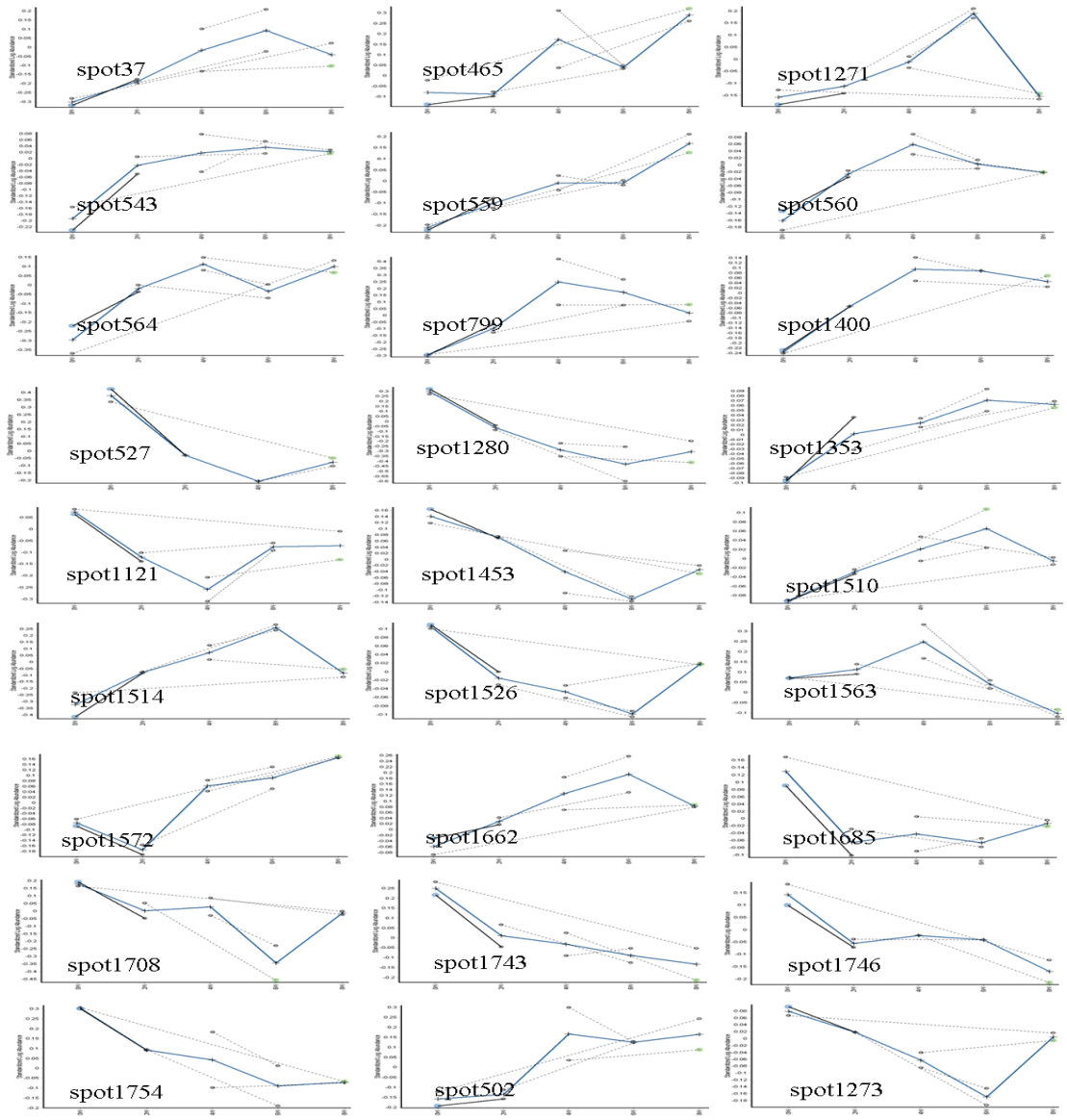
Supplemental data



Sport ID	Max	Anova	Wilcoxon		ratio>2 & Anova<0.05			
37	2.0789	0.0303203	0	1	"1"	"1"	"1"	"1"
465	3.8932	0.00104345	0	1	"1"	"1"	"1"	"1"
527	-3.52332	0.0124988	0	1	"1"	"1"	"1"	"1"
543	2.87164	0.00150523	0	1	"1"	"1"	"1"	"1"
559	2.26754	0.023475	0	1	"1"	"1"	"1"	"1"
560	2.64349	2.31345e-4	0	1	"1"	"1"	"1"	"1"
564	2.47844	0.0463818	0	1	"1"	"1"	"1"	"1"
502	2.23441	0.0148328	0	1	"1"	"1"	"1"	"1"
799	2.29926	0.0166998	0	1	"1"	"1"	"1"	"1"
1121	-2.39675	0.0231339	0	1	"1"	"1"	"1"	"1"
1271	3.02366	0.00121944	0	1	"1"	"1"	"1"	"1"
1273	-2.4166	0.0024406	0	1	"1"	"1"	"1"	"1"

1280	-2.2932	5.92003e-4	0	1	"1"	"1"	"1"	"1"
1353	2.02762	0.00764313	0	1	"1"	"1"	"1"	"1"
1400	2.20124	0.0123302	0	1	"1"	"1"	"1"	"1"
1453	-3.24803	2.03383e-4	0	1	"1"	"1"	"1"	"1"
1510	2.10708	7.60294e-5	0	1	"1"	"1"	"1"	"1"
1514	2.16199	0.0280563	0	1	"1"	"1"	"1"	"1"
1526	-2.97009	0.00582803	0	1	"1"	"1"	"1"	"1"
1563	-2.0115	0.0171667	0	1	"1"	"1"	"1"	"1"
1572	2.52943	0.0121619	0	1	"1"	"1"	"1"	"1"
1662	2.1056	0.00616959	0	1	"1"	"1"	"1"	"1"
1685	-2.13905	0.00174601	0	1	"1"	"1"	"1"	"1"
1708	-2.51956	0.0135997	0	1	"1"	"1"	"1"	"1"
1743	-2.14373	0.00749905	0	1	"1"	"1"	"1"	"1"
1746	-2.54728	0.0102367	0	1	"1"	"1"	"1"	"1"
1754	-3.50464	0.00260713	0	1	"1"	"1"	"1"	"1"

Supplemental data illustrates the MALDI-TOF-TOF MS/MS spectra of ions from the proteins that listed in Table 2, and the detailed information of mascot search results.

Spot 1572

Match to: **IPI00197703** Score: **270** Expect: **4e-023**

Tax_Id=10116 Gene_Symbol=Apoa1 Apolipoprotein A-I precursor

Nominal mass (M_r): **30043**; Calculated pI value: **5.52**

Sequence Coverage: **71%**

Matched peptides shown in **Bold Red**

1 MKAAVLAVAL VFLTGCQAWE FWQQDEPQSQ WDRVKDFATV YVDAVKDSGR

51 DYVSQFESST LGKQLNLNLL DNWDTLGSTV GRLQEQLGPV TQEFWANLEK

101 ETDWLRNEMN KDLENVKQKM QPHLDEFQEK WNEEVEAYRQ KLEPLGTELH

151 KNAKEMQRHL KVVAEEFRDR MRVNADALRA KFGLYSDQMR ENLAQRLTEI

201 KNHPTLIEYH TKASDHLKTL GEKAKPALDD LGQGLMPVLE AWKAKIMSMI

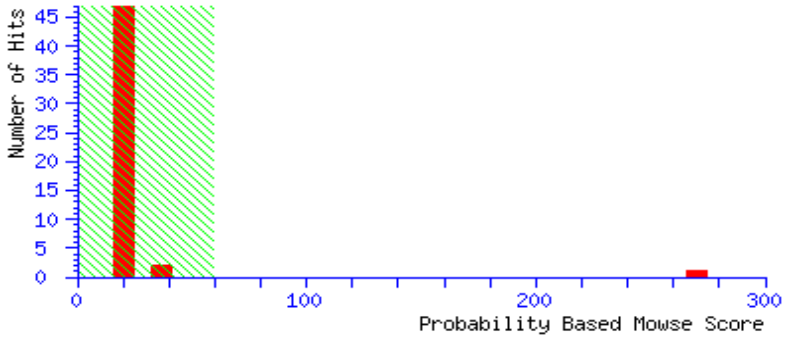
251 DEAKKKLNA

Probability Based Mowse Score

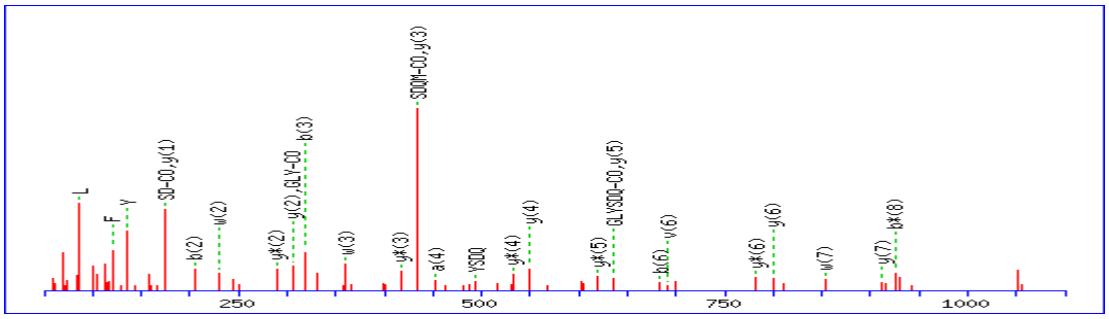
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 59 are significant (p<0.05).

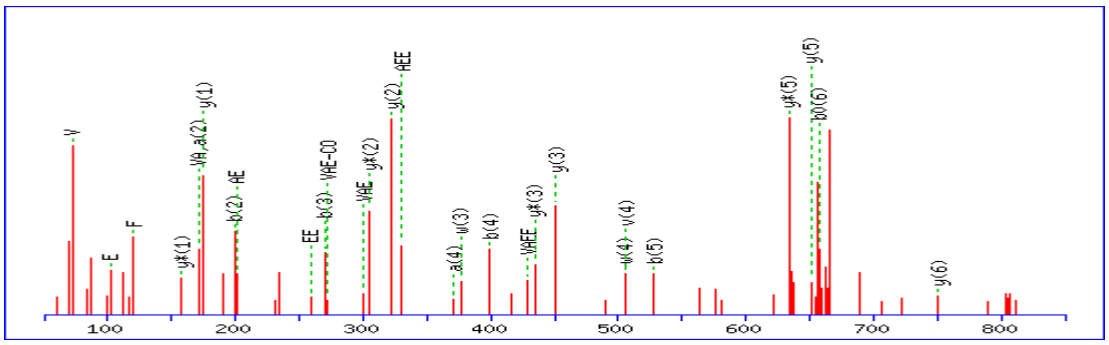
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



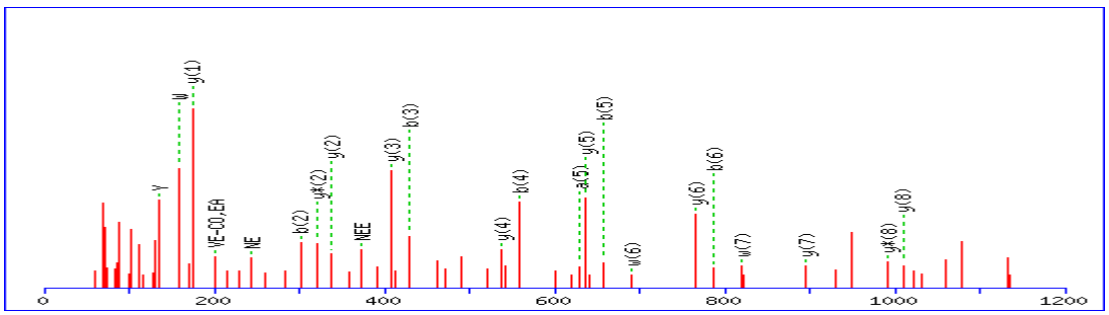
MS/MS Fragmentation of **FGLYSDQMR**



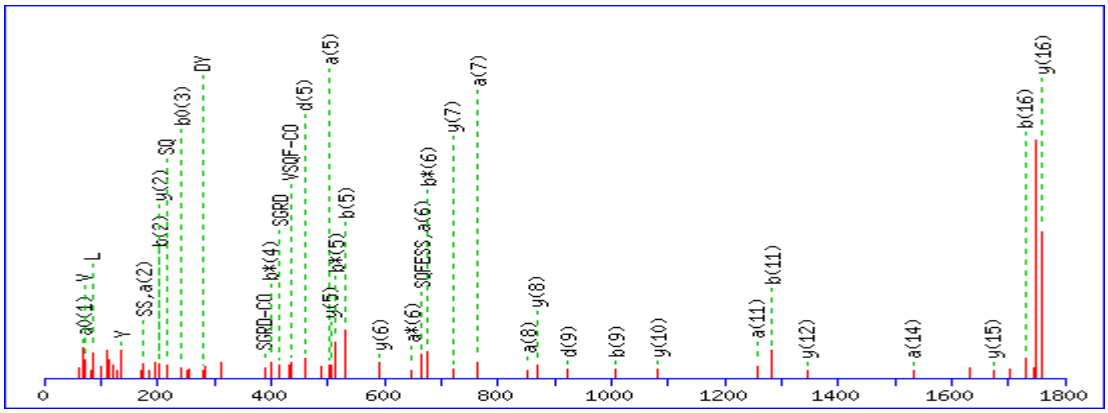
MS/MS Fragmentation of **VVAEEFR**



MS/MS Fragmentation of **WNEEVEAYR**



MS/MS Fragmentation of **DSGRDYVSQFESSTLGK**



Spot 1271

Match to: IPI00210823 Score: 498 Expect: 6.4e-046

Tax_Id=10116 Gene_Symbol=Akr1d1 3-oxo-5-beta-steroid 4-dehydrogenase

Nominal mass (M_r): 37354; Calculated pI value: 6.18

Sequence Coverage: 54%

Matched peptides shown in Bold Red

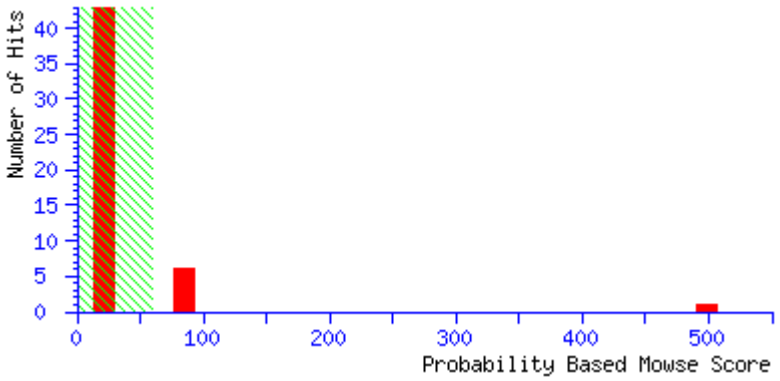
```
    1 MNLSTANHHI PLNDGNSIPI IGLGTYSDPR PVPGKTFIAV KTAIDEGYRH
   51 IDGAYVYRNE HEVGEAIREK VAEGKVKREE IFYCGKLWST DHDPEMVRPA
  101 LERTLQTLKL DYIDLYIIEM PMAFKPGEEF YPKDENGRVI YHKSNLCATW
  151 EALEACKDAG LVKSLGVSNF NRRQLEVILN KPGLKYKPVT NQVECHPYFT
  201 QTKLLEVSAS SMTSFIVAYS PLGTCRNPLW VNVSSPPLLK DELLTSLGKK
  251 YNKTQAQIVL RFDIQRGLVV IPKSTTPERI KENFQIFDFS LTKEEMKDIE
  301 ALNKNVRFVE MLMWSDHPEY PFHDEY
```

Probability Based Mowse Score

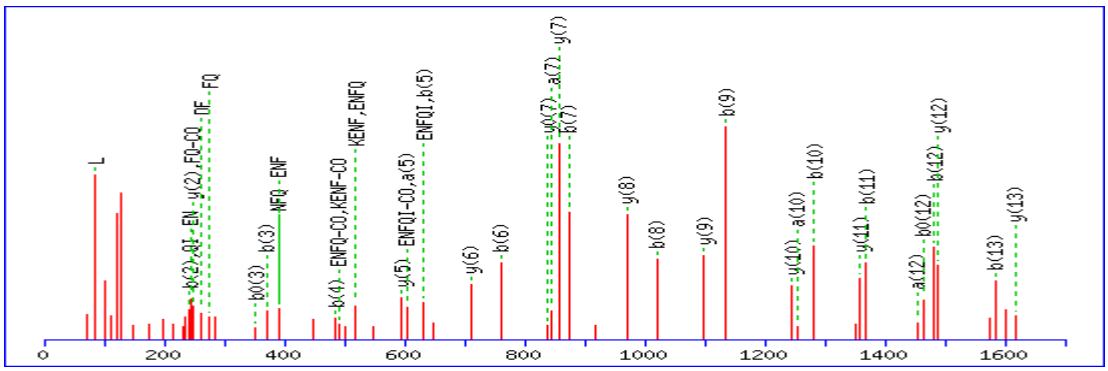
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 59 are significant (p<0.05).

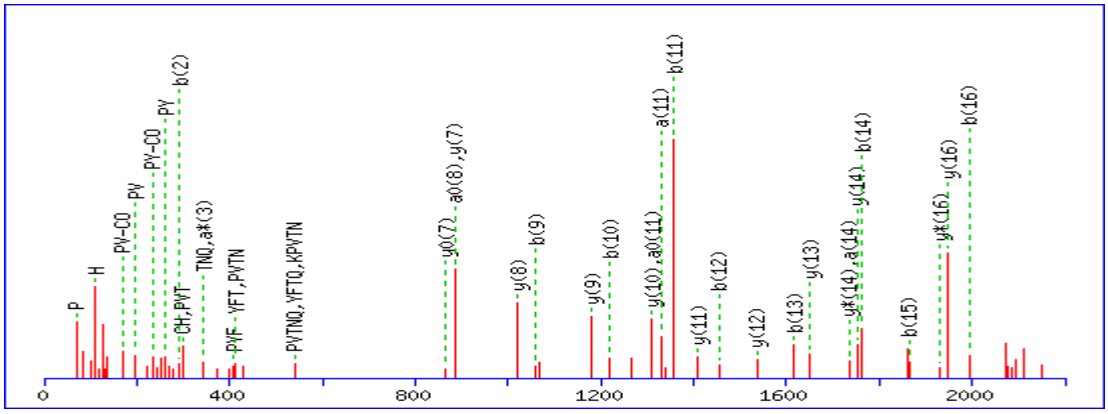
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



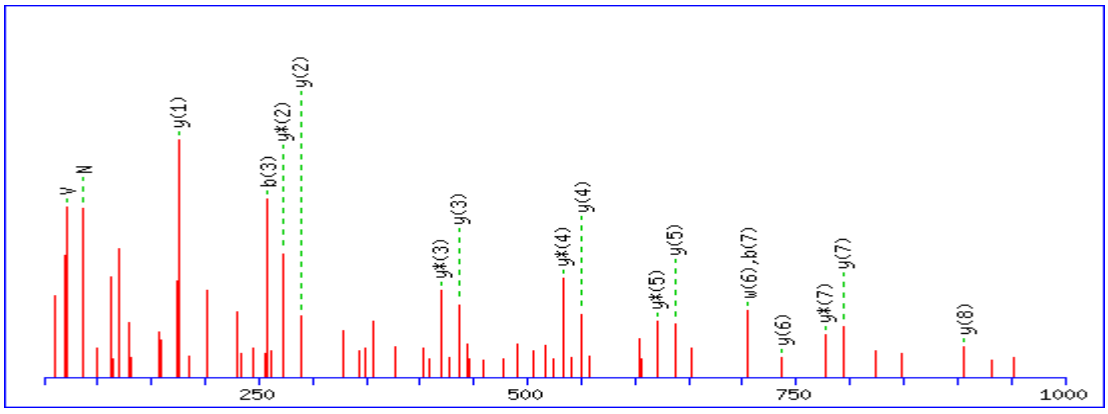
MS/MS Fragmentation of **IKENFQIFDFSLTK**



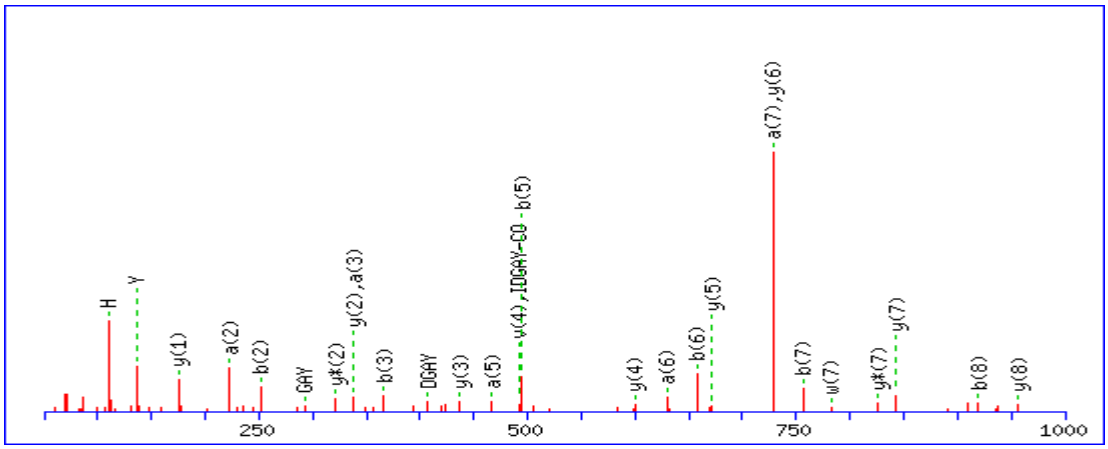
MS/MS Fragmentation of **YKPVTNQVECHPYFTQTK**



MS/MS Fragmentation of **SLGVSNFNR**



MS/MS Fragmentation of **HIDGAYVYR**



Spot 1510

Match to: IPI00231767 Score: 287 Expect: 8e-025

Tax_Id=10116 Gene_Symbol=Tpi1 Triosephosphate isomerase

Nominal mass (M_r): 26832; Calculated pI value: 6.89

Sequence Coverage: 75%

Matched peptides shown in **Bold Red**

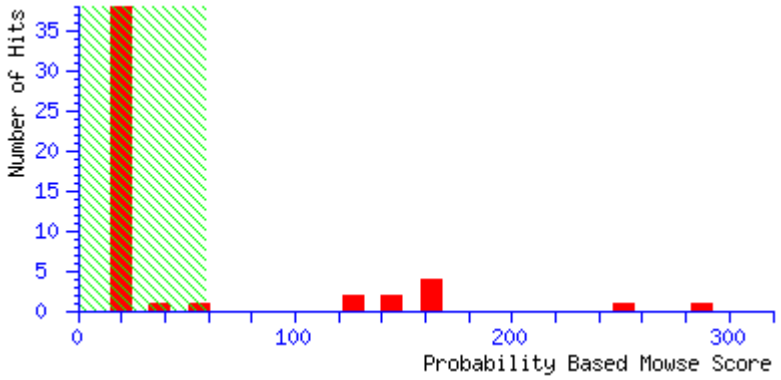
```
    1 MAPSRKFFVG GNWKMNGRKK CLGELICTLN AAKLPADTEV VCAPPTAYID
   51 FARQKLDPKI AVAAQNCYKV TNGAFTGEIS PGMIKDLGAT WVVLGHSERR
  101 HIFGESDELI GQKVNHALSE GLGVIACIGE KLDEREAGIT EKVVFEQTKA
  151 IADNVKDWCK VVLAYEPVWA IGTGKTATPQ QAQEVHEKLR GWLKCNVSEG
  201 VAQCTRIIYG GSVTGATCKE LASQPDVDGF LVGGASLKPE FVDIINAKQ
```

Probability Based Mowse Score

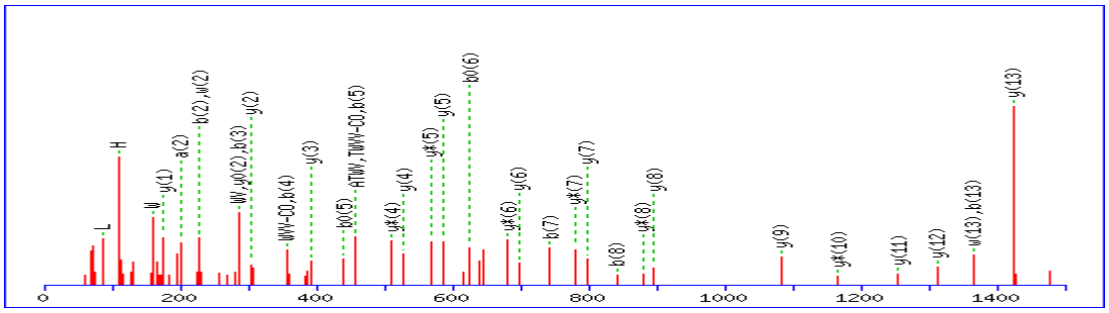
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 59 are significant (p<0.05).

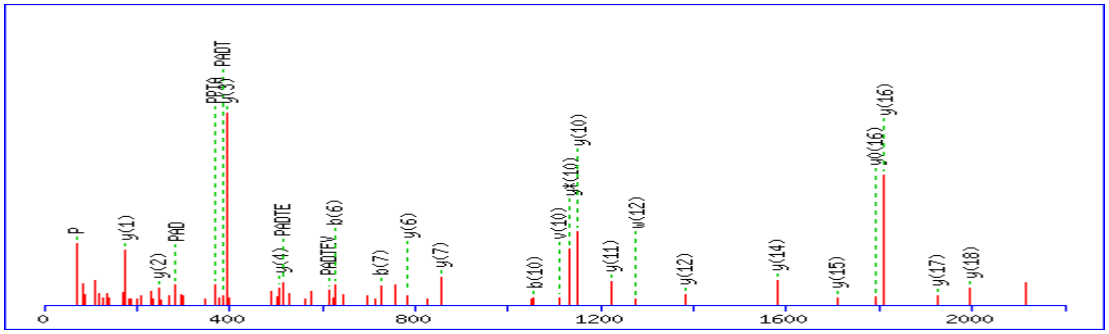
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



MS/MS Fragmentation of **DLGATWVVLGHSER**



MS/MS Fragmentation of **LPADTEVVCAPPTAYIDFAR**



Spot 1280

Match to: IPI00198717 Score: 428 Expect: 6.4e-039

Tax_Id=10116 Gene_Symbol=Mdh1 Malate dehydrogenase, cytoplasmic

Nominal mass (M_r): 36460; Calculated pI value: 6.16

Sequence Coverage: 46%

Matched peptides shown in **Bold Red**

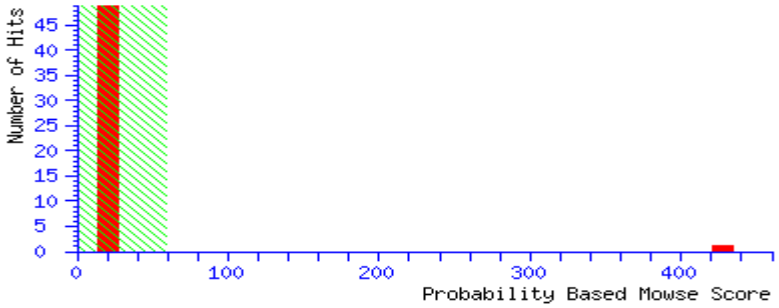
```
    1 MSEPIRVLVT GAAGQIAYSL LYSIGNGSVF GKDQPIILVL LDITPMMGVL
   51 DGVLMELQDC ALPLLQDVIA TDKEEVAFKD LDVAVLVGSM PRREGMERKD
  101 LLKANVKIFK SQGAALEKYA KKSVKVIVVG NPANTNCLTA SKSAPSIPKE
  151 NFSCLTRLDH NRAKSQIALK LGVTADDVKN VIIWGNHSST QYPDVNHAKV
  201 KLQGKEVGVY EALKDDSWLK GEFITTVQQR GAAVIKARKL SSAMSAAKAI
  251 SDHIRDIWFG TPEGEFVSMG VISDGNSYGV PDDLLYSFPV VIKNKTWKFV
  301 EGLPINDFSR EKMDLTAKEL TEEKETAFEF LSSA
```

Probability Based Mowse Score

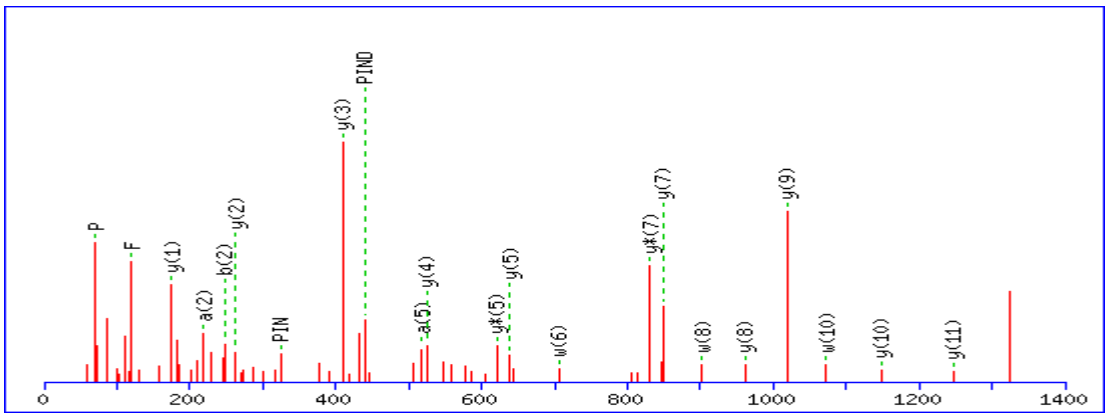
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 59 are significant (p<0.05).

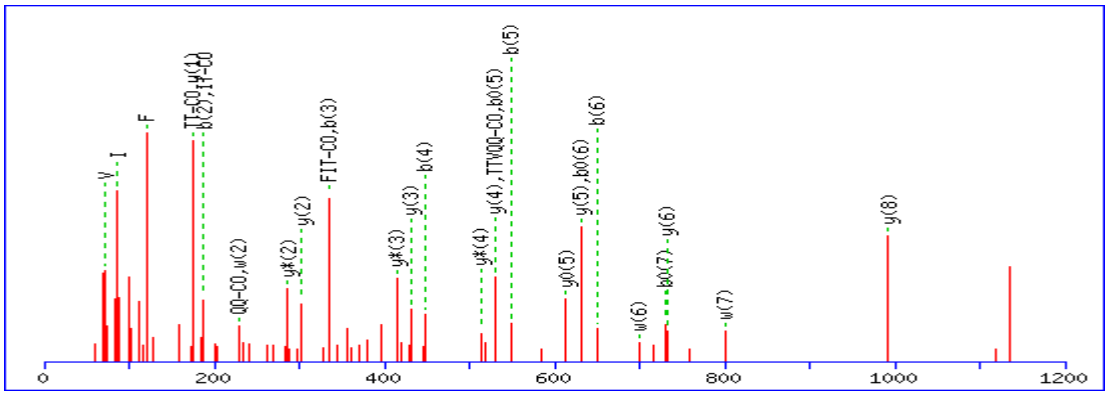
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



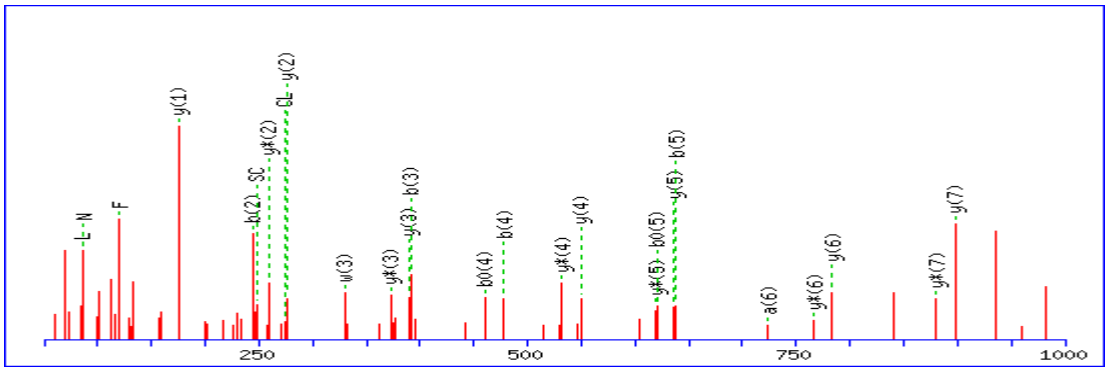
MS/MS Fragmentation of **FVEGLPINDFSR**



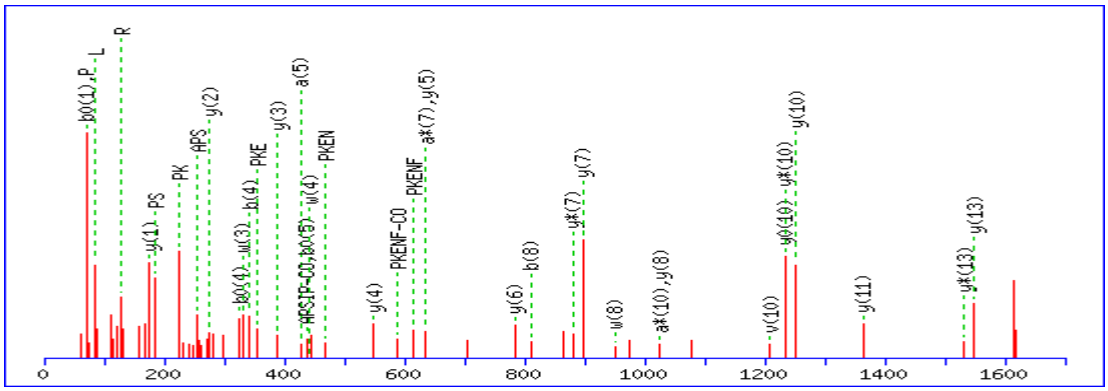
MS/MS Fragmentation of **GEFITTVQQR**



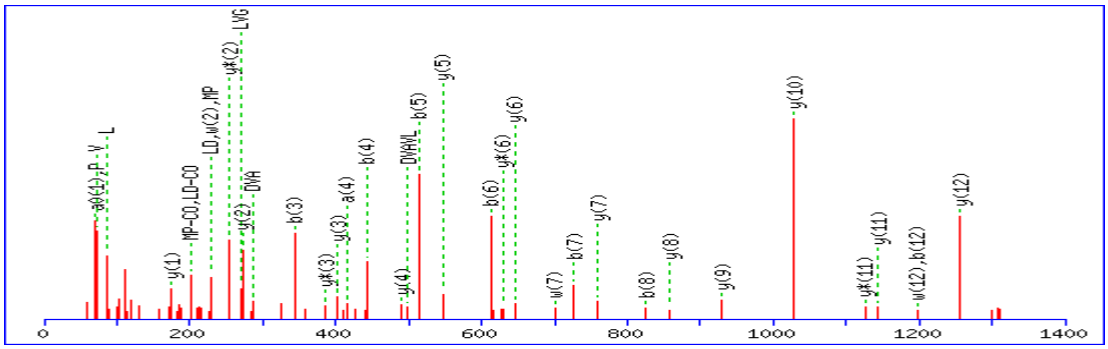
MS/MS Fragmentation of **ENFSCLTR**



MS/MS Fragmentation of **SAPSIPKENFSCLTR**



MS/MS Fragmentation of **DLDVAVLVGSMPR**



Spot 1121

Match to: IPI00360056 Score: 325 Expect: 1.3e-028

Tax_Id=10116 Gene_Symbol=Galm Aldose 1-epimerase

Nominal mass (M_r): 37869; Calculated pI value: 6.18

Sequence Coverage: 51%

Matched peptides shown in **Bold Red**

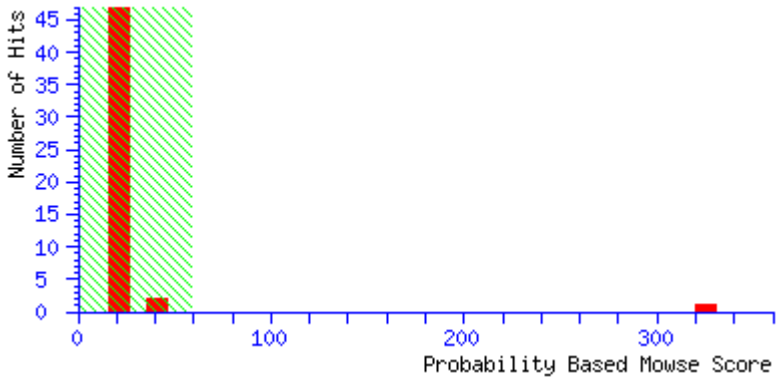
```
   1 MVSVTRTVFG ELPSGGGAVE KFQLRSDQLN VDIISWGCTI TALQVKDRQG
  51 KASDVVLGFA ELEGYLQKQP YFGAVVGRVA NRIAKGRFTV DGKEYHLPIN
 101 REPNSLHGGF RGFDKVLWTP QVLSNGVQFS RVSPDGEEGY PGELKVWVTY
 151 TLDGGELVVN YRAQASQTTP VNLTNHSYFN LAGQGSPDIY DHEVTIAADA
 201 YLPVDETLIP TGVIAPVEGT AFDLRKPVEL GKHLQSYHIH GFDHNFCLKE
 251 SKEKKFCARV HHAASGRILE VYTTQPGVQF YTGNFLDGTL KGKSGEVYPK
 301 HSGFCLETQN WPDAVNQPQF PPILLRPGEE YNHTTWFKFS VA
```

Probability Based Mowse Score

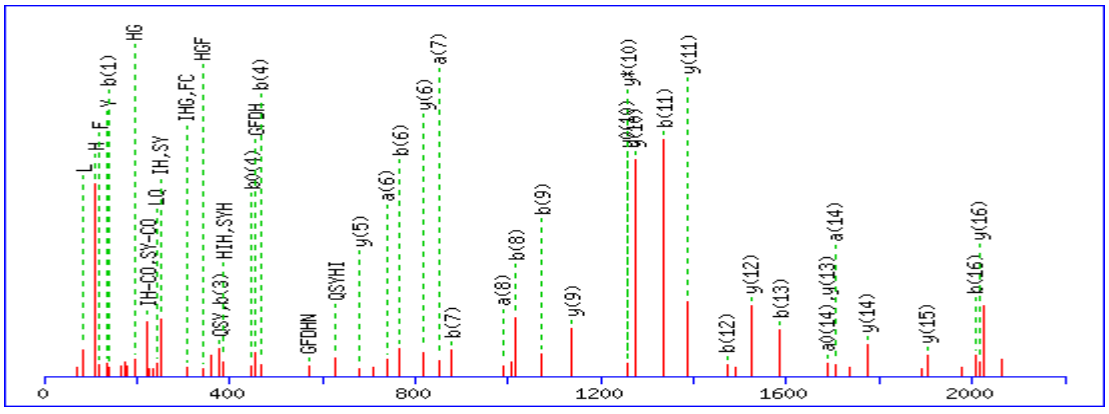
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 59 are significant (p<0.05).

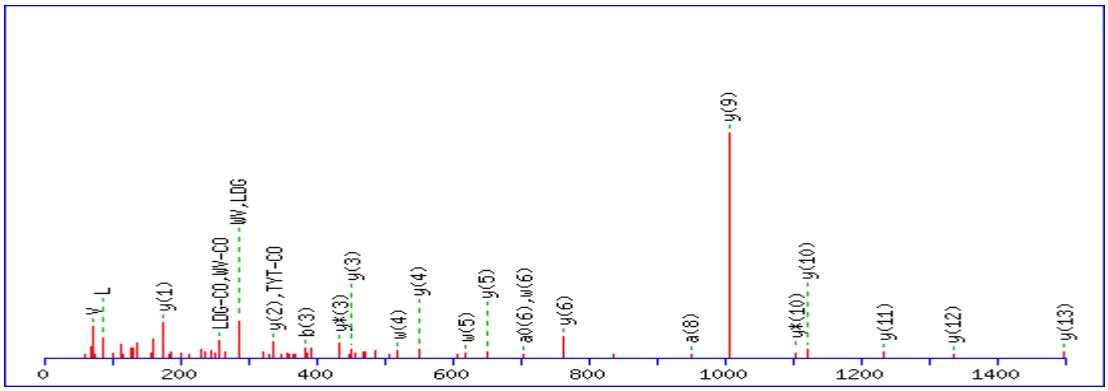
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



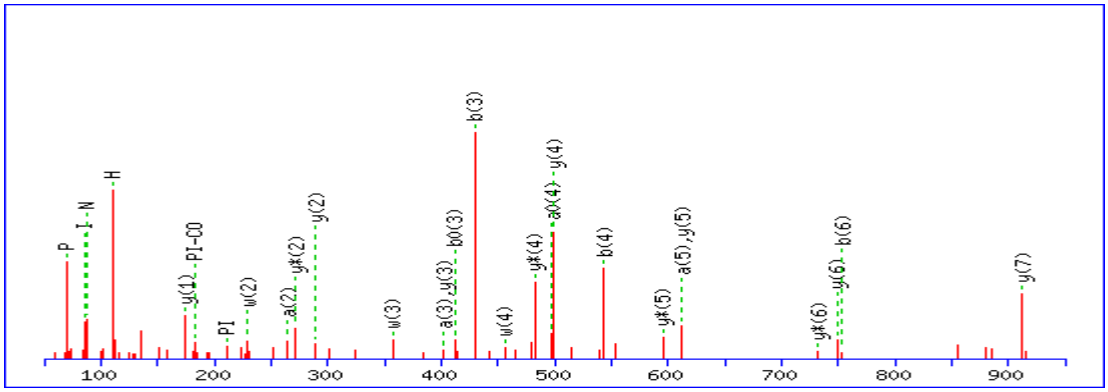
MS/MS Fragmentation of **HLQSYHIHGFDHNFCLK**



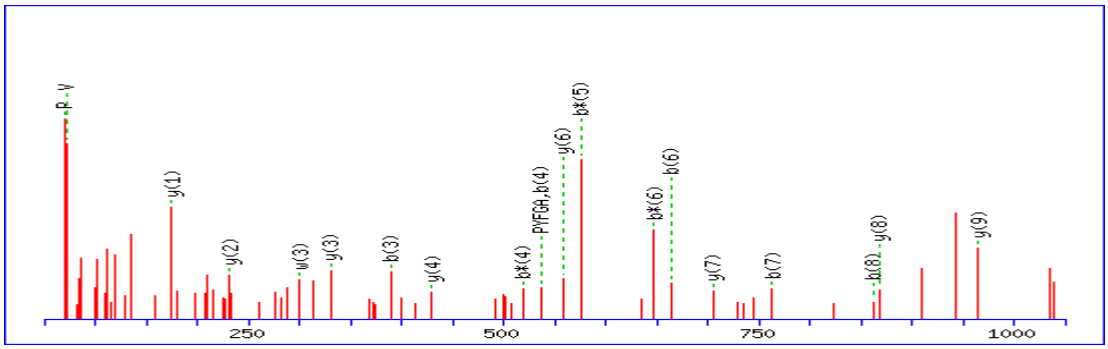
MS/MS Fragmentation of **VWVTYTLDGGELVVNYR**



MS/MS Fragmentation of **EYHLPINR**



MS/MS Fragmentation of **QPYFGAVVGR**



Spot 1353

Match to: IPI00194324 Score: 151 Expect: 3.2e-011

Tax_Id=10116 Gene_Symbol=Pdhb Pyruvate dehydrogenase E1 component subunit beta, mitochondrial precu

Nominal mass (M_r): 38957; Calculated pI value: 6.20

Sequence Coverage: 34%

Matched peptides shown in Bold Red

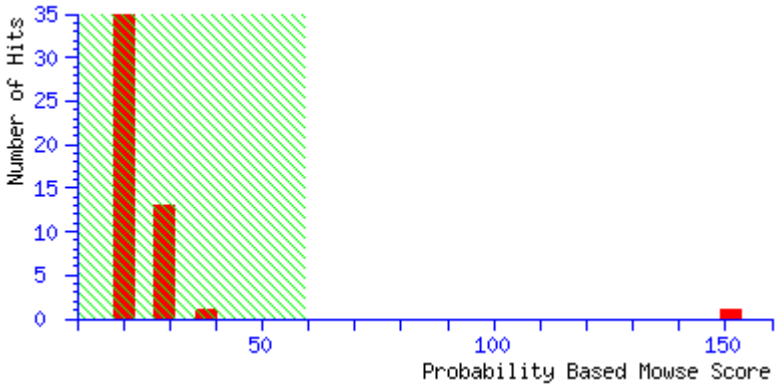
```
   1 MAAVAGLVRG PLRQASGLLK RRFHRSAPAA VQLTVREAIN QGMDEELERD
  51 EKVFLLGEEV AQYDGAYKVS RGLWKKYGDK RIIDTPISEM GFAGIAVGAA
 101 MAGLRPICEF MTFNFSMQAI DQVINSAAKT YYMSAGLQPV PIVFRGPNGA
 151 SAGVAAQHSQ CFAAWYGHCP GLKVVSPWNS EDAKGLIKSA IRDDNPVVML
 201 ENELMYGVAF ELPTEAQSKD FLIPIGKAKI ERQGTHITVV AHSRPVGHCL
 251 EAAAVLSKEG IECEVINLRT IRPMDIEAIE ASVMKTNHLV TVEGGWPQFG
 301 VGAEICARIM EGPAFNFLDA PAVRVTGADV PMPYAKILED NSIPQVKDII
 351 FAIKKTLNI
```

Probability Based Mowse Score

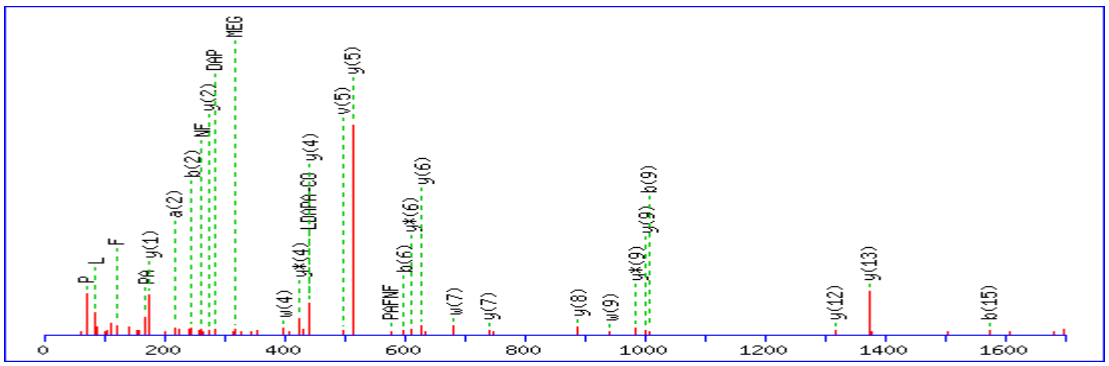
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 59 are significant (p<0.05).

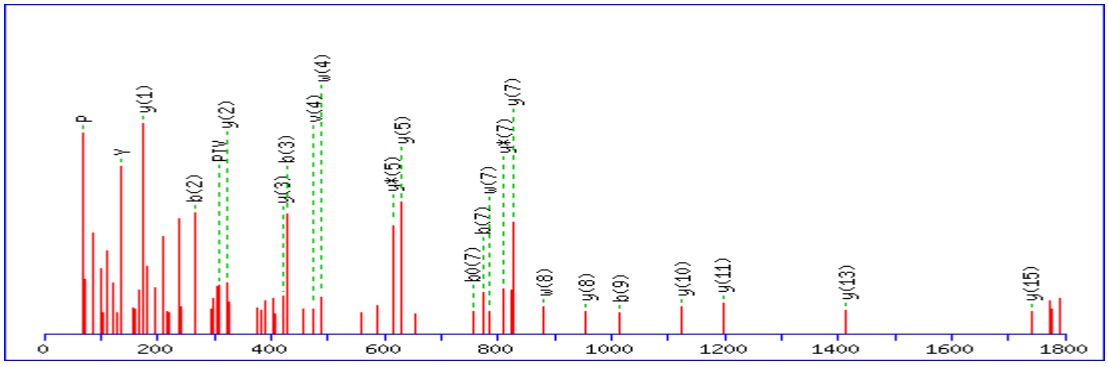
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



MS/MS Fragmentation of **IMEGPAFNFLDAPAVR**



MS/MS Fragmentation of **TYYMSAGLQPVPIVFR**



Spot 1273

Match to: IPI00197900 Score: 183 Expect: 2e-014

Tax_Id=10116 Gene_Symbol=Eef1d Translation elongation factor 1-delta subunit

Nominal mass (M_r): 28748; Calculated pI value: 4.86

Sequence Coverage: 49%

Matched peptides shown in Bold Red

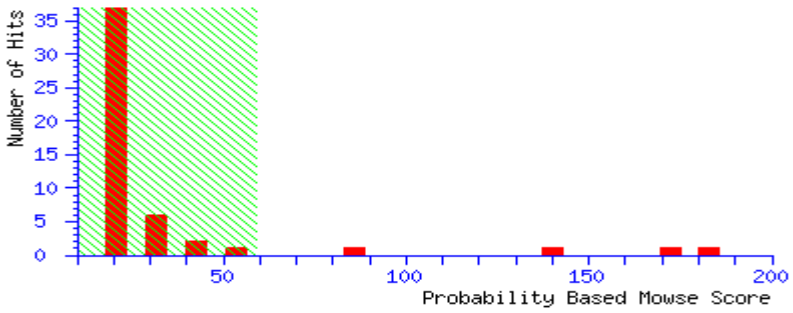
```
  1 MATNFLMHEK IWFDKFKYDD AERRFYEQMN GPVTAGSRQS SGPGASSGPG
 51 GDHSDLIVRI ASLEVENQNL RGVVQDLQQA ISKLEVRLST LEKSSPTHRA
101 TAPQTQHVSP MRQVEPPAKK GATPAEDDED NDIDLFGSDE EEEDKEAARL
151 REERLRQYAE KKAKKPTLVA KSSILLDVKP WDDETDMAQL ETCVRSIQLD
201 GLVWGASKLV PVGYGIRKLQ IQCVVEDDKV GTDLLEEEIT KFEEHVQSVD
251 IAAFNKI
```

Probability Based Mowse Score

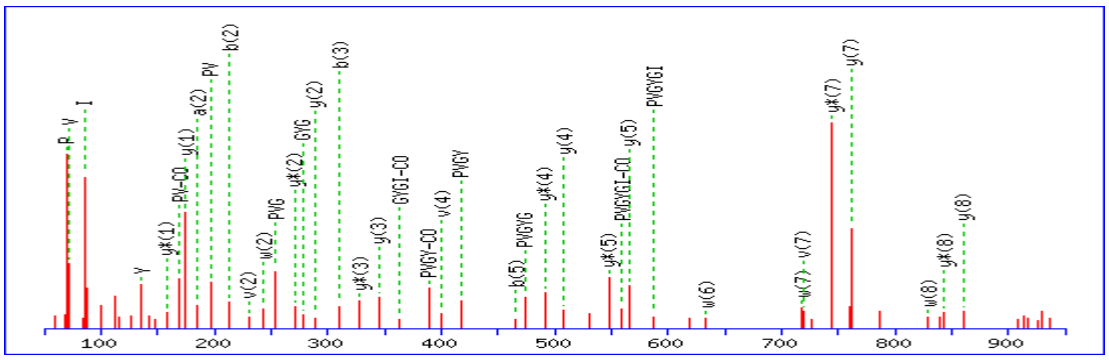
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 59 are significant (p<0.05).

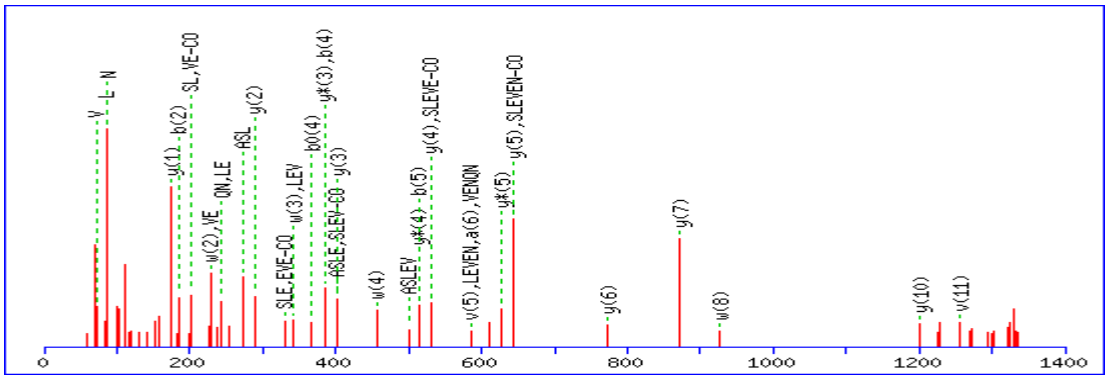
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



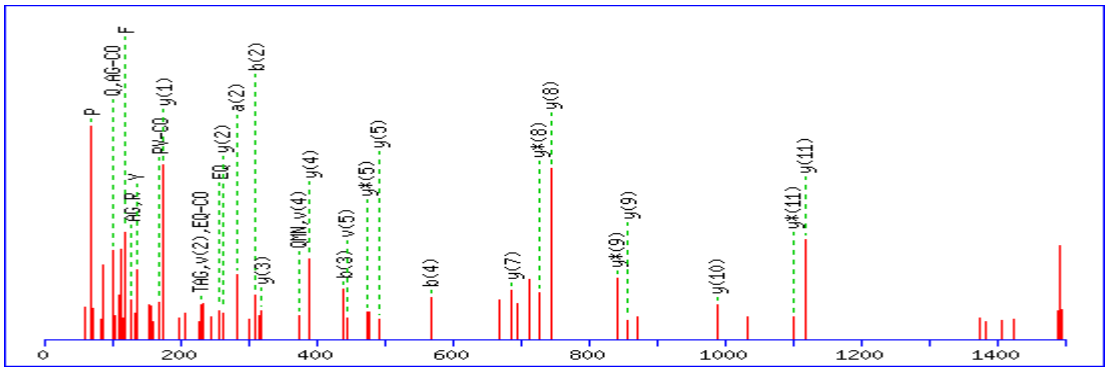
MS/MS Fragmentation of **LVPVGYGIR**



MS/MS Fragmentation of **IASLEVENQNLR**



MS/MS Fragmentation of **FYEQMNGPVTAGSR**



Spot 502

Match to: IPI00515829 Score: 191 Expect: 3.2e-015

Tax_Id=10116 Gene_Symbol=Kng1 Kininogen 1

Sequence Coverage: 37%

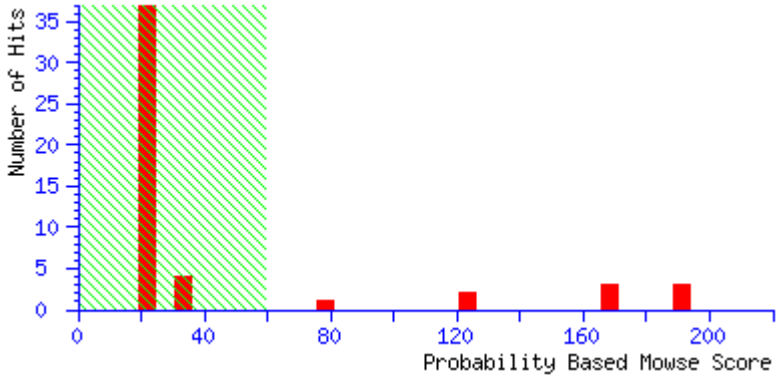
Matched peptides shown in Bold Red

```
  1 MKLITILLLC SRLLPSLAQE EGAQELNCND ETVFQAVDTA LKKYNAELES
 51 GNQFVLYRVT KGTKKDGAET LYSFKYQIKE GNCSVQSGLT WQDCDFKDAE
101 EAATGECTTT LGKKENKFSV ATQICNITPG KGPKKTEEDL CVGCFQPIPM
151 DSSDLKPVLK HAVEHFNNNT KHTHLFALRE VKSAHSQVVA GMNYKIIYSI
201 VQTNCSKEDF PSLREDCVPL PYGDHGECTG HTHVDIHNTI AGFSQSCDLY
251 PGDDLFELLP KNCRGCPREI PVDSPELKEA LGHSIAQLNA QHNHIFYFKI
301 DTVKKATSQV VAGVIYVIEF IARETNCSKQ SKTELTADCE TKHLGQSLNC
351 NANVYMRPWE NKVVPTVRCQ ALDMMISRPP GFSPFRLVRV QETKEGTTRL
```

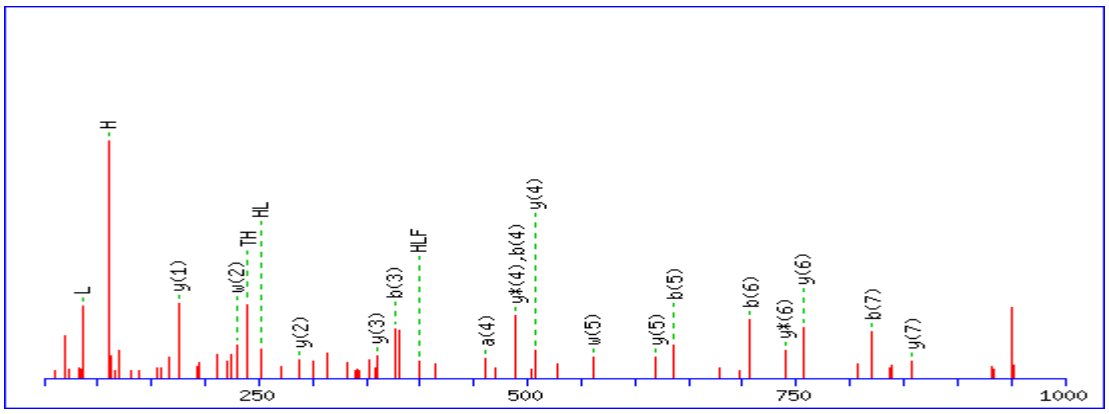
401 LNSCEYKGRL SKARAGPAPD HQAEASTVTS

Probability Based Mowse Score

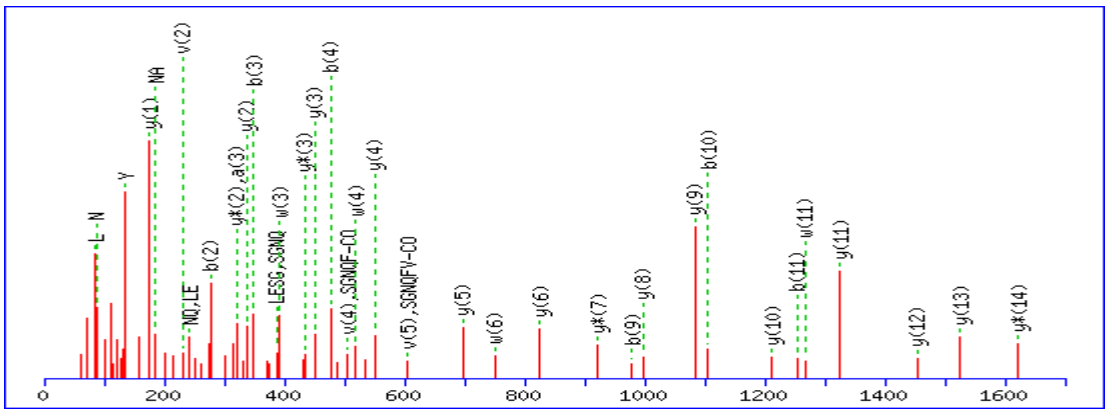
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 59 are significant (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



MS/MS Fragmentation of **HTHLFALR**



MS/MS Fragmentation of **YNAELESGNQFVLYR**



Spot 37

Match to: IPI00210644 Score: 179 Expect: 5e-014

Tax_Id=10116 Gene_Symbol=Cps1 Carbamoyl-phosphate synthase [ammonia], mitochondrial precursor

Nominal mass (M_r): 164476; Calculated pI value: 6.33

Sequence Coverage: 22%

Matched peptides shown in Bold Red

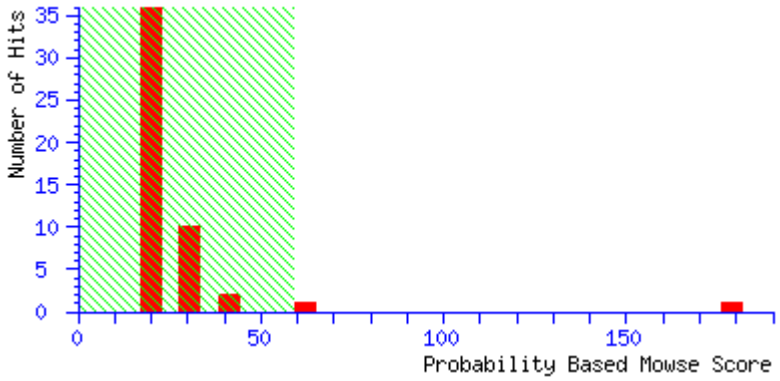
```
   1 MTRILTACKV VKTLKSGFGL ANVTSKRQWD FSRPGIRLLS VKAQTAHIVL
  51 EDGTKMKGYS FGHPSSVAGE VVFNTGLGGY SEALTDPAYK GQILTMANPI
 101 IGNGGAPDTT ARDELGLNKY MESDGIKVAG LLVLNYSHDY NHWLATKSLG
 151 QWLQEEKVPA IYGVDTRMLT KIIRDKGTML GKIEFEGQSV DFVDPNKQNL
 201 IAEVSTKDVK VFGKGNPTKV VAVDCGIKNN VIRLLVKRGA EVHLVPWNHD
 251 FTQMDYDGLL IAGGPGNPAL AQPLIQNVKK ILESDRKEPL FGISTGNIIT
 301 GLAAGAKSYK MSMANRGQNQ PVLNITNRQA FITAQNHGYA LDNTLPAGWK
 351 PLFVNVNDQT NEGIMHESKP FFAVQFHPEV SPGPTDTEYL FDSFFSLIKK
 401 GKGTTITSVL PKPALVASRV EVSKVLILGS GGLSIGQAGE FDYSGSQAVK
 451 AMKEENVKTV LMNPNIASVQ TNEVGLKQAD AVYFLPITPQ FVTEVIKAER
 501 PDGLILGMGG QTALNCGVEL FKRGVLKEYG VKVLGTSVES IMATEDRQLF
 551 SDKLNEINEK IAPSFAVESM EDALKAADTI GYPVMIRSAY ALGGLGSGIC
 601 PNKETLMDLG TKAFAMTNQI LVERSVTGWK EIEYEVVRDA DDNCVTVCNM
 651 ENVDAMGVHT GDSVVVAPAQ TLSNAEFQML RRTSINVVRH LGIVGECNIQ
 701 FALHPTSMEY CIIEVNARLS RSSALASKAT GYPLAFIAAK IALGIPLPEI
 751 KNVVSGKTSA CFEPSLDYMV TKIPRWDLDR FHGTSSRIGS SMKSVGEVMA
 801 IGRTFEESFQ KALRMCHPSV DGFTPRLPMN KEWPANLDLR KELSEPSSTR
 851 IYAIAKALEN NMSLDEIVKL TSIDKWFLYK MRDILNMDKT LKGLNSESVT
 901 EETLRQAKEI GFSDKQISKC LGLTEAQTRE LRLKKNIHPW VKQIDTLAAE
 951 YPSVTNYLYV TYNGQEHDIK FDEHGIMVLG CGPYHIGSSV EFDWCAVSSI
1001 RTLRQLGKKT VVVNCNPETV STDFDECDKL YFEELSLERI LDIYHQEACN
1051 GCIISVGGQI PNNLAVPLYK NGVKIMGTSP LQIDRAEDRS IFSAVLDELK
1101 VAQAPWKAVN TLNEALEFAN SVGYPCLLRP SYVLSGSAMN VVFSEDEMKR
1151 FLEEATRVSQ EHPVVLTKFI EGAREVEMDA VGKEGRVISH AISEHVEDAG
1201 VHSGDATLML PTQTISQGAI EKVKDATRKI AKAFAISGPF NVQFLVKGND
1251 VLVIECNLRA SRSFPFVSKT LGVDFIDVAT KVMIGESVDE KHLPTLEQPI
1301 IPSDYVAIKA PMFSWPRLRD ADPILRCEMA STGEVACFGE GIHTAFLKAM
1351 LSTGFKIPQK GILIGIQQSF RPRFLGVAEQ LHNEGFKLFA TEATSDWLNA
1401 NNVPATPVAW PSQEGQNPSL SSIRKLIRDG SIDLVINLPN NNTKFVHDNY
1451 VIRRTAVDSG IALLTNFQVT KLFAEAVQKA RTVDSKSLFH YRQYSAGKAA
1501
```

Probability Based Mowse Score

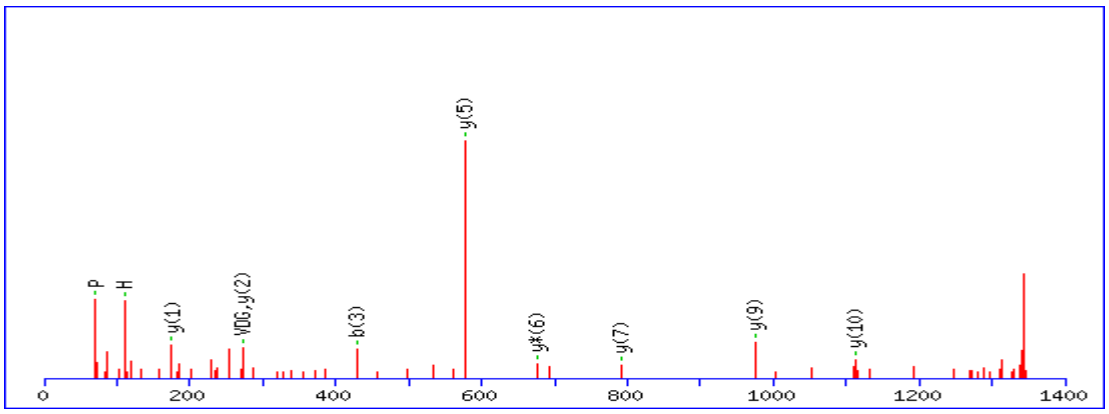
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 59 are significant (p<0.05).

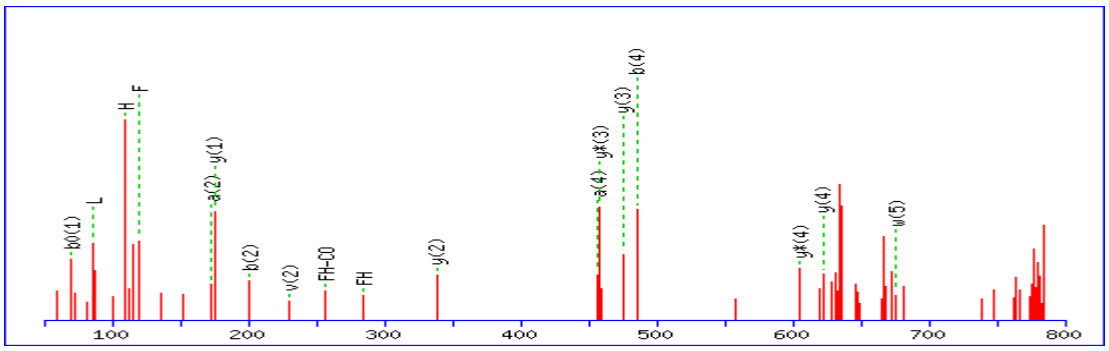
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



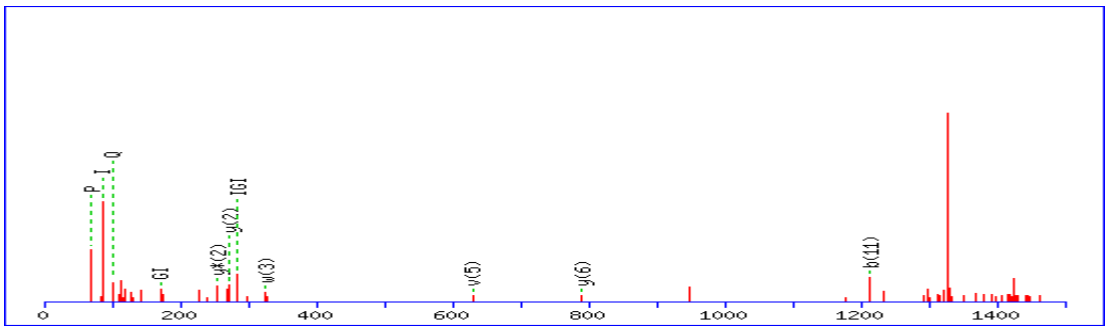
MS/MS Fragmentation of **MCHPSVDGFTPR**



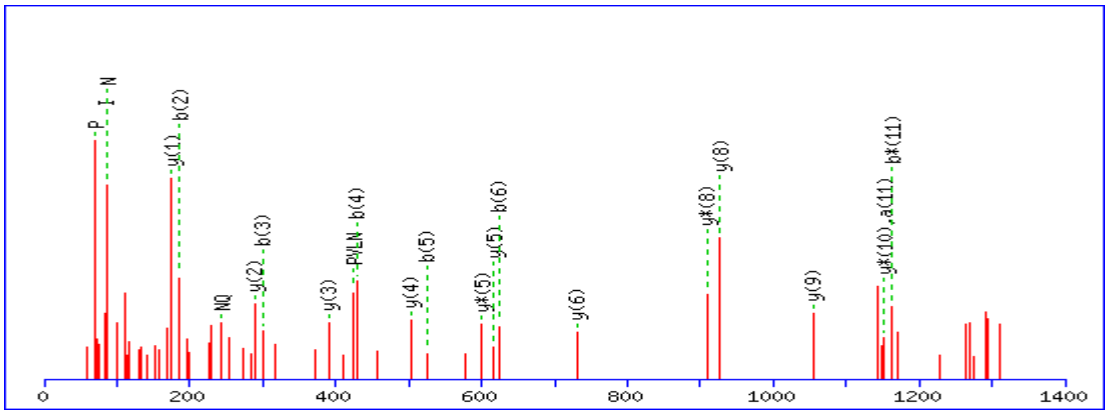
MS/MS Fragmentation of **SLFHYR**



MS/MS Fragmentation of **GILIGIQQSFRPR**



MS/MS Fragmentation of **GQNQPVLNITNR**


P
I
N
y(1)
b(2)
NQ
y(2)
b(3)
y(3)
PVEN
b(4)
y(4)
b(5)
y*(5)
y(5)
b(6)
y(6)
y*(8)
y(8)
y(9)
y*(10),a(11)
b*(11)
0
200
400
600
800
1000
1200
1400

Spot 1743

Match to: IPI00231963 Score: 376 Expect: 1e-033

Tax_Id=10116 Gene_Symbol=Ddt D-dopachrome decarboxylase

Nominal mass (M_r): 13125; Calculated pI value: 6.09

Sequence Coverage: 79%

Matched peptides shown in Bold Red

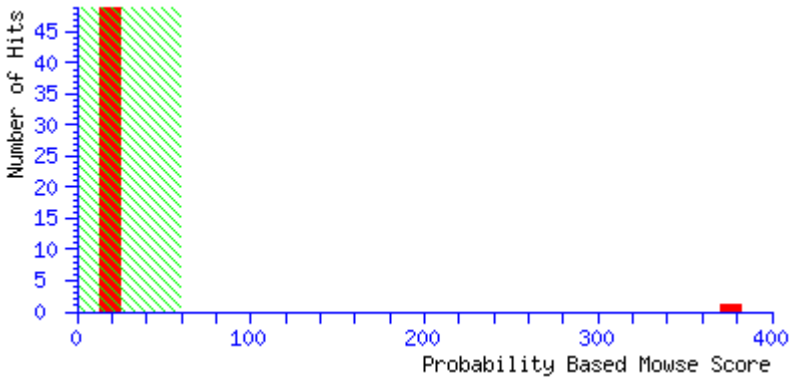
```
   1 MPFVELETNL PASRIPAGLE NRLCAATATI LDKPEDRVSV TIRPGMTLLM
  51 NKSTEPCAHL LISSIGVVGT AEQNRSHSSS FFKFLTEELS LDQDRIIIRF
 101 FPLEPWQIGK KGTVMTFL
```

Probability Based Mowse Score

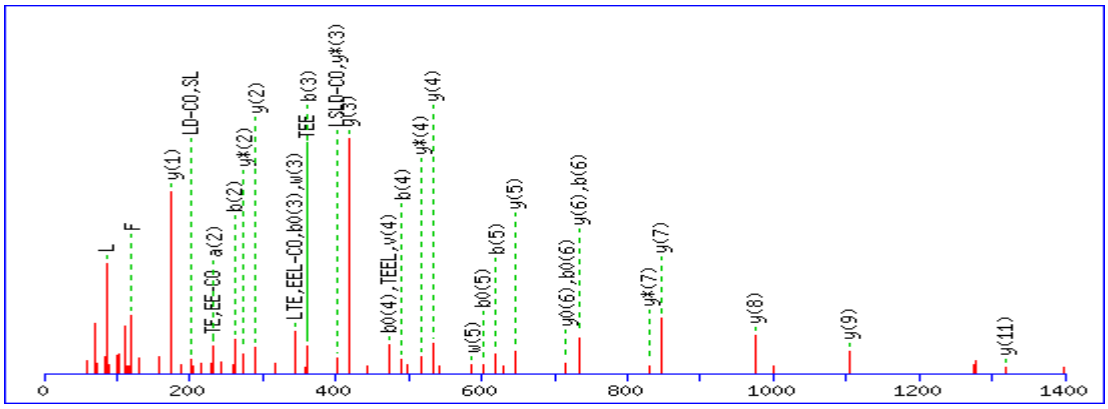
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 59 are significant (p<0.05).

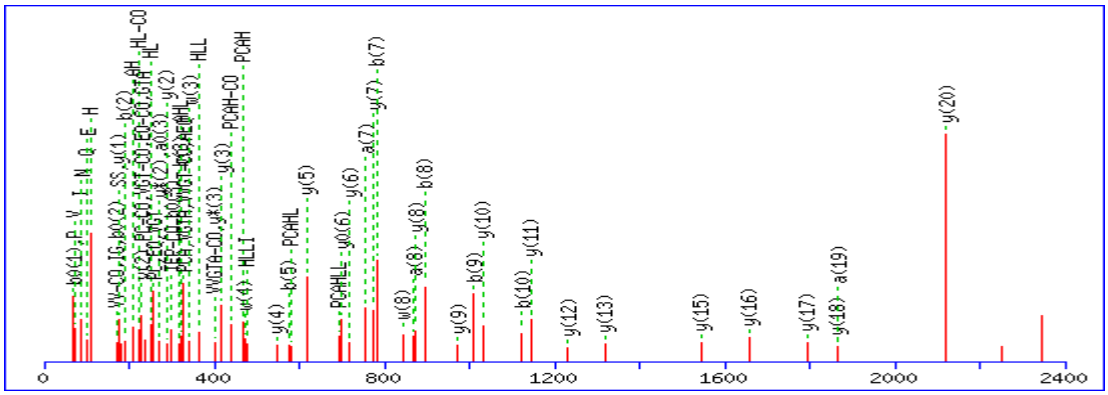
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



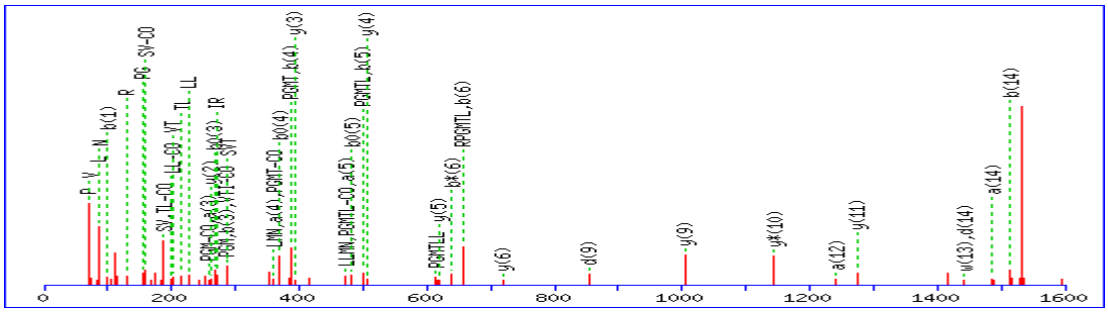
MS/MS Fragmentation of **FLTEELSLDQDR**



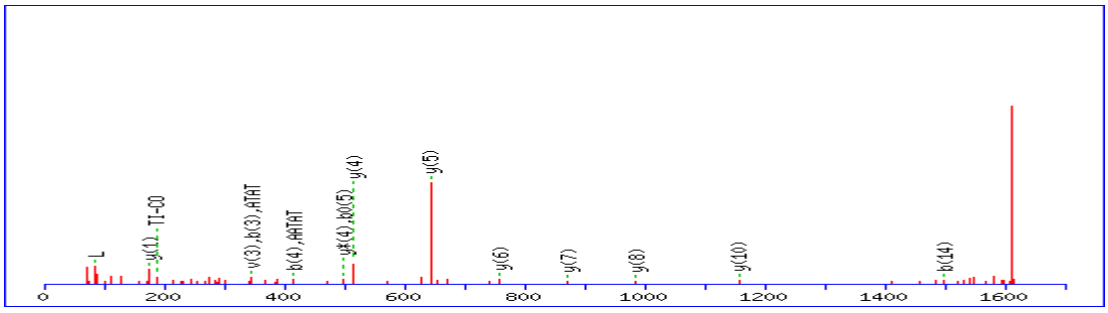
MS/MS Fragmentation of **STEPCAHLLISSIGVVGTAEQNR**



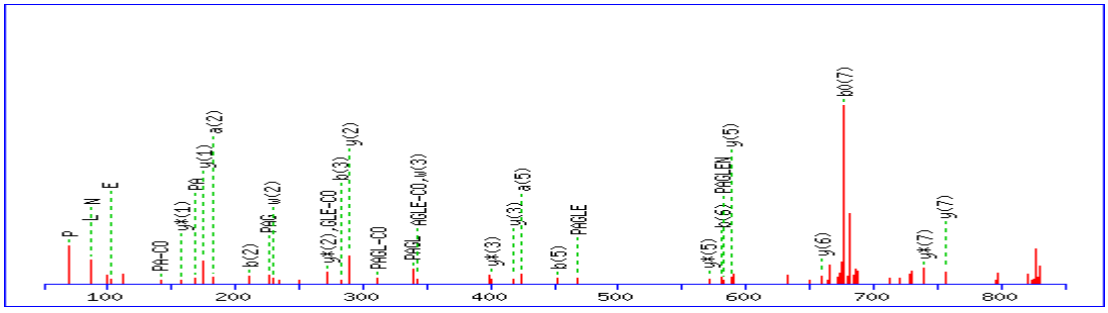
MS/MS Fragmentation of **VSVTIRPGMTLLMNK**



MS/MS Fragmentation of **LCAATATILDKPEDR**



MS/MS Fragmentation of **IPAGLENR**



Spot 1708

Match to: IPI00324380 Score: 146 Expect: 1e-010

Tax_Id=10116 Gene_Symbol=Ttr Transthyretin precursor

Nominal mass (M_r): 15710; Calculated pI value: 5.77

Sequence Coverage: 20%

Matched peptides shown in **Bold Red**

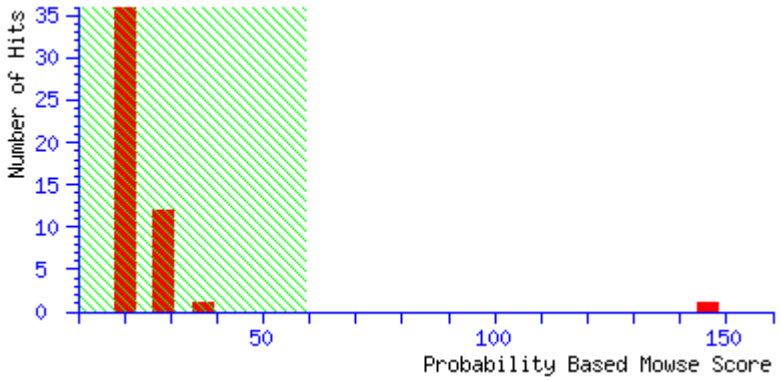
```
    1 MASLRLFLLC LAGLIFASEA GPGGAGESKC PLMVKVLDAV RGSPAVDVAV
   51 KVFKKTADGS WEPFASGKTA ESGELHGLTT DEKFTEGVYR VELDTKSYWK
  101 ALGISPFHEY AEVVFTANDS GHRHYTIAAL LSPYSYSTTA VVSNPQN
```

Probability Based Mowse Score

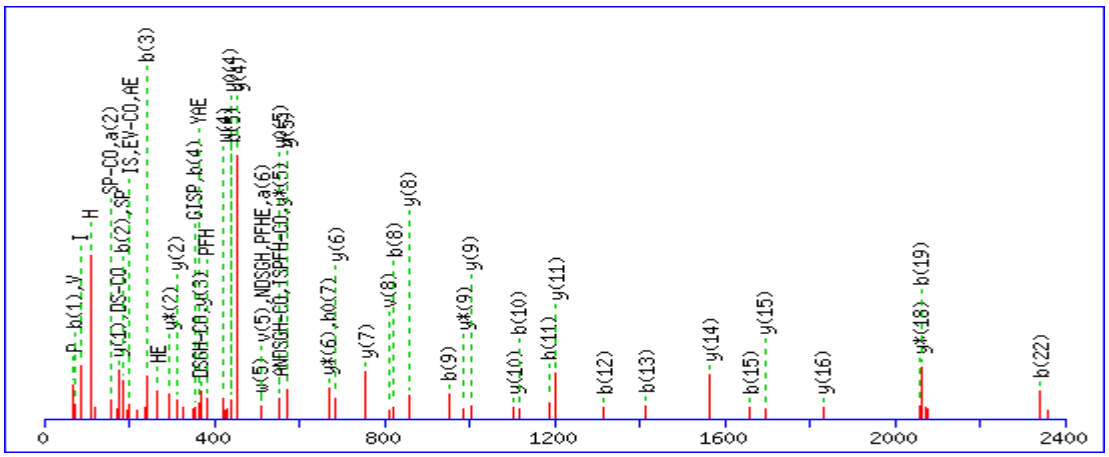
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 59 are significant (p<0.05).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



MS/MS Fragmentation of **ALGISPFHEYAEVVFTANDSGHR**



Spot 1168

Match to: IPI00327518 Score: 334 Expect: 1.6e-029

Tax_Id=10116 Gene_Symbol=Arg1 Arginase-1

Nominal mass (M_r): 36481; Calculated pI value: 6.51

Sequence Coverage: 62%

Matched peptides shown in **Bold Red**

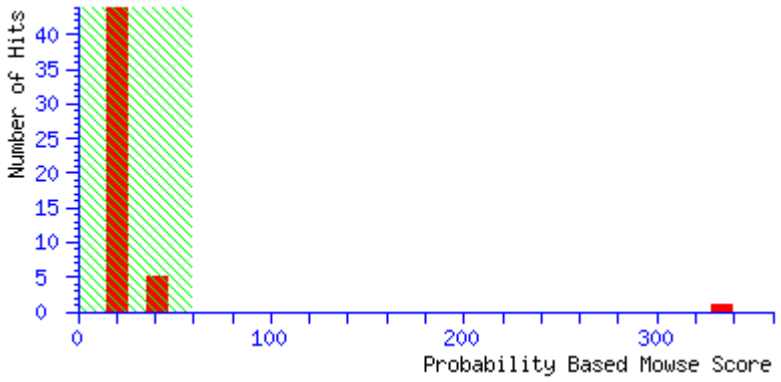
```
    1 MQQQQQQEPW MSMSSKPKPI EIIGAPFSKG QPRGGVEKGP AALRKAGLVE
   51 KLKETEYNVR DHGDLAFVDV PNDSPFQIVK NPRSVGKANE QLAAVVAETQ
  101 KNGTISVVLG GDHSMAIGSI SGHARVHPDL CVIWVDAHTD INTPLTTSSG
  151 NLHGQPVAFL LKELKGKFPD VPGFSWVTPC ISAKDIVYIG LRDVDPGEHY
  201 IIKTLGIKYF SMTEVDKLGI GKVMEETFSY LLGRKKRPIH LSFDVDGLDP
  251 VFTPATGTPV VGGLSYREGL YITEEIYKTG LLSGLDIMEV NPTLGKTPEE
  301 VTRTVNTAVA LTLSCFGTKR EGNHKPETDY LKPPK
```

Probability Based Mowse Score

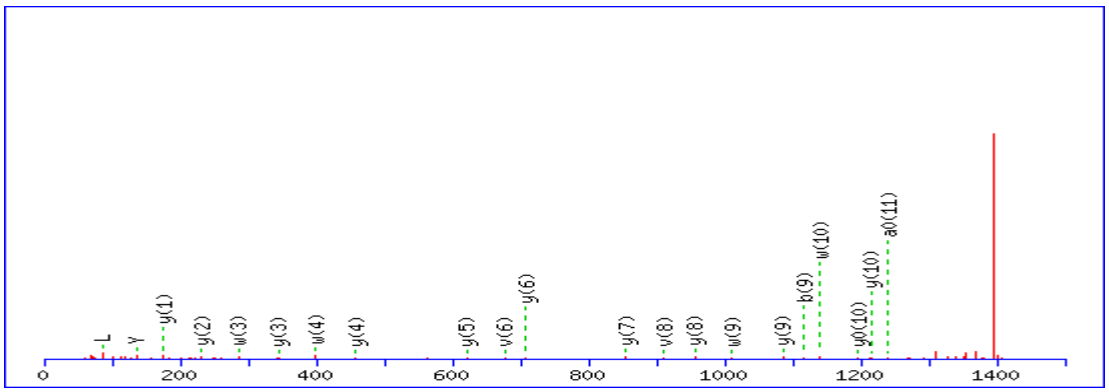
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 59 are significant (p<0.05).

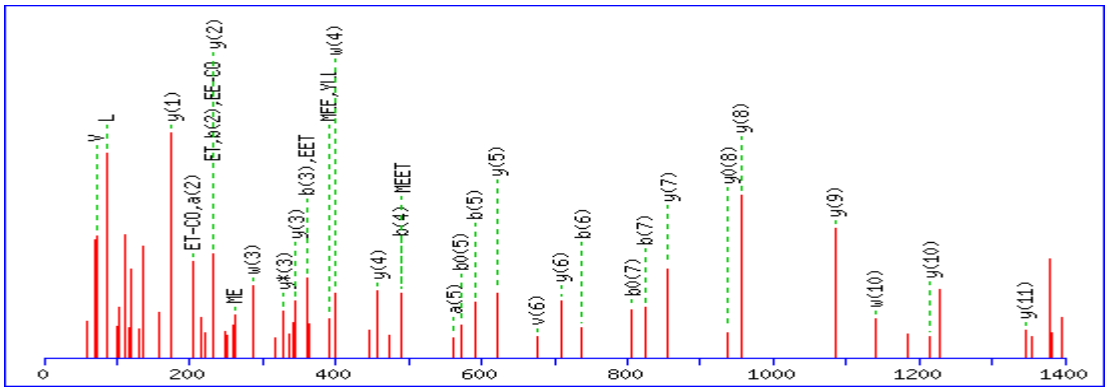
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



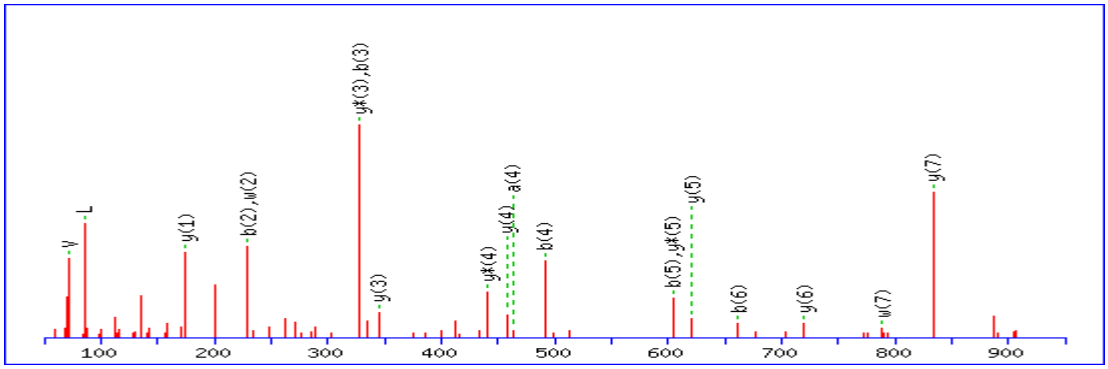
MS/MS Fragmentation of **VMEETFSYLLGR**



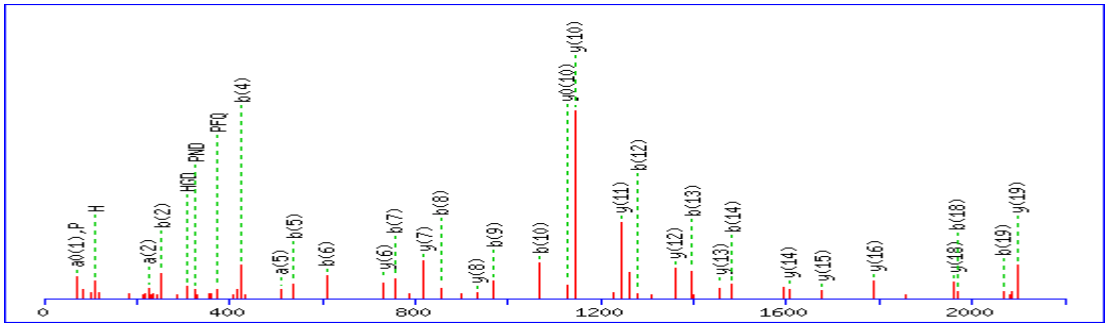
MS/MS Fragmentation of **VMEETFSYLLGR**



MS/MS Fragmentation of **DIVYIGLR**



MS/MS Fragmentation of **DHGDLAFVDVPNDSPFQIVK**



Spot 564

Match to: IPI00475676 Score: 125 Expect: 1.3e-008

Tax_Id=10116 Gene_Symbol=Tas1r2 Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial precur

Nominal mass (M_r): 61830; Calculated pI value: 7.14

Sequence Coverage: 26%

Matched peptides shown in **Bold Red**

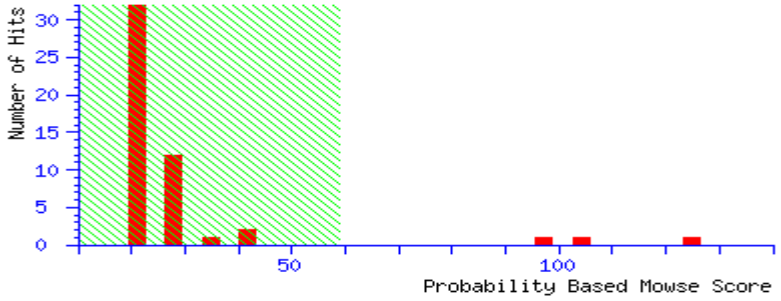
```
   1 MLPPALLRRS LLSYAWRGSG LRWKHASSLK VANEPILAFT QGSPERDALQ
  51 KALNDLKDQT EAIPCVVGDE EVWTSDVRYQ LSPFNHGHKV AKFCYADKAL
 101 LNKAIEAAVL ARKEWDLKPV ADRAQIFLKA ADMLSGPRRA EILAKTMVGQ
 151 GKTVIQAEID AAAELIDFFR FNAKFAVELE GEQPISVPPS TNHVVYRGLE
 201 GFVAAISPFN FTAIGGNLAG APALMGNVVL WKPSDTAMLA SYAVYRILRE
 251 AGLPPNVIQF VPADGPTFGD TVTSSEHLCG INFTGSVPTF KHLWKQVAQN
 301 LDRFRTFPRL AGECGGKNFH FVHSSADVDS VVSGTLRSAF EYGGQKCSAC
 351 SRLYVPQSLW PQIKGRLLEE HSRIKVGNPA EDFGTFFSAV IDAKAFARIK
 401 KWLEHARSSP SLSILAGGQC NESVGYFVEP CIIESKDPQE PIMKEEIFGP
 451 VLTVYVYPDE KYRETLQLVD STTSYGLTGA VFAQDKTIVQ EATRMLRNAA
 501 GNFYINDKST GSVVGQQPFG GARASGERDI PGQPRLVQLW TEPPFTPLAV
 551 SPPLGDWRYS YMQ
```

Probability Based Mowse Score

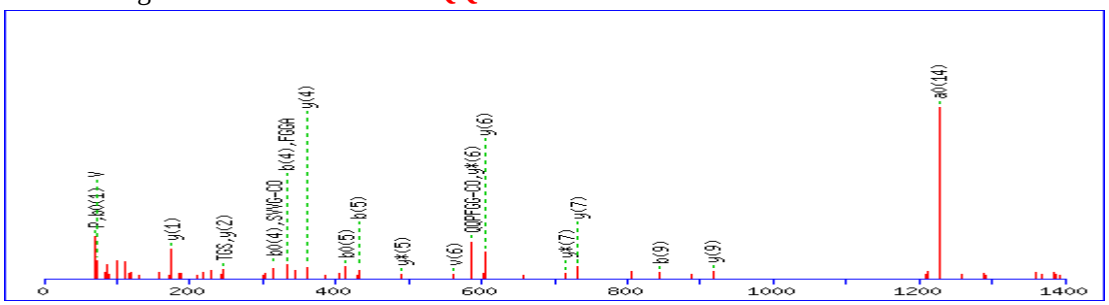
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 59 are significant (p<0.05).

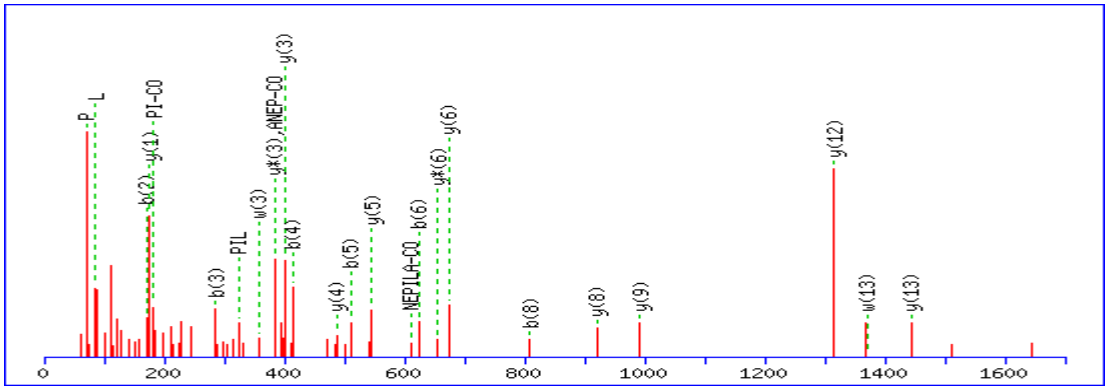
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



MS/MS Fragmentation of **STGSVVGQQPFGGAR**



MS/MS Fragmentation of **VANEPILAFTQGSPER**



Spot 1400

Match to: IPI00365297 Score: 290 Expect: 4e-025

Tax_Id=10116 Gene_Symbol=Agmat Agmatinase, mitochondrial precursor

Nominal mass (M_r): 37963; Calculated pI value: 6.71

Sequence Coverage: 32%

Matched peptides shown in **Bold Red**

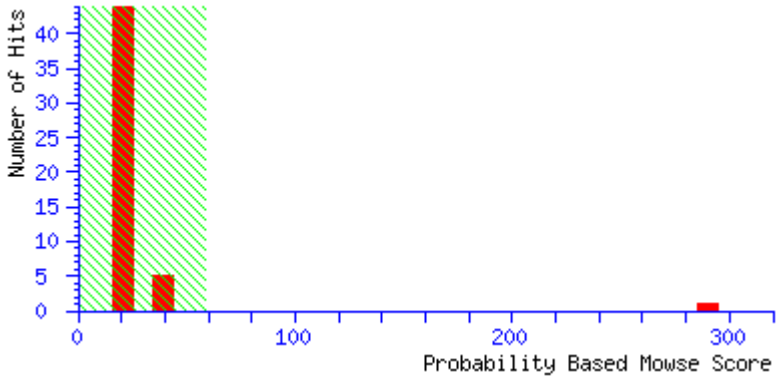
```
   1 MLQLLKSSWV RSAGSGVVTW RASAGLFCPG TRQASDTSDT LHHPSPSSES
  51 QVQPVRVCSM MHLPLQSSPE GLDAAFVGVP LDTGTSNRPG ARFGPRRIRE
 101 ESLMLGTVNP STGALPFQSL RVADLGNVNV NLYNLQDSCR LIREAYQNIL
 151 ATGCIPLTLG GDHTITYPIL QAVAKEHGPV GLVHVGAHSN TSDKPLEDKV
 201 YHRTPFRRSV DEGLLDSKRV VQIGIRGSSR TLDPYRYSRS QGFRVVLAED
 251 CWMKSLVPLM AEIRQQMGGV PLYISFAIDA LDPAYAPGTG TPEIAGLTPS
 301 QALEIIRGCQ GLNVVGCDLV EVSPPYDLSG NTALLAANLL FEMLCALPKV
 351 TTV
```

Probability Based Mowse Score

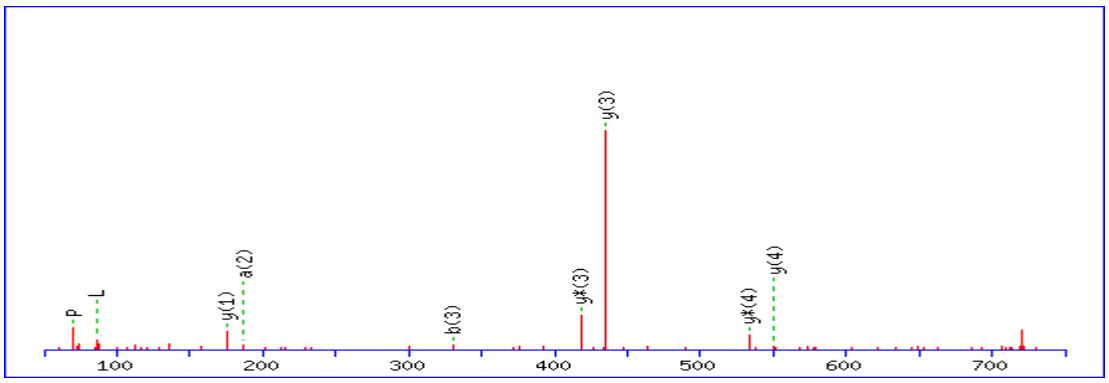
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 59 are significant (p<0.05).

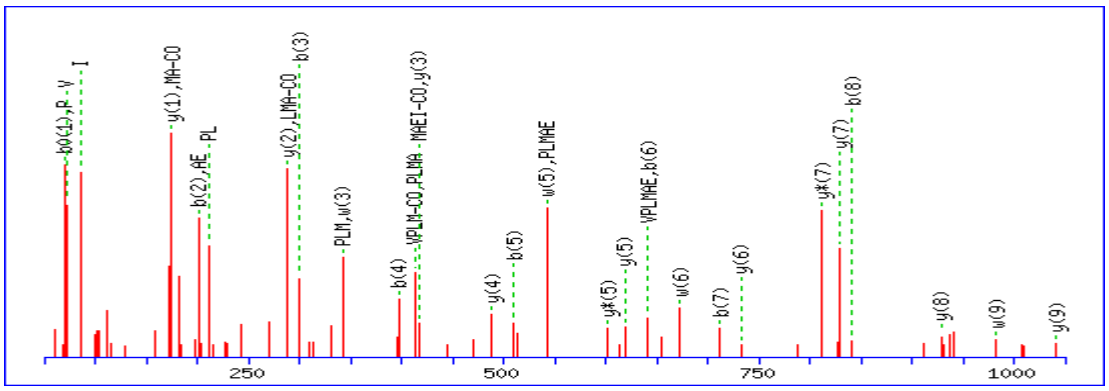
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



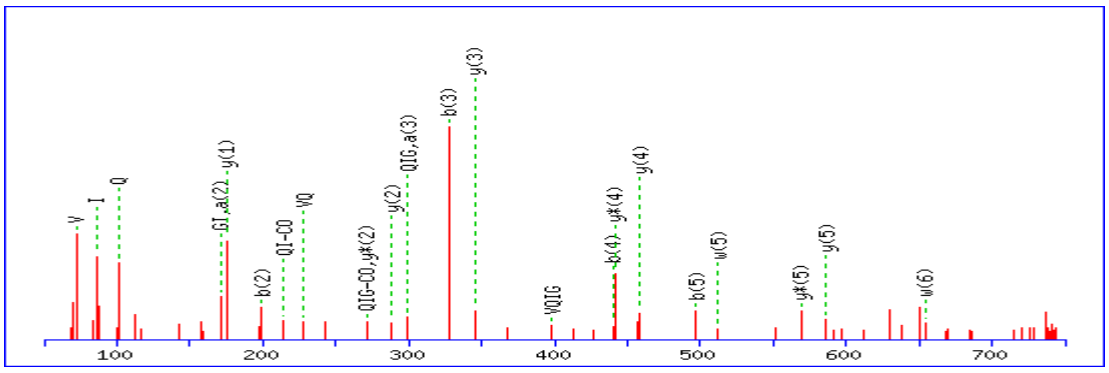
MS/MS Fragmentation of **TLDPYR**



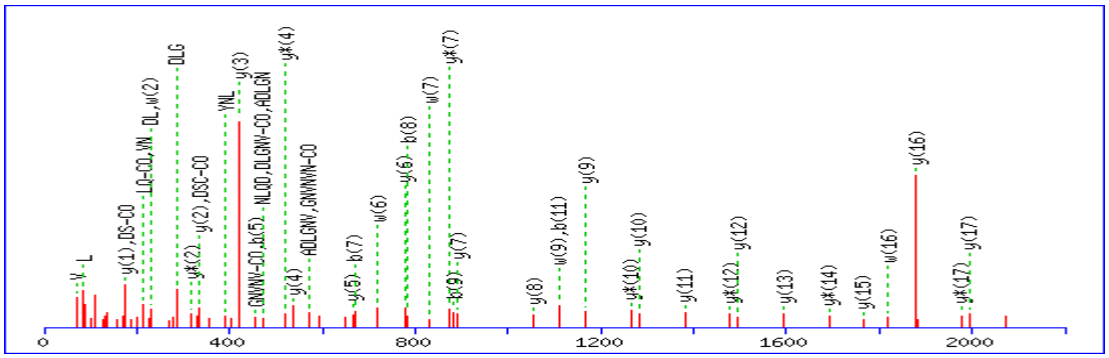
MS/MS Fragmentation of **SLVPLMAEIR**



MS/MS Fragmentation of **VVQIGIR**



MS/MS Fragmentation of **VADLGNVNVNLYNLQDSCR**



Spot 560

Match to: **IPI00231742** Score: **71** Expect: **0.0031**

Tax_Id=10116 Gene_Symbol=Cat Catalase

Nominal mass (M_r): **59719**; Calculated pI value: **7.07**

Sequence Coverage: **22%**

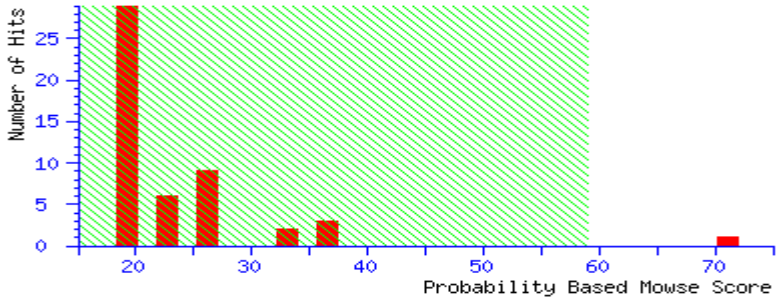
Matched peptides shown in **Bold Red**

```
    1 MADSRDPASD QMKQWKEQRA PQKPDVLTTG GGNPIGDKLN IMTAGPRGPL
   51 LVQDVVFTDE MAHFDRERIP ERVVHAKGAG AFGYFEVTHD ITRYSKAKVF
  101 EHIGKRTPIA VRFSTVAGES GSADTVRDPR GFAVKFYTED GNWDLVGNNT
  151 PIFFIRDAML FPSFIHSQKR NPQTHLKDPD MVWDFWSLCP ESLHQVTFLF
  201 SDRGIPDGHR HMNGYGSHTF KLVNANGEAV YCKFHYKTDQ GIKNLPVEEA
  251 GRLAQEDPDY GLRDLFNAIA SGNYPSWTFY IQVMTFKEAE TFPFNPFDLT
  301 KVWPHKDYPL IPVGKLVLNR NPANYFAEVE QMAFDPSNMP PGIEPSPDKM
  351 LQGRLFAYPD THRHRLGPNY LQIPVNCPYR ARVANYQRDG PMCMHDNQGG
  401 APNYYPNSFS APEQQGSALE HHSQCSADVK RFNSANEDNV TQVRTFYTKV
  451 LNEEERKRLC ENIANHLKDA QLFIQRKAVK NFTDVHPDYG ARVQALLDQY
  501 NSQKPKNAIH TYVQAGSHIA AKGKANL
```

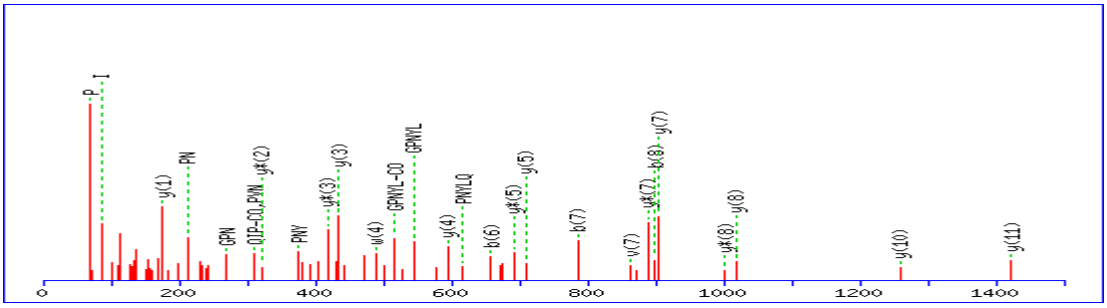
Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 59 are significant (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



MS/MS Fragmentation of **LGPNYLQIPVNCPYR**



Spot 527

Match to: **IPI00327469** Score: **101** Expect: **3.2e-006**

Tax_Id=10116 Gene_Symbol=Ahsg Alpha-2-HS-glycoprotein precursor

Nominal mass (M_r): **37958**; Calculated pI value: **6.05**

Sequence Coverage: **21%**

Matched peptides shown in **Bold Red**

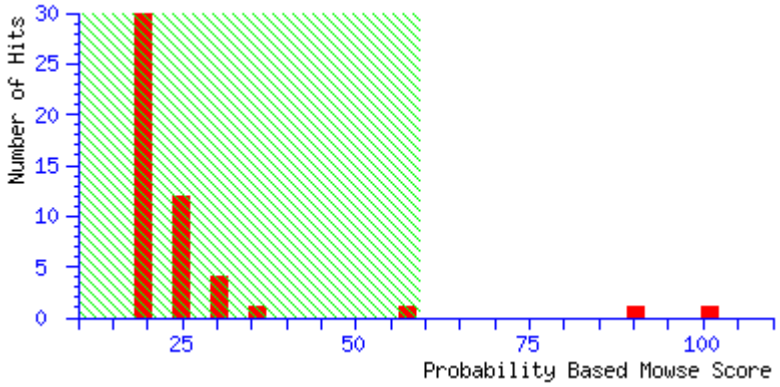
```
   1 MKSLVLLLCF AQLWSCQSAP QGAGLGFREL ACDDPETEHV ALIAVDYLNK
  51 HLLQGFRQIL NQIDKVKVWS RRPFGEVYEL EIDTLETTCH ALDPTPLANC
 101 SVRQQAEHAV EGDCDFHILK QDGQFRVLHA QCHSTPDSAE DVRKFCPRCP
 151 ILIRFNDTNV VHTVKTALAA FNAQNNGTYF KLVEISRAQN VPFPVSTLVE
 201 FVIAATDCTG QEVTDPAKCN LLAEKQYGFC KATLIHRLGG EEVSVACKLF
 251 QTQPQPANAN PAGPAPTVGQ AAPVAPPAGP PESVVVGPVA VPLGLPDHRT
 301 HHDLRHAFSP VASVESASGE VLHSPKVGQP GDAGAAGPVA PLCPGRVRYF
 351 KI
```

Probability Based Mowse Score

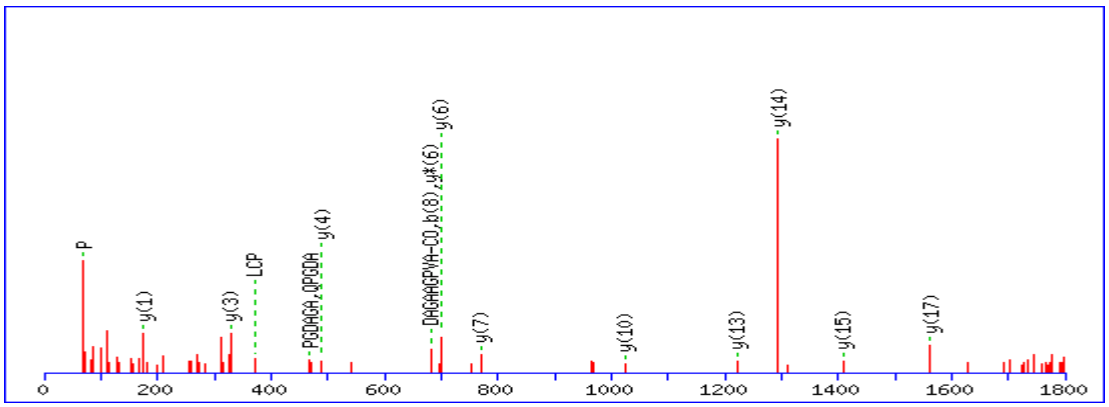
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 59 are significant (p<0.05).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



MS/MS Fragmentation of **VGQPGDAGAAGPVAPLCPGR**



Spot 543

Match to: IPI00206624 Score: 206 Expect: 1e-016

Tax_Id=10116 Gene_Symbol=Hspa5 78 kDa glucose-regulated protein precursor

Nominal mass (M_r): 72302; Calculated pI value: 5.07

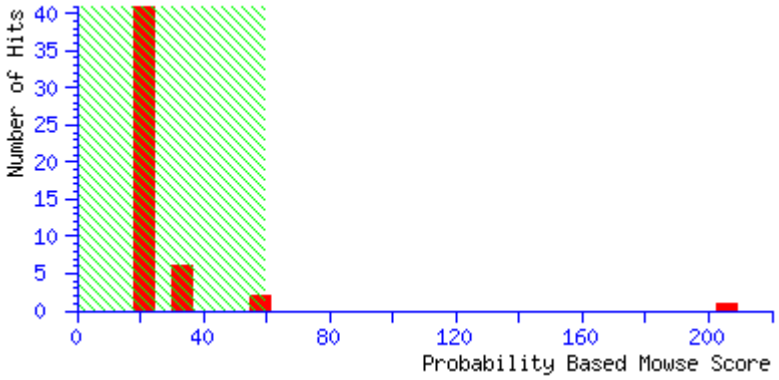
Sequence Coverage: 41%

Matched peptides shown in Bold Red

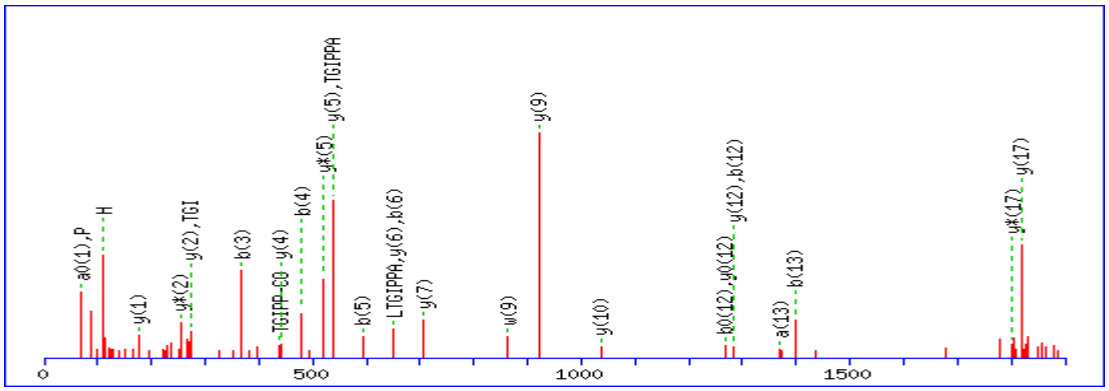
```
   1 MKFTVVAAAL LLLCAVRAEE EDKKEDVGTV VGIDLGTTYS CVGVFKNGRV
  51 EIIANDQGNR ITPSYVAFTP EGERLIGDAA KNQLTSNPEN TVFDAKRLIG
 101 RTWNDPSVQQ DIKFLPFKVV EKKTKPYIQV DIGGGQTKTF APEEISAMVL
 151 TKMKETAEAY LGKKVTHAVV TVPAYFNDAQ RQATKDAGTI AGLNVMRIIN
 201 EPTAAAIAYG LDKREGEKNI LVFDLGGGTF DVSLLTIDNG VFEVVATNGD
 251 THLGGEDFDQ RVMEHFIKLY KKKTGKDVRK DNRAVQKLRR EVEKAKRALS
 301 SQHQARIEIE SFFEGEDFSE TLTRAKFEEL NMDLFRSTMK PVQKVLEDSD
 351 LKKSDIDEIV LVGGSTRIPK IQQLVKEFFN GKEPSRGINP DEAVAYGAAV
 401 QAGVLSGDQD TGDLVLLDVC PLTLGIETVG GVMTKLIPRN TVVPTKKSQI
 451 FSTASDNQPT VTIKVYEGER PLTKDNHLLG TFDLTGIPPA PRGVPQIEVT
 501 FEIDVNGILR VTAEDKGTGN KNKITITNDQ NRLTPEEIER MVNDAEKFAE
 551 EDKKLKERID TRNELESYAY SLKNQIGDKE KLGGKLSPED KETMEKAVEE
 601 KIEWLESHQD ADIEDFKAKK KELEEIVQPI ISKLYGSGGP PPTGEEDTSE
 651 KDEL
```

Probability Based Mowse Score

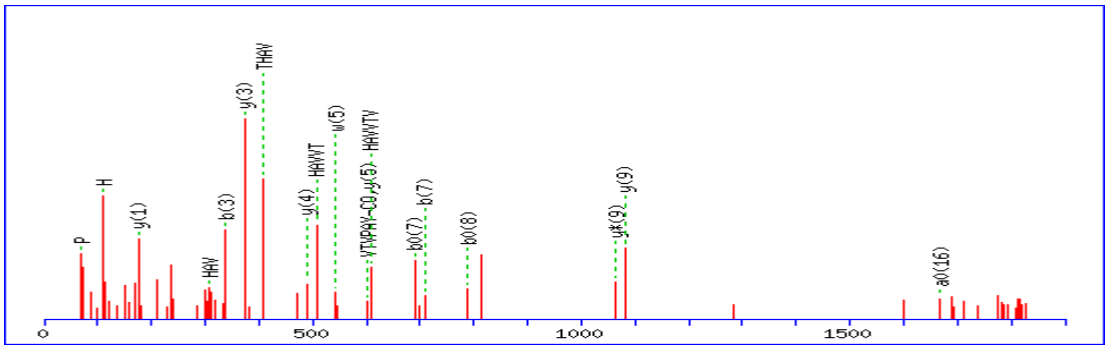
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 59 are significant (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



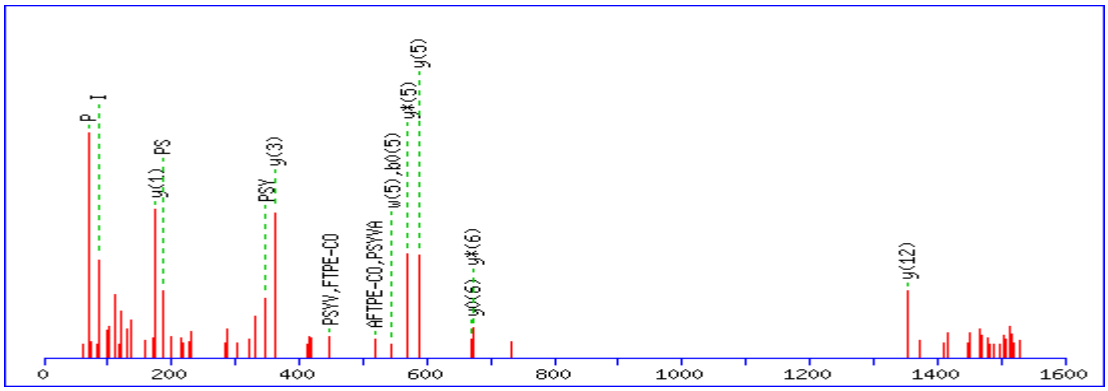
MS/MS Fragmentation of **DNHLLGTFDLTGIPPAPR**



MS/MS Fragmentation of **VTHAVVTVPAYFNDAQR**



MS/MS Fragmentation of **ITPSYVAFTPEGER**



Spot 1514

Match to: IPI00230788 Score: 468 Expect: 6.4e-043

Tax_Id=10116 Gene_Symbol=Ca3 Carbonic anhydrase 3

Nominal mass (M_r): 29413; Calculated pI value: 6.89

Sequence Coverage: 85%

Matched peptides shown in **Bold Red**

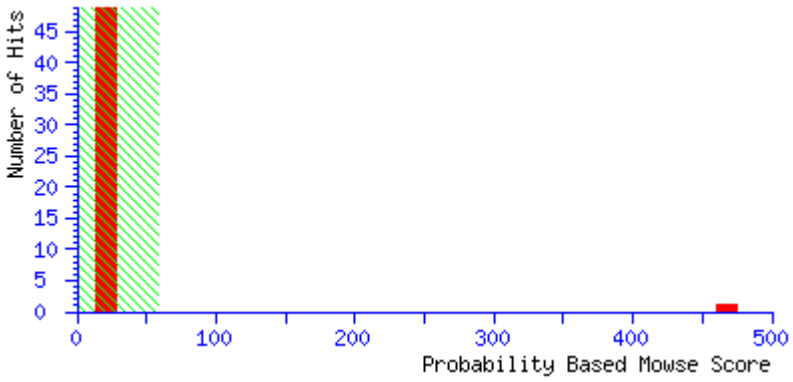
```
   1 MAKEWGYASH NGPEHWHELY PIAKGDNQSP IELHTKDIRH DPSLQPWSVS
  51 YDPGSAKTIL NNGKTCRVVF DDTFDRSMLR GGPLSGPYRL RQFHLHWGSS
 101 DDHGSEHTVD GVKYAAELHL VHWNPKYNTF GEALKQPDGI AVVGIFLKIG
 151 REKGEFQILL DALDKIKTKG KEAPFNHFDP SCLFPACRDY WTYHGSFTTP
 201 PCEECIVWLL LKEPMTVSSD QMAKLRSLFA SAENEPPVPL VGNWRPPQPI
 251 KGRVVRASFK
```

Probability Based Mowse Score

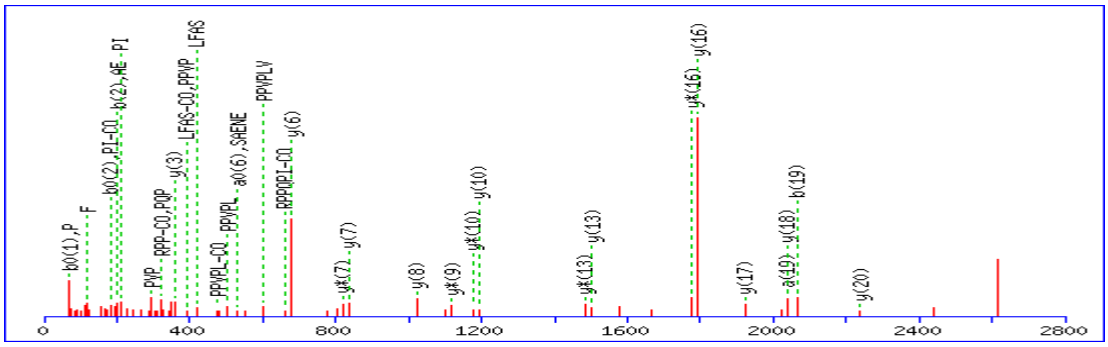
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 59 are significant (p<0.05).

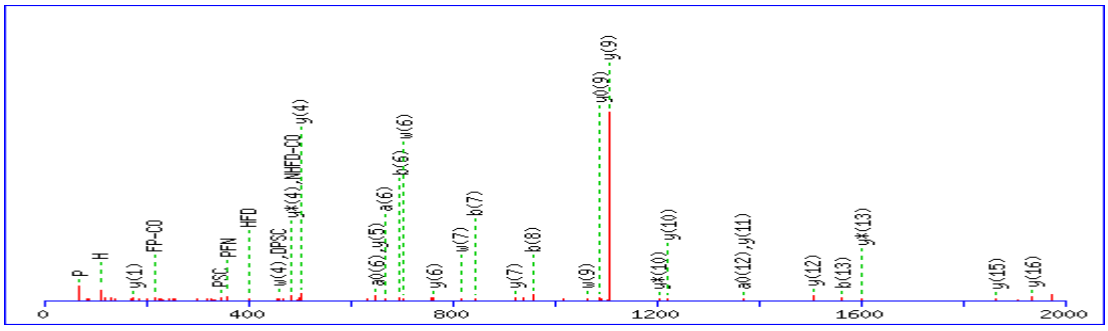
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



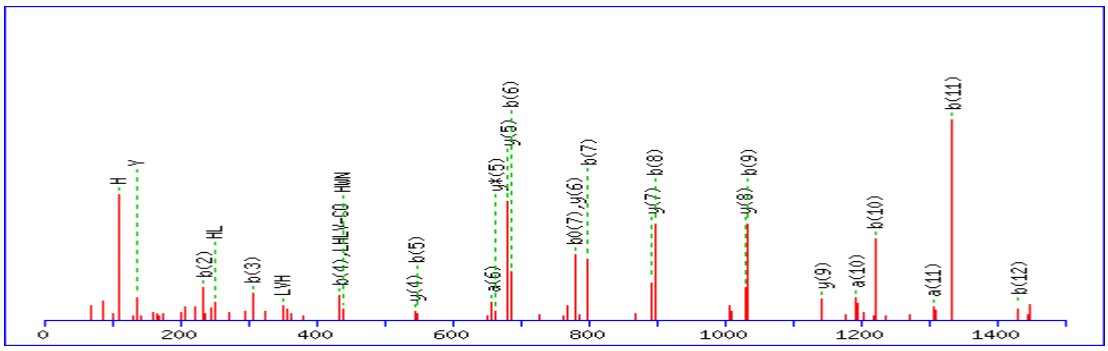
MS/MS Fragmentation of **SLFASAENEPPVPLVGNWRPPQPIK**



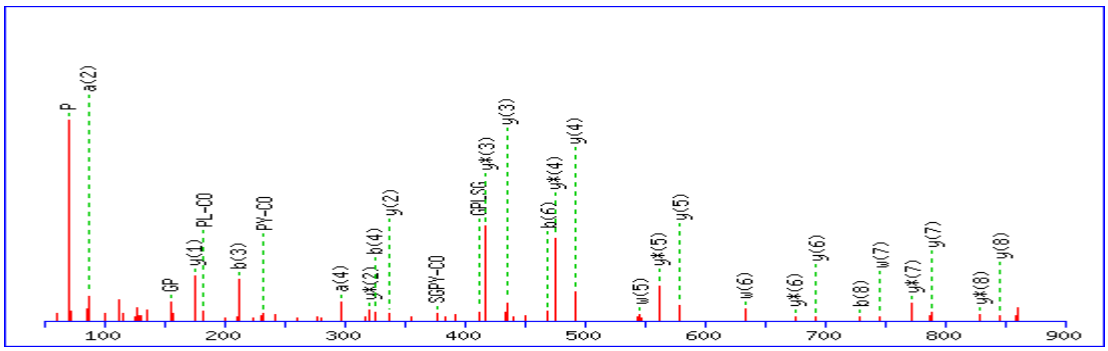
MS/MS Fragmentation of **EAPFNHFDPSCLFPACR**



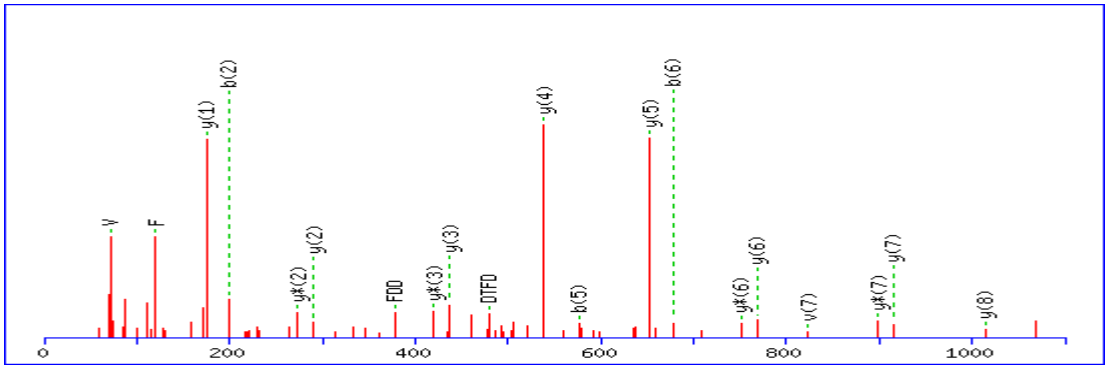
MS/MS Fragmentation of **YAAELHLVHWNPK**



MS/MS Fragmentation of **GGPLSGPYR**



MS/MS Fragmentation of **VVFDDTFDR**



Spot 799

Match to: IPI00389571 Score: 465 Expect: 1.3e-042

Tax_Id=10116 Gene_Symbol=Krt2-8 Keratin, type II cytoskeletal 8

Nominal mass (M_r): 53985; Calculated pI value: 5.83

Sequence Coverage: 55%

Matched peptides shown in Bold Red

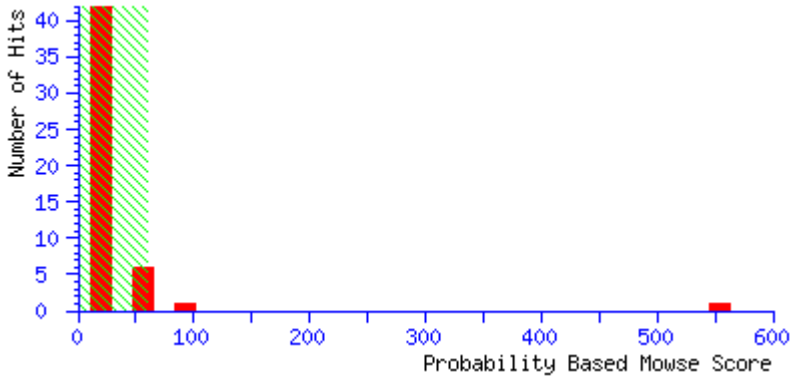
```
   1 MSVRVTQKSY KMSTSGPRAF SSRSFTSGPG ARISSSSFSR VGSSSSSFRG
  51 SLGGFGGAGV GGITAVTVNQ SLLNPLKLEV DPNIQAVRTQ EKEQIKTLNN
 101 KFASFIDKVR FLEQQNKMLE TKWSLLQQQK TSRSNMDNMF ESYINNLRRQ
 151 LEALGQEKLK LEVELGNMQG LVEDFKNKYE DEINKRTEME NEFVLIKKDV
 201 DEAYMNKVEL ESRLEGLTDE INFLRQIHEE EIRELQSQIS DTSVVLSMDN
 251 SRSLDMDSII AEVRAQYEEI ANRSRAEAET MYQIKYEELQ TLAGKHGDDL
 301 RRSKTEISEM NRNISRLQAE IDALKGQRAT LEAAIADAEQ RGELAVKDAN
 351 AKLEDLKNAL QKAKQDMARQ LREYQELMNV KLALDIEIAT YRKLLEGEES
 401 RLESGMQNMS IHTKTTSGYA GGLSSSYGGL TSPGFSYGMS SFQPGFGSVG
 451 GSSTYSRTKA VVVKKIETRD GKLVSESSDI MSK
```

Probability Based Mowse Score

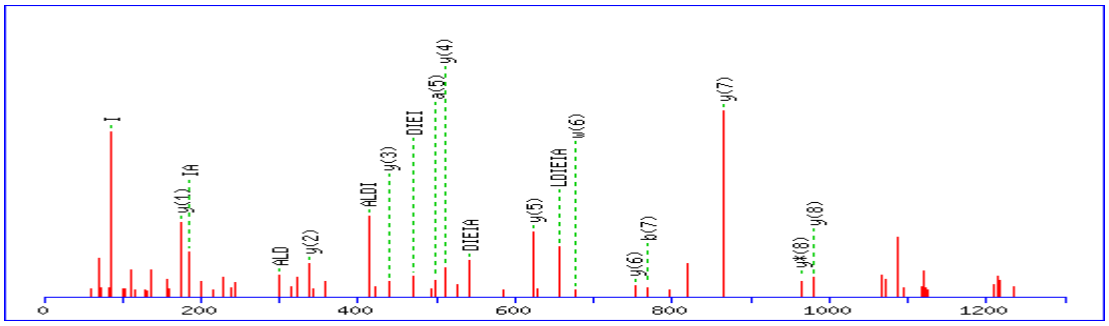
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 59 are significant (p<0.05).

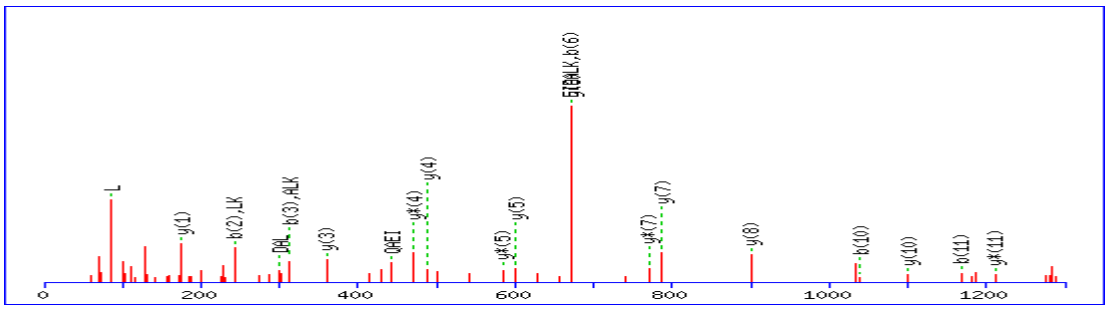
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



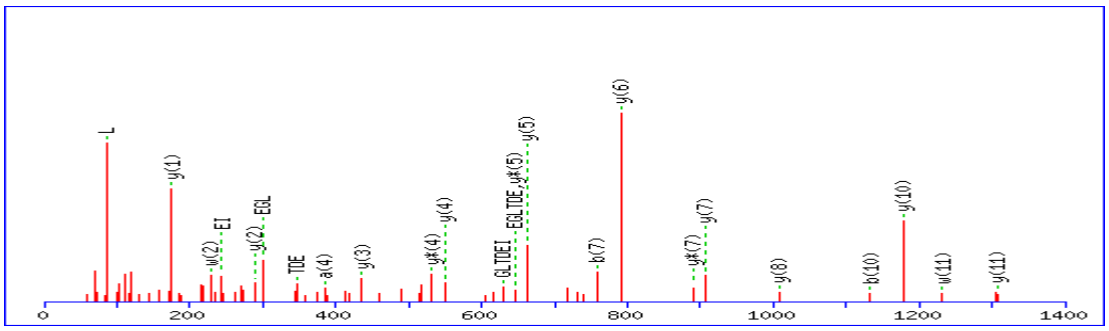
MS/MS Fragmentation of **LALDIEIATYR**



MS/MS Fragmentation of **LQAEIDALKGQR**



MS/MS Fragmentation of **LEGLTDEINFLR**



Spot 1662

Match to: **IPI00561017** Score: **488** Expect: **6.4e-045**

Tax_Id=10116 Gene_Symbol=Prdx5 22 kDa protein

Nominal mass (M_r): **22255**; Calculated pI value: **8.54**

Sequence Coverage: **55%**

Matched peptides shown in **Bold Red**

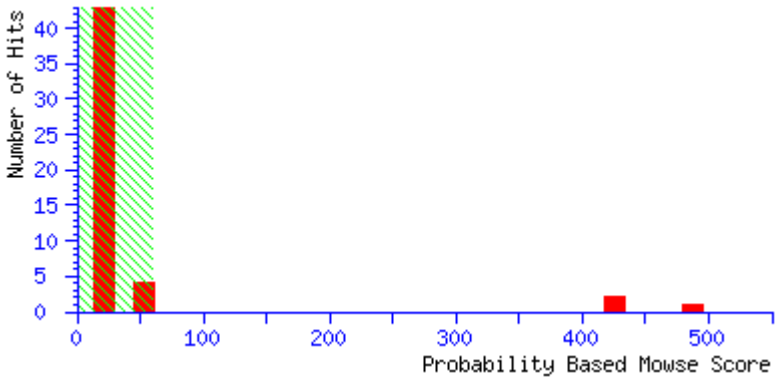
```
    1 MVQLRFCVLG SIAGSVLRAS ATWTCVAGRA GRKGAGWECG GARSFSSRGD
   51 YGPDQGVGDT IPSVEVFEGE PGKKVNLAEL FKDKKGVLFG VPGAFTPGCS
  101 KTHLPGFVEQ AGALKAKGAQ VVACLSVNDV FVTAEWGRAH QAEGKVQLLA
  151 DPTGAFGKET DLLLDDSLVS LFGNRRLKRF SMVIDKGVVK ALNVEPDGTG
  201 LTCSLAPNIL SQL
```

Probability Based Mowse Score

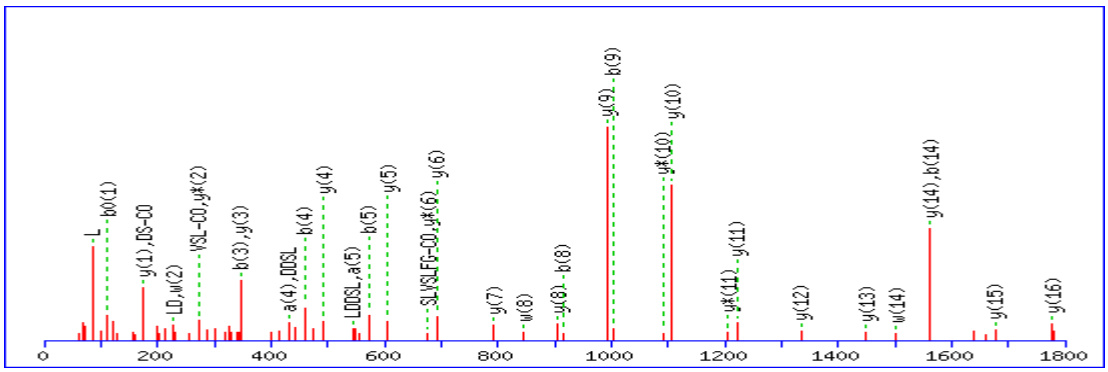
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 59 are significant (p<0.05).

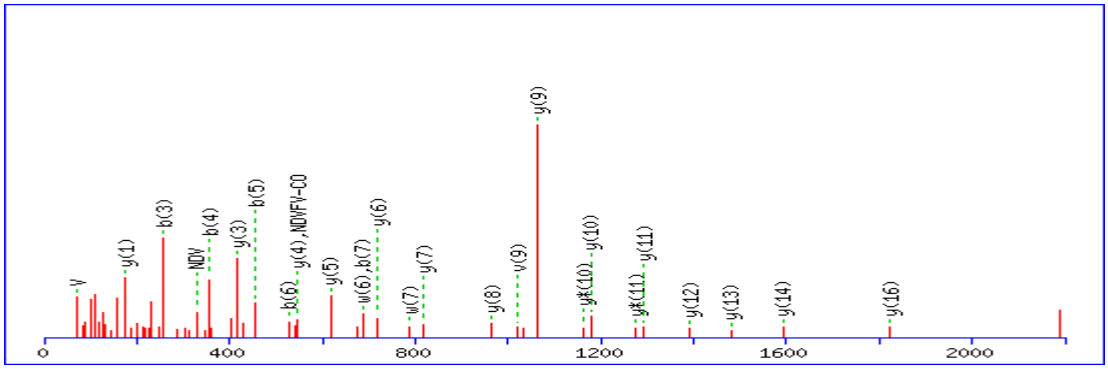
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



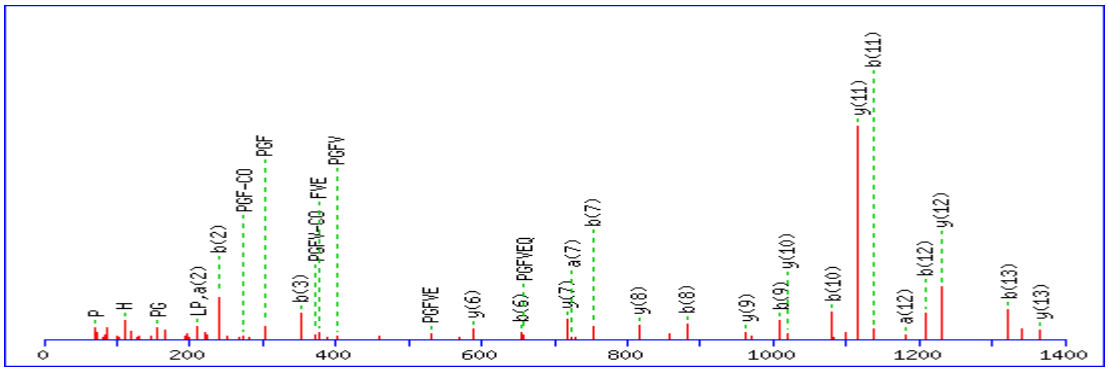
MS/MS Fragmentation of **ETDLLLDDSLVSLFGNR**



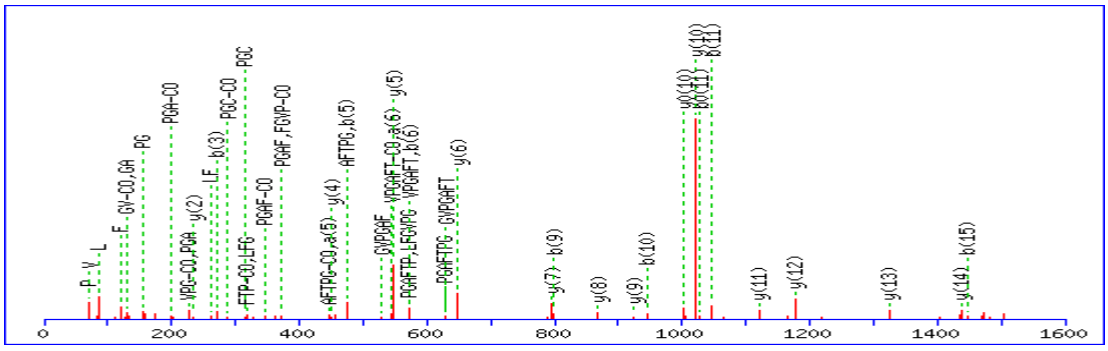
MS/MS Fragmentation of **GAQVVACLSVNDVFVTAEWGR**



MS/MS Fragmentation of **THLPGFVEQAGALK**



MS/MS Fragmentation of **GVLFGVPGAFTPGCSK**



Spot 1526

Match to: IPI00760117 Score: 143 Expect: 2e-010

Tax_Id=10116 Gene_Symbol=Comt Isoform 2 of Catechol O-methyltransferase

Nominal mass (M_r): 24731; Calculated pI value: 5.11

Sequence Coverage: 55%

Matched peptides shown in **Bold Red**

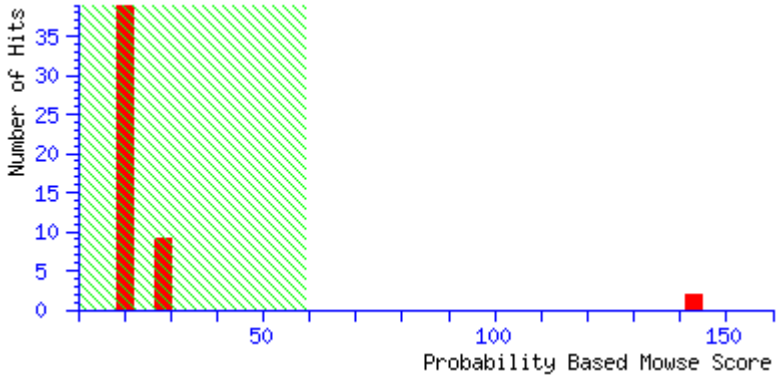
```
  1 MGDTKEQRIL RYVQQNAKPG DPQSVLEAID TYCTQKEWAM NVGDAKGQIM
 51 DAVIREYSPS LVLELGAYCG YSAVRMARLL QPGARLLTME MNPDYAAITQ
101 QMLNFAGLQD KVTILNGASQ DLIPQLKKKY DVDTLDMVFL DHWKDRYLPD
151 TLLLEKCGLL RKGTVLLADN VIVPGTPDFL AYVRGSSSFE CTHYSSYLEY
201 MKVVDGLEKA IYQGPSSPDK S
```

Probability Based Mowse Score

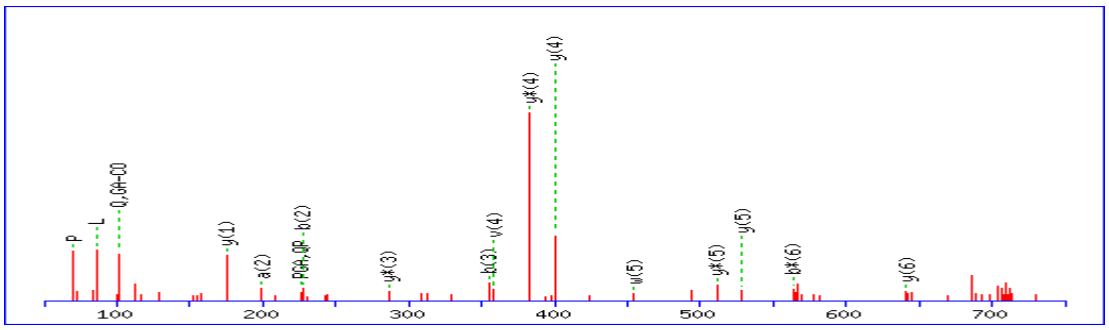
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 59 are significant (p<0.05).

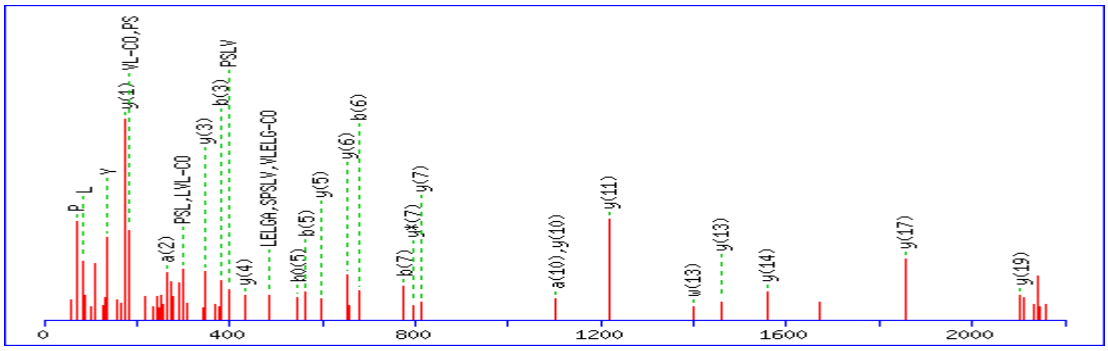
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



MS/MS Fragmentation of **LLQPGAR**



MS/MS Fragmentation of **EYSPSLVLELGAYCGYSAVR**


-P
-L
-V
-yk(1)
-VL-CO,PS
a(2)
-PSL,LVL-CO
y(3)
b(3)
-PSLV
y(4)
-LELGA,SPSLV,VLELG-CO
bk(5)
b(5)
y(5)
y(6)
b(6)
bk(7)
yk(7)
y(7)
a(10),yk(10)
y(11)
wk(13)
y(13)
y(14)
y(17)
y(19)
0
400
800
1200
1600
2000

Spot 1563

Match to: IPI00392676 Score: 233 Expect: 2e-019

Tax_Id=10116 Gene_Symbol=Blvrb_predicted biliverdin reductase B

Nominal mass (M_r): 22083; Calculated pI value: 6.29

Sequence Coverage: 62%

Matched peptides shown in Bold Red

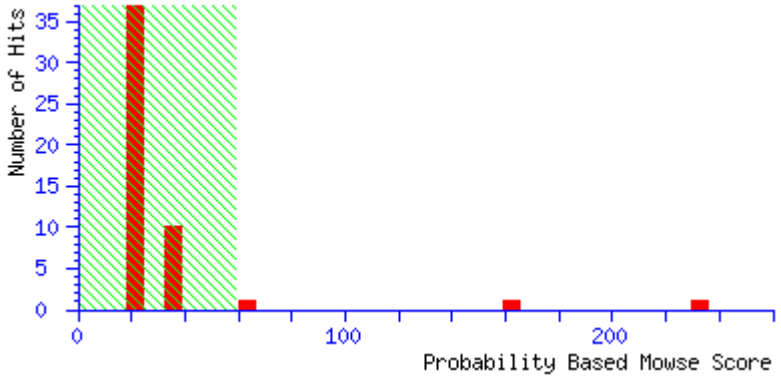
```
   1 MAVKKIAIFG ATGRTGLTTL AQASPSSYEV TVLVRDSSRL PSEGPQPAHV
  51 VVGDVLQAGD VDKTVAGQDA VIVLLGTGND LSPTTVMSEG TRNIVAAMKA
 101 HGVDKVVACT SAFLLWDPSK VPPRLQDVTD DHIRMHKILE ESGLKYVAVM
 151 PPHIGDQPLT GAYTVTLDGR GPSRVISKHD LGHFMLRCLT THEYDGQKTY
 201 PSHQYD
```

Probability Based Mowse Score

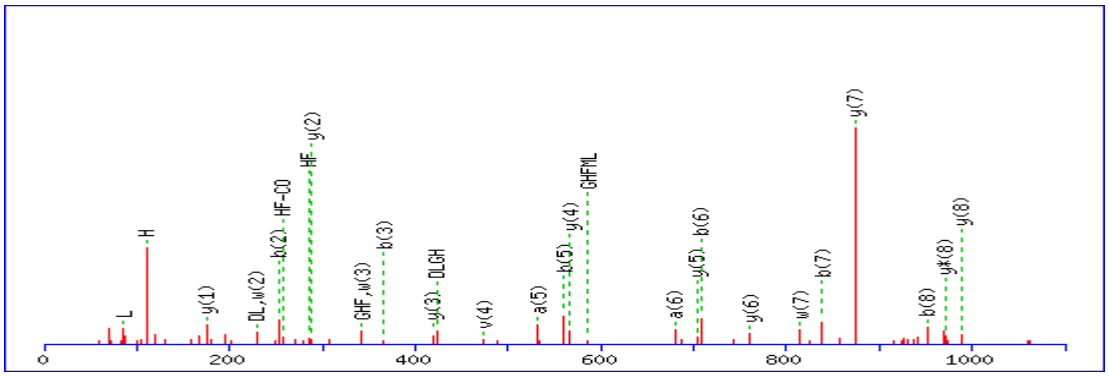
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 59 are significant (p<0.05).

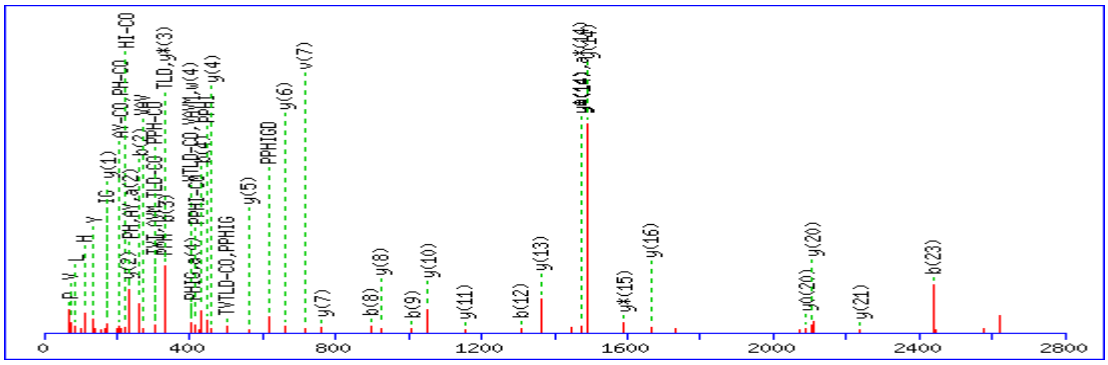
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



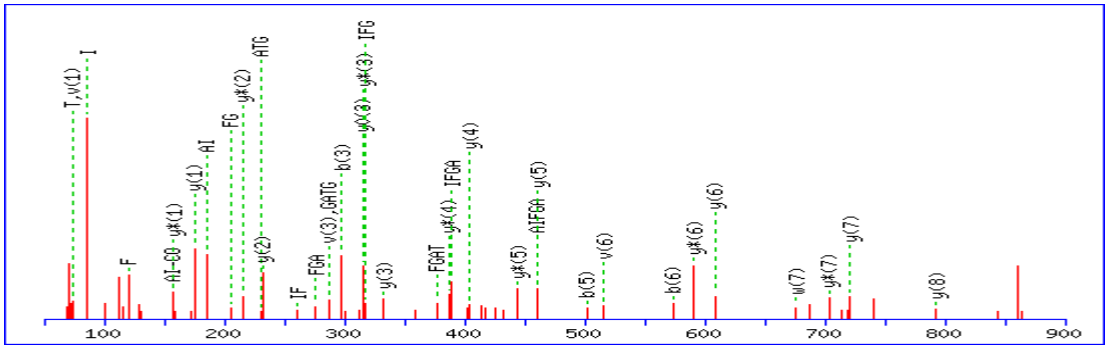
MS/MS Fragmentation of **HDLGHFMLR**



MS/MS Fragmentation of **YVAVMPPHIGDQPLTGAYTVTLDGR**



MS/MS Fragmentation of **IAIFGATGR**



Spot 1746

Match to: IPI00205036 Score: 534 Expect: 1.6e-049

Tax_Id=10116 Gene_Symbol=LOC360504 hemoglobin alpha 2 chain

Nominal mass (M_r): 15275; Calculated pI value: 8.45

Sequence Coverage: 88%

Matched peptides shown in **Bold Red**

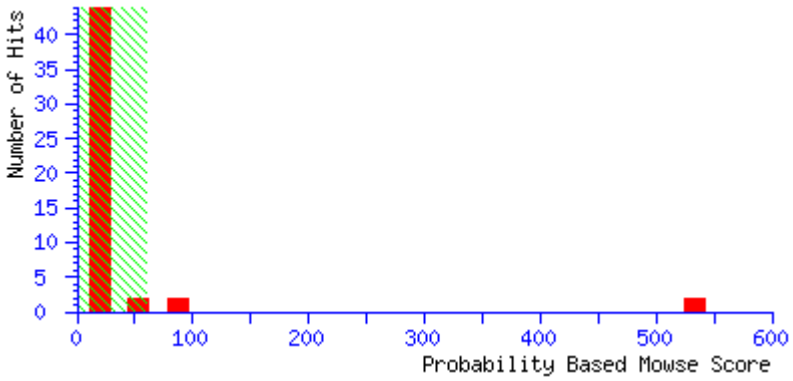
```
  1 MVLSAADKTN IKNCWGKIGG HGGEYGEEAL QRMFAAFPTT KTYFSHIDVS
 51 PGSAQVKAHG KKVADALAKA ADHVEDLPGA LSTLSDLHAH KLRVDPVNFK
101 FLSHCLLVTL ACHHPGDFTP AMHASLDKFL ASVSTVLTSK YR
```

Probability Based Mowse Score

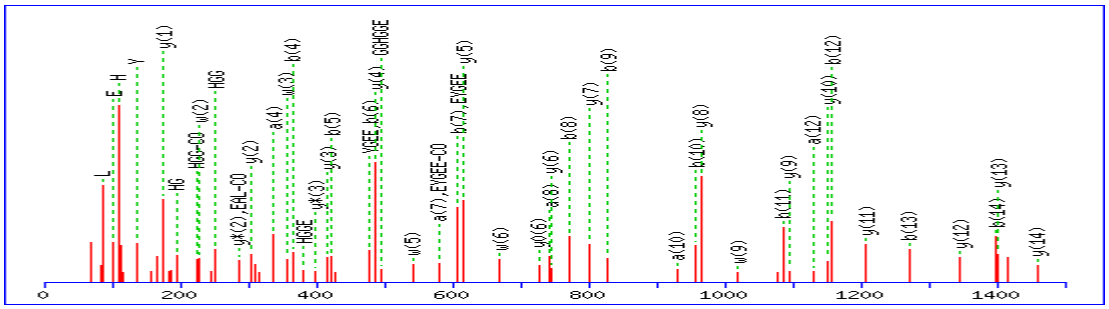
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 59 are significant (p<0.05).

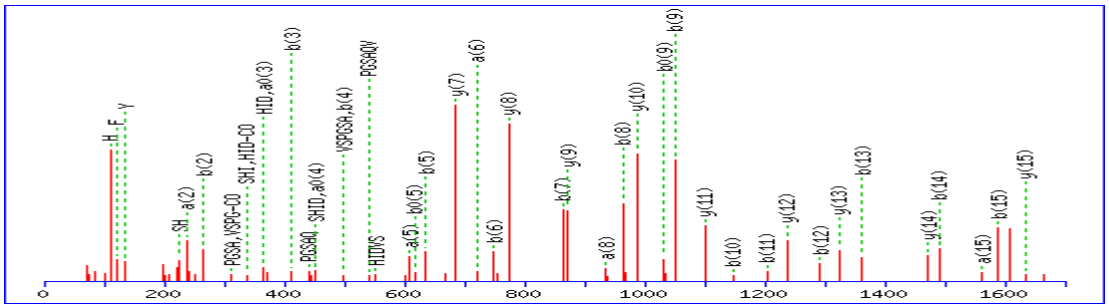
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



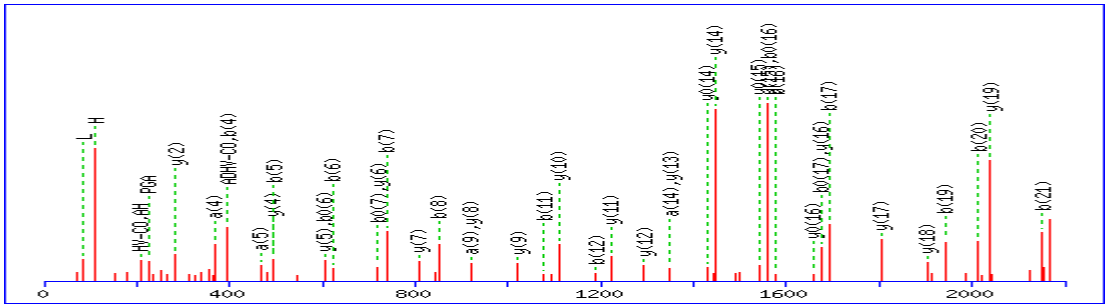
MS/MS Fragmentation of **IGGHGGEYGEEALQR**



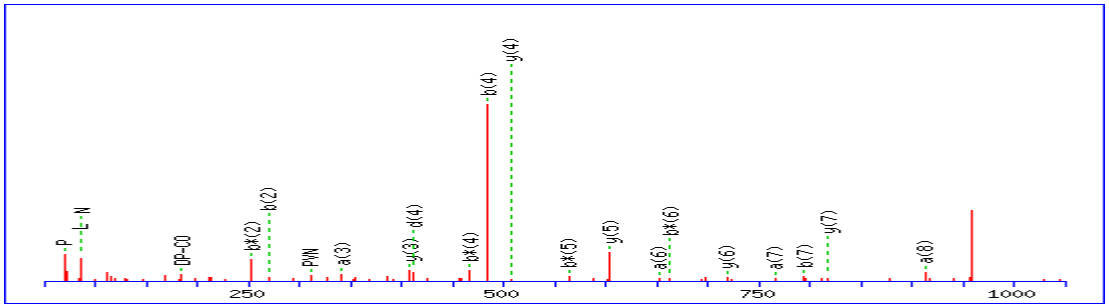
MS/MS Fragmentation of **TYFSHIDVSPGSAQVK**



MS/MS Fragmentation of **AADHVEDLPGALSTLSDLHAHK**



MS/MS Fragmentation of **LRVDPVNFK**



Spot 1453

Match to: IPI00231106 Score: 405 Expect: 1.3e-036

Tax_Id=10116 Gene_Symbol=Mpst 3-mercaptopyruvate sulfurtransferase

Nominal mass (M_r): 32919; Calculated pI value: 5.88

Sequence Coverage: 57%

Matched peptides shown in **Bold Red**

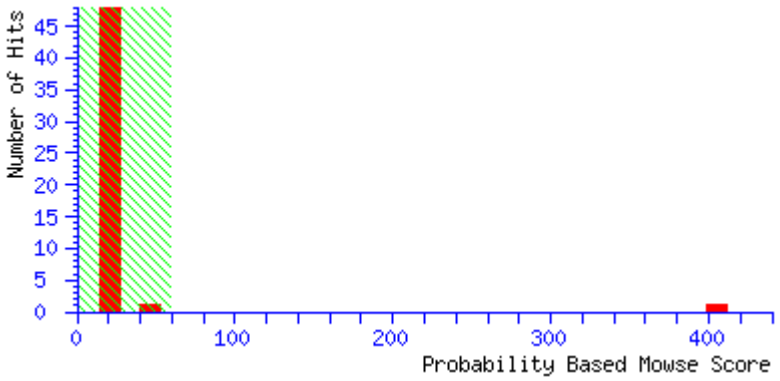
```
   1 MAAPQLFRAL VSAQWVAEAL KSPRASQPLK LLDASWYLPK LGRDARREFE
  51 ERHIPGAAFF DIDRCSDHTS PYDHMLPSAT HFADYAGSLG VSAATHVVIY
 101 DGSDQGLYSA PRVWWMFRAF GHHSVSLLDG GFRYWLSQNL PISSGKSPSE
 151 PAEFCAQLDP SFIKTHEDIL ENLDARRFQV VDARAAGRFQ GTQPEPRDGI
 201 EPGHIPGSVN IPFTEFLTSE GLEKSPEEIQ RLFQEKKVDL SKPLVATCGS
 251 GVTACHVVLG AFLCGKPDVP VYDGSWVEWY MRAQPEHVIS QGRGKTL
```

Probability Based Mowse Score

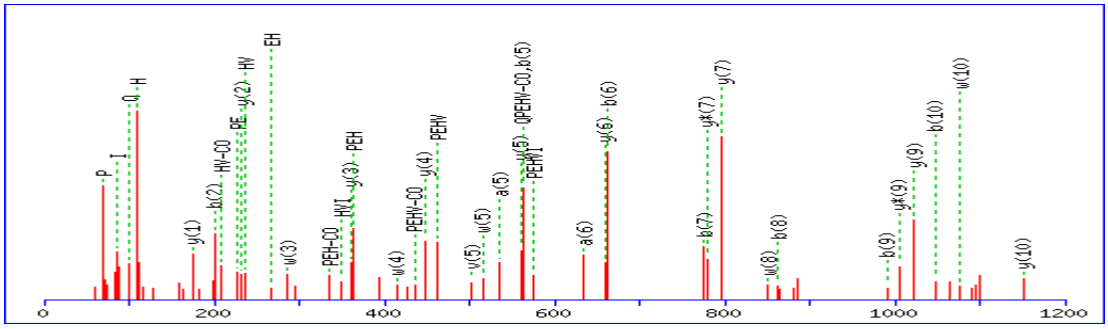
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 59 are significant (p<0.05).

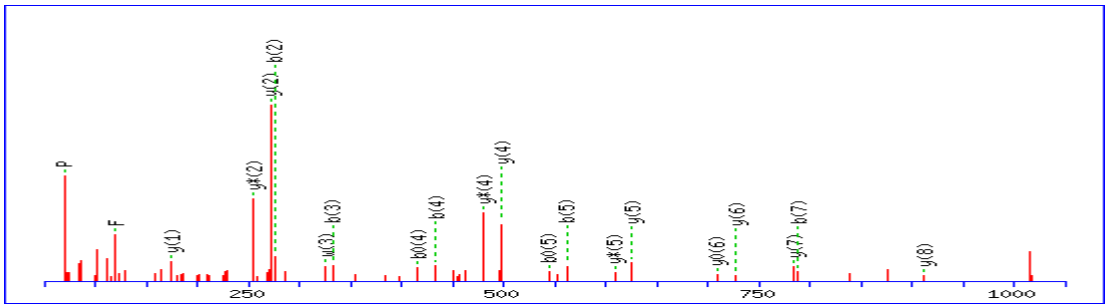
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



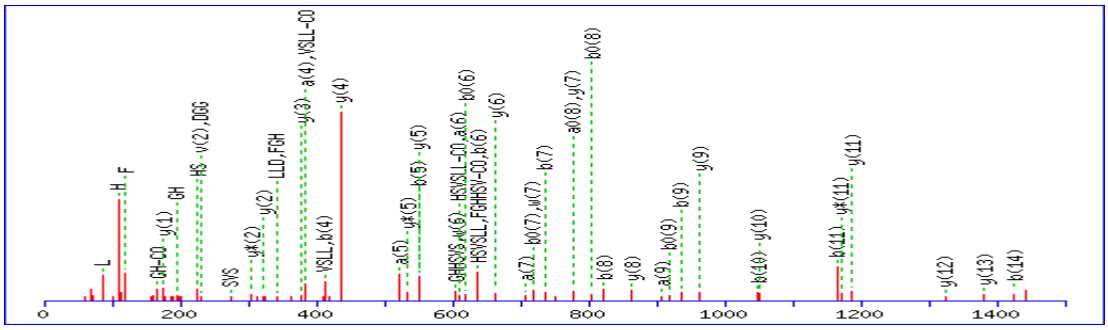
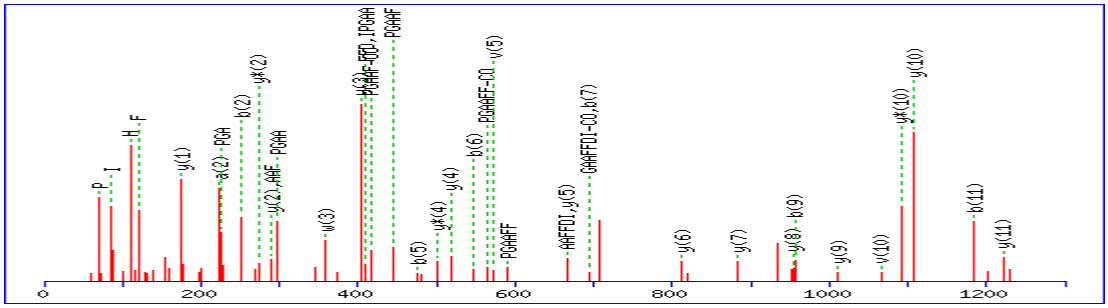
MS/MS Fragmentation of **AQPEHVISQGR**



MS/MS Fragmentation of **FQGTQPEPR**



MS/MS Fragmentation of **AFGHHSVSLLDGGFR**



MS/MS Fragmentation of **HIPGAAFFDIDR**