSAFSSR.S
  151 - 163     1254.6418   1253.6345   1253.6840       -39      0   R.SLGGSRPGLPTGR.L
  164 - 175     1370.7345   1369.7272   1369.8082       -59      0   R.LIPVTLGQVFQR.I
  210 - 217      967.4446    966.4374    966.4845       -49      0   K.FELLGTCK.I
  229 - 243     1641.7879   1640.7806   1640.8522       -44      0   K.TSGNLSQIPPFDIPR.L
  273 - 279      802.3879    801.3806    801.4093       -36      1   R.GDRGELR.V
```

Spot No.: **194**

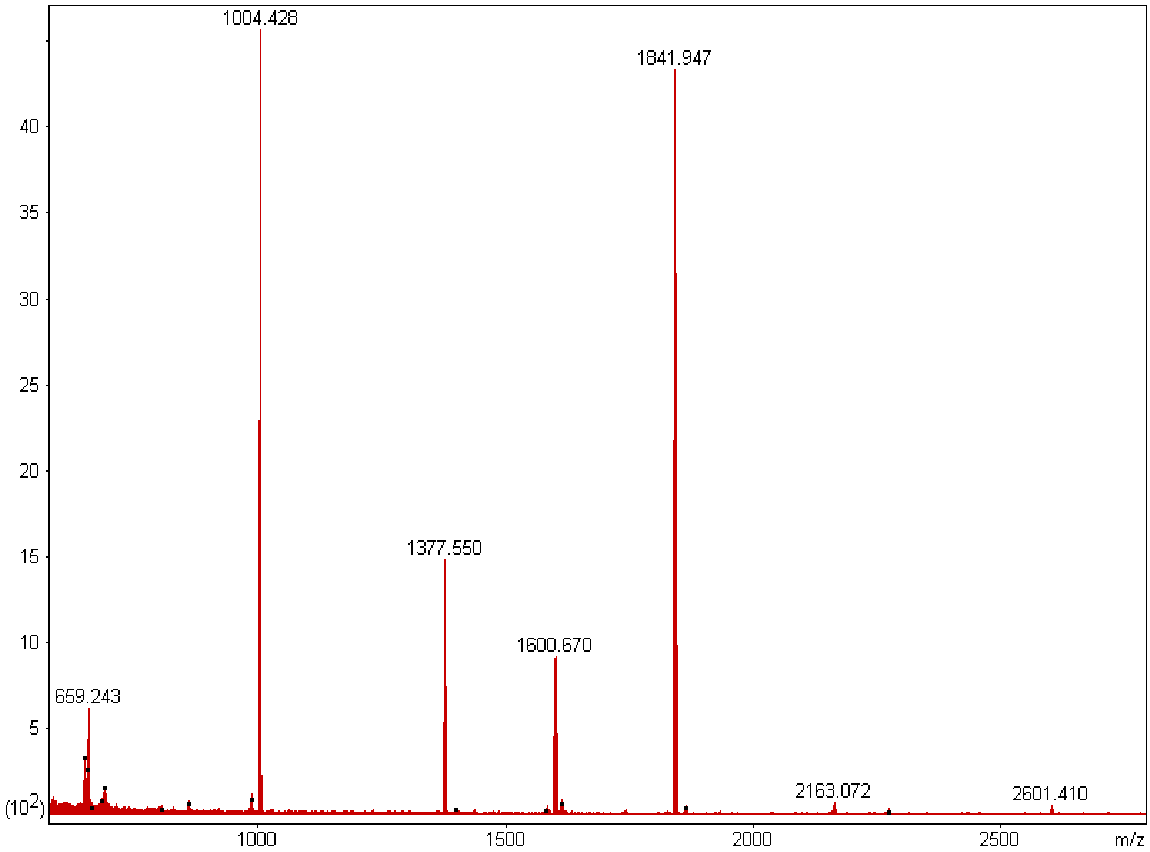
Mascot score: **81** Sequence coverage %: **29**

NCBI accession No.: **gi| 148515008**

Matched peptides No.: **6** Total peptides No.: **13**

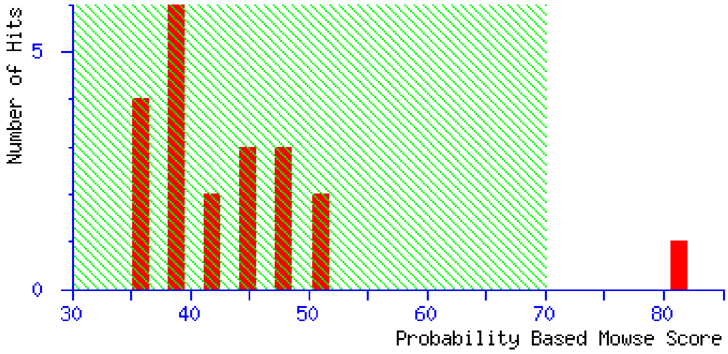
Calculated Mr: **25544** Calculated *p*I: **8.77**

Annotated PMF **spectra:**

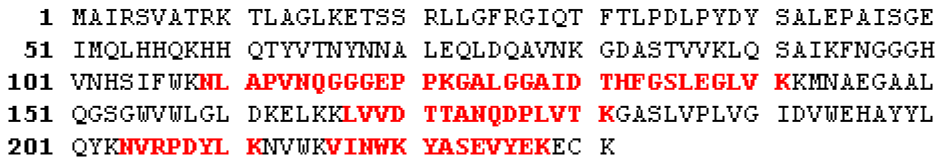


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

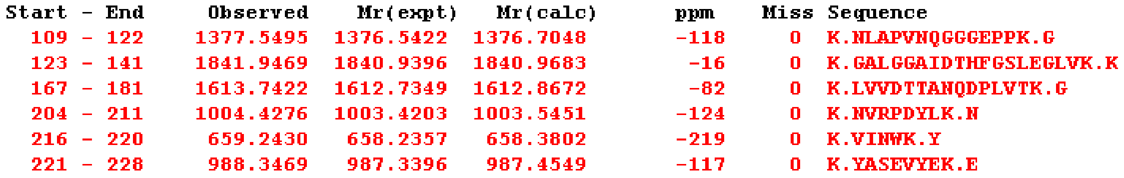


Matched peptide sequences: shown in Bold Red



```
  1 MAIRSVATRK TLAGLKETSS RLLGFRGIQT FTLPDLPYDY SALEPAISGE
 51 IMQLHHQKHH QTYVTNYNNA LEQLDQAVNK GDASTVVKLQ SAIKFNGGGH
101 VNHSIFWKNL APVNQGGGEP PKGALGGAID THFGSLEGLV KKMNAEGAAL
151 QGSGWVWLGL DKELKKLVVD TTANQDPLVT KGASLVPLVG IDVWEHAYYL
201 QYKNVRPDYL KNVWKVINWK YASEVYEKEC K
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
  109 - 122    1377.5495  1376.5422  1376.7048     -118      0  K.NLAPVNQGGGEPPK.G
  123 - 141    1841.9469  1840.9396  1840.9683      -16      0  K.GALGGAIDTHFGSLEGLVK.K
  167 - 181    1613.7422  1612.7349  1612.8672      -82      0  K.LVVDTTANQDPLVTK.G
  204 - 211    1004.4276  1003.4203  1003.5451     -124      0  K.NVRPDYLK.N
  216 - 220     659.2430   658.2357   658.3802     -219      0  K.VINWK.Y
  221 - 228     988.3469   987.3396   987.4549     -117      0  K.YASEVYEK.E
```

Spot No.: **195**

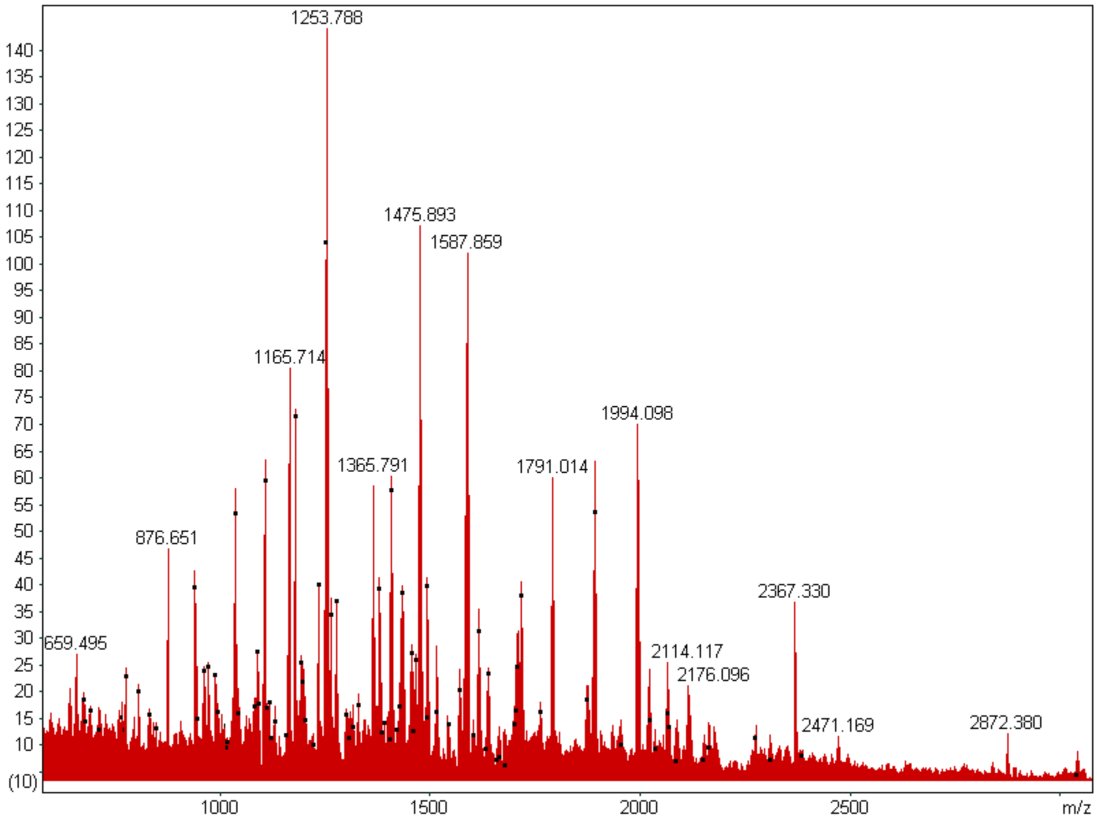
Mascot score: **98** Sequence coverage %: **50**

NCBI accession No.: **gi| 1405561**

Matched peptides No.: **11** Total peptides No.: **57**

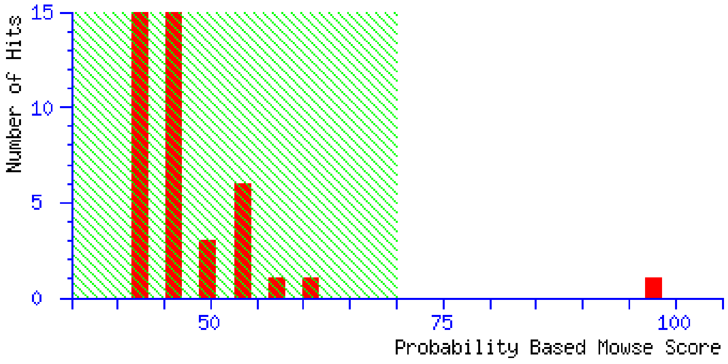
Calculated Mr: **24147** Calculated p*I*: **9.23**

Annotated PMF **spectra:**

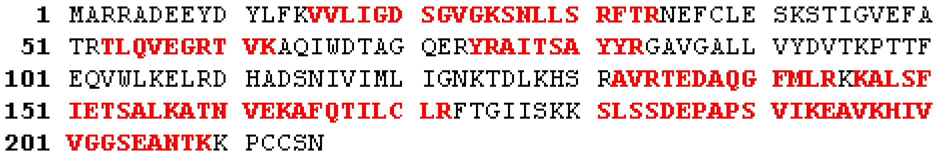


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

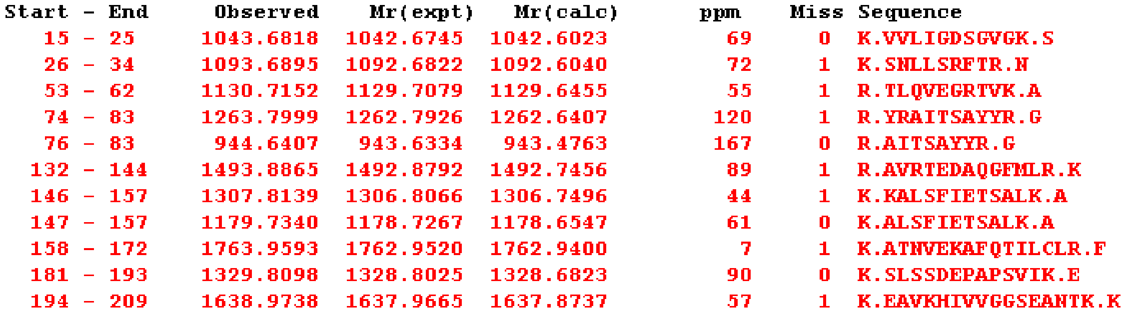


Matched peptide sequences: shown in Bold Red



```
  1 MARRADEEYD YLFKVVLIGD SGVGKSNLLS RFTRNEFCLE SKSTIGVEFA
 51 TRTLQVEGRT VKAQIWDTAG QERYRAITSA YYRGAVGALL VYDVTKPTTF
101 EQVWLKELRD HADSNIVIML IGNKTDLKHS RAVRTEDAQG FMLRKKALSF
151 IETSALKATN VEKAFQTILC LRFTGIISKK SLSSDEPAPS VIKEAVKHIV
201 VGGSEANTKK PCCSN
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss  Sequence
   15 - 25     1043.6818  1042.6745  1042.6023       69     0   K.VVLIGDSGVGK.S
   26 - 34     1093.6895  1092.6822  1092.6040       72     1   K.SNLLSRFTR.N
   53 - 62     1130.7152  1129.7079  1129.6455       55     1   R.TLQVEGRTVK.A
   74 - 83     1263.7999  1262.7926  1262.6407      120     1   R.YRAITSAYYR.G
   76 - 83      944.6407   943.6334   943.4763      167     0   R.AITSAYYR.G
  132 - 144    1493.8865  1492.8792  1492.7456       89     1   R.AVRTEDAQGFMLR.K
  146 - 157    1307.8139  1306.8066  1306.7496       44     1   K.KALSFIETSALK.A
  147 - 157    1179.7340  1178.7267  1178.6547       61     0   K.ALSFIETSALK.A
  158 - 172    1763.9593  1762.9520  1762.9400        7     1   K.ATNVEKAFQTILCLR.F
  181 - 193    1329.8098  1328.8025  1328.6823       90     0   K.SLSSDEPAPSVIK.E
  194 - 209    1638.9738  1637.9665  1637.8737       57     1   K.EAVKHIVVGGSEANTK.K
```

Spot No.: **196**

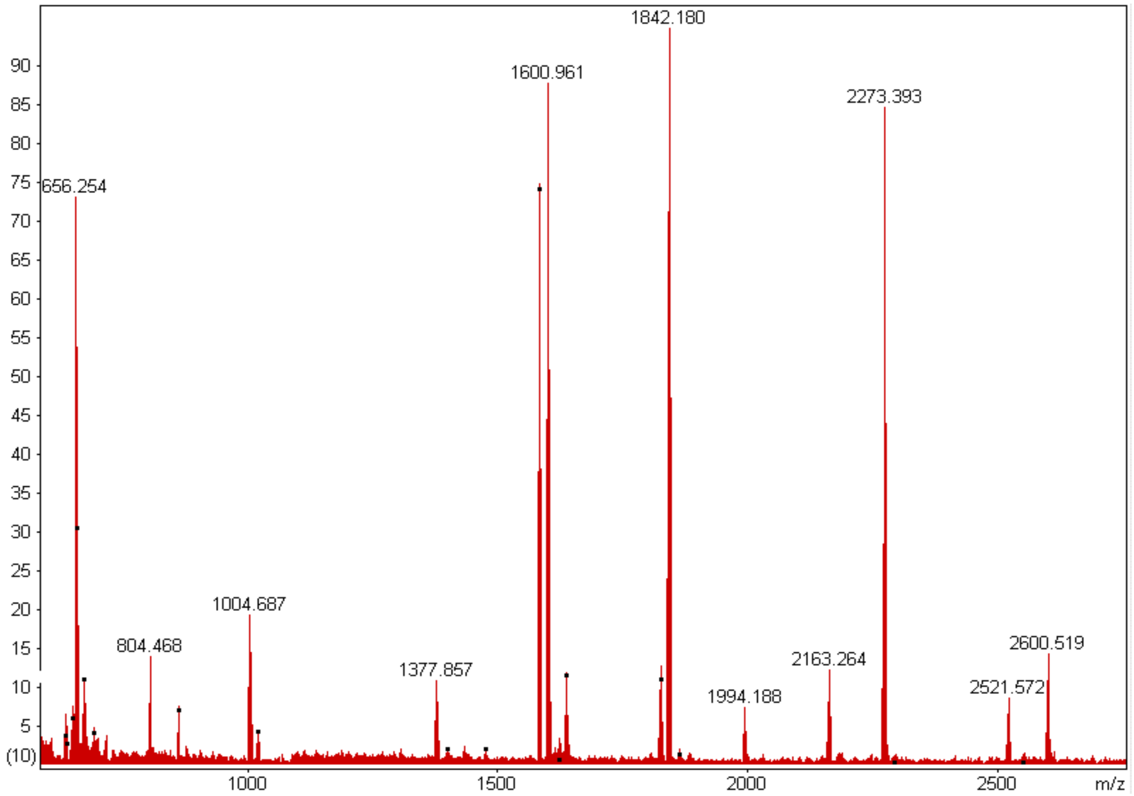
Mascot score: **89**   Sequence coverage %: **39**

NCBI accession No.: **gi| 148515008**

Matched peptides No.: **7**   Total peptides No.: **12**

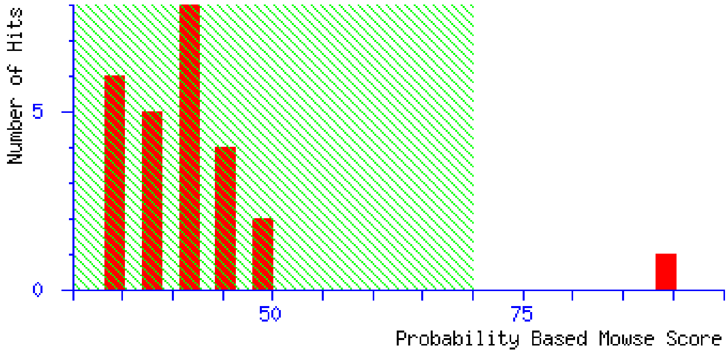
Calculated Mr: **25544**   Calculated *p*I: **8.77**

Annotated PMF **spectra:**

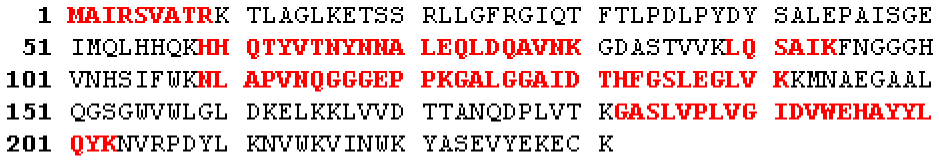


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

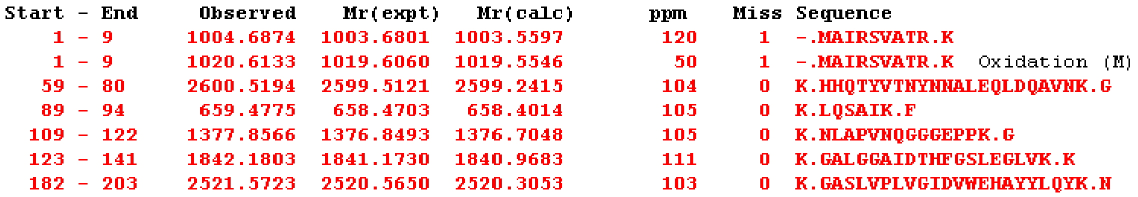


Matched peptide sequences: shown in Bold Red



1 **MAIRSVATR**K TLAGLKETSS RLLGFRGIQT FTLPDLPYDY SALEPAISGE
51 IMQLHHQK**HH QTYVTNYNNA LEQLDQAVNK** GDASTVVK**LQ SAIK**FNGGGH
101 VNHSIFWK**NL APVNQGGGEP PKGALGGAID THFGSLEGLV K**KMNAEGAAL
151 QGSGWVWLGL DKELKKLVVD TTANQDPLVT K**GASLVPLVG IDVWEHAYYL**
201 **QYK**NVRPDYL KNVWKVINWK YASEVYEKEC K

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
1 - 9	1004.6874	1003.6801	1003.5597	120	1	-.MAIRSVATR.K
1 - 9	1020.6133	1019.6060	1019.5546	50	1	-.MAIRSVATR.K Oxidation (M)
59 - 80	2600.5194	2599.5121	2599.2415	104	0	K.HHQTYVTNYNNALEQLDQAVNK.G
89 - 94	659.4775	658.4703	658.4014	105	0	K.LQSAIK.F
109 - 122	1377.8566	1376.8493	1376.7048	105	0	K.NLAPVNQGGGEPPK.G
123 - 141	1842.1803	1841.1730	1840.9683	111	0	K.GALGGAIDTHFGSLEGLVK.K
182 - 203	2521.5723	2520.5650	2520.3053	103	0	K.GASLVPLVGIDVWEHAYYLQYK.N

Spot No.: **197**

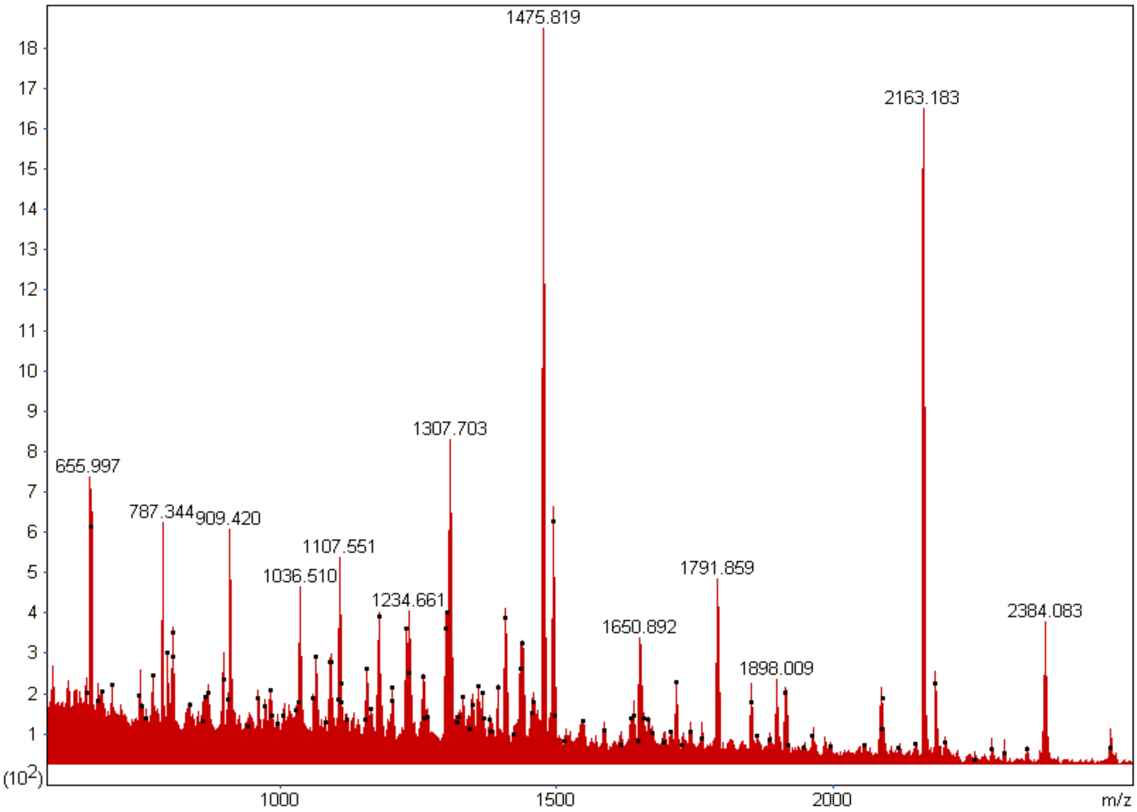
Mascot score: **88** Sequence coverage %: **42**

NCBI accession No.: **gi| 2792230**

Matched peptides No.: **8** Total peptides No.: **38**

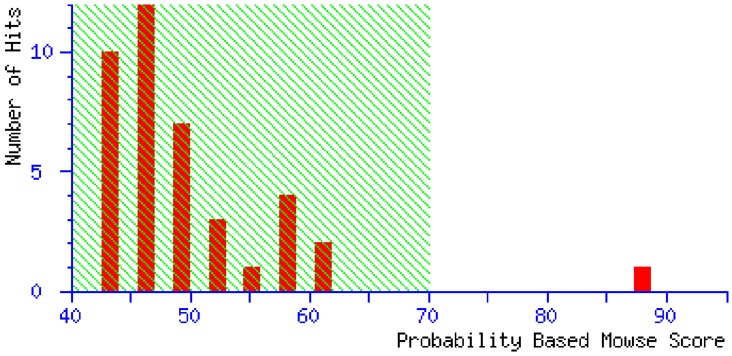
Calculated Mr: **19967** Calculated *p*I: **7.00**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 **GGWGKTTLAA NVYRNER**EKF ECHAWVSISQ TYSIKDVLK**C LSLELDLK**KE
51 IQGNIGDMDS ATLQNELYK**F LMDQK**YLIVL DDVWVPETVN DLFSIFVSNL
101 KGSRVLVTTR **IDGVAHLAFP DKRITLEPLS EKK**SWELFCK TAFPRDKNHE
151 RPTK**LTVLAQ QIVSKCEGFP LAL**

Matched peptides information:

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
1 - 14	1493.7956	1492.7883	1492.7787	6	1	-.GGWGKTTLAANVYR.N
6 - 17	1407.7434	1406.7361	1406.7266	7	1	K.TTLAANVYRNER.E
40 - 48	1090.5271	1089.5198	1089.5740	-50	0	K.CLSLELDLK.K
70 - 75	797.2867	796.2794	796.3789	-125	0	K.FLMDQK.Y Oxidation (M)
111 - 123	1438.7456	1437.7383	1437.7728	-24	1	R.IDGVAHLAFPDKR.I
124 - 133	1157.5816	1156.5743	1156.6703	-83	1	R.ITLEPLSEKK.S
155 - 173	2087.0935	2086.0862	2086.1496	-30	1	K.LTVLAQQIVSKCEGFPLAL.-
166 - 173	906.3922	905.3849	905.4317	-52	0	K.CEGFPLAL.-

Spot No.: **198**

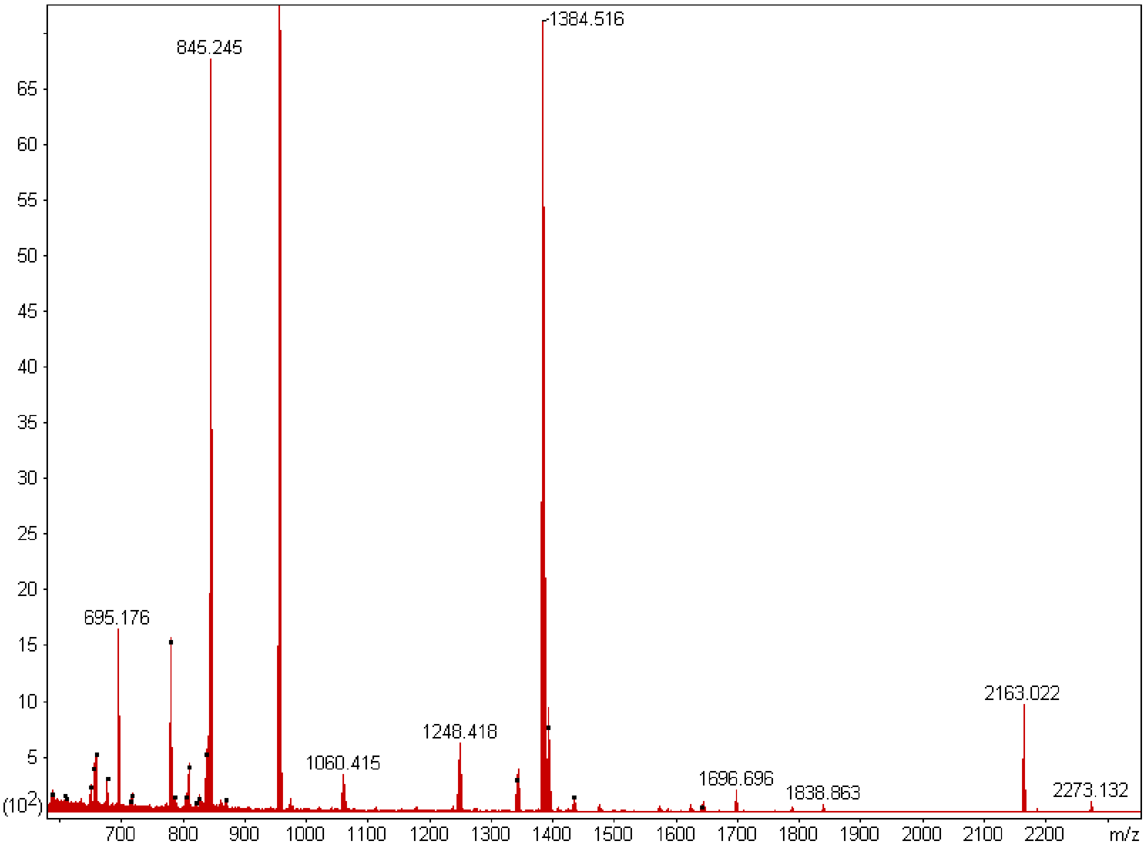
Mascot score: **82** Sequence coverage %: **15**

NCBI accession No.: **gi| 21592994**

Matched peptides No.: **8** Total peptides No.: **15**

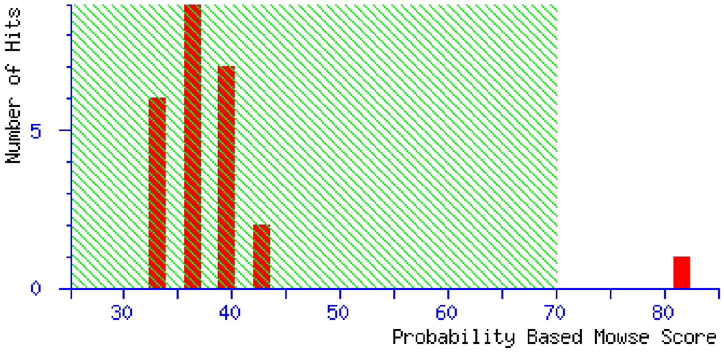
Calculated Mr: **34061** Calculated *p*I: **9.04**

Annotated PMF **spectra:**

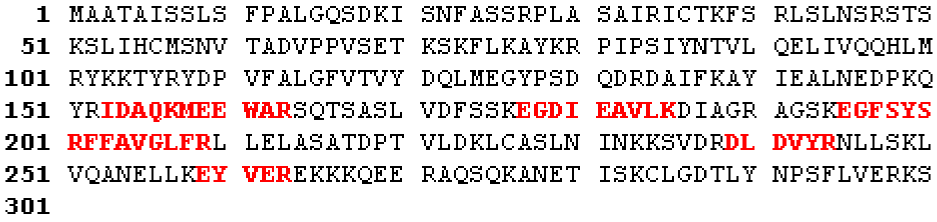


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).

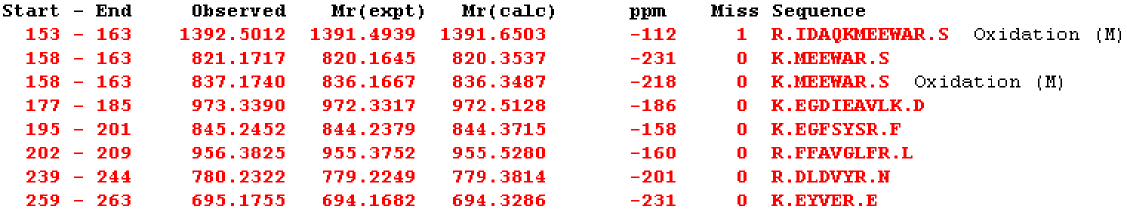


Matched peptide sequences: shown in **Bold Red**



1 MAATAISSLS FPALGQSDKI SNFASSRPLA SAIRICTKFS RLSLNSRSTS
51 KSLIHCMSNV TADVPPVSET KSKFLKAYKR PIPSIYNTVL QELIVQQHLM
101 RYKKTYRYDP VFALGFVTVY DQLMEGYPSD QDRDAIFKAY IEALNEDPKQ
151 YR**IDAQKMEE WAR**SQTSASL VDFSSK**EGDI EAVLK**DIAGR AGSK**EGFSYS**
201 **RFFAVGLFR**L LELASATDPT VLDKLCASLN INKKSVDR**DL DVYR**NLLSKL
251 VQANELLK**EY VER**EKKKQEE RAQSQKANET ISKCLGDTLY NPSFLVERKS
301

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
153 - 163	1392.5012	1391.4939	1391.6503	-112	1	R.IDAQKMEEWAR.S Oxidation (M)
158 - 163	821.1717	820.1645	820.3537	-231	0	K.MEEWAR.S
158 - 163	837.1740	836.1667	836.3487	-218	0	K.MEEWAR.S Oxidation (M)
177 - 185	973.3390	972.3317	972.5128	-186	0	K.EGDIEAVLK.D
195 - 201	845.2452	844.2379	844.3715	-158	0	K.EGFSYSR.F
202 - 209	956.3825	955.3752	955.5280	-160	0	R.FFAVGLFR.L
239 - 244	780.2322	779.2249	779.3814	-201	0	R.DLDVYR.N
259 - 263	695.1755	694.1682	694.3286	-231	0	K.EYVER.E

Spot No.: **199**

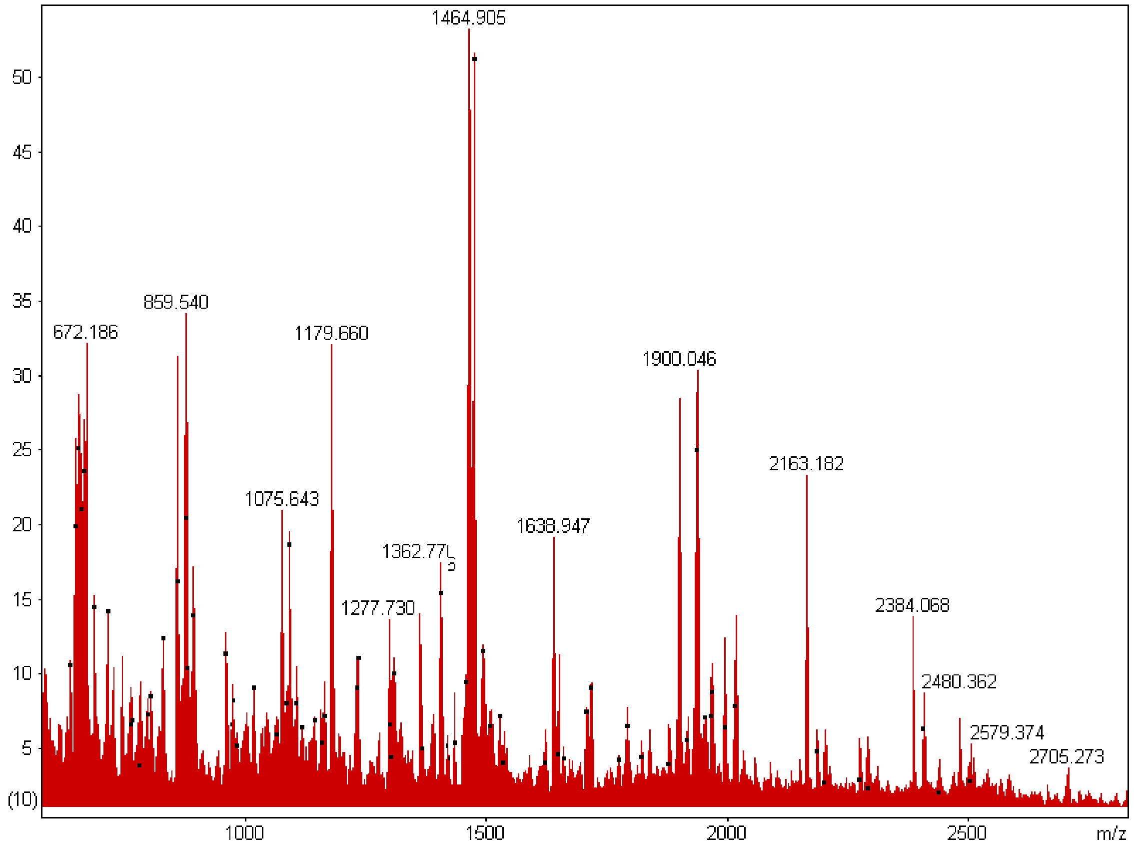
Mascot score: **116**   Sequence coverage %: **49**

NCBI accession No.: **gi| 21593565**

Matched peptides No.: **16**   Total peptides No.: **62**

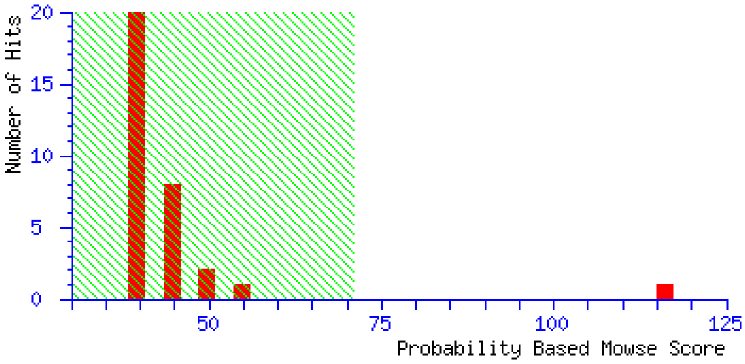
Calculated Mr: **35982**   Calculated *p*I: **7.00**

Annotated PMF **spectra:**

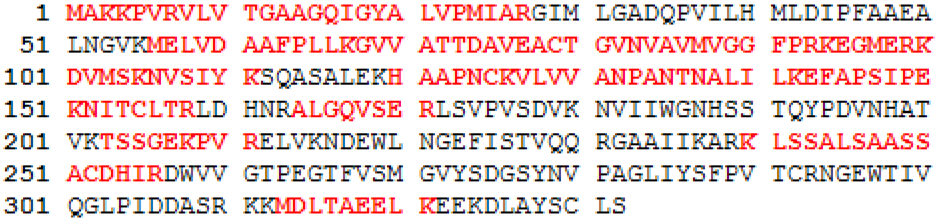


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant ($p<0.05$).

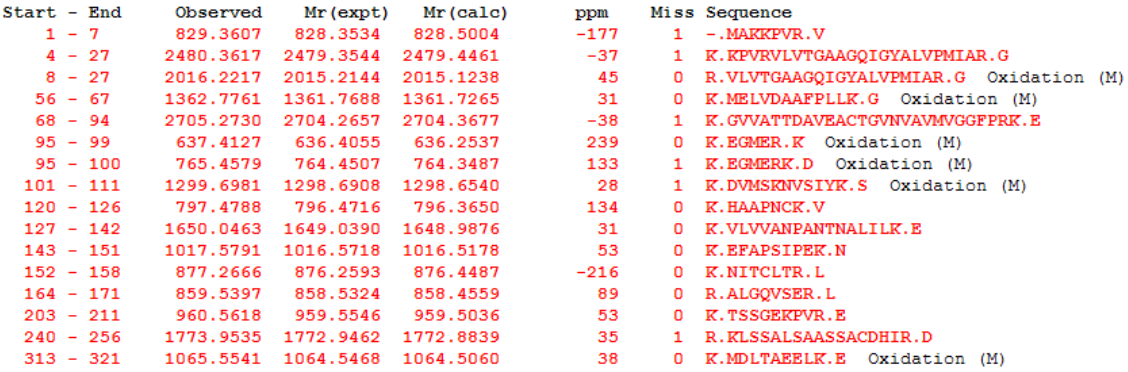


Matched peptide sequences: shown in Bold Red



1 **MAKKPVRVLV TGAAGQIGYA LVPMIAR**GIM LGADQPVILH MLDIPFAAEA
51 LNGVK**MELVD AAFPLLKGVV ATTDAVEACT GVNVAVMVGG FPRKEGMERK**
101 **DVMSKNVSIY K**SQASALEK**H AAPNCKVLVV ANPANTNALI LKEFAPSIPE**
151 **KNITCLTR**LD HNR**ALGQVSE R**LSVPVSDVK NVIIWGNHSS TQYPDVNHAT
201 VK**TSSGEKPV R**ELVKNDEWL NGEFISTVQQ RGAAIIKAR**K LSSALSAASS**
251 **ACDHIR**DWVV GTPEGTFVSM GVYSDGSYNV PAGLIYSFPV TCRNGEWTIV
301 QGLPIDDASR KK**MDLTAEEL K**EEKDLAYSC LS

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
1 - 7	829.3607	828.3534	828.5004	-177	1	-.MAKKPVR.V
4 - 27	2480.3617	2479.3544	2479.4461	-37	1	K.KPVRVLVTGAAGQIGYALVPMIAR.G
8 - 27	2016.2217	2015.2144	2015.1238	45	0	R.VLVTGAAGQIGYALVPMIAR.G Oxidation (M)
56 - 67	1362.7761	1361.7688	1361.7265	31	0	K.MELVDAAFPLLK.G Oxidation (M)
68 - 94	2705.2730	2704.2657	2704.3677	-38	1	K.GVVATTDAVEACTGVNVAVMVGGFPRK.E
95 - 99	637.4127	636.4055	636.2537	239	0	K.EGMER.K Oxidation (M)
95 - 100	765.4579	764.4507	764.3487	133	1	K.EGMERK.D Oxidation (M)
101 - 111	1299.6981	1298.6908	1298.6540	28	1	K.DVMSKNVSIYK.S Oxidation (M)
120 - 126	797.4788	796.4716	796.3650	134	0	K.HAAPNCK.V
127 - 142	1650.0463	1649.0390	1648.9876	31	0	K.VLVVANPANTNALILK.E
143 - 151	1017.5791	1016.5718	1016.5178	53	0	K.EFAPSIPEK.N
152 - 158	877.2666	876.2593	876.4487	-216	0	K.NITCLTR.L
164 - 171	859.5397	858.5324	858.4559	89	0	R.ALGQVSER.L
203 - 211	960.5618	959.5546	959.5036	53	0	K.TSSGEKPVR.E
240 - 256	1773.9535	1772.9462	1772.8839	35	1	R.KLSSALSAASSACDHIR.D
313 - 321	1065.5541	1064.5468	1064.5060	38	0	K.MDLTAEELK.E Oxidation (M)

Spot No.: **200**

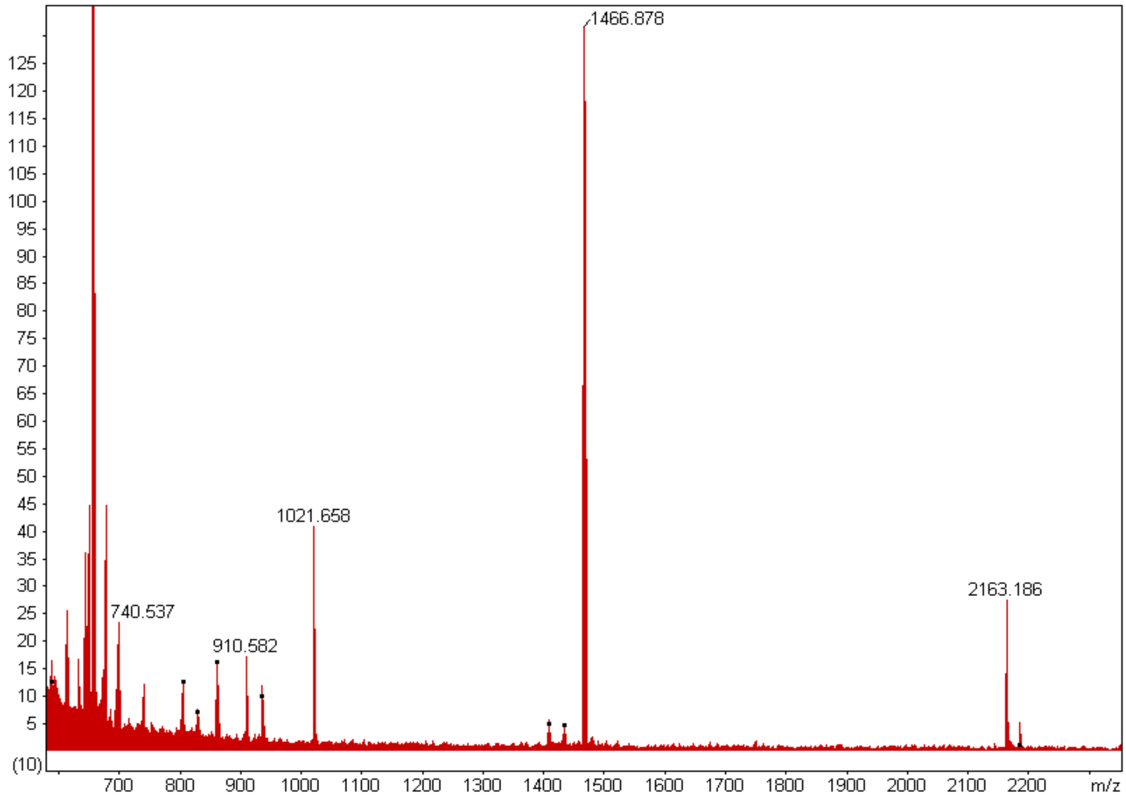
Mascot score: **85** Sequence coverage %: **20**

NCBI accession No.: **gi| 167891400**

Matched peptides No.: **6** Total peptides No.: **13**

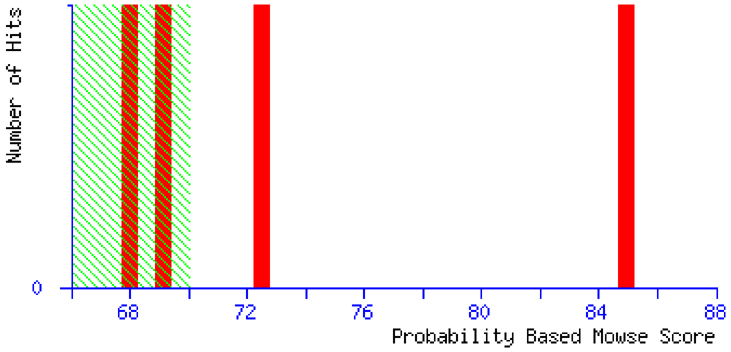
Calculated Mr: **26275** Calculated *p*I: **7.01**

Annotated PMF **spectra:**

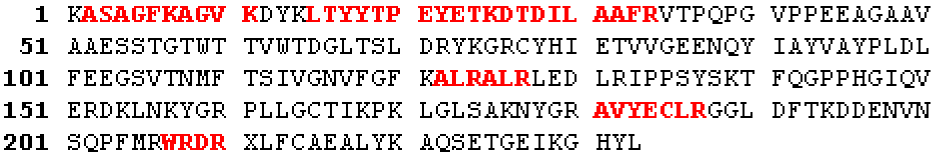


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

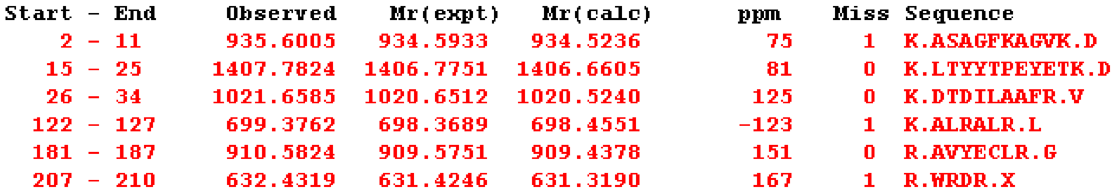


Matched peptide sequences: shown in Bold Red



```
  1 KASAGFKAGV KDYKLTYYTP EYETKDTDIL AAFRVTPQPG VPPEEAGAAV
 51 AAESSTGTWT TVWTDGLTSL DRYKGRCYHI ETVVGEENQY IAYVAYPLDL
101 FEEGSVTNMF TSIVGNVFGF KALRALRLED LRIPPSYSKT FQGPPHGIQV
151 ERDKLNKYGR PLLGCTIKPK LGLSAKNYGR AVYECLRGGL DFTKDDENVN
201 SQPFMRWRDR XLFCAEALYK AQSETGEIKG HYL
```

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
2 - 11	935.6005	934.5933	934.5236	75	1	K.ASAGFKAGVK.D
15 - 25	1407.7824	1406.7751	1406.6605	81	0	K.LTYYTPEYETK.D
26 - 34	1021.6585	1020.6512	1020.5240	125	0	K.DTDILAAFR.V
122 - 127	699.3762	698.3689	698.4551	-123	1	K.ALRALR.L
181 - 187	910.5824	909.5751	909.4378	151	0	R.AVYECLR.G
207 - 210	632.4319	631.4246	631.3190	167	1	R.WRDR.X

Spot No.: **201**

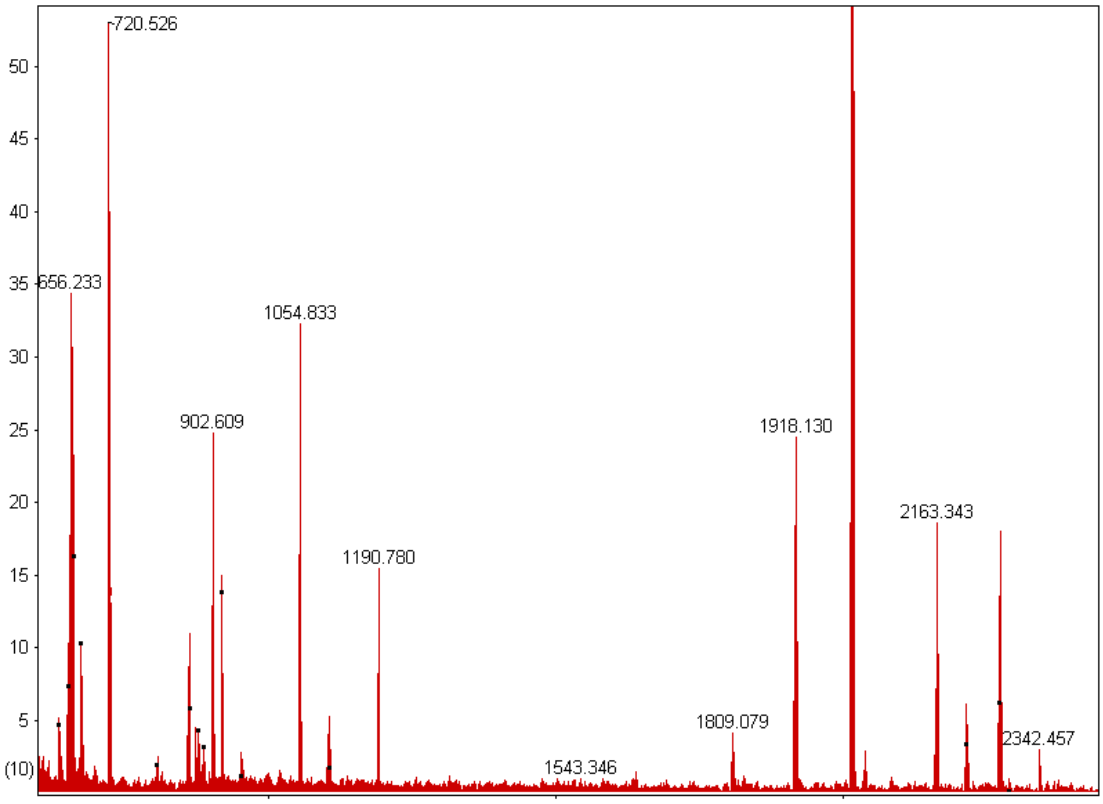
Mascot score: **112** Sequence coverage %: **53**

NCBI accession No.: **gi| 20230245**

Matched peptides No.: **12** Total peptides No.: **25**

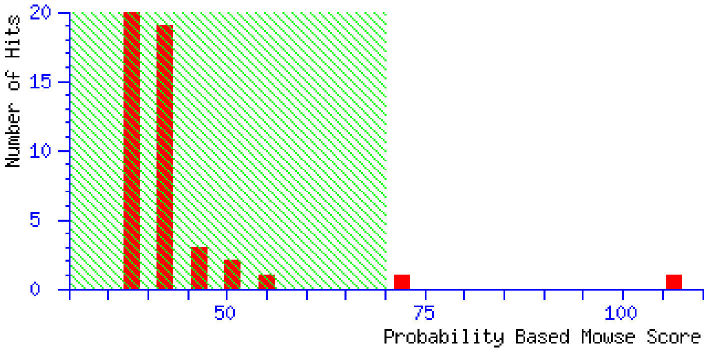
Calculated Mr: **26115** Calculated *p*I: **6.47**

Annotated PMF **spectra:**

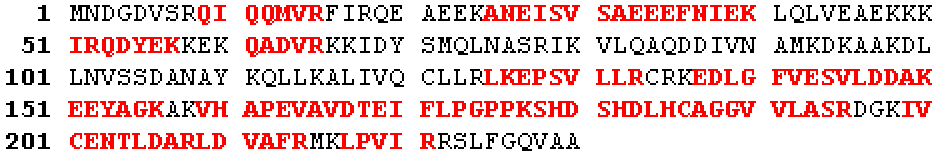


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

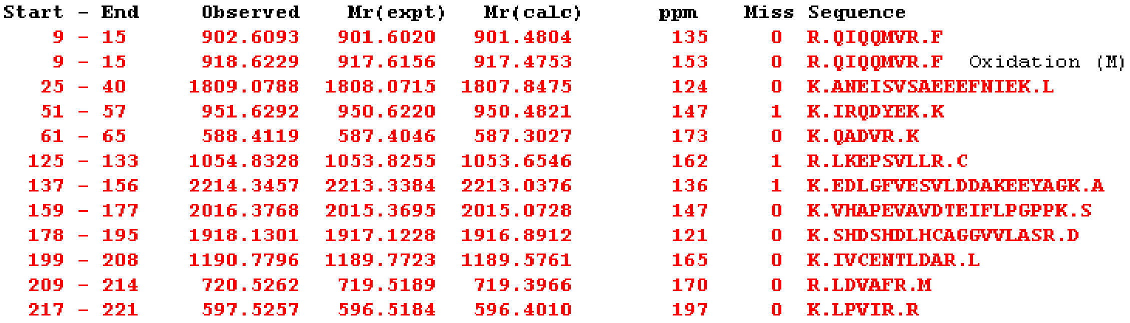


Matched peptide sequences: shown in Bold Red



```
  1 MNDGDVSRQI QQMVRFIRQE AEEKANEISV SAEEEFNIEK LQLVEAEKKK
 51 IRQDYEKKEK QADVRKKIDY SMQLNASRIK VLQAQDDIVN AMKDKAAKDL
101 LNVSSDANAY KQLLKALIVQ CLLRLKEPSV LLRCRKEDLG FVESVLDDAK
151 EEYAGKAKVH APEVAVDTEI FLPGPPKSHD SHDLHCAGGV VLASRDGKIV
201 CENTLDARLD VAFRMKLPVI RRSLFGQVAA
```

Matched peptides information:



```
Start - End     Observed    Mr(expt)    Mr(calc)      ppm    Miss  Sequence
    9 - 15      902.6093    901.6020    901.4804      135      0   R.QIQQMVR.F
    9 - 15      918.6229    917.6156    917.4753      153      0   R.QIQQMVR.F   Oxidation (M)
   25 - 40     1809.0788   1808.0715   1807.8475      124      0   K.ANEISVSAEEEFNIEK.L
   51 - 57      951.6292    950.6220    950.4821      147      1   K.IRQDYEK.K
   61 - 65      588.4119    587.4046    587.3027      173      0   K.QADVR.K
  125 - 133    1054.8328   1053.8255   1053.6546      162      1   R.LKEPSVLLR.C
  137 - 156    2214.3457   2213.3384   2213.0376      136      1   K.EDLGFVESVLDDAKEEYAGK.A
  159 - 177    2016.3768   2015.3695   2015.0728      147      0   K.VHAPEVAVDTEIFLPGPPK.S
  178 - 195    1918.1301   1917.1228   1916.8912      121      0   K.SHDSHDLHCAGGVVLASR.D
  199 - 208    1190.7796   1189.7723   1189.5761      165      0   K.IVCENTLDAR.L
  209 - 214     720.5262    719.5189    719.3966      170      0   R.LDVAFR.M
  217 - 221     597.5257    596.5184    596.4010      197      0   K.LPVIR.R
```

Spot No.: **202**

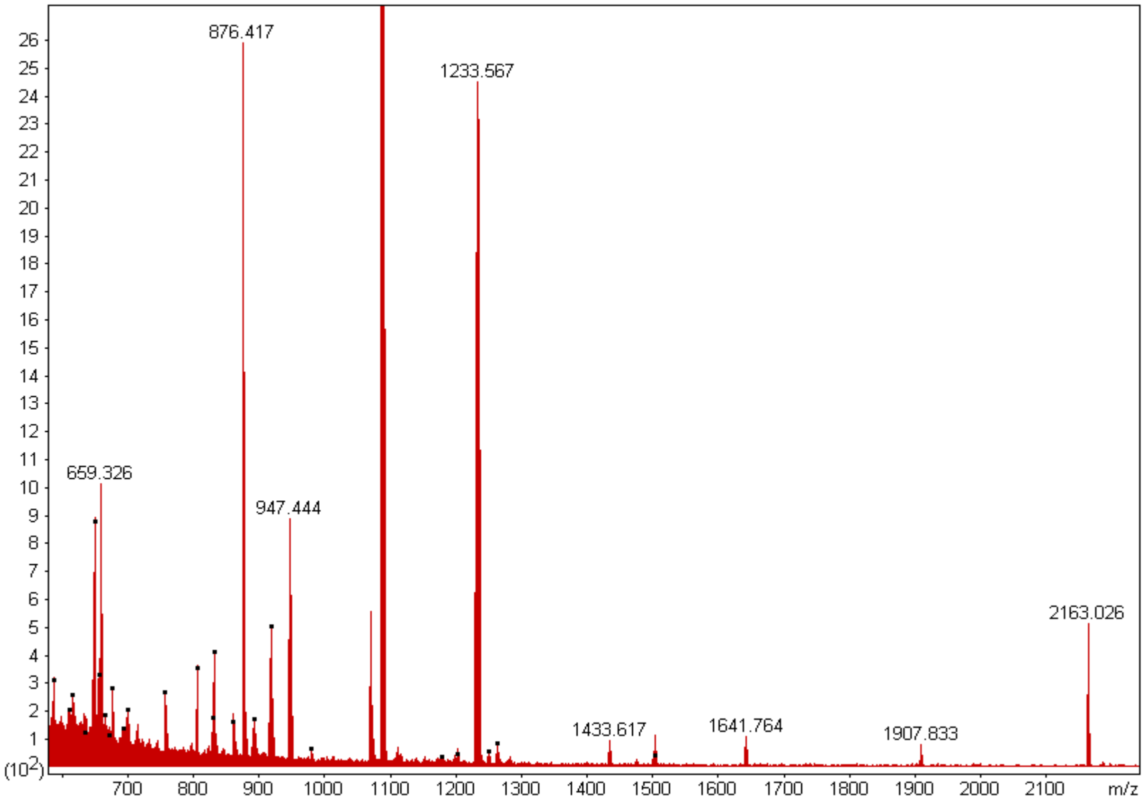
Mascot score: **86** Sequence coverage %: **17**

NCBI accession No.: **gi| 15222251**

Matched peptides No.: **10** Total peptides No.: **24**

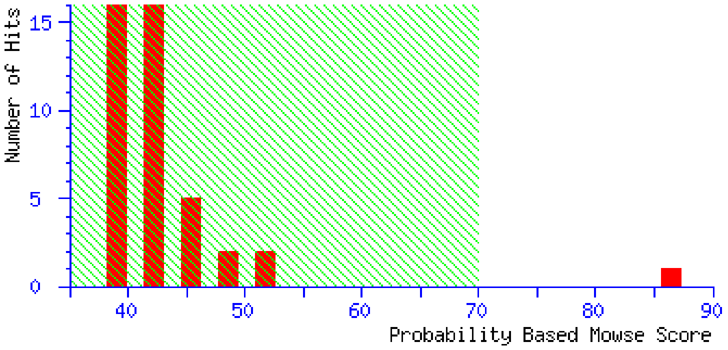
Calculated Mr: **45544** Calculated *p*I: **5.96**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 MGKK**LDALLG R**SFKTNK**FKS LITLALTR**LS ILKNQRQARL SQAISDVTEL
51 LKLGQHEHAY HRVDQVVKDQ NTLDVLFFIH GYFTLCLDRI HLFEHNRDCP
101 EELLEAVSGL LFAASRIGEF PELQEIRNVL ISRFGKDLAA RSIELRSNCG
151 VDPKIIQKLS TRPPPKEVRM KALKEIAAEN NIVLKLDQAS TSTEGTTNMQ
201 GTSDVSK**TKL TSK**DGR**GEGY GLSDSVK**RGK KKYKDVADAA QAAFESAAHA
251 AEAAQAAVEL SQFSPRGHDS PGNIGGENSF HGSENKESEQ EQEGNDDSSE
301 GEGDVMSESK RSMSDSEDII DVPVMSFR**ED PVKLLEK**DTI IYDSEEETQP
351 SVETITISK**S KDEQNR**MVGS NRADTR**HVDH MVRSIEDPIM RK**AGLKGPVS
401 VR**TRQVR**GY

Matched peptides information:

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
5 - 11	757.4073	756.4001	756.4494	-65	0	K.LDALLGR.S
18 - 28	1262.5305	1261.5232	1261.7758	-200	1	K.FKSLITLALTR.L
208 - 213	677.2529	676.2456	676.4119	-246	1	K.TKLTSK.D
217 - 227	1111.4741	1110.4668	1110.5193	-47	0	R.GEGYGLSDSVK.R
329 - 333	587.1636	586.1563	586.2962	-239	0	R.EDPVK.L
329 - 337	1070.4635	1069.4562	1069.6019	-136	1	R.EDPVKLLEK.D
360 - 366	876.4169	875.4096	875.4097	-0	1	K.SKDEQNR.M
377 - 383	893.3443	892.3371	892.4338	-108	0	R.HVDHMVR.S
384 - 392	1088.4928	1087.4855	1087.5695	-77	1	R.SIEDPIMRK.A
403 - 407	659.3257	658.3184	658.3875	-105	1	R.TRQVR.G

Spot No.: **203**

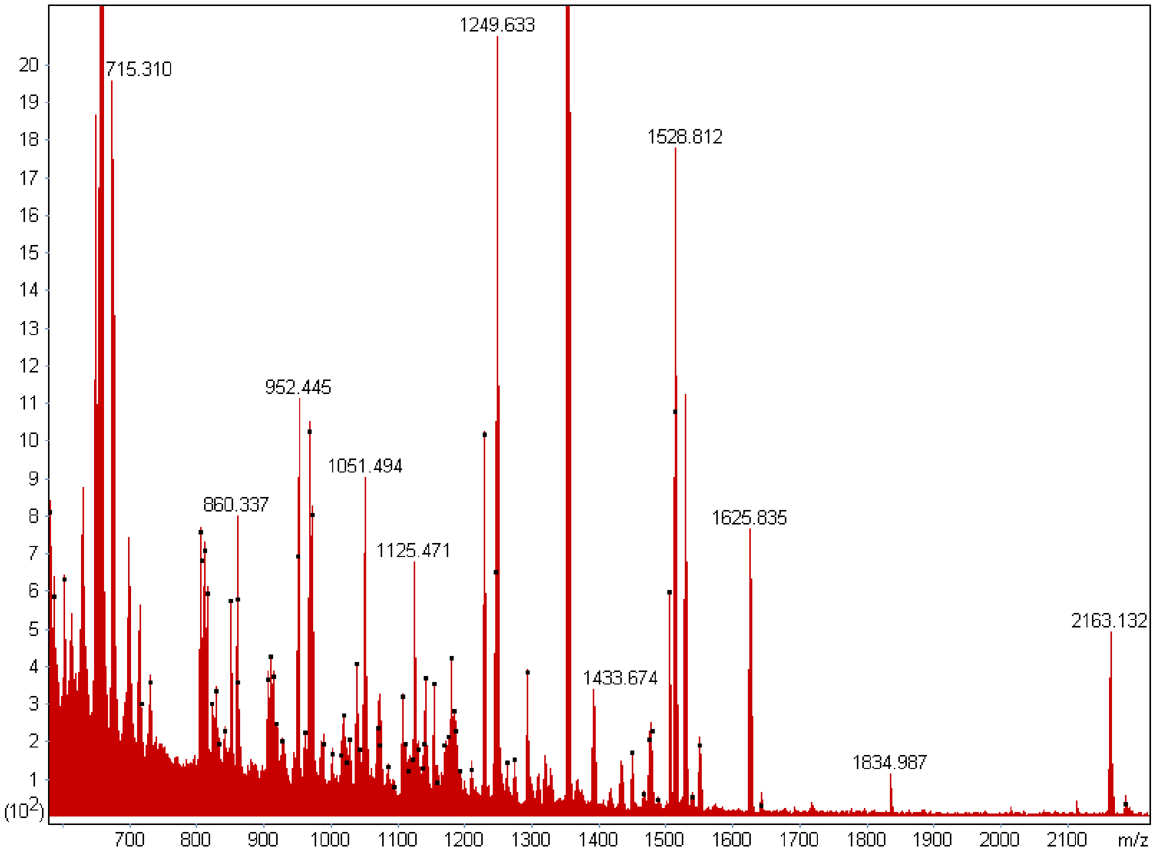
Mascot score: **111**   Sequence coverage %: **23**

NCBI accession No.: **gi| 11072026**

Matched peptides No.: **27**   Total peptides No.: **79**

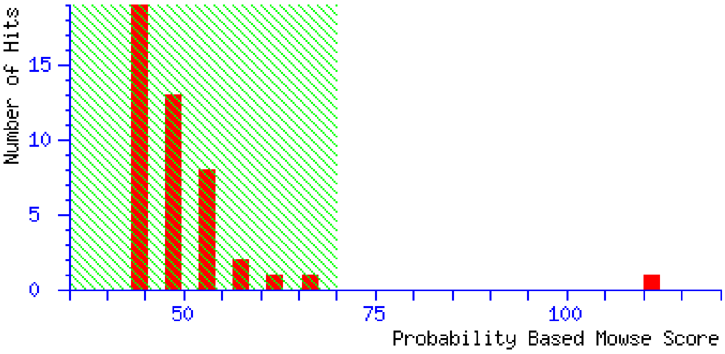
Calculated Mr: **114361**   Calculated *p*I: **6.69**

Annotated PMF **spectra:**

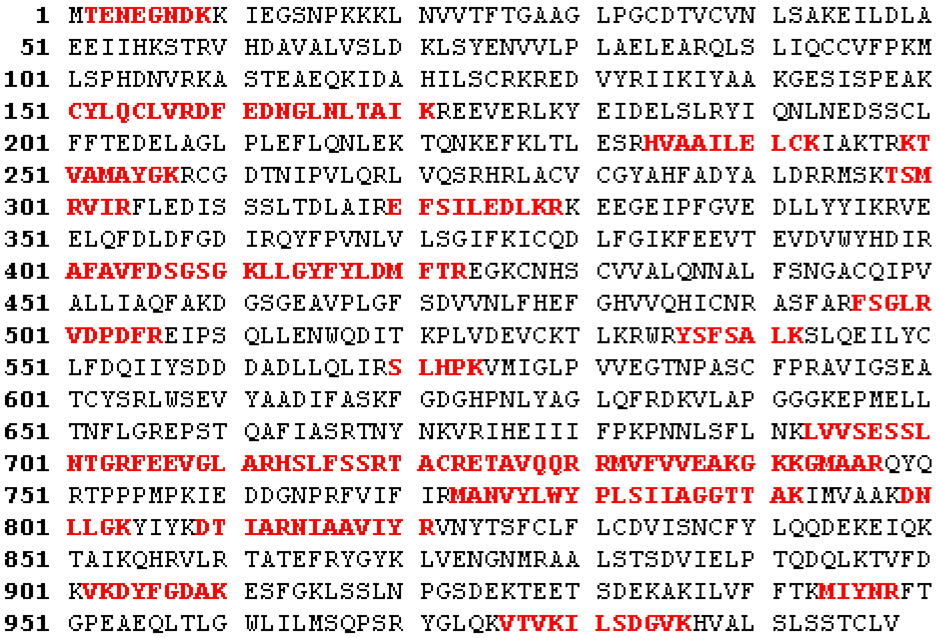


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

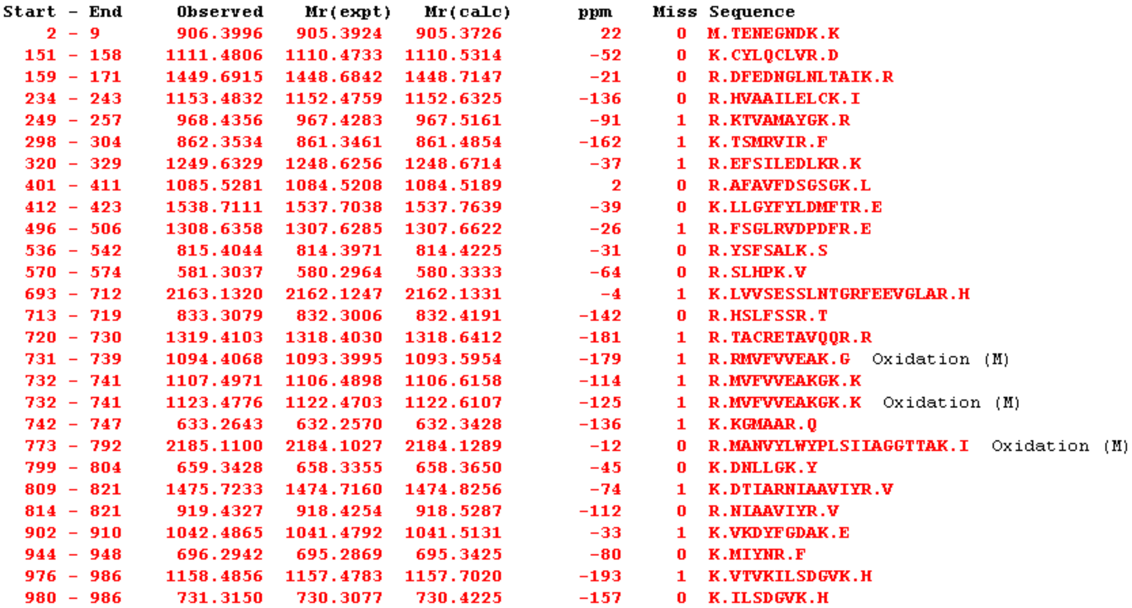


Matched peptide sequences: shown in Bold Red



1 M**TENEGNDK**K IEGSNPKKKL NVVTFTGAAG LPGCDTVCVN LSAKEILDLA
51 EEIIHKSTRV HDAVALVSLD KLSYENVVLP LAELEARQLS LIQCCVFPKM
101 LSPHDNVRKA STEAEQKIDA HILSCRKRED VYRIIKIYAA KGESISPEAK
151 **CYLQCLVRDF** **EDNGLNLTAI** **K**REEVERLKY EIDELSLRYI QNLNEDSSCL
201 FFTEDELAGL PLEFLQNLEK TQNKEFKLTL ESR**HVAAILE** **LCK**IAKTR**KT**
251 **VAMAYGK**RCG DTNIPVLQRL VQSRHRLACV CGYAHFADYA LDRRMSK**TSM**
301 **RVIR**FLEDIS SSLTDLAIR**E** **FSILEDLKR**K EEGEIPFGVE DLLYYIKRVE
351 ELQFDLDFGD IRQYFPVNLV LSGIFKICQD LFGIKFEEVT EVDVWYHDIR
401 **AFAVFDSGSG** **KLLGYFYLDM** **FTR**EGKCNHS CVVALQNNAL FSNGACQIPV
451 ALLIAQFAKD GSGEAVPLGF SDVVNLFHEF GHVVQHICNR ASFAR**FSGLR**
501 **VDPDFR**EIPS QLLENWQDIT KPLVDEVCKT LKRWR**YSFSA** **LK**SLQEILYC
551 LFDQIIYSDD DADLLQLIR**S** **LHPK**VMIGLP VVEGTNPASC FPRAVIGSEA
601 TCYSRLWSEV YAADIFASKF GDGHPNLYAG LQFRDKVLAP GGGKEPMELL
651 TNFLGREPST QAFIASRTNY NKVRIHEIII FPKPNNLSFL NK**LVVSESSL**
701 **NTGRFEEVGL** **ARHSLFSSRT** **ACRETAVQQR** **RMVFVVEAKG** **KKGMAAR**QYQ
751 RTPPPMPKIE DDGNPRFVIF IR**MANVYLWY** **PLSIIAGGTT** **AK**IMVAAK**DN**
801 **LLGK**YIYK**DT** **IARNIAAVIY** **R**VNYTSFCLF LCDVISNCFY LQQDEKEIQK
851 TAIKQHRVLR TATEFRYGYK LVENGNMRAA LSTSDVIELP TQDQLKTVFD
901 K**VKDYFGDAK** ESFGKLSSLN PGSDEKTEET SDEKAKILVF FTK**MIYNR**FT
951 GPEAEQLTLG WLILMSQPSR YGLQK**VTVKI** **LSDGVK**HVAL SLSSTCLV

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
2 - 9	906.3996	905.3924	905.3726	22	0	M.TENEGNDK.K
151 - 158	1111.4806	1110.4733	1110.5314	-52	0	K.CYLQCLVR.D
159 - 171	1449.6915	1448.6842	1448.7147	-21	0	R.DFEDNGLNLTAIK.R
234 - 243	1153.4832	1152.4759	1152.6325	-136	0	R.HVAAILELCK.I
249 - 257	968.4356	967.4283	967.5161	-91	1	R.KTVAMAYGK.R
298 - 304	862.3534	861.3461	861.4854	-162	1	K.TSMRVIR.F
320 - 329	1249.6329	1248.6256	1248.6714	-37	1	R.EFSILEDLKR.K
401 - 411	1085.5281	1084.5208	1084.5189	2	0	R.AFAVFDSGSGK.L
412 - 423	1538.7111	1537.7038	1537.7639	-39	0	K.LLGYFYLDMFTR.E
496 - 506	1308.6358	1307.6285	1307.6622	-26	1	R.FSGLRVDPDFR.E
536 - 542	815.4044	814.3971	814.4225	-31	0	R.YSFSALK.S
570 - 574	581.3037	580.2964	580.3333	-64	0	R.SLHPK.V
693 - 712	2163.1320	2162.1247	2162.1331	-4	1	K.LVVSESSLNTGRFEEVGLAR.H
713 - 719	833.3079	832.3006	832.4191	-142	0	R.HSLFSSR.T
720 - 730	1319.4103	1318.4030	1318.6412	-181	1	R.TACRETAVQQR.R
731 - 739	1094.4068	1093.3995	1093.5954	-179	1	R.RMVFVVEAK.G Oxidation (M)
732 - 741	1107.4971	1106.4898	1106.6158	-114	1	R.MVFVVEAKGK.K
732 - 741	1123.4776	1122.4703	1122.6107	-125	1	R.MVFVVEAKGK.K Oxidation (M)
742 - 747	633.2643	632.2570	632.3428	-136	1	K.KGMAAR.Q
773 - 792	2185.1100	2184.1027	2184.1289	-12	0	R.MANVYLWYPLSIIAGGTTAK.I Oxidation (M)
799 - 804	659.3428	658.3355	658.3650	-45	0	K.DNLLGK.Y
809 - 821	1475.7233	1474.7160	1474.8256	-74	1	K.DTIARNIAAVIYR.V
814 - 821	919.4327	918.4254	918.5287	-112	0	R.NIAAVIYR.V
902 - 910	1042.4865	1041.4792	1041.5131	-33	1	K.VKDYFGDAK.E
944 - 948	696.2942	695.2869	695.3425	-80	0	K.MIYNR.F
976 - 986	1158.4856	1157.4783	1157.7020	-193	1	K.VTVKILSDGVK.H
980 - 986	731.3150	730.3077	730.4225	-157	0	K.ILSDGVK.H

Spot No.: **204**

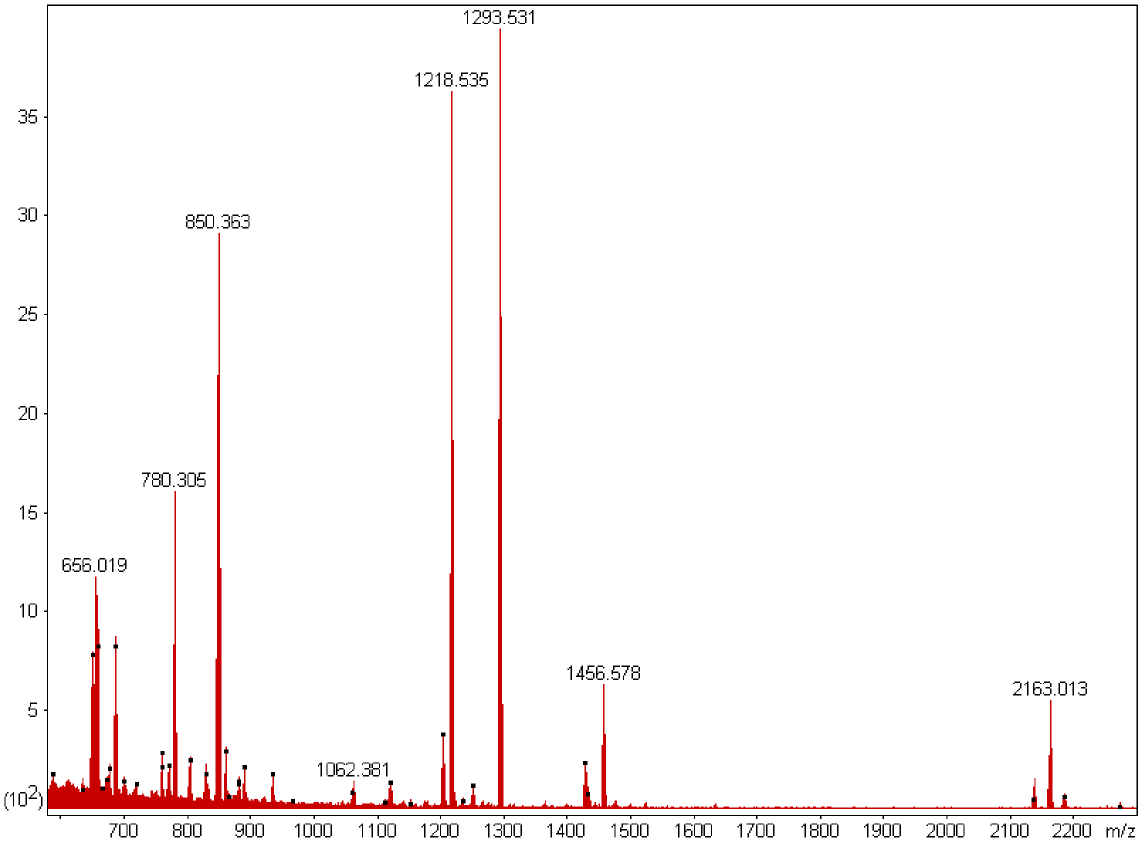
Mascot score: **117** Sequence coverage %: **23**

NCBI accession No.: **gi| 31593440**

Matched peptides No.: **11** Total peptides No.: **29**

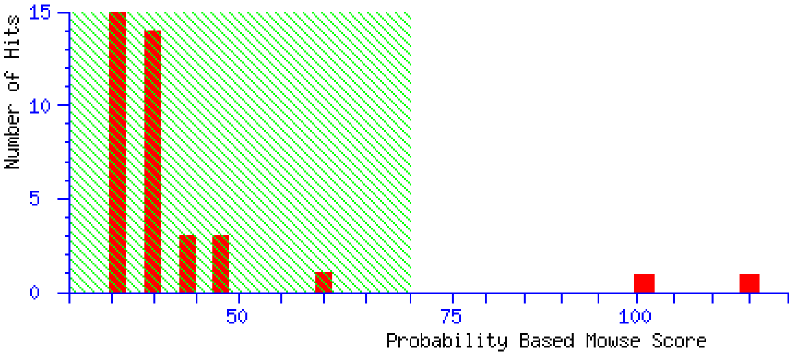
Calculated Mr: **36256** Calculated *p*I: **7.07**

Annotated PMF **spectra:**

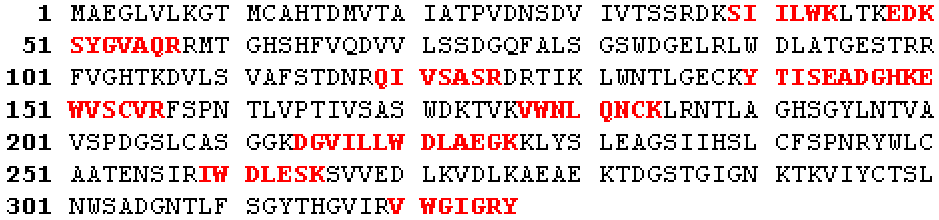


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

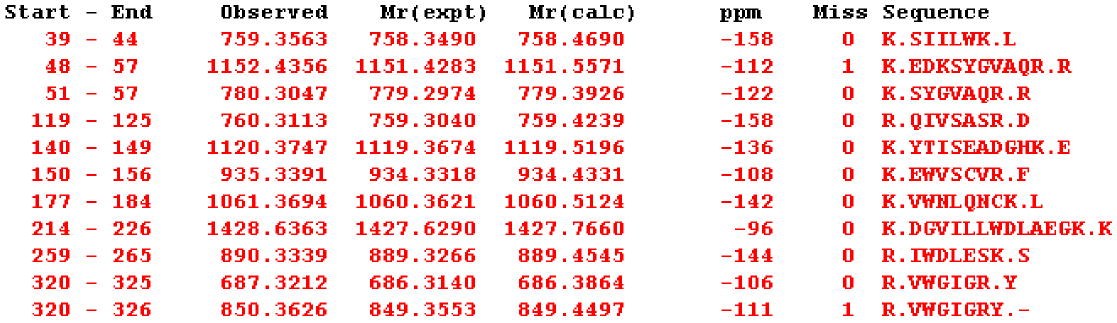


Matched peptide sequences: shown in Bold Red



1 MAEGLVLKGT MCAHTDMVTA IATPVDNSDV IVTSSRDK**SI** **ILWK**LTK**EDK**
51 **SYGVAQR**RMT GHSHFVQDVV LSSDGQFALS GSWDGELRLW DLATGESTRR
101 FVGHTKDVLS VAFSTDNR**QI** **VSASR**DRTIK LWNTLGECK**Y** **TISEADGHKE**
151 **WVSCVR**FSPN TLVPTIVSAS WDKTVK**VWNL** **QNCK**LRNTLA GHSGYLNTVA
201 VSPDGSLCAS GGK**DGVILLW** **DLAEGK**KLYS LEAGSIIHSL CFSPNRYWLC
251 AATENSIR**IW** **DLESK**SVVED LKVDLKAEAE KTDGSTGIGN KTKVIYCTSL
301 NWSADGNTLF SGYTHGVIR**V** **WGIGRY**

Matched peptides information:



Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
39 - 44	759.3563	758.3490	758.4690	-158	0	K.SIILWK.L
48 - 57	1152.4356	1151.4283	1151.5571	-112	1	K.EDKSYGVAQR.R
51 - 57	780.3047	779.2974	779.3926	-122	0	K.SYGVAQR.R
119 - 125	760.3113	759.3040	759.4239	-158	0	R.QIVSASR.D
140 - 149	1120.3747	1119.3674	1119.5196	-136	0	K.YTISEADGHK.E
150 - 156	935.3391	934.3318	934.4331	-108	0	K.EWVSCVR.F
177 - 184	1061.3694	1060.3621	1060.5124	-142	0	K.VWNLQNCK.L
214 - 226	1428.6363	1427.6290	1427.7660	-96	0	K.DGVILLWDLAEGK.K
259 - 265	890.3339	889.3266	889.4545	-144	0	R.IWDLESK.S
320 - 325	687.3212	686.3140	686.3864	-106	0	R.VWGIGR.Y
320 - 326	850.3626	849.3553	849.4497	-111	1	R.VWGIGRY.-

Spot No.: **205**

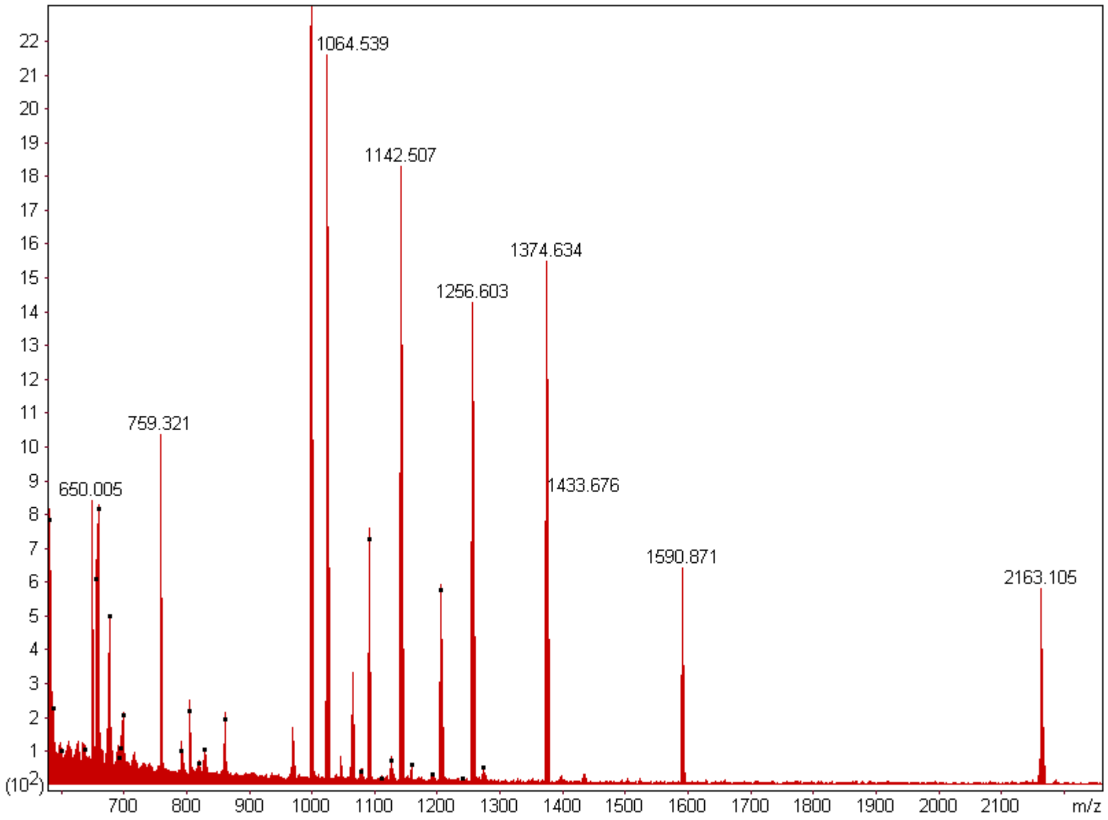
Mascot score: **107** Sequence coverage %: **32**

NCBI accession No.: **gi| 312282483**

Matched peptides No.: **13** Total peptides No.: **27**

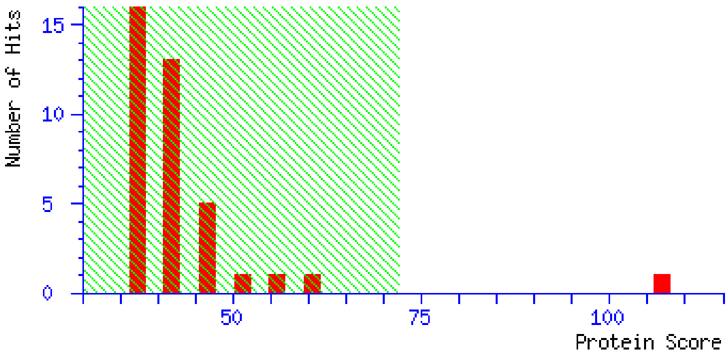
Calculated Mr: **34165** Calculated *p*I: **8.40**

Annotated PMF **spectra:**

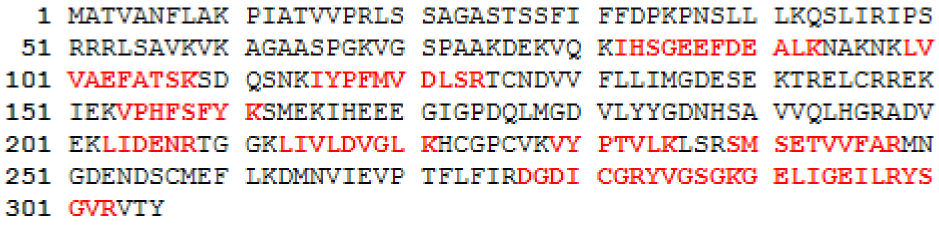


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

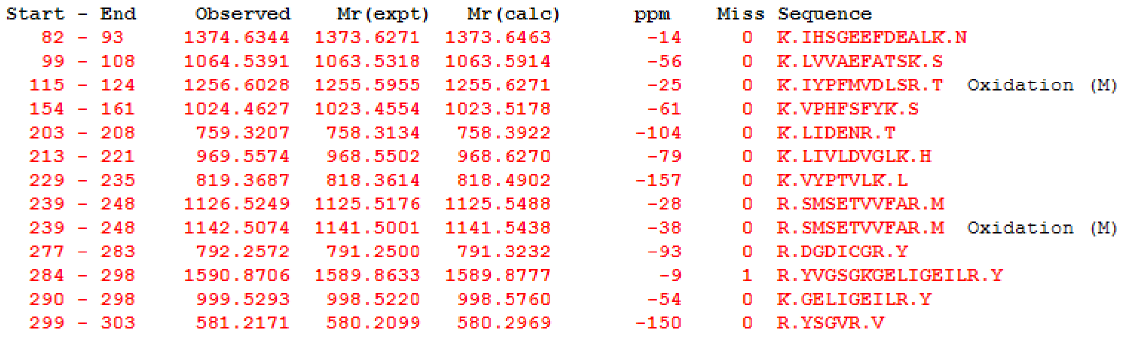


Matched peptide sequences: shown in Bold Red



1 MATVANFLAK PIATVVPRLS SAGASTSSFI FFDPKPNSLL LKQSLIRIPS
51 RRRLSAVKVK AGAASPGKVG SPAAKDEKVQ K**IHSGEEFDE** **ALK**NAKNK**LV**
101 **VAEFATSK**SD QSNK**IYPFMV** **DLSR**TCNDVV FLLIMGDESE KTRELCRREK
151 IEK**VPHFSFY** **K**SMEKIHEEE GIGPDQLMGD VLYYGDNHSA VVQLHGRADV
201 EK**LIDENR**TG GK**LIVLDVGL** **K**HCGPCVK**VY** **PTVLK**LSR**SM** **SETVVFAR**MN
251 GDENDSCMEF LKDMNVIEVP TFLFIR**DGDI** **CGRYVGSGKG** **ELIGEILRYS**
301 **GVR**VTY

Matched peptides information:



```
Start - End      Observed     Mr(expt)    Mr(calc)       ppm     Miss  Sequence
   82 - 93      1374.6344    1373.6271   1373.6463       -14      0   K.IHSGEEFDEALK.N
   99 - 108     1064.5391    1063.5318   1063.5914       -56      0   K.LVVAEFATSK.S
  115 - 124     1256.6028    1255.5955   1255.6271       -25      0   K.IYPFMVDLSR.T   Oxidation (M)
  154 - 161     1024.4627    1023.4554   1023.5178       -61      0   K.VPHFSFYK.S
  203 - 208      759.3207     758.3134    758.3922      -104      0   K.LIDENR.T
  213 - 221      969.5574     968.5502    968.6270       -79      0   K.LIVLDVGLK.H
  229 - 235      819.3687     818.3614    818.4902      -157      0   K.VYPTVLK.L
  239 - 248     1126.5249    1125.5176   1125.5488       -28      0   R.SMSETVVFAR.M
  239 - 248     1142.5074    1141.5001   1141.5438       -38      0   R.SMSETVVFAR.M   Oxidation (M)
  277 - 283      792.2572     791.2500    791.3232       -93      0   R.DGDICGR.Y
  284 - 298     1590.8706    1589.8633   1589.8777        -9      1   R.YVGSGKGELIGEILR.Y
  290 - 298      999.5293     998.5220    998.5760       -54      0   K.GELIGEILR.Y
  299 - 303      581.2171     580.2099    580.2969      -150      0   R.YSGVR.V
```

Spot No.: **206**

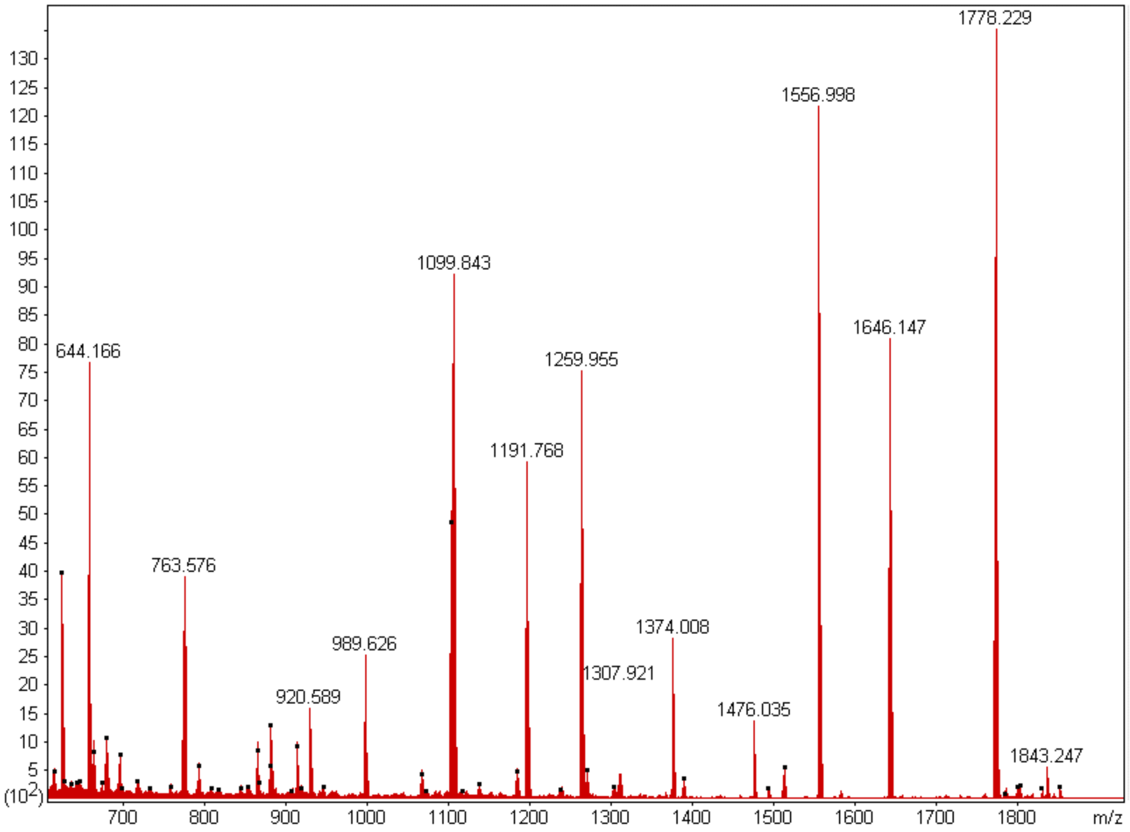
Mascot score: **137** Sequence coverage %: **38**

NCBI accession No.: **gi| 15237225**

Matched peptides No.: **19** Total peptides No.: **59**

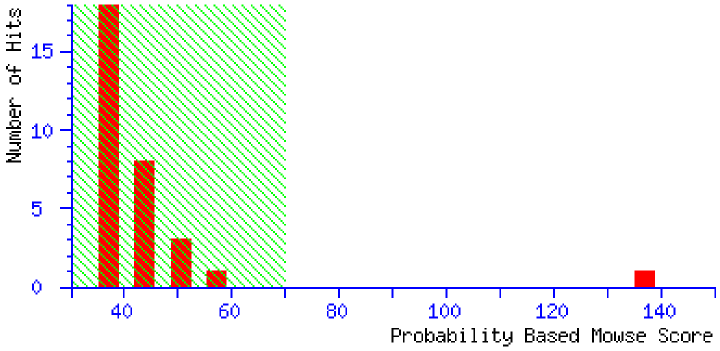
Calculated Mr: **44133** Calculated *p*I: **6.79**

Annotated PMF **spectra:**

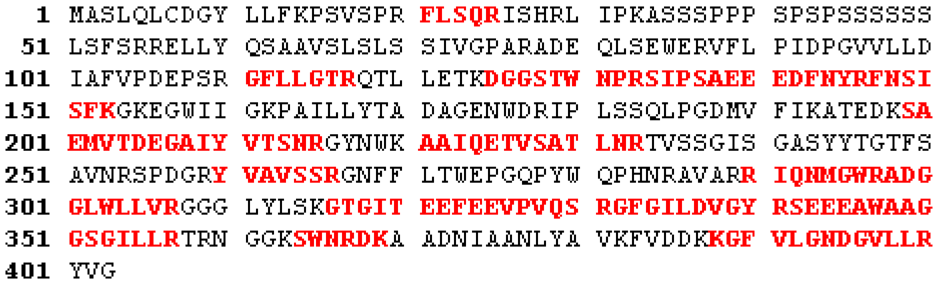


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

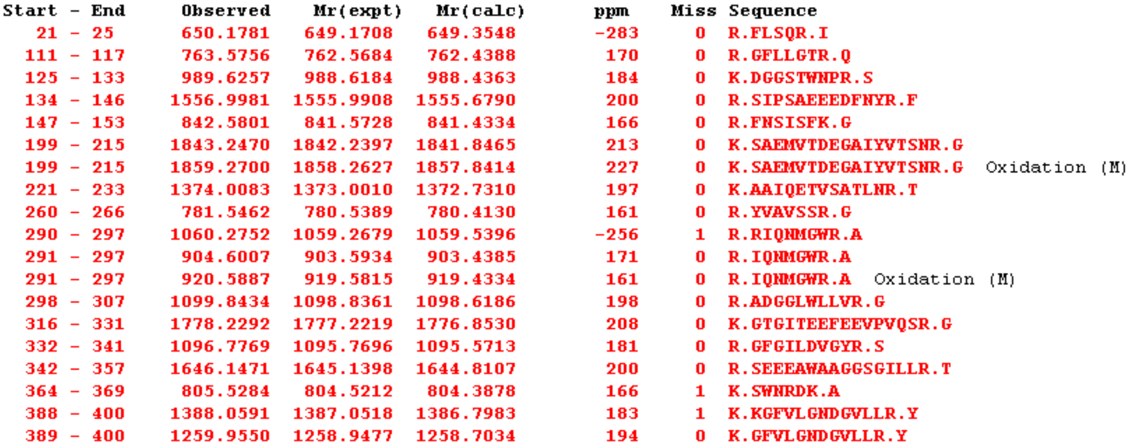


Matched peptide sequences: shown in Bold Red



1 MASLQLCDGY LLFKPSVSPR **FLSQR**ISHRL IPKASSSPPP SPSPSSSSSS
51 LSFSRRELLY QSAAVSLSLS SIVGPARADE QLSEWERVFL PIDPGVVLLD
101 IAFVPDEPSR **GFLLGTR**QTL LETK**DGGSTW NPRSIPSAEE EDFNYRFNSI**
151 **SFK**GKEGWII GKPAILLYTA DAGENWDRIP LSSQLPGDMV FIKATEDK**SA**
201 **EMVTDEGAIY VTSNR**GYNWK **AAIQETVSAT LNR**TVSSGIS GASYYTGTFS
251 AVNRSPDGR**Y VAVSSR**GNFF LTWEPGQPYW QPHNRAVAR**R IQNMGWRADG**
301 **GLWLLVR**GGG LYLSK**GTGIT EEFEEVPVQS RGFGILDVGY RSEEEAWAAG**
351 **GSGILLR**TRN GGK**SWNRDK**A ADNIAANLYA VKFVDDK**KGF VLGNDGVLLR**
401 YVG

Matched peptides information:



```
Start - End      Observed    Mr(expt)    Mr(calc)       ppm    Miss Sequence
   21 - 25       650.1781    649.1708    649.3548      -283      0  R.FLSQR.I
  111 - 117      763.5756    762.5684    762.4388       170      0  R.GFLLGTR.Q
  125 - 133      989.6257    988.6184    988.4363       184      0  K.DGGSTWNPR.S
  134 - 146     1556.9981   1555.9908   1555.6790       200      0  R.SIPSAEEEDFNYR.F
  147 - 153      842.5801    841.5728    841.4334       166      0  R.FNSISFK.G
  199 - 215     1843.2470   1842.2397   1841.8465       213      0  K.SAEMVTDEGAIYVTSNR.G
  199 - 215     1859.2700   1858.2627   1857.8414       227      0  K.SAEMVTDEGAIYVTSNR.G  Oxidation (M)
  221 - 233     1374.0083   1373.0010   1372.7310       197      0  K.AAIQETVSATLNR.T
  260 - 266      781.5462    780.5389    780.4130       161      0  R.YVAVSSR.G
  290 - 297     1060.2752   1059.2679   1059.5396      -256      1  R.RIQNMGWR.A
  291 - 297      904.6007    903.5934    903.4385       171      0  R.IQNMGWR.A
  291 - 297      920.5887    919.5815    919.4334       161      0  R.IQNMGWR.A  Oxidation (M)
  298 - 307     1099.8434   1098.8361   1098.6186       198      0  R.ADGGLWLLVR.G
  316 - 331     1778.2292   1777.2219   1776.8530       208      0  K.GTGITEEFEEVPVQSR.G
  332 - 341     1096.7769   1095.7696   1095.5713       181      0  R.GFGILDVGYR.S
  342 - 357     1646.1471   1645.1398   1644.8107       200      0  R.SEEEAWAAGGSGILLR.T
  364 - 369      805.5284    804.5212    804.3878       166      1  K.SWNRDK.A
  388 - 400     1388.0591   1387.0518   1386.7983       183      1  K.KGFVLGNDGVLLR.Y
  389 - 400     1259.9550   1258.9477   1258.7034       194      0  K.GFVLGNDGVLLR.Y
```

Spot No.: **207**

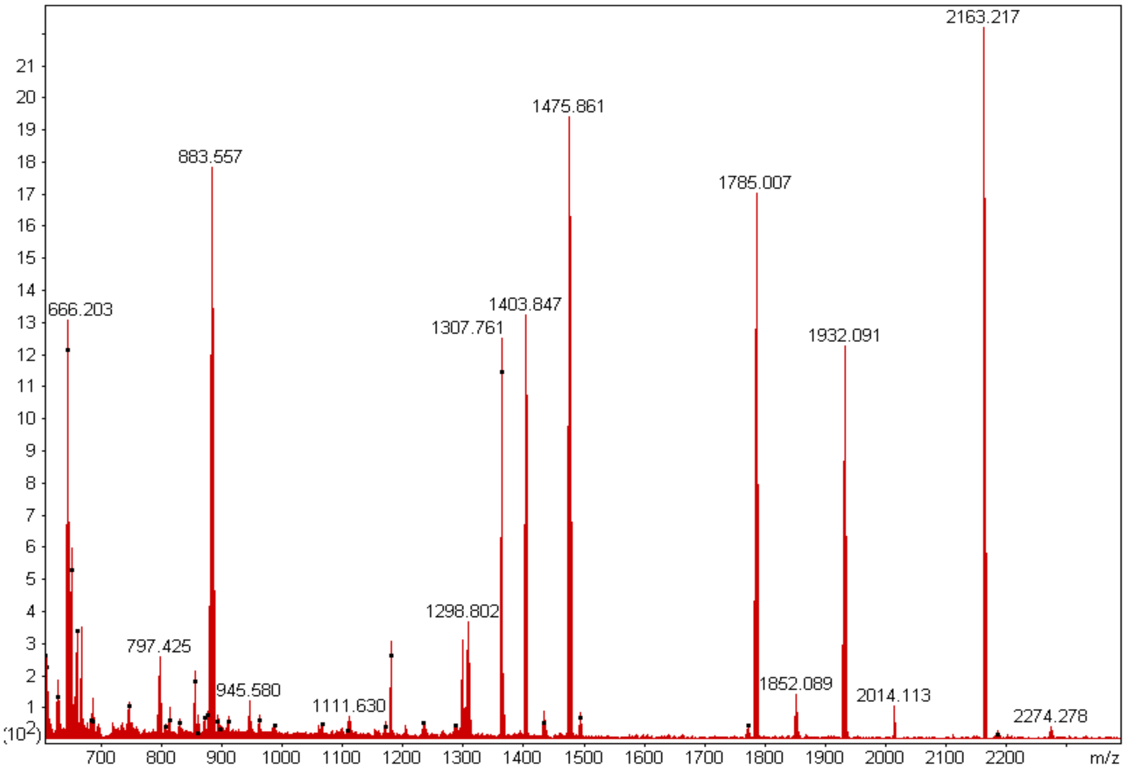
Mascot score: **81**　　Sequence coverage %: **27**

NCBI accession No.: **gi| 308802434**

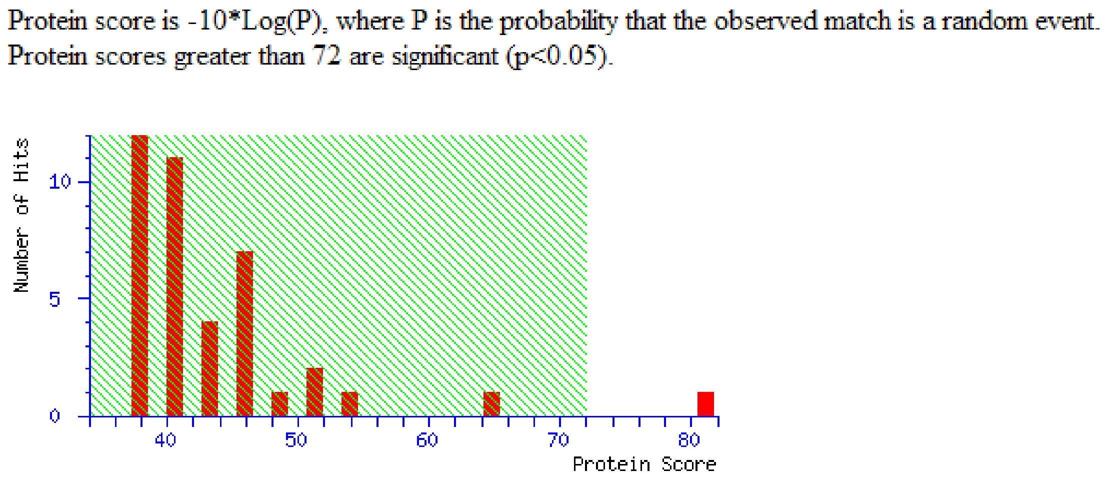
Matched peptides No.: **8**　　Total peptides No.: **25**

Calculated Mr: **34223**　　Calculated *p*I: **6.02**

Annotated PMF **spectra:**

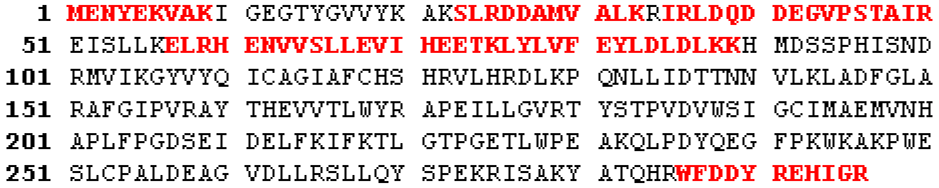


Probability Based Mowse Score:



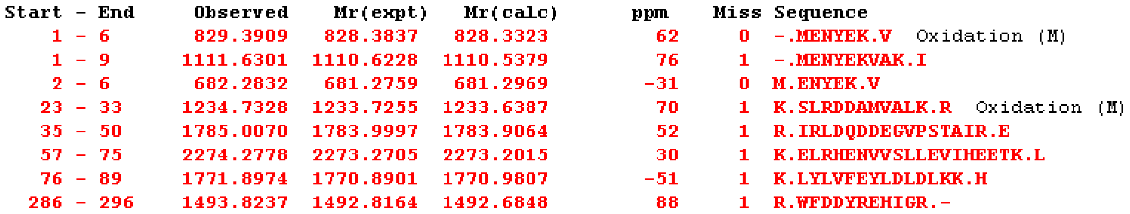
Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

Matched peptide sequences: shown in Bold Red



```
  1 MENYEKVAKI GEGTYGVVYK AKSLRDDAMV ALKRIRLDQD DEGVPSTAIR
 51 EISLLKELRH ENVVSLLEVI HEETKLYLVF EYLDLDLKKH MDSSPHISND
101 RMVIKGYVYQ ICAGIAFCHS HRVLHRDLKP QNLLIDTTNN VLKLADFGLA
151 RAFGIPVRAY THEVVTLWYR APEILLGVRT YSTPVDVWSI GCIMAEMVNH
201 APLFPGDSEI DELFKIFKTL GTPGETLWPE AKQLPDYQEG FPKWKAKPWE
251 SLCPALDEAG VDLLRSLLQY SPEKRISAKY ATQHRWFDDY REHIGR
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm    Miss Sequence
    1 - 6       829.3909   828.3837   828.3323       62     0   -.MENYEK.V   Oxidation (M)
    1 - 9      1111.6301  1110.6228  1110.5379       76     1   -.MENYEKVAK.I
    2 - 6       682.2832   681.2759   681.2969      -31     0   M.ENYEK.V
   23 - 33     1234.7328  1233.7255  1233.6387       70     1   K.SLRDDAMVALK.R   Oxidation (M)
   35 - 50     1785.0070  1783.9997  1783.9064       52     1   R.IRLDQDDEGVPSTAIR.E
   57 - 75     2274.2778  2273.2705  2273.2015       30     1   K.ELRHENVVSLLEVIHEETK.L
   76 - 89     1771.8974  1770.8901  1770.9807      -51     1   K.LYLVFEYLDLDLKK.H
  286 - 296   1493.8237  1492.8164  1492.6848       88     1   R.WFDDYREHIGR.-
```

Spot No.: **208**

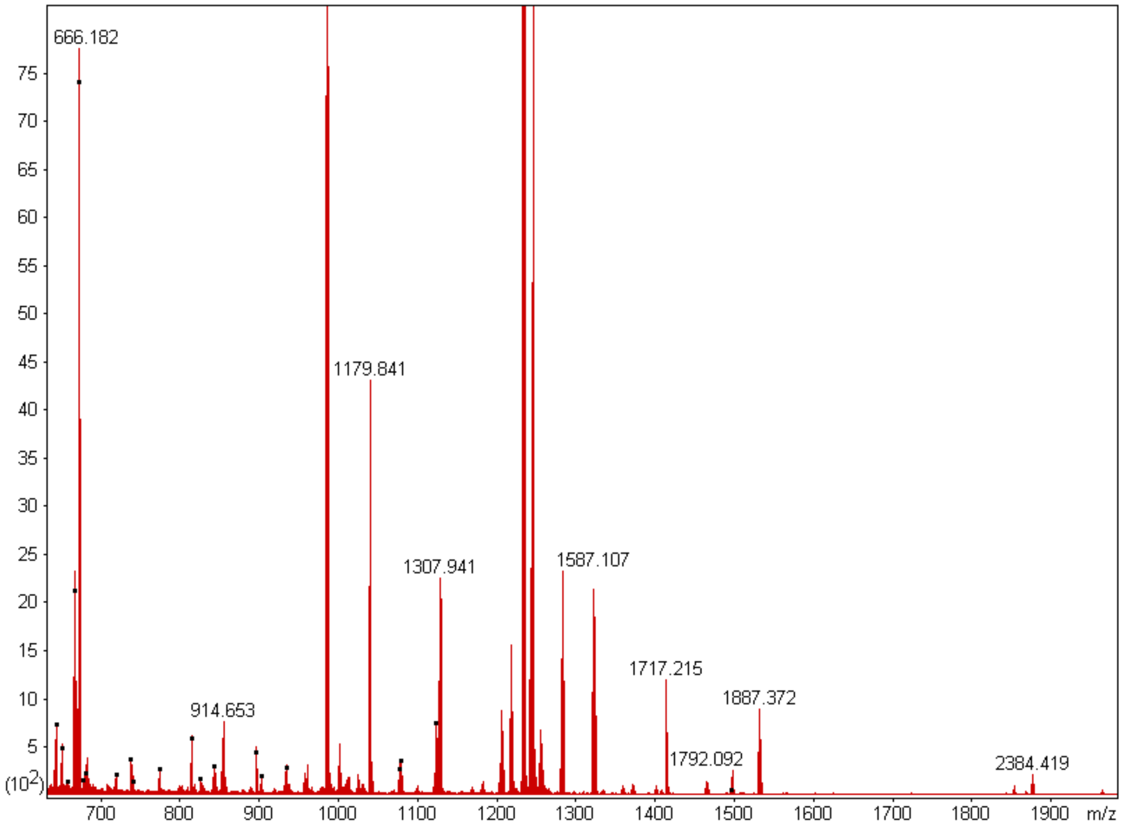
Mascot score: **133**　　Sequence coverage %: **36**

NCBI accession No.: **gi| 166359602**

Matched peptides No.: **12**　　Total peptides No.: **25**

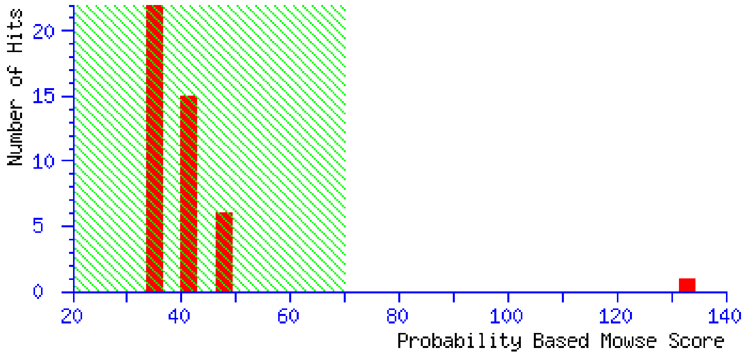
Calculated Mr: **24136**　　Calculated *p*I: **6.17**

Annotated PMF **spectra:**

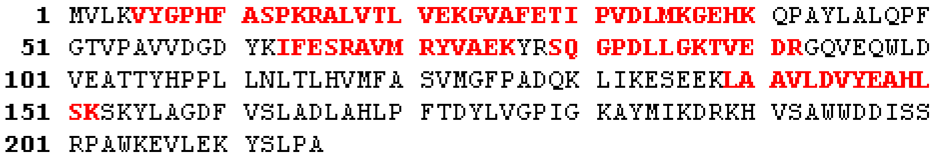


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 72 are significant (p<0.05).

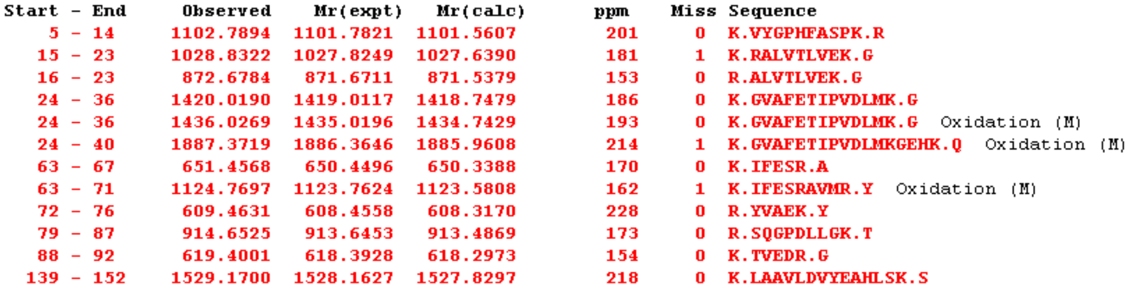


Matched peptide sequences: shown in Bold Red



```
  1 MVLKVYGPHF ASPKRALVTL VEKGVAFETI PVDLMKGEHK QPAYLALQPF
 51 GTVPAVVDGD YKIFESRAVM RYVAEKYRSQ GPDLLGKTVE DRGQVEQWLD
101 VEATTYHPPL LNLTLHVMFA SVMGFPADQK LIKESEEKLA AVLDVYEAHL
151 SKSKYLAGDF VSLADLAHLP FTDYLVGPIG KAYMIKDRKH VSAWWDDISS
201 RPAWKEVLEK YSLPA
```

Matched peptides information:



```
Start - End      Observed   Mr(expt)   Mr(calc)       ppm     Miss Sequence
    5 - 14      1102.7894  1101.7821  1101.5607       201       0  K.VYGPHFASPK.R
   15 - 23      1028.8322  1027.8249  1027.6390       181       1  K.RALVTLVEK.G
   16 - 23       872.6784   871.6711   871.5379       153       0  R.ALVTLVEK.G
   24 - 36      1420.0190  1419.0117  1418.7479       186       0  K.GVAFETIPVDLMK.G
   24 - 36      1436.0269  1435.0196  1434.7429       193       0  K.GVAFETIPVDLMK.G  Oxidation (M)
   24 - 40      1887.3719  1886.3646  1885.9608       214       1  K.GVAFETIPVDLMKGEHK.Q  Oxidation (M)
   63 - 67       651.4568   650.4496   650.3388       170       0  K.IFESR.A
   63 - 71      1124.7697  1123.7624  1123.5808       162       1  K.IFESRAVMR.Y  Oxidation (M)
   72 - 76       609.4631   608.4558   608.3170       228       0  R.YVAEK.Y
   79 - 87       914.6525   913.6453   913.4869       173       0  R.SQGPDLLGK.T
   88 - 92       619.4001   618.3928   618.2973       154       0  K.TVEDR.G
  139 - 152     1529.1700  1528.1627  1527.8297       218       0  K.LAAVLDVYEAHLSK.S
```

Spot No.: **209**

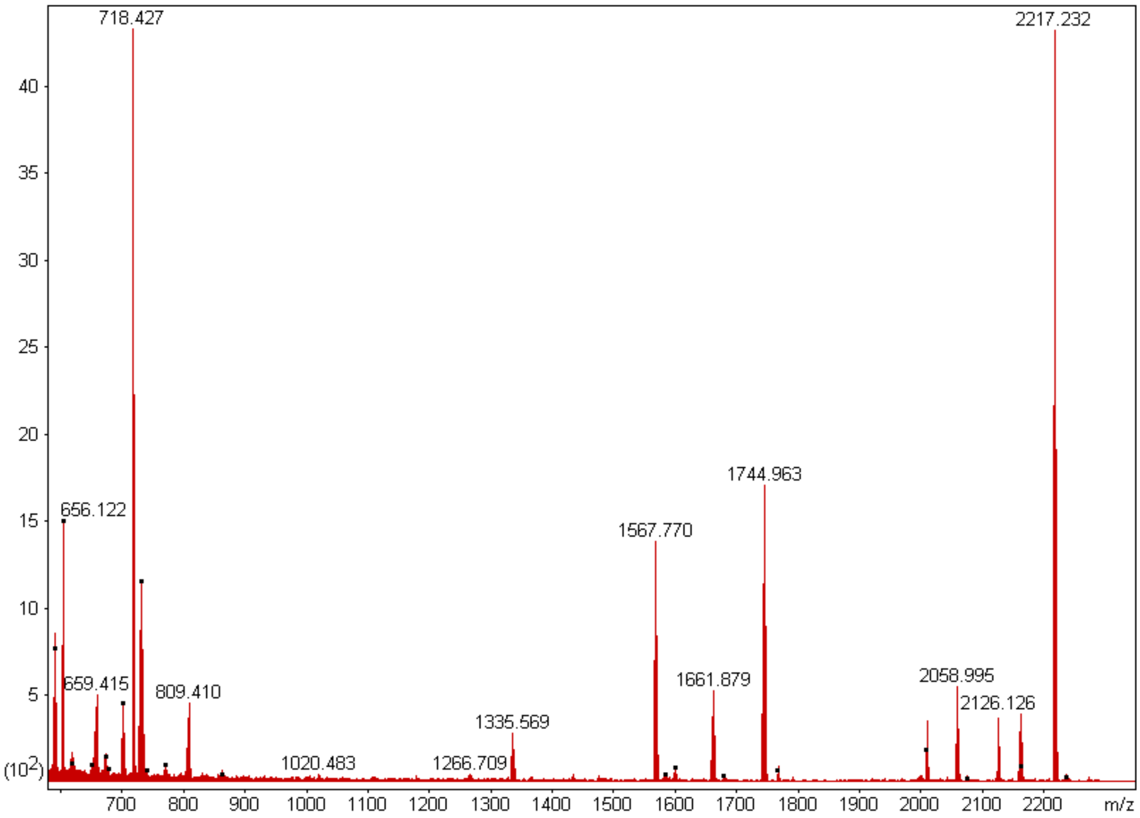
Mascot score: **115**   Sequence coverage %: **32**

NCBI accession No.: **gi| 15240250**

Matched peptides No.: **9**   Total peptides No.: **32**

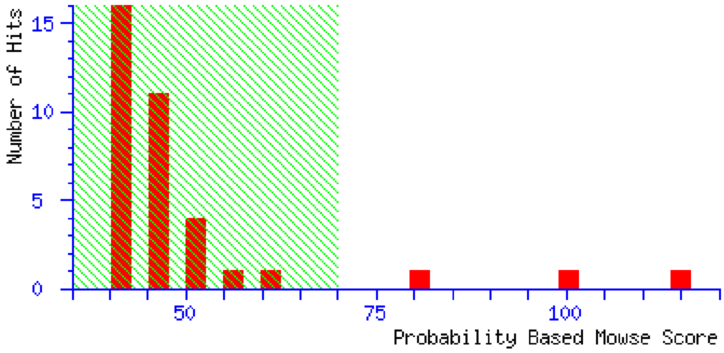
Calculated Mr: **30275**   Calculated *p*I: **8.24**

Annotated PMF **spectra:**

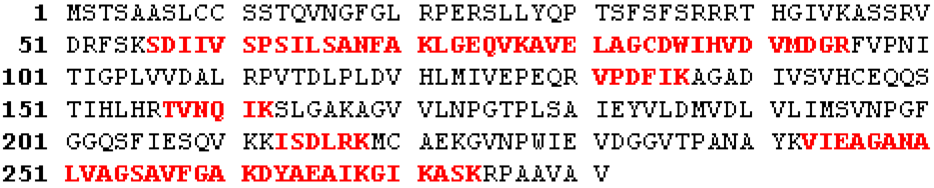


Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 72 are significant (p<0.05).

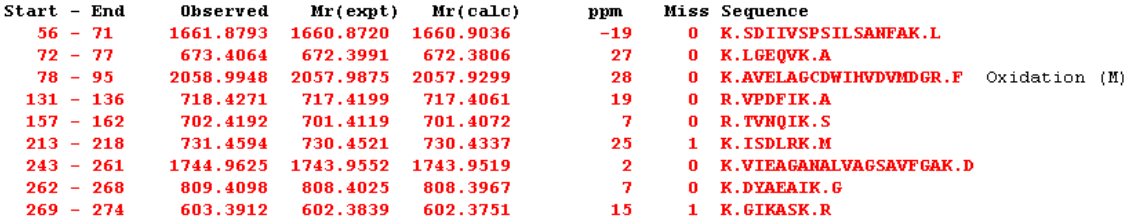


Matched peptide sequences: shown in Bold Red



```
  1 MSTSAASLCC SSTQVNGFGL RPERSLLYQP TSFSFSRRRT HGIVKASSRV
 51 DRFSKSDIIV SPSILSANFA KLGEQVKAVE LAGCDWIHVD VMDGRFVPNI
101 TIGPLVVDAL RPVTDLPLDV HLMIVEPEQR VPDFIKAGAD IVSVHCEQQS
151 TIHLHRTVNQ IKSLGAKAGV VLNPGTPLSA IEYVLDMVDL VLIMSVNPGF
201 GGQSFIESQV KKISDLRKMC AEKGVNPWIE VDGGVTPANA YKVIEAGANA
251 LVAGSAVFGA KDYAEAIKGI KASKRPAAVA V
```

Matched peptides information:



```
Start - End     Observed   Mr(expt)   Mr(calc)      ppm  Miss Sequence
   56 - 71     1661.8793  1660.8720  1660.9036      -19    0  K.SDIIVSPSILSANFAK.L
   72 - 77      673.4064   672.3991   672.3806       27    0  K.LGEQVK.A
   78 - 95     2058.9948  2057.9875  2057.9299       28    0  K.AVELAGCDWIHVDVMDGR.F  Oxidation (M)
  131 - 136     718.4271   717.4199   717.4061       19    0  R.VPDFIK.A
  157 - 162     702.4192   701.4119   701.4072        7    0  R.TVNQIK.S
  213 - 218     731.4594   730.4521   730.4337       25    1  K.ISDLRK.M
  243 - 261    1744.9625  1743.9552  1743.9519        2    0  K.VIEAGANALVAGSAVFGAK.D
  262 - 268     809.4098   808.4025   808.3967        7    0  K.DYAEAIK.G
  269 - 274     603.3912   602.3839   602.3751       15    1  K.GIKASK.R
```