Supplemental Information

Title: Comprehensive Proteomics Analysis of Laticifer Latex Reveals New Insights into Ethylene Stimulation of Natural Rubber Production

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Supplementary Figures and Tables

Supplementary Figure S1: Identification of the high abundant latex proteins in 2-DE gels.

Supplementary Figure S2: Classification and functional analysis of the identified main latex proteins.

Supplementary Figure S3: Identification of the differentially expressed latex proteins in DIGE gels.

Supplementary Figure S4: Identification of ethylene responsive latex proteins by iTRAQ.

Supplementary Figure S5: Information of the 59 phosphorlated latex proteins.

Supplementary Figure S6: Antibody information.

Supplementary Figure S7: Primers used in RT-PCR.

Supplementary Table S1: MS identification of high abundant rubber latex proteins 2-DE gels.

Supplementary Table S2: MS identification of the differential latex proteins in DIGE gels.

Supplementary Table S3: MS information of ethylene responsive latex proteins by iTRAQ.

Supplementary Table S4: MS identification of the phosphorlated latex proteins.

Supplementary Figure S1:

Annotated spectra for the 252 total latex protein spots and 35 bands identified by PMF and the combination results of PMF and PFF.

Spot numbers of the **252** proteins correspond to the proteins that listed in detail.

CID: collision induced desorption;

MALDI TOF:

matrix assisted laser desorption/ionization time of flight;

MS: mass spectrometry;

PMF: peptide mass fingerprinting;

PFF: peptide fragment fingerprinting.

Spot No.: **1**

NCBI accession No.: **gi|132270** Species: *Hevea brasiliensis*

Protein name：Rubber elongation factor protein; Short=REF; AltName: Allergen=Hev b 1

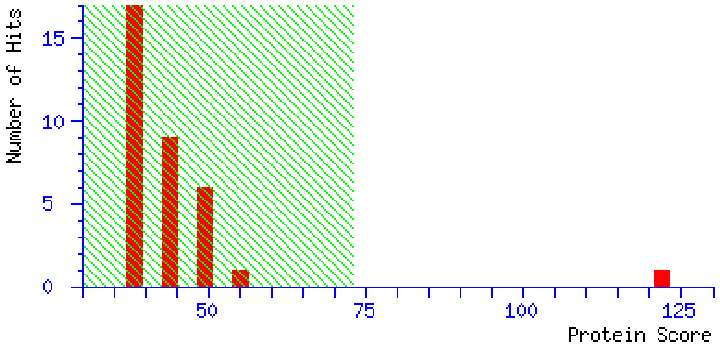
Mascot score: **122** Sequence coverage %: **73**

Matched peptides No.: 9 Total peptides No.: **23**

Calculated Mr: **14713** Calculated *p*I: **5.04**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 MAEDEDNQQG QGEGLK**YLGF** **VQDAATYAVT** **TFSNVYLFAK** **DKSGPLQPGV**
51 **DIIEGPVKNV** **AVPLYNR**FSY IPNGALK**FVD** **STVVASVTII** **DRSLPPIVKD**
101 **ASIQVVSAIR** **AAPEAARSLA** **SSLPGQTKIL** AKVFYGEN

Spot No.: **2**

NCBI accession No.: **gi|132270** Species: *Hevea brasiliensis*

Protein name： Rubber elongation factor protein; Short=REF;

AltName: Allergen=Hev b 1

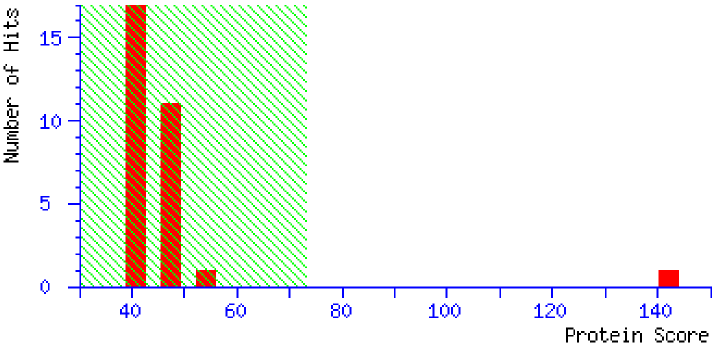
Mascot score: **142** Sequence coverage %: **81**

Matched peptides No.: **10** Total peptides No.: **17**

Calculated Mr: **14713** Calculated *p*I: **5.04**

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 73 are significant ($p<0.05$).



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

1 MAEDEDNQQG QGEGLK**YLGF** **VQDAATYAVT** **TFSNVYLFAK** **DKSGPLQPGV**
51 **DIIEGPVKNV** **AVPLYNRFSY** **IPNGALKFVD** **STVVASVTII** **DRSLPPIVKD**
101 **ASIQVVSAIR** **AAPEAARSLA** **SSLPGQTK**IL AKVFYGEN

Spot No.: **3**

NCBI accession No.: **gi|132270** Species: *Hevea brasiliensis*

Protein name：Rubber elongation factor protein; Short=REF; AltName: Allergen=Hev b 1

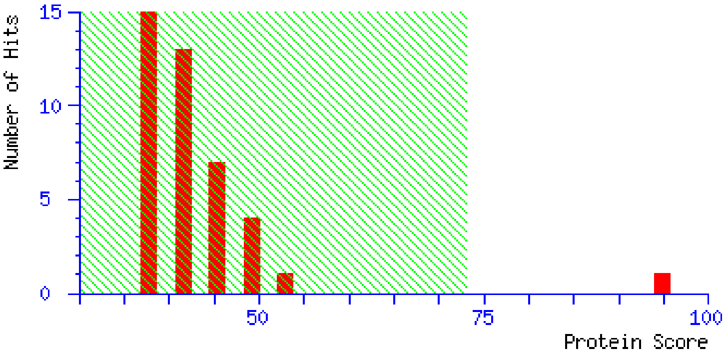
Mascot score: **95** Sequence coverage %: **56**

Matched peptides No.: **8** Total peptides No.: **42**

Calculated Mr: **14713** Calculated *p*I: **5.04**

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 73 are significant ($p<0.05$).



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

1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK **DKSGPLQPGV**
51 **DIIEGPVKNV AVPLYNR**FSY IPNGALK**FVD STVVASVTII DRSLPPIVKD**
101 **ASIQVVSAIR AAPEAARSLA SSLPGQTK**IL AKVFYGEN

Spot No.: **4**

NCBI accession No.: **gi|14423933** Species: *Hevea brasiliensis*

Protein name：Small rubber particle protein; Short=SRPP; AltName: Full=22 kDa rubber particle protein; Short=22 kDa RPP; AltName: Full=27 kDa natural rubber allergen; AltName: Full=Latex allergen Hev b 3

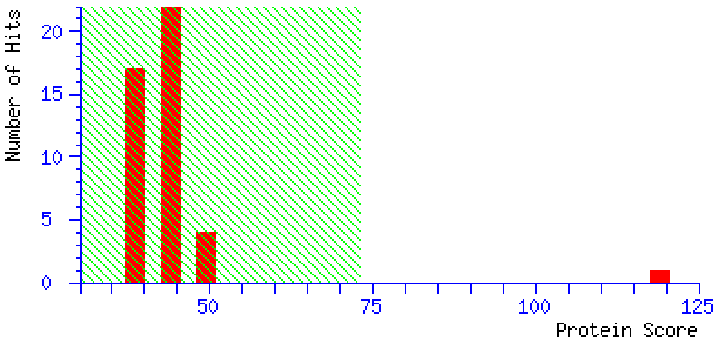
Mascot score: **119** Sequence coverage %: **75**

Matched peptides No.: **12** Total peptides No.: **52**

Calculated Mr: **22331** Calculated *p*I: **4.80**

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red:

1 MAEEVEEERL K**YLDFVRAAG** **VYAVDSFSTL** **YLYAKDISGP** **LKPGVDTIEN**
51 **VVKTVVTPVY** **YIPLEAVK**FV DK**TVDVSVTS** **LDGVVPPVIK** **QVSAQTYSVA**
101 **QDAPRIVLDV** **ASSVFNTGVQ** **EGAKALYANL** **EPKAEQYAVI** **TWR**ALNKLPL
151 VPQVANVVVP TAVYFSEK**YN** **DVVRGTTEQG** **YRVSSYLPLL** **PTEK**ITKVFG
201 DEAS

Spot No.: **5**

NCBI accession No.: **gi|14423933** Species: *Hevea brasiliensis*

Protein name：Small rubber particle protein; Short=SRPP; AltName: Full=22 kDa rubber particle protein; Short=22 kDa RPP; AltName: Full=27 kDa natural rubber allergen; AltName: Full=Latex allergen Hev b 3

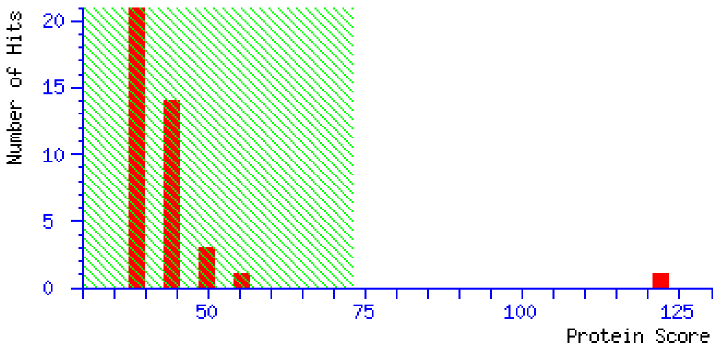
Mascot score: **122** Sequence coverage %: **85**

Matched peptides No.: **13** Total peptides No.: **55**

Calculated Mr: **22331** Calculated *p*I: **4.80**

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red:

1 MAEEVEEERL K**YLDFVRAAG** **VYAVDSFSTL** **YLYAKDISGP** **LKPGVDTIEN**
51 **VVKTVVTPVY** **YIPLEAVK**FV DK**TVDVSVTS** **LDGVVPPVIK** **QVSAQTYSVA**
101 **QDAPRIVLDV** **ASSVFNTGVQ** **EGAKALYANL** **EPKAEQYAVI** **TWR**ALNK**LPL**
151 **VPQVANVVVP** **TAVYFSEKYN** **DVVRGTTEQG** **YRVSSYLPLL** **PTEK**ITKVFG
201 DEAS

Spot No.: **6**

NCBI accession No.: **gi|14423933** Species: *Hevea brasiliensis*

Protein name：Small rubber particle protein; Short=SRPP; AltName: Full=22 kDa rubber particle protein; Short=22 kDa RPP; AltName: Full=27 kDa natural rubber allergen; AltName: Full=Latex allergen Hev b 3

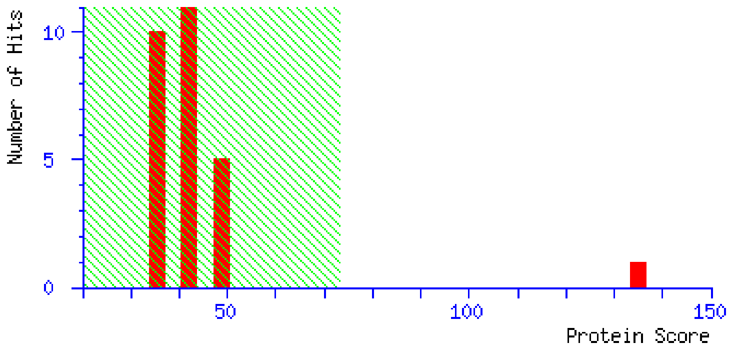
Mascot score: **135** Sequence coverage %: **75**

Matched peptides No.: **12** Total peptides No.: **31**

Calculated Mr: **22331** Calculated *p*I: **4.80**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MAEEVEEERL K**YLDFVRAAG** **VYAVDSFSTL** **YLYAKDISGP** **LKPGVDTIEN**

51 **VVKTVVTPVY** **YIPLEAVK**FV DK**TVDVSVTS** **LDGVVPPVIK** **QVSAQTYSVA**

101 **QDAPRIVLDV** **ASSVFNTGVQ** **EGAKALYANL** **EPKAEQYAVI** **TWR**ALNKLPL

151 VPQVANVVVP TAVYFSEK**YN** **DVVRGTTEQG** **YRVSSYLPLL** **PTEK**ITKVFG

201 DEAS

Spot No.: **7**

NCBI accession No.: **gi| 29170601** Species: *Hevea brasiliensis*

PFF score: **[121]** Protein name: small rubber particle protein

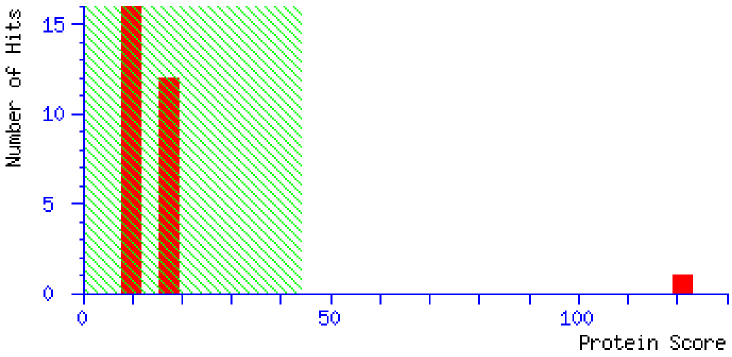
Matched peptides No.: [2] Sequence coverage %: [23]

Matched sequences: K.ENENFQQEANEQEEK.L;
K.QLPTQACDTSVK.E

Calculated Mr: **12769** Calculated *p*I: **4.61**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red

1 MAEGK**ENENF** **QQEANEQEEK** LKYLEFVQAT TDNAVTALSN IYLYAKDNSG
51 PLKPGVETIE GVAKTVVIPA SKIPTEAIKF ADRAVDASFT TLQNIVPSVL
101 **KQLPTQACDT** **SVK**ESAE

Spot No.: **8**

NCBI accession No.: **gi| 29170601** Species: *Hevea brasiliensis*

PFF score: **[110]** Protein name: small rubber particle protein

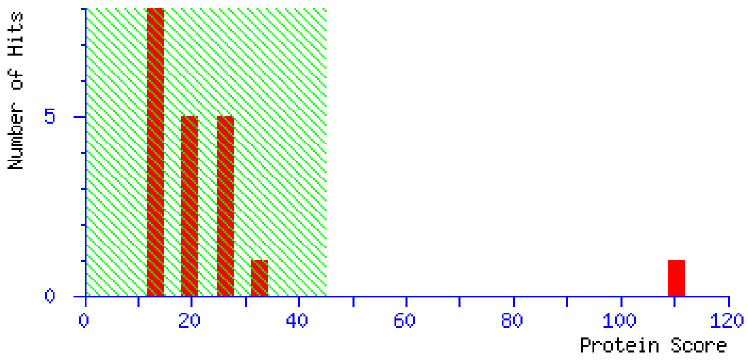
Matched peptides No.: [1] Sequence coverage %: [15]

Matched sequences: K.DNSGPLKPGVETIEGVAK.T

Calculated Mr: **12769** Calculated *p*I: **4.61**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEGKENENF QQEANEQEEK LKYLEFVQAT TDNAVTALSN IYLYAK**DNSG**
51 **PLKPGVETIE** **GVAK**TVVIPA SKIPTEAIKF ADRAVDASFT TLQNIVPSVL
101 KQLPTQACDT SVKESAE

Spot No.: **9**

NCBI accession No.: **gi|388503664** Species: *Lotus japonicus*

Protein name： **unknown**

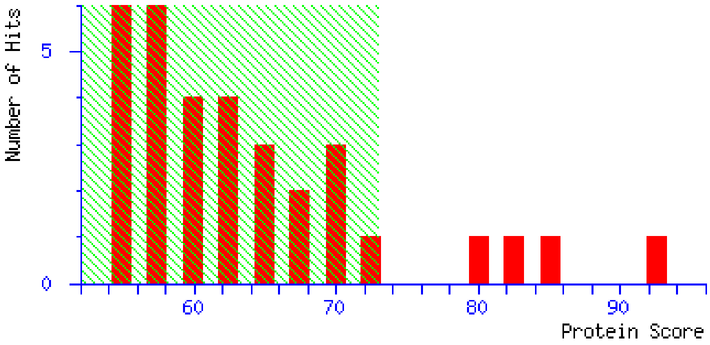
Mascot score: **93** Sequence coverage %: **45**

Matched peptides No.: **13** Total peptides No.: **48**

Calculated Mr: **29537** Calculated *p*I: **4.79**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MASSK**DRGTF** **VYVAKLAEQA** **ER**YEEMVDSM KKVANLDVEL TVEER**NLLSV**
51 **GYKNVIGAR**R ASWR**ILSSIE** **QK**EETKGNDV NAKR**IKEYR**Q KVESELADIC
101 NDVMRVIDEH LIPSATAGES TVFYYKMK**GD** **YYRYLAEFK**S GNEK**KEAADQ**
151 **SMKAYESATT** **AAEAELPPTH** **PIRLGLALNF** **SVFYYEILNS** **PERACHLAK**Q
201 AFDEAISELD TLNEESYK**DS** **TLIMQLLR**DN LTLWTSDIPE EGEDSLKAND
251 TAKVGGGEDA E

Spot No.: **10**

NCBI accession No.: **gi|3288200** Species: ***Hevea brasiliensis***

Protein name: **latex allergen**

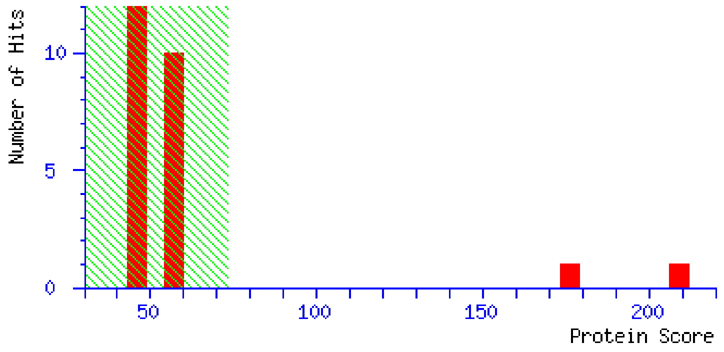
Mascot score: **209** Sequence coverage %: **68**

Matched peptides No.: **22** Total peptides No.: **42**

Calculated Mr: **43020** Calculated *p*I: **5.00**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MATGSTTLTQ GKK**ITVLSID** **GGGIRGIIPG** **IILASLESKL** **QDLDGPDARI**
51 **ADYFDIIAGT** **STGGLITTML** **TAPNEDKKPI** **YQAKDIKDFY** **LENCPK**IFPK
101 ESR**DTYDPIH** **SIGPIYDGEY** **LRELCNNLLK** DLTVK**DTLTD** **VIIPAFDIKL**
151 **LLPVIFSSDD** **AK**CNALKNAR **LADVCISTSA** **APVLLPAHSF** **TTEDDK**NIHT
201 FELIDGGVAA ANPTLLALTH IR**NEIIR**QNP R**FIGANLTES** **K**SRLVLSLGT
251 GKSEYK**EKYN** **ADMTSK**WRLY NWALYNGNSP AVDIFSNASS DMVDFHLSAL
301 FK**SLDCEDYY** **LRIQDDTLTG** **EESSGHIATE** **ENLQRLVEIG** **TELLEKQESR**
351 **INLDTGRLES** **IPGAPTNEAA** **IAK**FAK**LLSE** **ER**KLRQLK

Spot No.: **11**

NCBI accession No.: **gi|6707018**   Species: *Hevea brasiliensis*

Protein name: **latex protein allergen Hev b 7**

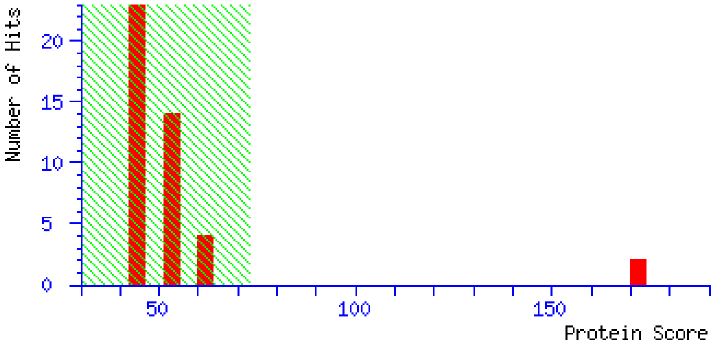
Mascot score: **172**   Sequence coverage %: **45**

Matched peptides No.: **17**   Total peptides No.: **45**

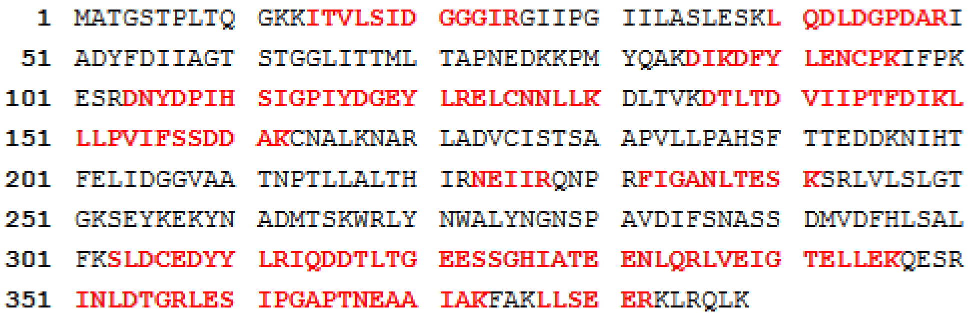
Calculated Mr: **43107**   Calculated *p*I: **5.00**

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 73 are significant (p<0.05).



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



1 MATGSTPLTQ GKK**ITVLSID** **GGGIR**GIIPG IILASLESK**L** **QDLDGPDARI**
51 ADYFDIIAGT STGGLITTML TAPNEDKKPM YQAK**DIKDFY** **LENCPK**IFPK
101 ESR**DNYDPIH** **SIGPIYDGEY** **LRELCNNLLK** DLTVK**DTLTD** **VIIPTFDIKL**
151 **LLPVIFSSDD** **AK**CNALKNAR LADVCISTSA APVLLPAHSF TTEDDKNIHT
201 FELIDGGVAA TNPTLLALTH IR**NEIIR**QNP R**FIGANLTES** **K**SRLVLSLGT
251 GKSEYKEKYN ADMTSKWRLY NWALYNGNSP AVDIFSNASS DMVDFHLSAL
301 FK**SLDCEDYY** **LRIQDDTLTG** **EESSGHIATE** **ENLQRLVEIG** **TELLEK**QESR
351 **INLDTGRLES** **IPGAPTNEAA** **IAK**FAKLLSE **ER**KLRQLK

Spot No.: **12**

NCBI accession No.: **gi|4235430** Species: *Hevea brasiliensis*

Protein name: **latex-abundant protein**

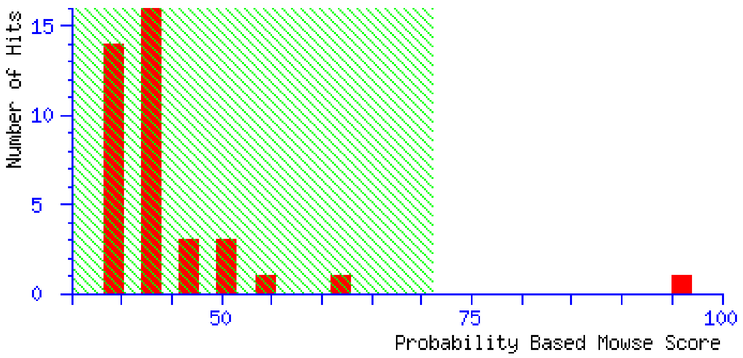
Mascot score: **82** Sequence coverage %: **49**

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

Calculated Mr: **46443** Calculated *p*I: **5.01**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MAKKAVLIGI NYPGTKAELK GCINDVKRMY RCLVDR**YGFS** **EEDITVLIDI**
51 **DESYIQPTGK** NIR**RVLTDLV** **RSAEPGDLLF** **VHYSGHGTRL** **PAETGEDDDT**
101 **GFDECIVPCD** **MNLITDDDFR** **EFVDQVPHGC** **R**ITVVSDSCH SGGLIDEAKE
151 QIGESTKRKE EESESGFGFK SFLK**QTIQDA** **FESRGVHLPS** **DLHHHHGHRD**
201 **EEDFDNRVVE** **EDYGDSGYVK** SK**SLPLSTLI** **EILK**QKTGKD DIDVGK**LRPT**
251 **LFDMFGDDAS** **PK**VKKFMKVI LNKLR**HGDGE** **SGGGGFLGMV** **GSLAQEFLK**H
301 KLDENDESYV KPALETEVDS KQEVYAGKTK RSLPDGGILI SGCQTDQTSA
351 DASPSGKSSE AYGALSNAIQ TIIAETDGAV TNQELVLKAR KMLKKQGFTQ
401 K**PGLYCSDDH** **VEASFVC**

Spot No.: **13**

NCBI accession No.: **gi|4235430** Species: *Hevea brasiliensis*

Protein name: **latex-abundant protein**

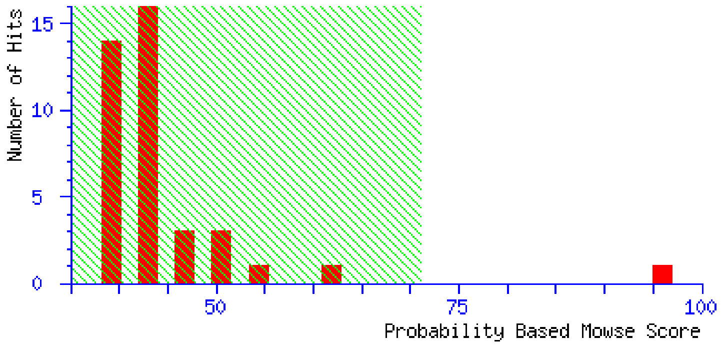
Mascot score: **96** Sequence coverage %: **54**

Matched peptides No.: **15** Total peptides No.: **37**

Calculated Mr: **46443** Calculated *p*I: **5.01**

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red:

1 MAKKAVLIGI NYPGTKAELK GCINDVKRMY RCLVDR**YGFS** **EEDITVLIDI**
51 **DESYIQPTGK** NIR**RVLTDLV** **RSAEPGDLLF** **VHYSGHGTRL** **PAETGEDDDT**
101 **GFDECIVPCD** **MNLITDDDFR** **EFVDQVPHGC** **RITVVSDSCH** **SGGLIDEAK**E
151 QIGESTKRKE EESESGFGFK SFLK**QTIQDA** **FESRGVHLPS** **DLHHHHGHRD**
201 **EEDFDNRVVE** **EDYGDSGYVK** SK**SLPLSTLI** **EILK**QKTGKD DIDVGK**LRPT**
251 **LFDMFGDDAS** **PK**VKKFMKVI LNKLRHGDGE SGGGGFLGMV GSLAQEFLK**H**
301 **KLDENDESYV** **KPALETEVDS** **K**QEVYAGKTK RSLPDGGILI SGCQTDQTSA
351 DASPSGKSSE AYGALSNAIQ TIIAETDGAV TNQELVLKAR KMLK**KQGFTQ**
401 **KPGLYCSDDH** **VEASFVC**

Spot No.: **14**

NCBI accession No.: **gi|20559**   Species: *Petunia x hybrida*

Protein name: **hsp70 (AA 6 - 651)**

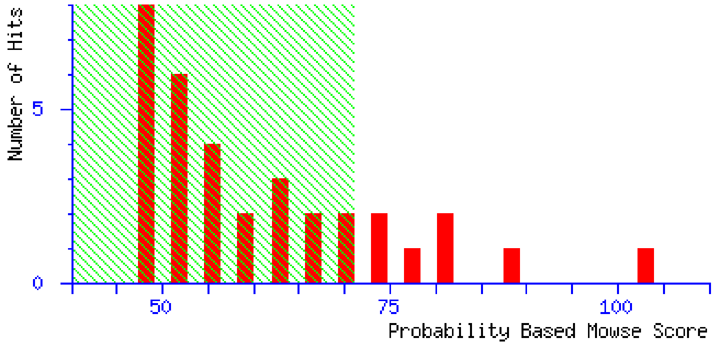
Mascot score: **103**   Sequence coverage %: **40**

Matched peptides No.: **24**   Total peptides No.: **41**

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

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red:

1 EGPAIGIDLG TTYSCVGVWQ HDRVEIIAND QGNRTTPSYV GFTDTERLIG

51 DAAKNQVAMN PINTVFDAKR LIGRRFSDPS VQSDIKLWPF KVIPGPGDKP

101 MIVVTYKGEE KQFAAEEISS MVLTK**MKEIA EAYLGTTIKN AVVTVPAYFN**

151 **DSQ**RQATK**DA GVIAGLNVMR IINEPTAAAI AYGLDKK**ASS AGEKNVLIFD

201 LGGGTFDVSL LTIEEGIFEV **KATAGDTHLG GEDFDNRMVN HFVQEFK**RKN

251 KK**DISGNPRA** LRRLRTACER AKR**TLSSTAQ TTIEIDSLYE GIDFYSTITR**

301 **ARFEELNMDL FRKCMEPVEK** CLRDAKMDK**S SVHDVVLVGG STR**IPKVQQL

351 LQDFFNGKEL CKSINPDEAV AYGAAVQAAI LSGEGNEKVQ DLLLLDVTPL

401 SLGLETAGGG MTVLIPRNTT IPTKK**EQVFS TYSDNQPGVL IQVYEGERAR**

451 TKDNNLLGKF ELSGIPPAPR **GVPQITVCFD IDANGILNVS AEDK**TTGQKN

501 KITITNDKGR LSK**EEIERMV QEAEK**YKSED EELKKKVEAK **NALENYAYNM**

551 **RNTIKDDKIN SQLSAADKKR IEDAIDEAIK** WLDNNQLAEA DEFEDK**MKEL**

601 **ESICNPIIAK** MYQGGAGGAT MDEDGPSVGG SAGSQTGAGP KIEEVD

Spot No.: **15**

NCBI accession No.: **gi|58013197** Species: *Isatis tinctoria*

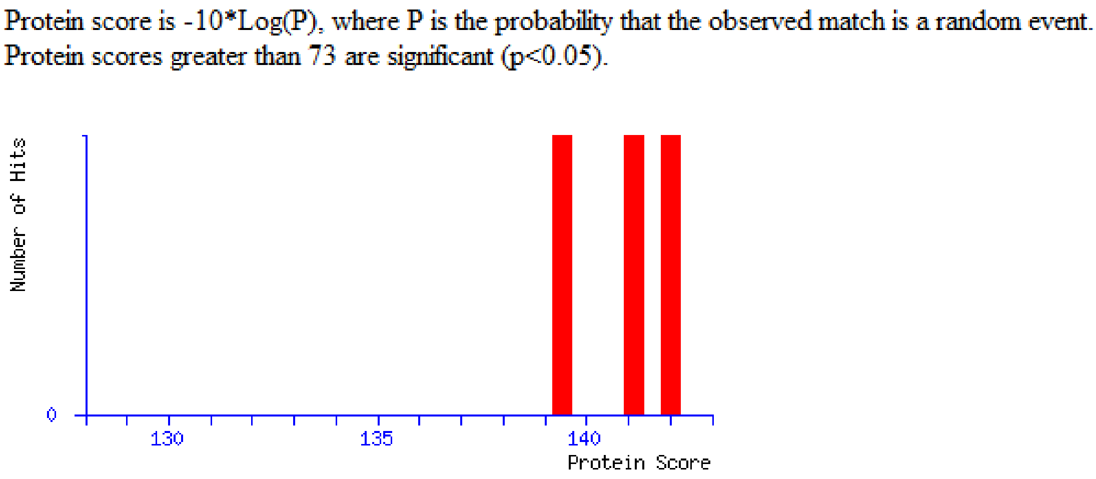
Protein name: **actin**

Mascot score: **142** Sequence coverage %: **51**

Matched peptides No.: **16** Total peptides No.: **36**

Calculated Mr: **42020** Calculated *p*I: **5.31**

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 73 are significant ($p<0.05$).

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

1 MADGEDIQPL VCDNGTGMVK **AGFAGDDAPR** **AVFPSIVGRP** **R**HTGVTVWMG
51 QKDAYVGDEA QSKRGILTLK **YPIEHGIVSN** **WDDMEK**IWHH TFYNELR**VAP**
101 **EEHPVLLTEA** **PLNPK**ANREK MTQIMFETFN VPAMYVAIQA VLSLYASGR**T**
151 **TGIVLDSGDG** **VSHTVPIYEG** **YALPHAILRL** **DLAGRDLTDS** **LMKILTERGY**
201 **MFTTTAEREI** VRDIKEK**LAY** **VALDYEQELE** **TAK**SSSSVEK **NYELPDGQVI**
251 **TIGAER**FRCP EILFQPSLIG MEAPGIHETT YNSIMK**CDVD** **IRKDLYGNIV**
301 **LSGGSTMFPG** **IADR**MSKEIT ALAPSSMKIK **VVAPPERK**YS VWIGGSILAS
351 LSTFQQMWIS K**GEYDESGPS** **IVHR**KCF

Spot No.: **16**

NCBI accession No.: gi|2506211

Species: *Vigna radiata var. radiata*

Protein name: V-type proton ATPase catalytic subunit A

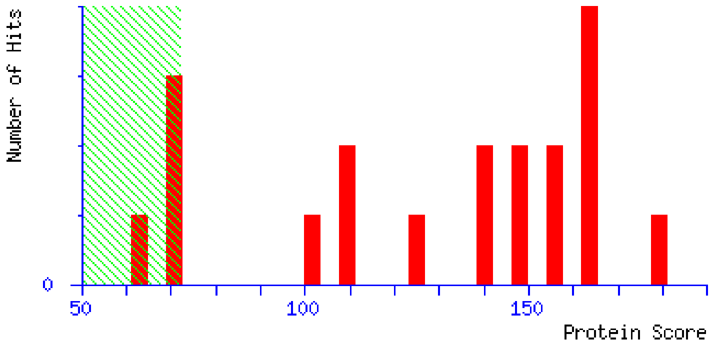
PMF Mascot score: **145** Sequence coverage %: **45**

Matched peptides No.: **27** Total peptides No.: **69**

Calculated Mr: **68923** Calculated *p*I: **5.30**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MPAVYGAR**LT** **TFEDSEKESE** **YGYVRKVSGP** **VVVADGMAGA** **AMYELVR**VGR

51 DNLIGEIIR**L** **EGDSATIQVY** **EETAGLMVND** **PVLRTHKPLS** **VELGPGILGN**

101 **IFDGIQRPLK** TIAKRSGDVY IPR**GVSVPAL** **DKDTLWEFQP** **K**KIGEGDLLT

151 GGDLYATVFE NTLMQHHIAL PPDAMGKITY IAPPGQYSIT DTVLELEFQG

201 VKK**KFTMLQT** **WPVR**TPRPVA SK**LAADTPLL** **TGQRVLDALF** **PSVLGGTCAI**

251 **PGAFGCGK**TV ISQALSKYSN SDAVVYVGCG ER**GNEMAEVL** **MDFPQLTMTL**

301 **PDGR**EESVMK RTTLVANTSN MPVAAR**EASI** **YTGITLAEYF** **R**DMGYNVSMM

351 ADSTSR**WAEA** **LR**EISGR**LAE** **MPADSGYPAY** **LAAR**LASFYE RPGKVKCLGG

401 PERTGSVTIV GAVSPPGGDF SDPVTSATLS IVQVFWGLDK KLAQR**KHFPS**

451 **VNWLISYSK**Y STALESFYEQ FDPDFINIRT KAR**EVLQRED** **DLNEIVQLVG**

501 **K**DALAEGDKI TLETAK**LLRE** **DYLAQNAFTP** **YDKFCPFYK**S VWMMR**NIIHF**

551 **YNLANQAVER** GAGSDGQKIT YSLIKHRVGD LFYRLVSQKF EDPAEGEAAL

601 VGQFQKLHED LSTGFRNLED ETR

Spot No.: **17**

NCBI accession No.: **gi|357480067** Species: *Medicago truncatula*

Protein name: Leucine aminopeptidase

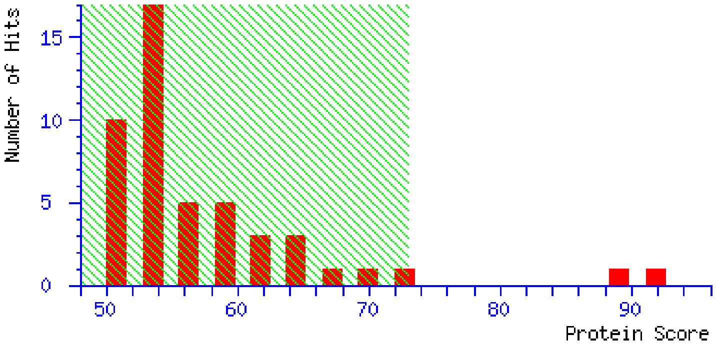
Mascot score: **92** Sequence coverage %: **31**

Matched peptides No.: **16** Total peptides No.: **69**

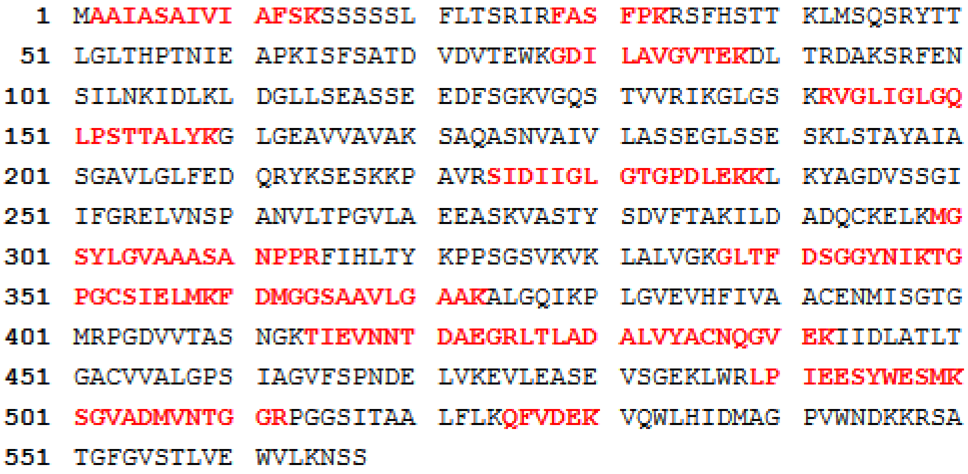
Calculated Mr: **59856** Calculated *p*I: **7.56**

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red:



1 **MAAIASAIVI** **AFSK**SSSSSL FLTSRIR**FAS** **FPK**RSFHSTT KLMSQSRYTT
51 LGLTHPTNIE APKISFSATD VDVTEWK**GDI** **LAVGVTEK**DL TRDAKSRFEN
101 SILNKIDLKL DGLLSEASSE EDFSGKVGQS TVVRIKGLGS K**RVGLIGLGQ**
151 **LPSTTALYK**G LGEAVVAVAK SAQASNVAIV LASSEGLSSE SKLSTAYAIA
201 SGAVLGLFED QRYKSESKKP AVR**SIDIIGL** **GTGPDLEKK**L KYAGDVSSGI
251 IFGRELVNSP ANVLTPGVLA EEASKVASTY SDVFTAKILD ADQCKELK**MG**
301 **SYLGVAAASA** **NPPR**FIHLTY KPPSGSVKVK LALVGK**GLTF** **DSGGYNIKTG**
351 **PGCSIELMKF** **DMGGSAAVLG** **AAK**ALGQIKP LGVEVHFIVA ACENMISGTG
401 MRPGDVVTAS NGK**TIEVNNT** **DAEGRLTLAD** **ALVYACNQGV** **EK**IIDLATLT
451 GACVVALGPS IAGVFSPNDE LVKEVLEASE VSGEKLWR**LP** **IEESYWESMK**
501 **SGVADMVNTG** **GR**PGGSITAA LFLK**QFVDEK** VQWLHIDMAG PVWNDKKRSA
551 TGFGVSTLVE WVLKNSS

Spot No.: **18**

NCBI accession No.: **gi|219885949** Species: *Zea mays*

Protein name: unknown

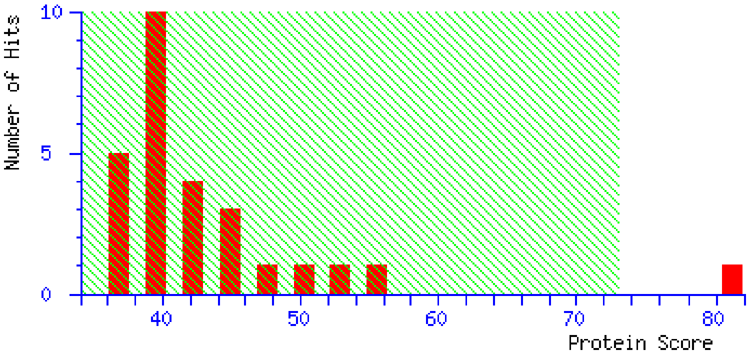
Mascot score: **81** Sequence coverage %: **35**

Matched peptides No.: **8** Total peptides No.: **46**

Calculated Mr: **30752** Calculated *p*I: **5.91**

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 73 are significant ($p<0.05$).



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

1 **MALAAVIRSS** **RATTMMELEI** **ELK**KASDKLK **SWDATSISLS** **AACDLFMRFV**
51 **TRTSHLEHEK** **FDAAK**SRLIE RGEK**FGEISL** **KARKTIAMLS** **QDFIYDGCTI**
101 **LVHGYSRVVL** **EVLK**LAASNR KLFRVLCTEG RPDRTGLRMS NELAALGIPV
151 KVLIDSAVAY SIDEVDMVFV GADGVVESGG IINMMGTYQI ALVAHTMDKP
201 VYVAAESHKF ARLYPLDQKD MTPAHRPIDF GVPIPIGVEV ETSARDYTPP
251 QYLTLLLTDL GVLTPSVVSD ELIQLYL

Spot No.: **19**

NCBI accession No.: **gi|242059605** Species: *Sorghum bicolor*

PFF score: **[101]**

Protein name：hypothetical protein SORBIDRAFT_03g043200

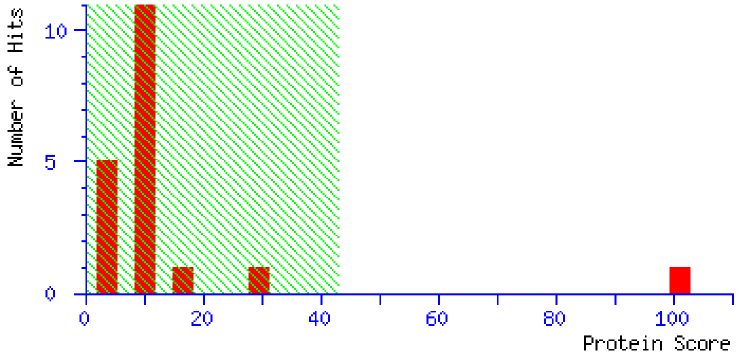
Matched peptides No.: [1] Sequence coverage %: [6]

Matched sequences: R.FFPSEFGNDVDHVHAVEPAK.S;

Calculated Mr: **34294** Calculated *p*I: **5.93**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 43 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red：

1 MSSAAGHKER SRVLVIGGTG YIGRFIVAAS AREGHPTYVL VRDPAPADPA
51 KAAVLQGFRD AGVTLVKGDL YNHESLVVAM ESADVVISAV GYAQLPDQTR
101 IISAIKDAGN IKR**FFPSEFG** **NDVDHVHAVE** **PAK**SVFAAKA SIRRAVEAEG
151 IPYTYISSNF FAGRFLPAIG QIGVTGLPID KVLILGDGNV KAIFGTEEDV
201 GTYTIKAVDD PRTLNKILYL RPPSNILSHN ELISLWEKKV GKTFERVYIP
251 EDDVLKKIQE SPIPLNRALS ISHSAWVKGD HTNFEIDPFF GVEATDLYPD
301 VKYTTVDEYL NKFL

Spot No.: **20**

NCBI accession No.: **gi|30575570** Species: *Citrus x paradisi*

PFF score: **[86]** Protein name：HSP19 class II, partial

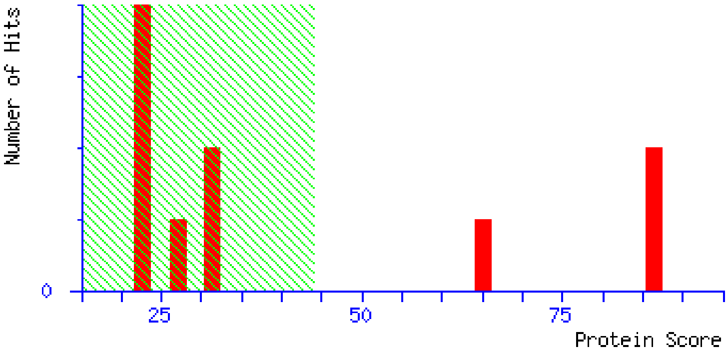
Matched peptides No.: [1] Sequence coverage %: [15]

Matched sequences: K.VQVEDDNVLLISGER.K;

Calculated Mr: **11191** Calculated *p*I: **8.01**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red：

```
 1  YVFIVDMPGL  KSGDIKVQVE  DDNVLLISGE  RKREEEKDGA  KYVRMERRVG
51  KFMRKFVLPE  NANVEAISAV  CQDGVLTVTV  DKLPPPEPKK  PKTIEVKIA
```

Spot No.: **21**

NCBI accession No.: **gi|27449246** Species: *Hevea brasiliensis*

Protein name: Cu/Zn superoxide dismutase

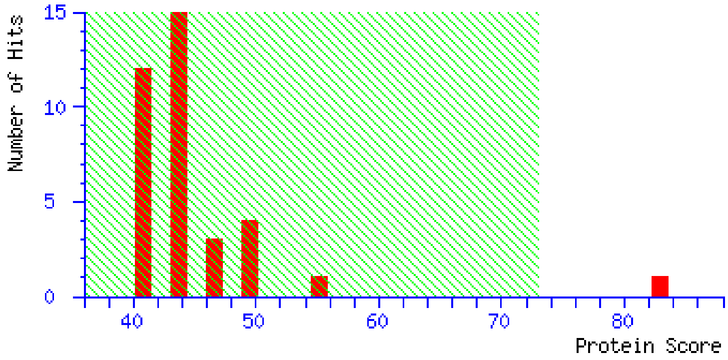
Mascot score: **83** Sequence coverage %:**48**

Matched peptides No.: **7** Total peptides No.: **21**

Calculated Mr: **15726** Calculated *p*I: **5.73**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MLKAVAVITS SEGISGKIFF TQEGDGPTTV TGSVSGLKPG LHGFHVHTFG
51 DTTNGCLSTG LHFNPASK**DH** **GGPEDENRHA** **GDLGNVNVGD** **DGTANFTIVD**
101 **KHIPLSGPHS** **IAGRSVVFHE** **GRDDLGKGGH** **ELSKITGNAG** DRIACGIIGL
151 QE

Spot No.: **22**

NCBI accession No.: **gi|37806305**

Species: *Oryza sativa Japonica Group*

PFF score: **[60]** Protein name：hypothetical protein

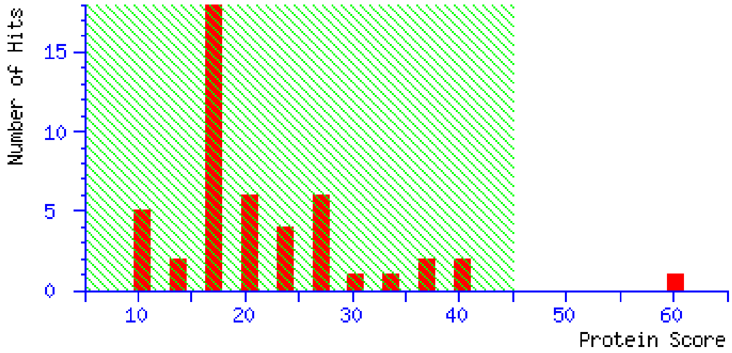
Matched peptides No.: [2] Sequence coverage %: [3]

Matched sequences: K.LGTLVLGDRPR.L ; K.LGTLVLGDRPR.L

Calculated Mr: **35105** Calculated *p*I: **8.29**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red：

1 MEVFQGVQFA RLRNWWEETY VTADEDGRSV YHYAPDRHRP AHEAIWAVQM
51 VLAGAPPTQY VLLRGAYGRY LGAPDAVVRR WPLSCCWPAP VVGQRDFDQP
101 EVDAIMWRAV RRADHVLCLH DKSGRYLRGK **LGTLVLGDRP** **R**LTVGDGRLN
151 DDEKALRWEV LPVLPNPGRP ELPISIVPEA DLVGRLVKAC FLPLQREIQF
201 VEADDDGNIG EGQEVWDSFQ YEGRSVQLLR NELEDRVGYA ITVCVRAGRH
251 GQHSPLLINL PHSRETLHIV VLRRNSEADN QLTFPDPKAS SRRRYRHRRR
301 AIIQ

Spot No.: **23**

NCBI accession No.: **gi|10946499** Species: *Hevea brasiliensis*

Protein name: beta-1,3-glucanase

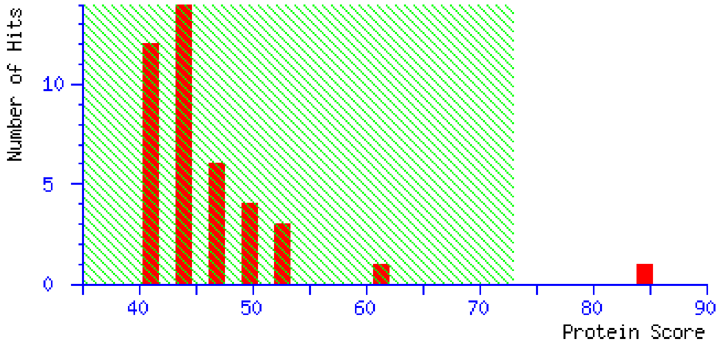
Mascot score: **85** Sequence coverage %:**43**

Matched peptides No.: **14** Total peptides No.: **53**

Calculated Mr: **35295** Calculated *p*I: **9.46**

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 73 are significant ($p<0.05$).



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

1 QVGVCYGMQG NNLPPVSEVI ALYKKSNITR MR**IYDPNRAV** **LEALR**GSNIE
51 LILGVPNSDL QSLTNPSNAK SWVQKNVRGF WSSVLFR**YIA** **VGNEISPVNR**
101 **GTAWLAQFVL** **PAMRNIHDAI** **RSAGLQDQIK** **VSTAIDLTLV** **GNSYPPSAGA**
151 **FRDDVRSYLN** **PIIRFLSSIR** SPLLANIYPY FTYAGNPRDI SLPYALFTSP
201 SVVVWDGQRG YK**NLFDATLD** **VLYSALER**AS GGSLEVVVSE SGWPSAGAFA
251 ATFDNGR**TYL** **SNLIQHVK**RG TPKRPNR**AIE** **TYLFAMFDEN** **K**KQPEVEKQF
301 GLFFPDKWQK YNLNFG

Spot No.: **24**

NCBI accession No.: **gi|78216493** Species: *Malus x domestica*

Protein name: cytosolic malate dehydrogenase

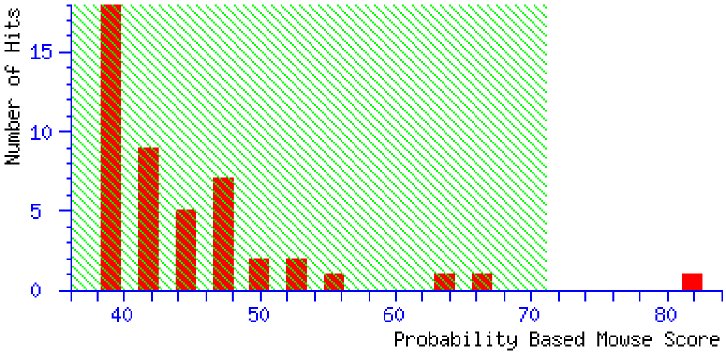
Mascot score: **82** Sequence coverage %:54

Matched peptides No.: **15** Total peptides No.: **50**

Calculated Mr: **35970** Calculated *p*I: **6.01**

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 73 are significant ($p<0.05$).



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

1 M**AKEPVRVLV TGAAGQIGYA LVPMIARGIM LGADQPVILH LLDIPPAAEA**

51 **LNGVKMELVD AAFPLLK**GVV ATTDVVEACT GVNIAVMVGG FPRK**EGMERK**

101 **DVMTK**NVSIY KSQASALEKH AAPNCK**VLVV ANPANTNALI LKEFAPSIPE**

151 **K**NVTCLTRLD HNRALGQVSE R**LNVQVSDVK NVIIWGNHSS SQYPDVNHAT**

201 **VK**TPSGEKCV R**ELVADDAWL NGEFISTVQQ R**GAAIIKARK **LSSALSAASS**

251 **ACDHIR**DWVL GTPEGTWVSM GVYSDGSYDV PSGLIFSFPV TCQHGEWK**IV**

301 **QGLSIDEFSR K**KLDATAEEL SEEKALAYSC LS

Spot No.: **25**

NCBI accession No.: **gi|257219562** Species: *Jatropha curcas*

PFF score: [81] Protein name： annexin-like protein

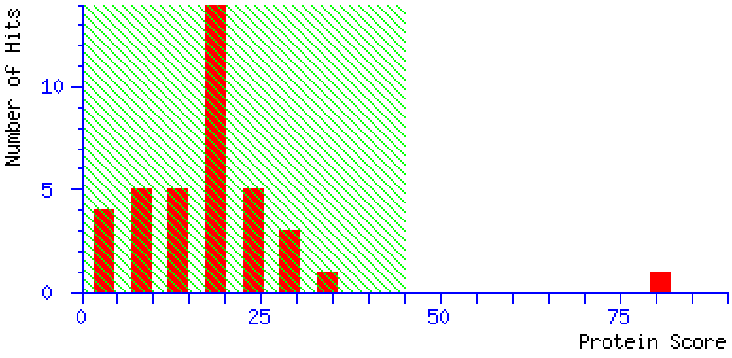
Matched peptides No.: [2] Sequence coverage %: [5]

Matched sequences: K.AFEGWGTNEK.A ; R.WILDPEDR.D

Calculated Mr: **36015** Calculated *p*I: **6.41**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red：

1 MATIVVPANV SYVEDAETLR K**AFEGWGTNE** **K**AVIAVLGHR NAVQKKHIRQ
51 AYWDLYQEDL VKRLESELGG DFERAMYR**WI** **LDPEDR**DAVL ANVALRKSGD
101 FHVIVEIACA RSAEELLLVR RAYQARYKHS LEEDVATHTT GDIRKLLVGL
151 VTAFMYEGAE INTRLAKSEA DVLQEAIKDK HFNHDEVIRI LTTRSKTQLN
201 TTFNHFKDDH GTSITKALLG EKADNEFVRL LSIAIRTMNE PLKYYEKVLR
251 NAIKRIGTDE DALTRVIVTR AEKDLLHIKE LYPKRNNVPL DHAVDKEIHG
301 DYKHFLLALL GHQD

Spot No.: **26**

NCBI accession No.: **gi|3451147** Species: *Hevea brasiliensis*

PFF score: [56] Protein name： chitinase

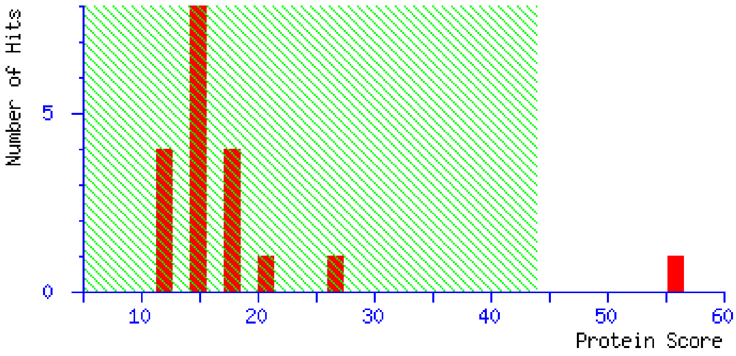
Matched peptides No.: [1] Sequence coverage %: [4]

Matched sequences: K.VYLTAAPQCPFPDR.Y

Calculated Mr: **34138** Calculated *p*I: **8.72**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MAKRTQAILL LLLAISLIMS SSHVDGGGIA IYWGQNGNEG TLTQTCSTRK
51 YSYVNIAFLN KFGNGQTPQI NLAGHCNPAA GGCTIVSNGI RSCQIQGIKV
101 MLSLGGGIGS YTLASQADAK NVADYLWNNF LGGKSSSRPL GDAVLDGIDF
151 DIEHGSTLYW DDLARYLSAY SKQGKK**VYLT** **AAPQCPFPDR** YLGTALNTGL
201 FDYVWVQFYN NPPCQYSSGN INNIINSWNR WTTSINAGKI FLGLPAAPEA
251 AGSGYVPPDV LISRILPEIK KSPKYGGVML WSKFYDDKNG YSSSIRDSVL
301 FLHSEKCMTV L

Spot No.: **27**

NCBI accession No.: **gi|4469175** Species: *Hevea brasiliensis*

Protein name: beta-1,3-glucanase

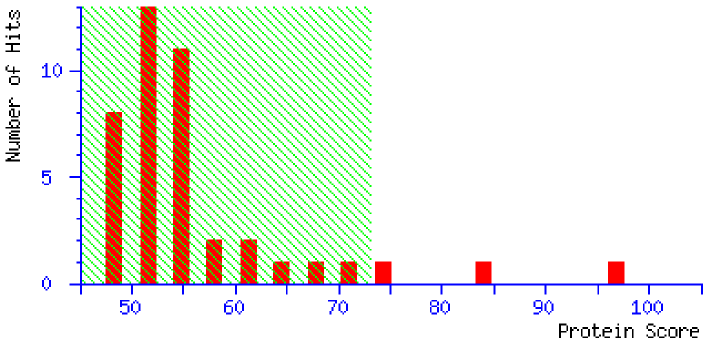
Mascot score: **97** Sequence coverage %:46

Matched peptides No.: **16** Total peptides No.: **107**

Calculated Mr: **38930** Calculated *p*I: **9.45**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 **MAISSSTSGT** **SSSLPSR**TTV MLLLFFFAAS VGITDAQVGV CYGMQGNNLP
51 PVSEVIALYK KSNITRMR**IY** **DPNRAVLEAL** **RGSNIELILG** **VPNSDLQSLT**
101 **NPSNAK**SWVQ KNVR**GFWSSV** **LFRYIAVGNE** **ISPVNRGTAW** **LAQFVLPAMR**
151 **NIHDAIRSAG** **LQDQIK**VSTA IDLTLVGNSY PPSAGAFRDD VR**SYLNPIIR**
201 **FLSSIR**SPLL ANIYPYFTYA GNPRDISLPY ALFTSPSVVV WDGQRGYK**NL**
251 **FDATLDVLYS** **ALER**ASGGSL EVVVSESGWP SAGAFAATFD NGR**TYLSNLI**
301 **QHVK**RGTPKR PNR**AIETYLF** **AMFDENKK**QP EVEKQFGLFF PDKWQKYNLN
351 FG

Spot No.: **28**

NCBI accession No.: **gi|124365253** Species: *Hevea brasiliensis*

Protein name: beta-1,3-glucanase

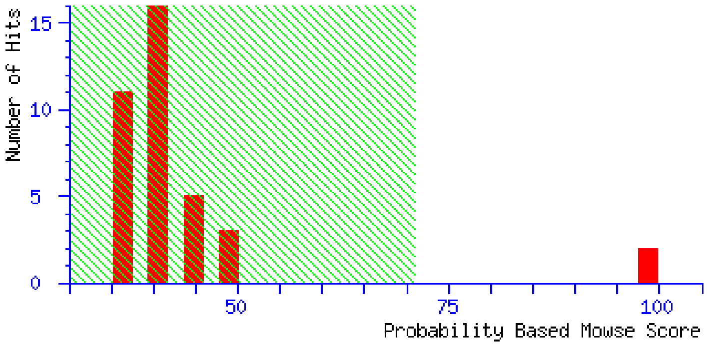
Mascot score: **99** Sequence coverage %:**37**

Matched peptides No.: **15** Total peptides No.: **44**

Calculated Mr: **41543** Calculated *p*I: **9.40**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MAISSSTSGT SSSLPSRTTV MLLLFFFTAS VGITDAQVGV CYGMQGNNLP

51 PVSEVIALYK K**SNITRMRIY** **DPNQAVLEAL** **R**GSNIELILG VPNSDLQSLT

101 NPSNAKSWVQ KNVRGFWSSV RFR**YIAVGNE** **ISPVNR**GTAW LAQFVLPAMR

151 **NIHDAIRSAG** **LQDQIKVSTA** **IDLTLVGNSY** **PPSAGAFRDD** **VRSYLNPIIR**

201 **FLSSIR**SPLL ANIYPYFTYA GNPRDISLPY ALFTSPSVVV WDGQRGYK**NL**

251 **FDATLDALYS** **ALER**ASGGSL EVVVSESGWP SAGAFAATFD NGR**TYLSNLI**

301 **QHVK**RGTPKR PKR**AIETYLF** **AMFDENKK**QP EVEK**HFGLFF** **PNK**WQKYNLN

351 FSAEKNWDIS TEHNATILFL KSDM

Spot No.: **29**

NCBI accession No.: **gi|124365253** Species: *Hevea brasiliensis*

Protein name: beta-1,3-glucanase

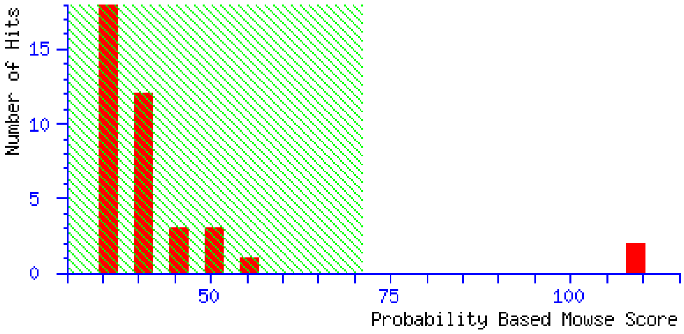
Mascot score: **109** Sequence coverage %:**38**

Matched peptides No.: **15** Total peptides No.: **35**

Calculated Mr: **41543** Calculated *p*I: **9.40**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MAISSSTSGT SSSLPSRTTV MLLLFFFTAS VGITDAQVGV CYGMQGNNLP
51 PVSEVIALYK KSNITRMR**IY** **DPNQAVLEAL** **R**GSNIELILG VPNSDLQSLT
101 NPSNAKSWVQ KNVRGFWSSV RFR**YIAVGNE** **ISPVNR**GTAW LAQFVLPAMR
151 **NIHDAIRSAG** **LQDQIKVSTA** **IDLTLVGNSY** **PPSAGAFRDD** **VRSYLNPIIR**
201 **FLSSIRSPLL** **ANIYPYFTYA** **GNPR**DISLPY ALFTSPSVVV WDGQRGYK**NL**
251 **FDATLDALYS** **ALER**ASGGSL EVVVSESGWP SAGAFAATFD NGR**TYLSNLI**
301 **QHVK**RGTPKR PK**RAIETYLF** **AMFDENKK**QP EVEKHFGLFF PNKWQKYNLN
351 FSAEKNWDIS TEHNATILFL KSDM

Spot No.: **30**

NCBI accession No.: **gi|255540341** Species: *Ricinus communis*

Protein name: **glyceraldehyde 3-phosphate dehydrogenase, putative**

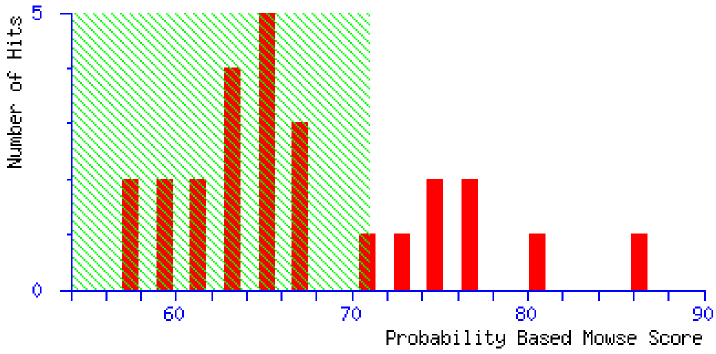
Mascot score: **86** Sequence coverage %:**42**

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

Calculated Mr: **36930** Calculated *p*I: **7.10**

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 73 are significant ($p<0.05$).



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

1 MAKIK**IGING** **FGR**IGRLVAR **VALQR**DDVEL VAVNDPFIST EYMTYMFK**YD**
51 **TVHGQWK**HHE LKIKDDKTLL FGEKPVTVFG VR**NPEEIPWA** **ETGAEYIVES**
101 **TGVFTDKDK**A AAHLKGGAKK VIISAPSK**DA** **PMFVVGVNEK** EYTPDLHIIS
151 NASCTTNCLA PLAKVINDRF GIVEGLMTTV HSITATQK**TV** **DGPSMK**DWRG
201 GR**AASFNIIP** **SSTGAAKAVG** **K**VLPSLNGK**L** **TGMSFRVPTV** **DVSVVDLTVR**
251 LEKSATYEQI KAAIK**EESEG** **KLK**GILGYTE DDVVSTDFIG DKRSSIFDAK
301 **AGIALNDKFV** **KLVSWYDNEW** **GYSTR**VVDLI VHVASVH

Spot No.: **31**

NCBI accession No.: **gi|4539543** Species: *Nicotiana tabacum*

Protein name: glyceraldehyde-3-phosphate dehydrogenase

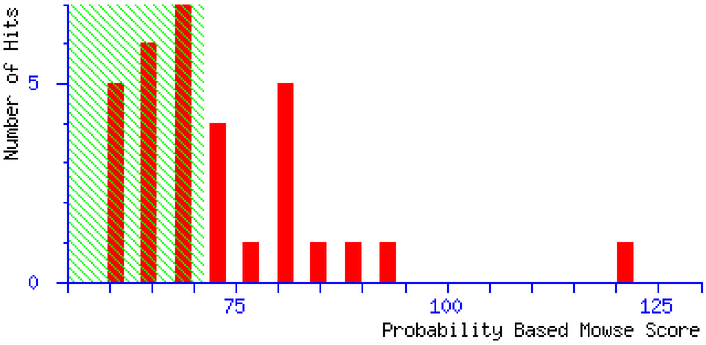
Mascot score: **121** Sequence coverage %:**47**

Matched peptides No.: **19** Total peptides No.: **89**

Calculated Mr: **36816** Calculated *p*I: **7.70**

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 73 are significant ($p<0.05$).



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

1 **MAKVKIGING** **FGR**IGRLVAR **VALQR**DDVEL VAVNDPFISV EYMTYMFKYD
51 SVHGQWKHHE LK**VKDDKTLL** **FGEK**AVTVFG FRNPEEIPWG QTGADYIVES
101 TGVFTDKDKA AAHLKGGAKK VIISAPSK**DA** **PMFVVGVNEK** EYKPELNIVS
151 NASCTTNCLA PLAKVINDR**F** **GIVEGLMTTV** **HSITATQK**TV DGPSAKDWRG
201 GR**AASFNIIP** **SSTGAAK**AVG KVLPALNGK**L** **TGMAFRVPTV** **DVSVVDLTVR**
251 LEKEATYDEI KAAIK**EESEG** **KLKGILGYTE** **DDVVSTDFVG** **DNRSSIFDAK**
301 **AGIALSK**NFV K**LVSWYDNEW** **GYSTR**VVDLI K**HMASVQ**

Spot No.: **32**

NCBI accession No.: **gi|32527831**

Species: *Populus tremula x Populus tremuloides*

Protein name: UDP-glucose pyrophosphorylase

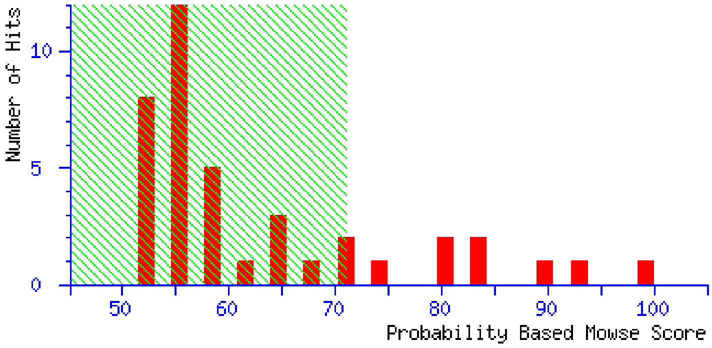
Mascot score: **99** Sequence coverage %:**40**

Matched peptides No.: **18** Total peptides No.: **102**

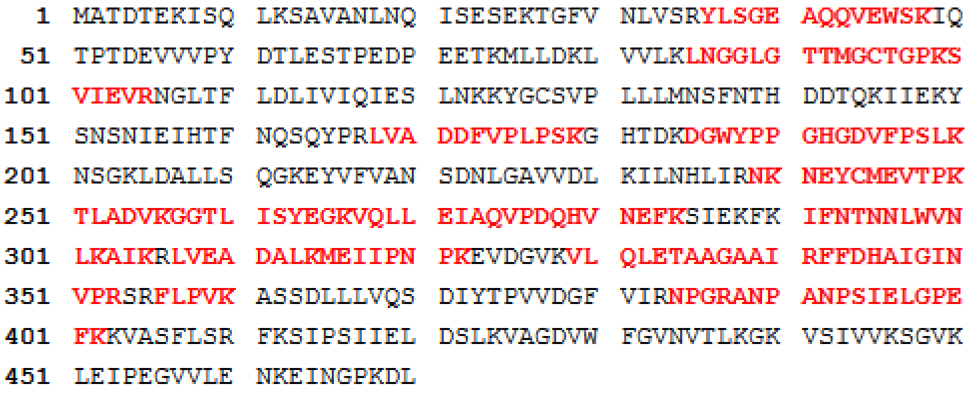
Calculated Mr: **51949** Calculated *p*I: **5.68**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:



1 MATDTEKISQ LKSAVANLNQ ISESEKTGFV NLVSR**YLSGE** **AQQVEWSK**IQ
51 TPTDEVVVPY DTLESTPEDP EETKMLLDKL VVLK**LNGGLG** **TTMGCTGPKS**
101 **VIEVR**NGLTF LDLIVIQIES LNKKYGCSVP LLLMNSFNTH DDTQKIIEKY
151 SNSNIEIHTF NQSQYPR**LVA** **DDFVPLPSK**G HTDK**DGWYPP** **GHGDVFPSLK**
201 NSGKLDALLS QGKEYVFVAN SDNLGAVVDL KILNHLIR**NK** **NEYCMEVTPK**
251 **TLADVKGGTL** **ISYEGKVQLL** **EIAQVPDQHV** **NEFK**SIEKFK **IFNTNNLWVN**
301 **LKAIK**R**LVEA** **DALKMEIIPN** **PK**EVDGVK**VL** **QLETAAGAAI** **RFFDHAIGIN**
351 **VPRSRFLPVK** ASSDLLLVQS DIYTPVVDGF VIR**NPGRANP** **ANPSIELGPE**
401 **FK**KVASFLSR FKSIPSIIEL DSLKVAGDVW FGVNVTLKGK VSIVVKSGVK
451 LEIPEGVVLE NKEINGPKDL

Spot No.: **33**

NCBI accession No.: **gi|6707018** Species: *Hevea brasiliensis*

Protein name: latex protein allergen Hev b 7

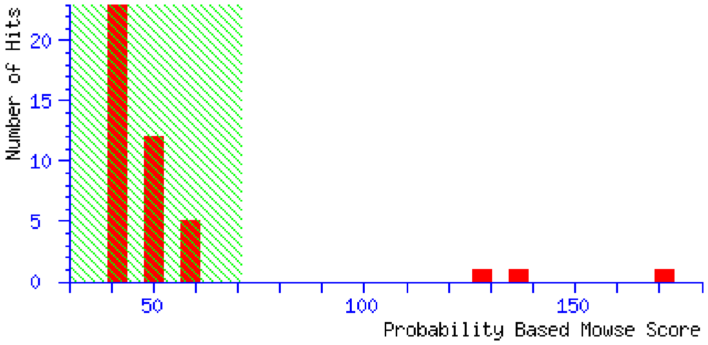
Mascot score: **171** Sequence coverage %:**79**

Matched peptides No.: **26** Total peptides No.: **67**

Calculated Mr: **43107** Calculated *p*I: **5.00**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 **MATGSTPLTQ GKKITVLSID GGGIRGIIPG IILASLESKL QDLDGPDARI**
51 **ADYFDIIAGT STGGLITTML TAPNEDKKPM YQAKDIKDFY LENCPK**IFPK
101 ESR**DNYDPIH SIGPIYDGEY LRELCNNLLK DLTVKDTLTD VIIPTFDIKL**
151 **LLPVIFSSDD AK**CNALKNAR **LADVCISTSA APVLLPAHSF TTEDDKNIHT**
201 **FELIDGGVAA TNPTLLALTH IRNEIIR**QNP R**FIGANLTES K**SRLVLSLGT
251 GKSEYK**EKYN ADMTSK**WRLY NWALYNGNSP AVDIFSNASS DMVDFHLSAL
301 FK**SLDCEDYY LRIQDDTLTG EESSGHIATE ENLQRLVEIG TELLEKQESR**
351 **INLDTGRLES IPGAPTNEAA IAK**FAK**LLSE ER**KLRQLK

Spot No.: **34**

NCBI accession No.: **gi|158144895** Species:*Gossypium hirsutum*

Protein name: enolase

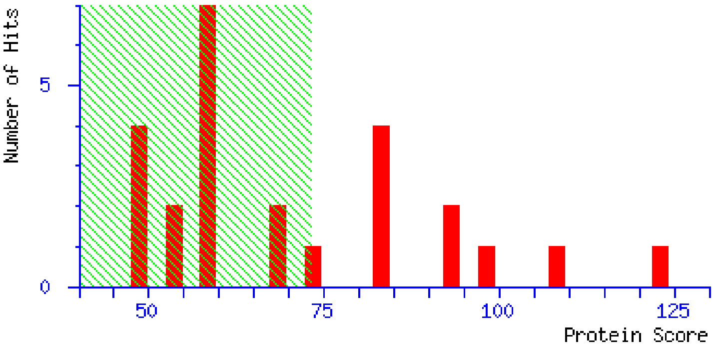
Mascot score: **123** Sequence coverage %:**39**

Matched peptides No.: **14** Total peptides No.: **48**

Calculated Mr: **47982** Calculated *p*I: **5.49**

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 73 are significant ($p<0.05$).



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

1 MAATIVSVKA R**QIFDSR**GNP TVEVDVETSN GIKAR**AAVPS** **GASTGIYEAL**
51 **ELR**DGDFDYL GKGVSK**AVAN** **VNTIIGPALI** **GK**DPTEQTAI DNFMVQQLDG
101 TQNEWGWCKQ KLGANAILAV SLAVCKAGAE VKKLPLYKHI ANLAGNSKLV
151 LPVPAFNVIN GGSHAGNK**LA** **MQEFMILPVG** **ASSFK**EAMKM GVEVYHHLKS
201 VIKK**KYGQDA** **TNVGDEGGFA** **PNIQENK**EGL ELLNTAIAKA GYTGKVVIGM
251 DVAASEFYGT DKTYDLNFKE ENNDGK**QKIS** **GDALK**DLYK**S** **FVAEYPIVSI**
301 **EDPFDQDDWE** **HYSK**LTNEIG EK**VQIVGDDL** **LVTNPK**RVAK AIAEKTCNAL
351 LLK**VNQIGSV** **TESIEAVK**MS KQAGWGVMAS HR**SGETEDTF** **IADLSVGLAT**
401 **GQIKTGAPCR** SERLAK**YNQL** **LR**IEEELGAE AVYAGASFRA PVAPY

Spot No.: 35

NCBI accession No.: **gi|3288200** Species: *Hevea brasiliensis*

PFF score: [81]

Protein name: **latex allergen**

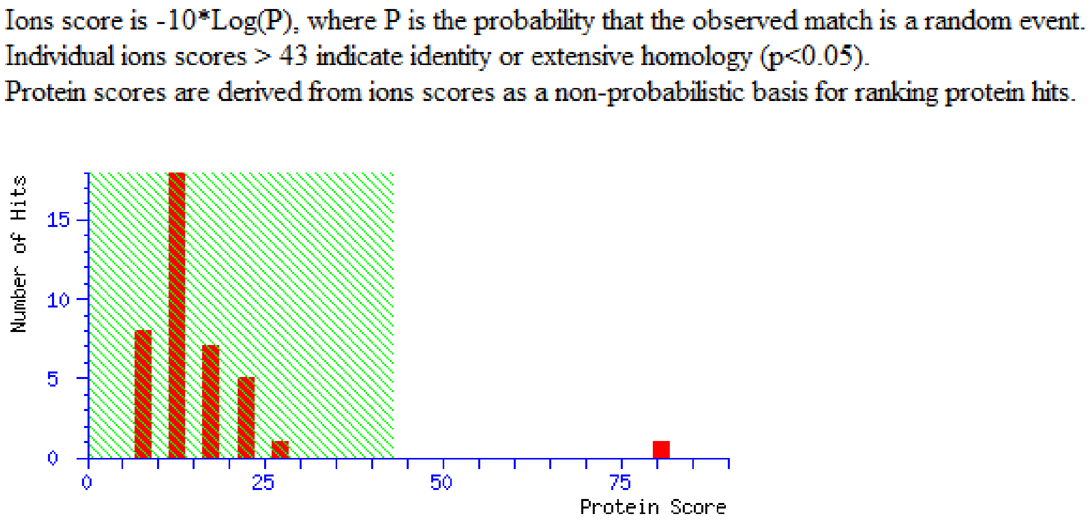
Matched peptides No.: [2] Sequence coverage %: [4]

Matched sequences: R.DTYDPIHSIGPIYDGEYLR.E;

R.DTYDPIHSIGPIYDGEYLR.E

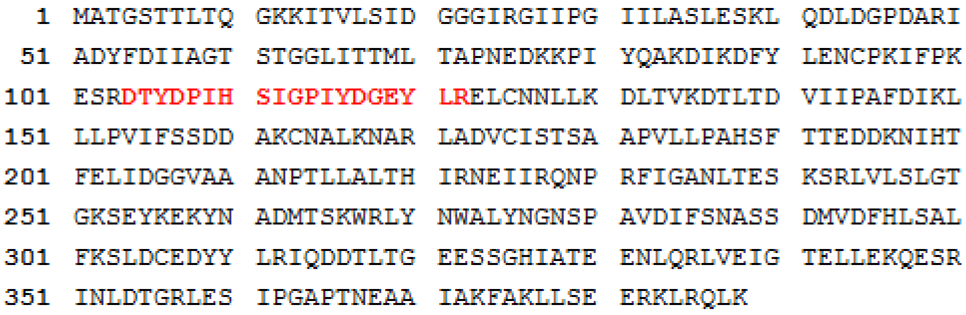
Calculated Mr: **43020** Calculated *p*I: **5.00**

Probability Based Mowse Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 43 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Matched peptide sequences: shown in Bold Red:



1 MATGSTTLTQ GKKITVLSID GGGIRGIIPG IILASLESKL QDLDGPDARI
51 ADYFDIIAGT STGGLITTML TAPNEDKKPI YQAKDIKDFY LENCPKIFPK
101 ESR**DTYDPIH SIGPIYDGEY LR**ELCNNLLK DLTVKDTLTD VIIPAFDIKL
151 LLPVIFSSDD AKCNALKNAR LADVCISTSA APVLLPAHSF TTEDDKNIHT
201 FELIDGGVAA ANPTLLALTH IRNEIIRQNP RFIGANLTES KSRLVLSLGT
251 GKSEYKEKYN ADMTSKWRLY NWALYNGNSP AVDIFSNASS DMVDFHLSAL
301 FKSLDCEDYY LRIQDDTLTG EESSGHIATE ENLQRLVEIG TELLEKQESR
351 INLDTGRLES IPGAPTNEAA IAKFAKLLSE ERKLRQLK

Spot No.: 36

NCBI accession No.: **gi|1916805**   Species: *Hevea brasiliensis*

PFF score: [138]

Protein name：**latex patatin homolog**

Matched peptides No.: [2]   Sequence coverage %: [8]

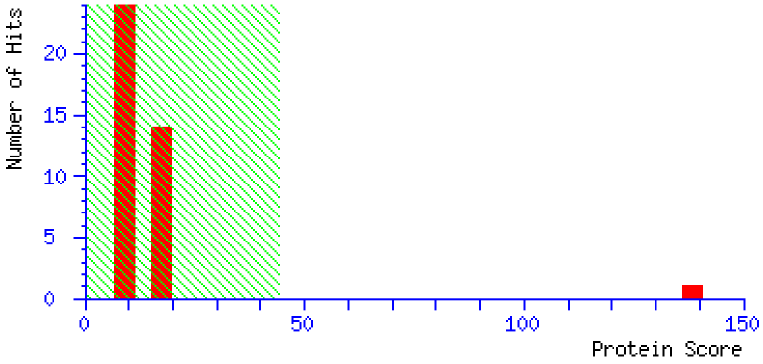
Matched sequences: K.SLDCEDYYLR.I；

R.IQDDTLTGEESSGHIATEENLQR.L

Calculated Mr: **43035**   Calculated *p*I: **5.00**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MATGSTTLTQ GKKITVLSID GGGIRGIIPG IILASLESKL QDLDGPDARI
51 ADYFDIIAGT STGGLITTML TAPNEDKKPM YQAKDIKDFY LENCPKIFPK
101 ESRDNYDPIH SIGPIYDGEY LRELCNNLLK DLTVKDTSTD VIIPTFDIKL
151 LLPVIFPSDD AKCNALKNAR LADVCISTSA APVLLPAHSF TTEDDKNIHT
201 FELIDGGVAA TNPTLLALTH IRNEIIRQNP RFIGANLTES KSRLVLSLGT
251 GKSEYKEKYN ADMTSKWRLY NWALYNGNSP AVDIFSNASS DMVDSHLSAL
301 FK**SLDCEDYY** **LRIQDDTLTG** **EESSGHIATE** **ENLQR**LVEIG TELLEKQESR
351 INLDTGRLES IPGAPTNEAA IAKFAKLLSE ERKLRQLK

Spot No.: 37

NCBI accession No.: **gi|41581137** Species: *Hevea brasiliensis*

Protein name：**putative latex allergen hev b 7.02**

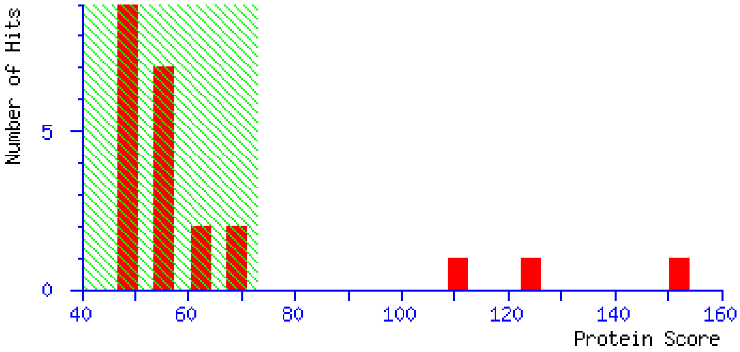
PMF score: **152** Sequence coverage %: **44**

Matched peptides No.: **16** Total peptides No.: **39**

Calculated Mr: **43027** Calculated *p*I: **5.12**

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 73 are significant ($p<0.05$).



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

1 ATGSTTLTQG KK**ITVLSIDG** **GGIRGIIPGI** **ILASLESKLQ** **DLDGPDAR**IA
51 DYFDIIAGTS TGGLITTMLT APNEDK**KPMY** **QAK**DIK**DFYL** **ENCPK**IFPKE
101 SR**DNYDPIHS** **IGPIYDGEYL** **RELCNNLLK**D LTVK**DTLTDV** **IIPTFDIKLL**
151 **LPVIFSSDDA** **K**CNALKNARL ADVCISTSAA PVLLPAHSFT TEDDKNIHTF
201 ELIDGGVAAT NPTLLALTHI R**NEIIR**QNPR **FIGANLTESK** SRLVLSLGTG
251 KSEYKEKYNA DMTSKWRLYN WALYNGNSPA VDIFSNASSD MVDFHLSALF
301 K**SLDCEDYYL** **RIQDDTLTGE** **ESSGHIATEE** **NLQRLVEIGT** **R**LLEKQESR**I**
351 **NLDTGR**LESI PGASTNEAAI TKFAK**LLSEE** **R**KLRQLK

Spot No.: 38

NCBI accession No.: **gi|41581137** Species: *Hevea brasiliensis*

Protein name：**putative latex allergen hev b 7.02**

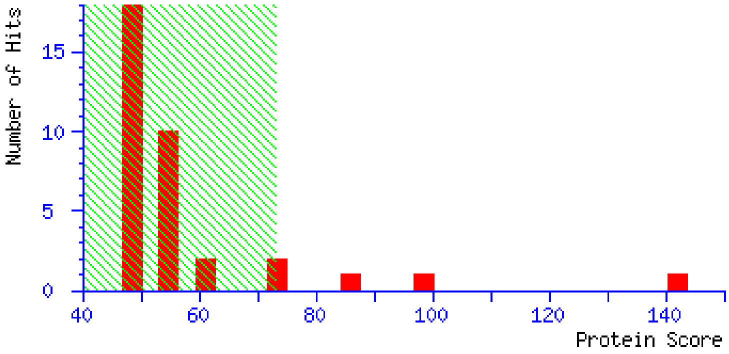
PMF score: **142** Sequence coverage %: **42**

Matched peptides No.: **15** Total peptides No.: **51**

Calculated Mr: **43027** Calculated *p*I: **5.12**

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 73 are significant (p<0.05).



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

1 ATGSTTLTQG KK**ITVLSIDG GGIRGIIPGI ILASLESKLQ DLDGPDARI**A
51 DYFDIIAGTS TGGLITTMLT APNEDKKPMY QAKDIK**DFYL ENCPK**IFPKE
101 SR**DNYDPIHS IGPIYDGEYL R**ELCNNLLK**D LTVKDTLTDV IIPTFDIKLL**
151 **LPVIFSSDDA K**CNALKNARL ADVCISTSAA PVLLPAHSFT TEDDKNIHTF
201 ELIDGGVAAT NPTLLALTHI R**NEIIR**QNPR **FIGANLTESK** SRLVLSLGTG
251 KSEYKEKYNA DMTSKWRLYN WALYNGNSPA VDIFSNASSD MVDFHLSALF
301 K**SLDCEDYYL RIQDDTLTGE ESSGHIATEE NLQRLVEIGT R**LLEKQESR**I**
351 **NLDTGR**LESI PGASTNEAAI TKFAK**LLSEE R**KLRQLK

Spot No.: 39

NCBI accession No.: **gi|255556934** Species: *Ricinus communis*

Protein name：**Transitional endoplasmic reticulum ATPase, putative**

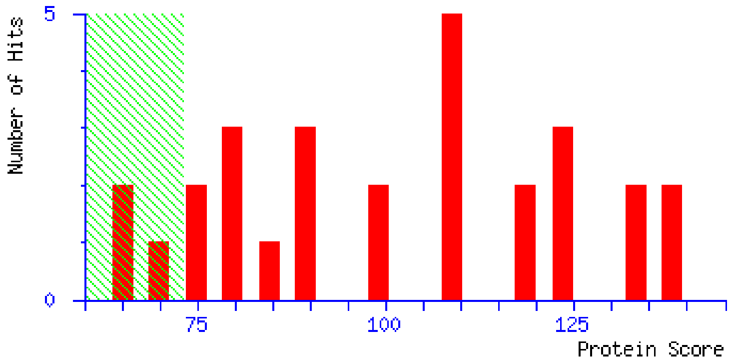
PMF score: **136** Sequence coverage %: **31**

Matched peptides No.: **25** Total peptides No.: **59**

Calculated Mr: **90355** Calculated *p*I: **5.13**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

```
  1 MSNQAESSDS KGTKRDFSTA ILERKKSPNR LVVDEAINDD NSVVSLHPET
 51 MEKLQLFRGD TILIKGKKRK DTICIALADD SCDEPKIRMN KVVRSNLRVR
101 LGDVVSVHQC PDVKYGKRVH ILPIDDTIEG VTGNLFDAYL KPYFLEAYRP
151 VRKGDLFLVR GGMRSVEFKV IETDPAEYCV VAPDTEIFCE GEPVRREDEN
201 RLDEVGYDDV GGVRKQMAQI RELVELPLRH PQLFKSIGVK PPKGILLYGP
251 PGSGKTLIAR AVANETGAFF FCINGPEIMS KLAGESESNL RKAFEEAEKN
301 APSIIFIDEI DSIAPKREKT HGEVERRIVS QLLTLMDGLK SRAHVIVIGA
351 TNRPNSIDPA LRRFGRFDRE IDIGVPDEVG RLEVLRIHTK NMKLAEDVDL
401 ERISKDTHGY VGADLAALCT EAALQCIREK MDVIDLEDET IDAEILNSMA
451 VSNEHFQTAL GTSNPSALRE TVVEVPNVSW EDIGGLENVK RELQETVQYP
501 VEHPEKFEKF GMSPSKGVLF YGPPGCGKTL LAKAIANECQ ANFISVKGPE
551 LLTMWFGESE ANVREIFDKA RQSAPCVLFF DELDSIATQR GSSVGDAGGA
601 ADRVLNQLLT EMDGMSAKKT VFIIGATNRP DIIDPALLRP GRLDQLIYIP
651 LPDEDSRHQI FKACLRKSPV SKDVDLRALA KYTQGFSGAD ITEICQRACK
701 YAIRENIEKD IERERRRDN  PEAMEEDVED DVAEIKAAHF EESMKYARRS
751 VSDADIRKYQ AFAQTLQQSR GFGSEFRFSE ATGAAAGADP FAASAGGEAD
801 DDDLYS
```

Spot No.: 40

NCBI accession No.: **gi|149938964** Species: *Actinidia deliciosa*

Protein name：**ACT1**

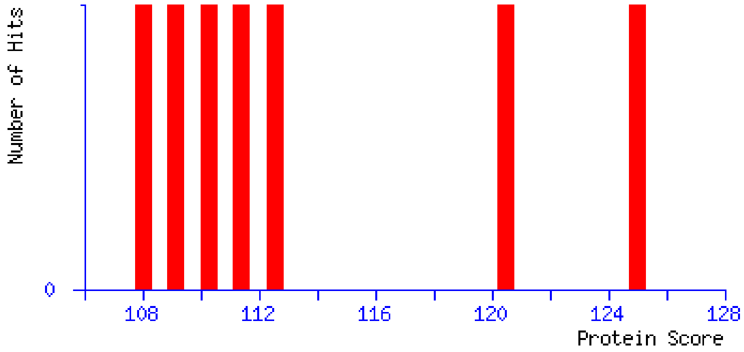
PMF score: **125** Sequence coverage %: **57**

Matched peptides No.: **19** Total peptides No.: **56**

Calculated Mr: **41865** Calculated *p*I: **5.31**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 **MADAEDIQPL** **VCDNGTGMVK** **AGFAGDDAPR** **AVFPSIVGRP** **RHTGVMVGMG**

51 **QKDAYVGDEA** **QSK**R**GILTLK** **YPIEHGIVSN** **WDDMEKIWHH** **TFYNELRVAP**

101 **EEHPVLLTEA** **PLNPK**ANREK MTQIMFETFN VPAMYVAIQA VLSLYASGRT

151 TGIVLDSGDG VSHTVPIYEG YALPHAILR**L** **DLAGRDLTDA** **LMK**ILTER**GY**

201 **MFTTTAERE**I VRDVKEK**LAY** **VALDYEQELE** **TAK**SSSSVEK **NYELPDGQVI**

251 **TIGAER**FR**CP** **EVLFQPSLIG** **MEAAGIHETT** **YNSIMK**CDVD IRKDLYGNIV

301 LSGGSTMFPG IADRMSKEIT ALAPSSMKIK **VVAPPER**KYS VWIGGSILAS

351 LSTFQQMWIS K**GEYDESGPS** **IVHR**KCF

Spot No.: 41

NCBI accession No.: **gi|159489771**

Species: *Chlamydomonas reinhardtii*

Protein name: **predicted protein**

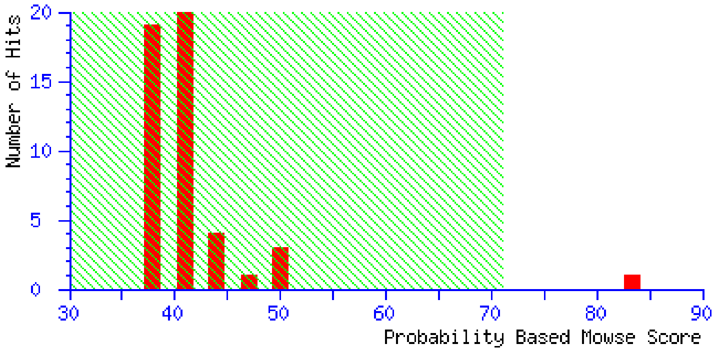
PMF score: **83** Sequence coverage %: **37**

Matched peptides No.: **13** Total peptides No.: **42**

Calculated Mr: **41375** Calculated *p*I: **9.34**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

```
  1  SGAAFIKWGQ  WAATRVDLFP  DDFCDTLANL  HDRAPTHSFA  FTRKQVERSF
 51  GLALERMFES  FEQQPVASGS  IAQIHRAVMR  GSDGSRLQVA  VKVVHPRVAL
101  RIRQDFALLR  PAAAALGRLR  SLRSLSLPET  VSQFSATMTA  QADLRVEAAH
151  LRRFYANFAA  VAAHVTTPRP  LPGLVRPEVM  VETWEDGRSV  SHYIRYPHPS
201  LNGRVVCLGL  DTYLKMLLQD  NFVHTDLHPG  NIMVRANRSS  RSSCRRAGVQ
251  LVLLDFGLAE  ELSPVVRHHF  ISFLQHLLRG  DGVAAAGHLL  RWTSRRQACA
301  DPAALTADMV  ALAATQCDLR  SEEGIDLDKV  MKDVLRLARK  HGVTIDSCYA
351  ALVIAVCVIV  GFATSLDPGV  NL
```

Spot No.: 42

NCBI accession No.: **gi|14423688**

Species: *Hevea brasiliensis*

Protein name: **Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1; AltName: Allergen=Hev b 9**

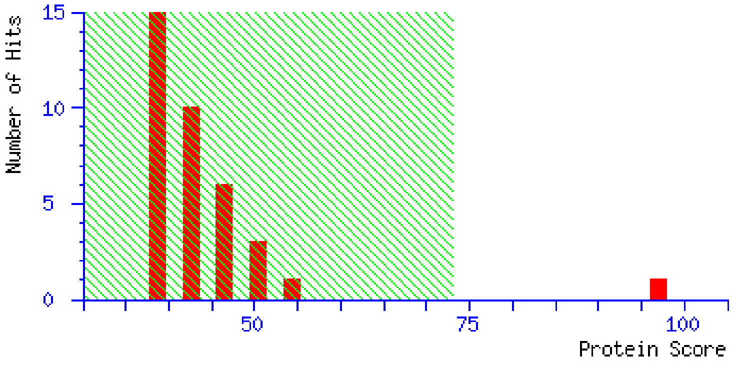
PMF score: **97** Sequence coverage %: **39**

Matched peptides No.: **14** Total peptides No.: **24**

Calculated Mr: **48029** Calculated *p*I: **5.57**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 M**AITIVSVRA** **RQIFDSR**GNP TVEADVK**LSD** **GYLARAAVPS** **GASTGIYEAL**
51 **ELR**DGGSDYL GKGVSKAVEN VNIIIGPALV GKDPTDQVGI DNFMVQQLDG
101 TVNEWGWCKQ KLGANAILAV SLAVCKAGAH VKGIPLYEHI ANLAGNKNLV
151 LPVPAFNVIN GGSHAGNK**LA** **MQEFMILPVG** **ASSFK**EAMKM GAEVYHHLKS
201 VIKKK**YGQDA** **TNVGDEGGFA** **PNIQENK**EGL ELLKTAIAKA GYTGKVVIGM
251 DVAASEFYGS DQTYDLNFKE ENNNGSQKIS GEALKDLYK**S** **FVAEYPIVSI**
301 **EDPFDQDDWA** **HYAK**LTSEIG EKVQIVGDDL LVTNPKRVEK AIKEKACNAL
351 LLK**VNQIGSV** **TESIEAVK**MS KR**AGWGVMAS** **HRSGETEDTF** **IADLSVGLAT**
401 **GQIK**TGAPCR SERLAKYNQL LR**IEEELGSE** **AVYAGANFRK** **PVEPY**

Spot No.: 44

NCBI accession No.: gi|382929047 Species: *Hypselodelphys hirsuta*

Protein name：maturase K (chloroplast)

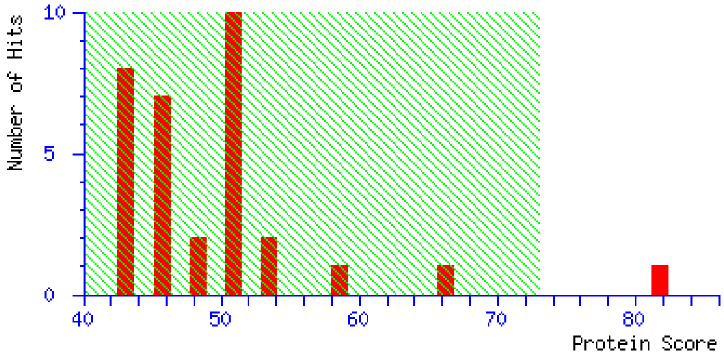
PMF score: **82** Sequence coverage %: **28**

Matched peptides No.: **15** Total peptides No.: **41**

Calculated Mr: **62643** Calculated *p*I: **9.61**

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 73 are significant (p<0.05).



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

1 **MEELQRYLEK** DRSRQQHFLY PLLFQEYIYV FAYDHGLTSS IFYESVKLK**S**
51 **LGYDNKSSSI** **LVK**RLIIR**MY** **QQNFLIYSVI** **YSVNDSYQNR** **FVR**HNNYFYS
101 HFFSQMISEG FAVIVEIPFS LQLVSSLEEK EIPKSHNLQS IHSVFPFLED
151 KLLHLNYLSD ILIPHFIHIE ILVQILKSWI QDVPSLHLLR FFLHEDYNWN
201 NLITPK**KSIY** **VFSK**ENK**RIF** **WVLYNSYLSE** **CEFVFIFLRK** **QSSYLR**LTSS
251 GVFLERTYFY GK**IEHLLVCR** **IFFQK**TLWVF KDPFMHYVRY QGK**AILGSRG**
301 **THSLMK**KWKY YLVNFWQYHF HFWSQSCRIH INQLSKYSFY FLGYLSSVLI
351 NSLAVRNQML ENSFLMETLT RKFDTIIPRI PLIRSLFKAK **FCTVSGHPIS**
401 **K**PIWTDLSDC DIINRFGRVC R**NLSHYHSGS** **SKKQSLYRMK** YILRLSCART
451 LARK**HKSTVR** SFLQRLSSGL LEEFFTEEKQ VLSLIFPKIT FFSLYRSSRE
501 RIWYLDIIRI NDLVNNL

Spot No.: 45

NCBI accession No.: gi|4469175 Species: *Hevea brasiliensis*

Protein name： beta-1,3-glucanase

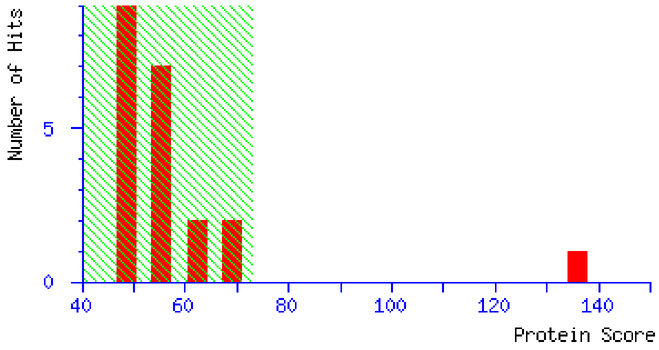
PMF score: **156** Sequence coverage %: **55**

Matched peptides No.: **19** Total peptides No.: **37**

Calculated Mr: **38930** Calculated *p*I: **9.45**

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 73 are significant ($p<0.05$).



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

1 **MAISSSTSGT** **SSSLPSR**TTV MLLLFFFAAS VGITDAQVGV CYGMQGNNLP
51 PVSEVIALYK KSNITRMR**IY** **DPNRAVLEAL** **R**GSNIELILG VPNSDLQSLT
101 NPSNAKSWVQ KNVR**GFWSSV** **LFRYIAVGNE** **ISPVNR**GTAW LAQFVLPAMR
151 **NIHDAIRSAG** **LQDQIKVSTA** **IDLTLVGNSY** **PPSAGAFRDD** **VRSYLNPIIR**
201 **FLSSIRSPLL** **ANIYPYFTYA** **GNPRDISLPY** **ALFTSPSVVV** **WDGQR**GYK**NL**
251 **FDATLDVLYS** **ALER**ASGGSL EVVVSESGWP SAGAFAATFD NGR**TYLSNLI**
301 **QHVK**R**GTPKR** **PNRAIETYLF** **AMFDENKK**QP EVEKQFGLFF PDKWQKYNLN
351 FG

Spot No.: 46

NCBI accession No.: gi|4469175 Species: *Hevea brasiliensis*

Protein name： beta-1,3-glucanase

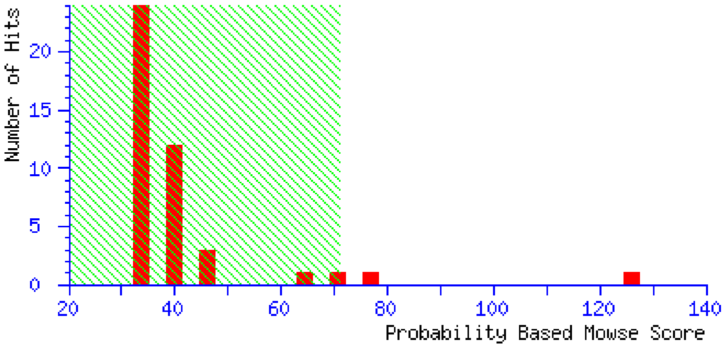
PMF score: **126** Sequence coverage %: **55**

Matched peptides No.: **19** Total peptides No.: **37**

Calculated Mr: **38930** Calculated *p*I: **9.45**

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 73 are significant ($p<0.05$).



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

1 **MAISSSTSGT SSSLPSR**TTV MLLLFFFAAS VGITDAQVGV CYGMQGNNLP

51 PVSEVIALYK KSNITRMR**IY DPNRAVLEAL R**GSNIELILG VPNSDLQSLT

101 NPSNAKSWVQ KNVR**GFWSSV LFRYIAVGNE ISPVNR**GTAW LAQFVLPAMR

151 **NIHDAIRSAG LQDQIKVSTA IDLTLVGNSY PPSAGAFRDD VRSYLNPIIR**

201 **FLSSIRSPLL ANIYPYFTYA GNPRDISLPY ALFTSPSVVV WDGQR**GYK**NL**

251 **FDATLDVLYS ALER**ASGGSL EVVVSESGWP SAGAFAATFD NGR**TYLSNLI**

301 **QHVK**R**GTPKR PNRAIETYLF AMFDENKK**QP EVEKQFGLFF PDKWQKYNLN

351 FG

Spot No.: 47

NCBI accession No.: gi|225438145 Species: *Vitis vinifera*

PFF score: [65]

Protein name： PREDICTED: malate dehydrogenase, cytoplasmic

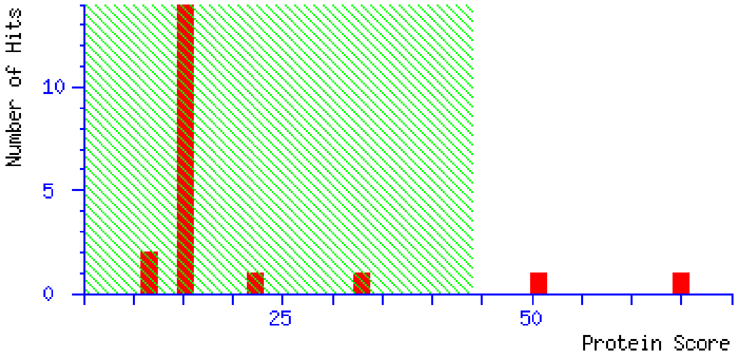
Matched peptides No.: [1] Sequence coverage %: [3]

Matched sequences: K.IVQGLHIDEFSR.K

Calculated Mr: **35881** Calculated *p*I: **6.18**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAKEPVRVLV TGAAGQIGYA LVPMIARGVM LGADQPVILH MLDIPPAAEA
51 LNGVKMELVD AAFPLLKGVV ATTDVVEACT GVNIAVMVGG FPRKEGMERK
101 DVMSKNVSIY KSQASALENH AAANCKVLVV ANPANTNALI LKEFAPSIPE
151 KNISCLTRLD HNRALGQVSE RLNVQVSDVK NVIIWGNHSS TQYPDVNHAT
201 VKTPAGEKPV RGLVGDDAWL NGEFITTVQQ RGAAIIKARK LSSALSAASA
251 ACDHIRDWVL GTPEGTWVSM GVYSDGSYNV PAGLIYSFPV TCCAGEWK**IV**
301 **QGLHIDEFSR** KKLDLTAQEL SEEKELAYSC LS

Spot No.: 48

NCBI accession No.: gi|225438145 Species: *Vitis vinifera*

PFF score: [85]

Protein name：PREDICTED: malate dehydrogenase, cytoplasmic

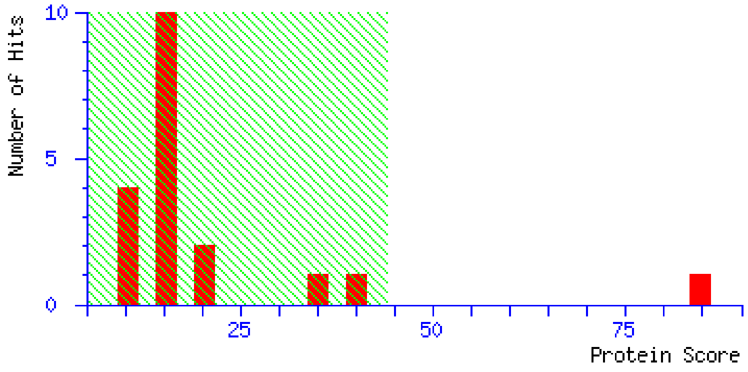
Matched peptides No.: [1] Sequence coverage %: [3]

Matched sequences: K.IVQGLHIDEFSR.K

Calculated Mr: **35881** Calculated *p*I: **6.18**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

```
  1  MAKEPVRVLV  TGAAGQIGYA  LVPMIARGVM  LGADQPVILH  MLDIPPAAEA
 51  LNGVKMELVD  AAFPLLKGVV  ATTDVVEACT  GVNIAVMVGG  FPRKEGMERK
101  DVMSKNVSIY  KSQASALENH  AAANCKVLVV  ANPANTNALI  LKEFAPSIPE
151  KNISCLTRLD  HNRALGQVSE  RLNVQVSDVK  NVIIWGNHSS  TQYPDVNHAT
201  VKTPAGEKPV  RGLVGDDAWL  NGEFITTVQQ  RGAAIIKARK  LSSALSAASA
251  ACDHIRDWVL  GTPEGTWVSM  GVYSDGSYNV  PAGLIYSFPV  TCCAGEWKIV
301  QGLHIDEFSR  KKLDLTAQEL  SEEKELAYSC  LS
```

Spot No.: 49

NCBI accession No.: gi|255552291 Species: *Ricinus communis*

PFF score: [75]

Protein name： short chain dehydrogenase, putative

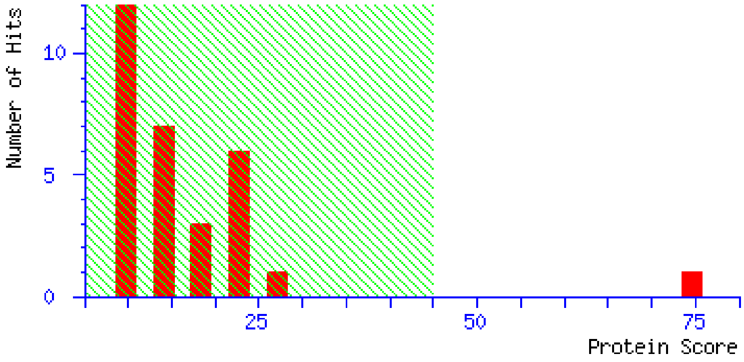
Matched peptides No.: [1] Sequence coverage %: [5]

Matched sequences: K.DPIAIPTDVGFEENCR.K

Calculated Mr: **32148** Calculated *p*I: **6.50**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MATRRGYRFP PQSQDKQPGK EYLMHPLPEF INPHYKPSNK LQDKVALVTG
51 GDSGIGRAVS YYFTLEGATV AFTYVKGRED KDKDHILKIL HEVKAEGAK**D**
101 **PIAIPTDVGF** **EENCR**KVIDQ IMSEYGKIDI LVNNAGEAHY STTIEDITDP
151 MLERVFRTNI FGHFFMSRHA LKHMKEGGCI INTASVAAYA GFSFMVDYSS
201 TKGAVVAFTR SLALQLIDRG IRVNAVAPGS VWTPFQPSTL SAEQVAQVGS
251 GVPMDRAAQP YEIAPSFVFL ASNDCSSYFT GQVLHPNGMF

Spot No.: 50

NCBI accession No.: gi|29170601 Species: *Hevea brasiliensis*

PFF score: [240]

Protein name： small rubber particle protein

Matched peptides No.: [2] Sequence coverage %: [28]

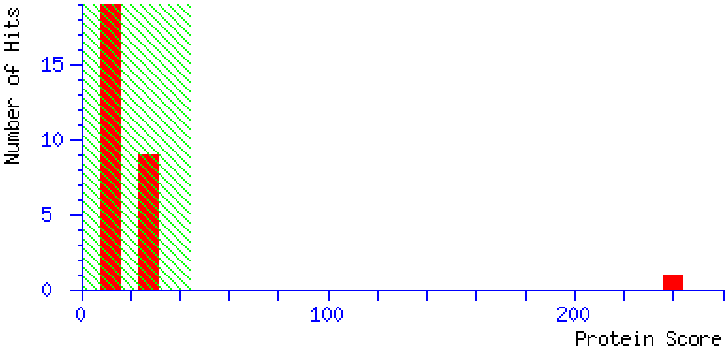
Matched sequences: K.ENENFQQEANEQEEK.L；

K.DNSGPLKPGVETIEGVAK.T

Calculated Mr: **12769** Calculated *p*I: **4.61**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEGK**ENENF** **QQEANEQEEK** LKYLEFVQAT TDNAVTALSN IYLYAK**DNSG**
51 **PLKPGVETIE** **GVAK**TVVIPA SKIPTEAIKF ADRAVDASFT TLQNIVPSVL
101 KQLPTQACDT SVKESAE

Spot No.: 51

NCBI accession No.: **gi|132270**　　Species: *Hevea brasiliensis*

Protein name：　**Rubber elongation factor protein**

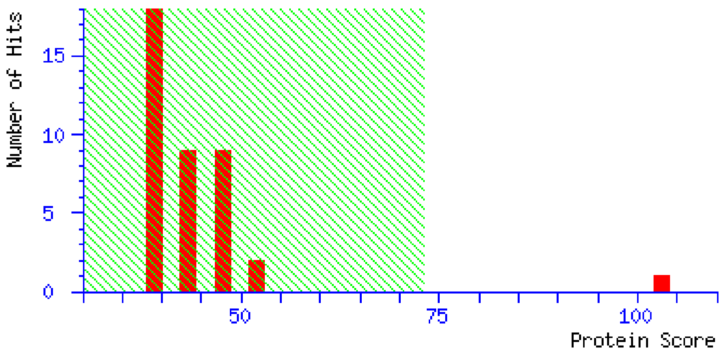
PMF score: **103**　　Sequence coverage %: **78**

Matched peptides No.: **10**　　Total peptides No.: **43**

Calculated Mr: **14713**　　Calculated *p*I: **5.04**

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 73 are significant ($p<0.05$).



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

1 MAEDEDNQQG QGEGLK**YLGF** **VQDAATYAVT** **TFSNVYLFAK** **DKSGPLQPGV**

51 **DIIEGPVKNV** **AVPLYNR**FSY IPNGALK**FVD** **STVVASVTII** **DRSLPPIVKD**

101 **ASIQVVSAIR** **AAPEAARSLA** **SSLPGQTK**IL AK**VFYGEN**

Spot No.: 52

NCBI accession No.: **gi|132270** Species: *Hevea brasiliensis*

Protein name： **Rubber elongation factor protein**

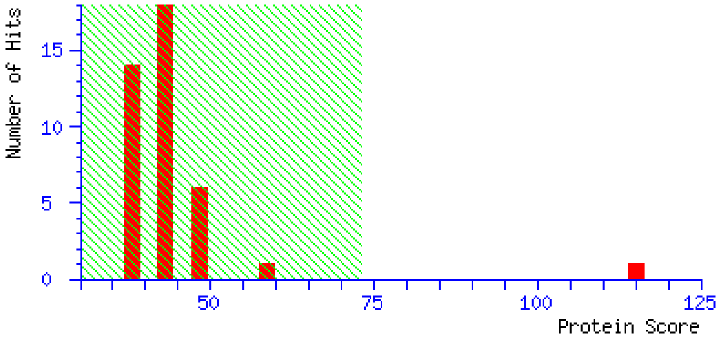
PMF score: **115** Sequence coverage %: **78**

Matched peptides No.: **10** Total peptides No.: **33**

Calculated Mr: **14713** Calculated *p*I: **5.04**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 MAEDEDNQQG QGEGLK**YLGF VQDAATYAVT TFSNVYLFAK DKSGPLQPGV**
51 **DIIEGPVKNV AVPLYNR**FSY IPNGALK**FVD STVVASVTII DRSLPPIVKD**
101 **ASIQVVSAIR AAPEAARSLA SSLPGQTK**IL A**KVFYGEN**

Spot No.: 53

NCBI accession No.: **gi|115187464** Species: *Arachis hypogaea*

PFF score: [61]

Protein name: **thioredoxin fold**

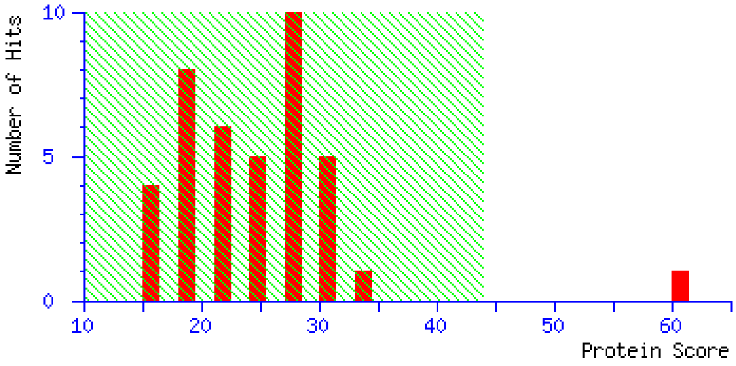
Matched peptides No.: [1] Sequence coverage %: [4]

Matched sequences: K.HVPGFIER.A

Calculated Mr: **17525** Calculated *p*I: **5.57**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAPIAVGDVI PDGTLAFLDN DNKPQSVSIH SLAKGKKVII FGVPGAFTPT
51 CSLK**HVPGFI** **ER**AEELKGKG VDEIICISVN DPFVMKSWAN TFPENKHVTF
101 LADGSAKYTH DLGLELDLSE KGLGIRSKRF ALLVEDLKVK VANIESGGEF
151 TVSSAEEIIK AL

Spot No.: 54

NCBI accession No.: **gi|34538473** Species: *Hordeum vulgare*

Protein name： **caleosin 1**

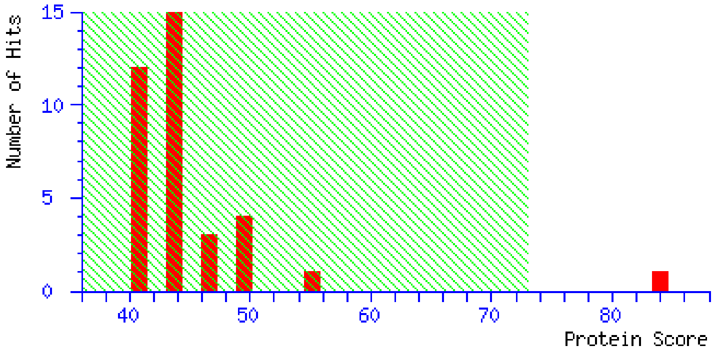
PMF score: **84** Sequence coverage %: **19**

Matched peptides No.: **10** Total peptides No.: **37**

Calculated Mr: **34330** Calculated *p*I: **6.11**

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 73 are significant ($p<0.05$).



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

1 **MATKAR**KVEV R**DASRAEGKG** **DAADVHVLRE** **AMRADGK**GDH DTAGGANRAD
51 GHGDAGGRVG DSRGVDGKDS LKMVALQAPV TVERPVRGDL EEHVPKPYLA
101 RALAAPDMYH PEGTTTDDHQ HHNMSVLQQH VAFFDRDNNG IIYPWETYDG
151 CRAVGFNVFM SAFIAFLVNL VMSYPTLPGW LPNPLFPIYV HNIHKSK**HGS**
201 **DSGTYDK**EGR FMPVNFENIF SKYARTYPDR LSYR**EMWR**MT EGCREVFDFF
251 GWVAMKLEWS ILYALARDDE GYLSR**EAIRR** MYDGSLFEYM ERQR**MEHVKM**
301 **S**

Spot No.: 55

NCBI accession No.: **gi|225440278** Species: *Vitis vinifera*

Protein name：**PREDICTED: hypothetical protein**

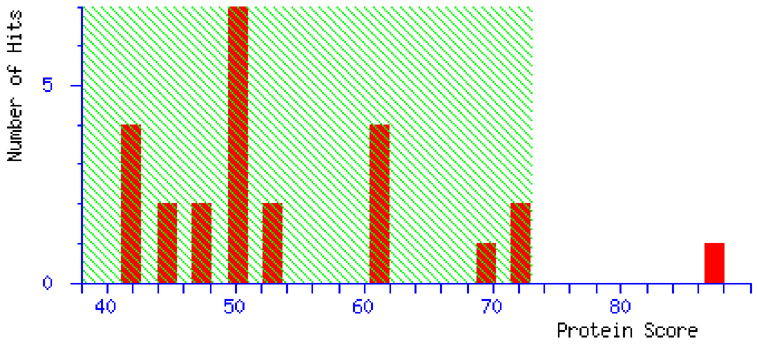
PMF score: **88** Sequence coverage %: **41**

Matched peptides No.: **7** Total peptides No.: **14**

Calculated Mr: **19226** Calculated *p*I: **9.57**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 **MDHYEALGIG RNASK**GEIK**E AFRK**LALK**YH PDKHAQSPK**A VRDGATLRFK
51 QVSEAYEVLS DDRKRSLYNL RSSTAPPGFS GGYAHSYHYN NERPR**YSSRP**
101 **NADAFVSKFE VVLR**FLTTR**A FLLNVAFAGA LLGGMAIIDR** SGETLWKMNN
151 SGKSFDEAME SIGKAKAHKD DM

Spot No.: **56**

NCBI accession No.: **gi|2213877** Species: *Hevea brasiliensis*

Protein name：glutamine synthetase

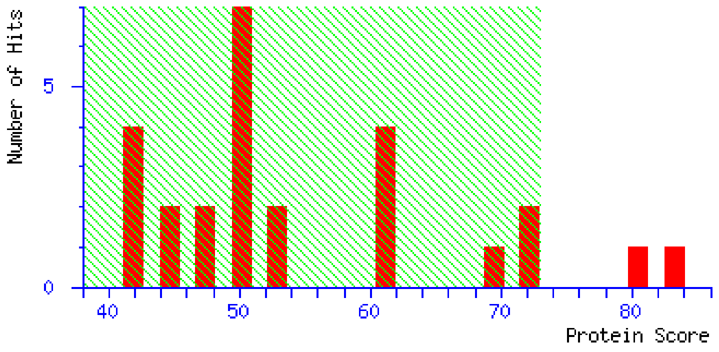
PMF score: **83** Sequence coverage %: **38**

Matched peptides No.: **14** Total peptides No.: **76**

Calculated Mr: **39504** Calculated *p*I: **5.81**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MSLLSDLINL NLSDTTDK**II** **AEYIWIGGSG** **MDMR**SKARTL SGPVSDPSKL

51 PKWNYDGSST GQAPGEDSEV ILYPQAIFKD PFRR**GNNILV** **MCDAYTPAGE**

101 **PIPTNKR**HAA AKIFSHPDVV AEEPWYGIEQ EYTLLQRDVK **WPIGWPLGGY**

151 **PGPQGPYYCS** **IGADK**SFGRD VVDSHYKSCL YAGINISGIN GEVMPGQWEF

201 QVGPAVGISA GDELWVAR**YI** **LERITEIAGV** **VLSFDPKPIQ** **GDWNGAGAHT**

251 **NYSTK**SMRHD GGYEVIKKAI EKLGLR**HKEH** **IAAYGEGNER** RLTGR**HETAD**

301 **INTFLWGVAN** **R**GASIRVGRD TEKQGK**GYFE** **DR**RPASNMDP YVVTSMIAET

351 TILWKP

Spot No.: **57**

NCBI accession No.: **gi|172050753**   Species: *Capparis spinosa*

Protein name： 70 kDa heat shock protein

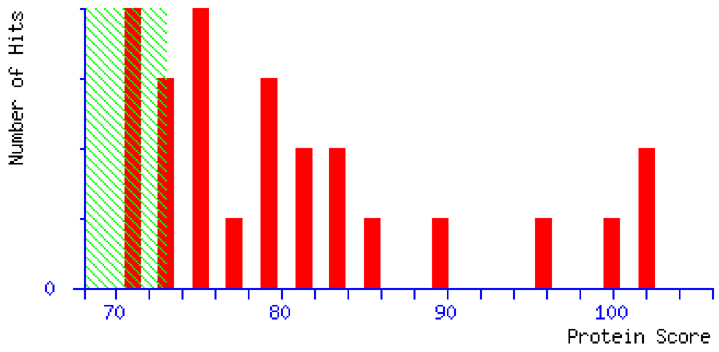
PMF score: **102**   Sequence coverage %: **36**

Matched peptides No.: **19**   Total peptides No.: **58**

Calculated Mr: **71456**   Calculated *p*I: **5.21**

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 73 are significant ($p<0.05$).



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

1 MAGKGEGPAI GIDLGTTYSC VGVWQHDR**VE** **IIANDQGNRT** **TPSYVAFTDT**

51 **ER**LIGDAAKN QVAMNPINTV FDAKRLIGRR YSDSSVQADM KLWPFKVVPG

101 SGDKPMIVVN YKGEEKQFAA EEISSMVLIK **MREIAEAFLG** **CTIK**NGVVTV

151 PAYFNDSQRQ ATK**DAGVIAG** **LNVMRIINEP** **TAAAIAYGLD** **K**KAASVGEKN

201 VLIFDLGGGT FDVSLLTIEE GIFEVK**ATAG** **DTHLGGEDFD** **NRMVNHFVQE**

251 **FK**RKNKRDIS GNPRALRR**LR** **TACERAKRTL** **SSTAQTTIEI** **DSLYEGIDFY**

301 **TTITRARFEE** **LNMDLFRKCM** **EPVEK**CLRDA KMDKSNVHDI VLVGGSTRIP

351 K**VQQLLQDFF** **NGK**ELCK**SIN** **PDEAVAYGAA** **VQAAILSGEG** **NEK**VQDLLLL

401 DVTPLSLGLE TAGGVMTVLI PRNTTIPTKK EQIFSTYSDN QPGVLIQVYE

451 GERARTK**DNN** **LLGKFELTGI** **PPAPRGVPQI** **NVCFDIDANG** **ILNVSAEDK**T

501 TGQKNKITIT NDKGRLSKEE IEKMVQEAEK YKSEDEEHKK KVEAK**NALEN**

551 **YAYNMR**NTIK DEKIGSKLDP ADKKKIEDAI DQAIQWLDGN QLAEADEFKD

601 KMKELESICN PIIARMYQGA GGDMGGAGGA DDASPAGGSG AGPKIEEVD

Spot No.: **58**

NCBI accession No.: **gi|762844**   Species: *Solanum lycopersicum*

PFF score: [151]   Protein name：Hsc70

Matched peptides No.: [3]   Sequence coverage %: [10]

Matched sequences: K.ATAGDTHLGGEDFDNR.M;

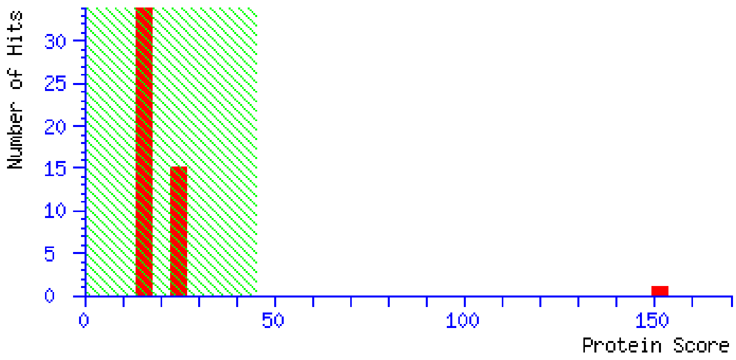
R.TLSSTAQTTIEIDSLYEGIDFYTTITR.A;

K.EQVFSTYSDNQPGVLIQVYEGER.A

Calculated Mr: **71869**   Calculated *p*I: **5.18**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAGKGEGPAI GIDLGTTYSC VGVWQHDRVE IIANDQGNRT TPSYVAFTDT

51 ERLIGDAAKN QVAMNPTNTV FDAKRLIGRR FSDPSVQSDM KLWPFKVIPG

101 PADKPMIVVN YKGEEKQFSA EEISSMVLIK MKEIAEAFLG TTIKNAVVTV

151 PAYFNDSQRQ ATKDAGTISG LNVMRIINEP TAAAIAYGLD KKISSTGEKT

201 VLIFDLGGGT FDVSLLTIEE GIFEVK**ATAG** **DTHLGGEDFD** **NR**MVNHFVQE

251 FKRKHKKDIS GNPRALRRLR TACERAKR**TL** **SSTAQTTIEI** **DSLYEGIDFY**

301 **TTITR**ARFEE LNMDLFRKCM EPVEKCLRDA KIDKSGVHDI VLVGGSTRIP

351 KVQQLLQDFF NGRELCKSIN PDEAVAYGAA VQAAILSGEG NEKVQDLLLL

401 DVTPLSLGLE TAGGVMTTLI PRNTTIPTKK **EQVFSTYSDN** **QPGVLIQVYE**

451 **GER**ARTRDNN LLGKFELTGI PPAPRGVPQI TVCFDIDANG ILNVSAEDKT

501 TGQKNKITIT NDKGRLSKDE IEKMVQEAEK YKAEDEEHKK KVEAKNALEN

551 YAYNMRNTIK DDKIASKLSP DEKKKIEDSV EQAIQWLDGN QLAEADEFED

601 KMKELESICN PIIAKMYQGR AGPDMAGGMD EDGPSAGASS AGAGPKIEEV

651 D

Spot No.: **59**

NCBI accession No.: **gi|356552478** Species: *Glycine max*

Protein name：PREDICTED: heat shock cognate protein 80-like

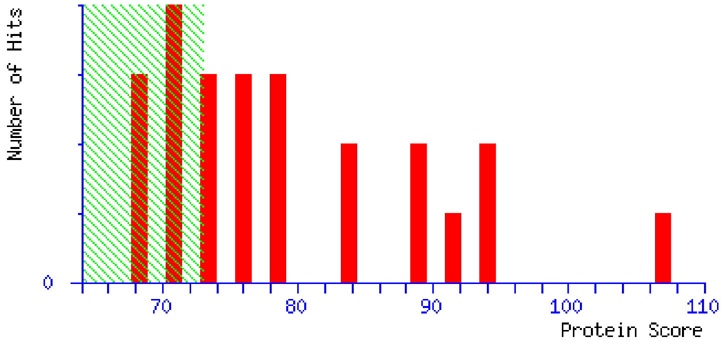
Mascot score: **107** Sequence coverage %: **25**

Matched peptides No.: **21** Total peptides No.: **54**

Calculated Mr: **80422** Calculated *p*I: **4.98**

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 73 are significant ($p<0.05$).



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

1 MASETETFAF QAEINQLLSL IINTFYSNK**E** **IFLR**ELISNA SDALDKIRFE
51 SLTDKSKLDA QPELFIHIIP DKTNNTLSII DSGIGMTK**AD** **LVNNLGTIAR**
101 SGTKEFMEAL AAGADVSMIG QFGVGFYSAY LVADKVIVTT KHNDDEQYVW
151 ESHAGGSFTV TR**DTSGENLG** **RGTKITLFLK** **EDQLEYLEER** RLKDLIKKHS
201 EFISYPISLW IEKTTEKEIS DDEDEEEKKD EEGKVEDVDE DKEKEEKKKK
251 TIKEVSHEWS LVNK**QKPIWM** **R**KPEEITKEE YAAFYK**SLTN** **DWEEHLAVKH**
301 **FSVEGQLEFK** AVLFIPK**RAP** **FDLFDTR**KKP NNIKLYVRRV FIMDNCEELM
351 PEYLSFVK**GI** **VDSEDLPLNI** **SR**EMLQQNKI LKVIRK**NLVK** **K**CIEMFFEIA
401 ENKEDYNK**FY** **EAFSK**NLKLG IHEDSQNKTK **LAELLR**YHST KSGDEMTSLK
451 DYVTRMKEGQ NDIYYITGES KKAVENSPFL EKLKKK**GYEV** **LYMVDAIDEY**
501 **AVGQLK**EFEG KKLVSATKEG LKLDESEDEK KKKEELKDKF EGLCHVIKDV
551 LGDKVEKVVV SDRVVDSPCC LVTGEYGWTA NMERIMK**AQA** **LRDSSMAGYM**
601 **SSKKTMEINP** **ENPIMEELR**K RADADKNDKS VKDLVLLLFE TALLTSGFSL
651 DDPNTFGNR**I** **HRMLK**LGLSI DEDAGEADAD MPPLEDADAD AEGSKMEEVD

Spot No.: **60**

NCBI accession No.: **gi|356510919**   Species: *Glycine max*

PFF score: [51]

Protein name：PREDICTED: UDP-glycosyltransferase 75D1-like

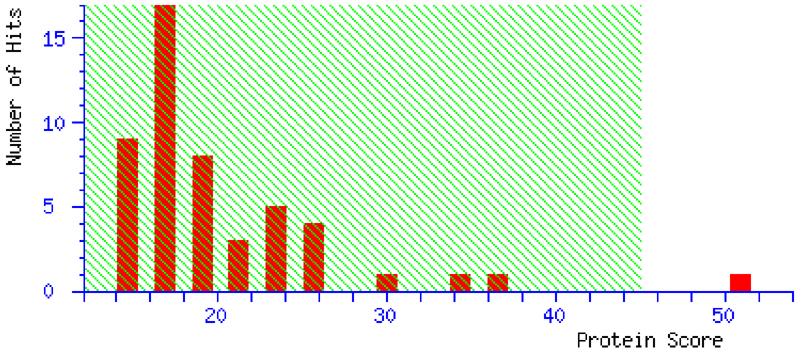
Matched peptides No.: [1]   Sequence coverage %: [2]

Matched sequences: K.CVEEVMGSGELR.R

Calculated Mr: **52131**   Calculated *p*I: **5.07**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MLHHRFLLVI YPGQGQINPA LQFAKRLTAM GARVTIPITL DMHRRMTNTT
51 AVPGLSLAPF SDGYDDGFHA IRGTDSDYNL YASELKRRAS VFVSNLILSS
101 ANEGHPFTCL LYTLLVPWAP QVARGLNLPT AMLWIQPATV LDILYHYFHG
151 YADYINDETK ENIVLPGLSF SLSPRDIPSF LLTSKPSLLS FVFPLFEEQI
201 KQLDLEANPK VLVNTFEALE EEALRAVDKL NMIPIGPLIP TAFLGGKDPE
251 DTSFGGDLLQ VSNGYVEWLD SKEDKSVVYV SFGSYFELSK RQTEEIARAL
301 LGCSFPFLWV IRVKEEEKEE EEELCFREEL EGKGKLVKWC SQVEVLSHGS
351 VGCFVTHCGW NSTMESLVSG VPMVAFPQWS DQKTNAKLIE DVWKIGVRVE
401 NDGDGIVEKE EIRK**CVEEVM** **GSGELR**RNAE KWKGLAREAA KEGGPSERNL
451 KAFLDAMAAL QF

Spot No.: **61**

NCBI accession No.: **gi|255560725**   Species: *Ricinus communis*

Protein name： dead box ATP-dependent RNA helicase, putative

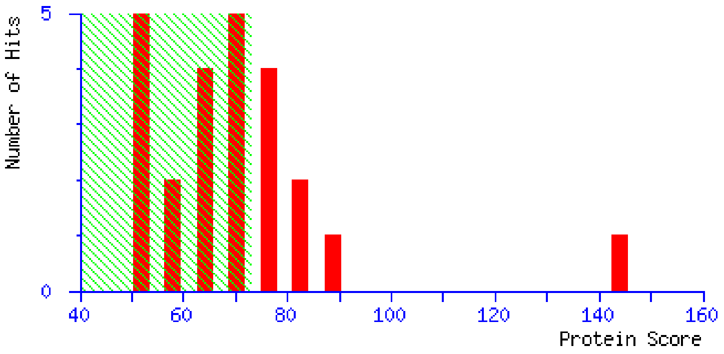
Mascot score: **144**   Sequence coverage %: **68**

Matched peptides No.: **25**   Total peptides No.: **91**

Calculated Mr: **47097**   Calculated *p*I: **5.49**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 M**AGLAPEGSQ** **FDAKQYDAKM** **SELLSTEGQE** **FFTTYDEVYD** **SFDAMGLQEN**
51 **LLRGIYAYGF** **EKPSAIQQR**G IVPFCK**GLDV** **IQQAQSGTGK** **TATFCSGILQ**
101 **QLDYGLVQCQ** **ALVLAPTR**EL AQQIEKVMR**A** **LGDYLGVKVH** **ACVGGTSVR**E
151 DQR**ILQAGVH** **VVVGTPGRVF** **DMLR**RQSLRP DYIK**MFVLDE** **ADEMLSR**GFK
201 **DQIYDIFQLL** **PAK**VQVGVFS ATMPPEALEI TRKFMNKPVR ILVK**RDELTL**
251 **EGIKQFYVNV** **EKEEWKLETL** **CDLYETLAIT** **QSVIFVNTR**R K**VDWLTDKMR**
301 SRDHTVSATH GDMDQNTRDI IMREFRSGSS R**VLITTDLLA** **RGIDVQQVSL**
351 **VINYDLPTQP** **ENYLHR**IGRG GRFGR**KGVAI** **NFVTR**DDER**M** **LFDIQK**FYNV
401 VIEELPSNVA DLL

Spot No.: **62**

NCBI accession No.: **gi|4235430** Species: *Hevea brasiliensis*

PFF score: [142] Protein name：latex-abundant protein

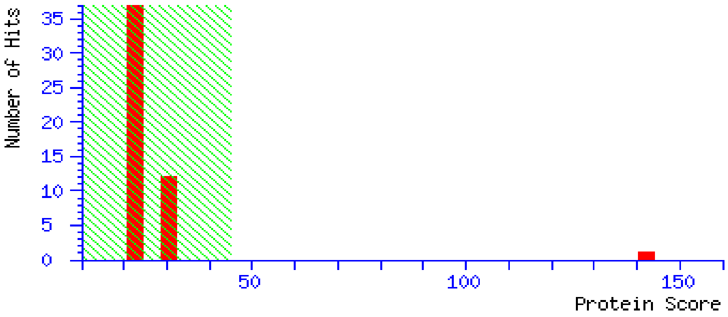
Matched peptides No.: [9] Sequence coverage %: [16]

Matched sequences: R.SAEPGDLLFVHYSGHGTR.L;
R.EFVDQVPHGCR.I;
R.EFVDQVPHGCR.I;
K.QTIQDAFESR.G;
K.QTIQDAFESR.G;
R.VVEEDYGDSGYVK.S;
R.VVEEDYGDSGYVK.S;
K.LRPTLFDMFGDDASPK.V +Oxidation(M);
K.LRPTLFDMFGDDASPK.V + Oxidation (M)

Calculated Mr: **46443** Calculated *p*I: **5.01**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MAKKAVLIGI NYPGTKAELK GCINDVKRMY RCLVDRYGFS EEDITVLIDI
51 DESYIQPTGK NIRRVLTDLV R**SAEPGDLLF** **VHYSGHGTR**L PAETGEDDDT
101 GFDECIVPCD MNLITDDDFR **EFVDQVPHGC** **R**ITVVSDSCH SGGLIDEAKE
151 QIGESTKRKE EESESGFGFK SFLK**QTIQDA** **FESR**GVHLPS DLHHHHGHRD
201 EEDFDNR**VVE** **EDYGDSGYVK** SKSLPLSTLI EILKQKTGKD DIDVGK**LRPT**
251 **LFDMFGDDAS** **PK**VKKFMKVI LNKLRHGDGE SGGGGFLGMV GSLAQEFLKH
301 KLDENDESYV KPALETEVDS KQEVYAGKTK RSLPDGGILI SGCQTDQTSA
351 DASPSGKSSE AYGALSNAIQ TIIAETDGAV TNQELVLKAR KMLKKQGFTQ
401 KPGLYCSDDH VEASFVC

Spot No.: **63**

NCBI accession No.: **gi|255578278** Species: *Ricinus communis*

PFF score: [76]

Protein name:hypothetical protein RCOM_0537780

Matched peptides No.: [3] Sequence coverage %: [6]

Matched sequences: K.QESEYGSGGYGR.R;

R.KPSYGEEGGYGER.T ;

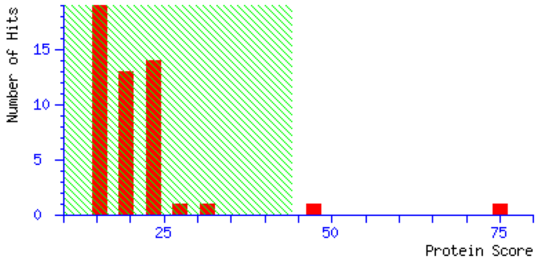
R.KPSYGEEGGYGER.T

Calculated Mr: **41389** Calculated *p*I: **4.65**

Probability Based Mowse Score:

Mascot Score Histogram

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MPYYTRSEDD VNDFDEFDPT PYGGGYDLAL TYGRPLPPSD ETCYQNSAIA
51 DDDVDYDRPN FTSYAEPSAY NDDILQEEYN SYSRPKPRPG FIPGGGIGGD
101 PYSRPHAAPG FQPGSGGYGG VSEYEKPSGY GRRPDSEYGS GGYGGGTEYE
151 RPSGEDYGSG HGRKQDSEYG SGGYGRRPES EYGSGGGYER PSSEEYGSGY
201 GRK**QESEYGS** **GGYGR**RPEAE YGSGYGGRPE TEYGGGGGSE YGGGYGR**KPS**
251 **YGEEGGYGER** TEYERPSYGD DPPRRPGYGR QDDEYERPSY ERKSDDDNDG
301 SRRKYGGDDD EKGYQKKYGG YGDDDDEEGS RRKYGYGGEE ESYGRKKYGD
351 DGSDDDEKKH HRHKHHQHKH SDDE

Spot No.: **64**

NCBI accession No.: **gi|5302811** Species: *Arabidopsis thaliana*

PFF score: [98] Protein name:putative serine protease-like protein

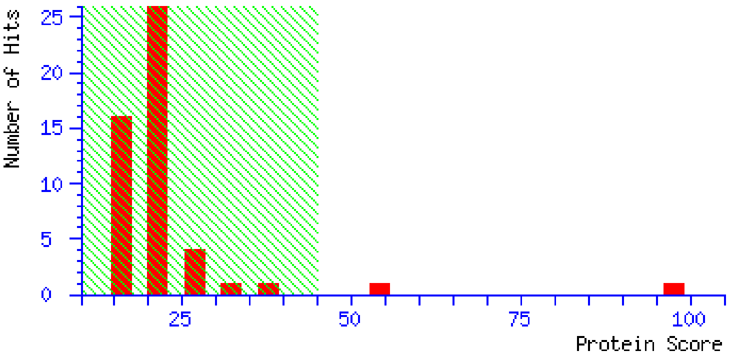
Matched peptides No.: [1] Sequence coverage %: [2]

Matched sequences: R.QEQAAFIEEISR.T

Calculated Mr: **47129** Calculated *p*I: **5.15**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MVVMMKATRG TRDPDLLGLM FVHHQFLFCV ISFFYLLLRD FEFLLNDSSS
51 GIWTWSQVVS ETQALPYLQK AFNIQHFDFP TQEDQEENTY AAKVSEKQDF
101 SKEQWQDYKR PASEQHYSDE VETYGNLEPS QLELSGLSEA CNKLWELDLN
151 RLVPGRIIKS TAEMGKGSMR ELIWLKDYCS LGFCSLLDNY NPNEGYKEVV
201 TEEER**QEQAA** **FIEEISR**TSV IKYLHRYLVL KDVAPGSYLE FKRMLTSLWF
251 DLYGRGGTSG SSSAFEHVFV GEIKQSGGNK SLDSITGFST SKPVTDRETT
301 LLLRMQPDSE TQLLTIQFEW NGVLKSVSST LVGVSPEFEL ALYTMCFFMG
351 TEDNHIQLGP YNVNVKCYRL GNNRIALSFP HCRILKPLLM ALVTKYLPLA
401 QYCIELL

Spot No.: **65**

NCBI accession No.: **gi|2506277**   Species: *Pisum sativum*

Protein name： RuBisCO large subunit-binding protein subunit beta

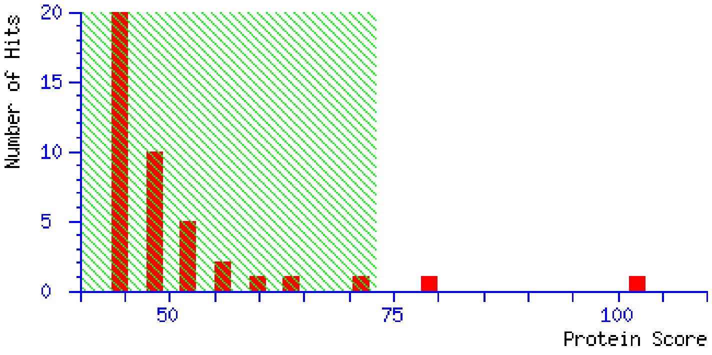
PMF score: **102**   Sequence coverage %: **34**

Matched peptides No.: **17**   Total peptides No.: **54**

Calculated Mr: **63287**   Calculated *p*I: **5.85**

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 73 are significant ($p<0.05$).



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

1 MASTFSATTS SCNLSSSAAI SSFPLAAGKR NANKVVLPRK NRNVKVSAMA
51 KELHFNKDGS AIKKLQNGVN K**LADLVGVTL** **GPKGRNVVLE** **SKYGSPK**IVN
101 DGVTVAK**EVE** **LEDPVENIGA** **K**LVRQAAAKT **NDLAGDGTTT** **SVVLAQGLIA**
151 **EGVKVVAAGA** **NPVLITRGIE** **K**TSKALVAEL KKMSKEVEDS ELADVAAVSA
201 GNNHEVGNMI AEALSKVGRK GVVTLEEGK**S** **AENSLYVVEG** **MQFDRGYISP**
251 **YFVTDSEKMT** **VEFENCK**LLL VDKKITNAR**D** **LINILEDAIR** SGFPIVIIAE
301 DIEQEALATL VVNKLRGSLK IAALK**APGFG** **ERKSQYLDDI** **AILTGGTVIR**
351 EEVGLTLDKA DKEVLGNAAK VVLTKDTTTI VGDGSTQEAV NKRVSQIKNQ
401 IEAAEQEYEK EKLSERIAKL SGGVAVIQVG AQTETELKEK KLRVEDALNA
451 TK**AAVEEGIV** **VGGGCTLLR**L ASKVDAIK**DT** **LANDEEKVGA** **DIVK**RALSYP
501 LKLIAKNAGV NGSVVSEKVL SSDNPKYGYN AATGK**YEDLM** **AAGIIDPTKV**
551 **VR**CCLEHASS VAKTFLMSDC VVVEIKEPES APVGNPMDNS GYGNI

Spot No.: **66**

NCBI accession No.: **gi|255543357** Species: *Ricinus communis*

Protein name： heat shock protein, putative

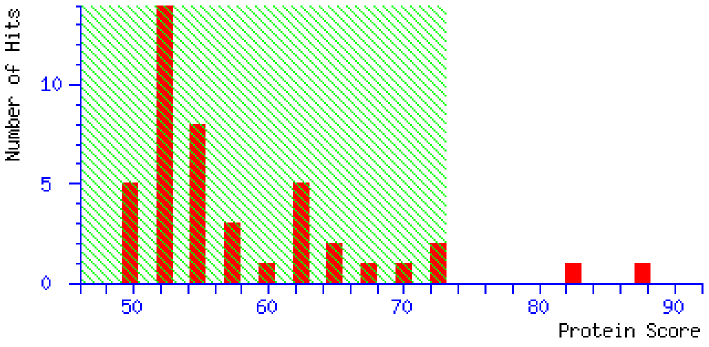
PMF score: **88** Sequence coverage %: **29**

Matched peptides No.: **18** Total peptides No.: **79**

Calculated Mr: **71965** Calculated *p*I: **5.27**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MAKTEGKAVG IDLGTTYSCV GVWQNDRVEI IANDQGNR**TT** **PSYVAFTDTE**
51 **R**LIGDAAKNQ VAMNPQNTVF DAKRLIGRRF SDPSVQSDMK HWPFKVVPGP
101 GDKPMIVVLY KGEEKQFAPE EISSMVLIKM KEIAEAYLGQ TVK**NAVITVP**
151 **AYFNDSQR**QA TK**DAGAISGL** **NVMRIINEPT** **AAAIAYGLDK** KGSRSGEKNV
201 LIFDLGGGTF DVSLLTIEEG IFEVK**ATAGD** **THLGGEDFDN** **R**LVNHFVAEF
251 RRKHKKDIST NARALRRLRT ACERAKRTLS STSQTTIEID SLYEGIDFYS
301 TITR**ARFEEL** **NMDLFRKCME** **PVEK**CLRDSK IDK**SQVDDIV** **LVGGSTRIPK**
351 **VQQLLQDFFN** **GK**ELCKSINP DEAVAYGAAV QAAILSGEGD QKVQELLLLD
401 VTPLSLGIET AGGVMTVLIP RNTTIPAKKE QIFSTYSDNQ PGVLIQVYEG
451 ERARTK**DNNL** **LGTFELK**GIP PAPR**GVPQIN** **VCFDIDANGI** **LNVSAEDK**TA
501 GVKNKITITN DKGRLSKEDI ERMVQEAEK**Y** **KAEDEQVK**KK VEAKNALENY
551 AYNMRNTVKD EKFAGKLDSA DKQKIEK**AID** **ETIEWLDGNQ** **LAEVDEFEDK**
601 **LK**ELEGLCNP IVSKMYQGGA GGDVPMGGGA KPGSGYGNAS SGGSGSGPKI
651 EEVD

Spot No.: **67**

NCBI accession No.: **gi|224100473** Species: *Populus trichocarpa*

PFF score: [91] Protein name: predicted protein

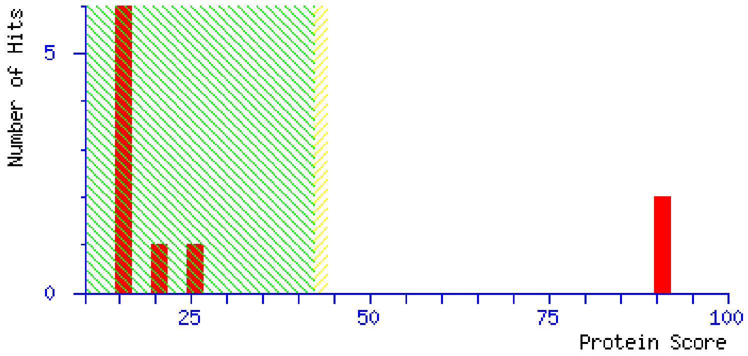
Matched peptides No.: [1] Sequence coverage %: [3]

Matched sequences: R.SPPIEEVIQAGVVPR.F

Calculated Mr: **46093** Calculated *p*I: **4.54**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 42 indicate peptides with significant homology.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

```
  1  GVWSEDGNLQ  LESTTQFRKL  LSIERSPPIE  EVIQAGVVPR  FVEFLVREDF
 51  PQLQFEAAWA  LTNIASGTSE  NTKVVIDHGA  VPIFVKLLGS  PSDDVREQAV
101  WALGNVAGDS  PKCRDLVLSH  GALIPLLAQL  NEHAKLSMLR  NATWTLSNFC
151  RGKPQPPFEQ  VRPALPALER  LVHSTDEEVL  TDSCWALSYL  SDGTDDKIQA
201  VIEAGVCPRL  VELLLHPSPS  VLVPALRTVG  NIVTGDDMQT  QVKALLAFCL
251  FVPSFAVIEN  GLIGPLVNLL  QNAEFDIKKE  AAWAVSNATS  GGTHEQIKFL
301  VSQGCIKPLC  DLLVSPDPRI  VTVSLEGLEN  ILKVGEAEKN  LGNSGDANFY
351  AQMIDDAEGL  EKIENLQSHD  NNEIYEKAVK  ILETYWLEED  DETLPSGDGA
401  QQGFQFGGNG  VQVPSGGFNF
```

Spot No.: **68**

NCBI accession No.: **gi|31580730** Species: *Hevea brasiliensis*

Protein name： latex cyanogenic beta glucosidase

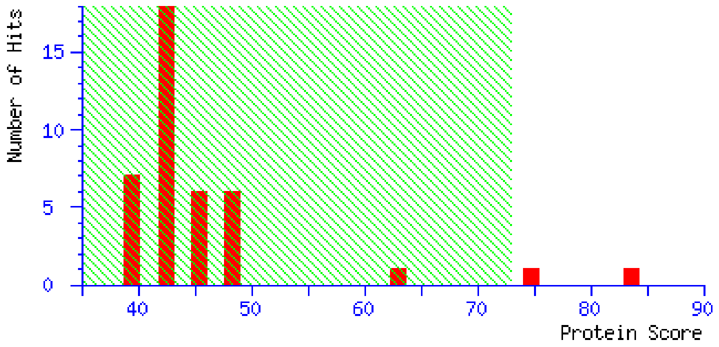
PMF score: **84** Sequence coverage %: **27**

Matched peptides No.: **12** Total peptides No.: **51**

Calculated Mr: **56325** Calculated *p*I: **5.72**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MMKEKFLKEH PYLLEKEVSR **SDFPPNFLFG** **VATSAYQIEG** **GCREGGRGPS**
51 **IWDAFSHTKG** **TILDGSNGDV** **AVDHYHR**YKE DIELIAK**LGF** **DAYRFSLSWS**
101 **R**IFPDGLGTK VNEEGIAFYN NIINALLEKG IEPYITLYHW DLPLHLQESM
151 GGWLNKEIVK **YFAIYADTCF** **ASFGDR**VKKW ITLNEPLQTA VNGFDTGILA
201 PGKHEHSYTE PFLASHHQIL AHATAVSIYR SMYKDNQGGE VGLVVDCEWA
251 ESNSDKIEDK AAAAKRLEFQ LGWYLHPLYY GDYPEVMRKI LGGGLPK**FSE**
301 **EDKELLRNSL** **DFIGLNHYSS** **R**FIKHVTDSP AECYYYKAQE IERLAK**WEDG**
351 **EPIGER**AASE WLYVRPWGLR K**VLNYIVQR**Y NNPIIYVTEN GMDDEDSSAP
401 LHEMLDDKLR VRYFKGYLAA VAQAIKDGAD VRGYFAWSLL DNFEWAQGYT
451 KRFGLIYVDY KNGLARHPK**S** **SAYWFMR**FLK GDEGKNGKE

Spot No.: **69**

NCBI accession No.: **gi|2501850** Species: *Nicotiana tabacum*

Protein name: GDP dissociation inhibitor

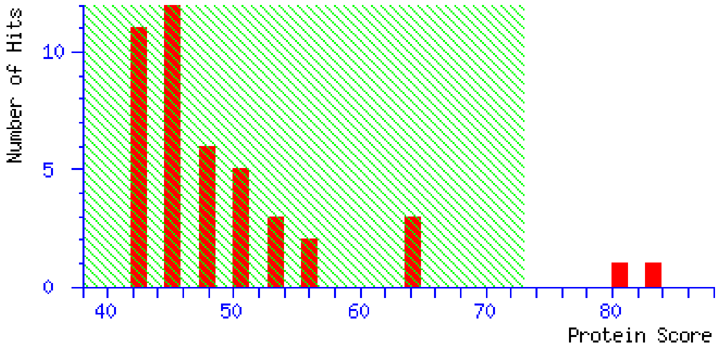
PMF score: **83** Sequence coverage %: **34**

Matched peptides No.: **16** Total peptides No.: **62**

Calculated Mr: **50127** Calculated *p*I: **5.44**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MDEEYDVIVL GTGLK**ECILS** **GLLSVDGLK**V LHMDRNDYYG GESTSLNLVQ
51 LWKRFR**GSDK** **PPAELGSSR**D FNVDMIPKFI MANGALVR**VL** **IHTDVTKYLY**
101 **FKAVDGSFVY** **NK**GKVHK**VPA** **TDMEALKSPL** **MGIFEK**RRAR KFFIYVQDYN
151 ESDPK**THEGM** **DLTR**VTTREL IAKYGLDDNT VDFIGHALAL HRDDR**YLDEP**
201 **AQDTVKR**MK**L** **YAESLARFQG** **GSPYIYPLYG** **LGELPQAFAR** **LSAVYGGTYM**
251 **LNKPECK**VEF DEEGKVCGVT SEGETAKCK**K** **VVCDPSYLPN** **K**VRKVGKVAR
301 AIAIMSHPIP NTNDSHSVQI ILPQKQLGRK SDMYLFCCSY THNVAPKGKF
351 IAFVSTEAET DNPESELKQG VNLLGPVDEI FYETYDRSEP VNEPSLDNCF
401 ISTSYDATTH FESTVDDVLN LYTKITGKVL DLNVDLSAAS AAEE

Spot No.: **70**

NCBI accession No.: **gi|2501850** Species: *Nicotiana tabacum*

PFF score: [202] Protein name: GDP dissociation inhibitor

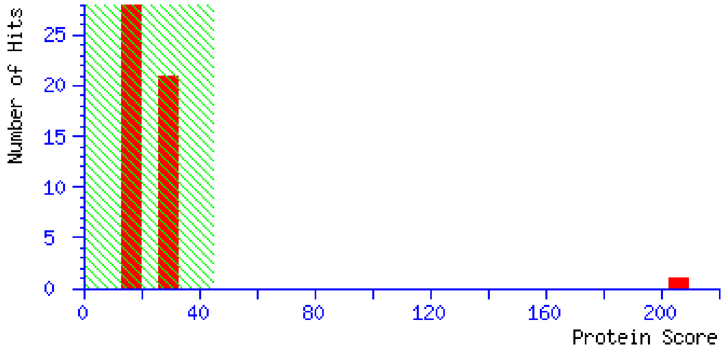
Matched peptides No.: [5] Sequence coverage %: [8]

Matched sequences: K.AVDGSFVYNK.G;
K.THEGMDLTR.V;
K.LYAESLAR.F;
K.KVVCDPSYLPNK.V;
K.VVCDPSYLPNK.V

Calculated Mr: **50127** Calculated *p*I: **5.44**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

```
  1 MDEEYDVIVL GTGLKECILS GLLSVDGLKV LHMDRNDYYG GESTSLNLVQ
 51 LWKRFRGSDK PPAELGSSRD FNVDMIPKFI MANGALVRVL IHTDVTKYLY
101 FKAVDGSFVY NKGKVHKVPA TDMEALKSPL MGIFEKRRAR KFFIYVQDYN
151 ESDPKTHEGM DLTRVTTREL IAKYGLDDNT VDFIGHALAL HRDDRYLDEP
201 AQDTVKRMKL YAESLARFQG GSPYIYPLYG LGELPQAFAR LSAVYGGTYM
251 LNKPECKVEF DEEGKVCGVT SEGETAKCKK VVCDPSYLPN KVRKVGKVAR
301 AIAIMSHPIP NTNDSHSVQI ILPQKQLGRK SDMYLFCCSY THNVAPKGKF
351 IAFVSTEAET DNPESELKQG VNLLGPVDEI FYETYDRSEP VNEPSLDNCF
401 ISTSYDATTH FESTVDDVLN LYTKITGKVL DLNVDLSAAS AAEE
```

Spot No.: **71**

NCBI accession No.: **gi|359478860** Species: *Vitis vinifera*

Protein name： PREDICTED: 26S protease regulatory subunit 6B homolog

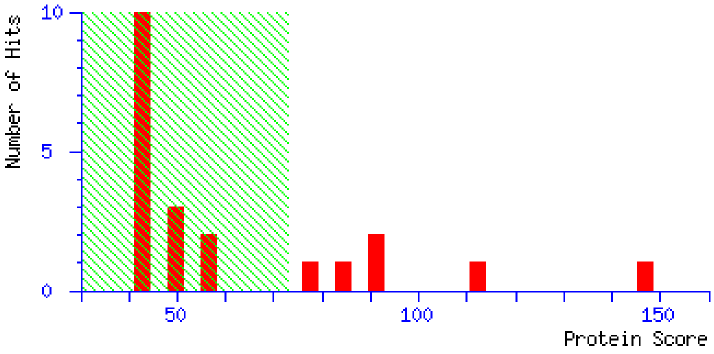
PMF score: **147** Sequence coverage %: **47**

Matched peptides No.: **18** Total peptides No.: **44**

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

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MAVVLEPKPS SEPPPSFPST RSDIQGFSDQ SSSFSDEDDL YGRLKSLQR**Q**
51 **LEFIDIQEEY** **VKDEQK**NLKR ELLRAQEEVK RIQSVPLVIG QFMEMVDQNN
101 GIVGSTTGSN YYVRILSTIN R**ELLKPSASV** **ALHR**HSNALV DVLPPEADSS
151 ISLLSQSEKP DVTYNDIGGC DIQKQEIR**EA** **VELPLTHHEL** **YKQIGIDPPR**
201 **GVLLYGPPGT** **GK**TMLAK**AVA** **NHTTAAFIR**V VGSEFVQK**YL** **GEGPR**MVRDV
251 FRLAK**ENAPA** **IIFIDEVDAI** **ATARFDAQTG** **ADR**EVQR**ILM** **ELLNQMDGFD**
301 **QTVNVK**VIMA TNR**ADTLDPA** **LLRPGR**LDR**K** **IEFPLPDR**RQ KRLVFQVCTA
351 K**MNLSDEVDL** **EDYVSRPDKI** **SAAEIAAICQ** **EAGMHAVR**KN RYVILPKDFE
401 KGYRTNVK**KP** **DTDFEFYK**

Spot No.: **72**

NCBI accession No.: **gi|224071449** Species: *Populus trichocarpa*

PFF score: [128] Protein name:predicted protein

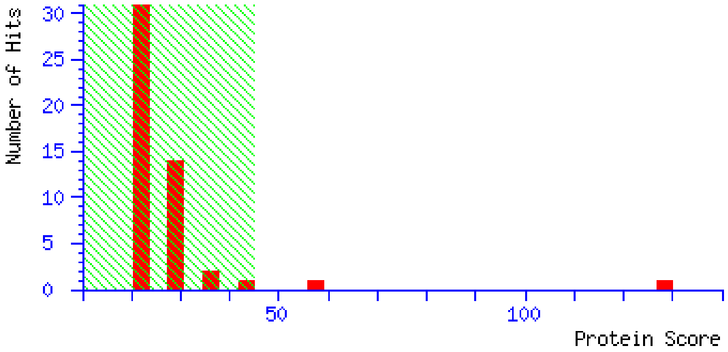
Matched peptides No.: [3] Sequence coverage %: [4]

Matched sequences:R.EIYIAFR.G ;
K.NKIDVIPHYPGR.L ;
K.IDVIPHYPGR.L ;

Calculated Mr: **47121** Calculated *p*I: **5.28**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MDGTSEATWP EILGSRNWDN LLDPLDLSLR KLILRCGDFC QATYDAFNND
51 QNSRYCGTSR YGKRNFFHKV MLDNPENYQV SSFLYATARV SLPEAFLLHS
101 LSRDSWDRET NWIGYIAVTS DEQTKTLGRR **EIYIAFR**GTT RNYEWVDILG
151 AKLKSAKPLL RGATSTTHDQ ESSSSSDDDD DKVPKVMLGW LTMYISDDPN
201 SPFTKLSARA QLLAHIKELR ERYKDDDLSI IFTGHSLGAS LSILSAFDLV
251 ENGITDIPVS AFVFGSPQVG NKEFNERFNK YPNLKVLHIK **NKIDVIPHYP**
301 **GR**LMGYVYTG IEFEIDTRKS PSLKDSKNPS DWHNLQAMLH IVAGWNGEEQ
351 EFELKVKRSL ALVNKSSEFL KDECLVPGIW WVEKNKGMVR NEDGEWVLAP
401 PDEEDLPVPE C

Spot No.: **73**

NCBI accession No.: **gi|32186912** Species: *Gossypium hirsutum*

Protein name： **actin**

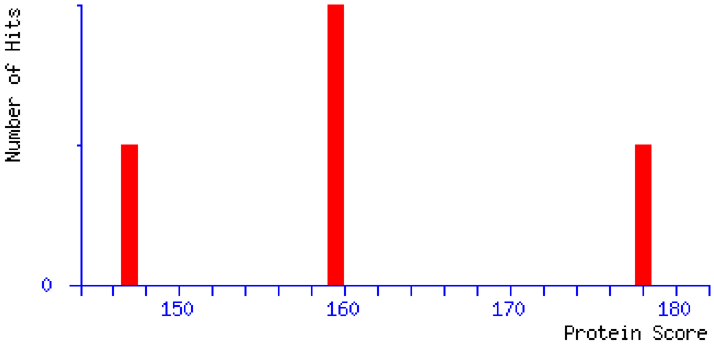
PMF score: **178** Sequence coverage %: **57**

Matched peptides No.: **19** Total peptides No.: **35**

Calculated Mr: **41936** Calculated *p*I: **5.37**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MADGEDIQPL VCDNGTGMVK **AGFAGDDAPR** **AVFPSIVGRP** **RHTGVMVGMG**
51 **QK**DAYVGDEA QSKRGILTLK **YPIEHGIVSN** **WDDMEKIWHH** **TFYNELRVAP**
101 **EEHPVLLTEA** **PLNPK**ANREK MTHIIFETFN VPAMYVAIQA VLSLYASGR**T**
151 **TGIVLDSGDG** **VSHTVPIYEG** **YALPHAILRL** **DLAGRDLTDA** **LMK**ILTERGY
201 **MFTTTAER**EI VRDMKEK**LAY** **VALDYEQELE** **TAK**SSSSVEK **NYELPDGQVI**
251 **TIGAER**FRCP EVLFQPSFIG MEAAGIHETT YNSIMKCDVD IR**KDLYGNIV**
301 **LSGGSTMFPG** **IADR**MSK**EIT** **ALVPSSMKIK** **VVAPPER**KYS VWIGGSILAS
351 LSTFQQMWIS K**GEYDESGPS** **IVHR**KCF

Spot No.: **74**

NCBI accession No.: **gi|297816956**

Species: Arabidopsis lyrata subsp. lyrata

PFF score: [70]

Protein name:hypothetical protein ARALYDRAFT_486071

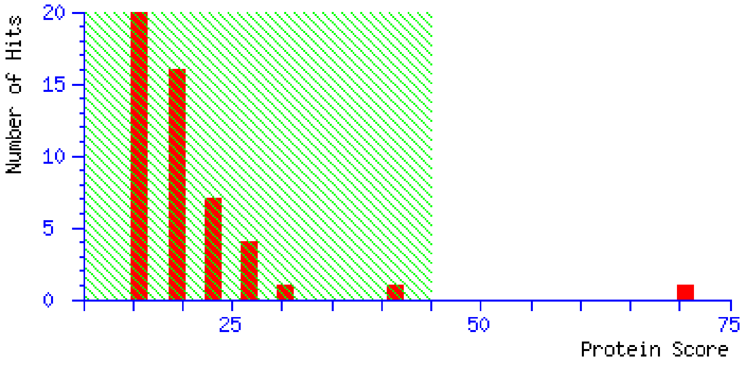
Matched peptides No.: [3]   Sequence coverage %: [5]

Matched sequences:K.APLLIGCDVR.N ;
K.EVIAVNQDPLGVQGR.K;
K.EVIAVNQDPLGVQGR.K

Calculated Mr: **48033**   Calculated *p*I: **4.79**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

```
  1  MKDSVLFLVG  LFSLSVLVSQ  SISGRVKAPL  LQSNTGGLVF  SKSFNSIYDT
 51  SMYGRLQLNN  GLARTPQMGW  NSWNFFACNI  NETVIKETAD  ALLSSGLADL
101  GYIHVNIDDC  WSNLLRDSKG  QLVPHPETFP  SGIKLLADYV  HSKGLKLGIY
151  SDAGVFTCQV  RPGSLFHEVD  DADIFASWGV  DYLKYDNCFN  LGIKPIKRYP
201  PMRDALNATG  RSIFYSLCEW  GVDDPALWAK  EVGNSWRTTD  DINDTWASMT
251  TIADLNNKWA  AYAGPGGWND  PDMLEIGNGG  MTYEEYRGHF  SIWALMKAPL
301  LIGCDVRNMT  AETFEILSNK  EVIAVNQDPL  GVQGRKIQAN  GEDDCQQVWS
351  GPLSGDRIVV  ALWNRCSEQA  TITASWDVIG  LESTISVSVR  DLWQHKDVTE
401  NASGSFEAQV  DAHDCHMYVL  TPQTVSHSDV
```

Spot No.: **75**

NCBI accession No.: **gi|3264769** Species: *Prunus armeniaca*

PFF score: [74] Protein name: late embryogenesis-like protein

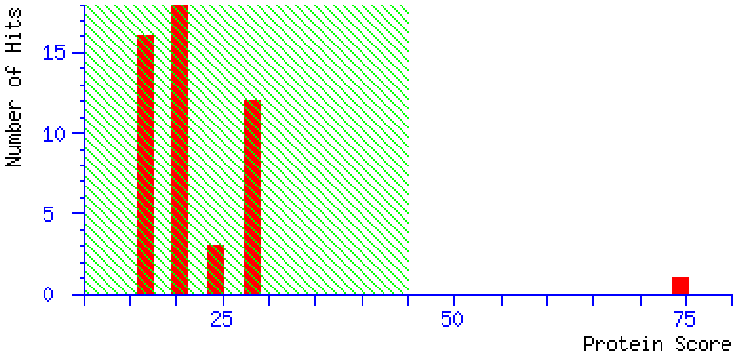
Matched peptides No.: [1] Sequence coverage %: [8]

Matched sequences: K.LVSGLIPDAGTIHAHGEETVK.V

Calculated Mr: **28937** Calculated *p*I: **4.72**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 DVTAIHIPSI NLEKAEIVVD VLIKNPNPVP IPLIDINYLI ESDGRK**LVSG**
51 **LIPDAGTIHA** **HGEETVK**VPV HLVYDDIKNT YDDIKPGSII PYRFKVDLIV
101 DVPVLGRLTL PLEKTGEIPI PYKPDVDVEK IKFQAFSFEE TVAVLHVKLE
151 NMNDFDLGLN ALDYEIWLSE VNIGGAQLSQ SANLAKKGVT FIELPITFRP
201 KDFGSALWDM IRGKGTGYTI KGNINVDTPF GAMKLPIVKE GGTTRLRKNK
251 EDGGDDDDED ED

Spot No.: **76**

NCBI accession No.: **gi|168066110**

Species: **Physcomitrella patens subsp. patens**

Protein name： **predicted protein**

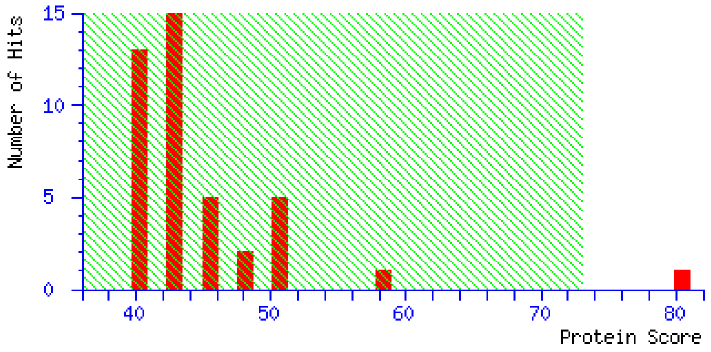
PMF score: **81** Sequence coverage %: **39**

Matched peptides No.: **15** Total peptides No.: **82**

Calculated Mr: **41963** Calculated *p*I: **5.24**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 **MEASSHYIRK** **HWTRATTEVL** **VK**AGDIEEPI VALVDHGFEI NLMSKDLYKK
51 R**KWPIDIEHR** **WVILAANNTR** **GELYRACSDV** **KIWIGDVATK** RHFFVQDTTS
101 YPLILGQSYI TATR**METKVL** **DDGSTYARNY** **GGTK**EEILSQ DEGTFDASFI
151 DIFESRNIIY KKVDDSKRKE IKRLYSIERE LRKLETLEDG EKILGVYEEN
201 GLEDSLELIA SIELGDNDKI VEIHSTEVYS ILESFQAPEV IVETKYKIVD
251 K**KVKPLVRPL** **IEDSK**EKMEE ASK**EESLRDP** **KKIGHEFTKE** **TFEELK**IGYD
301 GSLFPTEIEY FKKILAKR**GK** **SFAFGSHEIG** **CVDPNIVALM** **LSR**SFIDAAL
351 TSHVPLIDFL D

Spot No.: **77**

NCBI accession No.: **gi|388503664** Species: *Lotus japonicus*

Protein name： **unknown**

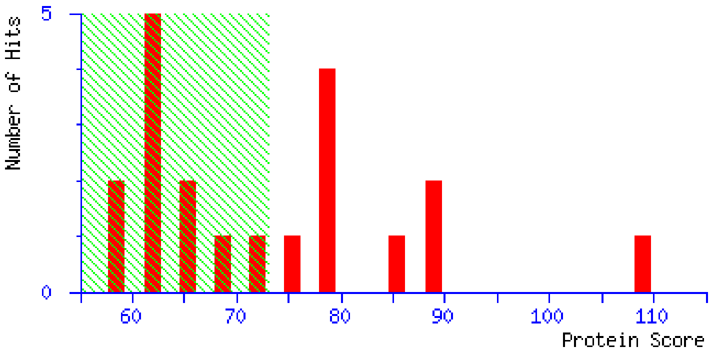
PMF score: **109** Sequence coverage %: **43**

Matched peptides No.: **13** Total peptides No.: **37**

Calculated Mr: **29537** Calculated *p*I: **4.79**

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red:

1 MASSK**DRGTF** **VYVAKLAEQA** **ERYEEMVDSM** **KK**VANLDVEL TVEERNLLSV
51 GYK**NVIGAR**R ASWR**ILSSIE** **QK**EETKGNDV NAKR**IKEYR**Q KVESELADIC
101 NDVMRVIDEH LIPSATAGES TVFYYK**MKGD** **YYRYLAEFK**S GNEKKEAADQ
151 SMK**AYESATT** **AAEAELPPTH** **PIR**LGLALNF SVFYYEILNS PERACHLAKQ
201 AFDEAISELD TLNEESYK**DS** **TLIMQLLRDN** **LTLWTSDIPE** **EGEDSLKAND**
251 **TAK**VGGGEDA E

Spot No.: **78**

NCBI accession No.: **gi|115468882**

Species: *Oryza sativa Japonica Group*

PFF score: [71] Protein name:Os06g0608500

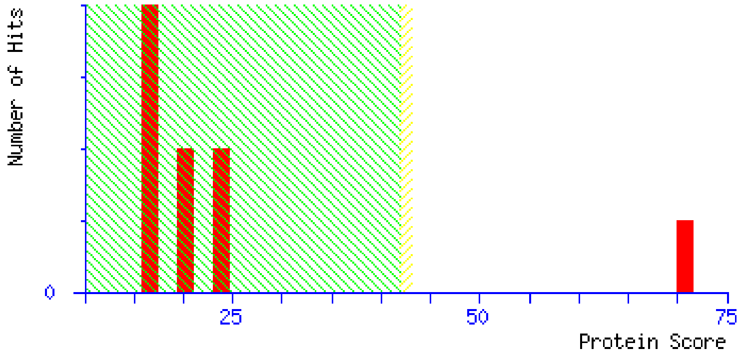
Matched peptides No.: [1] Sequence coverage %: [6]

Matched sequences: R.LYEQQIEQLGNFQLR.I

Calculated Mr: **24269** Calculated *p*I: **4.84**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 42 indicate peptides with significant homology.
Individual ions scores > 43 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MSGVFGKVFG KSKAQSQATA LASIDKLSET LEMLEKKENL LVKKANLEVE
51 KAKTFTKAKN KRAAIQCLKR KR**LYEQQIEQ** **LGNFQLR**IHD QMIMLEGAKA
101 TTETVDALRT GASAMKAMHK ATNIDDVDKT MDEINDNMEN MRQIQDLLSA
151 PIGAAADFDE DELEAELADL EGEELEAELL APTTTAPTAP VRVQQPTRPS
201 AQSSKTEDDE LAALQAEMAM

Spot No.: **79**

NCBI accession No.: **gi|356532109** Species: *Glycine max*

PFF score: [104]

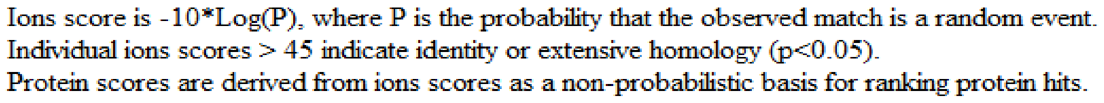
Protein name: 2,3-bisphosphoglycerate-independent phosphoglycerate mutase-like

Matched peptides No.: [3] Sequence coverage %: [7]

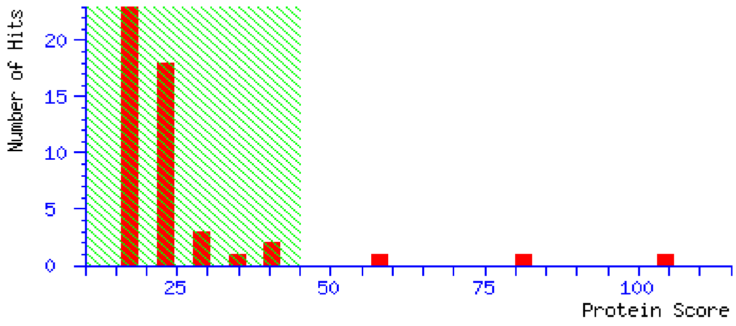
Matched sequences: K.ALEYENFDKFDR.V ;
K.ALEYENFDKFDR.V;
R.AHGTAVGLPTEDDMGNSEVGHNALGAGR.I + Oxidation (M)

Calculated Mr: **61059** Calculated *p*I: **5.51**

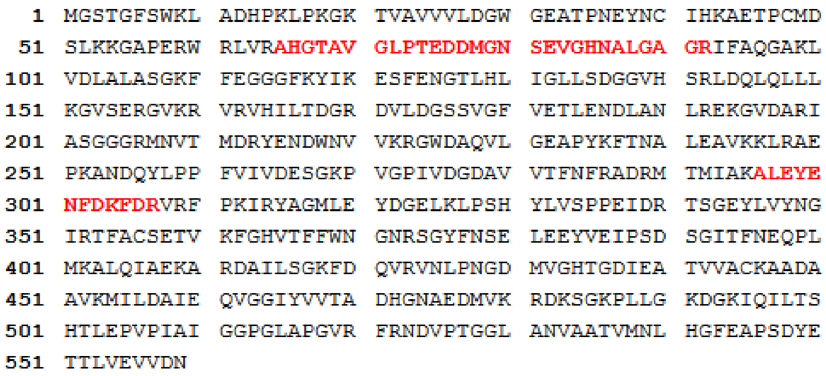
Probability Based Mowse Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:



1 MGSTGFSWKL ADHPKLPKGK TVAVVVLDGW GEATPNEYNC IHKAETPCMD
51 SLKKGAPERW RLVR**AHGTAV** **GLPTEDDMGN** **SEVGHNALGA** **GR**IFAQGAKL
101 VDLALASGKF FEGGGFKYIK ESFENGTLHL IGLLSDGGVH SRLDQLQLLL
151 KGVSERGVKR VRVHILTDGR DVLDGSSVGF VETLENDLAN LREKGVDARI
201 ASGGGRMNVT MDRYENDWNV VKRGWDAQVL GEAPYKFTNA LEAVKKLRAE
251 PKANDQYLPP FVIVDESGKP VGPIVDGDAV VTFNFRADRM TMIAK**ALEYE**
301 **NFDKFDR**VRF PKIRYAGMLE YDGELKLPSH YLVSPPEIDR TSGEYLVYNG
351 IRTFACSETV KFGHVTFFWN GNRSGYFNSE LEEYVEIPSD SGITFNEQPL
401 MKALQIAEKA RDAILSGKFD QVRVNLPNGD MVGHTGDIEA TVVACKAADA
451 AVKMILDAIE QVGGIYVVTA DHGNAEDMVK RDKSGKPLLG KDGKIQILTS
501 HTLEPVPIAI GGPGLAPGVR FRNDVPTGGL ANVAATVMNL HGFEAPSDYE
551 TTLVEVVDN

Spot No.: **80**

NCBI accession No.: **gi|224056489** Species: *Populus trichocarpa*

Protein name: **predicted protein**

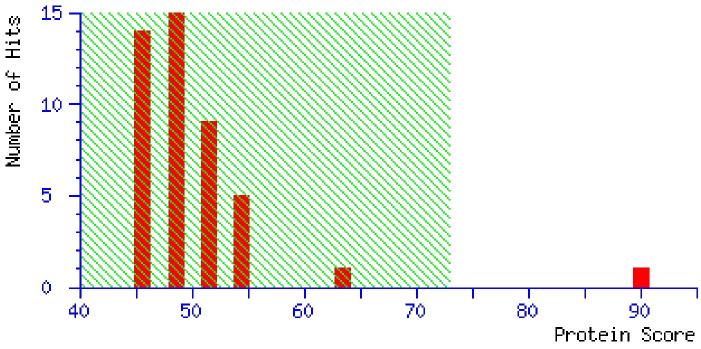
Mascot score: **90** Sequence coverage %: **32**

Matched peptides No.: **17** Total peptides No.: **86**

Calculated Mr: **59210** Calculated *p*I: **5.11**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 **MEESESRK**QT LLSSLESAGI WIPDNVTSIG DLSPETFVSI CAQCVNLIDQ
51 TASLPTTLPD AAIDKLK**MCA** **DMGLAIKR**LG FIGDMSYIKV IKPVTNCFVI
101 K**LLYPSEDDL** **HKLTRFLVER** LTESTRPVKI AEVKDVNARG KTKEDGSDIG
151 GRLDLNHQRE K**LADPSLHNA** **VPEAEDIPFI** **GLSR**QNLGKD KLPAFFYGEL
201 FDEEGKSGRD LFGNEETAAA GDDKDVQKAI SIK**EQPSMVI** **IEKEELR**NEE
251 KVLTEEVTAK TSELQHLEEE LELLKAAAEM AYGDQNSIDF CFEQLKGQVD
301 AKRCNITELK **SQWDAFRMPL** **EDKKRNLEES** **LYANIPGSQE** **K**LQKLRELEH
351 EKQLVLSEIT KREEEHSKLS ADLEKQPKLP SRTSYIERIK EITKSSQKQD
401 ADIKRILK**ET** **RELQLESNSI** **QDRLHR**TYAV LDEIVCREAK RDLVGRKAYR
451 LLTSLHDCFG QISEK**ILTTD** **RISR**EMTELE K**KLAAMASRS** **LNVDKLQADL**
501 **DAIVKENECL** **ELRLAENP**

Spot No.: **81**

NCBI accession No.: **gi|255552291** Species: *Ricinus communis*

PFF score: [174]

Protein name:short chain dehydrogenase, putative

Matched peptides No.: [2] Sequence coverage %: [10]

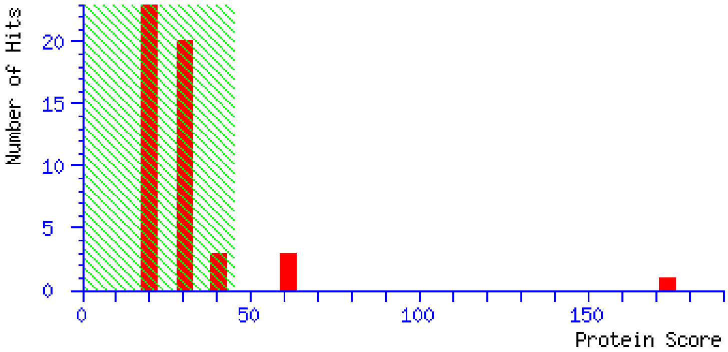
Matched sequences: K.VALVTGGDSGIGR.A ;

K.DPIAIPTDVGFEENCR.K

Calculated Mr: **32148** Calculated *p*I: **6.50**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MATRRGYRFP PQSQDKQPGK EYLMHPLPEF INPHYKPSNK LQDK**VALVTG**
51 **GDSGIGR**AVS YYFTLEGATV AFTYVKGRED KDKDHILKIL HEVKAEGAK**D**
101 **PIAIPTDVGF** **EENCR**KVIDQ IMSEYGKIDI LVNNAGEAHY STTIEDITDP
151 MLERVFRTNI FGHFFMSRHA LKHMKEGGCI INTASVAAYA GFSFMVDYSS
201 TKGAVVAFTR SLALQLIDRG IRVNAVAPGS VWTPFQPSTL SAEQVAQVGS
251 GVPMDRAAQP YEIAPSFVFL ASNDCSSYFT GQVLHPNGMF

Spot No.: **82**

NCBI accession No.: **gi|2073448** Species: *Lotus japonicus*

Protein name：glutamine synthetase

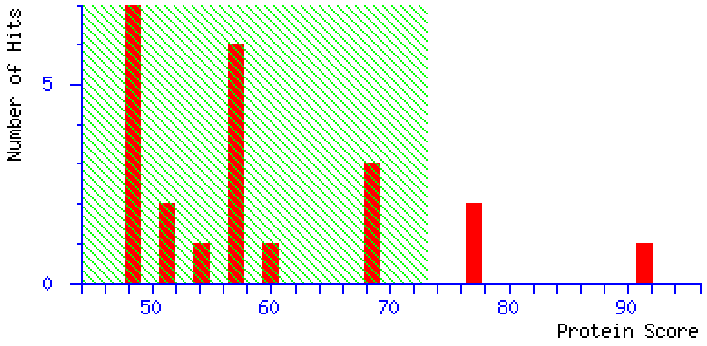
PMF score: **91** Sequence coverage %: **46**

Matched peptides No.: **13** Total peptides No.: **89**

Calculated Mr: **39308** Calculated *p*I: **5.49**

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red:

1 M**SLLSDLINL** **NLSETTDKII** **AEYIWIGGSG** **LDMR**TKARTL PGPVSDPSQL
51 PK**WNYDGSST** **GQAPGEDSEV** **ILYPQAIFRD** **PFR**RGSNILV ICDAYTPAGE
101 PIPTNKRHAA AKVFSHPDVV AEVPWYGIEQ EYTLLQK**EVN** **WPVGWPIGGF**
151 **PGPQGPYYCG** **IGADK**AFGRD IVDAHYKACL YAGVNISGIN GEVMPGQWEF
201 QVGPSVGISA GDEVWVAR**YI** **LER**ITEIAGV VLSFDPKPIK GDWNGAGAHT
251 NYSTKTMRED GGYEVIKKAI DKLGLR**HKEH** **IAAYGEGNER** RLTGR**HETAD**
301 **INTFLWGVAN** **RGASIRVGR**D TEKEGK**GYFE** **DRRPASNMDP** **YVVTSMIADT**
351 **TILWKP**

Spot No.: **83**

NCBI accession No.: **gi|192912956** Species: *Elaeis guineensis*

PFF score: [204]

Protein name: aluminum-induced protein

Matched peptides No.: [2] Sequence coverage %: [9]

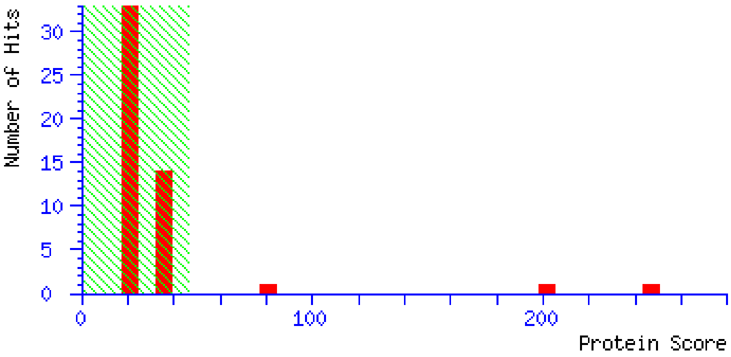
Matched sequences: K.TANEVIIVIEAYR.S ;

R.GPYPADKVVR.D

Calculated Mr: 27466 Calculated *p*I: **6.07**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MLAVFDRTVA KCPEGLRNMD SGPGEKGVGG VASLVDHFSA TREGAVTIRL
51 GSSGAVAYTA EKQNLLLPRL FAAVDDIYCL FQGHIENIAH LKQQYGLNK**T**
101 **ANEVIIVIEA** **YR**SLRDR**GPY** **PADKVVR**DLN GKFAFILFDC SAKSTFIAAD
151 ADGSVPFYWG TDSGSHLVLS DDVDVIKKGC GKSFAPFPKG CFFTTSGGLQ
201 SFEHPLNEVK LMPRVDSQGE VCGATYEIDA QTKKESSMPR VGSAANWSSH
251 Y

Spot No.: 84

NCBI accession No.: gi|255559601 Species: ***Ricinus communis***

PFF score: [254]

Protein name：**alpha-soluble nsf attachment protein, putative**

Matched peptides No.: [6]   Sequence coverage %: [12]

Matched sequences: H EAAQAYVDAA HCYK ;

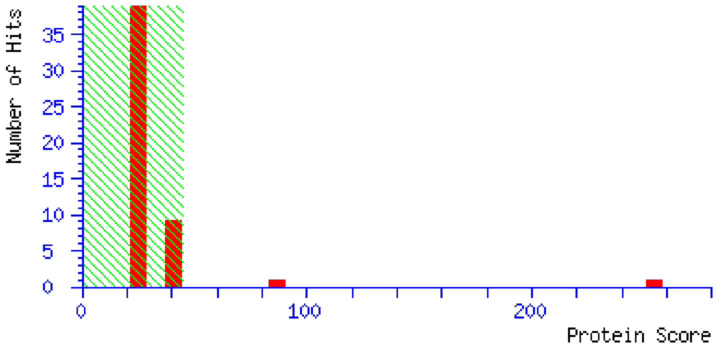
AIEIYEEIAR;

YQ DLDPTFSGTR

Calculated Mr: **32914**   Calculated *p*I: **5.12**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MSDQIAKGEE FEKKAEKKLN GWGLFGSKYE DASDLFDKAA NSFKLAKSWD
51 RAGSTYVKLA NCHLKLDSK**H** **EAAQAYVDAA** **HCYK**KTTTNE AISCLGQAVE
101 MFCDIGRISM AARYYKEIAE LYESEANVEK AMDFYEKAAD FFQGEEVTTS
151 ANQCKQKVAQ FAAQLEQYQK **AIEIYEEIAR** HSLSNNLLKY GVKGHLLNAG
201 ICHLCKGDVV SVTNALER**YQ** **DLDPTFSGTR** EYRLLADVAA AIDEEDVAKF
251 TDVVKEFDSM TPLDSWKTTL LLRVKEKLKA KELEEDDLT

Spot No.: 85

NCBI accession No.: **gi|224099853** Species: ***Populus trichocarpa***

PFF score: [69] Protein name: **putative protein**

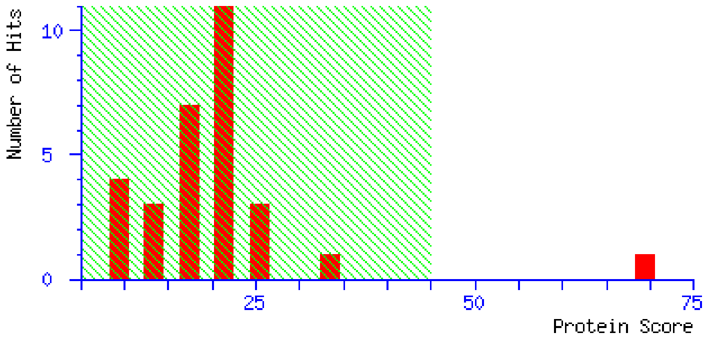
Matched peptides No.: [2] Sequence coverage %: [5]

Matched sequences: S FEHPLNELKP VPR

Calculated Mr: **27448** Calculated *p*I: **5.84**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MLAVFDNTVA KCPDALQSPH SAPASSALKD GFLANHFASQ HPGSVTVNLG
51 TSGLISHSVE KQNPFLPRLF AVVDDIFCLF QGHIDNVAVL KQQYGLNKTA
101 NEVIVVIEAY RTLRDRGPYP ADQVVKDIQG KFAFILYDST SKATFFAADA
151 DGSVPFFWGA DSEGNLVLSD DVQIVQKGCG KSFAPFPKGC FFTTSGGLR**S**
201 **FEHPLNELKP** **VPR**VDSSGQV CGATFKVDAE TKKESVGMPR VDSSYNWSSN
251 Y

Spot No.: 86

NCBI accession No.: **gi|38122474** Species: *Hevea brasiliensis*

PFF score: [410] Protein name： rubber elongation factor

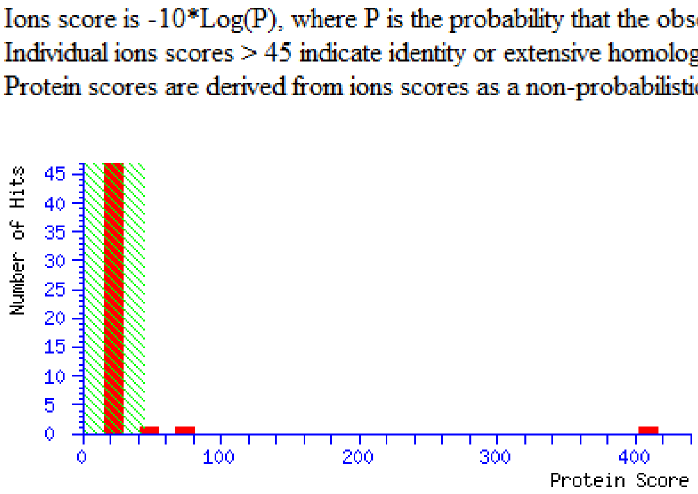
Matched peptides No.: [4] Sequence coverage %: [26]

Matched sequences: YLDFVQAATVYAR ;

SGPFKPGVNTVESR;
SVVRPVYNK ;
RVDAYVTVLDR

Calculated Mr: **19570** Calculated *p*I: **5.06**

Probability Based Mowse Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

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

1 MAEGEEEVNI QEEANKGEEN PQEEANIQEE TNKGEENIQE EANIEEEANK
51 EEESLK**YLDF** **VQAATVYAR**A SFSKLYLFAK DK**SGPFKPGV** **NTVESR**FK**SV**
101 **VRPVYNK**FQP VPNKVLKFAD R**RVDAYVTVL** **DR**IVPPIVKR ASIQAYSVAP
151 GAALAVASYL PLHTKRLSKV LYGDG

Spot No.: 87

NCBI accession No.: **gi|38122474** Species: *Hevea brasiliensis*

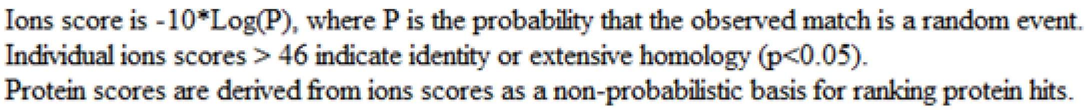
PFF score: [226] Protein name： rubber elongation factor

Matched peptides No.: [4] Sequence coverage %: [26]

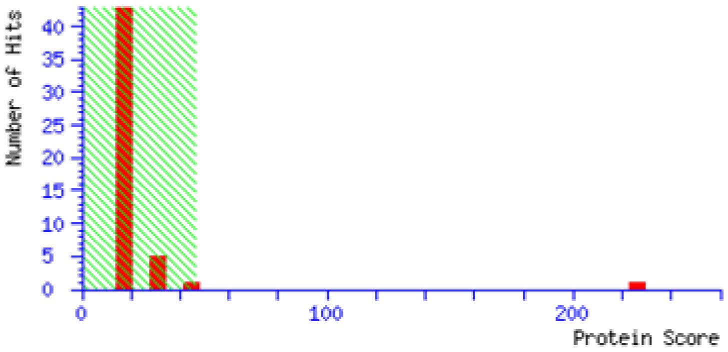
Matched sequences: YLDFVQAATVYAR ;
SGPFKPGVNTVESR;
SVVRPVYNK ;
RVDAYVTVLDR

Calculated Mr: **19570** Calculated *p*I: **5.06**

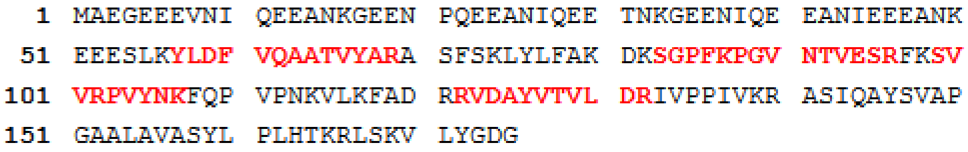
Probability Based Mowse Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red



1 MAEGEEEVNI QEEANKGEEN PQEEANIQEE TNKGEENIQE EANIEEEANK
51 EEESLK**YLDF** **VQAATVYAR**A SFSKLYLFAK DK**SGPFKPGV** **NTVESR**FK**SV**
101 **VRPVYNK**FQP VPNKVLKFAD R**RVDAYVTVL** **DR**IVPPIVKR ASIQAYSVAP
151 GAALAVASYL PLHTKRLSKV LYGDG

Spot No.: 88

NCBI accession No.: **gi|38122474** Species: *Hevea brasiliensis*

Protein name： rubber elongation factor

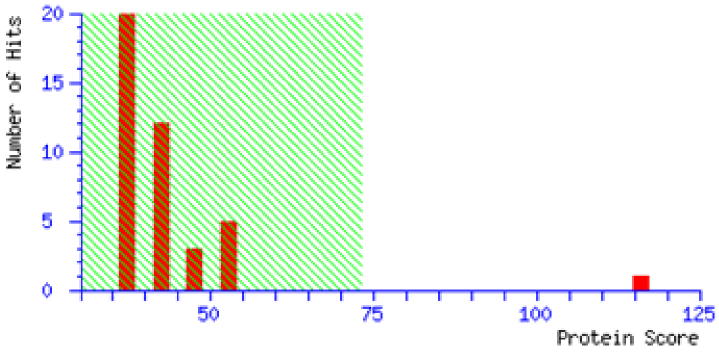
PMF score: **116** Sequence coverage %: **54**

Matched peptides No.: **11** Total peptides No.: **60**

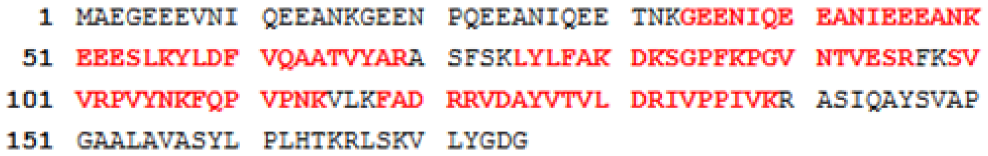
Calculated Mr: **19570** Calculated *p*I: **5.06**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red


1 MAEGEEEVNI QEEANKGEEN PQEEANIQEE TNK**GEENIQE** **EANIEEEANK**
51 **EEESLKYLDF** **VQAATVYAR**A SFSK**LYLFAK** **DKSGPFKPGV** **NTVESRFKSV**
101 **VRPVYNKFQP** **VPNKVLKFAD** **RRVDAYVTVL** **DRIVPPIVK**R ASIQAYSVAP
151 GAALAVASYL PLHTKRLSKV LYGDG

Spot No.: 88

NCBI accession No.: **gi|38122474** Species: *Hevea brasiliensis*

Protein name：rubber elongation factor

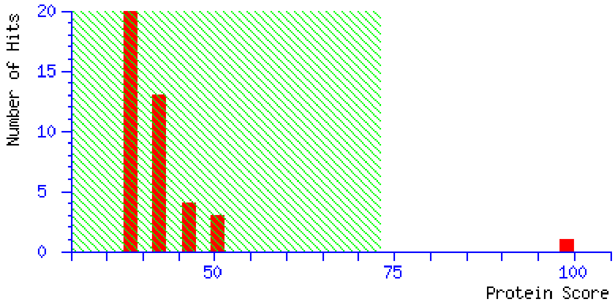
PMF score: **99** Sequence coverage %: **455**

Matched peptides No.: **8** Total peptides No.: **39**

Calculated Mr: **19570** Calculated *p*I: **5.06**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 MAEGEEEVNI QEEANKGEEN PQEEANIQEE TNK**GEENIQE** **EANIEEEANK**
51 **EEESLKYLDF** **VQAATVYAR**A SFSK**LYLFAK** DK**SGPFKPGV** **NTVESR**FK**SV**
101 **VRPVYNK**FQP VPNKVLK**FAD** **RRVDAYVTVL** **DR**IVPPIVKR ASIQAYSVAP
151 GAALAVASYL PLHTKRLSKV LYGDG

Spot No.: 90

NCBI accession No.: **gi|334854634** Species: *Hevea brasiliensis*

PFF score: [496] Protein name： elicitor-responsive protein

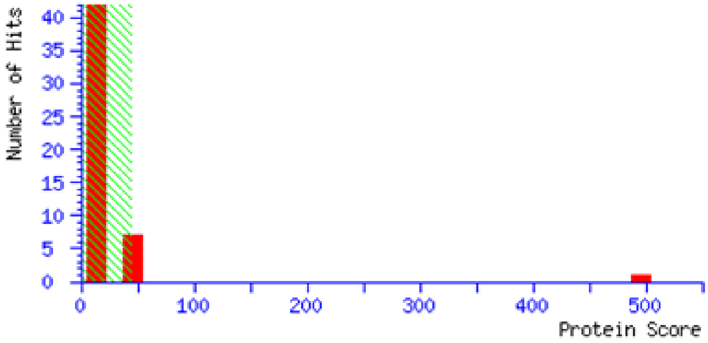
Matched peptides No.: [3] Sequence coverage %: [59]

Matched sequences: PLGTVEVLLVGAKGLENTDFLNGVDPYVVLACR;
GSEP EWNEKFSFEVSDGDTELTLK;
GEITVGLTFTPEVEMDNVGVDGYDFRL

Calculated Mr: **15249** Calculated *p*I: **4.06**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 M**PLGTVEVLL** **VGAKGLENTD** **FLNGVDPYVV** **LACR**TQEQKS SVASGK**GSEP**
51 **EWNEKFSFEV** **SDGDTELTLK** IMDSDVGAAD DFVGEATIPL EPLFLEGNLP
101 STAYKVVKEQ EYK**GEITVGL** **TFTPEVEMDN** **VGVDGYDFRL**

Spot No.: 91

NCBI accession No.: **gi|334854634** Species: *Hevea brasiliensis*

PFF score: [95]

Protein name:eukaryotic translation initiation factor 5A isoform VII

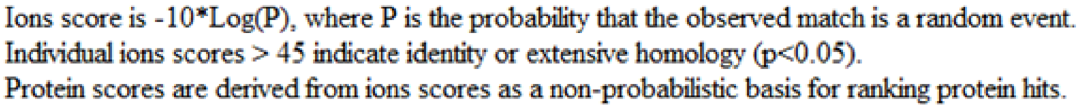
Matched peptides No.: [3] Sequence coverage %: [28]

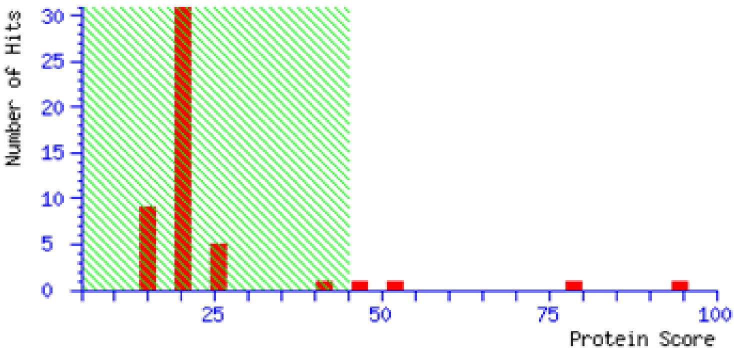
Matched sequences: TYPQQAGTIR;

K LEDIVPSSHNCDVPHVTR ;
TKDDLRLPTDENLLSQIK

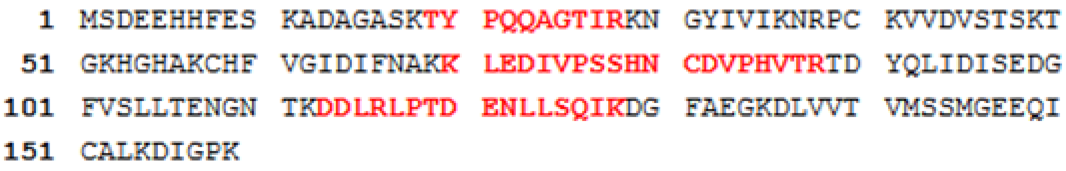
Calculated Mr: **17689** Calculated *p*I: **5.60**

Probability Based Mowse Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red


1 MSDEEHHFES KADAGASK**TY** **PQQAGTIR**KN GYIVIKNRPC KVVDVSTSKT

51 GKHGHAKCHF VGIDIFNAK**K** **LEDIVPSSHN** **CDVPHVTR**TD YQLIDISEDG

101 FVSLLTENGN TK**DDLRLPTD** **ENLLSQIK**DG FAEGKDLVVT VMSSMGEEQI

151 CALKDIGPK

Spot No.: 92

NCBI accession No.: **gi|224144943** Species: *Populus trichocarpa*

PFF score: [180] Protein name: predicted protein

Matched peptides No.: [2] Sequence coverage %: [28]

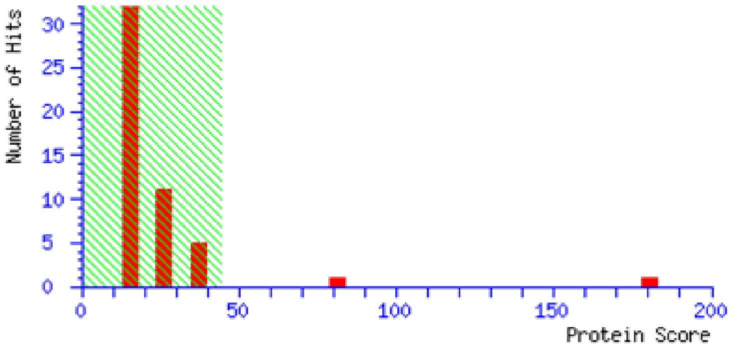
Matched sequences: VFEDNVLIRVLVVDGGGSLR;

HVPITIG GTRISDGEWLYADTDGILISR

Calculated Mr: **17971** Calculated *p*I: **5.39**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red

1 MALVTTAEVC DANPQLIVSG ELRALQPIFQ IYGRRQVFSG PVVTLK**VFED**
51 **NVLIREFLEE** KGNGR**VLVVD** **GGGSLR**CAIL GGNPVVQAQN NGWAGIVVNG
101 CIRDVDEIMG CDIGVRALAS HPMKANKKGI GEK**HVPITIG** **GTRISDGEWL**
151 **YADTDGILIS** **R**TELAV

Spot No.: 93

NCBI accession No.: gi|253760141

Species: *Hevea brasiliensis*

Protein name：nucleoside diphosphate kinase 1

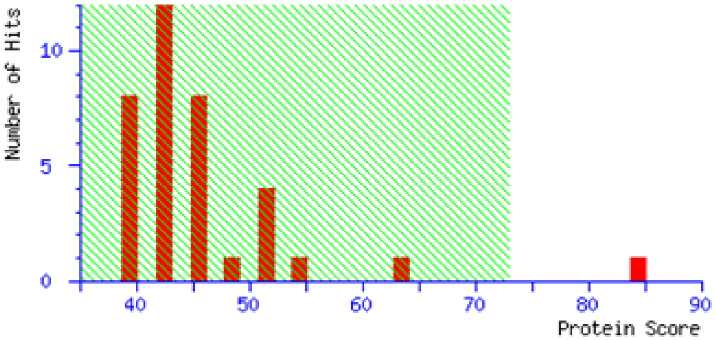
PMF score:84　　Sequence coverage %: 44

Matched peptides No.: 8　　Total peptides No.: 76

Calculated Mr: 16338　　Calculated *p*I: 6.85

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold red:

1 MEQTFIMIKP DGVQR**GLVGE** **IIGR**FEKKGF SLKGLK**LITV** **ERLFAER**HYA
51 DLSAKPFFNG LVEYIISGPV VAMVWEGK**NV** **VTTGRKIIGA** **TNPADSAPGT**
101 **IRGDYAIDIG** **RNVIHGSDSV** **ESARK**EIALW FPEGPVSWSS SLHPWIYE

Spot No.: 94

NCBI accession No.: gi|123062 Species: *Hevea brasiliensis*

PFF score: [96]

Protein name: prohevein

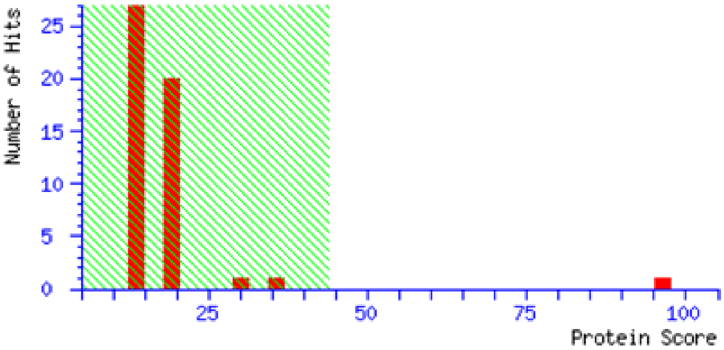
Matched peptides No.: [1] Sequence coverage %: [8]

Matched sequences: IVDQ CSNGGLDLDV NVFR

Calculated Mr: 22700 Calculated *p*I: 5.63

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red

1 MNIFIVVLLC LTGVAIAEQC GRQAGGKLCP NNLCCSQWGW CGSTDEYCSP
51 DHNCQSNCKD SGEGVGGGSA SNVLATYHLY NSQDHGWDLN AASAYCSTWD
101 ANKPYSWRSK YGWTAFCGPV GAHGQSSCGK CLSVTNTGTG AKTTVR**IVDQ**
151 **CSNGGLDLDV** **NVFR**QLDTDG KGYERGHITV NYQFVDCGDS FNPLFSVMKS
201 SVIN

Spot No.: 95

NCBI accession No.: **gi|313586569** Species: *Hevea brasiliensis*

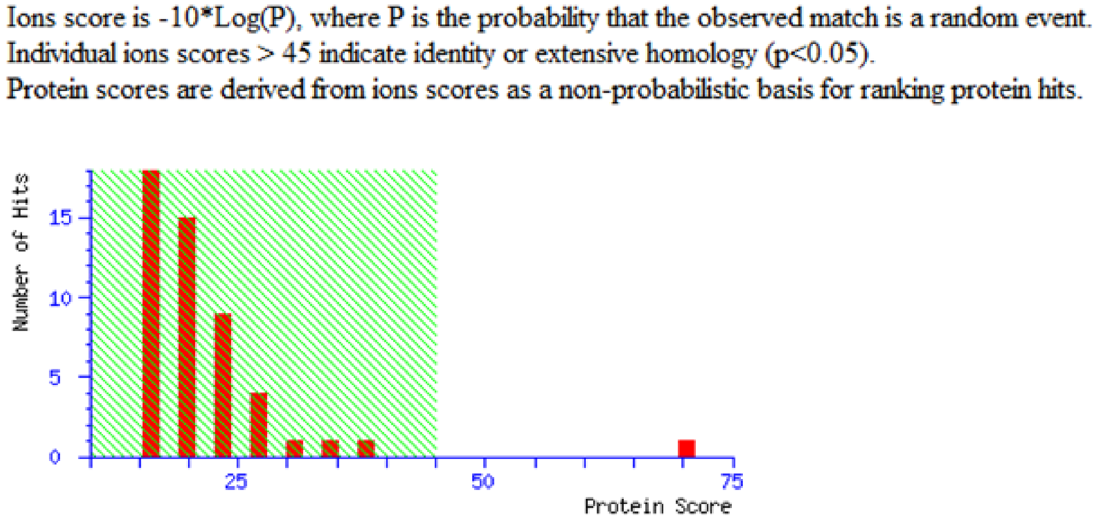
PFF score: [70] Protein name: hypothetical protein 19

Matched peptides No.: [1] Sequence coverage %: [5]

Matched sequences: ADPNFFLTIR

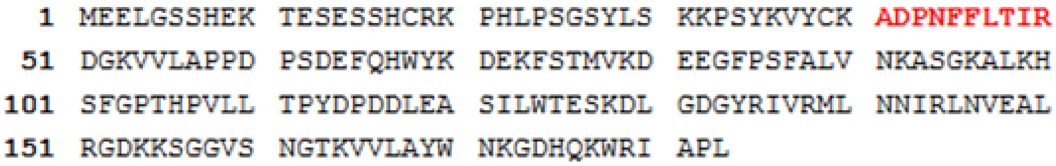
Calculated Mr: **20724** Calculated *p*I: **7.77**

Probability Based Mowse Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Matched peptide sequences: shown in Bold Red



1 MEELGSSHEK TESESSHCRK PHLPSGSYLS KKPSYKVYCK **ADPNFFLTIR**
51 DGKVVLAPPD PSDEFQHWYK DEKFSTMVKD EEGFPSFALV NKASGKALKH
101 SFGPTHPVLL TPYDPDDLEA SILWTESKDL GDGYRIVRML NNIRLNVEAL
151 RGDKKSGGVS NGTKVVLAYW NKGDHQKWRI APL

Spot No.: 96

NCBI accession No.: gi|313586569 Species: *Hevea brasiliensis*

Protein name: **hypothetical protein 19**

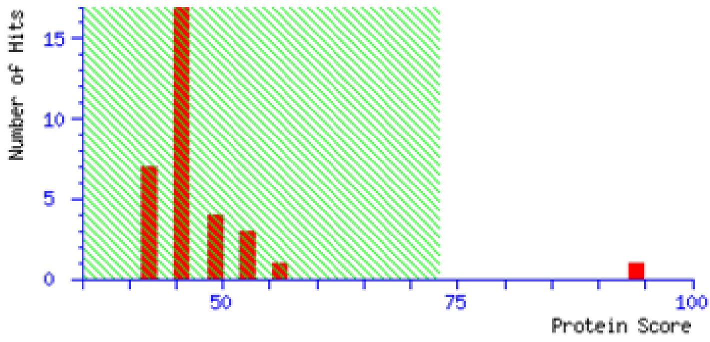
PMF score: **94** Sequence coverage %: **62**

Matched peptides No.: **11** Total peptides No.: **73**

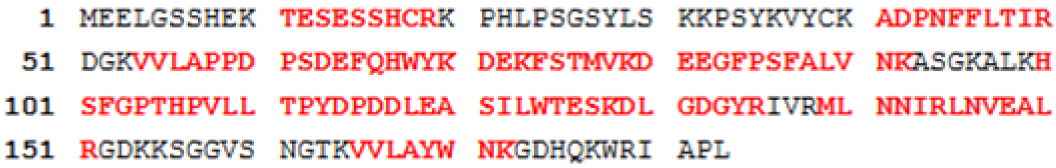
Calculated Mr: **20724** Calculated *p*I: **7.77**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red



```
  1 MEELGSSHEK TESESSHCRK PHLPSGSYLS KKPSYKVYCK ADPNFFLTIR
 51 DGKVVLAPPD PSDEFQHWYK DEKFSTMVKD EEGFPSFALV NKASGKALKH
101 SFGPTHPVLL TPYDPDDLEA SILWTESKDL GDGYRIVRML NNIRLNVEAL
151 RGDKKSGGVS NGTKVVLAYW NKGDHQKWRI APL
```

Spot No.: 97

NCBI accession No.: **gi|4835766** Species: ***Arabidopsis thaliana***

Protein name：Contains similarity to gb|AB017693 transfactor (WERBP-1) from Nicotiana tabacum

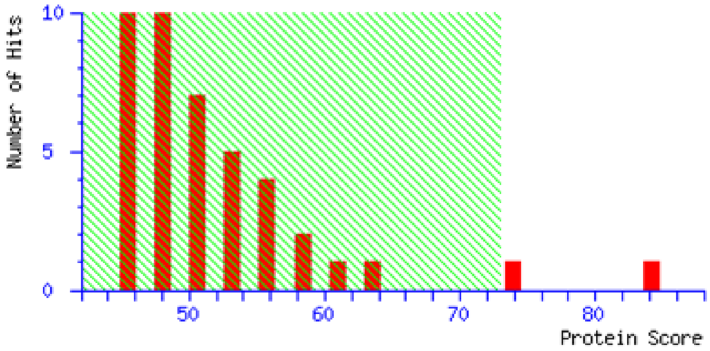
PMF score: **84** Sequence coverage %: **27**

Matched peptides No.: **11** Total peptides No.:**56**

Calculated Mr: **40677** Calculated *p*I: **8.94**

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 MFHAKKPSSM NGSYENR**AMC** **VQGDSGLVLT** **TDPKPR**LR**WT** **VELHERFVDA**
51 **VAQLGGPDKA** **TPK**TIMR**VMG** **VKGLTLYHLK** SHLQKFRLGK QPHK**EYGDHS**
101 **TKEGSRASAM** **DIQR**NVASSS GMMSRNMNDN SHQVGLIR**MQ** **MEVQRRLHEQ**
151 **LEVQR**HLQLR **IEAQGK**YMQS ILERACQTLA GENMAAATAA AAVGGGYKGN
201 LGSSSLSAAV GPPPHPLSFP PFQDLNIYGN TTDQVLDHHN FHHQNIENHF
251 TGNNAADTNI YLGKKRPNPN FGNDVRKGLL MWSDQDHDLS ANQSIDDEHR
301 IQIQMATHVS TDLDSLSEIY ERKSGLSGDE GNNGGKLLER PSPRRSPLSP
351 MMNPNGGLIQ GRNSPFG

Spot No.: 98

NCBI accession No.: gi|38122474   Species: *Hevea brasiliensis*

Protein name: rubber elongation factor

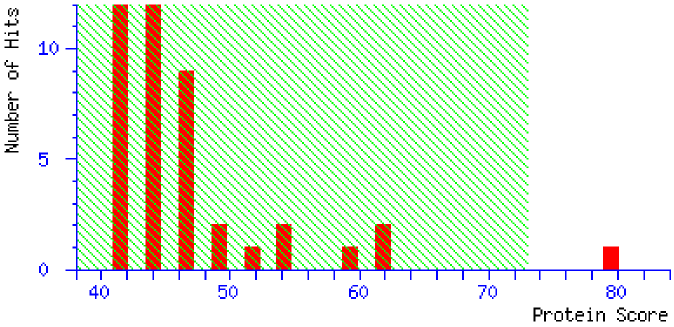
PMF score: 99   Sequence coverage %: 45

Matched peptides No.: 8   Total peptides No.: 39

Calculated Mr: 19570   Calculated *p*I: 5.06

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 73 are significant ($p<0.05$).



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

1 MAEGEEEVNI QEEANKGEEN PQEEANIQEE TNK**GEENIQE** **EANIEEEANK**
51 **EEESLKYLDF** **VQAATVYAR**A SFSK**LYLFAK** DK**SGPFKPGV** **NTVESR**FK**SV**
101 **VRPVYNK**FQP VPNKVLK**FAD** **RRVDAYVTVL** **DR**IVPPIVKR ASIQAYSVAP
151 GAALAVASYL PLHTKRLSKV LYGDG

Spot No.: **99**

NCBI accession No.: **gi|3377751**

Species: *Mesembryanthemum crystallinum*

PFF score: [73]		Protein name: glutathione S-transferase

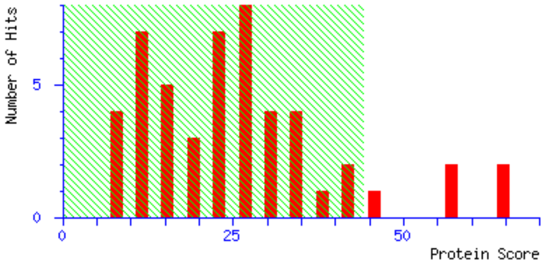
Matched peptides No.: [1]		Sequence coverage %: [4]

Matched sequences: R.FWADFIDKK.L

Calculated Mr: **26154**		Calculated *p*I: **5.71**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

```
  1  MGEEVILLDF  WPSMFGMRLR  IALAEKGVKH  ERKEEDLLIG  KSPLLLQLNP
 51  VHKKIPVLVH  NGKPINESMI  AVQYIDEVWN  EKSPSLLPSD  PYQRAQARFW
101  ADFIDKKLYD  ECRKIYTTKE  AEIGEETYKG  FLEIIKVLEA  EVGEKSYFGG
151  DTFGFVDVAL  IPFYSWFYAL  EMLGKFNIET  ECPKLIAWAK  RCMERESVSK
201  SLPDRHKIYD  FITLQLRKAL  GVDQ
```

Spot No.: **100**

NCBI accession No.: **gi|1709761**   Species: *Spinacia oleracea*

PFF score: [49]

Protein name: Proteasome subunit alpha type-4

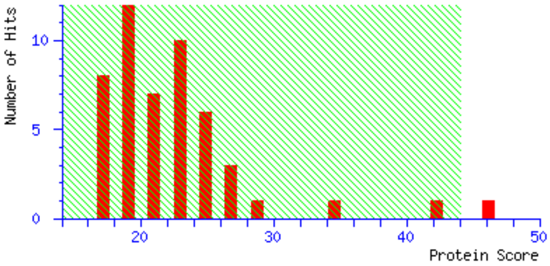
Matched peptides No.: [1]   Sequence coverage %: [3]

Matched sequences: R.TTIFSPEGR.L

Calculated Mr: **27545**   Calculated *p*I: **6.17**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MSRRYDSR**TT** **IFSPEGR**LYQ VEYAMEAIGN AGSAIGILAK DGVVLIGEKK
51 VTSKLLQTST STEKMYKIDD HVACAVAGIM SDANILINTA RVQAQRYTFS
101 YQEPMPVEQL VQSLCDTKQG YTQFGGLRPF GVSFLFAGWD KNYGFQLYMS
151 DPSGNYGGWK ATAIGANNQA AQSMLKQDYK DDVTREDAVK LALKALSKTM
201 DSTSLTSEKL ELAEVYLLPS GKVKYQVHSP ESLNRLLTES GLTQPAAETS

Spot No.: **101**

NCBI accession No.: **gi|27449248** Species: *Hevea brasiliensis*

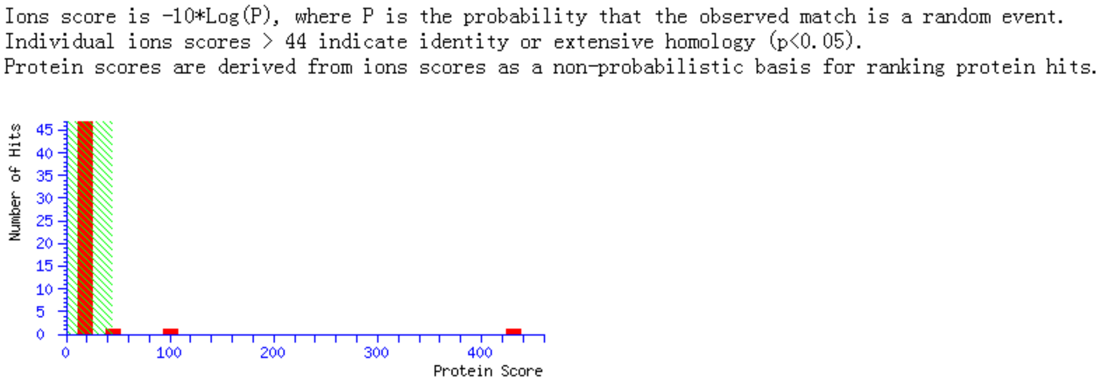
PFF score: [431] Protein name: ascorbate peroxidase

Matched peptides No.: [5] Sequence coverage %: [32]

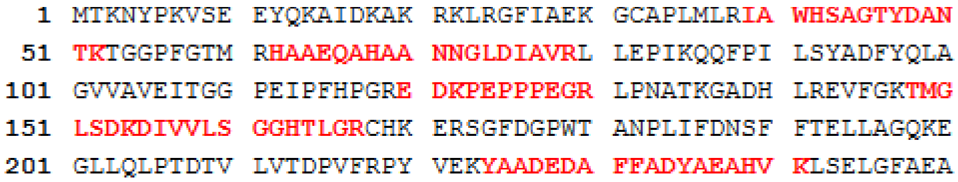
Matched sequences: R.EDKPEPPPEGR.L;
R.IAWHSAGTYDANTK.T;
R.HAAEQAHAANNGLDIAVR.L;
K.YAADEDAFFADYAEAHVK.L;
K.TMGLSDKDIVVLSGGHTLGR.C + Oxidation (M)

Calculated Mr: **27526** Calculated *p*I: **5.78**

Probability Based Mowse Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Matched peptide sequences: shown in Bold Red:


1 MTKNYPKVSE EYQKAIDKAK RKLRGFIAEK GCAPLMLR**IA** **WHSAGTYDAN**
51 **TK**TGGPFGTM R**HAAEQAHAA** **NNGLDIAVR**L LEPIKQQFPI LSYADFYQLA
101 GVVAVEITGG PEIPFHPGR**E** **DKPEPPPEGR** LPNATKGADH LREVFGK**TMG**
151 **LSDKDIVVLS** **GGHTLGR**CHK ERSGFDGPWT ANPLIFDNSF FTELLAGQKE
201 GLLQLPTDTV LVTDPVFRPY VEK**YAADEDA** **FFADYAEAHV** **K**LSELGFAEA

Spot No.: **102**

NCBI accession No.: **gi|211906460** Species: *Gossypium hirsutum*

PFF score: [193] Protein name: triosephosphate isomerase

Matched peptides No.: [3] Sequence coverage %: [18]

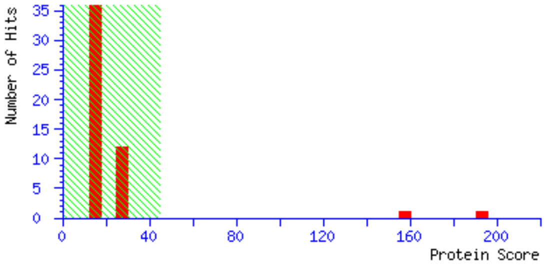
Matched sequences: K.FFVGGNWK.C;

K.VIACIGETLEQR.E;
K.ELAAQPDVDGFLVGGASLKPEFIDIIK.S

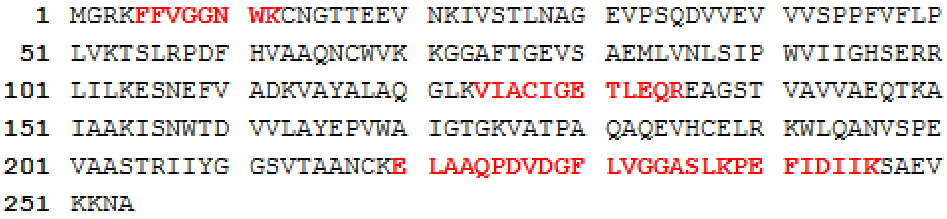
Calculated Mr: **27472** Calculated *p*I: **6.00**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:



```
  1 MGRKFFVGGN WKCNGTTEEV NKIVSTLNAG EVPSQDVVEV VVSPPFVFLP
 51 LVKTSLRPDF HVAAQNCWVK KGGAFTGEVS AEMLVNLSIP WVIIGHSERR
101 LILKESNEFV ADKVAYALAQ GLKVIACIGE TLEQREAGST VAVVAEQTKA
151 IAAKISNWTD VVLAYEPVWA IGTGKVATPA QAQEVHCELR KWLQANVSPE
201 VAASTRIIYG GSVTAANCKE LAAQPDVDGF LVGGASLKPE FIDIIKSAEV
251 KKNA
```

Spot No.: 103

NCBI accession No.: gi|38122474 Species: ***Hevea Brasiliensis***

Protein name： rubber elongation factor

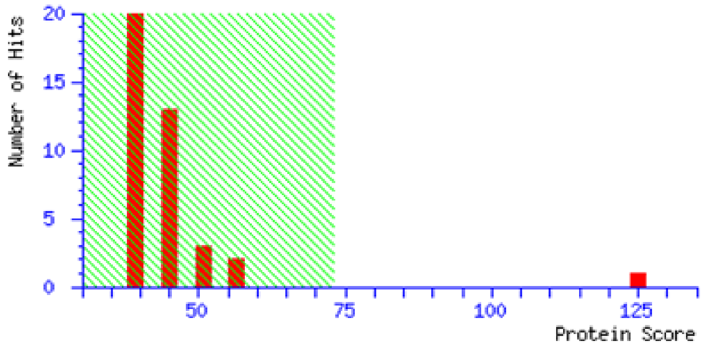
PMF score: **125** Sequence coverage %: **68**

Matched peptides No.: **11** Total peptides No.: **50**

Calculated Mr: **19570** Calculated *p*I: **5.06**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 M**AEGEEEVNI QEEANKGEEN PQEEANIQEE TNKGEENIQE EANIEEEANK**
51 **EEESLKYLDF VQAATVYAR**A SFSK**LYLFAK** DK**SGPFKPGV NTVESRFKSV**
101 **VRPVYNKFQP VPNK**VLK**FAD RRVDAYVTVL DR**IVPPIVKR ASIQAYSVAP
151 GAALAVASYL PLHTKRLSKV LYGDG

Spot No.: 104

NCBI accession No.: gi|3451147   Species: *Hevea Brasiliensis*

Protein name： chitinase

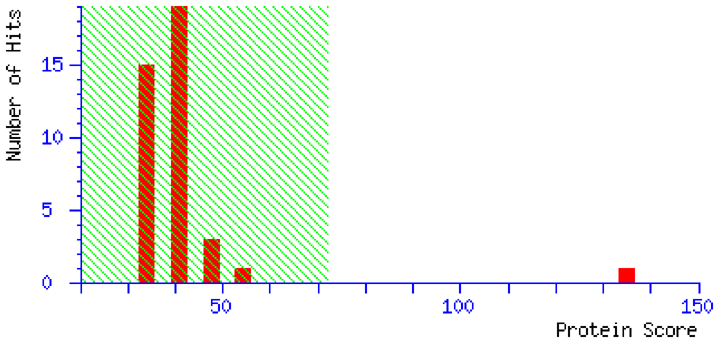
PMF score: **135**   Sequence coverage %: **66**

Matched peptides No.: **19**   Total peptides No.: **77**

Calculated Mr: **34138**   Calculated *p*I: **8.72**

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 73 are significant (p<0.05).



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

1 MAKRTQAILL LLLAISLIMS SSHVDGGGIA IYWGQNGNEG TLTQTCSTR**K**
51 **YSYVNIAFLN KFGNGQTPQI NLAGHCNPAA GGCTIVSNGI RSCQIQGIKV**
101 **MLSLGGGIGS YTLASQADAK NVADYLWNNF LGGKSSSRPL GDAVLDGIDF**
151 **DIEHGSTLYW DDLAR**YLSAY SKQGK**KVYLT AAPQCPFPDR** YLGTALNTGL
201 FDYVWVQFYN NPPCQYSSGN INNIINSWNR **WTTSINAGKI FLGLPAAPEA**
251 **AGSGYVPPDV LISRILPEIK** KSPK**YGGVML WSKFYDDKNG YSSSIRDSVL**
301 **FLHSEKCMTV L**

Spot No.:105

NCBI accession No.: gi|157831407   Species: *Hevea brasiliensis*

Protein name：Chain A, Crystal Structures Of Hevamine

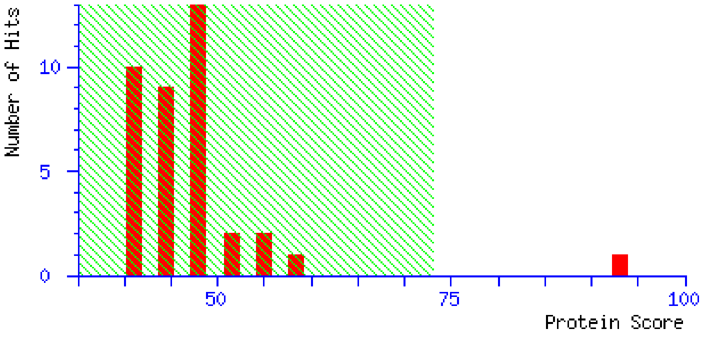
PMF score: 93   Sequence coverage %:51

Matched peptides No.: 13   Total peptides No.: 76

Calculated Mr: 29874   Calculated *p*I: 8.44

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold red:

1 GGIAIYWGQN GNEGTLTQTC STR**KYSYVNI** **AFLNK**FGNGQ TPQINLAGHC
51 NPAAGGCTIV SNGIR**SCQIQ** **GIKVMLSLGG** **GIGSYTLASQ** **ADAKNVADYL**
101 **WNNFLGGKSS** **SRPLGDAVLD** **GIDFDIEHGS** **TLYWDDLARY** LSAYSKQGK**K**
151 **VYLTAAPQCP** **FPDR**YLGTAL NTGLFDYVWV QFYNNPPCQY SSGNINNIIN
201 SWNRWTTSIN AGK**IFLGLPA** **APEAAGSGYV** **PPDVLISRIL** PEIKKSPK**YG**
251 **GVMLWSKFYD** **DK**NGYSSSIL DSV

Spot No.:106

NCBI accession No.: gi|157831407 Species: *Hevea brasiliensis*

Protein name：Chain A, Crystal Structures Of Hevamine

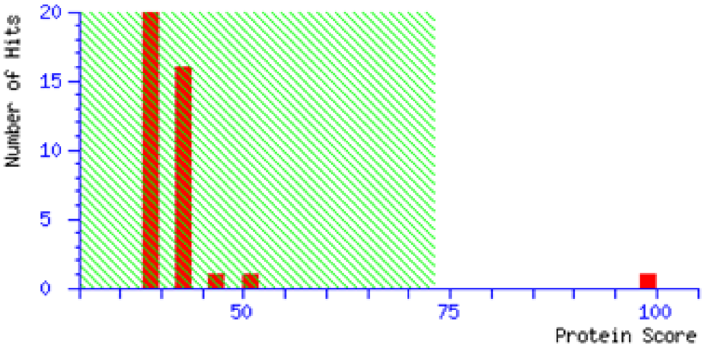
PMF score: 99 Sequence coverage %:42

Matched peptides No.: 12 Total peptides No.: 47

Calculated Mr: 29874 Calculated *p*I: 8.44

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 GGIAIYWGQN GNEGTLTQTC STR**KYSYVNI** **AFLNK**FGNGQ TPQINLAGHC
51 NPAAGGCTIV SNGIR**SCQIQ** **GIKVMLSLGG** **GIGSYTLASQ** **ADAKNVADYL**
101 **WNNFLGGKSS** **SRPLGDAVLD** **GIDFDIEHGS** **TLYWDDLAR**Y LSAYSKQGK**K**
151 **VYLTAAPQCP** **FPDR**YLGTAL NTGLFDYVWV QFYNNPPCQY SSGNINNIIN
201 SWNRWTTSIN AGKIFLGLPA APEAAGSGYV PPDVLISRIL PEIKKSPK**YG**
251 **GVMLWSKFYD** **DK**NGYSSSIL DSV

Spot No.:107

NCBI accession No.: gi|3451147 Species: *Hevea Brasiliensis*

Protein name： chitinase

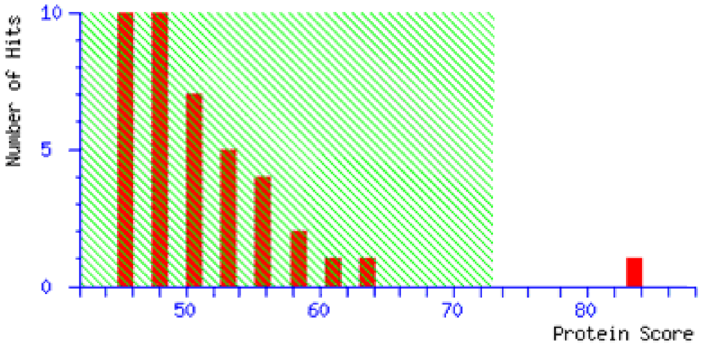
PMF score: **83** Sequence coverage %: **48**

Matched peptides No.: **12** Total peptides No.: **81**

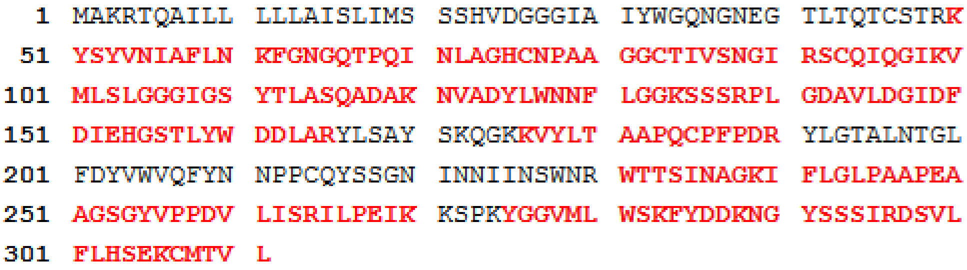
Calculated Mr: **34138** Calculated *p*I: **8.72**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red



1 MAKRTQAILL LLLAISLIMS SSHVDGGGIA IYWGQNGNEG TLTQTCSTR**K**
51 **YSYVNIAFLN KFGNGQTPQI NLAGHCNPAA GGCTIVSNGI RSCQIQGIKV**
101 **MLSLGGGIGS YTLASQADAK NVADYLWNNF LGGKSSSRPL GDAVLDGIDF**
151 **DIEHGSTLYW DDLAR**YLSAY SKQGK**KVYLT AAPQCPFPDR** YLGTALNTGL
201 FDYVWVQFYN NPPCQYSSGN INNIINSWNR **WTTSINAGKI FLGLPAAPEA**
251 **AGSGYVPPDV LISRILPEIK** KSPK**YGGVML WSKFYDDKNG YSSSIRDSVL**
301 **FLHSEKCMTV L**

Spot No.: **108**

NCBI accession No.: **gi|2493895** Species: *Citrullus lanatus*

PFF score: [89]

Protein name: cysteine synthase

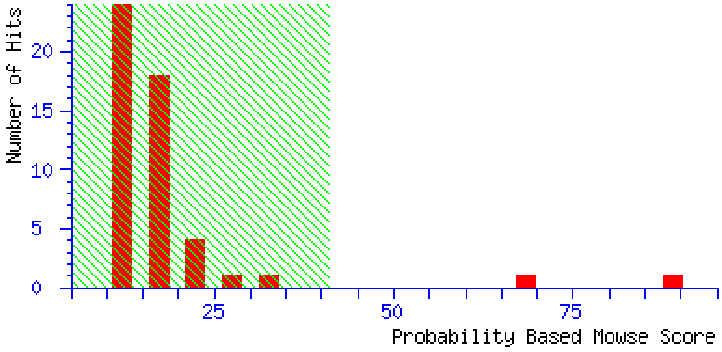
Matched peptides No.: [1] Sequence coverage %: [ ]

Matched sequences: K.EGLLVGISSGAAAAAAIR.I

Calculated Mr: **34495** Calculated *p*I: **6.26**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 41 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MADAKSTIAK DVTELIGNTP LVYLNRVVDG CVARVAAKLE MMEPCSSVKD RIGYSMISDA

61 ENKGLITPGE SVLIEPTSGN TGIGLAFIAA AKGYRLIICM PASMSLERRT ILRAFGAELV

121 LTDPARGMKG AVQKAEEIKA KTPNSYILQQ FENPANPKIH YETTGPEIWR GSGGKIDALV

181 SGIGTGGTVT GAGKYLKEQN PNIKLYGVEP VESAILSGGK PGPHKIQGIG AGFIPGVLDV

241 NLLDEVIQVS SEESIETAKL LAL**KEGLLVG ISSGAAAAAA IRI**AKRPENA GKLIVAVFPS

301 FGERYLSTVL FESVKRETEN MVFEP

Spot No.: **109**

NCBI accession No.: gi|114199044 Species: *Malus x domestica*

PFF score: [163]

Protein name: caffeic acid O-methyltransferase

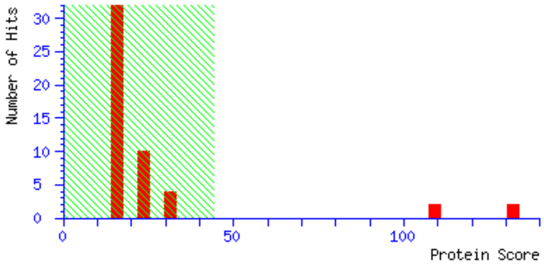
Matched peptides No.: [2] Sequence coverage %: [13]

Matched sequences: R.TEKEFEALAK.G;
K.AYGMTAFEYHGTDPR.F;
K.AYGMTAFEYHGTDPR.F + Oxidation (M);
K.WICHDWSDEHCLK.F

Calculated Mr: **39811** Calculated *p*I: **5.39**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MGSTSESQSN SLTHTEDEAF LFAMQLCSAS VLPMVLKSAV ELDLLELMAK
51 AGPGAAISPS ELAAQLSTQN PEAPVMLDRM LRLLASYSVL NCTLRTLPDS
101 SVERLYSLAP VCKYLTKNAD GVSVAPLLLM NQDKVLMESW YHLKDAVLDG
151 GIPFNK**AYGM** **TAFEYHGTDP** **R**FNKVFNRGM SDHSTMSMKK ILEDYKGFEG
201 LNSIVDVGGG TGATVNMIVS KYPSIKGINF DLPHVIGDAP TYPGVEHVGG
251 DMFASVPKAD AIFMK**WICHD** **WSDEHCLK**FL KNCYEALPAN GKVIIAECIL
301 PEAPDTSLAT KNTVHVDIVM LAHNPGGKER **TEKEFEALAK** GAGFTGFARL
351 VALTTLGSWN STSN

Spot No.: 110

NCBI accession No.: gi|14423688 Species: *Hevea brasiliensis*

Protein name： Enolase 1

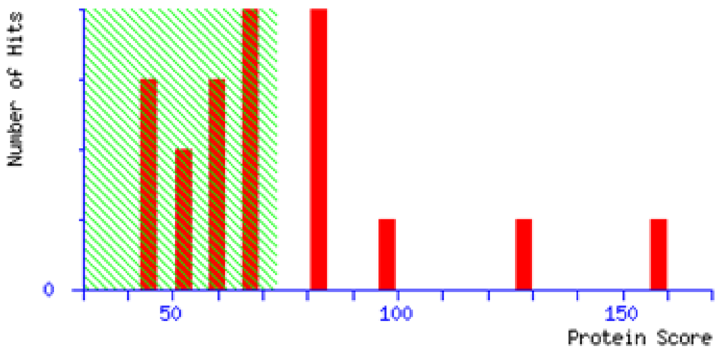
PMF score: 158 Sequence coverage %: 53

Matched peptides No.:18 Total peptides No.: 56

Calculated Mr: 48028 Calculated *p*I: 5.57

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold red

1 MAITIVSVRA R**QIFDSR**GNP TVEADVK**LSD GYLARAAVPS GASTGIYEAL**
51 **ELR**DGGSDYL GKGVSK**AVEN VNIIIGPALV GK**DPTDQVGI DNFMVQQLDG
101 TVNEWGWCKQ KLGANAILAV SLAVCKAGAH VKGIPLYEHI ANLAGNKNLV
151 LPVPAFNVIN GGSHAGNK**LA MQEFMILPVG ASSFK**EAMK**M GAEVYHHLK**S
201 VIKK**KYGQDA TNVGDEGGFA PNIQENK**EGL ELLKTAIAKA GYTGK**VVIGM**
251 **DVAASEFYGS DQTYDLNFK**E ENNNGSQKIS GEALKDLYK**S FVAEYPIVSI**
301 **EDPFDQDDWA HYAK**LTSEIG EK**VQIVGDDL LVTNPK**RVEK AIKEKACNAL
351 LLK**VNQIGSV TESIEAVK**MS K**RAGWGVMAS HRSGETEDTF IADLSVGLAT**
401 **GQIK**TGAPCR SERLAK**YNQL LRIEEELGSE AVYAGANFRK PVEPY**

Spot No.: 111

NCBI accession No.: gi|14423688 Species: *Hevea brasiliensis*

Protein name： Enolase 1

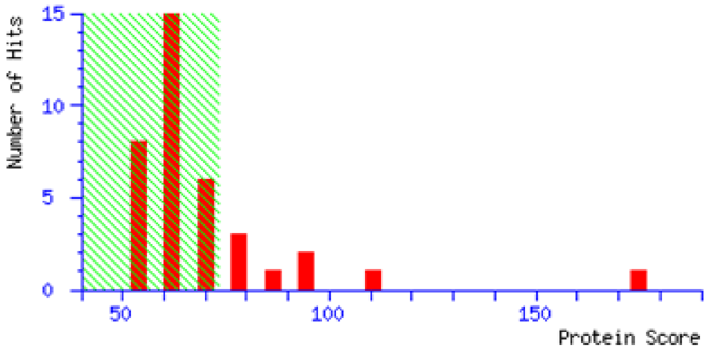
PMF score: 175 Sequence coverage %: 59

Matched peptides No.:25 Total peptides No.: 76

Calculated Mr: 48028 Calculated *p*I: 5.57

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 73 are significant ($p<0.05$).



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

1 **MAITIVSVR**A R**QIFDSR**GNP TVEADVK**LSD** **GYLARAAVPS** **GASTGIYEAL**
51 **ELR**DGGSDYL GKGVSKAVEN VNIIIGPALV GKDPTDQVGI DNFMVQQLDG
101 TVNEWGWCKQ KLGANAILAV SLAVCKAGAH VK**GIPLYEHI** **ANLAGNK**NLV
151 LPVPAFNVIN GGSHAGNK**LA** **MQEFMILPVG** **ASSFK**EAMK**M** **GAEVYHHLK**S
201 VIKK**KYGQDA** **TNVGDEGGFA** **PNIQENK**EGL ELLKTAIAKA GYTGK**VVIGM**
251 **DVAASEFYGS** **DQTYDLNFK**E ENNNGSQKIS GEALKDLYK**S** **FVAEYPIVSI**
301 **EDPFDQDDWA** **HYAKLTSEIG** **EKVQIVGDDL** **LVTNPK**RVEK AIKEKACNAL
351 LLK**VNQIGSV** **TESIEAVK**MS KR**AGWGVMAS** **HRSGETEDTF** **IADLSVGLAT**
401 **GQIKTGAPCR** **SERLAKYNQL** **LRIEEELGSE** **AVYAGANFRK** **PVEPY**

Spot No.: 112

NCBI accession No.: gi|226897734   Species: *Thalictrum flavum*

Protein name：norcoclaurine 6-O-methyltransferase

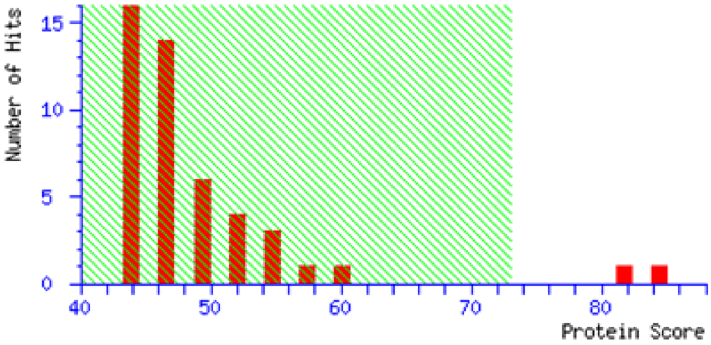
PMF score: 85   Sequence coverage %: 45

Matched peptides No.:9   Total peptides No.:100

Calculated Mr: 25178   Calculated *p*I:6.05

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold red:

1 **MEMINKENLS** **SQAK**LWNFIY GFADSLVLKS AVQLDLANII HNHGSPMTLS
51 ELSLHLPSQP VNQDALYRVL R**YLVHMKLFT** **KSSIDGELR**Y GLAPPAKFLV
101 K**GWDKCMLGA** **ILTITDKDFM** **APWHYLK**EGI LNDGSTSTAF EK**ALGTNIWD**
151 **YMAEHPEK**NQ LFNEGMANDT RLIMSALVK**E** **CSSMFDGITT** **IVDVGGGTGT**
201 **AVRNIAK**AFP HIKCTVYDLP HVIAD

Spot No.: **113**

NCBI accession No.: **gi| 255565071** Species: *Ricinus communis*

PFF score: [51]

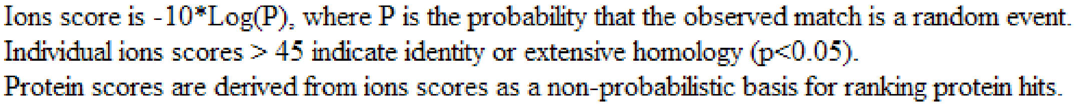
Protein name: conserved hypothetical protein

Matched peptides No.: [2] Sequence coverage %: [2]

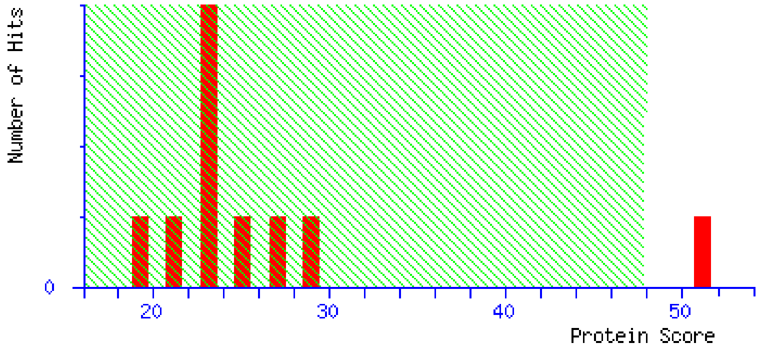
Matched sequences: R.LQVEELVFER.S; R.LQVEELVFER.S

Calculated Mr: **54103** Calculated *p*I: **5.53**

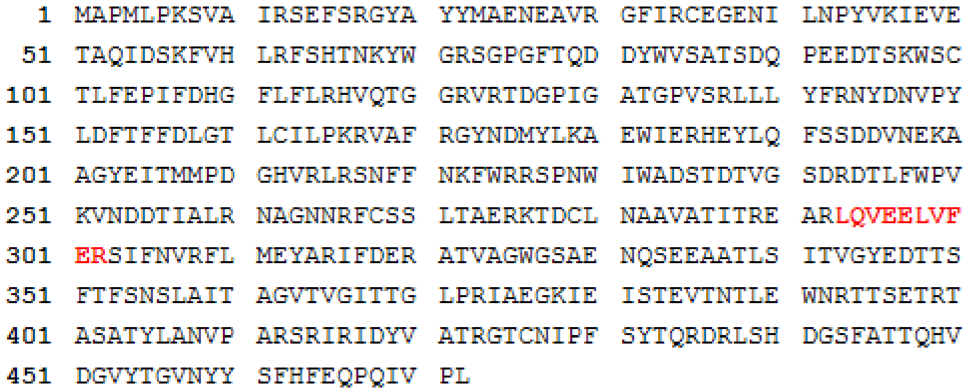
Probability Based Mowse Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:



```
  1 MAPMLPKSVA IRSEFSRGYA YYMAENEAVR GFIRCEGENI LNPYVKIEVE
 51 TAQIDSKFVH LRFSHTNKYW GRSGPGFTQD DYWVSATSDQ PEEDTSKWSC
101 TLFEPIFDHG FLFLRHVQTG GRVRTDGPIG ATGPVSRLLL YFRNYDNVPY
151 LDFTFFDLGT LCILPKRVAF RGYNDMYLKA EWIERHEYLQ FSSDDVNEKA
201 AGYEITMMPD GHVRLRSNFF NKFWRRSPNW IWADSTDTVG SDRDTLFWPV
251 KVNDDTIALR NAGNNRFCSS LTAERKTDCL NAAVATITRE ARLQVEELVF
301 ERSIFNVRFL MEYARIFDER ATVAGWGSAE NQSEEAATLS ITVGYEDTTS
351 FTFSNSLAIT AGVTVGITTG LPRIAEGKIE ISTEVTNTLE WNRTTSETRT
401 ASATYLANVP ARSRIRIDYV ATRGTCNIPF SYTQRDRLSH DGSFATTQHV
451 DGVYTGVNYY SFHFEQPQIV PL
```

Spot No.: **114**

NCBI accession No.: **gi|1346735** Species: *Ricinus communis*

PFF score: [96]

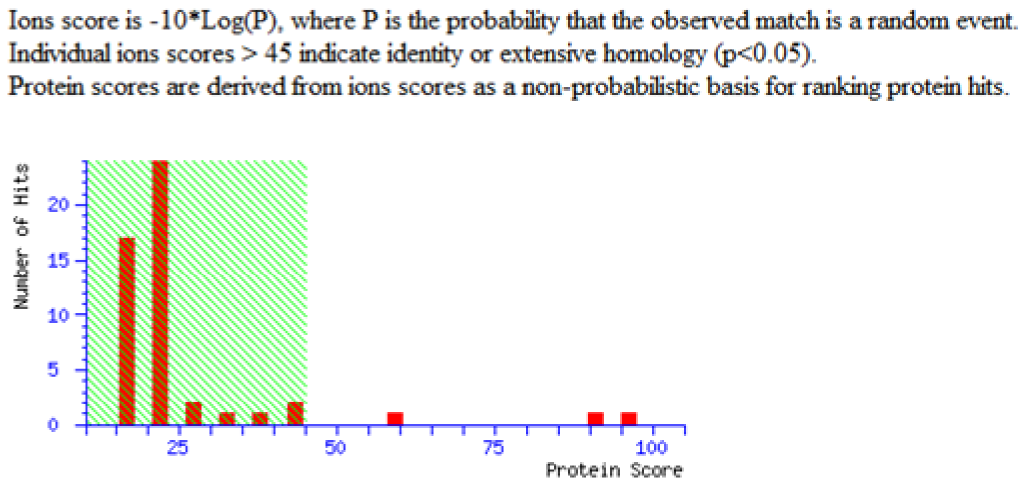
Protein name: 2,3-bisphosphoglycerate-independent phosphoglycerate mutase

Matched peptides No.: [1] Sequence coverage %: [2]

Matched sequences: K.LPSHYLVSPPEIER.T

Calculated Mr: **57374** Calculated *p*I: **5.60**

Probability Based Mowse Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

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

1 GEFTWKLADH PKLPKGKTIA MVVLDGWGEA KPDQYNCIHV AETPTMDSFK

51 KTAPERWRLI KAHGTAVGLP TEDDMGNSEV GHNALGAGRI YAQGAKLVDL

101 ALASGKIYEG EGFKYVKECF DKGTLHLIGL LSDGGVHSRL DQLQLLLKGA

151 AEHGAKRIRV HVLTDGRDVI DGTSVGFAET LEKDLENLRE KGVDAQVASG

201 GGRMYVTMDR YENDWNVVKR GWDAQVLGEA PYKFKSAVEA IKKLREEPKA

251 NDQYLPPFVI VDENGKPVGP IVDGDAVVTI NFRADRMVML AKALEYENFD

301 TFDRVRFPKI HYAGMLQYDG ELK**LPSHYLV** **SPPEIER**TSG EYLVHNGVHT

351 FACSETVKFG HVTFFWNGNR SGYFNPEMEE YVEIPSDVGI TFNVQPKMKA

401 IEIAEKARDA ILSGKFQQVR VNIPNGDMVG HTGDVEATVV GCKAADEAVK

451 MIIDAIEQVG GIYVVTADHG NAEDMVKRDK SGKPMADKSG KIQILTSHTL

501 QPVPIAIGGP GLTPGVRFRS DIPTGGLANV AATVMNLHGF EAPSDYEPTL

551 IEAVDN

Spot No.: 115

NCBI accession No.: gi|255565836 Species: *Ricinus communis*

Protein name： eukaryotic translation elongation factor, putative

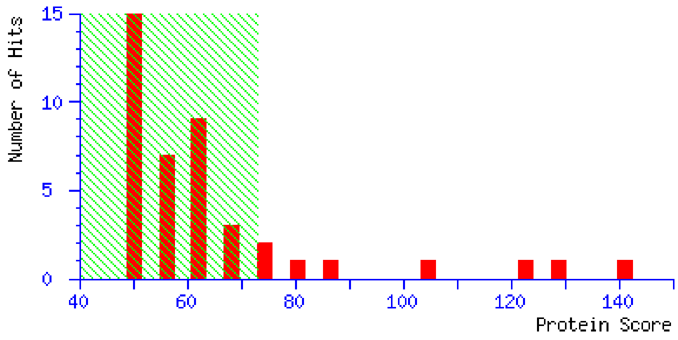
PMF score: 141 Sequence coverage %: 40

Matched peptides No.:36 Total peptides No.:121

Calculated Mr: 94981 Calculated *p*I:5.87

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold red:

1 MVK**FTAEELR** RIMDYKHNIR **NMSVIAHVDH** **GKSTLTDSLV** **AAAGIIAQEV**
51 **AGDVR**MTDTR QDEAERGITI KSTGISLYYE MTDEALKSFK GERQGNEYLI
101 NLIDSPGHVD FSSEVTAALR ITDGALVVVD CIEGVCVQTE TVLR**QALGER**
151 **IRPVLTVNK**M DRCFLELQVD GEEAYQTFSR VIENANVIMA TYEDPLLGDC
201 QVYPEK**GTVA** **FSAGLHGWAF** **TLTNFAK**MYA SKFGVDESKM MER**LWGENFF**
251 **DPATK**KWTSK **NTGSPTCKRG** **FVQFCYEPIK** **QIINTCMNDQ** **K**DKLWPMLQK
301 **LGVTMKSDEK** **ELMGK**ALMKR VMQTWLPASS ALLEMMIFHL PSPAKAQR**YR**
351 **VENLYEGPLD** **DPYATAIRNC** **DPEGPLMLYV** **SK**MIPASDKG R**FFAFGR**VFA
401 GKVSTGLK**VR** **IMGPNYVPGE** **K**KDLYVK**SVQ** **RTVIWMGK**KQ ETVEDVPCGN
451 TVALVGLDQF ITKNATLTNE KEVDAHPIRA MK**FSVSPVVR** VAVQCKVASD
501 LPKLVEGLKR LAKSDPMVVC TIEESGEHII AGAGELHLEI CLK**DLQDDFM**
551 **GGAEIIKSDP** **VVSFR**ETVLE K**SCRVVMSK**S PNKHNRLYME ARPMEEGLAE
601 AIDEGR**IGPR** **DDPK**ARAK**IL** **SEEFGWDKDL** **AK**KIWCFGPE TTGPNMVVDM
651 CKGVQYLNEI K**DSVVAGFQW** **ASKEGALAEE** **NMRGICFEVC** **DVVLHADAIH**
701 **RGGGQVIPTA** **RRVIYASQLT** **AKPR**LLEPVY LVEIQAPEQA LGGIYSVLNQ
751 KR**GHVFEELQ** **RPGTPLYNIK** AYLPVIESFG FSGTLRAATS GQAFPQCVFD
801 HWDMMSSDPM EPGSQAANLV TEIRKRKGLK EQMTPLSEFE DKL

Spot No.: **116**

NCBI accession No.: **gi|6707018** Species: *Hevea brasiliensis*

Protein name: latex protein allergen Hev b 7

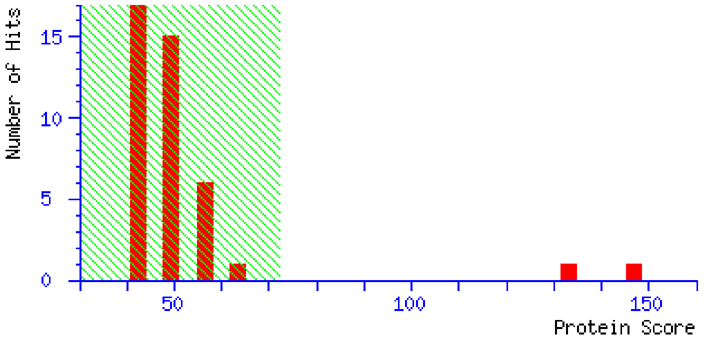
PMF score: **147** Sequence coverage %:**64**

Matched peptides No.: **17** Total peptides No.: **60**

Calculated Mr: **43107** Calculated *p*I: **5.00**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MATGSTPLTQ GKK**ITVLSID** **GGGIRGIIPG** **IILASLESKL** **QDLDGPDARI**
51 **ADYFDIIAGT** **STGGLITTML** **TAPNEDK**KPM YQAKDIK**DFY** **LENCPK**IFPK
101 ESR**DNYDPIH** **SIGPIYDGEY** **LR**ELCNNLLK DLTVK**DTLTD** **VIIPTFDIKL**
151 **LLPVIFSSDD** **AK**CNALKNAR **LADVCISTSA** **APVLLPAHSF** **TTEDDKNIHT**
201 **FELIDGGVAA** **TNPTLLALTH** **IRNEIIR**QNP RFIGANLTES KSRLVLSLGT
251 GKSEYKEKYN ADMTSKWRLY NWALYNGNSP AVDIFSNASS DMVDFHLSAL
301 FK**SLDCEDYY** **LRIQDDTLTG** **EESSGHIATE** **ENLQRLVEIG** **TELLEK**QESR
351 **INLDTGRLES** **IPGAPTNEAA** **IAK**FAK**LLSE** **ER**KLRQLK

Spot No.: **117**

NCBI accession No.: **gi|51315784** Species: *Hevea brasiliensis*

PFF score: [59]

Protein name: Esterase

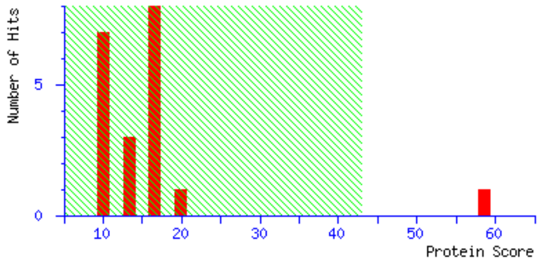
Matched peptides No.: [1] Sequence coverage %: [4]

Matched sequences: K.AAAFYPLNPPYGETFFHR.S

Calculated Mr: **43871** Calculated *p*I: **5.00**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 43 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MEFPETNNNP IITLSFLLCM LSLAYASETC DFPAIFNFGD SNSDTGGK**AA**
51 **AFYPLNPPYG ETFFHR**STGR YSDGRLIIDF IAESFNLPYL SPYLSSLGSN
101 FKHGADFATA GSTIKLPTTI IPAHGGFSPF YLDVQYSQFR QFIPRSQFIR
151 ETGGIFAELV PEEYYFEKAL YTFDIGQNDL TEGFLNLTVE EVNATVPDLV
201 NSFSANVKKI YDLGARTFWI HNTGPIGCLS FILTYFPWAE KDSAGCAKAY
251 NEVAQHFNHK LKEIVAQLRK DLPLATFVHV DIYSVKYSLF SEPEKHGFEF
301 PLITCCGYGG KYNFSVTAPC GDTVTADDGT KIVVGSCACP SVRVNWDGAH
351 YTEAANEYFF DQISTGAFSD PPVPLNMACH KTESLRTLAS V

Spot No.: 118

NCBI accession No.: **gi|38122474** Species: *Hevea brasiliensis*

Protein name： rubber elongation factor

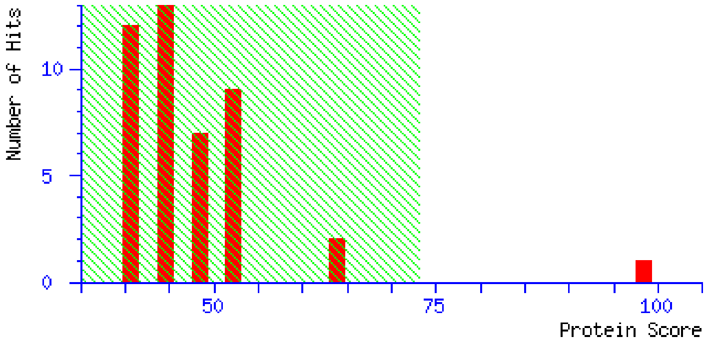
PMF score: **98** Sequence coverage %: **57**

Matched peptides No.: **9** Total peptides No.: **44**

Calculated Mr: **19570** Calculated *p*I: **5.06**

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 73 are significant ($p<0.05$).



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

1 M**AEGEEEVNI** **QEEANKGEEN** **PQEEANIQEE** **TNKGEENIQE** **EANIEEEANK**
51 **EEESLKYLDF** **VQAATVYAR**A SFSK**LYLFAK** DKSGPFKPGV NTVESRFK**SV**
101 **VRPVYNKFQP** **VPNK**VLKFAD R**RVDAYVTVL** **DR**IVPPIVKR ASIQAYSVAP
151 GAALAVASYL PLHTKRLSKV LYGDG

Spot No.: **119**

NCBI accession No.: **gi| 3023685** Species: *Alnus glutinosa*

PFF score: [51]

Protein name: **Enolase; AltName: Full=2-phospho-D-glycerate hydro-lyase; AltName: Full=2-phosphoglycerate dehydratase**

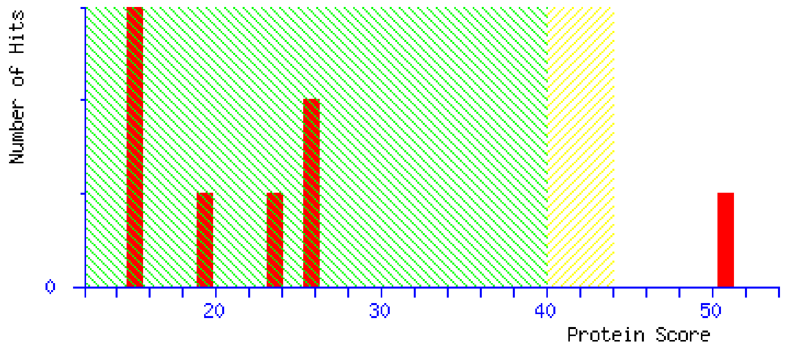
Matched peptides No.: [1] Sequence coverage %: [3]

Matched sequences: R.IEEELGSEAVYAGANFR.T

Calculated Mr: **47796** Calculated *p*I: **5.41**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 40 indicate peptides with significant homology.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEITHIKAR QIFDSRGNPT VEAEVTTANG VVSRAAVPSG ASTGVYEALE
51 LRDGGSDYLG KGVLKAVDNV NKIIGPALIG KDATEQTAID IDFMFQQLDG
101 TVNEWGWCKQ KLGANAILAV SLAVCKAGAS VKKIPLYKHI ANLAGNPKLV
151 LPVPAFNVIN GGSHAGNKLA MQEFMILPVG ASSFKEAMKM GVEVYHHLKA
201 VIKKKYGQDA TNVGDEGGFA PNIQENKEGL ELLKTAIAKA GYVVIGMDVA
251 ASEFYEKDKD ITNFKEENND GSQKISADQL KDLYKSFVDE YPIVSIEDPF
301 DQDDWEHYSK LTAEIGEKVQ IVGDDLLVTN PKRVEKAIKE KACNALLLKV
351 NQIGSVTESI EAVKMSKRAG WGVMAHRSGE TEDTFIADLS VGLATGQIKT
401 GAPCRSERLA KYNQLLR**IEE** **ELGSEAVYAG** **ANFR**TPVEPY

Spot No.: 120

NCBI accession No.: **gi**| 351723039 Species: *Glycine max*

Protein name： uncharacterized protein LOC100305754 precursor

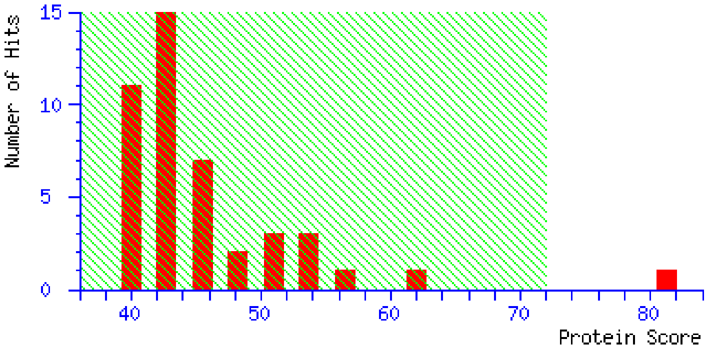
PMF score: **81** Sequence coverage %: **51**

Matched peptides No.: **8** Total peptides No.: **28**

Calculated Mr: **21968** Calculated *p*I: **4.83**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 **MSMRSIGTSL** **SLMVWLVIAT** **SALAK**SDNPP VLDTQGNPLE PGK**DYYIKPA**
51 **ITDVGGR**VTL LSRNNPCPLY VGQENSDAAE GLPLFFTPFA EEDDVVKVNR
101 DFKLTFSAAS ICVQGTNWNL AEK**DSESGRR** **LIAASGRDDY** **FRITETPIKG**
151 **SYYIGWCPTD** **VCPFCRFDCG** **IVGGLR**ENGK **ILLALDGNVL** **PVVFEK**AY

Spot No.: **121**

NCBI accession No.: **gi| 255554865** Species: *Ricinus communis*

PFF score: [55]

Protein name: lactoylglutathione lyase, putative

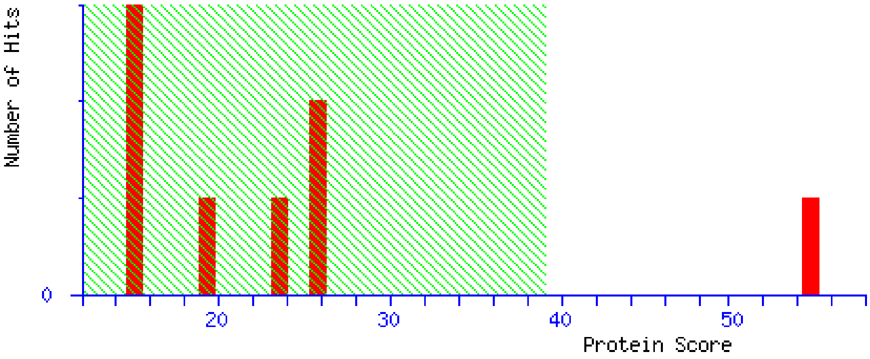
Matched peptides No.: [1] Sequence coverage %: [3]

Matched sequences: K.FYTECFGMK.L

Calculated Mr: **31641** Calculated *p*I: **7.63**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 40 indicate peptides with significant homology.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

```
  1  MAAEATAPNA  DVLEWPKKDK  RRLLHAVYRV  GDLDRTIKFY  TECFGMKLLR
 51  KRDIPEEKYS  NAFLGFGPEE  TNFVVELTYN  YGVTSYDIGT  GFGHFAIATQ
101  DVYKLVEEVL  AKGGAVTREP  GPVKGGTTVI  AFVKDPDGYI  FELIQRGPTP
151  EPLCQVMLRV  GDLDRSIRFY  EKALGMKLLR  KVDKPEYKYT  LAMMGYADEY
201  ETTVLELTYN  YGVTEYTKGN  AYAQVAISTD  DVYKSAEVVN  LVTQELGGKI
251  TRQPGPIPGL  NTKITSFLDP  DGWKTKRKRR
```

Spot No.: **122**

NCBI accession No.: **gi|118485535** Species: *Populus trichocarpa*

PFF score: [83]

Protein name: unknown

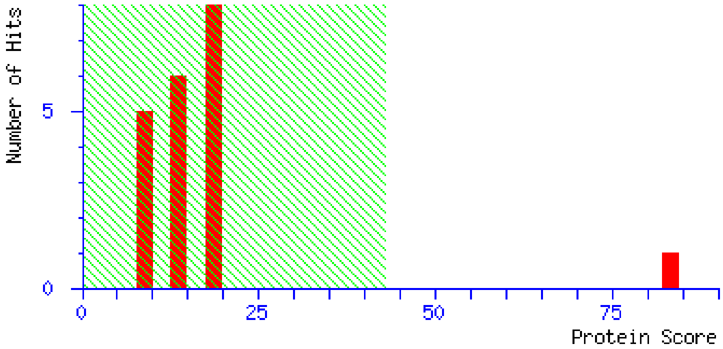
Matched peptides No.: [1] Sequence coverage %: [8]

Matched sequences: K.VATPAQAQEVHLELR.K

Calculated Mr: **18429** Calculated *p*I: **5.59**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MLVNLGIPWV ILGHSERRSL LNESNEFVGD KVAYALSLGL KVIACVGETL
51 QQRESGSTMA VVAAQTKAIA ANVSYWDNVV MAYEPVWAIG TGK**VATPAQA**
101 **QEVHLELR**KW FHDNVGAEVA ASTRIIYGGS VNGANCKELA GQPDVDGFLV
151 GGASLKPEFI DIIKSATVKS QL

Spot No.: **123**

NCBI accession No.: **gi|15225839** Species: *Arabidopsis thaliana*

Protein name: endopeptidase/ peptidase/ threonine-type endopeptidase

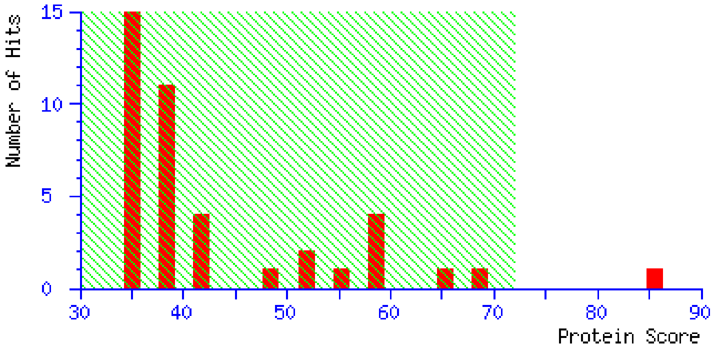
PMF Mascot score: **86** Sequence coverage %: **40**

Matched peptides No.: **14** Total peptides No.: **56**

Calculated Mr: **27645** Calculated *p*I: **5.93**

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 73 are significant ($p<0.05$).



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

1 MSSIGTGYDL SVTTFSPDGR **VFQIEYAAK**A VDNSGTVVGI KCKDGIVMGV

51 EKLIASK**MML** **PGSNRRIHSV** **HRHAGMAVAG** **LAADGRQIVA** **RAKSEARSYE**

101 **SVYGDAVPVK** ELSERVASYV HLCTLYWWLR PFGCGVILGG YDR**DGPQLYM**

151 **IEPSGISYRY** **FGAAIGK**GKQ AAKTEIEKLN LSEMTCKEGV IEVAKIIYKL

201 HDEAK**DKAFE** **LEMSWICEES** **K**REHQKVPDD LLEEAKTAAK TALEEMDAD

Spot No.: **124**

NCBI accession No.: **gi| 10862818** Species: *Hevea brasiliensis*

Protein name: IgE-binding protein Mn SOD

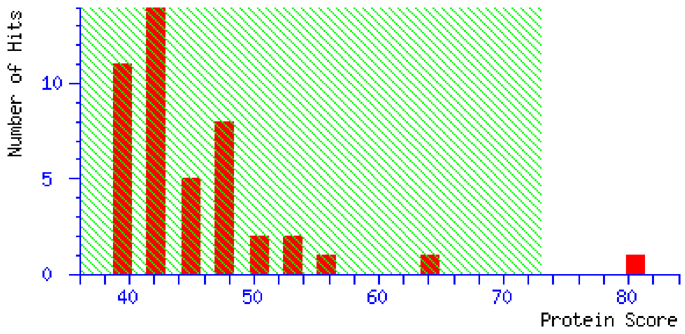
PMF Mascot score: **81** Sequence coverage %: **37**

Matched peptides No.: **5** Total peptides No.: **8**

Calculated Mr: **22958** Calculated *p*I: **6.06**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 QTFSLPDLPY DYGALEPAIS GEIMQLHHQK HHQTYITNYN KALEQLNDAI
51 EKGDSAAVVK **LQSAIK**FNGG GHVNHSIFWK **NLAPVREGGG** **ELPHGSLGWA**
101 **IDADFGSLEK** LIQLMNAEGA ALRGSGWVWL ALDKELK**KLV** **VETTANQDPL**
151 **VTK**GPTLVPL LGIDVWEHAY YLQYK**NVRPD** **YLKNIWKVMN** **WKYASEVYAK**
201 ECPSS

Spot No.: **125**

NCBI accession No.: **gi|1170781** Species: *Glycine max*

PFF score: [51]

Protein name: Glutathione S-transferase 3

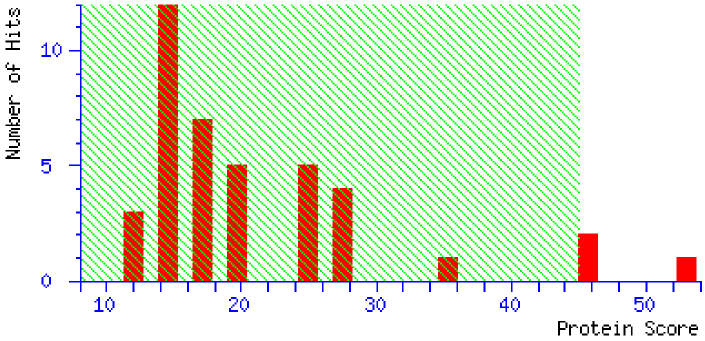
Matched peptides No.: [1] Sequence coverage %: [5]

Matched sequences: K.SPLMPSDPYKR.S+Oxidation (M)

Calculated Mr: **26112** Calculated *p*I: **5.58**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MSDEVVLLDT WASMYGMRAR IALAEKGVRY EYKEENLMNR SPLLLQMNPI
51 HKKIPVLIHN GKPICESAII VQYIDEVWND K**SPLMPSDPY KR**SQARFWVD
101 YIDKKIYDTW KKMWLSKGEE HEEGKKELIS IFKQLEETLT DKPFYGDDTF
151 GFVDLCLITF SSWFYTYETY GNFKMEEECP KLMAWVKRCM ERETVSNTLP
201 DAKKVYGLIV ELQKTLESK

Spot No.: **126**

NCBI accession No.: **gi|29170601** Species: *Hevea brasiliensis*

PFF score: [97]

Protein name: small rubber particle protein

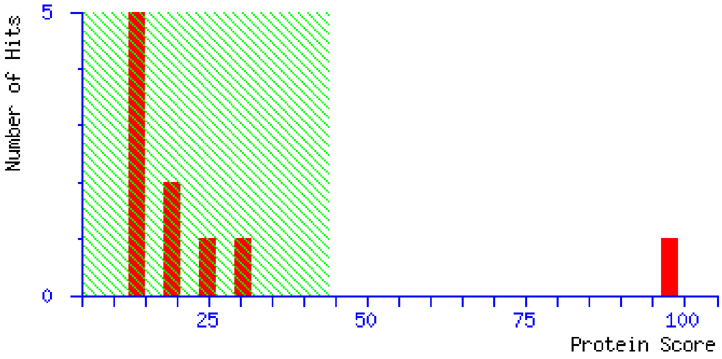
Matched peptides No.: [1] Sequence coverage %: [12]

Matched sequences: K.ENENFQQEANEQEEK.L

Calculated Mr: **12769** Calculated *p*I: **4.61**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MAEGK**ENENF** **QQEANEQEEK** LKYLEFVQAT TDNAVTALSN IYLYAKDNSG
51 PLKPGVETIE GVAKTVVIPA SKIPTEAIKF ADRAVDASFT TLQNIVPSVL
101 KQLPTQACDT SVKESAE

Spot No.: 127

NCBI accession No.: **gi|2832430** Species: *Hevea brasiliensis*

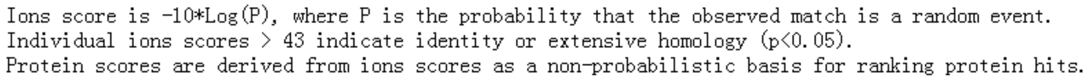
PFF score: [84] Protein name: prohevein

Matched peptides No.: [1] Sequence coverage %: [10]

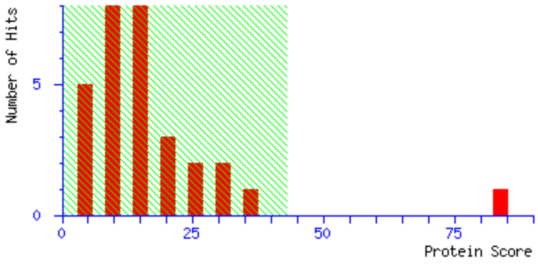
Matched sequences: K.YGWTAFCGPVGAHGQPSCGK.C

Calculated Mr: **20852** Calculated *p*I: **5.64**

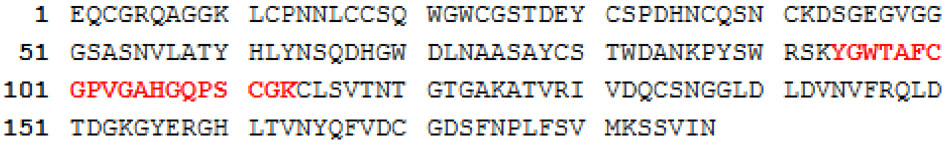
Probability Based Mowse Score:



```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 43 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:



```
  1 EQCGRQAGGK LCPNNLCCSQ WGWCGSTDEY CSPDHNCQSN CKDSGEGVGG
 51 GSASNVLATY HLYNSQDHGW DLNAASAYCS TWDANKPYSW RSKYGWTAFC
101 GPVGAHGQPS CGKCLSVTNT GTGAKATVRI VDQCSNGGLD LDVNVFRQLD
151 TDGKGYERGH LTVNYQFVDC GDSFNPLFSV MKSSVIN
```

Spot No.: **128**

NCBI accession No.: **gi|224054224** Species: *Populus trichocarpa*

PFF score: [68] Protein name: predicted protein

Matched peptides No.: [2] Sequence coverage %: [12]

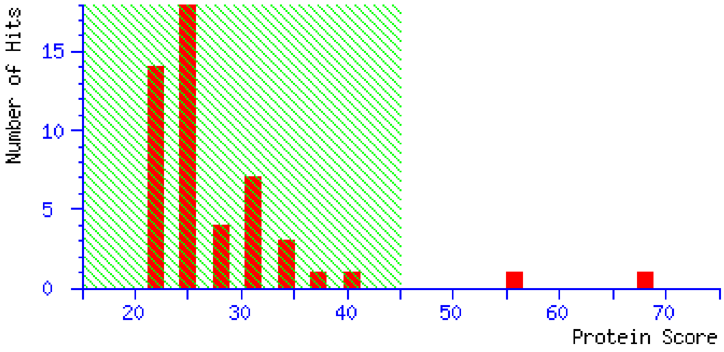
Matched sequences: R.AYVGDRPTWR.N;

R.NPQHPWR.V

Calculated Mr: **15003** Calculated *p*I: **6.82**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MTVKLVDATI SSFGSVFEKF KAEAPKNKVN LILFLADNDP STNLSWCPDC
51 VRAEPVILKK LEALPDDVAL LR**AYVGDRPT** **WRNPQHPWR**V DSRFKLKGVP
101 TLISWENDAV KGRLEDYEAH LEHKINALVS GN

Spot No.: **129**

NCBI accession No.: **gi| 329750601** Species: *Hevea brasiliensis*

PFF score: [61] Protein name: thioredoxin H-type 2

Matched peptides No.: [2] Sequence coverage %: [12]

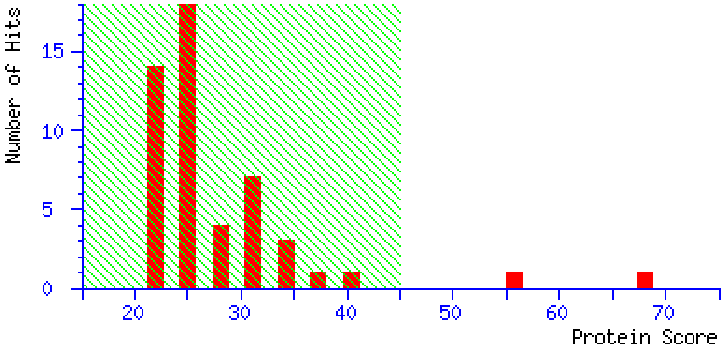
Matched sequences: R.AYVGDRPTWR.N;

R.NPQHPWR.V

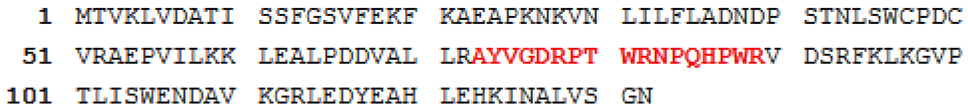
Calculated Mr: **13295** Calculated *p*I: **5.89**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:



1 MTVKLVDATI SSFGSVFEKF KAEAPKNKVN LILFLADNDP STNLSWCPDC
51 VRAEPVILKK LEALPDDVAL LR**AYVGDRPT** **WRNPQHPWR**V DSRFKLKGVP
101 TLISWENDAV KGRLEDYEAH LEHKINALVS GN

Spot No.: **130**

NCBI accession No.: **gi|268321205**

Plantspecies: ***Hevea brasiliensis*** Protein name：**latex cystatin**

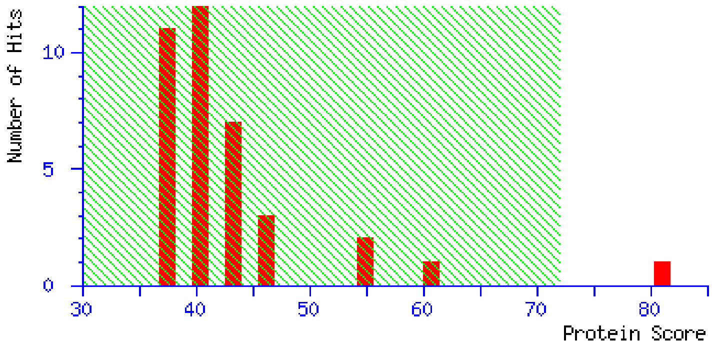
PMF score: **81** Sequence coverage %: **48**

Matched peptides No.: **6** Total peptides No.:**42**

Calculated Mr: **11248** Calculated *p*I: **5.45**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 MAKLGGVK**EV EGSANSVEIN SLARYAVDDY NQKQNALLEF K**KVVNAKQQV
51 VAGTIYYITL EVIDGGQKKV YEAK**VWEKPW LNFKEVQEFK** LIGDAPSDST
101 A

Spot No.: **131**

NCBI accession No.: **gi|132270** Species: *Hevea brasiliensis*

PFF score: [539]

Protein name: small rubber particle protein

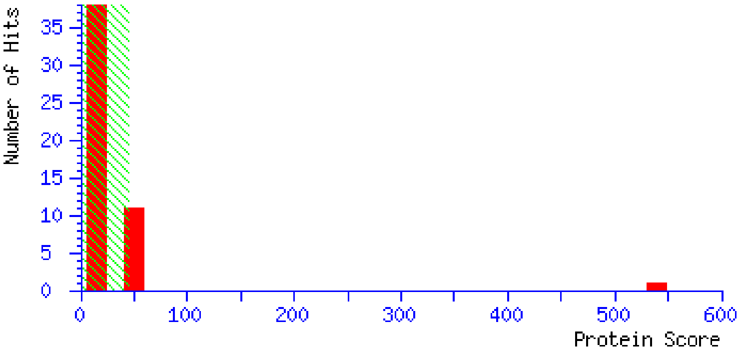
Matched peptides No.: [5] Sequence coverage %: [39]

Matched sequences: K.DKSGPLQPGVDIIEGPVK.N;
K.SGPLQPGVDIIEGPVK.N;
K.FVDSTVVASVTIIDR.S;
K.DASIQVVSAIR.A;
R.SLASSLPGQTK.I

Calculated Mr: **14713** Calculated *p*I: **5.04**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK **DKSGPLQPGV**
51 **DIIEGPVK**NV AVPLYNRFSY IPNGALK**FVD** **STVVASVTII** **DR**SLPPIVK**D**
101 **ASIQVVSAIR** AAPEAAR**SLA** **SSLPGQTK**IL AKVFYGEN

Spot No.: 132

NCBI accession No.: **gi|132270**   Species: *Hevea brasiliensis*

Protein name: **Rubber elongation factor protein**

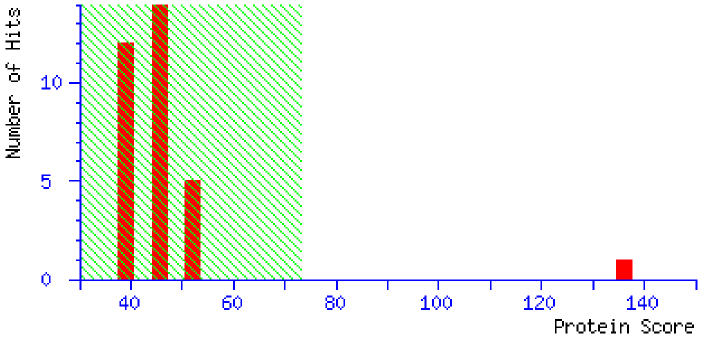
PMF score: **138**   Sequence coverage %: **81**

Matched peptides No.: **10**   Total peptides No.: **28**

Calculated Mr: **14713**   Calculated *p*I: **5.04**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 MAEDEDNQQG QGEGLK**YLGF VQDAATYAVT TFSNVYLFAK DKSGPLQPGV**
51 **DIIEGPVKNV AVPLYNRFSY IPNGALKFVD STVVASVTII DRSLPPIVKD**
101 **ASIQVVSAIR AAPEAARSLA SSLPGQTK**IL AKVFYGEN

Spot No.: **133**

NCBI accession No.: **gi|242083244**

Plantspecies: ***Sorghum bicolor***

Protein name：**hypothetical protein SORBIDRAFT_08g008236**

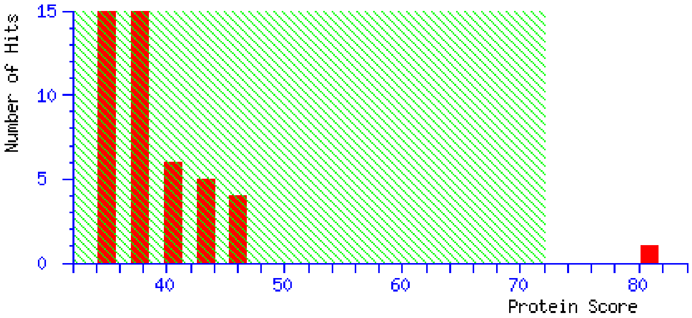
PMF score: **81** Sequence coverage %: **89**

Matched peptides No.: **7** Total peptides No.:**33**

Calculated Mr: **8620** Calculated *p*I: **6.4**

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

```
 1 CVENIILSVL FWSKVQLCLR ASQPLLVALR IVDGDETPID PKIMVAMDVA
51 KAIIKESLKD KPILLNEVLK YYDNR
```

Spot No.: **134**

NCBI accession No.: **gi|29170601** Species: *Hevea brasiliensis*

PFF score: [85]

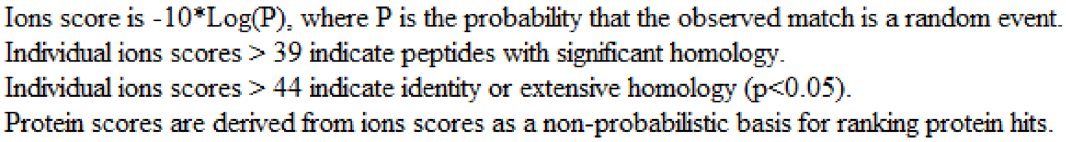
Protein name: small rubber particle protein

Matched peptides No.: [1] Sequence coverage %: [15]

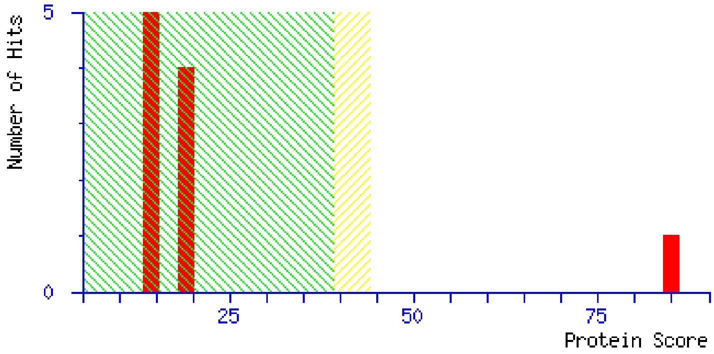
Matched sequences: R.AVDASFTTLQNIVPSVLK.Q

Calculated Mr: **12769** Calculated *p*I: **4.61**

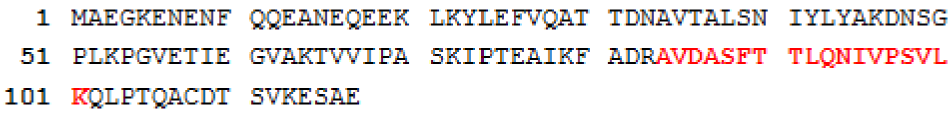
Probability Based Mowse Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 39 indicate peptides with significant homology.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:



1 MAEGKENENF QQEANEQEEK LKYLEFVQAT TDNAVTALSN IYLYAKDNSG
51 PLKPGVETIE GVAKTVVIPA SKIPTEAIKF ADR**AVDASFT TLQNIVPSVL**
101 **K**QLPTQACDT SVKESAE

Spot No.: **135**

NCBI accession No.: **gi|29170601** Species: *Hevea brasiliensis*

PFF score: [485]

Protein name: small rubber particle protein

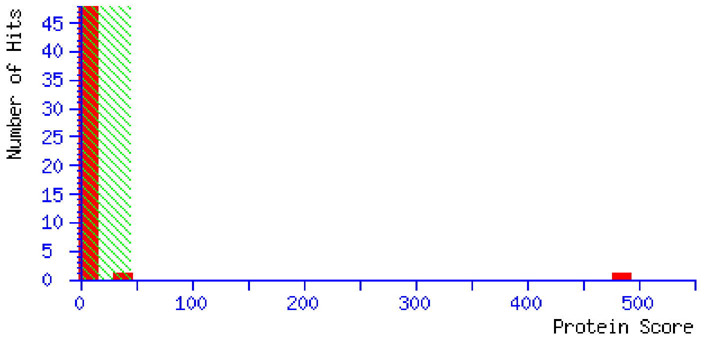
Matched peptides No.: [4] Sequence coverage %: [53]

Matched sequences: K.ENENFQQEANEQEEK.L;
K.DNSGPLKPGVETIEGVAK.T;
R.AVDASFTTLQNIVPSVLK.Q;
K.QLPTQACDTSVK.E

Calculated Mr: **12769** Calculated *p*I: **4.61**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEGK**ENENF** **QQEANEQEEK** LKYLEFVQAT TDNAVTALSN IYLYAK**DNSG**
51 **PLKPGVETIE** **GVAK**TVVIPA SKIPTEAIKF ADR**AVDASFT** **TLQNIVPSVL**
101 **KQLPTQACDT** **SVK**ESAE

Spot No.: 136

NCBI accession No.: **gi|354318** Species: *Triticum aestivum*

PFF score: [128] Protein name: calmodulin

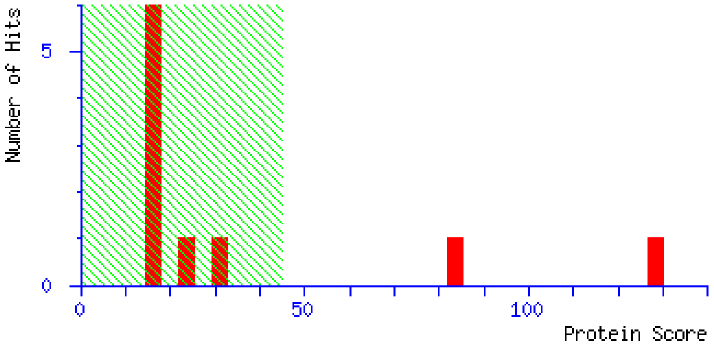
Matched peptides No.: [1] Sequence coverage %: [10]

Matched sequences: R.VFDKDQDGFISAAELR.H

Calculated Mr: **16876** Calculated *p*I: **4.10**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

```
  1 ADQLTDEQNI AEFKEAFSLF DKDGDGCITT KELGTVMRSL GQNPTEAELQ
 51 DMINEVDADG NGTIDFPEFL NLMARKMKDT DSEEELKEAF RVFDKDQDGF
101 ISAAELRHVM TNLGEKLTDE EVDEMIREAD VDGDGQINYE EFVKVMMAK
```

Spot No.: 137

NCBI accession No.: gi|14423933 Species: *Hevea brasiliensis*

Protein name： Small rubber particle protein

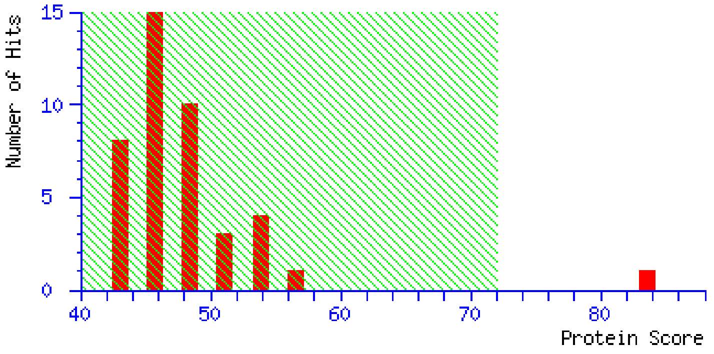
PMF score: **84** Sequence coverage %: **65**

Matched peptides No.: **9** Total peptides No.:**43**

Calculated Mr: **22331** Calculated *p*I: **4.80**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 MAEEVEEERL K**YLDFVRAAG VYAVDSFSTL YLYAKDISGP LKPGVDTIEN**
51 **VVKTVVTPVY YIPLEAVK**FV DKTVDVSVTS LDGVVPPVIK **QVSAQTYSVA**
101 **QDAPRIVLDV ASSVFNTGVQ EGAK**ALYANL EPK**AEQYAVI TWR**ALNK**LPL**
151 **VPQVANVVVP TAVYFSEK**YN DVVRGTTEQG YR**VSSYLPLL PTEK**ITKVFG
201 DEAS

Spot No.: 138

NCBI accession No.: gi|14423933 Species: *Hevea brasiliensis*

Protein name： Small rubber particle protein

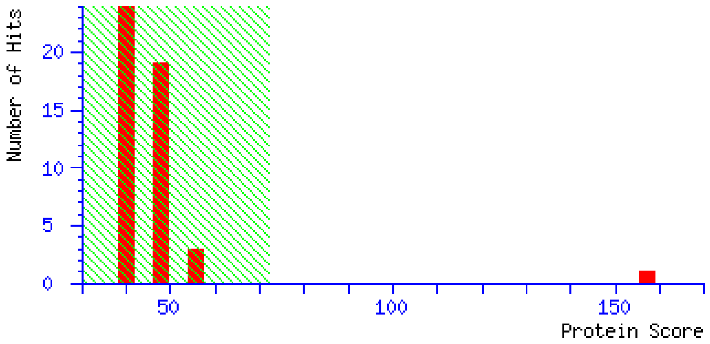
PMF score: **162** Sequence coverage %: **85**

Matched peptides No.: **13** Total peptides No.:**43**

Calculated Mr: **22331** Calculated *p*I: **4.80**

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

```
  1 MAEEVEEERL KYLDFVRAAG VYAVDSFSTL YLYAKDISGP LKPGVDTIEN
 51 VVKTVVTPVY YIPLEAVKFV DKTVDVSVTS LDGVVPPVIK QVSAQTYSVA
101 QDAPRIVLDV ASSVFNTGVQ EGAKALYANL EPKAEQYAVI TWRALNKLPL
151 VPQVANVVVP TAVYFSEKYN DVVRGTTEQG YRVSSYLPLL PTEKITKVFG
201 DEAS
```

Spot No.: 139

NCBI accession No.: gi|14423688   Species: *Hevea brasiliensis*

Protein name： **Enolase 1**

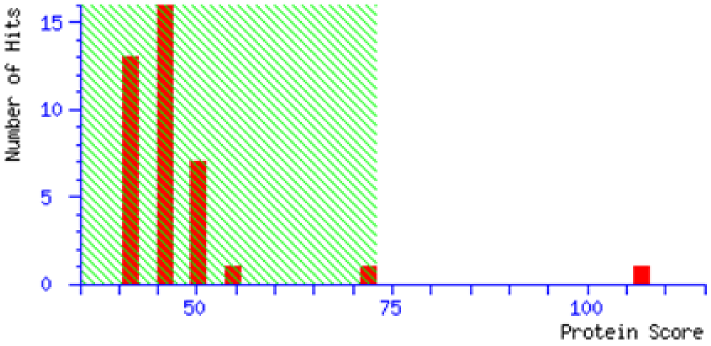
PMF score: 107   Sequence coverage %: 44

Matched peptides No.:14   Total peptides No.:47

Calculated Mr: 48029   Calculated *p*I:5.57

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold red:

1 M**AITIVSVR**A R**QIFDSR**GNP TVEADVK**LSD** **GYLARAAVPS** **GASTGIYEAL**
51 **ELR**DGGSDYL GKGVSK**AVEN** **VNIIIGPALV** **GK**DPTDQVGI DNFMVQQLDG
101 TVNEWGWCKQ KLGANAILAV SLAVCKAGAH VKGIPLYEHI ANLAGNKNLV
151 LPVPAFNVIN GGSHAGNK**LA** **MQEFMILPVG** **ASSFK**EAMKM GAEVYHHLKS
201 VIKKK**YGQDA** **TNVGDEGGFA** **PNIQENK**EGL ELLKTAIAKA GYTGKVVIGM
251 DVAASEFYGS DQTYDLNFKE ENNNGSQKIS GEALKDLYK**S** **FVAEYPIVSI**
301 **EDPFDQDDWA** **HYAK**LTSEIG EKVQIVGDDL LVTNPKRVEK AIKEKACNAL
351 LLK**VNQIGSV** **TESIEAVK**MS KR**AGWGVMAS** **HRSGETEDTF** **IADLSVGLAT**
401 **GQIK**TGAPCR SERLAK**YNQL** **LRIEEELGSE** **AVYAGANFRK** **PVEPY**

Spot No.: 140

NCBI accession No.: **gi|132270** Species: *Hevea brasiliensis*

PFF score: [52] Protein name：Rubber elongation factor protein

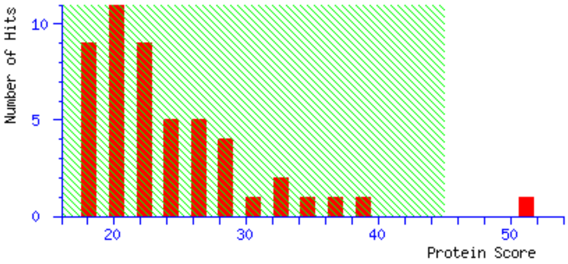
Matched peptides No.: [1] Sequence coverage %: [10]

Matched sequences: K.FVDSTVVASVTIIDR.S

Calculated Mr: **14713** Calculated *p*I: **5.04**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK DKSGPLQPGV
51 DIIEGPVKNV AVPLYNRFSY IPNGALK**FVD** **STVVASVTII** **DR**SLPPIVKD
101 ASIQVVSAIR AAPEAARSLA SSLPGQTKIL AKVFYGEN

Spot No.: **141**

NCBI accession No.: **gi|14423688** Species: *Hevea brasiliensis*

Protein name: Enolase 1

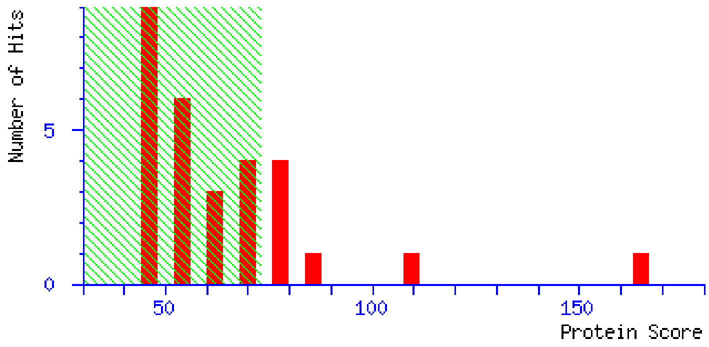
PMF Mascot score: **165** Sequence coverage %: **52**

Matched peptides No.: **22** Total peptides No.: **64**

Calculated Mr: **48029** Calculated *p*I: **5.57**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 M**AITIVSVR**A R**QIFDSR**GNP TVEADVK**LSD** **GYLARAAVPS** **GASTGIYEAL**
51 **ELR**DGGSDYL GKGVSKAVEN VNIIIGPALV GKDPTDQVGI DNFMVQQLDG
101 TVNEWGWCKQ KLGANAILAV SLAVCKAGAH VKGIPLYEHI ANLAGNKNLV
151 LPVPAFNVIN GGSHAGNK**LA** **MQEFMILPVG** **ASSFK**EAMK**M** **GAEVYHHLK**S
201 VIKK**KYGQDA** **TNVGDEGGFA** **PNIQENK**EGL ELLKTAIAKA GYTGK**VVIGM**
251 **DVAASEFYGS** **DQTYDLNFK**E ENNNGSQKIS GEALKDLYK**S** **FVAEYPIVSI**
301 **EDPFDQDDWA** **HYAK**LTSEIG EK**VQIVGDDL** **LVTNPK**RVEK AIKEKACNAL
351 LLK**VNQIGSV** **TESIEAVK**MS KR**AGWGVMAS** **HRSGETEDTF** **IADLSVGLAT**
401 **GQIKTGAPCR** SERLAK**YNQL** **LRIEEELGSE** **AVYAGANFRK** **PVEPY**

Spot No.: **142**

NCBI accession No.: **gi|14423687** Species: *Hevea brasiliensis*

PFF score: [766] Protein name: Enolase 2

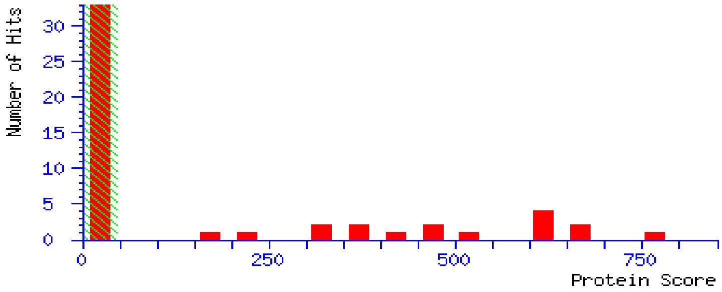
Matched peptides No.: [10] Sequence coverage %: [32]

Matched sequences: K.LAMQEFMILPVGASSFK.E + Oxidation (M);
K.MGAEVYHHLK.S;
K.MGAEVYHHLK.S + Oxidation (M);
K.YGQDATNVGDEGGFAPNIQENK.E;
K.VVIGMDVAASEFYGSDK.T;
K.VQIVGDDLLVTNPK.R;
K.VNQIGSVTESIEAVK.M;
R.AGWGVMASHR.S + Oxidation (M);
R.SGETEDTFIADLSVGLATGQIK.T;
R.IEEELGAEAVYAGANFR.T

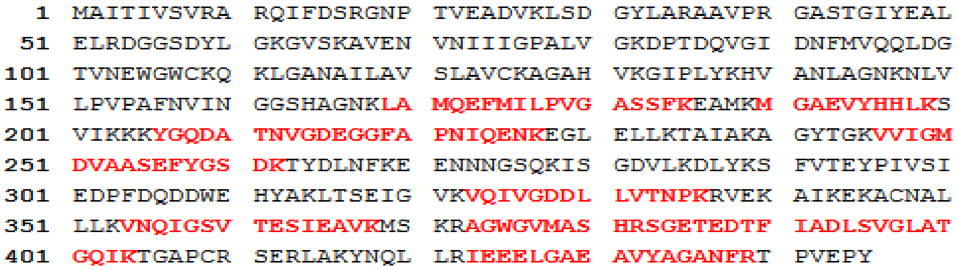
Calculated Mr: **48112** Calculated *p*I: **5.92**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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


1 MAITIVSVRA RQIFDSRGNP TVEADVKLSD GYLARAAVPR GASTGIYEAL
51 ELRDGGSDYL GKGVSKAVEN VNIIIGPALV GKDPTDQVGI DNFMVQQLDG
101 TVNEWGWCKQ KLGANAILAV SLAVCKAGAH VKGIPLYKHV ANLAGNKNLV
151 LPVPAFNVIN GGSHAGNK**LA** **MQEFMILPVG** **ASSFK**EAMK**M** **GAEVYHHLK**S
201 VIKKK**YGQDA** **TNVGDEGGFA** **PNIQENK**EGL ELLKTAIAKA GYTGK**VVIGM**
251 **DVAASEFYGS** **DK**TYDLNFKE ENNNGSQKIS GDVLKDLYKS FVTEYPIVSI
301 EDPFDQDDWE HYAKLTSEIG VK**VQIVGDDL** **LVTNPK**RVEK AIKEKACNAL
351 LLK**VNQIGSV** **TESIEAVK**MS KR**AGWGVMAS** **HRSGETEDTF** **IADLSVGLAT**
401 **GQIK**TGAPCR SERLAKYNQL LR**IEEELGAE** **AVYAGANFR**T PVEPY

Spot No.: **143**

NCBI accession No.: **gi|333690873** Species: *Hevea brasiliensis*

PFF score: [52]

Protein name: glutathione-S-transferase tau 1

Matched peptides No.: [2] Sequence coverage %: [10]

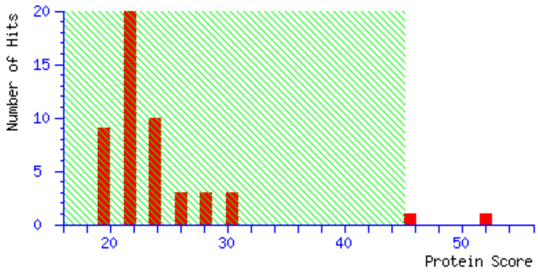
Matched sequences: K.YEYREEDLR.N;

K.DKSPFLPSDPYQR.A

Calculated Mr: 25595 Calculated *p*I: **5.48**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEEVILLDF WPSPFGMRVR IALAEKGVK**Y** **EYREEDLR**NK SPLLLQMNPV
51 HKKIPVLIHN GKPICESLIA VQYVDEVWK**D** **KSPFLPSDPY** **QR**AQARFWAD
101 FIDKKIYDIG RKIWTTKGDE QEAAKKEFIE ALKLLEGELG NKPYFGGESM
151 GYVDVALIPF YSWFYAYETC GNFSIEPECP VLIAWAKRCL QKESVSESVP
201 DPEKVYEFVL VLKKKFGIE

Spot No.: **144**

NCBI accession No.: **gi|242080619**   Species: *Sorghum bicolor*

Protein name: hypothetical protein SORBIDRAFT_07g003800

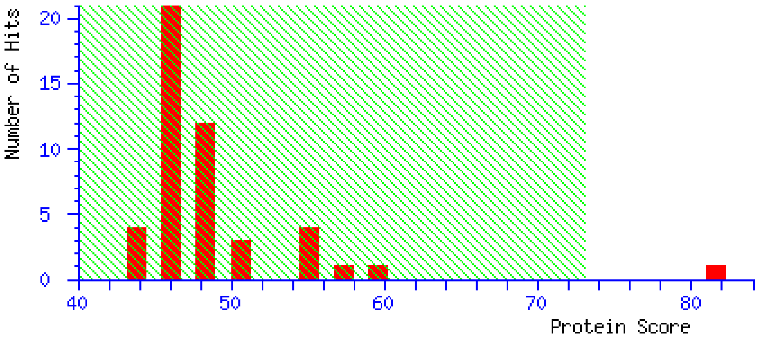
PMF Mascot score: **82**   Sequence coverage %: **34**

Matched peptides No.: **13**   Total peptides No.: **69**

Calculated Mr: **43483**   Calculated *p*I: **8.78**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 **MAEANVAAAS** **LFGADSRLCS** **ADILAPPEAK** VRARIEVAVL NFLAALASPS
51 SPAISVLPLI SRSSANCSLR SGLLNDVSSV YLSHTFCK**RS** **LMHNPK**AFVR
101 VWKVMEMCYK ILGEGK**LVHQ** **RELFYK**LLSD SPKYFSCQRH VNQAIQDVVS
151 LLRCTRQSLG VMASSRGALI GRLVLHEPDE EQIDCSILGA SGHAITGDLN
201 LLSK**LNLSSD** **ARYIIVVEK**D AIFQRLAEDR **LYNQLPCILI** **TAKGYPDIAT**
251 **R**FILHRLSQT FPNMPIFALV DWNPAGLAIM CTYKYGSISM GLESYRYACN
301 VK**WLGMRGDD** **LQLIPESAFQ** **VLK**PR**DLQTC** **TNYLRPQFHQ** **ESHRAELTLM**
351 **VEKGK**RADIE ALYSHGFDYL GKYIARKIVQ GDYI

Spot No.: **145**

NCBI accession No.: **gi|30575570** Species: *Citrus x paradisi*

PFF score: [87]

Protein name: HSP19 class II

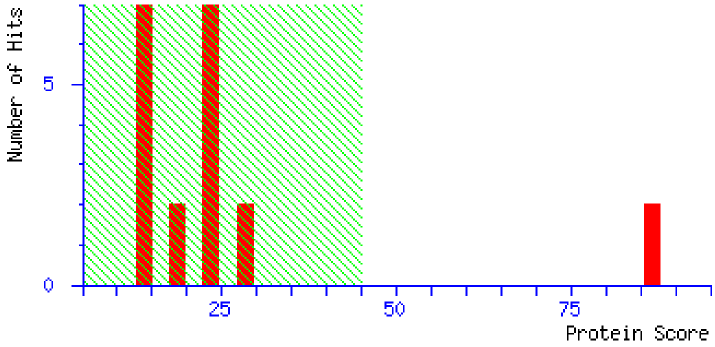
Matched peptides No.: [1] Sequence coverage %: [15]

Matched sequences: K.VQVEDDNVLLISGER.K

Calculated Mr: **11191** Calculated *p*I: **8.01**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 YVFIVDMPGL KSGDIK**VQVE** **DDNVLLISGE** **R**KREEEKDGA KYVRMERRVG
51 KFMRKFVLPE NANVEAISAV CQDGVLTVTV DKLPPPEPKK PKTIEVKIA

Spot No.: **146**

NCBI accession No.: **gi|37901124** Species: *Hevea brasiliensis*

PFF score: [88]

Protein name: latex abundant protein 1

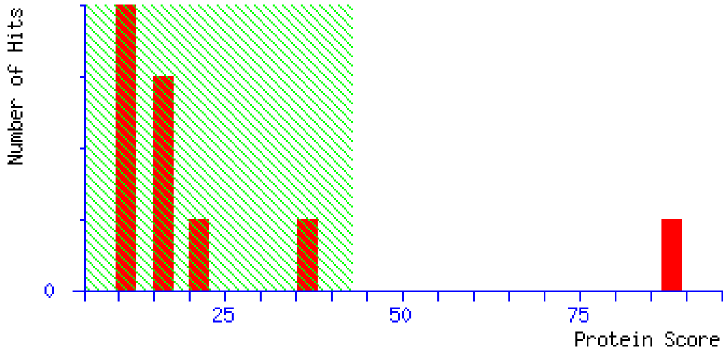
Matched peptides No.: [1] Sequence coverage %: [11]

Matched sequences: R.NKDDINCFNEYNPR.P

Calculated Mr: **14618** Calculated *p*I: **5.01**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 43 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MPYYTR**NKDD** **INCFNEYNPR** PYIGGYDMAL TYGRPISACE ETCYPRSSSA
51 NEIDYDYPDF TWYVEPSAYN DDHLQEEYTS YARPKPRPAP NSLGSCPILG
101 GNDEEKKHHH CHHQHEKHCD DE

Spot No.: **147**

NCBI accession No.: **gi|359806300** Species: *Glycine max*

PFF score: [173]

Protein name: uncharacterized protein LOC100784610

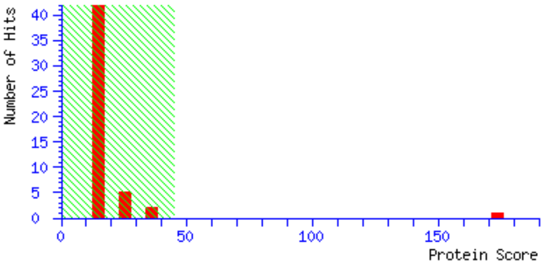
Matched peptides No.: [3] Sequence coverage %: [9]

Matched sequences: K.NTALHYAAGYGR.K;
R.YWNNEEVLQK.L;
R.TALHFACGYGEVK.C

Calculated Mr: **38027** Calculated *p*I: **4.53**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MASDSKKDFP ADDKAGTEES KTSKDETSSK DSPAEQRATA TFGPRPGPAG
51 HPGNPFDLSA MSGLLNDPSI KELAEQIAKD PSFNQMAEQL QKTFQGAPQD
101 AIPSFDNQQY FSTMQQVMQN PNFMTMAERL GNALMQDPSM SAMLESFSNP
151 SNKDQLEERM ARIKEDPSLK HILEEIETGG PAAMMR**YWNN** **EEVLQK**LGQA
201 MGLANSGDAG ASAENSGADE TEDLGNEDES IVHHTASVGD VEGLKNALAS
251 GADKDEEDSE GR**TALHFACG** **YGEVK**CAQVL LEAGAKVDAL DKNK**NTALHY**
301 **AAGYGR**KECV ALLLENGAAV TLQNMDGKTP IDVAKLNNQN EVLKLLEKDA
351 FL

Spot No.: **148**

NCBI accession No.: **gi|37625031** Species: *Vitis aestivalis*

PFF score: [166]

Protein name: putative ankyrin-repeat protein

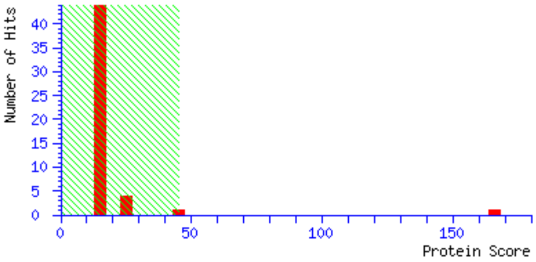
Matched peptides No.: [3] Sequence coverage %: [9]

Matched sequences: K.LNNQHEVLK.L;
K.NTALHYAAGYGR.K;
R.TALHFACGYGEVK.C

Calculated Mr: **38089** Calculated *p*I: **4.53**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MASNSDKDTP AGSAENSKSD SSSGESHSEQ RRAAAAASVP GAGLPTNPFD
51 FSAMTGLLND PSIKELAEQI AKDPAFNQMA EQLQKTFHGA AVEESIPQFD
101 TQQYYSTMQQ VMQNPQFMTM AERLGNALMQ DPSMSSMLEN LANPTHKDQL
151 EERMARIKED PSLKPILDEI ETGGPAAMMR YWNDKDVLQK LGEAMGLAVS
201 GDAAASADNS GLDEAEELAN EDESIAHHHS ESIVHDTASV GDVEGLKNAL
251 ASGADKDEED SEGR**TALHFA** **CGYGEVK**CAQ ILVEAGATVD ALDKNK**NTAL**
301 **HYAAGYGR**KE CVALLLENGA AVTLQNMDGK TPIDVAK**LNN** **QHEVLK**LLEK
351 DAFL

Spot No.: **149**

NCBI accession No.: **gi|13310811** Species: *Nicotiana tabacum*

PFF score: [71]

Protein name: putative ankyrin-repeat protein

Matched peptides No.: [2] Sequence coverage %: [7]

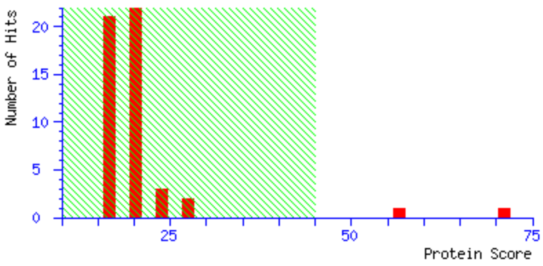
Matched sequences: K.NTALHYAAGYGR.K;

R.TALHFACGYGEVK.C

Calculated Mr: **37522** Calculated *p*I: **4.45**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MSEGEKVLPT ASADEKSGAS ENKKSSESSS TEAPSGEART TSTAAAGAGL
51 QNPFDFSAMS GLLNDPSIKE LAEQIAKDPA FNQMAEQLQK TFQGAAVEES
101 VPNFDSQQYY STMQQVMQNP QFMTMAERLG NALMQDPSMS GMLESLSNPA
151 QKEQIEERMA RIKEDPSLKP ILEEIESGGP AAMMRYWNDQ ETLKKIGEAM
201 GFAAGGEGAT SSAIPGTDET EEANEDESVV HQCASVGDAE GLKAALTAGA
251 DKDEEDSEGR **TALHFACGYG** **EVK**CAQILLE AGAKVDALDK NK**NTALHYAA**
301 **GYGR**KECVAL LLENGAAVTL QNLDGKTPID VAKLNNQQEV LKLLEKDVFL

Spot No.: **150**

NCBI accession No.: gi|129916   Species: *Triticum aestivum*

PFF score: [180]

Protein name: Phosphoglycerate kinase, cytosolic

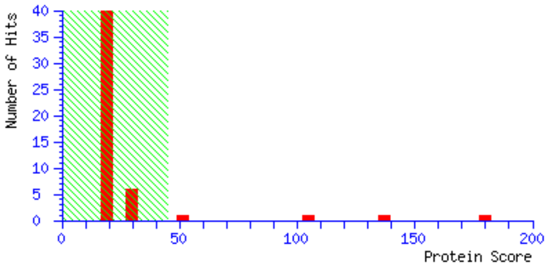
Matched peptides No.: [3]   Sequence coverage %: [7]

Matched sequences: K.KPFAAIVGGSK.V;
K.LASVADLYVNDAFGTAHR.A;
K.KLASVADLYVNDAFGTAHR.A

Calculated Mr: **42153**   Calculated *p*I: **5.64**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MATKRSVGTL GEADLKGKKV FVRADLNVPL DDAQKITDDT RIRASIPTIK
51 YLLEKGAKVI LASHLGRPKG VTPKFSLKPL VARLSELLGL EVVMAPDCIG
101 EEVEKLAAAL PDGGVLLLEN VRFYKEEEKN DPEFAK**KLAS** **VADLYVNDAF**
151 **GTAHR**AHAST EGVTKFLRPS VAGFLMQKEL DYLVGAVANP K**KPFAAIVGG**
201 **SK**VSSKIGVI ESLLAKVDIL ILGGGMIFTF YKAQGLAVGK SLVEEDKLEL
251 ATSLIETAKS KGVKLLLPTD VVVADKFAAD AESKIVPATA IPDGWMGLDV
301 GPDSIKTFAE ALDTTKTVIW NGPMGVFEFE KFAAGTDAIA KQLAELTGKG
351 VTTIIGGGDS VAAVEKAGLA DKMSHISTGG GASLELLEGK PLPGVLALDE
401 A

Spot No.: **151**

NCBI accession No.: **gi|378464888**

Species: *Ammopiptanthus mongolicus*

PFF score: [117]

Protein name: translation elongation factor

Matched peptides No.: [2] Sequence coverage %: [11]

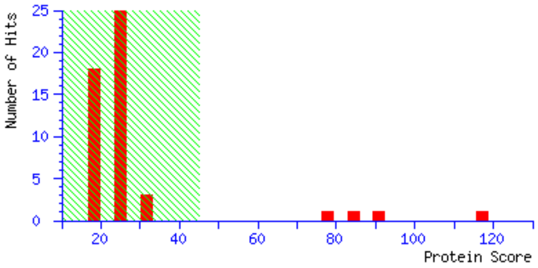
Matched sequences: R.WFNHIDALLR.I;

K.SSVLLDVKPWDDETDMK.K

Calculated Mr: **25300** Calculated *p*I: **4.50**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MVLTLYNLSS EPGLKKLDEY LLSRSYITGY QASKDDLTVY AALPEVPSDK
51 YVNVSR**WFNH** **IDALLR**ISGV SGEGSGVTVE GSAPVAEETI ATPPAADTKA
101 TAAEDDDDDV DLFGEETEEE KKAAEERAAS VKASVKKKES GK**SSVLLDVK**
151 **PWDDETDMK**K LKEAVRSVSM EGLHWGASKL VPVGYGIKKL QIMLTIVDDL
201 VSVDNLIEEQ LQVEPINEYV QSCDIVAFNK I

Spot No.: **152**

NCBI accession No.: **gi|225456295**   Species: *Vitis vinifera*

PFF score: [107]

Protein name: elongation factor 1-delta-like

Matched peptides No.: [4]   Sequence coverage %: [17]

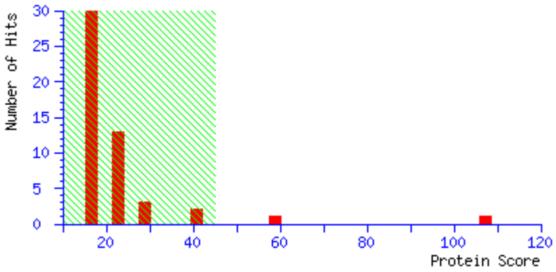
Matched sequences: K.APSSEYVNVSR.W;

R.SIKMEGLLWGASK.L;
R.SIKMEGLLWGASK.L + Oxidation (M);
K.SSVLLDVKPWDDETDMK.K

Calculated Mr: **25060**   Calculated *p*I: **4.50**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAVTFYGVNS GSGLKKLDEY LLTRSYISGY QASKDDITVH AALSK**APSSE**
51 **YVNVSR**WYNH IESLLRISGV SGEGCGVTIE GFAPVDAVAT PPAEDTKATA
101 AEDDDDDDVD LFGEETEEEK KAAEARAAAV KASGKKKESG K**SSVLLDVKP**
151 **WDDETDMK**KL EEAVR**SIKME** **GLLWGASK**LV PVGYGIKKLQ IMLTIVDDLV
201 SVDDLIEEQL TVEPTNEYVQ SCDIVAFNKI

Spot No.: **153**

NCBI accession No.: **gi|22261807** Species: *Solanum tuberosum*

PFF score: [132]

Protein name: Light-induced protein, chloroplastic

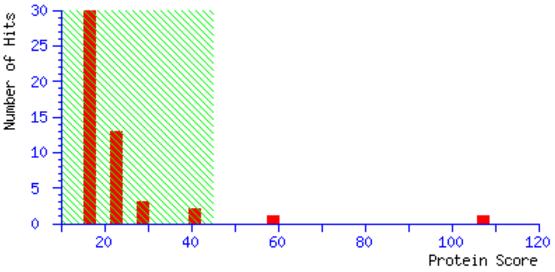
Matched peptides No.: [1] Sequence coverage %: [8]

Matched sequences: K.FEEGIIGTPQLTDSIVLPENVEFLGQK.I

Calculated Mr: **35671** Calculated *p*I: **5.26**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

```
  1 MAVTFYGVNS GSGLKKLDEY LLTRSYISGY QASKDDITVH AALSKAPSSE
 51 YVNVSRWYNH IESLLRISGV SGEGCGVTIE GFAPVDAVAT PPAEDTKATA
101 AEDDDDDDVD LFGEETEEEK KAAEARAAAV KASGKKKESG KSSVLLDVKP
151 WDDETDMKKL EEAVRSIKME GLLWGASKLV PVGYGIKKLQ IMLTIVDDLV
201 SVDDLIEEQL TVEPTNEYVQ SCDIVAFNKI
```

Spot No.: **154**

NCBI accession No.: **gi|345103803**   Species: *Gossypium thurberi*

Protein name: 14-3-3-like protein, partial

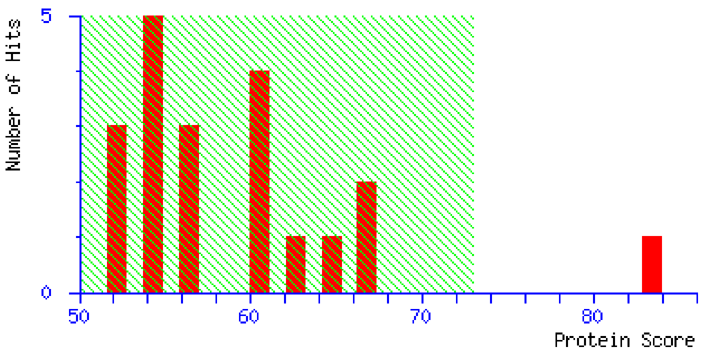
PMF Mascot score: **83**   Sequence coverage %: **37**

Matched peptides No.: **11**   Total peptides No.: **41**

Calculated Mr: **28861**   Calculated *p*I: **4.82**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MEKER**EQQVY** **LARLAEQAER** YDEMVEAMKS VAK**LDVELTV** **EER**NLLSVGY
51 K**NVIGARR**AS WR**ILSSIEQK** EEAKGNEQNV KRIKDYRQRV EDELSKICND
101 ILSVIDKHLI PSSSTGESTV FYYKMKGDYF R**YLAEFK**AGD DRKEAADQSL
151 K**AYEAATSTA** **SSDLPPTHPI** **R**LGLALNFSV FYYEILNSPE RACHLAK**QAF**
201 **DEAIAELDSL** **NEESYKDSTL** **IMQLLR**DNLT LWTSDLPEEG GEQSKADEPQ
251 AE

Spot No.: **155**

NCBI accession No.: **gi|326694865** Species: *Hevea brasiliensis*

PFF score: [384]

Protein name: 14-3-3 protein 2

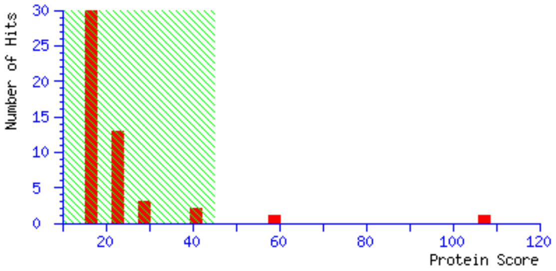
Matched peptides No.: [9] Sequence coverage %: [32]

Matched sequences: R.GNEDHVTIIK.E;
K.DSTLIMQLLR.D;
K.DSTLIMQLLR.D + Oxidation (M);
R.YEEMVEFMEK.V;
R.YEEMVEFMEK.V + Oxidation (M),K.TVDVEELTVEER.N;
K.SAQDIALADLAPTHPIR.L;
K.LAEQAERYEEMVEFMEK.V;
R.LGLALNFSVFYYEILNSPDR.A

Calculated Mr: **35671** Calculated *p*I: **5.26**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAVTFYGVNS GSGLKKLDEY LLTRSYISGY QASKDDITVH AALSK**APSSE**
51 **YVNVSR**WYNH IESLLRISGV SGEGCGVTIE GFAPVDAVAT PPAEDTKATA
101 AEDDDDDDVD LFGEETEEEK KAAEARAAAV KASGKKKESG K**SSVLLDVKP**
151 **WDDETDMK**KL EEAVR**SIKME** **GLLWGASK**LV PVGYGIKKLQ IMLTIVDDLV
201 SVDDLIEEQL TVEPTNEYVQ SCDIVAFNKI

Spot No.: **156**

NCBI accession No.: **gi|225458231** Species: *Vitis vinifera*

PFF score: [53]

Protein name: PREDICTED: proteasome subunit alpha type-1-B

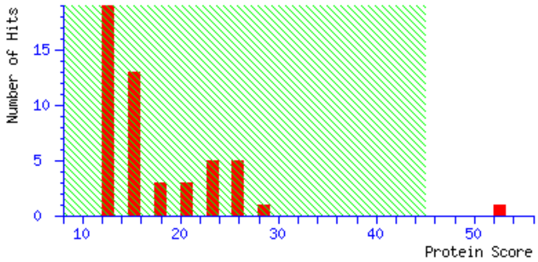
Matched peptides No.: [3] Sequence coverage %: [17]

Matched sequences: K.VDDHIGVAIAGLTADGR.V;
R.NQYDTDVTTWSPAGR.L;
R.SECINYSFTYESPLPVGR.L

Calculated Mr: **30912** Calculated *p*I: **5.02**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MFR**NQYDTDV** **TTWSPAGR**LF QVEYAMEAVK QGSAAIGLRS KTHVVLACVN
51 KANSELSSHQ KKIFK**VDDHI** **GVAIAGLTAD** **GR**VLSRYMRS **ECINYSFTYE**
101 **SPLPVGR**LVV QLADKAQVCT QRSWKRPYGV GLLVAGLDES GAHLYYNCPS
151 GNYFEYQAFA IGSRSQAAKT YLERRFGTFQ NSSREDLIKD ALFAIRETLQ
201 GEKLKSSICT VTVLGVGEPF HILDQETVQG LINAFEMAGE EAPAADQGAA
251 GEEGAAGEVV AAAEEGAAPE EGAATEEGAA PMDI

Spot No.: **157**

NCBI accession No.: **gi|211906514** Species: *Gossypium hirsutum*

PFF score: [80]

Protein name: lactoylglutathione lyase

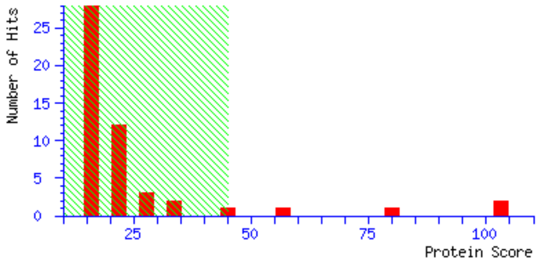
Matched peptides No.: [3]   Sequence coverage %: [6]

Matched sequences: K.FYTECFGMK.L;
K.FYTECFGMK.L + Oxidation (M);
K.ITSFLDPDGWK.T

Calculated Mr: **32609**   Calculated *p*I: **5.69**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEGSAAVPS TELLEWPKKD KRRFLHAVYR VGDLDRTIK**F** **YTECFGMK**LL
51 RKRDIPEEKY SNAFLGFGPE ESHFVVELTY NYGVTSYDIG TGFGHFAIAT
101 PDVYKMVEDI RAKGGNITRE PGPVKGGSSV IAFVKDPDGY IFELIQRAST
151 PEPLCQVMLR VGDLDRSVKF YEKALGMKLV KKVDRPEYKY SIAMMGYAEE
201 HETTVLELTY NYGVTEYTKG NAYAQVAIST DDVYKSGEVV EHVIQELGGK
251 VTRKPGPIPG INTK**ITSFLD** **PDGWK**TVLVD NEDFLKELK

Spot No.: **159**

NCBI accession No.: **gi|340033945** Species: *Crithmum maritimum*

Protein name: ATP synthase CF1 beta subunit

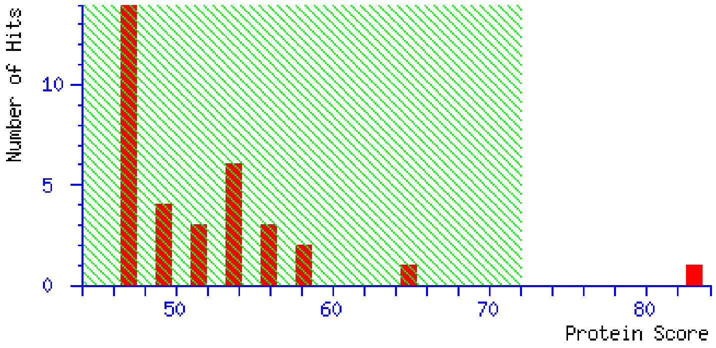
PMF Mascot score: **83** Sequence coverage %: **29**

Matched peptides No.: **15** Total peptides No.: **69**

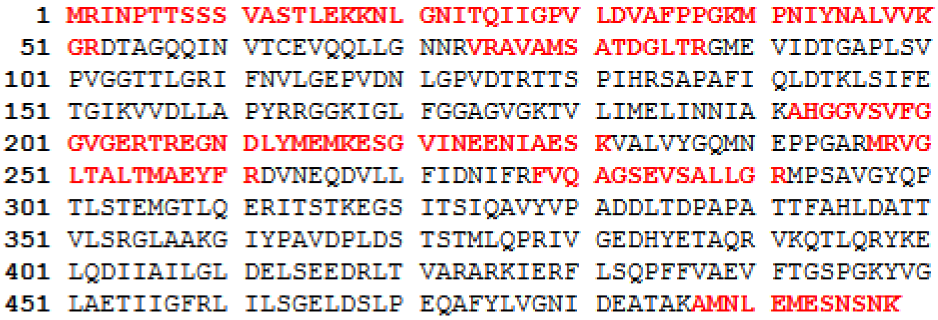
Calculated Mr: **53692** Calculated *p*I: **5.08**

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red:



```
  1 MRINPTTSSS VASTLEKKNL GNITQIIGPV LDVAFPPGKM PNIYNALVVK
 51 GRDTAGQQIN VTCEVQQLLG NNRVRAVAMS ATDGLTRGME VIDTGAPLSV
101 PVGGTTLGRI FNVLGEPVDN LGPVDTRTTS PIHRSAPAFI QLDTKLSIFE
151 TGIKVVDLLA PYRRGGKIGL FGGAGVGKTV LIMELINNIA KAHGGVSVFG
201 GVGERTREGN DLYMEMKESG VINEENIAES KVALVYGQMN EPPGARMRVG
251 LTALTMAEYF RDVNEQDVLL FIDNIFRFVQ AGSEVSALLG RMPSAVGYQP
301 TLSTEMGTLQ ERITSTKEGS ITSIQAVYVP ADDLTDPAPA TTFAHLDATT
351 VLSRGLAAKG IYPAVDPLDS TSTMLQPRIV GEDHYETAQR VKQTLQRYKE
401 LQDIIAILGL DELSEEDRLT VARARKIERF LSQPFFVAEV FTGSPGKYVG
451 LAETIIGFRL ILSGELDSLP EQAFYLVGNI DEATAKAMNL EMESNSNK
```

Spot No.: **160**

NCBI accession No.: gi|4388534   Species: *Sorghum bicolor*

Protein name: F1-ATP synthase, beta subunit

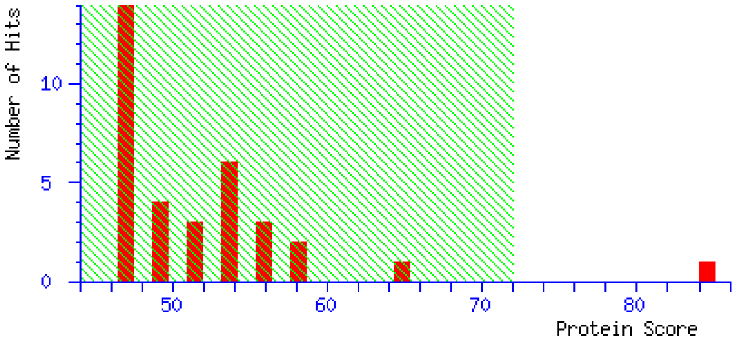
PMF Mascot score: **84**   Sequence coverage %: **19**

Matched peptides No.: **8**   Total peptides No.: **20**

Calculated Mr: **49239**   Calculated *p*I: **5.41**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 IGQVCQVIGA VVDVR**FDEGL** **PPILTALEVL** **DNNIR**LVLEV AQHLGENMVR
51 TIAMDGTEGL VRGQRVLNTG SPITVPVGRA TLGRIINVIG EPIDERGDIT
101 TNHFLPIHRE APAFVEQATE QQILVTGIKV VDLLAPYQRG GKIGLFGGAG
151 VGKTVLIMEL INNVAK**AHGG** **FSVFAGVGER** **TREGNDLYRE** **MIESGVIKLG**
201 **DK**QSESK**CAL** **VYGQMNEPPG** **AR**ARVGLTGL TVAEHFRDAE GQDVLLFIDN
251 IFRFTQANSE VSALLGRIPS AVGYQPTLAT DLGGLQERIT TTKKGSITSV
301 QAIYVPADDL TDPAPATTYA HLDATTVLSR QISER**GIYPA** **VDPLDSTSR**M
351 LSPHVLGEDH YNTARGVQKV LQKYKNLQDI IAILGMDELS EDDKLTVARA
401 RKIQRFLSQP FHVAEVFTGA PGKYVELKES VK**SFQGVLDG** **K**YDDLPAQSF
451 YMVG

Spot No.: **161**

NCBI accession No.: **gi|147805616** Species: *Vitis vinifera*

PFF score: [136]

Protein name: hypothetical protein VITISV_028800

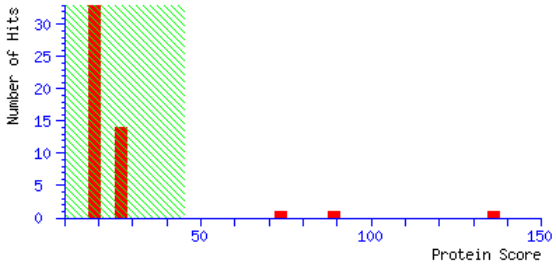
Matched peptides No.: [3] Sequence coverage %: [10]

Matched sequences: R.GPYPADQVVR.D;
R.DRGPYPADQVVR.D;
K.TANEVIIVIEAYR.T

Calculated Mr: 27385 Calculated *p*I: **5.64**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MLAVFHKSIA EAPEGLRTPD SASLPALKDG FLPQFFASLH PSAVTVNLGS
51 SGAISYSVDK QNPLLPRLFA VVDDIFCLFQ GHIENVALLK QQYGLNK**TAN**
101 **EVIIVIEAYR** TLR**DRGPYPA** **DQVVR**DLHGK FAFVLYDSSN RTAFLAADAD
151 ESVPFFWGVD SEGHLVLSDD EETVKKGCGK SFAPFPKGCF FTTSGGLRSF
201 EHPLNELRAE PRVDSSGQVC GANFKVDVEA KKETGMPRVG SAANWSTHY

Spot No.: **162**

NCBI accession No.: **gi|326492265**

Species: *Hordeum vulgare subsp. vulgare*

Protein name： **predicted protein**

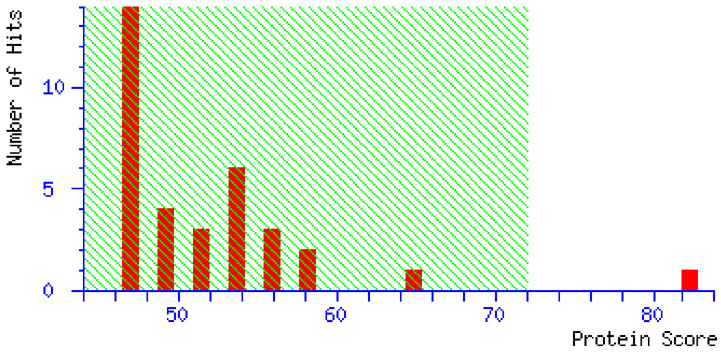
PMF score: **83** Sequence coverage %: **10**

Matched peptides No.: **58** Total peptides No.: **32**

Calculated Mr: **54666** Calculated *p*I: **8.89**

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 73 are significant ($p<0.05$).



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

1 **MSPYAVLVAV LLAFFYAVWK AR**GSSSSSSS RLPPSPPSRP LLGHLHLLGQ
51 LPHRSLRELH AR**YGTDGGLL LLQLGR**RRTL VVSTAAAAAD LYKNHDLAFA
101 SRVPSVPVDK LTYGSINISF SPYGDVWRRS KKIAVVHLLS PRRVDSFAPV
151 RAVEVAALVA GARRGAEAGE SVELRELLCA YSNAVVTRAT TGAAGATAEK
201 **LNKLLGNSAA LMSGLQADDV LPGAAAK**VVR WATGLEKR**LD AELELWDKFL**
251 **SQIIAEHLEK** KKCDGSAGEE DFLDVLLR**LR EEGGAGLELT DDRIKSIIKD**
301 **IIAAGTDTSS VTLEWAMAEL AGNPR**AMAKL QDEITR**VTQG KPTIQEADLS**
351 **R**MEYLKAVLK EVLRLHPAAP LLVPHQSTTT AVVQGYEIPA K**TALFVNAWA**
401 **IGRDPAAWGA TAEEFR**PERF LGSGGAEGVD LRGNDYQLLP FGAGRRLCPG
451 IGFAMPVLEI ALSSLVRHFD WELPAGARLD MSEAPGLTTP LLAPLRLVPK
501 CRRQQ

Spot No.: **163**

NCBI accession No.: **gi|225428086** Species: *Vitis vinifera*

PFF score: [343]

Protein name：V-type proton ATPase subunit B 1

Matched peptides No.: [10] Sequence coverage %: [30]

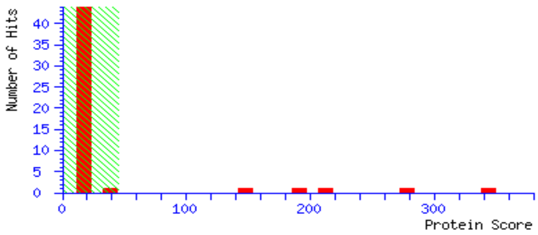
Matched sequences: K.YQEIVNIR.L;
K.FVAQGAYDTR.N;
R.RGQVLEVDGEK.A;
K.YTTVQFTGEVLK.T;
R.QIYPPINVLPSLSR.L;
R.VTLFLNLANDPTIER.I;
R.GYPGYMYTDLATIYER.A;
R.RDHADVSNQLYANYAIGK.D;
K.IPLFSAAGLPHNEIAAQICR.Q;
K.AVVGEEALSSEDLLYLEFLDKFER.K

Calculated Mr: **54367** Calculated *p*I: **5.04**

Probability Based Mowse Score:

Mascot Score Histogram

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MGVEQNNHDA EEGTLLVGME YRTVSGVAGP LVILEKVKGP K**YQEIVNIR**L
51 GDGTTR**RGQV** **LEVDGEK**AVV QVFEGTSGID NK**YTTVQFTG** **EVLK**TPVSLD
101 MLGRIFNGSG KPIDNGPPIL PEAYLDISGS SINPSERTYP EEMIQTGIST
151 IDVMNSIARG QK**IPLFSAAG** **LPHNEIAAQI** **CR**QAGLVKRL EKSGSLLEDV
201 EEDNFAIVFA AMGVNMETAQ FFKRDFEENG SMER**VTLFLN** **LANDPTIER**I
251 ITPRIALTTA EYLAYECGKH VLVILTDMSS YADALREVSA AREEVPGRR**G**
301 **YPGYMYTDLA** **TIYER**AGRIE GRKGSITQIP ILTMPNDDIT HPTPDLTGYI
351 TEGQIYIDRQ LHNR**QIYPPI** **NVLPSLSR**LM KSAIGEGMTR **RDHADVSNQL**
401 **YANYAIGK**DV QAMK**AVVGEE** **ALSSEDLLYL** **EFLDKFER**KF **VAQGAYDTR**N
451 IFQSLDLAWT LLRIFPRELL HRIPAKTLDQ YYSREASN

Spot No.: **164**

NCBI accession No.: **gi|225428086** Species: *Vitis vinifera*

PFF score: [377]

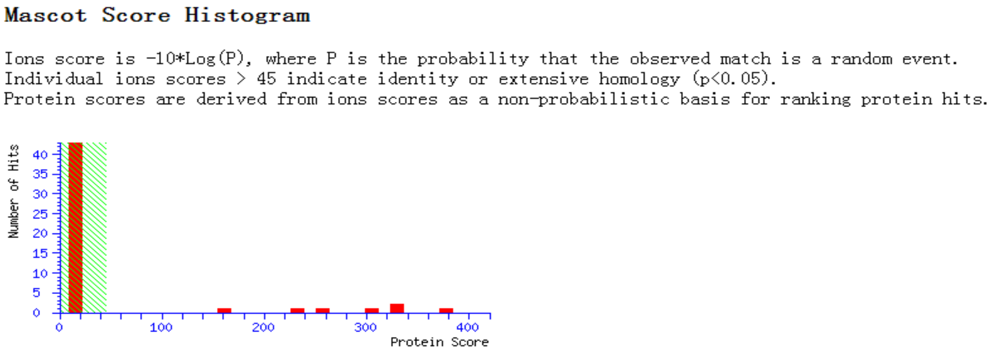
Protein name： V-type proton ATPase subunit B 1

Matched peptides No.: [10] Sequence coverage %: [23]

Matched sequences: K.YQEIVNIR.L;
K.FVAQGAYDTR.N;
R.DFEENGSMER.V;
R.RGQVLEVDGEK.A;
R.KFVAQGAYDTR.N;
K.YTTVQFTGEVLK.T;
R.QIYPPINVLPSLSR.L;
R.VTLFLNLANDPTIER.I;
R.GYPGYMYTDLATIYER.A;
R.RDHADVSNQLYANYAIGK.D

Calculated Mr: **54367** Calculated *p*I: **5.04**

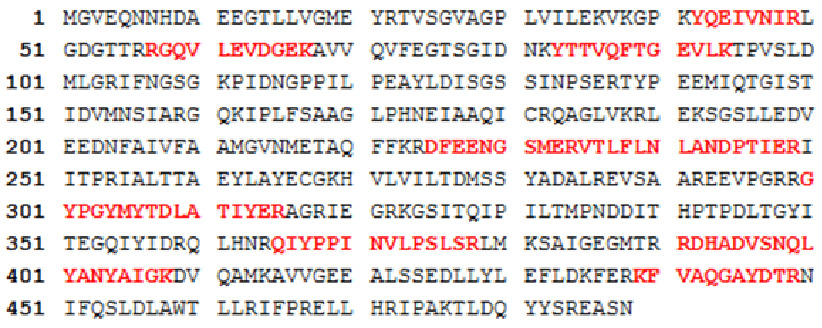
Probability Based Mowse Score:



Mascot Score Histogram

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Matched peptide sequences: shown in Bold Red:



1 MGVEQNNHDA EEGTLLVGME YRTVSGVAGP LVILEKVKGP K**YQEIVNIR**L
51 GDGTTR**RGQV** **LEVDGEK**AVV QVFEGTSGID NK**YTTVQFTG** **EVLK**TPVSLD
101 MLGRIFNGSG KPIDNGPPIL PEAYLDISGS SINPSERTYP EEMIQTGIST
151 IDVMNSIARG QKIPLFSAAG LPHNEIAAQI CRQAGLVKRL EKSGSLLEDV
201 EEDNFAIVFA AMGVNMETAQ FFKR**DFEENG** **SMERVTLFLN** **LANDPTIER**I
251 ITPRIALTTA EYLAYECGKH VLVILTDMSS YADALREVSA AREEVPGRR**G**
301 **YPGYMYTDLA** **TIYER**AGRIE GRKGSITQIP ILTMPNDDIT HPTPDLTGYI
351 TEGQIYIDRQ LHNR**QIYPPI** **NVLPSLSR**LM KSAIGEGMTR **RDHADVSNQL**
401 **YANYAIGK**DV QAMKAVVGEE ALSSEDLLYL EFLDKFER**KF** **VAQGAYDTR**N
451 IFQSLDLAWT LLRIFPRELL HRIPAKTLDQ YYSREASN

Spot No.: **165**

NCBI accession No.: **gi|224071449** Species: *Populus trichocarpa*

PFF score: [59]

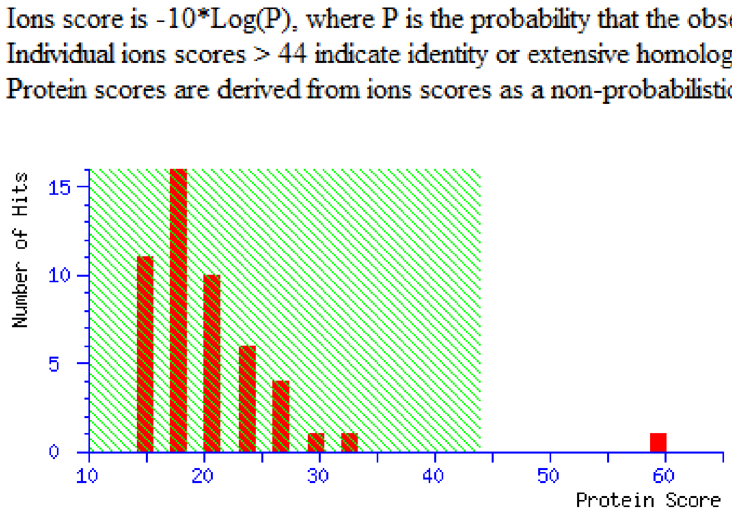
Protein name: predicted protein

Matched peptides No.: [1] Sequence coverage %: [2]

Matched sequences: K.IDVIPHYPGR.L

Calculated Mr: **47121** Calculated *p*I: **5.28**

Probability Based Mowse Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

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

1 MDGTSEATWP EILGSRNWDN LLDPLDLSLR KLILRCGDFC QATYDAFNND
51 QNSRYCGTSR YGKRNFFHKV MLDNPENYQV SSFLYATARV SLPEAFLLHS
101 LSRDSWDRET NWIGYIAVTS DEQTKTLGRR EIYIAFRGTT RNYEWVDILG
151 AKLKSAKPLL RGATSTTHDQ ESSSSSDDDD DKVPKVMLGW LTMYISDDPN
201 SPFTKLSARA QLLAHIKELR ERYKDDDLSI IFTGHSLGAS LSILSAFDLV
251 ENGITDIPVS AFVFGSPQVG NKEFNERFNK YPNLKVLHIK NK**IDVIPHYP**
301 **GR**LMGYVYTG IEFEIDTRKS PSLKDSKNPS DWHNLQAMLH IVAGWNGEEQ
351 EFELKVKRSL ALVNKSSEFL KDECLVPGIW WVEKNKGMVR NEDGEWVLAP
401 PDEEDLPVPE C

Spot No.: **166**

NCBI accession No.: **gi|116789736** Species: *Picea sitchensis*

Protein name: unknown

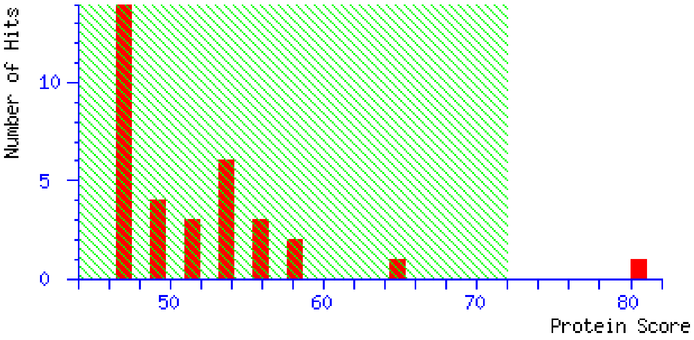
PMF Mascot score: **81** Sequence coverage %: **60**

Matched peptides No.: **6** Total peptides No.: **48**

Calculated Mr: **13436** Calculated *p*I: **5.91**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 **MPSHSLIGTT TTNRRGSMED YPNPFNPETI HELFKLVWSQ TNK**ARAQ**KEG**
51 **GETELEVGAA ASK**K**TRTTTA NSNALK**LSCE FLRLFVTEAV QRAAIVAEVE
101 GSTQIEGTHL ERILPQLLLD F

Spot No.: 167

NCBI accession No.: **gi|115392253**

Species: *Cercocarpus betuloides*

PFF score: [51] Protein name: polyphenol oxidase

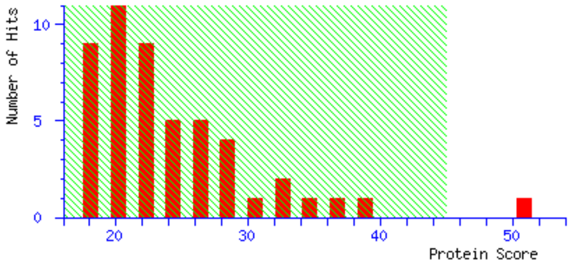
Matched peptides No.: [1] Sequence coverage %: [3]

Matched sequences: K.EKEQEEEILVIEGIEFDR.D

Calculated Mr: **51023** Calculated *p*I: **5.98**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

```
  1 PFAFAKPVAP PDVSKCGAAD LPTGAQPTNC CPPVASKIID FKLPSPTPLR VRPAAHAVDK
 61 AYIEKYSKAI ELMKALPDDD PRSFKQQANV HCAYCDGAYD QAGFPDLELQ IHNSWLFFPF
121 HRYYLYFHEK ILGSLIGDPT FALPFWNWDA PAGMPLPAIY ANPKSPLYDK FRAANHQPPT
181 LVDLDFNGTE DAASNETQIN ANLKIMYRQM VSNAKTPQLF FGNPYRAGDE PDPGGGSIEG
241 TPHGPVHLWT GDNTQPNFED MGNFYSAGRD PIFFAHHSNV DRLWSIWKTL GGKRTDITDT
301 DWLDSGFLFY DENAQMVRVK VRDCLESKNL GYVYQDANIP WLESKPTPRR VKAALGKIAK
361 KLHVAHAADN SSASKVVARA AFPIAKLDTK MSTVVARPKQ KKRSKKEKEQ EEEILVIEGI
421 EFDRDVAVKF DVYVNDEDDL PSGPDKSEFA GSFVS
```

Spot No.: 168

NCBI accession No.: **gi|225430941** Species: *Vitis vinifera*

PFF score: [210]

Protein name: regulator of ribonuclease-like protein 2

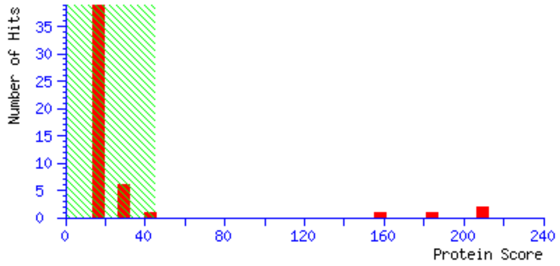
Matched peptides No.: [3] Sequence coverage %: [24]

Matched sequences: K.VFEDNVLIR.E;
R.DVDEINGCDIGVR.A;
R.ISDGEWLYADTDGILISR.T

Calculated Mr: **17984** Calculated *p*I: **5.39**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red

```
  1 MALVTTAEVC DANPQLIVSG ELRALQPVFQ IYGRRPVFSG PIVTLKVFED
 51 NVLIREFLEE KGNGRVLVVD GGGSMRCAIL GGNPVVQAQN NGWAGIVVNG
101 CIRDVDEING CDIGVRALNS HPMKANKKGI GEKHVPIAIA GTRISDGEWL
151 YADTDGILIS RTELSV
```

Spot No.: **169**

NCBI accession No.: **gi|2832430** Species: *Hevea brasiliensis*

PFF score: [152] Protein name: prohevein

Matched peptides No.: [2] Sequence coverage %: [20]

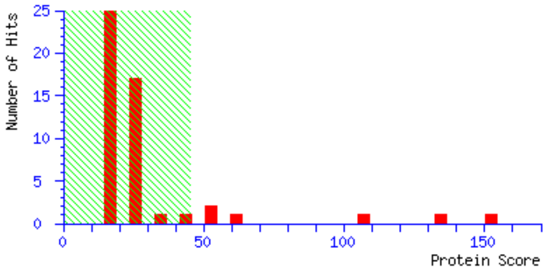
Matched sequences: R.IVDQCSNGGLDLDVNVFR.Q;

K.YGWTAFCGPVGAHGQPSCGK.C

Calculated Mr: **20852** Calculated *p*I: **5.64**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 EQCGRQAGGK LCPNNLCCSQ WGWCGSTDEY CSPDHNCQSN CKDSGEGVGG
51 GSASNVLATY HLYNSQDHGW DLNAASAYCS TWDANKPYSW RSK**YGWTAFC**
101 **GPVGAHGQPS** **CGK**CLSVTNT GTGAKATVR**I** **VDQCSNGGLD** **LDVNVFR**QLD
151 TDGKGYERGH LTVNYQFVDC GDSFNPLFSV MKSSVIN

Spot No.: **170**

NCBI accession No.: **gi|298362843** Species: *Hevea brasiliensis*

PFF score: [110]

Protein name: actin-depolymerizing factor

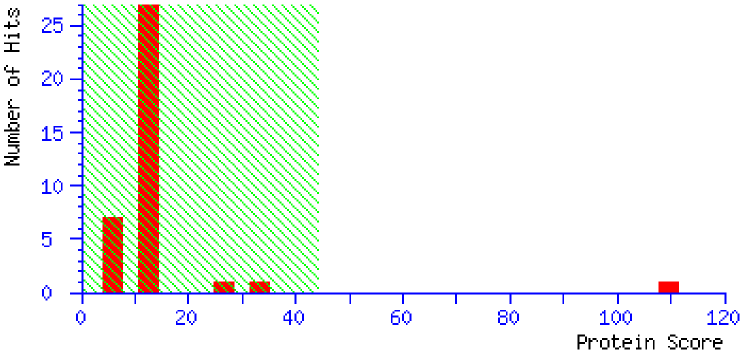
Matched peptides No.: [1] Sequence coverage %: [15]

Matched sequences: K.LGEPTQSYEDFTASLPADECR.Y

Calculated Mr: **16220** Calculated *p*I: **5.92**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MANAASGMAV HDDCKLRFLE LKAKRTYRYI VFKIEEKAKQ VIVEK**LGEPT**
51 **QSYEDFTASL** **PADECR**YAVY DFDFVTEENC QKSRIFFIAW SPDTSRVRSK
101 MIYASSKDRF KRELDGIQVE LQATDPTEMG LDVFKSRAS

Spot No.: 171

NCBI accession No.: **gi|115392253**

Species: *Cercocarpus betuloides*

PFF score: [104] Protein name: actin depolymerizing factor

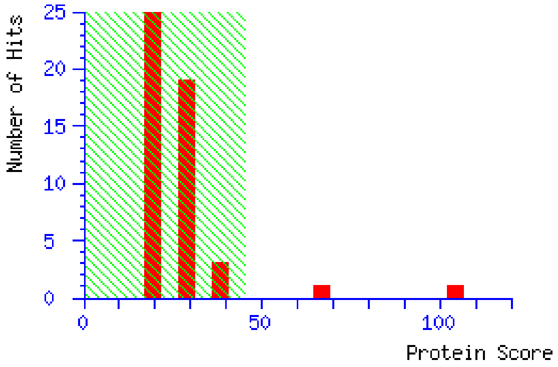
Matched peptides No.: [1] Sequence coverage %: [4]

Matched sequences: K.EKEQEEEILVIEGIEFDR.D

Calculated Mr: **58369** Calculated *p*I: **9.23**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 40 indicate peptides with significant homology.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 PFAFAKPVAP PDVSKCGAAD LPTGAQPTNC CPPVASKIID FKLPSPTPLR VRPAAHAVDK
61 AYIEKYSKAI ELMKALPDDD PRSFKQQANV HCAYCDGAYD QAGFPDLELQ IHNSWLFFPF
121 HRYYLYFHEK ILGSLIGDPT FALPFWNWDA PAGMPLPAIY ANPKSPLYDK FRAANHQPPT
181 LVDLDFNGTE DAASNETQIN ANLKIMYRQM VSNAKTPQLF FGNPYRAGDE PDPGGGSIEG
241 TPHGPVHLWT GDNTQPNFED MGNFYSAGRD PIFFAHHSNV DRLWSIWKTL GGKRTDITDT
301 DWLDSGFLFY DENAQMVRVK VRDCLESKNL GYVYQDANIP WLESKPTPRR VKAALGKIAK
361 KLHVAHAADN SSASKVVARA AFPIAKLDTK MSTVVARPKQ KKRSKK**EKEQ EEEILVIEGI**
421 **EFDR**DVAVKF DVYVNDEDDL PSGPDKSEFA GSFVS

Spot No.: 172

NCBI accession No.: **gi|2832430** Species: *Hevea brasiliensis*

PFF score: [252]

Protein name: prohevein

Matched peptides No.: [3] Sequence coverage %: [26]

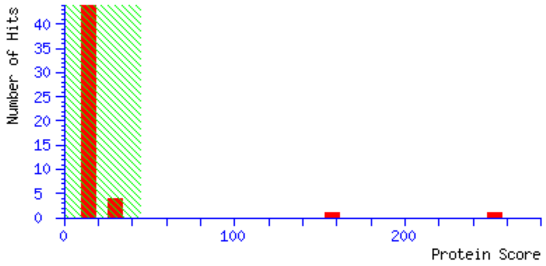
Matched sequences: R.QLDTDGKGYER.G;

R.IVDQCSNGGLDLDVNVFR.Q;
K.YGWTAFCGPVGAHGQPSCGK.C

Calculated Mr: **20852** Calculated *p*I: **5.64**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red

```
  1  EQCGRQAGGK LCPNNLCCSQ WGWCGSTDEY CSPDHNCQSN CKDSGEGVGG
 51  GSASNVLATY HLYNSQDHGW DLNAASAYCS TWDANKPYSW RSKYGWTAFC
101  GPVGAHGQPS CGKCLSVTNT GTGAKATVRI VDQCSNGGLD LDVNVFRQLD
151  TDGKGYERGH LTVNYQFVDC GDSFNPLFSV MKSSVIN
```

Spot No.: **173**

NCBI accession No.: **gi|255574159** Species: *Ricinus communis*

Protein name: proteasome subunit beta type 6,9, putative

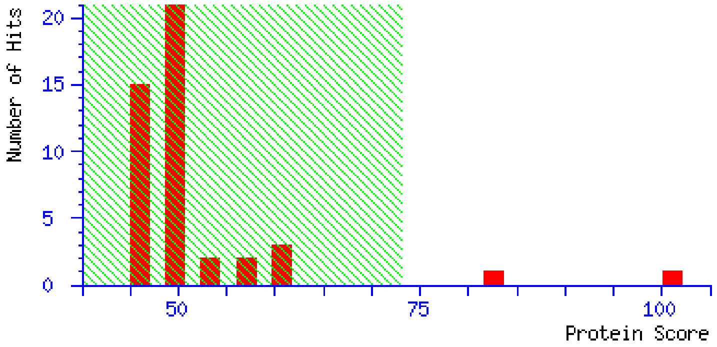
PMF Mascot score: **101** Sequence coverage %: **51**

Matched peptides No.: **14** Total peptides No.: **60**

Calculated Mr: **24912** Calculated *p*I: **5.17**

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red:

1 MDLKAPHSMG TTIIGVTYNG GVVLGADSR**T** **STGMYVANRA** SDK**ITQLTDN**
51 **VYVCRSGSAA** **DSQIVSDYVR** **YFLHQHTIQL** **GQPATVKVAA** **NLVRLISYNN**
101 **KNMLETGLIV** **GGWDK**YDGGK IYGIPLGGTI IEQPFAIGGS GSSYLYGFFD
151 QAWKEGMTK**D** **EAEQLVVKAV** **SLAMARDGAS** **GGVVRTVIIN** **SEGVTR**NFYP
201 GDSLPLWHEE LEPQNSLLDI LNASSPEPMN I

Spot No.: **174**

NCBI accession No.: gi|242059605   Species: *Sorghum bicolor*

PFF score: [117]

Protein name: hypothetical protein SORBIDRAFT_03g043200

Matched peptides No.: [2]   Sequence coverage %: [6]

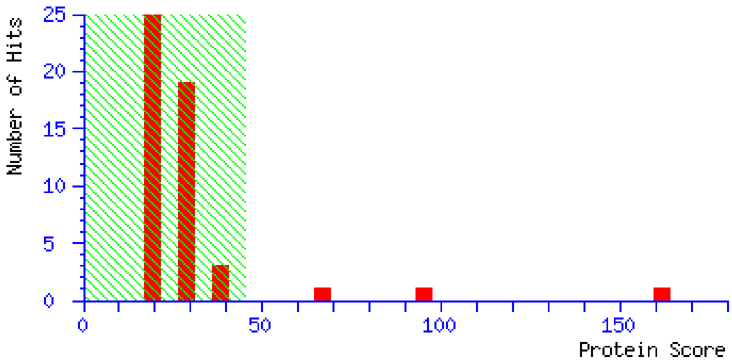
Matched sequences: K.RFFPSEFGNDVDHVHAVEPAK.S;

R.FFPSEFGNDVDHVHAVEPAK.S

Calculated Mr: **34294**   Calculated *p*I: **5.93**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MSSAAGHKER SRVLVIGGTG YIGRFIVAAS AREGHPTYVL VRDPAPADPA
51 KAAVLQGFRD AGVTLVKGDL YNHESLVVAM ESADVVISAV GYAQLPDQTR
101 IISAIKDAGN IK**RFFPSEFG** **NDVDHVHAVE** **PAK**SVFAAKA SIRRAVEAEG
151 IPYTYISSNF FAGRFLPAIG QIGVTGLPID KVLILGDGNV KAIFGTEEDV
201 GTYTIKAVDD PRTLNKILYL RPPSNILSHN ELISLWEKKV GKTFERVYIP
251 EDDVLKKIQE SPIPLNRALS ISHSAWVKGD HTNFEIDPFF GVEATDLYPD
301 VKYTTVDEYL NKFL

Spot No.: **175**

NCBI accession No.: **gi|2832654** Species: *Arabidopsis thaliana*

Protein name: chloroplast protein cs/ch-42

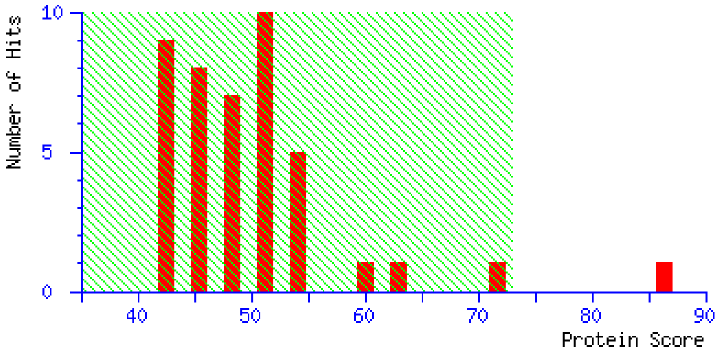
PMF Mascot score: **86** Sequence coverage %: **37**

Matched peptides No.: **16** Total peptides No.: **78**

Calculated Mr: **66408** Calculated *p*I: **6.44**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 **MLCFSASRLD** **DFDLGSSPPK** KGSK**TTTKSM** **DCEEICASSK** SDKSDDLDFG
51 LDLPITR**QVP** **SKANTDVQAK** ASAEK**ESQNY** **KTTDTLVVNK** SKNSNQAALE
101 SMGDFEAVES PQGSRKK**ASQ** **THTMCVQPQS** **VDTSPLK**TSC SKVEEKNEPC
151 PSNETIAPSP LHASEIAHIA VNRETSPDIH ELCRSGTK**ED** **CPIDPENANK**
201 K**MITTMESSY** **EK**IEQTSPSI SSHLCSDKIE HQQEEMGTDT QAEIQDNTK**G**
251 **ALYNSDAGHS** **LTTLSGK**ISP GTR**TSQTAKV** **QDLSEK**LPLD PSHSMAGLDN
301 LR**AMQNKDLG** **LIR**SRFFKKP EKPESHVLES SPIETEIQPV IRENIGSSLN
351 PTNDTSSHEK **IIHKDHSNGK** **TVENVAGQMD** **HLK**LQAKNTT REKSILQINI
401 SSK**LDASSLT** **QKLSNHLSSG** **VESLQK**PKLN SLGRPK**LGNI** **MADLRAVK**TQ
451 RNVEELTHRA VQGKVRFTNR SVILIVTRRK SFLCQESRID TKTTKEPVKE
501 SPQTKSHYQN INMANLEIPI TENADNIEK**A** **EAYTKELENV** **NR**ALFSIMNI
551 LNIICNILKK KHEEAKELLV RAVVDNNKLL MLNHPLYEDQ ISFL

Spot No.: **176**

NCBI accession No.: **gi|27449248**   Species: *Hevea brasiliensis*

PFF score: [487]   Protein name: ascorbate peroxidase

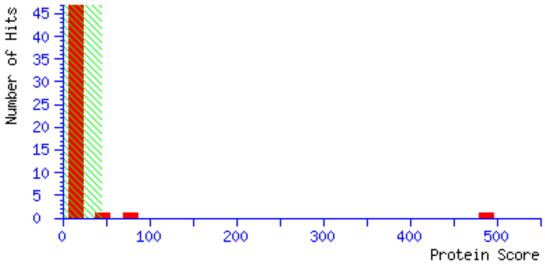
Matched peptides No.: [5]   Sequence coverage %: [34]

Matched sequences: R.EDKPEPPPEGR.L;
R.IAWHSAGTYDANTK.T;
R.HAAEQAHAANNGLDIAVR.L;
K.YAADEDAFFADYAEAHVK.L;
K.EGLLQLPTDTVLVTDPVFRPYVEK.Y

Calculated Mr: **27526**   Calculated *p*I: **5.78**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



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

```
  1  MTKNYPKVSE EYQKAIDKAK RKLRGFIAEK GCAPLMLRIA WHSAGTYDAN
 51  TKTGGPFGTM RHAAEQAHAA NNGLDIAVRL LEPIKQQFPI LSYADFYQLA
101  GVVAVEITGG PEIPFHPGRE DKPEPPPEGR LPNATKGADH LREVFGKTMG
151  LSDKDIVVLS GGHTLGRCHK ERSGFDGPWT ANPLIFDNSF FTELLAGQKE
201  GLLQLPTDTV LVTDPVFRPY VEKYAADEDA FFADYAEAHV KLSELGFAEA
```

Spot No.: **177**

NCBI accession No.: **gi|357480975** Species: *Medicago truncatula*

PFF score: [369]

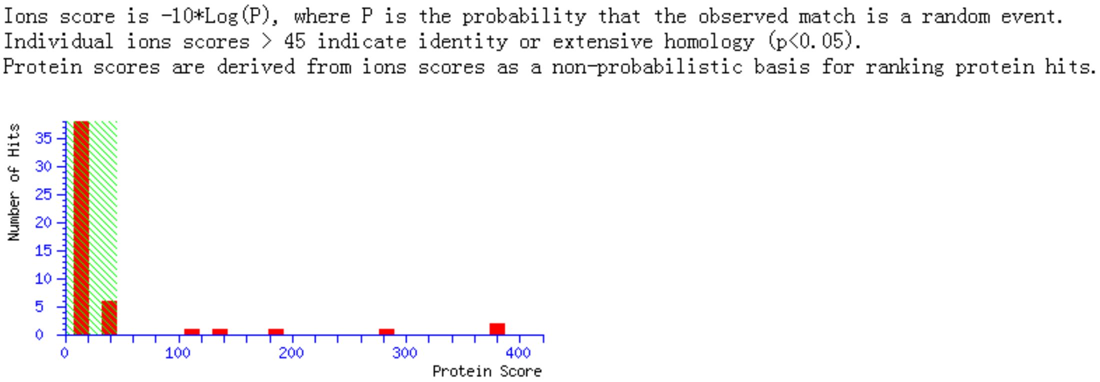
Protein name: Proteasome subunit beta type

Matched peptides No.: [7] Sequence coverage %: [42]

Matched sequences: K.NVALYQFR.N;
R.VQFTEYIQK.N;
R.LVVAPPNFVIK.I;
R.NGIPLTTAAAANFTR.G;
K.GAFGYGSYFSLSMMDR.H;
K.ETGPSLYYIDYIATLHK.L;
K.LIAASGEPGDRVQFTEYIQK.N

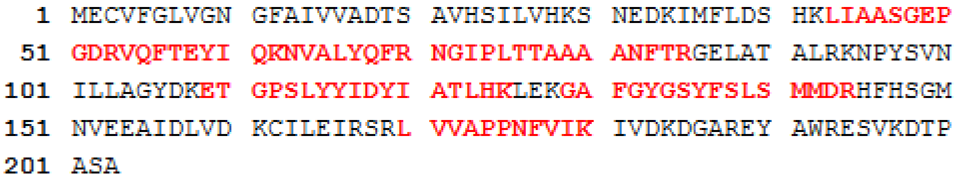
Calculated Mr: **22572** Calculated *p*I: **6.06**

Probability Based Mowse Score:



```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```

Matched peptide sequences: shown in Bold Red:



1 MECVFGLVGN GFAIVVADTS AVHSILVHKS NEDKIMFLDS HK**LIAASGEP**
51 **GDRVQFTEYI** **QKNVALYQFR** **NGIPLTTAAA** **ANFTR**GELAT ALRKNPYSVN
101 ILLAGYDK**ET** **GPSLYYIDYI** **ATLHK**LEK**GA** **FGYGSYFSLS** **MMDR**HFHSGM
151 NVEEAIDLVD KCILEIRSR**L** **VVAPPNFVIK** IVDKDGAREY AWRESVKDTP
201 ASA

Spot No.: **178**

NCBI accession No.: **gi|255541320** Species: *Ricinus communis*

PFF score: [302]

Protein name: proteasome subunit beta type, putative

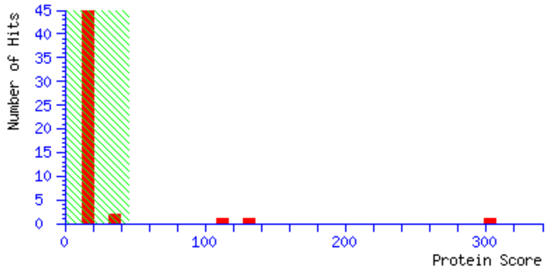
Matched peptides No.: [4] Sequence coverage %: [28]

Matched sequences: K.HLIYQHQHNK.Q;
K.GCVYTYDAVGSYER.V;
R.FFPYYAFNVLGGLDSEGK.G;
R.VGYSAQGSGSTLIMPFLDNQLK.S

Calculated Mr: **24880** Calculated *p*I: **6.08**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

1 MTKQQANWSP YDNNGGSCVA IAGADYCVIA ADTRMSTGYN ILTRDYSKIC
51 QLAEKSVMAS SGFQADVQAL QKHLKAK**HLI** **YQHQHNK**QMS CPAMGQLLSN
101 TLYFKR**FFPY** **YAFNVLGGLD** **SEGKGCVYTY** **DAVGSYERVG** **YSAQGSGSTL**
151 **IMPFLDNQLK** SPSPLLLPAQ DAVTPLSEPE AVDLVKTVFA SATERDIYTG
201 DKVEIVVLNA DGIRREYMEL RKD

Spot No.: 179

NCBI accession No.: gi|350537255

Species: *Solanum lycopersicum*

Protein name： small zinc finger-like protein

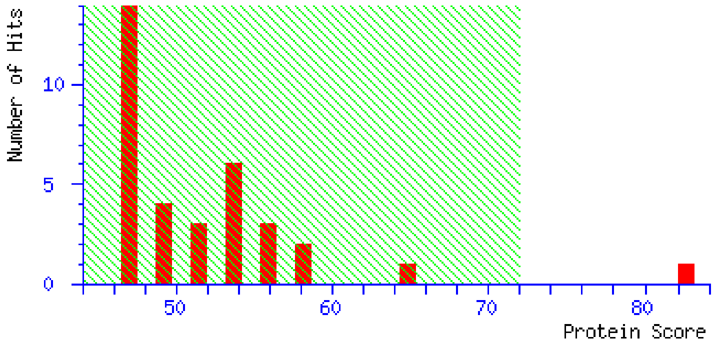
PMF score: 82 Sequence coverage %: 70

Matched peptides No.: 7 Total peptides No.: 40

Calculated Mr: 9669 Calculated *p*I: 6.56

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold red:

1 **MAGVPSNLER** **EQIFSMAEK**E MEYR**VEMFNK** **LTHTCFK**KCV **ENKYKDSELN**
51 **MGENSCIDRC** **VSK**YWQVTNL VGTLLGNTRP M

Spot No.: **180**

NCBI accession No.: **gi|37622210** Species: *Hevea brasiliensis*

Protein name: small rubber particle protein

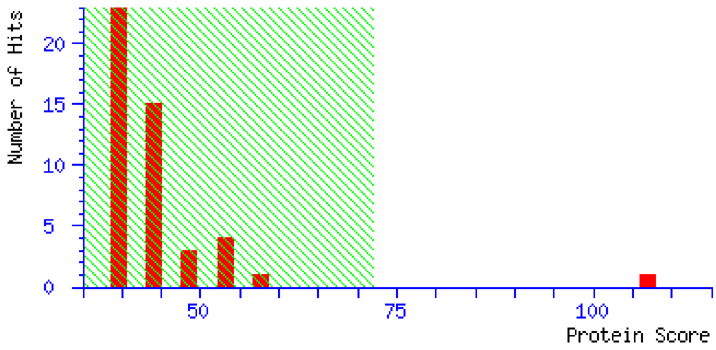
PMF Mascot score: **107** Sequence coverage %: **60**

Matched peptides No.: **10** Total peptides No.: **38**

Calculated Mr: **18929** Calculated *p*I: **8.99**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 K**FHDVPNEVL** **KFVDR**K**VDES** **VTSLDSR**VPP VVK**QVSAQAY** **SVAREAPVAA**
51 **RAVASEVHQS** **GVK**ETASGLA KTLYTKYEPK AKELYSKYEP K**AEQCAVTAW**
101 **R**RLNQLPLFP QVAQVVVPTA AYCSEK**YNQT** **VLSTFEK**GYR **VSSYLPLVPT**
151 **ERI**AK**VFSDD** **VAQSMPLVSS**

Spot No.: 181

NCBI accession No.: gi|168038495

Species: *Physcomitrella patens subsp. patens*

Protein name：predicted protein

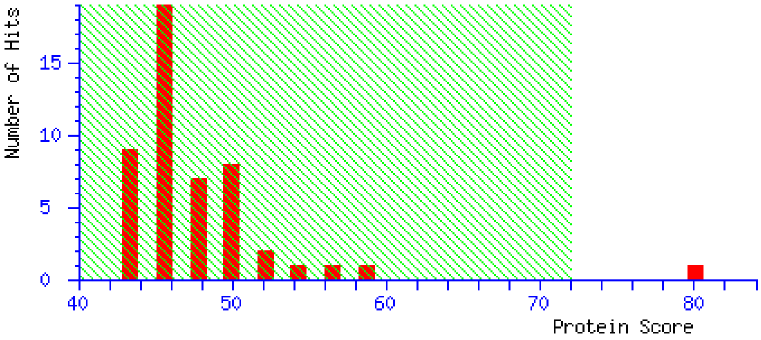
PMF score: **81** Sequence coverage %: **36**

Matched peptides No.: **18** Total peptides No.: **81**

Calculated Mr: **61349** Calculated *p*I:**5.80**

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold red:

1 MQAPVLVLNE STKR**ETGGRV** **HHANIQASK**A VADVIRTTLG PRSMLKMLLD
51 ASGGIVLTND GNAILRELDV SHPAAKSMIE LSRTQDEEVG DGTTSVIILA
101 GEMLYVAEQF LDR**QFHPTVI** **CRAYTKALED** **AVAALKEIAF** **DIDITDRTMM**
151 **LNIVRSCIGT** **K**FTSRFGTLI ADLAIDSVAT ISVDLGNGLR **EVDIK**KYIKV
201 EK**IPGGQLED** **SKVLK**GVMFN KDVVSPGKMR R**KILNPR**IIL LDSPLEYKK**G**
251 **ENQTNAEIMK** EEDWATLLRM EEEYIEQLCV QIIKFKPDLV ITEKGLSDLA
301 SHYLSKAGIS AIRRLRKTDN NRIAR**ACGAT** **IVNRPEELQE** **SDVGTRCGLF**
351 **EVK**KIGDEYF TFIVQCNEPK **ACTVLLRGPS** **KDLLNEVERN** **LADAMGVARN**
401 **VIK**DAKLVPG GGASEMAVSA ILKKNSMSIE GVEQWPYRAV AQALEVIPRT
451 LAQNCGVNVI RTMTALQAK**H** **ANAENPMFGI** **DGNTGELTDM** **K**ELGVWDSFG
501 VK**LQTFKTAI** **EAACMLLR**ID DIVSGIKKKQ APGAAPK**QPM** **TSTGEDVDSE**
551 **QMIPE**

Spot No.: **182**

NCBI accession No.: **gi|164472662** Species: *Triticum aestivum*

Protein name: calcium-dependent protein kinase

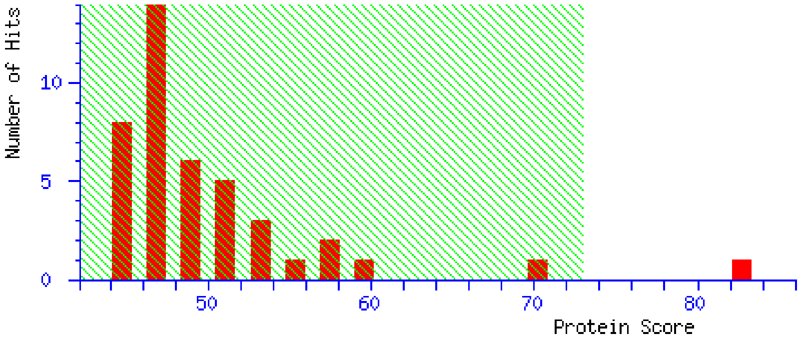
PMF Mascot score: **82** Sequence coverage %: **28**

Matched peptides No.: **17** Total peptides No.: **74**

Calculated Mr: **61353** Calculated *p*I: **6.04**

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 73 are significant ($p<0.05$).



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

1 **MGNCCRSPAA** **AAR**EDVSSSH FPASAGKRK**P** **HQARNGGGGG** **AGGGGGGGGA**
51 **GAGGEK**KRLS VLGEEGPDVS GGIDDK**YALD** **RELGRGEFGV** **TYLCMDR**GSK
101 ELLACKSISK RKLR**TPVDVE** **DVR**REVAIMR HLPRSASIVT LREACEDDGA
151 GHLVMELCEG GELFDRIVAR GHYTER**AAAA** **VTR**TIVEVVQ LCHHHGVIHR
201 **DLKPENFLFA** **NK**KENSPLKA IDFGLSIFFK PGEKFSEIVG SPYYMAPEVL
251 KRNYGPEIDI WSAGVILYIL LCGVPPFWAE TEQGVAQAIL R**GNIDFK**REP
301 WPHVSDNAKD LDRQMLQPDP KIRLTAKQVL EHTWLQNAKK **APNVPLGDIV**
351 **KSR**LKQFSRM NRFKRRALRV IADHLSAEEV EDIKEMFK**VM** **DTDNDGIVSY**
401 **EELK**SGIAKF GSHLAESEVQ MLIEAVDTNG RGALDYGEFL AVSLHLQR**MA**
451 **NDEHLRR**AFL FFDKDGDGFI EPEELQEALA EDGAVDITEV VK**DILQEVDT**
501 **DKDGKISFEE** **FVAMMK**TGTD WRKASRHYSR GRFNSLSIRL IKDGSVKMGN
551 E

Spot No.: **183**

NCBI accession No.: **gi|32527831**

Species: *Populus tremula x Populus tremuloides*

Protein name: UDP-glucose pyrophosphorylase

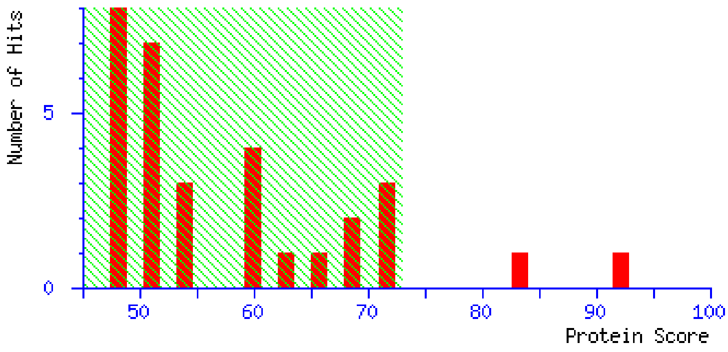
PMF Mascot score: **92** Sequence coverage %: **29**

Matched peptides No.: **12** Total peptides No.: **45**

Calculated Mr: **51949** Calculated *p*I: **5.68**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MATDTEKISQ LKSAVANLNQ ISESEKTGFV NLVSR**YLSGE** **AQQVEWSK**IQ
51 TPTDEVVVPY DTLESTPEDP EETKMLLDKL VVLK**LNGGLG** **TTMGCTGPKS**
101 **VIEVR**NGLTF LDLIVIQIES LNKKYGCSVP LLLMNSFNTH DDTQKIIEKY
151 SNSNIEIHTF NQSQYPR**LVA** **DDFVPLPSKG** HTDK**DGWYPP** **GHGDVFPSLK**
201 NSGKLDALLS QGKEYVFVAN SDNLGAVVDL KILNHLIR**NK** **NEYCMEVTPK**
251 TLADVK**GGTL** **ISYEGKVQLL** **EIAQVPDQHV** **NEFK**SIEKFK IFNTNNLWVN
301 LKAIKRLVEA DALK**MEIIPN** **PKEVDGVKVL** **QLETAAGAAI** **R**FFDHAIGIN
351 VPRSRFLPVK ASSDLLLVQS DIYTPVVDGF VIRNPGRANP ANPSIELGPE
401 FKKVASFLSR FKSIPSIIEL DSLKVAGDVW FGVNVTLKGK VSIVVKSGVK
451 LEIPEGVVLE NK**EINGPKDL**

Spot No.: **184**

NCBI accession No.: **gi|356576773** Species: *Glycine max*

Protein name: seryl-tRNA synthetase-like

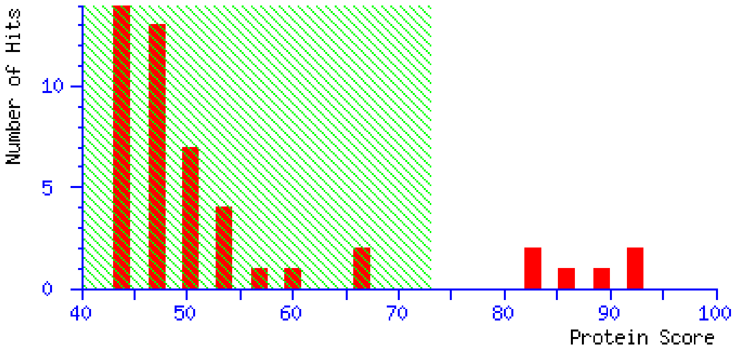
PMF Mascot score: **92** Sequence coverage %:**28**

Matched peptides No.: **17** Total peptides No.: **53**

Calculated Mr: **51822** Calculated *p*I:**6.04**

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red

1 **MLDINLFREE** **K**GHNPEFIRE SQRRRFASVE VVDEVINLDK **EWRK**RQFELE
51 NLRKEFNKIN KEVSKLKRAG EDATKFISES EETKK**SIGEK** **EVEVR**ETLNL
101 LNSKLETIGN LVHDSVPISQ DEANNVVVRS WGEKR**VEPKL** **K**NHVDLVELL
151 GIADTKKGAD VAGGR**GFYLK** GDGVR**LNQAL** **INFGLDFLEK** **R**EYTLLHTPF
201 FMRKDIMSK**C** **AQLAQFDEEL** **YK**VTGEGDDK YLIATAEQPL CAYHLDDWIH
251 PTQLPLR**YAG** **YSSCFR**KEAG SHGR**DTLGIF** **RVHQFEK**VEQ FCLTSPNDND
301 SWDMHEEMLK **NSEDFYK**ALN LPYQVVSIVS GALNDAAAKK **YDLEAWFPAS**
351 **QAYR**ELVSCS NCTDYQAR**RL** **EIR**YGQKKSN EQMK**QYVHLL** **NSTLTATER**T
401 ICCILENNQK EDGVEIPEAL RPFMGGKTFL PFKNQPSNEA KGKKSKA

Spot No.: **185**

NCBI accession No.: gi|357514973 Species: *Medicago truncatula*

PFF score: [51]

Protein name: annexin, putative

Matched peptides No.: [2] Sequence coverage %: [7]

Matched sequences: R.SSEELLGAR.K;

R.FENALVIWAMHPWER.D + Oxidation (M)

Calculated Mr: **35872** Calculated *p*I: **6.04**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
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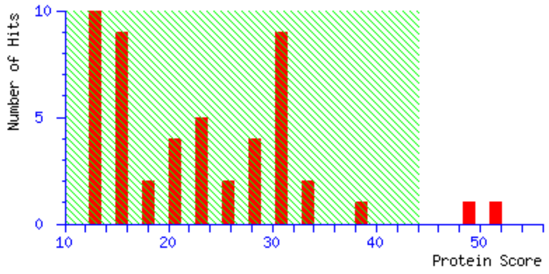


Matched peptide sequences: shown in Bold Red:

1 MAHPEELEAL TKAFSGLGVD EKSLISILGK SHPEHRKSFR KGSPHLFIED
51 ERSFERWDDD SVHLLRQEFA R**FENALVIWA** **MHPWER**DARL IYEALREGPQ
101 SYGVIVEIAC TR**SSEELLGA** **R**KAYHSLFDH SIEEDVATHI SGTERKLLVA
151 LASAYRYEGP KVKEDSAKFE AKIFANAVKN GDKTNPIEDD EVIRILSTRS
201 KPHLKAVYKH YKEISGNGII EDLGAANLIL KETVECLCTP HAFFSKVLDK
251 AMRKDADHNT KKALTRVIVT QADIDLKEIS EQYNSLYGIP LSKKVEETAN
301 GNYKDFLLAL ISREN

Spot No.: **186**

NCBI accession No.: **gi| 1351887** Species: *Malus x domestica*

PFF score: [63]

Protein name: Alcohol dehydrogenase

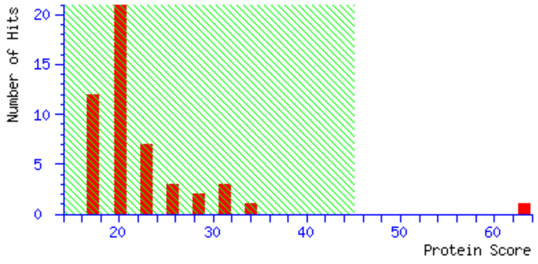
Matched peptides No.: [1] Sequence coverage %: [7]

Matched sequences: K.SMGMPDEDEAAVELAWSR.F

Calculated Mr: 42066 Calculated *p*I: **6.48**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MLAAAIRSLS PSSTSSIFNK SALPPLLRSL SPSLSNSRFQ IRSMADSASS
51 PFKKVQIHRD NTTFDAYVIG KDDAPGIVVV QEWWGVDFEI KNHAEKISQL
101 EPGFKALIPD LYRGKVGLDV AEAQHLMDGL DWQGAVKDIG ASVNWLKANG
151 SKKAGVTGFC MGGALAIASS VLVPEVDAVV AFYGVPPSEL ADATQAKAPI
201 QAHFGELDNF VGFADITAAK ALEEKLKASG VPSEVHIYPG NAHAFMNRSA
251 EGVKRRK**SMG** **MPDEDEAAVE** **LAWSR**FRSWM NQYLSA

Spot No.: **187**

NCBI accession No.: **gi|380468126** Species: *Hevea brasiliensis*

PFF score: [123]

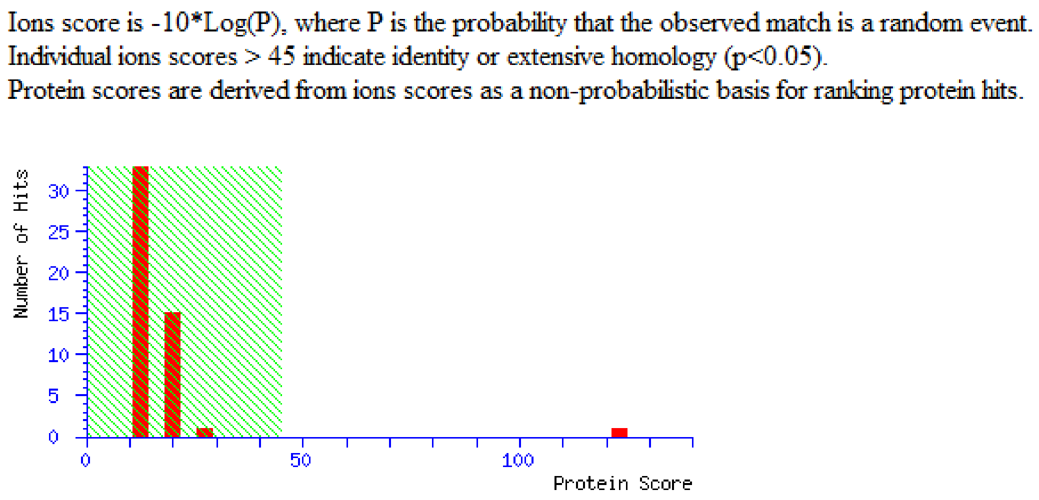
Protein name: caffeic acid 3-O-methyltransferase

Matched peptides No.: [3] Sequence coverage %: [11]

Matched sequences: K.NPEAPVLLDR.M;
K.SWYHLNEAILEGGTPFNR.A;
R.AYGMNQFEYPGTDQR.F + Oxidation (M)

Calculated Mr: **40957** Calculated *p*I: **5.54**

Probability Based Mowse Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Matched peptide sequences: shown in Bold Red:

1 MTGSEQSNSA SIMSGRSDEE TWNLAIDLAN TVILPMVLKS ALELNVIDII
51 STAGNSGASL SAPEIAQRIP EAK**NPEAPVL** **LDR**MLRLLAT YDIVKCSSNT
101 KENGEVERLY APGPICKFLT KNKNGSGSAA PLLLLHHDEV FMK**SWYHLNE**
151 **AILEGGTPFN** **RAYGMNQFEY** **PGTDQR**FNRV FNDAMSSYTT YLVKKILDAY
201 KGFDGLKSLV DVGGNSGVTL NSITSKYPHI KGINYDLPHV LADAPSYPGV
251 EHVAGDMFKS VPKGDAIILK WVLHDWNDDL CLKLLKNCWE ALPSNGKVIV
301 VESILPTVPE NNVTSQVLHK EDLMLLSFNV GGKERTRQEF EALASKSGFS
351 SCEFICCAYN SWVIEFHK

Spot No.: **188**

NCBI accession No.: **gi|380468126** Species: *Hevea brasiliensis*

PFF score: [117]

Protein name: caffeic acid 3-O-methyltransferase

Matched peptides No.: [2] Sequence coverage %: [8]

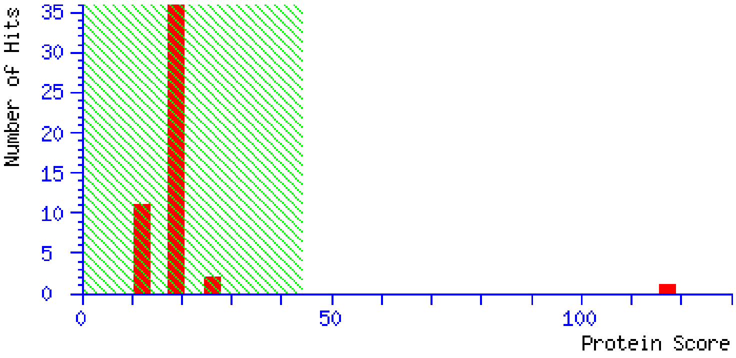
Matched sequences: K.SWYHLNEAILEGGTPFNR.A;

R.AYGMNQFEYPGTDQR.F + Oxidation (M)

Calculated Mr: **40957** Calculated *p*I: **5.54**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MTGSEQSNSA SIMSGRSDEE TWNLAIDLAN TVILPMVLKS ALELNVIDII
51 STAGNSGASL SAPEIAQRIP EAKNPEAPVL LDRMLRLLAT YDIVKCSSNT
101 KENGEVERLY APGPICKFLT KNKNGSGSAA PLLLLHHDEV FMK**SWYHLNE**
151 **AILEGGTPFN RAYGMNQFEY PGTDQR**FNRV FNDAMSSYTT YLVKKILDAY
201 KGFDGLKSLV DVGGNSGVTL NSITSKYPHI KGINYDLPHV LADAPSYPGV
251 EHVAGDMFKS VPKGDAIILK WVLHDWNDDL CLKLLKNCWE ALPSNGKVIV
301 VESILPTVPE NNVTSQVLHK EDLMLLSFNV GGKERTRQEF EALASKSGFS
351 SCEFICCAYN SWVIEFHK

Spot No.: **189**

NCBI accession No.: **gi|284433794** Species: *Jatropha curcas*

PFF score: [159]

Protein name: glutathione S-transferase omega

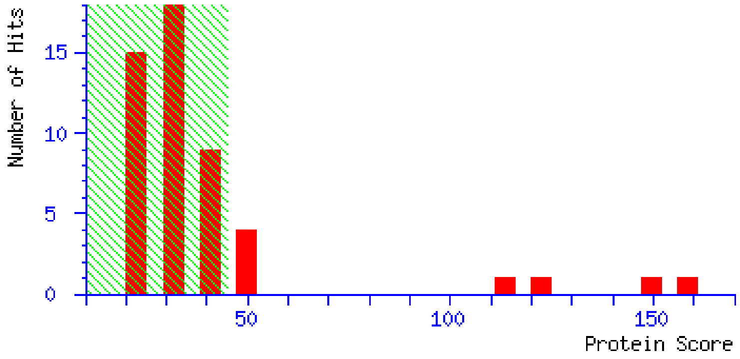
Matched peptides No.: [3] Sequence coverage %: [10]

Matched sequences: K.IIGESLDLIK.Y;
K.YDITAGRPK.L;
K.ELVEFYK.K

Calculated Mr: **27480** Calculated *p*I: **5.41**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAATALDKSL PEKLPPILDA TAEQPPLFDG TIRLYTSYAC PFAQRVWITR
51 NYKGLQDKIK LVPLNLQNRP SWYGEKVYPA NKVPALEHNG **KIIGESLDLI**
101 **K**YIDANFEGP SLLPDDPAKK EFAEELFSYT DTFTKTVFTS FKGDAVKDAS
151 PAFDYLENAL HKFEDGPFLL GQFSLVDIAY IPFVERFQIF FSEVFK**YDIT**
201 **AGRPK**LAAWI EEMNKIEAYK QTKTDPK**ELV** **EFYK**KRLLAQ

Spot No.: **190**

NCBI accession No.: **gi|255567721** Species: *Ricinus communis*

PFF score: [52]

Protein name: carboxymethylenebutenolidase, putative

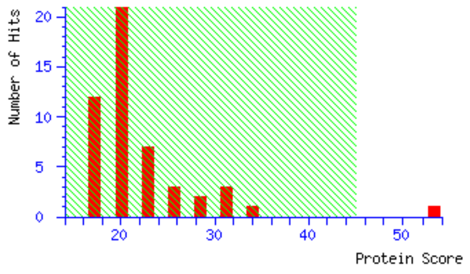
Matched peptides No.: [1] Sequence coverage %: [6]

Matched sequences: K.SMGMPDEDEAAVELAWSR.F + 2 Oxidation (M)

Calculated Mr: 30833 Calculated *p*I: **6.09**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MLAAAIRSLS PSSTSSIFNK SALPPLLRSL SPSLSNSRFQ IRSMADSASS
51 PFKKVQIHRD NTTFDAYVIG KDDAPGIVVV QEWWGVDFEI KNHAEKISQL
101 EPGFKALIPD LYRGKVGLDV AEAQHLMDGL DWQGAVKDIG ASVNWLKANG
151 SKKAGVTGFC MGGALAIASS VLVPEVDAVV AFYGVPPSEL ADATQAKAPI
201 QAHFGELDNF VGFADITAAK ALEEKLKASG VPSEVHIYPG NAHAFMNRSA
251 EGVKRRK**SMG MPDEDEAAVE LAWSR**FRSWM NQYLSA

Spot No.: **191**

NCBI accession No.: **gi|125573095**

Species: *Oryza sativa Japonica Group*

PFF score: [59] Protein name: hypothetical protein OsJ_04535

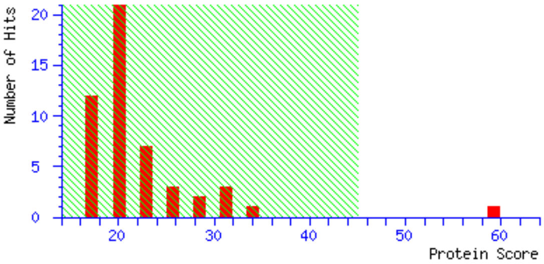
Matched peptides No.: [1] Sequence coverage %: [8]

Matched sequences: M.SSWNSPYYDTSSYGAGSGGGGGGGR.R

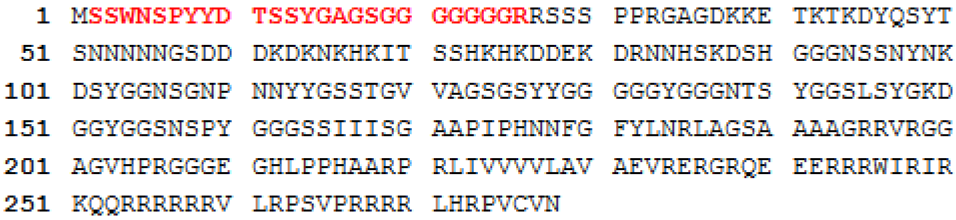
Calculated Mr: **29680** Calculated *p*I: **10.36**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:



```
  1 MSSWNSPYYD TSSYGAGSGG GGGGGRRSSS PPRGAGDKKE TKTKDYQSYT
 51 SNNNNNGSDD DKDKNKHKIT SSHKHKDDEK DRNNHSKDSH GGGNSSNYNK
101 DSYGGNSGNP NNYYGSSTGV VAGSGSYYGG GGGYGGGNTS YGGSLSYGKD
151 GGYGGSNSPY GGGSSIIISG AAPIPHNNFG FYLNRLAGSA AAAGRRVRGG
201 AGVHPRGGGE GHLPPHAARP RLIVVVVLAV AEVRERGRQE EERRRWIRIR
251 KQQRRRRRRV LRPSVPRRRR LHRPVCVN
```

Spot No.: **192**

NCBI accession No.: **gi|255542380** Species: *Ricinus communis*

Protein name: cysteine synthase, putative

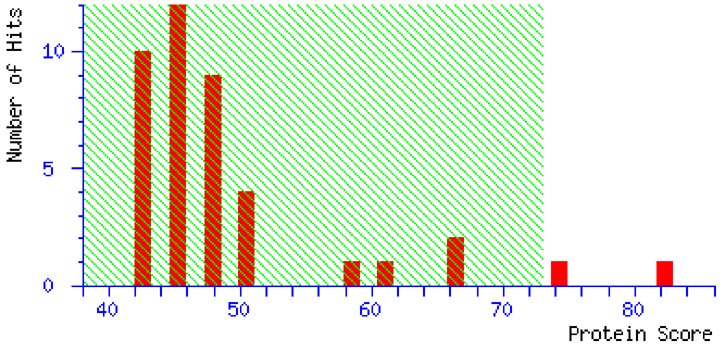
PMF Mascot score: **82** Sequence coverage %: **37**

Matched peptides No.: **13** Total peptides No.: **59**

Calculated Mr: **34435** Calculated *p*I: **5.50**

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 73 are significant ($p<0.05$).



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

1 MVEEKSAIAK DVTELVGK**TP** **LVYLNHVVDG** **CVARIAAKLE** **MMEPCSSVK**D
51 RIGYSMITDA EEK**GLIKPGE** **SVLIEPTSGN** **TGIGLAFMAA** **AK**GYK**LIITM**
101 **PASMSLERRM** **VLRAFGAELV** **LTDPAR**GMKG AVQKAEEILA KTPNSYILQQ
151 FENPANPKIH YETTGPEIWK GSGGKVDFFV SGIGTGGTVT GAGGYLREQN
201 PDIKLIGVEP VESAVLSGGK PGPHKIQGIG AGFIPGVLDV SLLDEVVQIS
251 SEEAIETAKL LALK**EGLLVG** **ISSGAAAAAA** **IK**IARR**PENA** **GK**LIVVIFPS
301 FGER**YLSSVL** **FESVKR**EAES MVFEP

Spot No.: **193**

NCBI accession No.: **gi|255562276** Species: *Ricinus communis*

PFF score: [57]

Protein name: pyridoxine kinase, putative

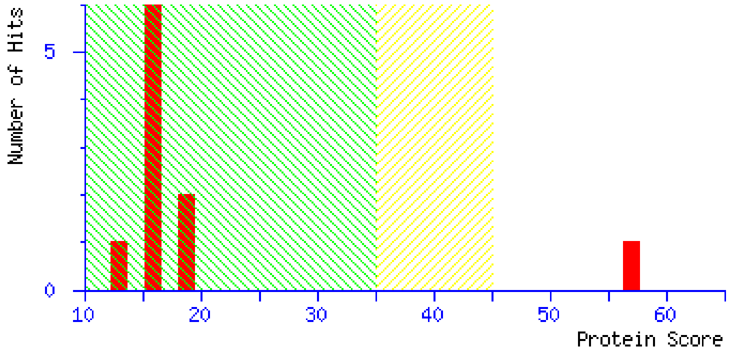
Matched peptides No.: [1] Sequence coverage %: [4]

Matched sequences: K.LYVPPELVAVYR.E

Calculated Mr: **32436** Calculated *p*I: **5.56**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 35 indicate peptides with significant homology.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAPPILSLAL PSGTGRVLSI QSHTVQGYVG NKSAVFPLQI LGYDVDPINS
51 VQFSNHTGYP SVKGQVLNGQ QLWDLIEGLE GNDLLYYTHL LTGYIGSVSF
101 LNTILEVVNK LRSINPKLTY VCDPVMGDEG K**LYVPPELVA VYR**EKVVPVA
151 SMLTPNQFEA EQLTGFRIVT EKDGREACNT LHAAGPSKVI ITSINIDGNL
201 LLVGSHQKEK DQPPEQFKIE IPKIPAYFTK YPDNLGTAAE LAVSSLQALL
251 QRTVNDYRSV GYDPQSSSLE IRLIQSQDDI RHPQVKFKAE KYD

Spot No.: **194**

NCBI accession No.: **gi|255552291** Species: *Ricinus communis*

PFF score: [303]

Protein name: short chain dehydrogenase, putative

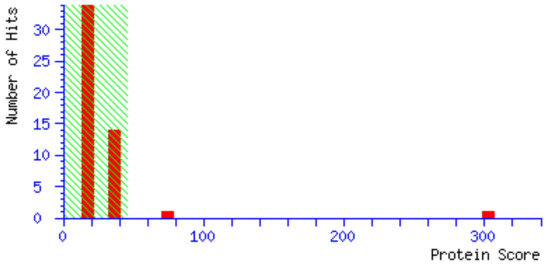
Matched peptides No.: [3] Sequence coverage %: [11]

Matched sequences: K.VALVTGGDSGIGR.A;
K.DPIAIPTDVGFEENCR.K;
K.AEGAKDPIAIPTDVGFEENCR.K

Calculated Mr: **32148** Calculated *p*I: **6.50**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MATRRGYRFP PQSQDKQPGK EYLMHPLPEF INPHYKPSNK LQDK**VALVTG**
51 **GDSGIGR**AVS YYFTLEGATV AFTYVKGRED KDKDHILKIL HEVK**AEGAKD**
101 **PIAIPTDVGF EENCR**KVIDQ IMSEYGKIDI LVNNAGEAHY STTIEDITDP
151 MLERVFRTNI FGHFFMSRHA LKHMKEGGCI INTASVAAYA GFSFMVDYSS
201 TKGAVVAFTR SLALQLIDRG IRVNAVAPGS VWTPFQPSTL SAEQVAQVGS
251 GVPMDRAAQP YEIAPSFVFL ASNDCSSYFT GQVLHPNGMF

Spot No.: **195**

NCBI accession No.: gi|255543357 Species: *Ricinus communis*

Protein name: heat shock protein, putative

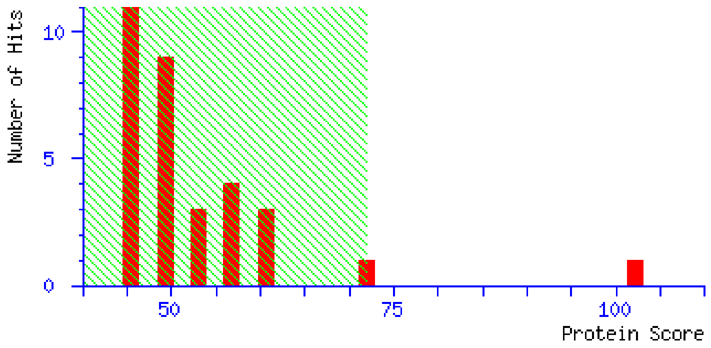
PMF Mascot score: **102** Sequence coverage %: **27**

Matched peptides No.: **18** Total peptides No.: **61**

Calculated Mr: **71.965** Calculated *p*I: **5.27**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MAKTEGKAVG IDLGTTYSCV GVWQNDR**VEI** **IANDQGNRTT** **PSYVAFTDTE**
51 **R**LIGDAAKNQ VAMNPQNTVF DAKRLIGRRF SDPSVQSDMK HWPFKVVPGP
101 GDK**PMIVVLY** **KGEEK**QFAPE EISSMVLIKM KEIAEAYLGQ TVK**NAVITVP**
151 **AYFNDSQR**QA TK**DAGAISGL** **NVMRIINEPT** **AAAIAYGLDK** KGSRSGEKNV
201 LIFDLGGGTF DVSLLTIEEG IFEVK**ATAGD** **THLGGEDFDN** **RLVNHFVAEF**
251 **R**RKHKKDIST NARALRRLRT ACERAKRTLS STSQTTIEID SLYEGIDFYS
301 TITR**ARFEEL** **NMDLFRKCME** **PVEK**CLRDSK IDKSQVDDIV LVGGSTRIPK
351 VQQLLQDFFN GKELCKSINP DEAVAYGAAV QAAILSGEGD QKVQELLLLD
401 VTPLSLGIET AGGVMTVLIP RNTTIPAKKE QIFSTYSDNQ PGVLIQVYEG
451 ERARTKDNNL LGTFELKGIP PAPR**GVPQIN** **VCFDIDANGI** **LNVSAEDK**TA
501 GVKNKITITN DKGRLSKEDI ERMVQEAEKY KAEDEQVKKK VEAKNALENY
551 AYNMR**NTVKD** **EK**FAGKLDSA DKQKIEK**AID** **ETIEWLDGNQ** **LAEVDEFEDK**
601 **LK**ELEGLCNP IVSKMYQGGA GGDVPMGGGA KPGSGYGNAS SGGSGSGPKI
651 EEVD

Spot No.: **196**

NCBI accession No.: **gi|224139936** Species: *Populus trichocarpa*

Protein name： predicted protein

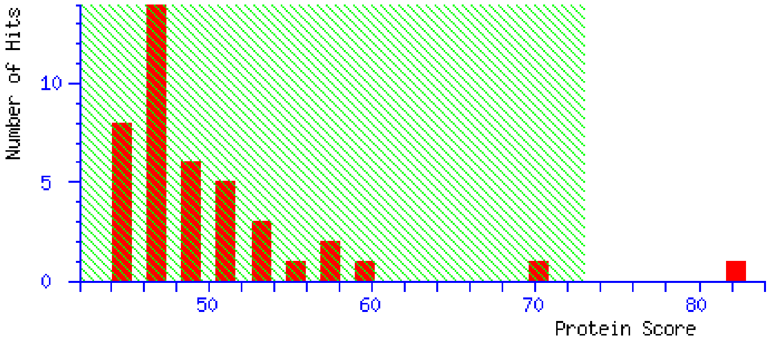
PMF score: **82** Sequence coverage %: **15**

Matched peptides No.: **80** Total peptides No.: **22**

Calculated Mr: **68859** Calculated *p*I: **7.90**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 **MGSMFLNSPL** **PASNK**LIRVS SK**CDWCFLRW** RKRNVVVYCQ GGGGKAIR**SS**
51 **GFPSVLTERS** AVVSDQEHIA SVRDAGSLVL SPNEKGQPEI AVEDFVPYGG
101 PTSSSLLEMQ DGIGIVKFLR GKGLFISGAT GFLAK**VLIEK** **ILRTMPDVGK**
151 IYVLIKAESK EAAITR**LKNE** **IINAELFKCL** **R**QTHGKSYQS FMLNKLVPVV
201 GNVCESNLGL EEDLADKIAN EVDIIVNSAA NTTFDER**YDV** **AIDVNTR**GTC
251 HLMSFAKKCP KLK**LFLQVST** **AYVNGQR**QGR IMEKPFLFGD CIARENLIIS
301 ESTPRFAPAL DIEHEMNLAL DSKEAFQENE VAQKMKELGL ERARK**YGWQD**
351 **TYVFTKAMGE** **MVVDNMRGDI** **PVVIIRPSVI** **ESTCK**EPFPG WMEGNR**MMDP**
401 **IVLYYGK**GQL TGFLVDPNGV LDVVPADMVV NATLAAMAWH GMEQKPDINV
451 YQIASSVVNP LVFQDLATLL HEHYNSSPYM DSNGRPIHVP SMKLFSSMEE
501 FSAHLWRYVT QRSRLAGMAT SDRKLSQKHE NICRKSVEQA KYLASIYEPY
551 TFYGGRFDNS NTQKLMERMS ENEKGIFGFD VGSIDWRDYI TNVHIPGLRR
601 HVMKGRGMCG

Spot No.: **197**

NCBI accession No.: **gi|351727028** Species: *Glycine max*

Protein name: cell division cycle protein 48 homolog

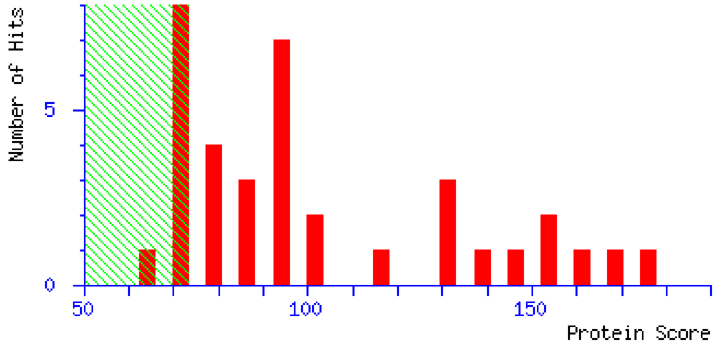
PMF Mascot score: **174** Sequence coverage %: **42**

Matched peptides No.: **37** Total peptides No.: **90**

Calculated Mr: **90512** Calculated *p*I: **5.18**

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red:

1 MSQQGESSDP KSGKK**DFSTA** **ILER**KKSPNR LVVDEAVNDD NSVVTMHPQT
51 MEK**LQLFR**GD TILIKGKKRK DTICIALADE NCEEPKIRMN KVVRSNLRVR
101 **LGDVVSVHQC** **PDVK**YGKRVH ILPIDDTIEG VTGNLFDAFL KPYFLEAYRP
151 VR**KGDLFLVR** GGMRSVEFKV VETDPGEYCV VAPDTEIFCE GEPLKREDEE
201 RLDEVGYDDV GGVR**KQMAQI** **RELVELPLRH** **PQLFK**SIGVK PPK**GILLYGP**
251 **PGSGK**TLIAR AVANETGAFF FCINGPEIMS K**LAGESESNL** **R**KAFEEAEKN
301 APSIIFIDEI DSIAPKREK**T** **HGEVERRIVS** **QLLTLMDGLK** **SRAHVIVIGA**
351 **TNRPNSIDPA** **LRRFGRFDRE** **IDIGVPDEVG** **RLEVLR**IHTK NMKLSDDVDL
401 ERIAK**DTHGY** **VGADLAALCT** **EAALQCIR**EK MDVIDLEDET IDAEVLNSMA
451 VTNEHFQTAL GTSNPSALR**E** **TVVEVPNVSW** **EDIGGLENVK** **RELQETVQYP**
501 **VEHPEKFEK**F GMSPSK**GVLF** **YGPPGCGK**TL LAK**AIANECQ** **ANFISVKGPE**
551 **LLTMWFGESE** **ANVR**EIFDKA R**QSAPCVLFF** **DELDSIATQR** **GSSVGDAGGA**
601 **ADRVLNQLLT** **EMDGMSAK**KT VFIIGATNRP DIIDPALLRP GR**LDQLIYIP**
651 **LPDEDSRHQI** **FK**ACLRKSPI AKNVDLRALA RHTQGFSGAD ITEICQRACK
701 YAIRENIEKD IERERKSREN PEAMDEDTVD DEVAEIKAAH FEESMKFARR
751 **SVSDADIRKY** **QAFAQTLQQS** **R**GFGSEFRFP ESGDRTTTGS DPFAASAGGA
801 DEDDLYS

Spot No.: **198**

NCBI accession No.: **gi|4235430** Species: *Hevea brasiliensis*

Protein name: latex-abundant protein

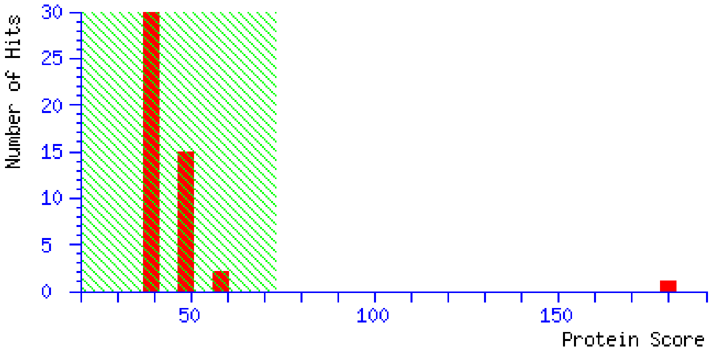
PMF Mascot score: **180** Sequence coverage %: **76**

Matched peptides No.: **22** Total peptides No.: **58**

Calculated Mr: **46443** Calculated *p*I: **5.01**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MAKKAVLIGI NYPGTKAELK GCINDVKRMY RCLVDR**YGFS** **EEDITVLIDI**

51 **DESYIQPTGK** NIRR**VLTDLV** **RSAEPGDLLF** **VHYSGHGTRL** **PAETGEDDDT**

101 **GFDECIVPCD** **MNLITDDDFR** **EFVDQVPHGC** **RITVVSDSCH** **SGGLIDEAK**E

151 QIGESTKR**KE** **EESESGFGFK** SFLK**QTIQDA** **FESRGVHLPS** **DLHHHHGHRD**

201 **EEDFDNRVVE** **EDYGDSGYVK** SK**SLPLSTLI** **EILK**QKTGKD DIDVGK**LRPT**

251 **LFDMFGDDAS** **PK**VKKFMKVI LNKLR**HGDGE** **SGGGGFLGMV** **GSLAQEFLKH**

301 **KLDENDESYV** **KPALETEVDS** **K**QEVYAGKTK R**SLPDGGILI** **SGCQTDQTSA**

351 **DASPSGKSSE** **AYGALSNAIQ** **TIIAETDGAV** **TNQELVLK**AR KMLK**KQGFTQ**

401 **KPGLYCSDDH** **VEASFVC**

Spot No.: **199**

NCBI accession No.: **gi|198400319** Species: *Camellia sinensis*

PFF score: [57]

Protein name: senescence-related protein

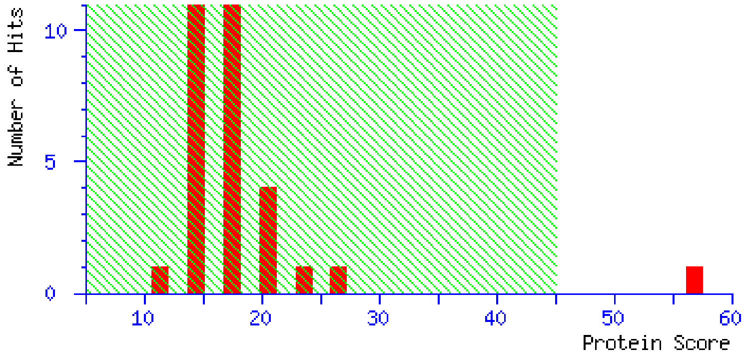
Matched peptides No.: [1] Sequence coverage %: [2]

Matched sequences: K.GILWCGDVTVDR.L

Calculated Mr: **48662** Calculated *p*I: **4.96**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MSSQNPKNSL YPQVDQSNPE AISSSSSSPS SSTIYPSIDM KDLAENLFPD
51 NDSQNPNSQS QLESSEEILI RVPGTIVHLI DKEQSVELAC GELTIVRLLQ
101 GGNVVAVLAR IDDQIQWPLA KDEAAVKLDE SHYFFTLRVP SEAGFDNEED
151 NDEVNMESEN LLNYGVTIAS KGQEGLLEAF DSILEHYSAF SVQKVSEAVD
201 GSVVARETSP EEMESEEEKR EMMEGSSAAY WTTLAPNVED YSGNVARMIA
251 VGSGQLIK**GI** **LWCGDVTVDR** LKWGNEFLKK KLGPASQTKI SPQAMRRMKR
301 VKLLTKMSEE VATGILSGVV KVSGFFTSSI VNSSVGKKFF SLLPGEIVLA
351 SLDGFNKVCD AVEVAGRNVM STTSVVTTGL VSQRYGEQAA KVTNEGFDAA
401 GHAIGIAWAV FKIRKALNPK SVIKPTTLAK AAAETNYAAL KAKSNKQT

Spot No.: **200**

NCBI accession No.: **gi|255570457** Species: *Ricinus communis*

PFF score: [282]

Protein name: protease C56, putative

Matched peptides No.: [3] Sequence coverage %: [8]

Matched sequences: R.APEYLAMNESVLDCVR.K;

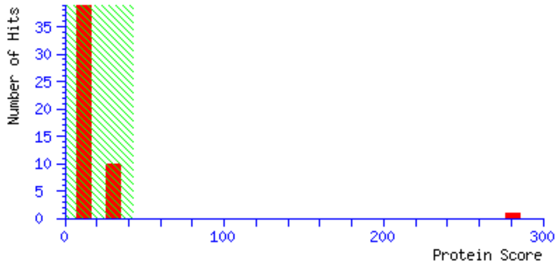
R.APEYLAMNESVLDCVR.K + Oxidation (M);

R.APEYLALDETVIALVK.Q

Calculated Mr: **42437** Calculated *p*I: **5.60**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 43 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MSHQKTVFLL CGDYMEDYEA MVPFQALLAY GVAVDAACPG KKAGDYCRTA
51 IHESSGHQTY SESRGHNFTL NSTFDDIDFG KYDGLVIPGG **RAPEYLAMNE**
101 **SVLDCVR**KFA DAGKPIASVC HGQLILAAAG LVKGRKCTAY PPVRPVLIAA
151 GAHWVEPETM ASCVADGNLI TGATYEGHPE FIQLFVKALG GSITGADKRI
201 LFLCGDYMED YEVTVPFQSL QALGCHVNAV CPKKKAGDSC PTAVHDFEGD
251 QTYSEKPGHH FTLTASYVGL DVSSYDALVL PGGR**APEYLA** **LDETVIALVK**
301 QFMQSKKPVA SICHGQQILA AAGVLKGKKC TAYPAVKLNV VLSGATWLEP
351 DPIDRCYTDE NLVTGAAWPG HPEFISQLMA LLGIRVSF

Spot No.: **201**

NCBI accession No.: **gi|32186896** Species: *Gossypium hirsutum*

Protein name: actin

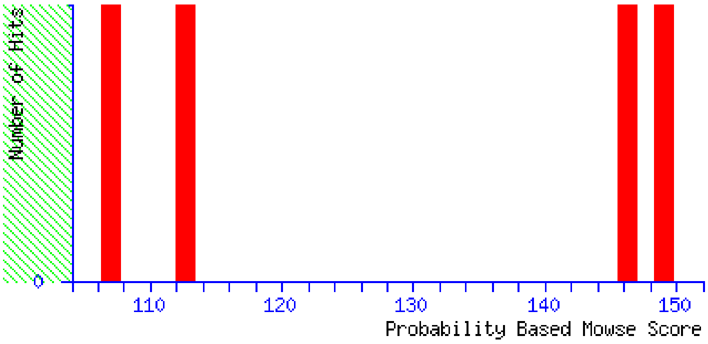
PMF Mascot score: **149** Sequence coverage %: **57**

Matched peptides No.: **21** Total peptides No.: **38**

Calculated Mr: **41935** Calculated *p*I: **5.44**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MADGEDIQPL VCDNGTGMVK **AGFAGDDAPR AVFPSIVGRP RHTGVMVGMG**
51 **HKDAYVGDEA QSKR**GILTLK YPIEHGIVSN WDDMEKIWHH TFYNELR**VAP**
101 **EEHPVLLTEA PLNPKANREK** MTHIMFETFN VPAMYVAIQA VLSLYASGRT
151 **TGIVLDSGDG VSHTVPIYEG YALPHAILRL DLAGRDLTDA LMKILTERGY**
201 **MFTTTAERE**I VR**DMKEKLAY VALDYEQELE TAKSSSSVEK NYELPDGQVI**
251 **TIGAER**FRCP EVLFQPSFIG MEAAGIHETT YNSIMKCDVD IR**KDLYGNIV**
301 **LSGGSTMFPG IADR**MSKEIT ALAPSSMK**IK VVAPPERK**YS VWIGGSILAS
351 LSTFQQMWIS K**GEYDESGPS IVHR**KCF

Spot No.: **202**

NCBI accession No.: **gi|255560725** Species: *Ricinus communis*

Protein name: dead box ATP-dependent RNA helicase, putative

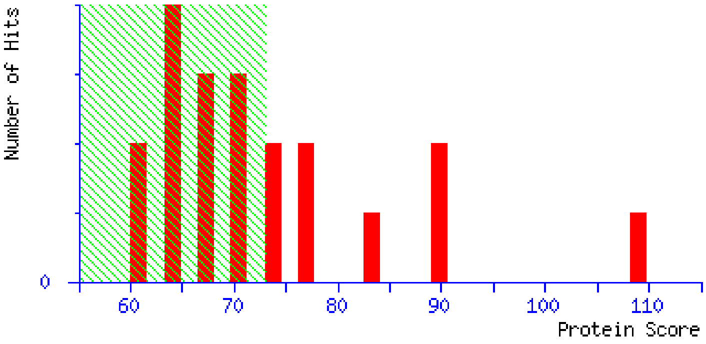
PMF Mascot score: **109** Sequence coverage %: **54**

Matched peptides No.: **21** Total peptides No.: **76**

Calculated Mr: **47097** Calculated *p*I: **5.49**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MAGLAPEGSQ FDAKQYDAKM SELLSTEGQE FFTTYDEVYD SFDAMGLQEN
51 LLR**GIYAYGF** **EKPSAIQQR**G IVPFCK**GLDV** **IQQAQSGTGK** TATFCSGILQ
101 QLDYGLVQCQ ALVLAPTREL AQQIEKVMR**A** **LGDYLGVKVH** **ACVGGTSVR**E
151 DQR**ILQAGVH** **VVVGTPGRVF** **DMLR**RQSLRP DYIK**MFVLDE** **ADEMLSRGFK**
201 **DQIYDIFQLL** **PAK**VQVGVFS ATMPPEALEI TRKFMNKPVR ILVK**RDELTL**
251 **EGIKQFYVNV** **EKEEWKLETL** **CDLYETLAIT** **QSVIFVNTR**R K**VDWLTDKMR**
301 SR**DHTVSATH** **GDMDQNTRDI** **IMR**EFRSGSS R**VLITTDLLA** **RGIDVQQVSL**
351 **VINYDLPTQP** **ENYLHRIGRG** **GR**FGRK**GVAI** **NFVTR**DDERM LFDIQKFYNV
401 VIEELPSNVA DLL

Spot No.: **203**

NCBI accession No.: **gi|14423688** Species: *Hevea brasiliensis*

PFF score: [229] Protein name: Enolase 1

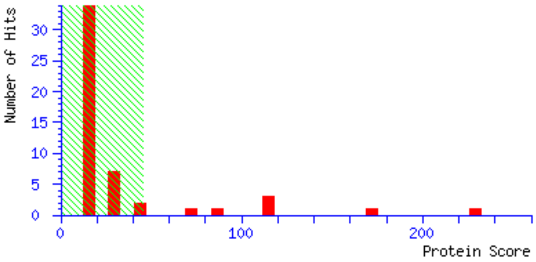
Matched peptides No.: [3] Sequence coverage %: [10]

Matched sequences: R.AGWGVMASHR.S + Oxidation (M);
R.AAVPSGASTGIYEALELR.D;
R.IEEELGSEAVYAGANFR.K

Calculated Mr: **48029** Calculated *p*I: **5.57**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAITIVSVRA RQIFDSRGNP TVEADVKLSD GYLAR**AAVPS** **GASTGIYEAL**
51 **ELR**DGGSDYL GKGVSKAVEN VNIIIGPALV GKDPTDQVGI DNFMVQQLDG
101 TVNEWGWCKQ KLGANAILAV SLAVCKAGAH VKGIPLYEHI ANLAGNKNLV
151 LPVPAFNVIN GGSHAGNKLA MQEFMILPVG ASSFKEAMKM GAEVYHHLKS
201 VIKKKYGQDA TNVGDEGGFA PNIQENKEGL ELLKTAIAKA GYTGKVVIGM
251 DVAASEFYGS DQTYDLNFKE ENNNGSQKIS GEALKDLYKS FVAEYPIVSI
301 EDPFDQDDWA HYAKLTSEIG EKVQIVGDDL LVTNPKRVEK AIKEKACNAL
351 LLKVNQIGSV TESIEAVKMS KR**AGWGVMAS** **HR**SGETEDTF IADLSVGLAT
401 GQIKTGAPCR SERLAKYNQL LR**IEEELGSE** **AVYAGANFR**K PVEPY

Spot No.: **204**

NCBI accession No.: **gi|186898205** Species: *Hevea brasiliensis*

PFF score: [311] Protein name: senescence-related protein

Matched peptides No.: [10] Sequence coverage %: [13]

Matched sequences: R.LSKEEIER.M;
R.LVNHFVAEFK.G;
R.FEELNMDLFR.K;
R.FEELNMDLFR.K + Oxidation (M);
R.TTPSYVAFTDTER.L;
R.ARFEELNMDLFR.K;
R.ARFEELNMDLFR.K + Oxidation (M);
K.ATAGDTHLGGEDFDNR.L;
K.NAVITVPAYFNDSQR.Q;
R.IINEPTAAAIAYGLDKK.G

Calculated Mr: **72036** Calculated *p*I: **5.27**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
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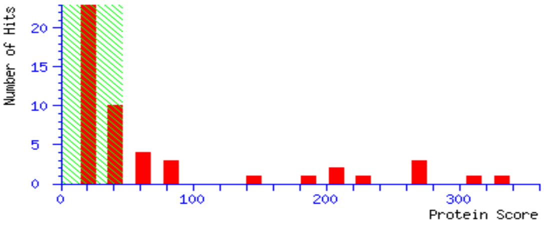


Matched peptide sequences: shown in Bold Red:

1 MAPKTEGKAI GIDLGTTYSC VGVWQNDRVE IIANDQGNR**T** **TPSYVAFTDT**
51 **ER**LIGDAAKN QVAMNPQNTV FDAKRLIGRR FSDPSVQSDM KHWPFKVISG
101 PGDKPMIVVQ YKGEEKQFAP EEISSMVLTK MKEIAEAYLG QTVK**NAVITV**
151 **PAYFNDSQR**Q ATKDAGAIAG VNVMR**IINEP** **TAAAIAYGLD** **KK**GSSTGEKN
201 VLIFDLGGGT FDVSLLTIEE GIFEVK**ATAG** **DTHLGGEDFD** **NRLVNHFVAE**
251 **FK**GKHKKDIS TNARALRRLR TARERAKRTL SSTSQTTIEI DSLYEGIDFY
301 ATITR**ARFEE** **LNMDLFR**KCM EPVEKCLRDS KIDKSQVHDV VLVGGSTRIP
351 KVQQLLQDIF NGKELCKSIN PDEAVAYGAA VQAAILSGEG DEKVQDLLLL
401 DVTPLSLGIE TAGGVMTVLI PRNTTIPTKK EQIFSTYSDN QPGVLIQVYE
451 GERARTKDNN LLGKFELTGI PPAPRGVPQI NVCFDIDANG IVNVSAEDKT
501 AGVKNKITIT NDKGR**LSKEE** **IER**MVQEAEK YKAEDEEVKK KVEAKNSLEN
551 YAYNMRNTVK DDKFAGKLAP ADKGKIEKAI DETIEWLDRN QLAEVEEFED
601 KLKELEGLCN PIIAKMYQGG AGGDVPVGGA EMPNSNYGKT SSGGSGAGPK
651 IEEVD

Spot No.: **205**

NCBI accession No.: **gi|255537027** Species: *Ricinus communis*

PFF score: [63]

Protein name: heat shock protein 70 (HSP70)-interacting protein,

Matched peptides No.: [2] Sequence coverage %: [5]

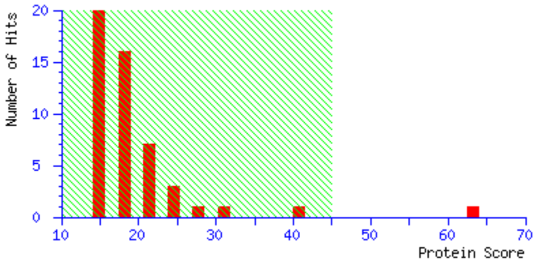
Matched sequences: K.LVNAGIVQIR.-;

K.HDPQNQELLDGVR.R

Calculated Mr: **65386** Calculated *p*I: **5.60**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEEAKAKGN AAFSAGDFTT AVKHFTEAIS IAPSNHVLYS NRSAALASLH
51 NYADALTDAK KTVELKPDWS KGYSRLGAAY LGLNQTQDAI SAYKKGLDID
101 PSNEALKSGL ADAQARFSAP PPPPSPFGDA FNGPEMWAKL TADPSTRMYL
151 QQPDFVKMMQ EIQKNPNNLN LYLKDQRVMQ ALGVLLNLKF RAPNAGAEDM
201 EVPQEDDHSS SPPPQAEQPA KKAPQPEPEP EPMDVITEED KEAKERKAQA
251 VKEKELGNAA YKQKDFETAI SHYTTALELD DEDISYLTNR AAVYLEMGKY
301 EDCIKDCDKA VERGRELRSD FKMIARALTR KGTALVKMAK SSKDYDSAIE
351 TFQKALTEHR NPETLKKLNE AERAKKELEQ QEYFDPKLAD EEREKGNEYF
401 KQQKYPEAVK HYTESLRRNP EDPRAYSNRA ACYTKLGALP EGLKDAEKCI
451 ELDPTFTKGY TRKGAVQFFM KEYDKALETY QEGLK**HDPQN** **QELLDGVR**RC
501 VEQLNKASRG DLSPEELKER QAKAMQDPEI QNILSDPVMR QVLVDFQENP
551 KSAQDHMKNP MVMNKIQK**LV** **NAGIVQIR**

Spot No.: 206

NCBI accession No.: gi|302853426

Species: *Volvox carteri f. nagariensis*

Protein name：**hypothetical protein VOLCADRAFT_77867**

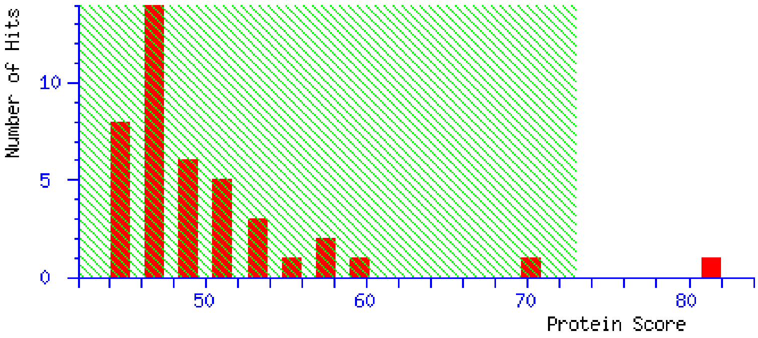
PMF score: 81   Sequence coverage %: 33

Matched peptides No.:14   Total peptides No.:69

Calculated Mr: 65036   Calculated *p*I:8.96

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold red:

1 **MIKQQYLGQE** **KIK**KRVSRNG GMGSRCSCRW RRGR**WSLKPI** **VTNTPLTPCS**
51 **EAALMFGRGM** **R**AGIDRREQK KAAASLEAEL LRKARSAAGL VETAETREHD
101 RERKR**LADQY** **DGFDMRIEK**H WTEKSLEEMT ERDWRIFRED FNIGYRGVNT
151 VLPIRKWEES GLPSLLIKAI DRVGYKK**PSP** **IQMAAIPLGL** **QQRDVIGIAE**
201 **TGSGK**TAAFV LPMLSYIMRQ PPMTEENEAD GPYAVVLAPT RELAQQIEEE
251 THKLAYYTNY R**IASVVGGQS** **IEEQGAK**LRK **GCEIVIATPG** **RLLDCIDR**HY
301 AVLNQCNYVV LDEADRMIDL GFEPQVIGVL DAMPSSFLKP DEDGAVLEAN
351 R**TYRTTYMFS** **ATMPPAVERL** **AK**KYLRRPVV VVIGSAGKVT DNVTQRVFVV
401 KENEK**PRVLE** **QEMESVDEK**R VIVFVNTQRQ CDNVHRHLEE LGYRCTILHG
451 GKTQDQREAG IKGFRDGTYN CLIATDVAGR **GIDVPDVALV** **INYDMPNNIE**
501 **NYTHR**IGRTG RAGKKGVAVT FLTLGDTGVF YDLKKLLEES **KAAVPPELAR**
551 **HEASK**LKPGS IEAKSRKDQT VFAA

Spot No.: **207**

NCBI accession No.: **gi|255537027** Species: *Ricinus communis*

PFF score: [266]

Protein name: heat shock protein 70 (HSP70)-interacting protein,

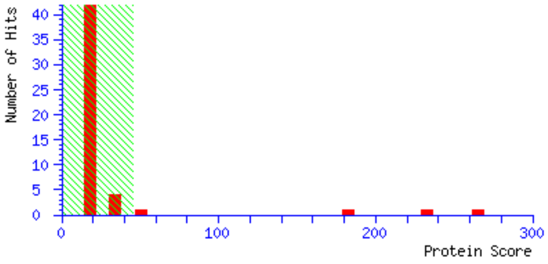
Matched peptides No.: [3] Sequence coverage %: [5]

Matched sequences: K.LVNAGIVQIR.-;
K.NPNNLNLYLK.D;
R.MYLQQPDFVK.M + Oxidation (M);
R.QVLVDFQENPK.S;
K.LGALPEGLKDAEK.C;
K.HDPQNQELLDGVR.R;
K.ALETYQEGLKHDPQNQELLDGVR.R

Calculated Mr: **65386** Calculated *p*I: **5.60**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEEAKAKGN AAFSAGDFTT AVKHFTEAIS IAPSNHVLYS NRSAALASLH
51 NYADALTDAK KTVELKPDWS KGYSRLGAAY LGLNQTQDAI SAYKKGLDID
101 PSNEALKSGL ADAQARFSAP PPPPSPFGDA FNGPEMWAKL TADPSTR**MYL**
151 **QQPDFVK**MMQ EIQK**NPNNLN** **LYLK**DQRVMQ ALGVLLNLKF RAPNAGAEDM
201 EVPQEDDHSS SPPPQAEQPA KKAPQPEPEP EPMDVITEED KEAKERKAQA
251 VKEKELGNAA YKQKDFETAI SHYTTALELD DEDISYLTNR AAVYLEMGKY
301 EDCIKDCDKA VERGRELRSD FKMIARALTR KGTALVKMAK SSKDYDSAIE
351 TFQKALTEHR NPETLKKLNE AERAKKELEQ QEYFDPKLAD EEREKGNEYF
401 KQQKYPEAVK HYTESLRRNP EDPRAYSNRA ACYTK**LGALP** **EGLKDAEK**CI
451 ELDPTFTKGY TRKGAVQFFM KEYDK**ALETY** **QEGLKHDPQN** **QELLDGVR**RC
501 VEQLNKASRG DLSPEELKER QAKAMQDPEI QNILSDPVMR **QVLVDFQENP**
551 **K**SAQDHMKNP MVMNKIQK**LV** **NAGIVQIR**

Spot No.: **208**

NCBI accession No.: **gi|255537027** Species: *Ricinus communis*

PFF score: [68]

Protein name: heat shock protein 70 (HSP70)-interacting protein,

Matched peptides No.: [2] Sequence coverage %: [5]

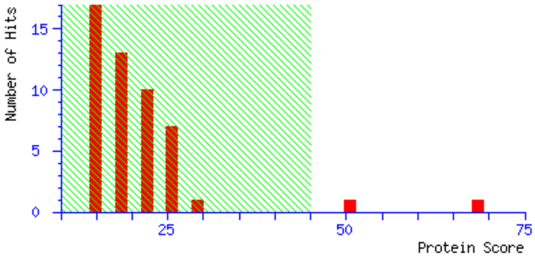
Matched sequences: K.LVNAGIVQIR.-;

K.HDPQNQELLDGVR.R

Calculated Mr: **65386** Calculated *p*I: **5.60**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MAEEAKAKGN AAFSAGDFTT AVKHFTEAIS IAPSNHVLYS NRSAALASLH
51 NYADALTDAK KTVELKPDWS KGYSRLGAAY LGLNQTQDAI SAYKKGLDID
101 PSNEALKSGL ADAQARFSAP PPPPSPFGDA FNGPEMWAKL TADPSTRMYL
151 QQPDFVKMMQ EIQKNPNNLN LYLKDQRVMQ ALGVLLNLKF RAPNAGAEDM
201 EVPQEDDHSS SPPPQAEQPA KKAPQPEPEP EPMDVITEED KEAKERKAQA
251 VKEKELGNAA YKQKDFETAI SHYTTALELD DEDISYLTNR AAVYLEMGKY
301 EDCIKDCDKA VERGRELRSD FKMIARALTR KGTALVKMAK SSKDYDSAIE
351 TFQKALTEHR NPETLKKLNE AERAKKELEQ QEYFDPKLAD EEREKGNEYF
401 KQQKYPEAVK HYTESLRRNP EDPRAYSNRA ACYTKLGALP EGLKDAEKCI
451 ELDPTFTKGY TRKGAVQFFM KEYDKALETY QEGLK**HDPQN** **QELLDGVR**RC
501 VEQLNKASRG DLSPEELKER QAKAMQDPEI QNILSDPVMR QVLVDFQENP
551 KSAQDHMKNP MVMNKIQK**LV** **NAGIVQIR**

Spot No.: **209**

NCBI accession No.: **gi|1346735** Species: *Ricinus communis*

PFF score: [161]

Protein name: 2,3-bisphosphoglycerate-independent phosphoglycerate mutase

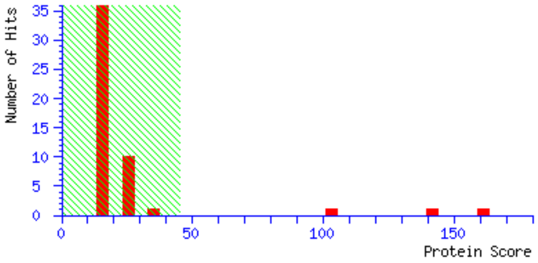
Matched peptides No.: [3] Sequence coverage %: [9]

Matched sequences: K.FGHVTFFWNGNR.S;
K.LPSHYLVSPPEIER.T;
K.AHGTAVGLPTEDDMGNSEVGHNALGAGR.I + Oxidation (M)

Calculated Mr: **57374** Calculated *p*I: **5.60**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 GEFTWKLADH PKLPKGKTIA MVVLDGWGEA KPDQYNCIHV AETPTMDSFK
51 KTAPERWRLI K**AHGTAVGLP** **TEDDMGNSEV** **GHNALGAGR**I YAQGAKLVDL
101 ALASGKIYEG EGFKYVKECF DKGTLHLIGL LSDGGVHSRL DQLQLLLKGA
151 AEHGAKRIRV HVLTDGRDVI DGTSVGFAET LEKDLENLRE KGVDAQVASG
201 GGRMYVTMDR YENDWNVVKR GWDAQVLGEA PYKFKSAVEA IKKLREEPKA
251 NDQYLPPFVI VDENGKPVGP IVDGDAVVTI NFRADRMVML AKALEYENFD
301 TFDRVRFPKI HYAGMLQYDG ELK**LPSHYLV** **SPPEIER**TSG EYLVHNGVHT
351 FACSETVK**FG** **HVTFFWNGNR** SGYFNPEMEE YVEIPSDVGI TFNVQPKMKA
401 IEIAEKARDA ILSGKFQQVR VNIPNGDMVG HTGDVEATVV GCKAADEAVK
451 MIIDAIEQVG GIYVVTADHG NAEDMVKRDK SGKPMADKSG KIQILTSHTL
501 QPVPIAIGGP GLTPGVRFRS DIPTGGLANV AATVMNLHGF EAPSDYEPTL
551 IEAVDN

Spot No.: **210**

NCBI accession No.: **gi|255537027** Species: *Ricinus communis*

PFF score: [69]

Protein name: heat shock protein 70 (HSP70)-interacting protein

Matched peptides No.: [3] Sequence coverage %: [5]

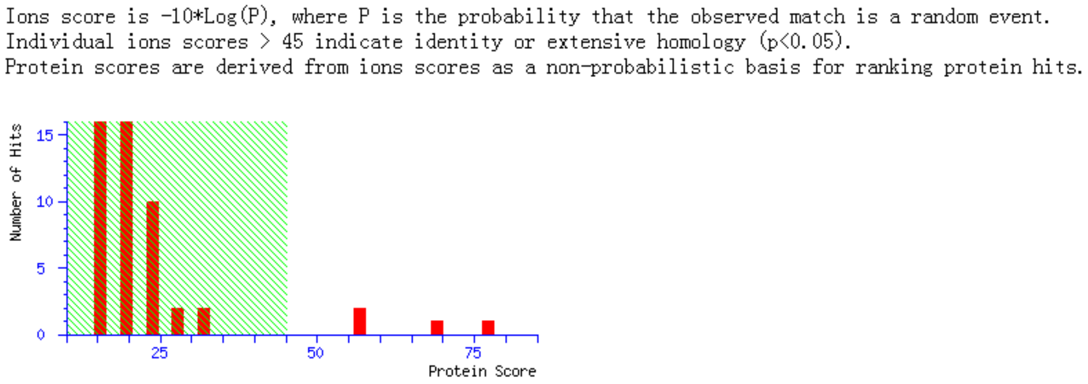
Matched sequences: K.LVNAGIVQIR.-;

K.HDPQNQELLDGVR.R;

K.ALETYQEGLKHDPQNQELLDGVR.R

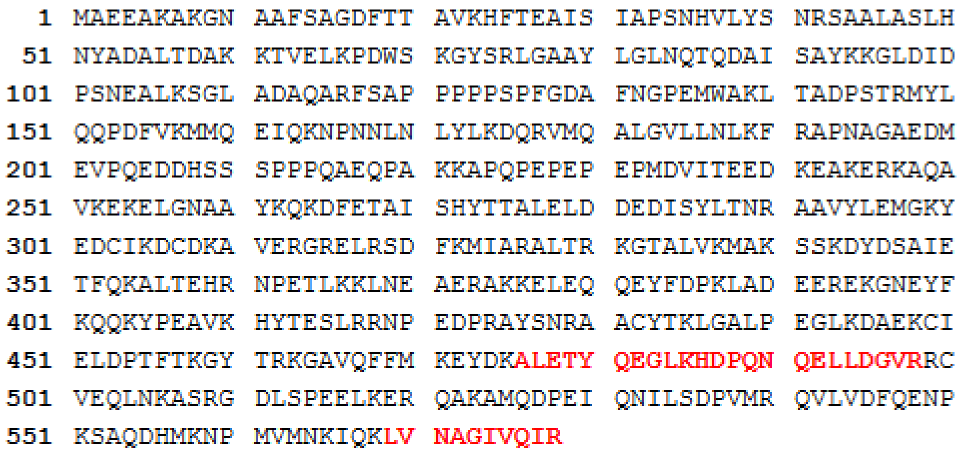
Calculated Mr: **65386** Calculated *p*I: **5.60**

Probability Based Mowse Score:



```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```

Matched peptide sequences: shown in Bold Red:



```
  1 MAEEAKAKGN AAFSAGDFTT AVKHFTEAIS IAPSNHVLYS NRSAALASLH
 51 NYADALTDAK KTVELKPDWS KGYSRLGAAY LGLNQTQDAI SAYKKGLDID
101 PSNEALKSGL ADAQARFSAP PPPPSPFGDA FNGPEMWAKL TADPSTRMYL
151 QQPDFVKMMQ EIQKNPNNLN LYLKDQRVMQ ALGVLLNLKF RAPNAGAEDM
201 EVPQEDDHSS SPPPQAEQPA KKAPQPEPEP EPMDVITEED KEAKERKAQA
251 VKEKELGNAA YKQKDFETAI SHYTTALELD DEDISYLTNR AAVYLEMGKY
301 EDCIKDCDKA VERGRELRSD FKMIARALTR KGTALVKMAK SSKDYDSAIE
351 TFQKALTEHR NPETLKKLNE AERAKKELEQ QEYFDPKLAD EEREKGNEYF
401 KQQKYPEAVK HYTESLRRNP EDPRAYSNRA ACYTKLGALP EGLKDAEKCI
451 ELDPTFTKGY TRKGAVQFFM KEYDKALETY QEGLKHDPQN QELLDGVRRC
501 VEQLNKASRG DLSPEELKER QAKAMQDPEI QNILSDPVMR QVLVDFQENP
551 KSAQDHMKNP MVMNKIQKLV NAGIVQIR
```

Spot No.: **211**

NCBI accession No.: gi|255556934   Species: *Ricinus communis*

PFF score: [1185]

Protein name：Transitional endoplasmic reticulum ATPase, putative

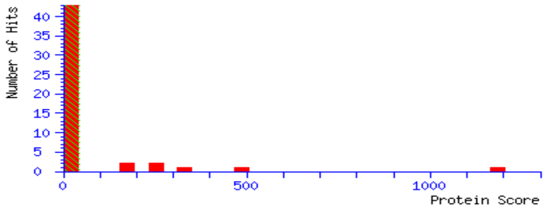
Matched peptides No.: [15]   Sequence coverage %: [26]

Matched sequences: R.DFSTAILER.K; K.GVLFYGPPGCGK.T;
R.EIDIGVPDEVGR.L; R.LDEVGYDDVGGVR.K;
K.YQAFAQTLQQSR.G; R.LGDVVSVHQCPDVK.Y;
R.KYQAFAQTLQQSR.G; R.LDQLIYIPLPDEDSR.H;
K.YTQGFSGADITEICQR.A; R.EDENRLDEVGYDDVGGVR.K;
R.AHVIVIGATNRPNSIDPALR.R; R.QSAPCVLFFDELDSIATQR.G;
R.ELQETVQYPVEHPEKFEK.F; R.ETVVEVPNVSWEDIGGLENVKR.E;
K.DTHGYVGADLAALCTEAALQCIR.E

Calculated Mr: **90355**   Calculated *p*I: **5.13**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MSNQAESSDS KGTKR**DFSTA** **ILER**KKSPNR LVVDEAINDD NSVVSLHPET
51 MEKLQLFRGD TILIKGKKRK DTICIALADD SCDEPKIRMN KVVRSNLRVR
101 **LGDVVSVHQC** **PDVK**YGKRVH ILPIDDTIEG VTGNLFDAYL KPYFLEAYRP
151 VRKGDLFLVR GGMRSVEFKV IETDPAEYCV VAPDTEIFCE GEPVRR**EDEN**
201 **RLDEVGYDDV** **GGVR**KQMAQI RELVELPLRH PQLFKSIGVK PPKGILLYGP
251 PGSGKTLIAR AVANETGAFF FCINGPEIMS KLAGESESNL RKAFEEAEKN
301 APSIIFIDEI DSIAPKREKT HGEVERRIVS QLLTLMDGLK SR**AHVIVIGA**
351 **TNRPNSIDPA** **LR**RFGRFDR**E** **IDIGVPDEVG** **R**LEVLRIHTK NMKLAEDVDL
401 ERISK**DTHGY** **VGADLAALCT** **EAALQCIR**EK MDVIDLEDET IDAEILNSMA
451 VSNEHFQTAL GTSNPSALR**E** **TVVEVPNVSW** **EDIGGLENVK** **RELQETVQYP**
501 **VEHPEKFEK**F GMSPSK**GVLF** **YGPPGCGK**TL LAKAIANECQ ANFISVKGPE
551 LLTMWFGESE ANVREIFDKA R**QSAPCVLFF** **DELDSIATQR** GSSVGDAGGA
601 ADRVLNQLLT EMDGMSAKKT VFIIGATNRP DIIDPALLRP GR**LDQLIYIP**
651 **LPDEDSR**HQI FKACLRKSPV SKDVDLRALA K**YTQGFSGAD** **ITEICQR**ACK
701 YAIRENIEKD IERERRRRDN PEAMEEDVED DVAEIKAAHF EESMKYARRS
751 VSDADIR**KYQ** **AFAQTLQQSR** GFGSEFRFSE ATGAAAGADP FAASAGGEAD
801 DDDLYS

Spot No.: **212**

NCBI accession No.: gi|4588474 Species: *Brassica napus*

PFF score: [166]

Protein name： phosphoinositide-specific phospholipase C

Matched peptides No.: [3] Sequence coverage %: [3]

Matched sequences: K.NDIDVLHGR.T;

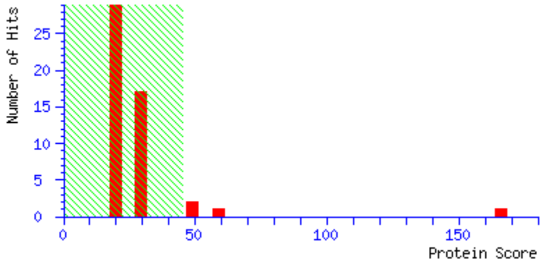
R.VIELDIWPNSNK.N;

R.VIELDIWPNSNKNDIDVLHGR.T

Calculated Mr: **66632** Calculated *p*I: **5.79**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MSKQTYKVCF CFNRRFRYTA SEAPRDVKTL FDKYSENGVM TVDHLQRFLI
51 DVQKQDKATK EDAQSIINAA SSLLHSNGLH LDAFFKYLFG DSNPPLALHE
101 VHQDMDAPIS HYFIFTGHNS YLTGNQLSSD CSEVPIIDAL KKGVR**VIELD**
151 **IWPNSNKNDI** **DVLHGR**TLTS PVELIKCLRA IKTHAFEVSD YPVVVTLEDH
201 LTPELQSKVA EMVTEIFGEI LFTPPVGESL KEFPSPNSLK RRIIISTKPP
251 KEYKEGKDED VVQKGKALGD EEVWGREVPS FIERNKSGDK DDLDDEEDND
301 EDDDVEKFKK NAPPQYKHLI AIHAGKPKGS ITACLKVDPD KVRRLSLSEE
351 QLEKAAEKYA KQIVRFTQQN LLRIYPKGTR VTSSNYNPLV GWSHGAQMVA
401 FNMQGYGRSL WLMQGMFRAN GGCGYIKKPD ILLKGGSDSD IFDPKTTLPV
451 KTTLRVTIYM GEGWYFDFRH THFDQYSPPD FYTRVGIAGV PADTVMKKTK
501 TLEDNWVPSW DEVFEFPLTV PELALLRLEV HEYDMSEKDD FGGQTCLPVW
551 ELQEGIRSFP LHNRKEEKYK SVKLLVKVEF V

Spot No.: **213**

NCBI accession No.: gi|4588474 Species: *Brassica napus*

PFF score: [116]

Protein name： phosphoinositide-specific phospholipase C

Matched peptides No.: [2] Sequence coverage %: [3]

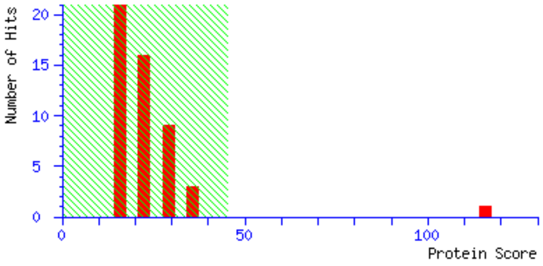
Matched sequences: K.NDIDVLHGR.T;

R.VIELDIWPNSNKNDIDVLHGR.T

Calculated Mr: **66632** Calculated *p*I: **5.79**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MSKQTYKVCF CFNRRFRYTA SEAPRDVKTL FDKYSENGVM TVDHLQRFLI
51 DVQKQDKATK EDAQSIINAA SSLLHSNGLH LDAFFKYLFG DSNPPLALHE
101 VHQDMDAPIS HYFIFTGHNS YLTGNQLSSD CSEVPIIDAL KKGVR**VIELD**
151 **IWPNSNKNDI** **DVLHGR**TLTS PVELIKCLRA IKTHAFEVSD YPVVVTLEDH
201 LTPELQSKVA EMVTEIFGEI LFTPPVGESL KEFPSPNSLK RRIIISTKPP
251 KEYKEGKDED VVQKGKALGD EEVWGREVPS FIERNKSGDK DDLDDEEDND
301 EDDDVEKFKK NAPPQYKHLI AIHAGKPKGS ITACLKVDPD KVRRLSLSEE
351 QLEKAAEKYA KQIVRFTQQN LLRIYPKGTR VTSSNYNPLV GWSHGAQMVA
401 FNMQGYGRSL WLMQGMFRAN GGCGYIKKPD ILLKGGSDSD IFDPKTTLPV
451 KTTLRVTIYM GEGWYFDFRH THFDQYSPPD FYTRVGIAGV PADTVMKKTK
501 TLEDNWVPSW DEVFEFPLTV PELALLRLEV HEYDMSEKDD FGGQTCLPVW
551 ELQEGIRSFP LHNRKEEKYK SVKLLVKVEF V

Spot No.: 215

NCBI accession No.: gi|32967699 Species: *Arabidopsis thaliana*

PFF score: [289]

Protein name：S-adenosyl-L-homocystein hydrolase

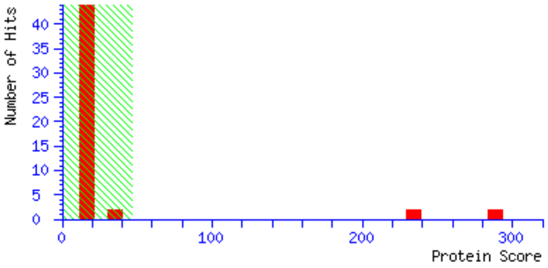
Matched peptides No.: [4] Sequence coverage %: [10]

Matched sequences: R.ITIKPQTDR.W;
K.SKFDNLYGCR.H;
K.GETLQEYWWCTER.A;
R.WVFPDTKSGIIVLAEGR.L

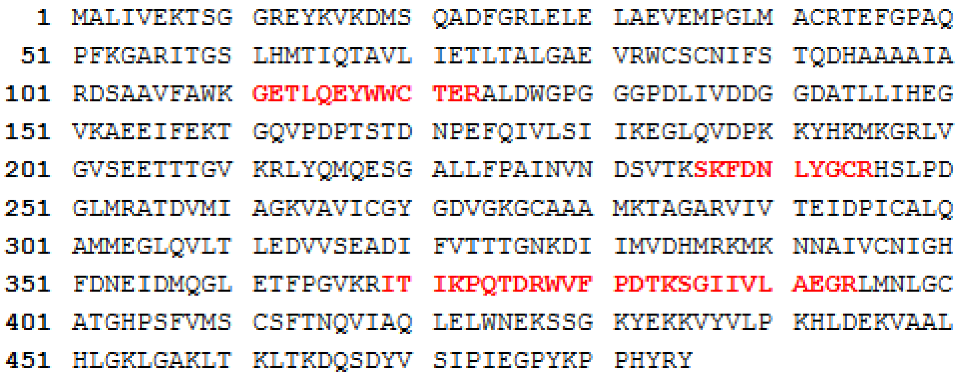
Calculated Mr: **53776** Calculated *p*I: **5.66**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:


1 MALIVEKTSG GREYKVKDMS QADFGRLELE LAEVEMPGLM ACRTEFGPAQ
51 PFKGARITGS LHMTIQTAVL IETLTALGAE VRWCSCNIFS TQDHAAAAIA
101 RDSAAVFAWK **GETLQEYWWC** **TER**ALDWGPG GGPDLIVDDG GDATLLIHEG
151 VKAEEIFEKT GQVPDPTSTD NPEFQIVLSI IKEGLQVDPK KYHKMKGRLV
201 GVSEETTTGV KRLYQMQESG ALLFPAINVN DSVTK**SKFDN** **LYGCR**HSLPD
251 GLMRATDVMI AGKVAVICGY GDVGKGCAAA MKTAGARVIV TEIDPICALQ
301 AMMEGLQVLT LEDVVSEADI FVTTTGNKDI IMVDHMRKMK NNAIVCNIGH
351 FDNEIDMQGL ETFPGVKR**IT** **IKPQTDRWVF** **PDTKSGIIVL** **AEGR**LMNLGC
401 ATGHPSFVMS CSFTNQVIAQ LELWNEKSSG KYEKKVYVLP KHLDEKVAAL
451 HLGKLGAKLT KLTKDQSDYV SIPIEGPYKP PHYRY

Spot No.: **216**

NCBI accession No.: gi|336390551   Species: *Glycine max*

PFF score: [327]

Protein name： adenosylhomocysteinase

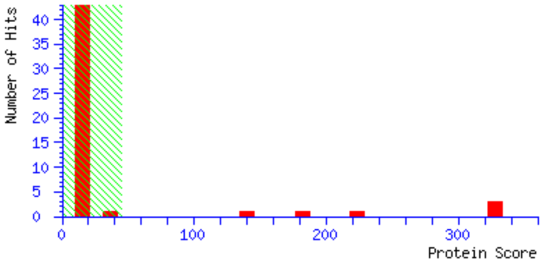
Matched peptides No.: [7]   Sequence coverage %: [21]

Matched sequences: R.HSLPDGLMR.A + Oxidation (M);
R.ITIKPQTDR.W;
K.SKFDNLYGCR.H;
K.GETLQEYWWCTER.A;
R.WVFPETNTGIIVLAEGR.L;
R.WCSCNIFSTQDHAAAAIAR.D;
R.ALDWGPGGGPDLIVDDGGDATLLIHEGVK.A

Calculated Mr: **53761**   Calculated *p*I: **5.69**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

```
  1 MALLVEKTTS GREYKVKDLS QADFGRLEIE LAEVEMPGLM ACRTEFGPSQ
 51 PFKGARITGS LHMTIQTAVL IETLTALGAE VRWCSCNIFS TQDHAAAAIA
101 RDSAAVFAWK GETLQEYWWC TERALDWGPG GGPDLIVDDG GDATLLIHEG
151 VKAEELYEKT GELPDPNSTD NAEFQIVLTI IRDGLKTDPT RYRKMKERLV
201 GVSEETTTGV KRLYQMQANG TLLFPAINVN DSVTKSKFDN LYGCRHSLPD
251 GLMRATDVMI AGKVAVVAGY GDVGKGCAAA MKQAGARVIV TEIDPICALQ
301 ALMEGLQVLT LEDVVSEADI FVTTTGNKDI IMVDHMRKMK NNAIVCNIGH
351 FDNEIDMLGL ENYPGVKRIT IKPQTDRWVF PETNTGIIVL AEGRLMNLGC
401 ATGHPSFVMS CSFTNQVIAQ LGLWKEKSIG KYEKKVYVLP KHLDEKVAAL
451 HLGKLGAKLT QLSKSQADYI SVPVEGPYKP AHYRY
```

Spot No.: **217**

NCBI accession No.: gi|6136111   Species: *Hordeum vulgare*

PFF score: [52]

Protein name：UTP--glucose-1-phosphate uridylyltransferase

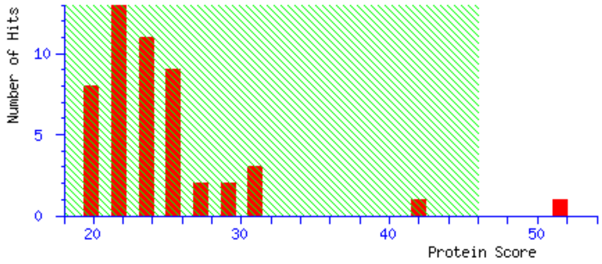
Matched peptides No.: [1]   Sequence coverage %: [2]

Matched sequences: R.FFEKAIGINVPR.S

Calculated Mr: **51783**   Calculated *p*I: **5.20**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAAAAVAADS KIDGLRDAVA KLGEISENEK AGFISLVSRY LSGEAEQIEW
51 SKIQTPTDEV VVPYDTLAPP PEDLDAMKAL LDKLVVLKLN GGLGTTMGCT
101 GPKSVIEVRN GFTFLDLIVI QIESLNKKYG CSVPLLLMNS FNTHDDTQKI
151 VEKYSNSNIE IHTFNQSQYP RIVTEDFLPL PSKGQTGKDG WYPPGHGDVF
201 PSLNNSGKLD TLLSQGKEYV FVANSDNLGA IVDIKILNHL IHNQNEYCME
251 VTPKTLADVK GGTLISYEGR VQLLEIAQVP DEHVDEFKSI EKFKIFNTNN
301 LWVNLKAIKR LVDAEALKME IIPNPKEVDG VKVLQLETAA GAAIR**FFEKA**
351 **IGINVPR**SRF LPVKATSDLL LVQSDLYTLV DGYVIRNPAR VKPSNPSIEL
401 GPEFKKVANF LARFKSIPSI VELDSLKVSG DVSFGSGVVL KGNVTIAAKA
451 GVKLEIPDGA VLENKDINGP EDI

Spot No.: 218

NCBI accession No.: gi|14916100 Species: *Hevea brasiliensis*

PFF score: [802]

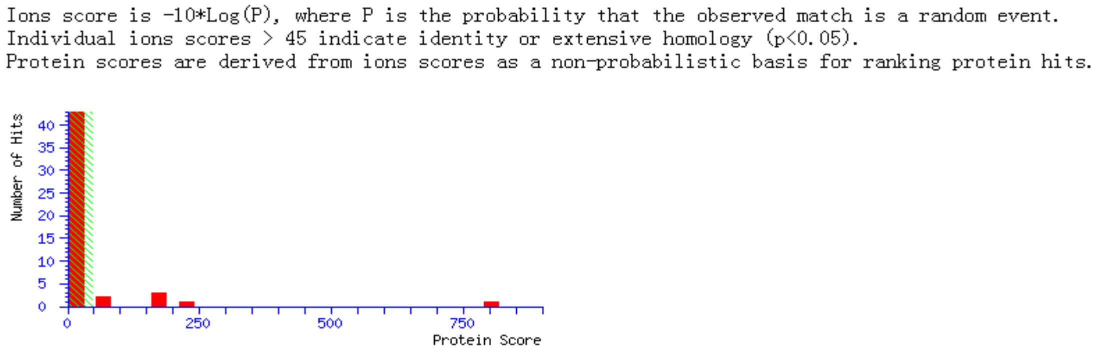
Protein name： hydroxymethylglutaryl coenzyme A

Matched peptides No.: [10] Sequence coverage %: [35]

Matched sequences: R.LVFNDFVR.N;
K.ARHELPPEK.F;
K.TFLMQIFEK.F + Oxidation (M);
K.VSQQVAKPLYDAK.V;
K.LAPFSNLSGDESYQNR.D;
R.YGLVVCTDSAVYAEGPAR.P;
K.QFSISDAEYFVFHSPYNK.L;
K.DCSLLASGTYYLTEVDSLYR.R;
R.GSHMSHAYDFYKPNLASEYPVVDGK.L + Oxidation (M);
K.NVGILAVDIYFPPTFVQQEALEAHDGASK.G

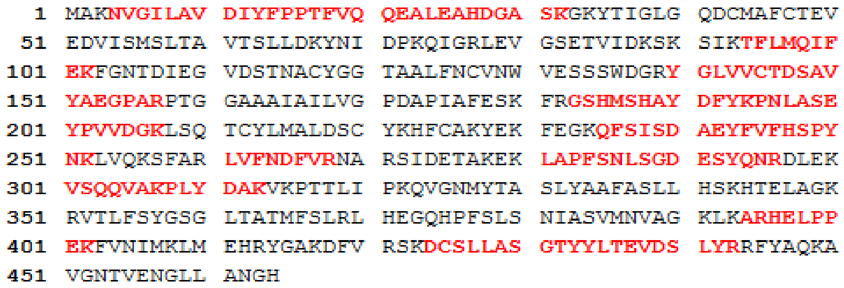
Calculated Mr: **51761** Calculated p*I*: **6.86**

Probability Based Mowse Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Matched peptide sequences: shown in Bold Red:



1 MAK**NVGILAV** **DIYFPPTFVQ** **QEALEAHDGA** **SK**GKYTIGLG QDCMAFCTEV
51 EDVISMSLTA VTSLLDKYNI DPKQIGRLEV GSETVIDKSK SIK**TFLMQIF**
101 **EK**FGNTDIEG VDSTNACYGG TAALFNCVNW VESSSWDGR**Y** **GLVVCTDSAV**
151 **YAEGPAR**PTG GAAAIAILVG PDAPIAFESK FR**GSHMSHAY** **DFYKPNLASE**
201 **YPVVDGK**LSQ TCYLMALDSC YKHFCAKYEK FEGK**QFSISD** **AEYFVFHSPY**
251 **NK**LVQKSFAR **LVFNDFVR**NA RSIDETAKEK **LAPFSNLSGD** **ESYQNR**DLEK
301 **VSQQVAKPLY** **DAK**VKPTTLI PKQVGNMYTA SLYAAFASLL HSKHTELAGK
351 RVTLFSYGSG LTATMFSLRL HEGQHPFSLS NIASVMNVAG KLK**ARHELPP**
401 **EK**FVNIMKLM EHRYGAKDFV RSK**DCSLLAS** **GTYYLTEVDS** **LYR**RFYAQKA
451 VGNTVENGLL ANGH

Spot No.: **219**

NCBI accession No.: **gi|307707110** Species: *Prunus armeniaca*

PFF score: [181]

Protein name：NAD-dependent malate dehydrogenase

Matched peptides No.: [4] Sequence coverage %: [19]

Matched sequences: R.LNVQVSDVK.N;
K.VLVVANPANTNALILK.E;
R.KLSSALSAASSACDHIR.D;
K.NVIIWGNHSSTQYPDVNHATVK.T

Calculated Mr: **34812** Calculated *p*I: **5.92**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
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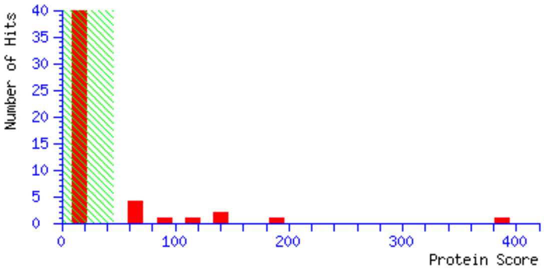


Matched peptide sequences: shown in Bold Red:

1 VTGAAGQIGY ALVPMIARGV MLGADQPVIL HLLDIPPAAE ALNGVKMELV
51 DAAFPLLKGV VATTDVVEAC TGVNIAVMVG GFPRKEGMER KDVMSKNVSI
101 YKSQASALEK HAAANCK**VLV** **VANPANTNAL** **ILK**EFAPSIP EKNITCLTRL
151 DHNRALGQVS ER**LNVQVSDV** **KNVIIWGNHS** **STQYPDVNHA** **TVK**TPSGEKA
201 VRELVADDAW LTGEFITTVQ QRGAAIIKAR **KLSSALSAAS** **SACDHIR**DWV
251 LGTPEGTWVS MGVYSDGSYN VPSGLIYSFP VTCQNGEWKN VQGLSIDEFS
301 RKKLDATADE LSEEKALAYS CLS

Spot No.: **220**

NCBI accession No.: **gi|357137038**

Species: *Brachypodium distachyon*

PFF score: [357]

Protein name：phosphoglycerate kinase, cytosolic-like

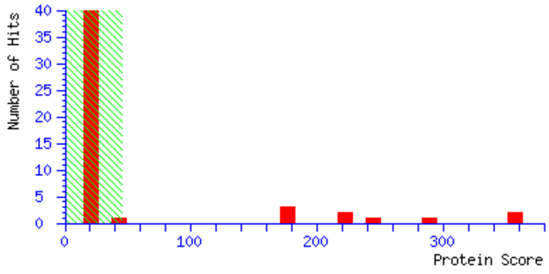
Matched peptides No.: [6] Sequence coverage %: [20]

Matched sequences: K.KPFAAIVGGSK.V;
K.ELDYLVGAVANPK.K;
K.GVTTIIGGGDSVAAVEK.A;
K.LASVADLYVNDAFGTAHR.A;
K.KLASVADLYVNDAFGTAHR.A;
K.VVPASAIPDGWMGLDVGPDAIK.T + Oxidation (M)

Calculated Mr: **42207** Calculated *p*I: **5.64**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MATKRSVGTL GEADLKGKKV FVRADLNVPL DDAQKITDDT RIRASVPTIK
51 FLLEKGAKVI LASHLGRPKG VTPKFSLKPL VPRLSELLGI DVVMANDCIG
101 EEVEKLAAAL PDGGVLLLEN VRFYKEEEKN DPEFAK**KLAS** **VADLYVNDAF**
151 **GTAHR**AHAST EGVTKFLRPS VAGFLMQK**EL** **DYLVGAVANP** **KKPFAAIVGG**
201 **SK**VSSKIGVI ESLLAKVDIL ILGGGMIFTF YKAQGLAVGK SLVEEDKLEL
251 ATSLIETAKA KGVKLLLPID VVVADKFAAD AESK**VVPASA** **IPDGWMGLDV**
301 **GPDAIK**TFSE ALDTCKTIIW NGPMGVFEFE KFAAGTDAIA KQLAELTAK**G**
351 **VTTIIGGGDS** **VAAVEK**AGLA DKMSHISTGG GASLELLEGK PLPGVLALDE
401 A

Spot No.: **221**

NCBI accession No.: **gi|357514973** Species: *Medicago truncatula*

PFF score: [99]

Protein name： **Annexin D4**

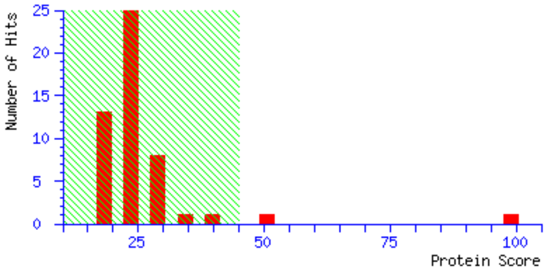
Matched peptides No.: [2] Sequence coverage %: [3]

Matched sequences: K.LLVALVSAYR.Y;
R.KLLVALVSAYR.Y

Calculated Mr: **36283** Calculated *p*I: **8.64**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAFNQELEAI TQAFSGHGVD EKSLIAVLGK WDPLERETYR KKTSHFFIED
51 HERQFQRWND HCVRLLKHEF VRFKNAVVLW SMHPWERDAR LAKEALKKGS
101 ISYGVLIEIA CTRSSEELLG ARKAYHSLFD HSIEEDVASH IHGNDR**KLLV**
151 **ALVSAYR**YEG TKVKDDTAKS EAKTLSNAIK NAQNKPIVED DEVIRILATR
201 SKLHLQAVYK HYKEISGKNL EEDLNDLRFK ETVQCLCTPQ VYFSKVLDAA
251 LKNDVNKNIK KSLTRVIVTR ADIDMKEIKA EYNNLYGVSL PQKIEETAKG
301 NYKDFLLTLI ARGG

Spot No.: 222

NCBI accession No.: gi|21536853 Species: *Arabidopsis thaliana*

PFF score: [314]

Protein name: phosphoglycerate kinase, putative

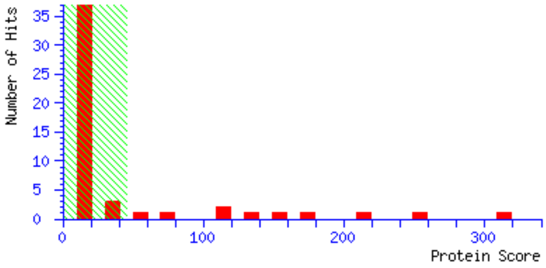
Matched peptides No.: [6] Sequence coverage %: [17]

Matched sequences: K.YSLKPLVPR.L;
K.ELDYLVGAVANPK.K;
K.YLKPSVAGFLMQK.E + Oxidation (M);
K.GVSLLLPTDVVIADK.F;
K.LAALADVYVNDAFGTAHR.A;
K.KLAALADVYVNDAFGTAHR.A

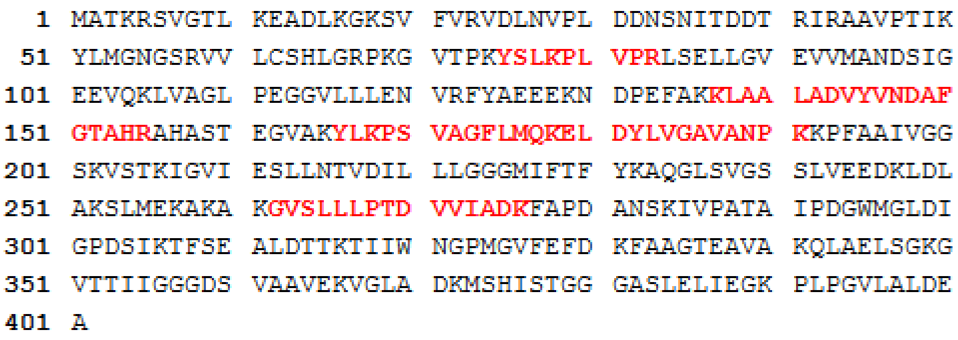
Calculated Mr: **42178** Calculated *p*I: **5.49**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:


```
  1 MATKRSVGTL KEADLKGKSV FVRVDLNVPL DDNSNITDDT RIRAAVPTIK
 51 YLMGNGSRVV LCSHLGRPKG VTPKYSLKPL VPRLSELLGV EVVMANDSIG
101 EEVQKLVAGL PEGGVLLLEN VRFYAEEEKN DPEFAKKLAA LADVYVNDAF
151 GTAHRAHAST EGVAKYLKPS VAGFLMQKEL DYLVGAVANP KKPFAAIVGG
201 SKVSTKIGVI ESLLNTVDIL LLGGGMIFTF YKAQGLSVGS SLVEEDKLDL
251 AKSLMEKAKA KGVSLLLPTD VVIADKFAPD ANSKIVPATA IPDGWMGLDI
301 GPDSIKTFSE ALDTTKTIIW NGPMGVFEFD KFAAGTEAVA KQLAELSGKG
351 VTTIIGGGDS VAAVEKVGLA DKMSHISTGG GASLELIEGK PLPGVLALDE
401 A
```

Spot No.: 223

NCBI accession No.: gi|255547137 Species: *Ricinus communis*

PFF score: [77]

Protein name：Alpha-1,4-glucan-protein synthase

Matched peptides No.: [2] Sequence coverage %: [5]

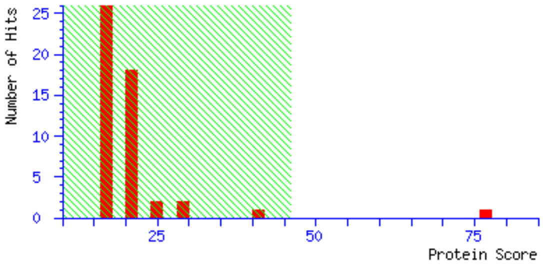
Matched sequences: K.DINALEQHIK.N;

K.VICDHLGFGVK.T

Calculated Mr: **41557** Calculated *p*I: **5.82**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MADFAAISPT PLLKDELDIV IPTIRNLDFL EMWRPFFQPY HLIIVQDGDP
51 SKIIKVPEGF DYELYNRNDI NRILGPKASC ISFKDSACRC FGYMVSKKKY
101 IYTIDDDCFV AKDPSGK**DIN** **ALEQHIK**NLL CPSTPFFFNT LYDPYRTGAD
151 FVRGYPFSLR EGVPTAVSHG LWLNIPDYDA PTQLVKPLER NTRYVDAVMT
201 IPKGTLFPMC GMNLAFNREL IGPAMYFGLM GDGQPIGRYD DMWAGWCTK**V**
251 **ICDHLGFGVK** TGLPYIYHSK ASNPFVNLKK EYKGIYWQEE LIPFFQSAVL
301 PKECTTVQKC YIELSKQVRA KLGKIDEYFV KLADAMVTWV EAWDELNPSG
351 NSGELPNGAA K

Spot No.: 224

NCBI accession No.: gi|380468126 Species: *Hevea brasiliensis*

PFF score: [922]

Protein name： caffeic acid 3-O-methyltransferase

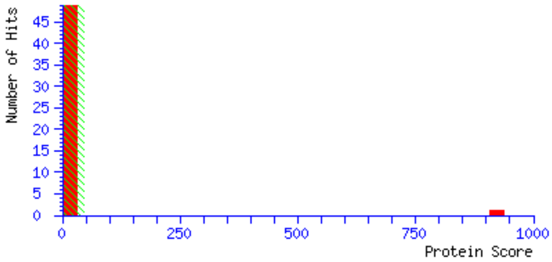
Matched peptides No.: [9] Sequence coverage %: [42]

Matched sequences: R.LYAPGPICK.F;
K.NPEAPVLLDR.M;
R.TRQEFEALASK.S;
K.WVLHDWNDDLCLK.L;
R.AYGMNQFEYPGTDQR.F + Oxidation (M);
K.SWYHLNEAILEGGTPFNR.A;
K.VIVVESILPTVPENNVTSQVLHK.E;
K.SALELNVIDIISTAGNSGASLSAPEIAQR.I;
K.GINYDLPHVLADAPSYPGVEHVAGDMFK.S + Oxidation (M)

Calculated Mr: **40957** Calculated *p*I: **5.54**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MTGSEQSNSA SIMSGRSDEE TWNLAIDLAN TVILPMVLK**S** **ALELNVIDII**
51 **STAGNSGASL** **SAPEIAQR**IP EAK**NPEAPVL** **LDR**MLRLLAT YDIVKCSSNT
101 KENGEVER**LY** **APGPICK**FLT KNKNGSGSAA PLLLLHHDEV FMK**SWYHLNE**
151 **AILEGGTPFN** **RAYGMNQFEY** **PGTDQR**FNRV FNDAMSSYTT YLVKKILDAY
201 KGFDGLKSLV DVGGNSGVTL NSITSKYPHI K**GINYDLPHV** **LADAPSYPGV**
251 **EHVAGDMFK**S VPKGDAIILK **WVLHDWNDDL** **CLK**LLKNCWE ALPSNGK**VIV**
301 **VESILPTVPE** **NNVTSQVLHK** EDLMLLSFNV GGKER**TRQEF** **EALASK**SGFS
351 SCEFICCAYN SWVIEFHK

Spot No.: 225

NCBI accession No.: gi|255570457   Species: *Ricinus communis*

PFF score: [237]

Protein name: protease C56, putative

Matched peptides No.: [3]   Sequence coverage %: [10]

Matched sequences: K.YDGLVIPGGR.A;

R.APEYLALDETVIALVK.Q;
R.APEYLAMNESVLDCVR.K + Oxidation (M)

Calculated Mr: **42437**   Calculated *p*I: **5.60**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
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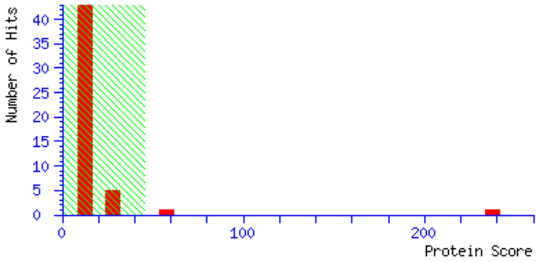


Matched peptide sequences: shown in Bold Red:

```
  1 MSHQKTVFLL CGDYMEDYEA MVPFQALLAY GVAVDAACPG KKAGDYCRTA
 51 IHESSGHQTY SESRGHNFTL NSTFDDIDFG KYDGLVIPGG RAPEYLAMNE
101 SVLDCVRKFA DAGKPIASVC HGQLILAAAG LVKGRKCTAY PPVRPVLIAA
151 GAHWVEPETM ASCVADGNLI TGATYEGHPE FIQLFVKALG GSITGADKRI
201 LFLCGDYMED YEVTVPFQSL QALGCHVNAV CPKKKAGDSC PTAVHDFEGD
251 QTYSEKPGHH FTLTASYVGL DVSSYDALVL PGGRAPEYLA LDETVIALVK
301 QFMQSKKPVA SICHGQQILA AAGVLKGKKC TAYPAVKLNV VLSGATWLEP
351 DPIDRCYTDE NLVTGAAWPG HPEFISQLMA LLGIRVSF
```

Spot No.: 226

NCBI accession No.: gi|224131618 Species: *Populus trichocarpa*

PFF score: [172]

Protein name：predicted protein

Matched peptides No.: [2] Sequence coverage %: [18]

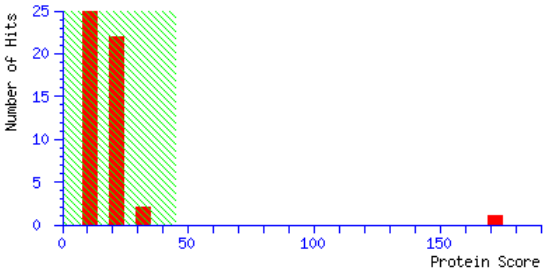
Matched sequences: K.ASGIPYEVHIYPGNAHAFMNR.S + Oxidation (M);

K.APVQAHFGELDNFVGFSDVTAAK.A

Calculated Mr: **26246** Calculated *p*I: **5.24**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAGSASQPFK KIQIQRDDTT FDAYVVGKED APGIVVLQEW WGVDFEIKNH
51 AVKISQLGPG FKALIPDLYR GKVGLDVAEA QHLMDGLDWQ GAVKDIQASV
101 NWLKTNGSSK AGVTGFCMGG ALSIASSVLV PEVDAVVAFY GVPSSQLADP
151 AQAK**APVQAH** **FGELDNFVGF** **SDVTAAK**ALE EKLK**ASGIPY** **EVHIYPGNAH**
201 **AFMNR**SPEGV MRRKGMGLPD EDEASAELAW SRFTTWMTRY LSA

Spot No.: 227

NCBI accession No.: gi|333690873 Species: *Hevea brasiliensis*

PFF score: [386]

Protein name： glutathione-S-transferase tau 1

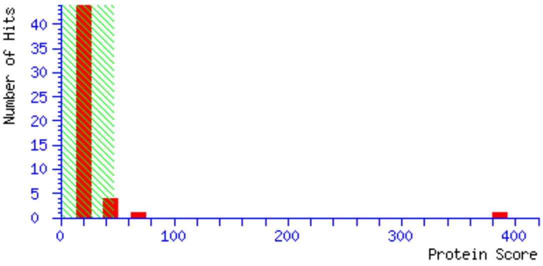
Matched peptides No.: [8] Sequence coverage %: [29]

Matched sequences: R.FWADFIDK.K;
K.VYEFVLVLK.K;
R.FWADFIDKK.I;
K.YEYREEDLR.N;
K.SPFLPSDPYQR.A;
K.SPLLLQMNPVHK.K + Oxidation (M);
K.DKSPFLPSDPYQR.A;
K.ESVSESVPDPEKVYEFVLVLK.K

Calculated Mr: **25595** Calculated *p*I: **5.48**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEEVILLDF WPSPFGMRVR IALAEKGVK**Y** **EYREEDLR**NK **SPLLLQMNPV**
51 **HK**KIPVLIHN GKPICESLIA VQYVDEVWK**D** **KSPFLPSDPY** **QR**AQAR**FWAD**
101 **FIDKK**IYDIG RKIWTTKGDE QEAAKKEFIE ALKLLEGELG NKPYFGGESM
151 GYVDVALIPF YSWFYAYETC GNFSIEPECP VLIAWAKRCL QK**ESVSESVP**
201 **DPEKVYEFVL** **VLK**KKFGIE

Spot No.: 228

NCBI accession No.: gi|211906460 Species: *Gossypium hirsutum*

PFF score: [243]

Protein name： triosephosphate isomerase

Matched peptides No.: [2] Sequence coverage %: [15]

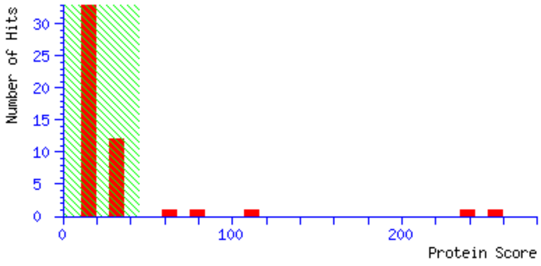
Matched sequences: K.VIACIGETLEQR.E;

K.ELAAQPDVDGFLVGGASLKPEFIDIIK.S

Calculated Mr: **27472** Calculated *p*I: **6.00**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MGRKFFVGGN WKCNGTTEEV NKIVSTLNAG EVPSQDVVEV VVSPPFVFLP
51 LVKTSLRPDF HVAAQNCWVK KGGAFTGEVS AEMLVNLSIP WVIIGHSERR
101 LILKESNEFV ADKVAYALAQ GLK**VIACIGE** **TLEQR**EAGST VAVVAEQTKA
151 IAAKISNWTD VVLAYEPVWA IGTGKVATPA QAQEVHCELR KWLQANVSPE
201 VAASTRIIYG GSVTAANCK**E** **LAAQPDVDGF** **LVGGASLKPE** **FIDIIK**SAEV
251 KKNA

Spot No.: 229

NCBI accession No.: gi|255568460 Species: *Ricinus communis*

PFF score: [93]

Protein name： glutathione-s-transferase omega, putative

Matched peptides No.: [2] Sequence coverage %: [13]

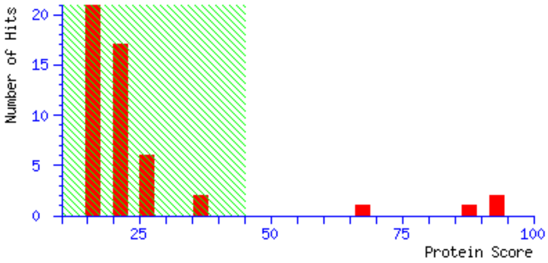
Matched sequences: K.YDITAGRPK.L;

K.FDDGPFLLGQFSLVDIAYIPFVER.L

Calculated Mr: **27477** Calculated *p*I: **5.13**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAAATALDKS AQENLPPILD AAADQPPLFD GTIRLYTAYA CPFAQRVWIT
51 RNYKGLQDSI KLVPLNLQNR PSWYPEKVYS VNKVPALEHN GKIIGESLDL
101 IKYVDSNFEG PSLFPDDPAK REFAEELFSY TDTFSRTVFT SFKGDVAKEA
151 GPAFDYLENA LQK**FDDGPFL** **LGQFSLVDIA** **YIPFVER**LEI FLSEVFK**YDI**
201 **TAGRPK**LAAW VGEVNKIGAY KQTKTDPKEL VEYYKKRFFA QQ

Spot No.: 230

NCBI accession No.: gi|2970051 Species: *Vigna radiata*

PFF score: [104]

Protein name：ARG10

Matched peptides No.: [2] Sequence coverage %: [12]

Matched sequences: K.SANEVILVIEAYK.A;

K.ITAVPAEEEEIWGATFK.V

Calculated Mr: **25750** Calculated *p*I: **5.62**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
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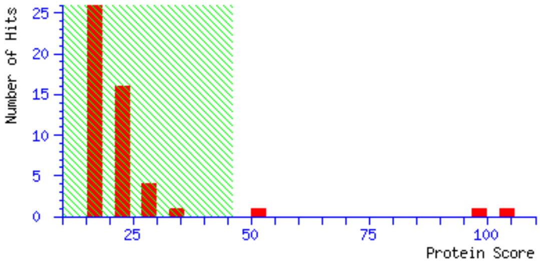


Matched peptide sequences: shown in Bold Red:

1 MLGIFSSSVV SPPEELVAAG SRTPSPKTTA GKLLTRFVES KASAVSLQVG
51 EHVQLAYTHH SESPWYPRSF AVKDEIFCLF EGALDNLGSL RQQYGLAK**SA**
101 **NEVILVIEAY** **K**ALRDRAPYP ANRVVCHLSG SFAFIVFDKS TSTVFVASDQ
151 AGKVPLYWGI TADGYVAFAD DADLLKGSCG KSLASFPQGC FYSTAVGGLR
201 CYENPKNK**IT** **AVPAEEEEIW** **GATFK**VEGSA VLAATEY

Spot No.: 231

NCBI accession No.: gi|2832430 Species: *Hevea brasiliensis*

PFF score: [217]

Protein name： prohevein

Matched peptides No.: [2] Sequence coverage %: [20]

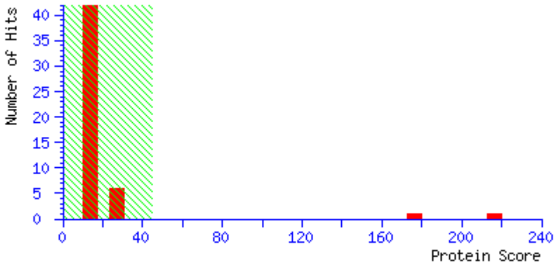
Matched sequences: R.IVDQCSNGGLDLDVNVFR.Q;

K.YGWTAFCGPVGAHGQPSCGK.C

Calculated Mr: **20852** Calculated *p*I: **5.64**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 EQCGRQAGGK LCPNNLCCSQ WGWCGSTDEY CSPDHNCQSN CKDSGEGVGG
51 GSASNVLATY HLYNSQDHGW DLNAASAYCS TWDANKPYSW RSK**YGWTAFC**
101 **GPVGAHGQPS** **CGK**CLSVTNT GTGAKATVR**I** **VDQCSNGGLD** **LDVNVFR**QLD
151 TDGKGYERGH LTVNYQFVDC GDSFNPLFSV MKSSVIN

Spot No.: 232

NCBI accession No.: gi|2832430 Species: *Hevea brasiliensis*

PFF score: [112]

Protein name： prohevein

Matched peptides No.: [2] Sequence coverage %: [16]

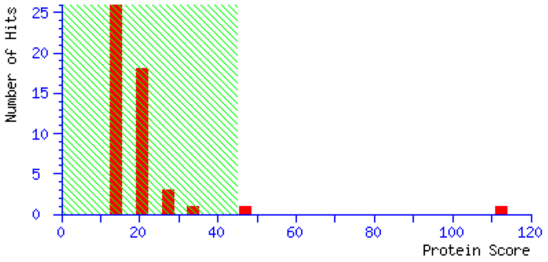
Matched sequences: R.QLDTDGKGYER.G;

K.YGWTAFCGPVGAHGQPSCGK.C

Calculated Mr: **20852** Calculated *p*I: **5.64**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 EQCGRQAGGK LCPNNLCCSQ WGWCGSTDEY CSPDHNCQSN CKDSGEGVGG
51 GSASNVLATY HLYNSQDHGW DLNAASAYCS TWDANKPYSW RSK**YGWTAFC**
101 **GPVGAHGQPS** **CGK**CLSVTNT GTGAKATVRI VDQCSNGGLD LDVNVFR**QLD**
151 **TDGKGYER**GH LTVNYQFVDC GDSFNPLFSV MKSSVIN

Spot No.: 233

NCBI accession No.: gi|14423933 Species: *Hevea brasiliensis*

PFF score: [384]

Protein name： Small rubber particle protein

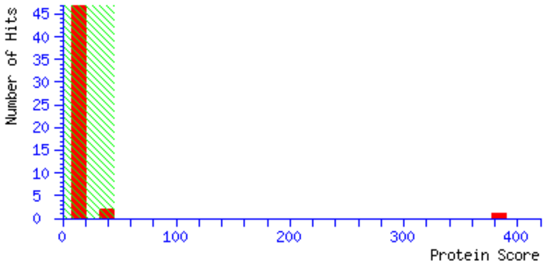
Matched peptides No.: [5] Sequence coverage %: [36]

Matched sequences: K.AEQYAVITWR.A;
R.VSSYLPLLPTEK.I;
K.QVSAQTYSVAQDAPR.I;
K.DISGPLKPGVDTIENVVK.T;
R.IVLDVASSVFNTGVQEGAK.A

Calculated Mr: **22331** Calculated *p*I: **4.80**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEEVEEERL KYLDFVRAAG VYAVDSFSTL YLYAK**DISGP** **LKPGVDTIEN**
51 **VVK**TVVTPVY YIPLEAVKFV DKTVDVSVTS LDGVVPPVIK **QVSAQTYSVA**
101 **QDAPRIVLDV** **ASSVFNTGVQ** **EGAK**ALYANL EPK**AEQYAVI** **TWR**ALNKLPL
151 VPQVANVVVP TAVYFSEKYN DVVRGTTEQG YR**VSSYLPLL** **PTEK**ITKVFG
201 DEAS

Spot No.: 234

NCBI accession No.: gi|132270 Species: *Hevea brasiliensis*

PFF score: [379]

Protein name： Rubber elongation factor protein

Matched peptides No.: [4] Sequence coverage %: [38]

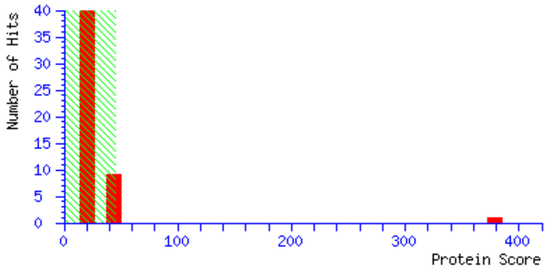
Matched sequences: K.NVAVPLYNR.F;

K.DASIQVVSAIR.A;
K.FVDSTVVASVTIIDR.S;
K.DKSGPLQPGVDIIEGPVK.N

Calculated Mr: **14713** Calculated *p*I: **5.04**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK **DKSGPLQPGV**
51 **DIIEGPVKNV** **AVPLYNR**FSY IPNGALK**FVD** **STVVASVTII** **DR**SLPPIVK**D**
101 **ASIQVVSAIR** AAPEAARSLA SSLPGQTKIL AKVFYGEN

Spot No.: 235

NCBI accession No.: gi|123550 Species: *Pisum sativum*

PFF score: [128]

Protein name: 17.1 kDa class II heat shock protein

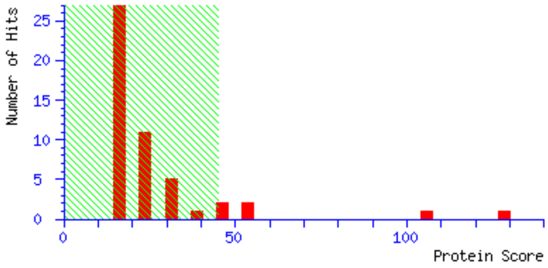
Matched peptides No.: [1] Sequence coverage %: [9]

Matched sequences: K.VQVEDENVLLISGER.K

Calculated Mr: **17059** Calculated *p*I: **6.32**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MDLDSPLFNT LHHIMDLTDD TTEKNLNAPT RTYVRDAKAM AATPADVKEH
51 PNSYVFMVDM PGVKSGDIK**V** **QVEDENVLLI** **SGER**KREEEK EGVKYLKMER
101 RIGKLMRKFV LPENANIEAI SAISQDGVLT VTVNKLPPPE PKKPKTIQVK
151 VA

Spot No.: 236

NCBI accession No.: gi|312985293 Species: *Hevea brasiliensis*

PFF score: [272]

Protein name: nucleoside diphosphate kinase 2

Matched peptides No.: [5] Sequence coverage %: [27]

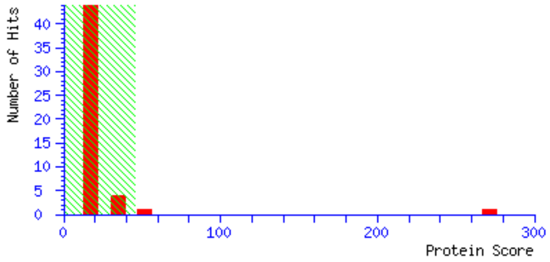
Matched sequences: K.LMSVERPFAEK.H;

K.LMSVERPFAEK.H + Oxidation (M);
R.NVIHGSDSVENAK.K;
R.NVIHGSDSVENAKK.E;
K.IIGATKPSESDPGTIR.G

Calculated Mr: **16463** Calculated *p*I: **5.96**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MEQTFIMIKP DGVQRGLVGE IISRFEKKGF SLKGLK**LMSV** **ERPFAEK**HYE
51 ELSSKPFFEG LVDYIISGPV AAMVWEGKNV VATGRK**IIGA** **TKPSESDPGT**
101 **IR**GDFAVEVG R**NVIHGSDSV** **ENAKK**EIALW FPDGTVNWQS SLHSWIYE

Spot No.: 237

NCBI accession No.: gi|132270 Species: *Hevea brasiliensis*

PFF score: [90]

Protein name：Rubber elongation factor protein

Matched peptides No.: [2] Sequence coverage %: [23]

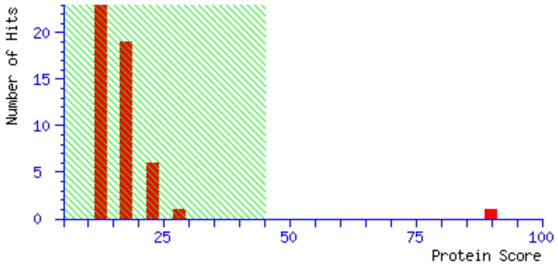
Matched sequences: K.FVDSTVVASVTIIDR.S;

K.DKSGPLQPGVDIIEGPVK.N

Calculated Mr: **14713** Calculated *p*I: **5.04**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK **DKSGPLQPGV**
51 **DIIEGPVK**NV AVPLYNRFSY IPNGALK**FVD** **STVVASVTII** **DR**SLPPIVKD
101 ASIQVVSAIR AAPEAARSLA SSLPGQTKIL AKVFYGEN

Spot No.: 238

NCBI accession No.: gi|2832430 Species: *Hevea brasiliensis*

PFF score: [344]

Protein name： prohevein

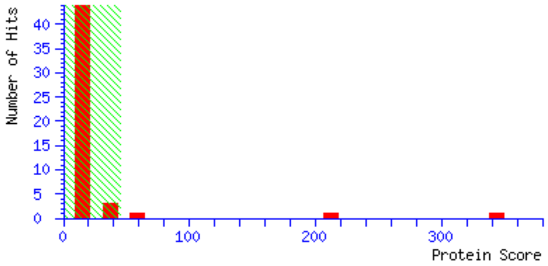
Matched peptides No.: [3] Sequence coverage %: [26]

Matched sequences: R.QLDTDGKGYER.G;
R.IVDQCSNGGLDLDVNVFR.Q;
K.YGWTAFCGPVGAHGQPSCGK.C

Calculated Mr: **20852** Calculated *p*I: **5.64**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 EQCGRQAGGK LCPNNLCCSQ WGWCGSTDEY CSPDHNCQSN CKDSGEGVGG
51 GSASNVLATY HLYNSQDHGW DLNAASAYCS TWDANKPYSW RSK**YGWTAFC**
101 **GPVGAHGQPS** **CGK**CLSVTNT GTGAKATVR**I** **VDQCSNGGLD** **LDVNVFRQLD**
151 **TDGKGYER**GH LTVNYQFVDC GDSFNPLFSV MKSSVIN

Spot No.: 239

NCBI accession No.: gi|255570457 Species: *Ricinus communis*

PFF score: [193]

Protein name： protease C56, putative

Matched peptides No.: [2] Sequence coverage %: [8]

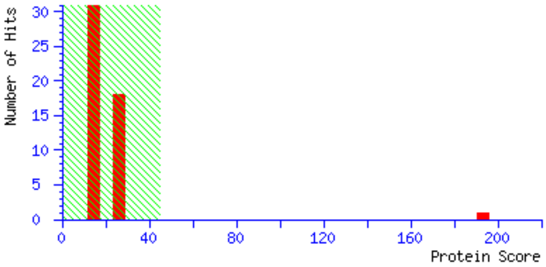
Matched sequences: R.APEYLALDETVIALVK.E;

R.APEYLAMNESVLDCVR.K + Oxidation (M)

Calculated Mr: **42437** Calculated *p*I: **5.60**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MSHQKTVFLL CGDYMEDYEA MVPFQALLAY GVAVDAACPG KKAGDYCRTA
51 IHESSGHQTY SESRGHNFTL NSTFDDIDFG KYDGLVIPGG R**APEYLAMNE**
101 **SVLDCVR**KFA DAGKPIASVC HGQLILAAAG LVKGRKCTAY PPVRPVLIAA
151 GAHWVEPETM ASCVADGNLI TGATYEGHPE FIQLFVKALG GSITGADKRI
201 LFLCGDYMED YEVTVPFQSL QALGCHVNAV CPKKKAGDSC PTAVHDFEGD
251 QTYSEKPGHH FTLTASYVGL DVSSYDALVL PGGR**APEYLA** **LDETVIALVK**
301 QFMQSKKPVA SICHGQQILA AAGVLKGKKC TAYPAVKLNV VLSGATWLEP
351 DPIDRCYTDE NLVTGAAWPG HPEFISQLMA LLGIRVSF

Spot No.: 240

NCBI accession No.: gi|727357 Species: *Arabidopsis thaliana*

PFF score: [58]

Protein name： DnaJ homolog

Matched peptides No.: [2] Sequence coverage %: [6]

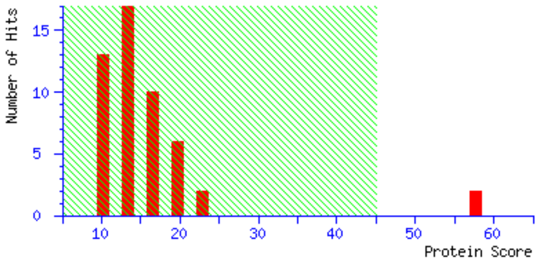
Matched sequences: R.EIYDQYGEDALK.E;

K.ELAQAYEVLSDPEKR.E

Calculated Mr: **47042** Calculated *p*I: **5.68**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MFGRGPSKKS DNTKFYEILG VPKSASPEDL KKAYKKAAIK NHPDKGGDPE
51 KFK**ELAQAYE** **VLSDPEKREI** **YDQYGEDALK** EGMGGGGGGH DPFDIFSSFF
101 GGGPFGGNTS RQRRQRRGED VVHPLKVSLE DVYLGTMKKL SLSRNALCSK
151 CNGKGSKSGA SLKCGGCQGS GMKVSIRQLG PGMIQQMQHA CNECKGTGET
201 INDRDRCPQC KGDKVIPEKK VLEVNVEKGM QHSQKITFEG QADEAPDTVT
251 GDIVFVLQQK EHPQFKRKGE DLFVEHTLSL TEALCGFQFV LTHLDGRSLL
301 IKSNPGEVVK PDSYKAISDE GMPIYQRPFM KGKLYIHFTV EFPDSLSPDQ
351 TKALEAVLPK PSTAQLSDME IDECEETTLH DVNIEDEMRR KAQAQREAYD
401 DDDEDDDHPG GAQRVQCAQQ

Spot No.: 241

NCBI accession No.: gi|255568794   Species: *Ricinus communis*

PFF score: [100]

Protein name： nucleoredoxin, putative

Matched peptides No.: [3]   Sequence coverage %: [5]

Matched sequences: K.LIEAYHEIK.A;
K.KCDFDLHPK.C;
R.VEYFRQEEENAK.K

Calculated Mr: **63728**   Calculated *p*I: **5.46**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
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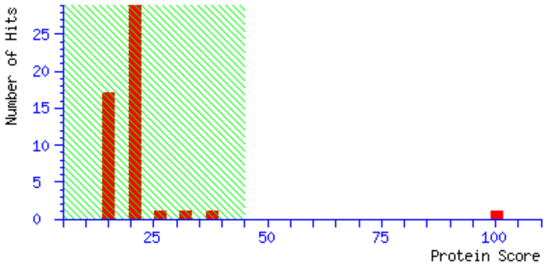


Matched peptide sequences: shown in **Bold Red:**

1 MADDPVIDVS HDLLSLLSSD DRDFLIRSNG DQVKISNLVG KIVGLYFSGS
51 WCGPCRHFTP NLVQVYEELS LKGDFEVVFI SSDRDAESFD AYFSKMPWLA
101 IPFSDQETCK HLKDLFKVRG IPNLVFLDAD GKVSCDQGVR FIREYGAEGY
151 PFTPER**VEYF** **RQEEENAK**KN QTLSSILVSS SRDFLISKDG TKIPVSELEG
201 KMVGLYFSVH SHRLCLDFTP RLEEVYKKLK EKGEKFEVVL ISMDYDENNF
251 KQGLETMPWL ALPFEDKSRE RLARYFELSA LPTLVIIGED GKTLNKNVAE
301 LIEGHGIQAY PFTPEKLVEL AEIEKARLEA QTLESVLVHG DKDFVIEESG
351 SKVPVSELVG KNILLYFSAK WCPPCRAFLP K**LIEAYHEIK** AKDNAFEIIF
401 ISSDRDQSSF DEFYTEMPWL ALPFGDDRKT ILQRKFKIKG IPAAIAISPT
451 GKTLTKEARE HITAYGADAY PFNEDHLKQL NDKQEEIAKG WPEKVRHELH
501 PEHELVRMKR NGYGCDGCKE AGSGWSFYCK **KCDFDLHPK**C ALKKEENGEK
551 VKK

Spot No.: **242**

NCBI accession No.: **gi| 37719658** Species: *Hevea brasiliensis*

Protein name： **50 kDa protein**

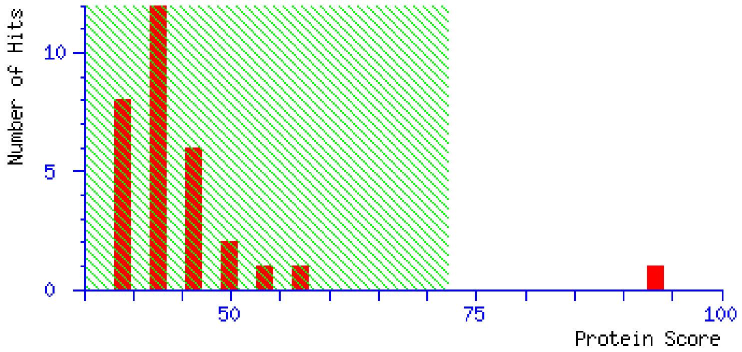
Mascot score: **93** Sequence coverage %: **31**

Matched peptides No.: **9** Total peptides No.: **33**

Calculated Mr: **41480** Calculated *p*I: **4.60**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MASLAYSLFI LSLFTFTLLN PVCSELDEYL FSFGDGLYDA GNAKFIYPDK
51 **YLPSYHHPYG TTFFDYPTGR** FSDGR**TVVDF VAENVSLPRI PPFK**NKEANF
101 TYGANFASEG ATASDSNPLI DFRSQIRDFG ELKLEWAVQL VNVTELARRL
151 KK**AVYLISFG ADDYLNYEIP SEASREQLES IVDVVLGNIS DRIKELYDFG**
201 **ARKFVVENVA PLGLIPFIK**Q TSDNSTLFYE LASLHAMKLP QILEKIQDGY
251 LFPEFNYTVF NYFGIIK**EII DAPGEHGFK**Y GDIACCGNST YRGQACGFLD
301 YEFCVCGNKT EYLFFDGTHN TDAANNLLAE LMWDKESGFI SPYGVKDFFP
351 SPTTIQTLLT EATALG

Spot No.: **243**

NCBI accession No.: **gi|37719658** Species: ***Hevea brasiliensis***

Protein name： **50 kDa protein**

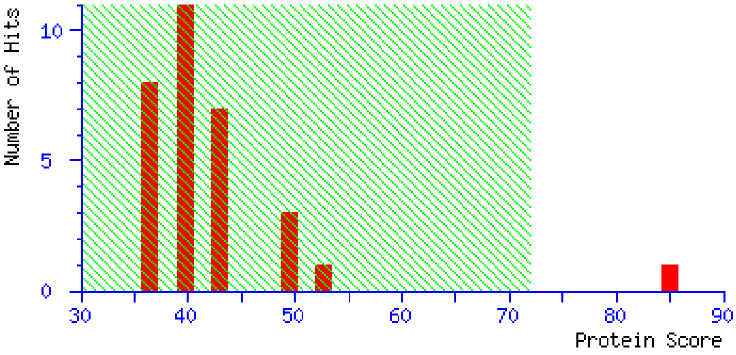
Mascot score: **93** Sequence coverage %: **36**

Matched peptides No.: **11** Total peptides No.: **44**

Calculated Mr: **41480** Calculated *p*I: **4.60**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MASLAYSLFI LSLFTFTLLN PVCSELDEYL FSFGDGLYDA GNAKFIYPDK
51 **YLPSYHHPYG TTFFDYPTGR FSDGRTVVDF VAENVSLPRI PPFK**NKEANF
101 TYGANFASEG ATASDSNPLI DFRSQIRDFG ELKLEWAVQL VNVTELARRL
151 KK**AVYLISFG ADDYLNYEIP SEASREQLES IVDVVLGNIS DRIKELYDFG**
201 **ARKFVVENVA PLGLIPFIK**Q TSDNSTLFYE LASLHAMKLP QILEKIQDGY
251 LFPEFNYTVF NYFGIIK**EII DAPGEHGFK**Y GDIACCGNST YRGQACGFLD
301 YEFCVCGNKT EYLFFDGTHN TDAANNLLAE LMWDK**ESGFI SPYGVK**DFFP
351 SPTTIQTLLT EATALG

Spot No.: **244**

NCBI accession No.: **gi|37719658** Species: *Hevea brasiliensis*

Protein name：**50 kDa protein**

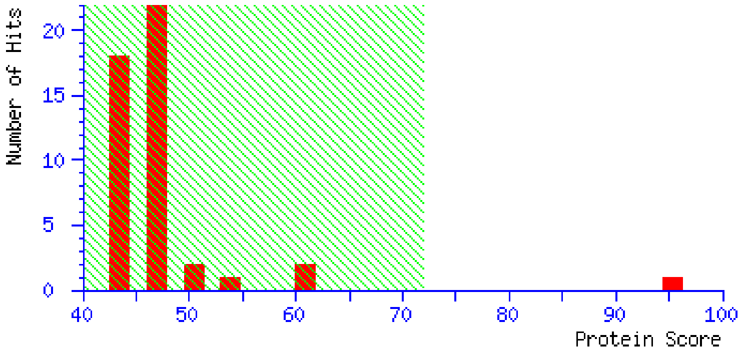
Mascot score: **95** Sequence coverage %: **42**

Matched peptides No.: **14** Total peptides No.: **66**

Calculated Mr: **41480** Calculated *p*I: **4.60**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MASLAYSLFI LSLFTFTLLN PVCSELDEYL FSFGDGLYDA GNAK**FIYPDK**
51 **YLPSYHHPYG TTFFDYPTGR FSDGRTVVDF VAENVSLPRI PPFK**NKEANF
101 TYGANFASEG ATASDSNPLI DFRSQIR**DFG ELK**LEWAVQL VNVTELARRL
151 KK**AVYLISFG ADDYLNYEIP SEASREQLES IVDVVLGNIS DRIKELYDFG**
201 **ARKFVVENVA PLGLIPFIK**Q TSDNSTLFYE LASLHAMK**LP QILEK**IQDGY
251 LFPEFNYTVF NYFGIIK**EII DAPGEHGFKY GDIACCGNST YR**GQACGFLD
301 YEFCVCGNKT EYLFFDGTHN TDAANNLLAE LMWDKESGFI SPYGVKDFFP
351 SPTTIQTLLT EATALG

Spot No.: **245**

NCBI accession No.: **gi| 37719658** Species: *Hevea brasiliensis*

Protein name: **50 kDa protein**

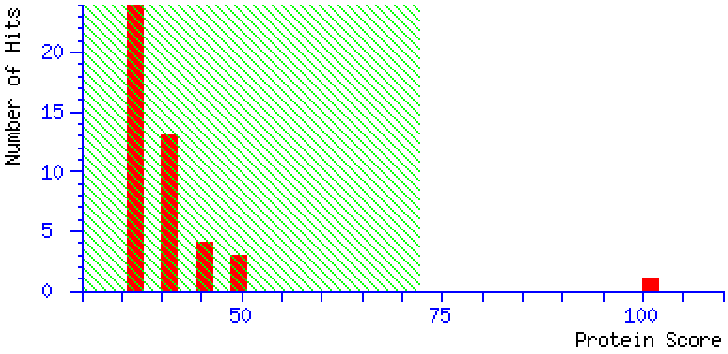
Mascot score: **101** Sequence coverage %: **49**

Matched peptides No.: **16** Total peptides No.: **67**

Calculated Mr: **41480** Calculated *p*I: **4.60**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MASLAYSLFI LSLFTFTLLN PVCSELDEYL FSFGDGLYDA GNAK**FIYPDK**
51 **YLPSYHHPYG TTFFDYPTGR FSDGRTVVDF VAENVSLPRI PPFK**NKEANF
101 TYGANFASEG ATASDSNPLI DFRSQIR**DFG ELK**LEWAVQL VNVTELARRL
151 KK**AVYLISFG ADDYLNYEIP SEASREQLES IVDVVLGNIS DRIKELYDFG**
201 **ARKFVVENVA PLGLIPFIK**Q TSDNSTLFYE LASLHAMK**LP QILEK**IQDGY
251 LFPEFNYTVF NYFGIIK**EII DAPGEHGFKY GDIACCGNST YRGQACGFLD**
301 **YEFCVCGNK**T EYLFFDGTHN TDAANNLLAE LMWDK**ESGFI SPYGVK**DFFP
351 SPTTIQTLLT EATALG

Spot No.: **246**

NCBI accession No.: **gi| 37719658** Species: *Hevea brasiliensis*

Protein name：**50 kDa protein**

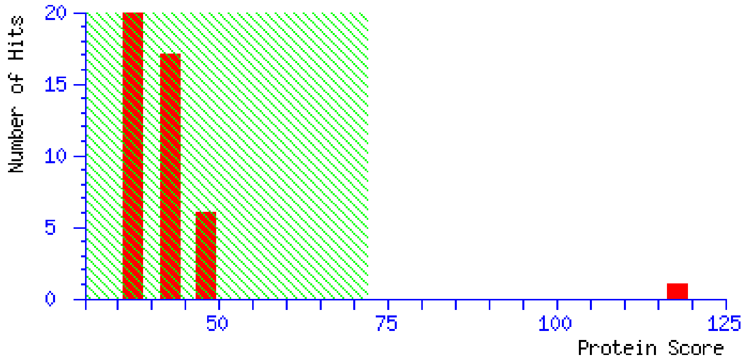
Mascot score: **118** Sequence coverage %: **47**

Matched peptides No.: **15** Total peptides No.: **46**

Calculated Mr: **41480** Calculated *p*I: **4.60**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MASLAYSLFI LSLFTFTLLN PVCSELDEYL FSFGDGLYDA GNAKFIYPDK
51 **YLPSYHHPYG TTFFDYPTGR FSDGRTVVDF VAENVSLPRI PPFK**NKEANF
101 TYGANFASEG ATASDSNPLI DFR**SQIR**DFG ELKLEWAVQL VNVTELARRL
151 KK**AVYLISFG ADDYLNYEIP SEASREQLES IVDVVLGNIS DRIKELYDFG**
201 **ARKFVVENVA PLGLIPFIK**Q TSDNSTLFYE LASLHAMK**LP QILEK**IQDGY
251 LFPEFNYTVF NYFGIIK**EII DAPGEHGFKY GDIACCGNST YRGQACGFLD**
301 **YEFCVCGNK**T EYLFFDGTHN TDAANNLLAE LMWDK**ESGFI SPYGVK**DFFP
351 SPTTIQTLLT EATALG

Spot No.: **247**

NCBI accession No.: **gi|123062** Species: *Hevea brasiliensis*

PFF score: [158]

Protein name: Pro-hevein

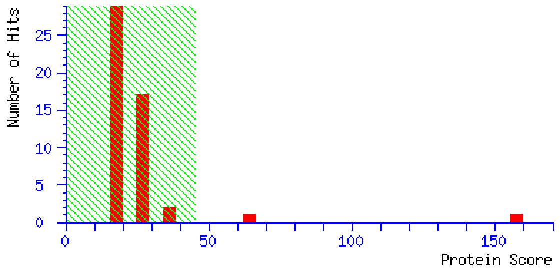
Matched peptides No.: [2] Sequence coverage %: [11]

Matched sequences: K.CLSVTNTGTGAK.T;
R.QLDTDGKGYER.G

Calculated Mr: **22700** Calculated *p*I: **5.63**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MNIFIVVLLC LTGVAIAEQC GRQAGGKLCP NNLCCSQWGW CGSTDEYCSP
51 DHNCQSNCKD SGEGVGGGSA SNVLATYHLY NSQDHGWDLN AASAYCSTWD
101 ANKPYSWRSK YGWTAFCGPV GAHGQSSCGK **CLSVTNTGTG** **AK**TTVRIVDQ
151 CSNGGLDLDV NVFR**QLDTDG** **KGYER**GHITV NYQFVDCGDS FNPLFSVMKS
201 SVIN

Spot No.: **248**

NCBI accession No.: **gi|2832430** Species: *Hevea brasiliensis*

PFF score: [446] Protein name: prohevein

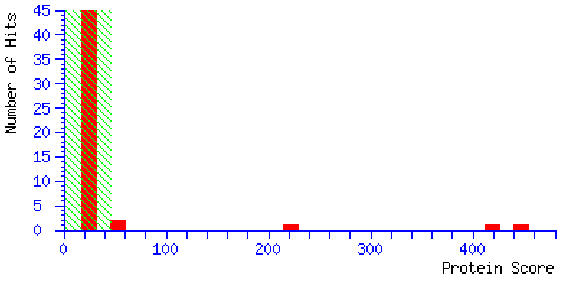
Matched peptides No.: [4] Sequence coverage %: [32]

Matched sequences: K.CLSVTNTGTGAK.A;
R.QLDTDGKGYER.G;
R.IVDQCSNGGLDLDVNVFR.Q;
K.YGWTAFCGPVGAHGQPSCGK.C

Calculated Mr: **20852** Calculated *p*I: **5.64**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 EQCGRQAGGK LCPNNLCCSQ WGWCGSTDEY CSPDHNCQSN CKDSGEGVGG
51 GSASNVLATY HLYNSQDHGW DLNAASAYCS TWDANKPYSW RSK**YGWTAFC**
101 **GPVGAHGQPS** **CGKCLSVTNT** **GTGAK**ATVR**I** **VDQCSNGGLD** **LDVNVFRQLD**
151 **TDGKGYER**GH LTVNYQFVDC GDSFNPLFSV MKSSVIN

Spot No.: **249**

NCBI accession No.: **gi|132270**   Species: *Hevea brasiliensis*

PFF score: [405]

Protein name: Rubber elongation factor protein

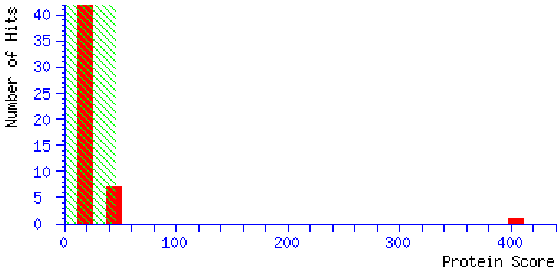
Matched peptides No.: [4]   Sequence coverage %: [38]

Matched sequences: K.NVAVPLYNR.F;
K.DASIQVVSAIR.A;
K.FVDSTVVASVTIIDR.S;
K.DKSGPLQPGVDIIEGPVK.N

Calculated Mr: **14713**   Calculated *p*I: **5.04**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK **DKSGPLQPGV**
51 **DIIEGPVKNV** **AVPLYNR**FSY IPNGALK**FVD** **STVVASVTII** **DR**SLPPIVKD
101 **ASIQVVSAIR** AAPEAARSLA SSLPGQTKIL AKVFYGEN

Spot No.: **250**

NCBI accession No.: **gi|132270**　　Species: *Hevea brasiliensis*

PFF score: [340]

Protein name: Rubber elongation factor protein

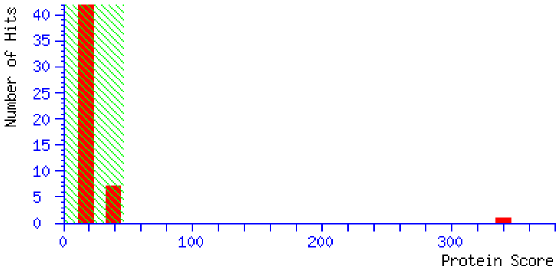
Matched peptides No.: [4]　　Sequence coverage %: [38]

Matched sequences: K.NVAVPLYNR.F;
K.DASIQVVSAIR.A;
K.FVDSTVVASVTIIDR.S;
K.DKSGPLQPGVDIIEGPVK.N

Calculated Mr: **14713**　　Calculated *p*I: **5.04**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK **DKSGPLQPGV**
51 **DIIEGPVKNV** **AVPLYNR**FSY IPNGALK**FVD** **STVVASVTII** **DR**SLPPIVK**D**
101 **ASIQVVSAIR** AAPEAARSLA SSLPGQTKIL AKVFYGEN

Spot No.: **251**

NCBI accession No.: **gi|132270** Species: *Hevea brasiliensis*

PFF score: [470]

Protein name: Rubber elongation factor protein

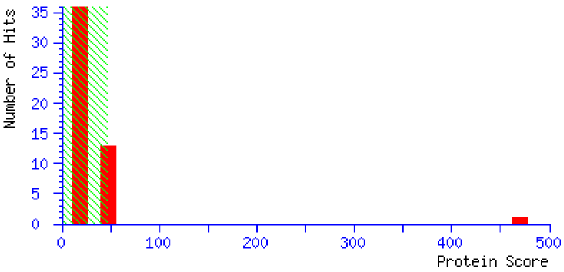
Matched peptides No.: [4] Sequence coverage %: [27]

Matched sequences: K.NVAVPLYNR.F;
K.DASIQVVSAIR.A;
K.SGPLQPGVDIIEGPVK.N;
K.DKSGPLQPGVDIIEGPVK.N

Calculated Mr: **14713** Calculated *p*I: **5.04**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK **DKSGPLQPGV**
51 **DIIEGPVKNV** **AVPLYNR**FSY IPNGALKFVD STVVASVTII DRSLPPIVK**D**
101 **ASIQVVSAIR** AAPEAARSLA SSLPGQTKIL AKVFYGEN

Spot No.: **252**

NCBI accession No.: **gi|132270** Species: *Hevea brasiliensis*

PFF score: [402]

Protein name: Rubber elongation factor protein

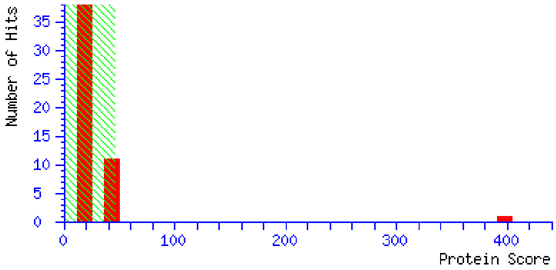
Matched peptides No.: [4] Sequence coverage %: [38]

Matched sequences: K.NVAVPLYNR.F;
K.DASIQVVSAIR.A;
K.FVDSTVVASVTIIDR.S;
K.DKSGPLQPGVDIIEGPVK.N

Calculated Mr: **14713** Calculated *p*I: **5.04**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK **DKSGPLQPGV**
51 **DIIEGPVKNV** **AVPLYNR**FSY IPNGALK**FVD** **STVVASVTII** **DR**SLPPIVK**D**
101 **ASIQVVSAIR** AAPEAARSLA SSLPGQTKIL AKVFYGEN

Band No.: B1

NCBI accession No.: **gi|132270** Species: *Hevea brasiliensis*

PFF score: [282]

Protein name: **Rubber elongation factor protein; Short=REF;**

AltName: Allergen=Hev b 1

Matched peptides No.: [4] Sequence coverage %: [38]

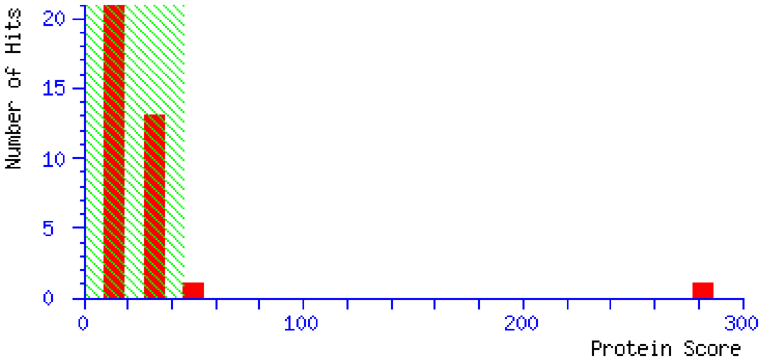
Matched sequences: K.DKSGPLQPGVDIIEGPVK.N; K.NVAVPLYNR.F;

K.FVDSTVVASVTIIDR.S; K.DASIQVVSAIR.A

Calculated Mr: **14713** Calculated *p*I: **5.04**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK **DKSGPLQPGV**
51 **DIIEGPVKNV** **AVPLYNR**FSY IPNGALK**FVD** **STVVASVTII** **DR**SLPPIVKD
101 **ASIQVVSAIR** AAPEAARSLA SSLPGQTKIL AKVFYGEN

Band No.: **B2**

NCBI accession No.: **gi|225440045** Species: ***Vitis vinifera***

Protein name： **cell division cycle protein 48 homolog**

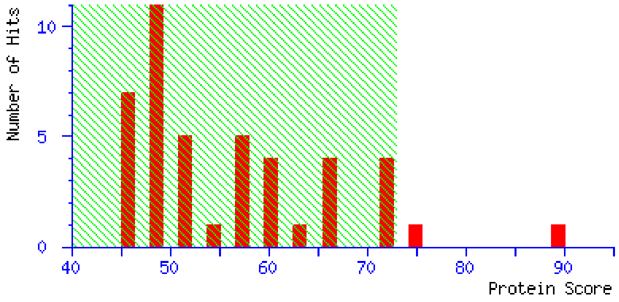
PMF score: **90** Sequence coverage %: **32**

Matched peptides No.: **23** Total peptides No.: **49**

Calculated Mr: **90331** Calculated *p*I: **5.14**

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 73 are significant ($p<0.05$).



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

1 MSNQAESSDS KGTKR**DFSTA** **ILERK**KAANR LVVDEAVNDD NSVVALHPDT

51 MEKLQLFRGD TILIKGKKRK DTICIALADD TCDEPKIRMN KVVR**SNLRVR**

101 **LGDVVSVHQC** **PDVK**YGKRVH ILPVDDTIEG VTGNLFDAYL KPYFLEAYRP

151 VR**KGDLFLVR** GGMRSVEFKV IETDPAEYCV VAPDTEIFCE GEPVRR**EDED**

201 **RLDEVGYDDV** **GGVRKQMAQI** **RELVELPLRH** **PQLFK**SIGVK PPK**GILLYGP**

251 **PGSGK**TLIAR AVANETGAFF FCINGPEIMS K**LAGESESNL** **R**KAFEEAEKN

301 APSIIFIDEI DSIAPKREKT HGEVERRIVS QLLTLMDGLK SRAHVIVIGA

351 TNRPNSIDPA LRR**FGRFDRE** **IDIGVPDEVG** **RLEVLR**IHTK **NMKLSEDVDL**

401 **ER**IAKDTHGY VGADLAALCT EAALQCIREK MDVIDLEDES IDAEILNSMA

451 VTDEHFKTAL GTSNPSALR**E** **TVVEVPNVSW** **EDIGGLENVK** **RELQETVQYP**

501 **VEHPEKFEK**F GMSPSKGVLF YGPPGCGKTL LAKAIANECQ ANFISVKGPE

551 LLTMWFGESE ANVR**EIFDKA** **R**QSAPCVLFF DELDSIATQR GSSVGDAGGA

601 ADR**VLNQLLT** **EMDGMSAK**K**T** **VFIIGATNRP** **DIIDPALLR**P GRLDQLIYIP

651 LPDEDSR**HQI** **FK**ACLRKSPV SKDVDLRALA KYTQGFSGAD ITEICQRACK

701 YAIRENIEKD IERERRR**REN** **PEAMEEDVDE** **EVAEIK**AAHF EESMKYARRS

751 VSDADIR**KYQ** **AFAQTLQQSR** **GFGTEFR**FSE TSTGAAGSDP FAASAGGAAD

801 EDDLYS

Band No.: **B3**

NCBI accession No.: **gi|** 88193697 Species: *Arachis hypogaea*

PFF score: **[100]** Protein name： phospholipase D alpha 2

Matched peptides No.: [2] Sequence coverage %: [2]

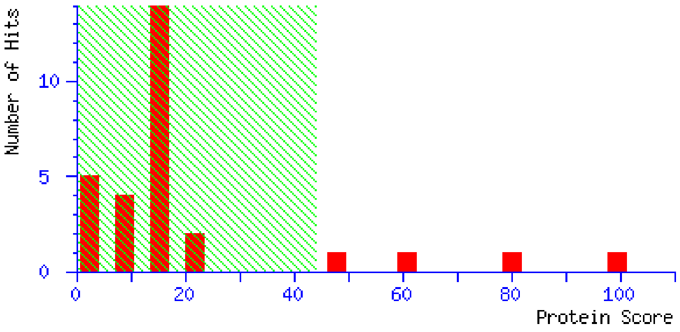
Matched sequences: R.SIDGGAAFGFPETPEDAAR.A;

R.SIDGGAAFGFPETPEDAAR.A

Calculated Mr: **92340** Calculated *p*I: **5.54**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MAQILLHGTL HVTIYEVDKL KTSGGNVFTK LVQNIEETVG FGKGVTKLYA

51 TIDLEKARVG RTRIIEKDHS NPRWYESFHI YCAHMASNII FTVKDDNPIG

101 ATLIGRAYVP VEDVLDGEEV DRWVEILDED KNPIHGNSKI HVKLQYFDVT

151 KDKNWARGVR SAKFPGVPYT FFSQRRGCKV SLYQDAHVPD NFVPKIPLAG

201 GQTYQPHRCW EDVFDAIEKA RHLIYITGWS VYTEITLVRD SRRPKPGGDL

251 TIGELLKKKA NEGVRVLMLV WDDRTSVPLL KKDGLMATHD EETEKYFQGT

301 EVHCILCPRN PDDGGSIIQD LQISTMFTHH QKIVVVDSDM PSGDSGKRRI

351 VSFVGGIDLC DGRYDTQFHS LFRTLDTAHH DDFHQPNFAG ASIMKGGPRE

401 PWHDIHSRLE GPIAWDVLFN FEQRWRKQGG KDLLIPLREL EDVIIPPSPV

451 TFAEDQETWN VQLFR**SIDGG AAFGFPETPE DAAR**AGLVSG KDNIIDRSIQ

501 DAYIHAIRRA KNFIYIENQY FLGSCFGWSP DDIKPEDIGA LHLIPKELSL

551 KIVSKIEAGE RFTVYIVVPM WPEGFPESGS VQAILDWQRR TMEMMYKDIV

601 EALNAKGIVE DPRNYLTFFC LGNREVKKPG EYEPSERPDP DSDYIKAQEN

651 RRFMIYVHAK MMIVDDEYII IGSANINQRS MDGARDSEIA MGAYQPYYLS

701 ARELARGQIH GFRLALWYEH LGMIRESFLQ PESEECIKMV NQVADKYWDL

751 YSSESLDHDL PGHLLRYPVG ISGDGTVTEL PGFEFFPDTK GRVLGTKTDY

801 LPPILTT

Band No.: B4

NCBI accession No.: **gi| 225440324** Species: ***Vitis vinifera***

Protein name： heat shock cognate 70 kDa protein isoform 1

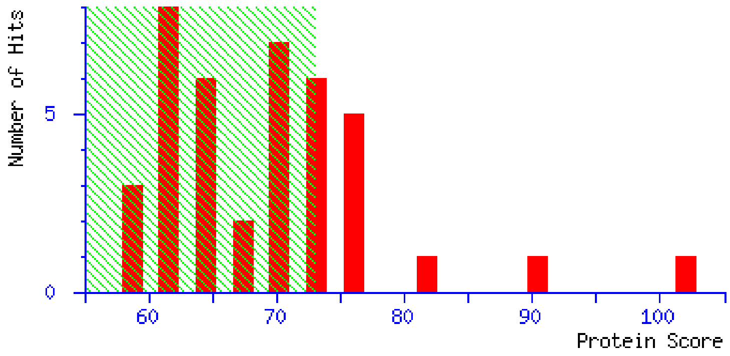
Mascot score: **102** Sequence coverage %: **36**

Matched peptides No.: **22** Total peptides No.: **68**

Calculated Mr: **71420** Calculated *p*I: **5.17**

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 73 are significant ($p<0.05$).



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

1 MAGKGEGPAI GIDLGTTYSC VGVWQHDRVE IIANDQGNR**T** **TPSYVAFTDT**
51 **ER**LVGDAAK**N** **QVAMNPINTV** **FDAKR**LIGRR FSDATVQSDI KLWPFKVVAG
101 PGDKPMIVVN YKGEEK**QFAA** **EEISSMVLMK** **MREIAEAYLG** **SAVKNAVVTV**
151 **PAYFNDSQRQ** **ATKDAGVIAG** **LNVMRIINEP** **TAAAIAYGLD** **KK**ATSVGEKN
201 VLIFDLGGGT FDVSLLTIEE GIFEVK**ATAG** **DTHLGGEDFD** **NRMVNHFVQE**
251 **FKR**KHKK**DIS** **GNPR**ALRRLR TACERAKRTL SSTAQTTIEI DSLYEGVDFY
301 TTITR**ARFEE** **LNMDLFR**KCM EPVEKCLRDA KMDK**SSVHDV** **VLVGGSTRIP**
351 KVQQLLQDFF NGKELCKSIN PDEAVAYGAA VQAAILSGEG NDKVQDLLLL
401 DVTPLSLGLE TAGGVMTVLI PRNTTIPTKK **EQVFSTFSDN** **QPGVLIQVYE**
451 **GERTR**TRDNN LLGKFELSGI PPAPRGVPQI TVCFDIDANG ILNVSAEDKT
501 TGQKNKITIT NDKGRLSKEE IEK**MVQEAEK** YKSEDEEHKK KVDAK**NALEN**
551 **YAYNMR**NTVK DEKIGAKLPP ADKKKIEDAI EQAIQWLDNN QLAEADEFED
601 KMKELESICN PIIAK**MYQGA** **GGPDMGGGMD** **EDGPSAGGSG** **AGPK**IEEVD

Band No.: B5

NCBI accession No.: gi|253760141 Species: *Sorghum bicolor*

Protein name: hypothetical protein SORBIDRAFT_1058s002010

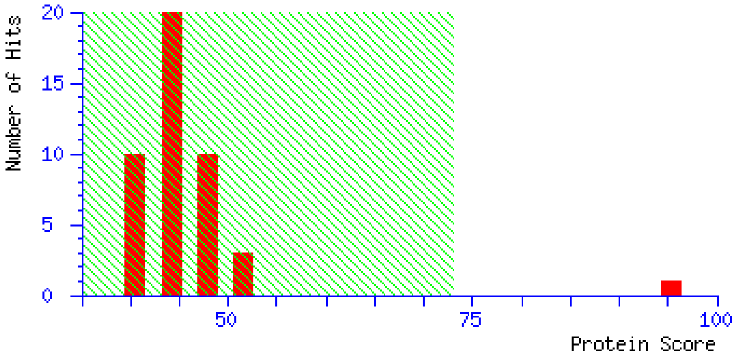
Mascot score: 95 Sequence coverage %: 57

Matched peptides No.: 15 Total peptides No.: 59

Calculated Mr: 23743 Calculated *p*I: 6.77

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold red:

1 **MASAVASMVA** **APKPVFLMDL** **LASPSASSRH** **LFR**TGDARPR SSSDGVKDST
51 GK**DDAAAADG** **RPERDPSIPK** **LFTGDVLDLF** **PEAAKR**DLLL ALAEDGGGAG
101 SMITGLAPRG WWISKKDGDA LQLK**VAMPGL** **GKEHVK**MRAE KNVLVIKGEG
151 DK**DAEGDKDA** **EGDDDKVPVP** **VPVPAR**YIYR IGLPSQAFK**M** **DQIKAEMKNG**
201 **VLILTMPKIK** **GEGR**KDVFGI KIE

Band No.: B6

NCBI accession No.: gi|14423933   Species: *Hevea brasiliensis*

PFF score: [348]

Protein name: **Small rubber particle protein; Short=SRPP; AltName: Full=22 kDa rubber particle protein; Short=22 kDa RPP; AltName: Full=27 kDa natural rubber allergen; AltName: Full=Latex allergen Hev b 3; AltName: Allergen=Hev b 3**

Matched peptides No.:   [4]   Sequence coverage %:   [21]

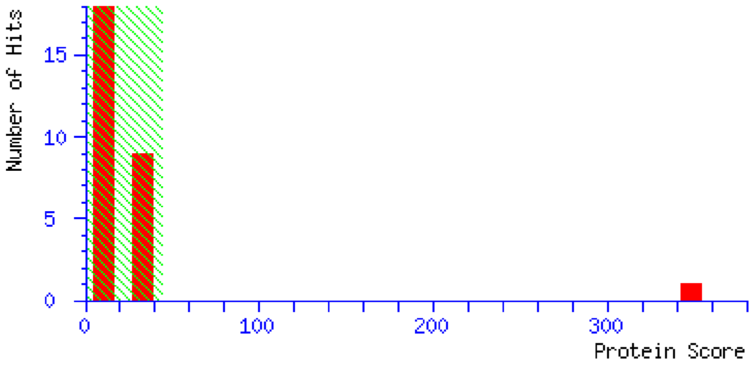
Matched sequences: K.QVSAQTYSVAQDAPR.I; R.IVLDVASSVFNTGVQEGAK.A;

R.IVLDVASSVFNTGVQEGAK.A; K.AEQYAVITWR.A

Calculated Mr: 22331   Calculated *p*I: 4.80

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

```
  1  MAEEVEEERL  KYLDFVRAAG  VYAVDSFSTL  YLYAKDISGP  LKPGVDTIEN
 51  VVKTVVTPVY  YIPLEAVKFV  DKTVDVSVTS  LDGVVPPVIK  QVSAQTYSVA
101  QDAPRIVLDV  ASSVFNTGVQ  EGAKALYANL  EPKAEQYAVI  TWRALNKLPL
151  VPQVANVVVP  TAVYFSEKYN  DVVRGTTEQG  YRVSSYLPLL  PTEKITKVFG
201  DEAS
```

Band No.: B7

NCBI accession No.: **gi|260099871** Species: ***Hevea Brasiliensis***

Protein name: **beta-1,3-glucanase**

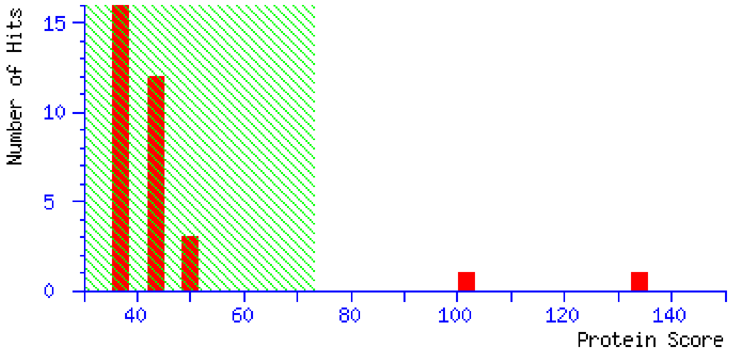
Mascot score: **125** Sequence coverage %: **40**

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

Calculated Mr: **41543** Calculated *p*I: **9.40**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 MAISSSTSGT SSSLPSRTTV MLLLFFFTAS VGITDAQVGV CYGMQGNNLP

51 PVSEVIALYK KSNITRMR**IY** **DPNQAVLEAL** **RGSNIELILG** **VPNSDLQSLT**

101 **NPSNAK**SWVQ KNVRGFWSSV RFR**YIAVGNE** **ISPVNR**GTAW LAQFVLPAMR

151 **NIHDAIRSAG** **LQDQIKVSTA** **IDLTLVGNSY** **PPSAGAFRDD** **VRSYLNPIIR**

201 **FLSSIRSPLL** **ANIYPYFTYA** **GNPR**DISLPY ALFTSPSVVV WDGQRGYKNL

251 FDATLDALYS ALERASGGSL EVVVSESGWP SAGAFAATFD NGR**TYLSNLI**

301 **QHVK**RGTPKR PK**RAIETYLF** **AMFDENKK**QP EVEKHFGLFF PNKWQKYNLN

351 FSAEKNWDIS TEHNATILFL KSDM

Band No.: **B8**

NCBI accession No.: **gi| 10946499** Species: ***Hevea Brasiliensis***

Protein name: **beta-1,3-glucanase**

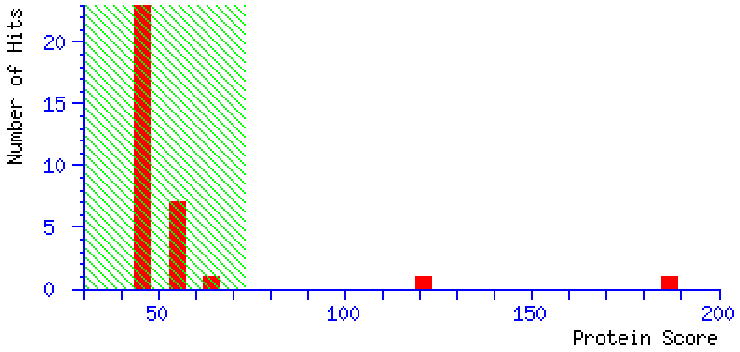
Mascot score: **187** Sequence coverage %: **61**

Matched peptides No.: **20** Total peptides No.: **62**

Calculated Mr: **35295** Calculated *p*I: **9.46**

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 73 are significant ($p<0.05$).



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

1 QVGVCYGMQG NNLPPVSEVI ALYKKSNITR MR**IYDPNRAV** **LEALRGSNIE**
51 **LILGVPNSDL** **QSLTNPSNAK** **SWVQK**NVR**GF** **WSSVLFRYIA** **VGNEISPVNR**
101 **GTAWLAQFVL** **PAMRNIHDAI** **RSAGLQDQIK** **VSTAIDLTLV** **GNSYPPSAGA**
151 **FRDDVRSYLN** **PIIRFLSSIR** **SPLLANIYPY** **FTYAGNPR**DI SLPYALFTSP
201 SVVVWDGQRG YK**NLFDATLD** **VLYSALER**AS GGSLEVVVSE SGWPSAGAFA
251 ATFDNGR**TYL** **SNLIQHVK**RG TPKRPNR**AIE** **TYLFAMFDEN** **KK**QPEVEKQF
301 GLFFPDKWQK YNLNFG

Band No.: B9

NCBI accession No.: gi|255540341 Species: *Ricinus communis*

Protein name： glyceraldehyde 3-phosphate dehydrogenase, putative

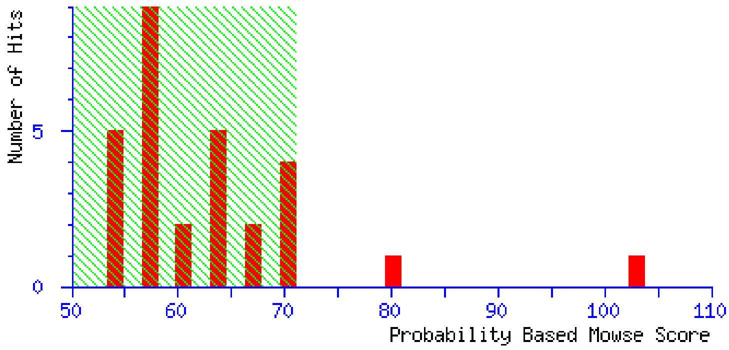
Mascot score: 103 Sequence coverage %: 48

Matched peptides No.: 15 Total peptides No.: 82

Calculated Mr: 36930 Calculated *p*I: 7.10

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 73 are significant (p<0.05).



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

1 MAKIK**IGING** **FGR**IGRLVAR **VALQR**DDVEL VAVNDPFIST EYMTYMFK**YD**
51 **TVHGQWK**HHE LKIKDDKTLL FGEKPVTVFG VR**NPEEIPWA** **ETGAEYIVES**
101 **TGVFTDKDK**A AAHLKGGAKK VIISAPSK**DA** **PMFVVGVNEK** EYTPDLHIIS
151 NASCTTNCLA PLAKVINDR**F** **GIVEGLMTTV** **HSITATQKTV** **DGPSMK**DWRG
201 GR**AASFNIIP** **SSTGAAK**AVG KVLPSLNGK**L** **TGMSFRVPTV** **DVSVVDLTVR**
251 LEKSATYEQI KAAIK**EESEG** **KLK**GILGYTE DDVVSTDFIG DKR**SSIFDAK**
301 **AGIALNDKFV** **KLVSWYDNEW** **GYSTR**VVDLI VHVASVH

Band No.: **B10**

NCBI accession No.: **gi|14423933** Species: ***Hevea Brasiliensis***

Protein name： **Small rubber particle protein**

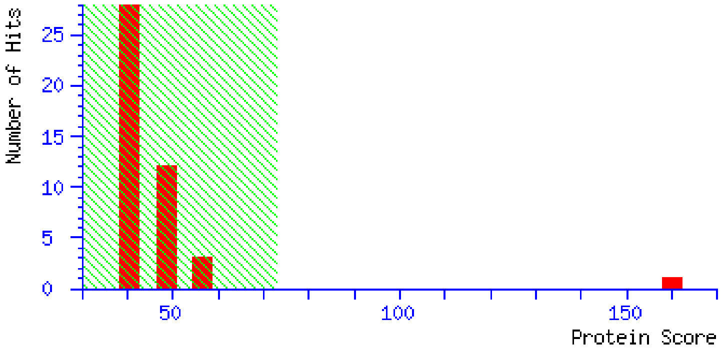
Mascot score: **160** Sequence coverage %: **77**

Matched peptides No.: **13** Total peptides No.: **44**

Calculated Mr: **22331** Calculated *p*I: **4.80**

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 73 are significant ($p<0.05$).



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

1 MAEEVEEERL K**YLDFVRAAG** **VYAVDSFSTL** **YLYAKDISGP** **LKPGVDTIEN**
51 **VVKTVVTPVY** **YIPLEAVKFV** **DKTVDVSVTS** **LDGVVPPVIK** **QVSAQTYSVA**
101 **QDAPRIVLDV** **ASSVFNTGVQ** **EGAKALYANL** **EPKAEQYAVI** **TWR**ALNKLPL
151 VPQVANVVVP TAVYFSEK**YN** **DVVRGTTEQG** **YRVSSYLPLL** **PTEK**ITKVFG
201 DEAS

Band No.: B**11**

NCBI accession No.: **gi| 38122474** Species: ***Hevea Brasiliensis***

Protein name: **rubber elongation factor**

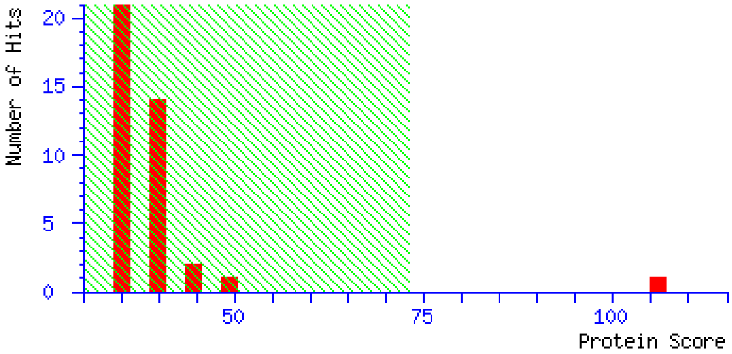
Mascot score: **106** Sequence coverage %: **42**

Matched peptides No.: **10** Total peptides No.: **29**

Calculated Mr: **19570** Calculated *p*I: **5.06**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 MAEGEEEVNI QEEANKGEEN PQEEANIQEE TNKGEENIQE EANIEEEANK
51 EEESLK**YLDF** **VQAATVYAR**A SFSK**LYLFAK** **DKSGPFKPGV** **NTVESRFKSV**
101 **VRPVYNKFQP** **VPNK**VLK**FAD** **RRVDAYVTVL** **DRIVPPIVKR** ASIQAYSVAP
151 GAALAVASYL PLHTKRLSKV LYGDG

Band No.: B12

NCBI accession No.: gi|3288200 Species: *Hevea brasiliensis*

Protein name： latex allergen

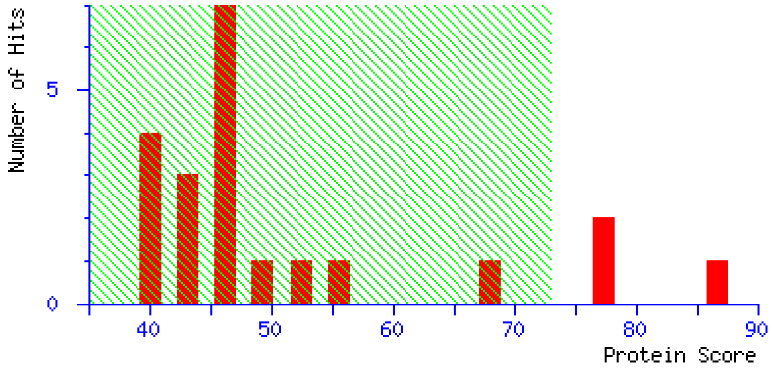
Mascot score: 87 Sequence coverage %: 41

Matched peptides No.: 12 Total peptides No.: 43

Calculated Mr: 43020 Calculated *p*I: 5.00

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 73 are significant ($p<0.05$).



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

1 MATGSTTLTQ GK**KITVLSID** **GGGIRGIIPG** **IILASLESKL** **QDLDGPDAR**I
51 ADYFDIIAGT STGGLITTML TAPNEDKKPI YQAKDIKDFY LENCPKIFPK
101 ESR**DTYDPIH** **SIGPIYDGEY** **LR**ELCNNLLK DLTVK**DTLTD** **VIIPAFDIKL**
151 **LLPVIFSSDD** **AK**CNALKNAR LADVCISTSA APVLLPAHSF TTEDDKNIHT
201 FELIDGGVAA ANPTLLALTH IRNEIIRQNP R**FIGANLTES** **K**SRLVLSLGT
251 GKSEYKEKYN ADMTSKWRLY NWALYNGNSP AVDIFSNASS DMVDFHLSAL
301 FKSLDCEDYY LR**IQDDTLTG** **EESSGHIATE** **ENLQRLVEIG** **TELLEKQESR**
351 **INLDTGRLES** **IPGAPTNEAA** **IAK**FAKLLSE **ER**KLRQLK

Band No.: B13

NCBI accession No.: **gi| 334854628** Species: ***Hevea brasiliensis***

PFF score: [271] Protein name：**rubber elongation factor**

Matched peptides No.: [3] Sequence coverage %: [27]

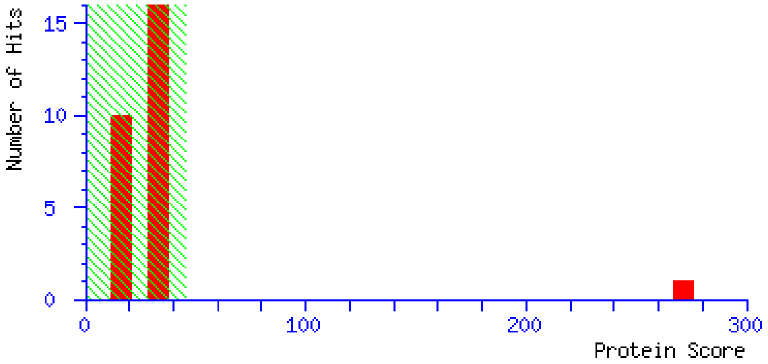
Matched sequences: K.DKSGPLQPGVDIIEGPVK.N; K.NVAVPLYNR.F;

K.DASIQVVSAIR.A

Calculated Mr: **14889** Calculated *p*I: **5.04**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red

1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK **DKSGPLQPGV**
51 **DIIEGPVKNV** **AVPLYNR**FSY IPNGALKFVD SPVVASVTII DRSLPPIVKD
101 **ASIQVVSAIR** AAPEAARFLA FFLPGQTKIL AKVFYGEN

Band No.: B14

NCBI accession No.: gi|14423688 Species: *Hevea brasiliensis*

Protein name：Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1; AltName: Allergen=Hev b 9

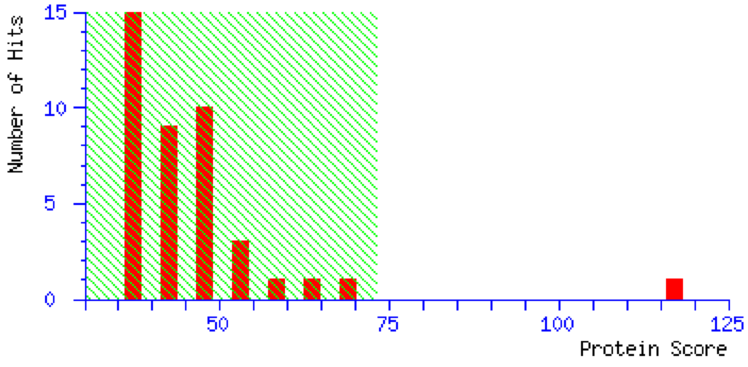
Mascot score: 117 Sequence coverage %: 48

Matched peptides No.: 20 Total peptides No.: 71

Calculated Mr: 48029 Calculated *p*I: 5.57

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 73 are significant ($p<0.05$).



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

1 MAITIVSVR**A** **RQIFDSRGNP** **TVEADVKLSD** **GYLARAAVPS** **GASTGIYEAL**
51 **ELRDGGSDYL** **GK**GVSKAVEN VNIIIGPALV GKDPTDQVGI DNFMVQQLDG
101 TVNEWGWCKQ KLGANAILAV SLAVCKAGAH VKGIPLYEHI ANLAGNKNLV
151 LPVPAFNVIN GGSHAGNKLA MQEFMILPVG ASSFKEAMK**M** **GAEVYHHLKS**
201 VIKKK**YGQDA** **TNVGDEGGFA** **PNIQENKEGL** **ELLK**TAIAKA GYTGKVVIGM
251 DVAASEFYGS DQTYDLNFKE ENNNGSQKIS GEALKDLYK**S** **FVAEYPIVSI**
301 **EDPFDQDDWA** **HYAKLTSEIG** **EKVQIVGDDL** **LVTNPK**RVEK AIKEKACNAL
351 LLK**VNQIGSV** **TESIEAVK**MS K**RAGWGVMAS** **HRSGETEDTF** **IADLSVGLAT**
401 **GQIK**TGAPCR SERLAK**YNQL** **LRIEEELGSE** **AVYAGANFRK** **PVEPY**

Band No.: B15

NCBI accession No.: gi|255543357 Species: *Ricinus communis*

Protein name： heat shock protein, putative

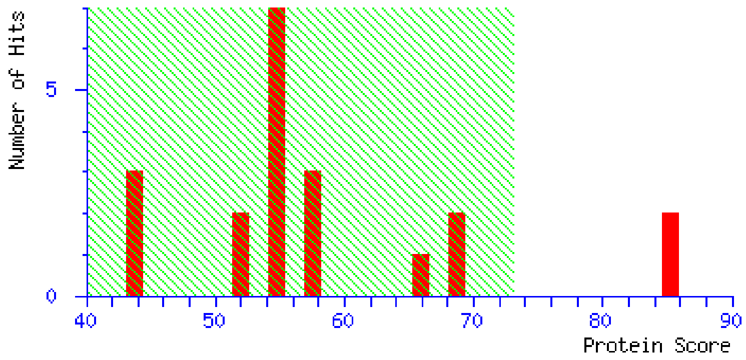
Mascot score: 85 Sequence coverage %: 22

Matched peptides No.: 9 Total peptides No.: 17

Calculated Mr: 71965 Calculated *p*I: 5.27

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 73 are significant ($p<0.05$).



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

1 MAK**TEGKAVG** **IDLGTTYSCV** **GVWQNDR**VEI IANDQGNR**TT** **PSYVAFTDTE**

51 **RLIGDAAKNQ** **VAMNPQNTVF** **DAKR**LIGRRF SDPSVQSDMK HWPFKVVPGP

101 GDKPMIVVLY KGEEKQFAPE EISSMVLIKM KEIAEAYLGQ TVK**NAVITVP**

151 **AYFNDSQR**QA TK**DAGAISGL** **NVMRIINEPT** **AAAIAYGLDK** **K**GSRSGEKNV

201 LIFDLGGGTF DVSLLTIEEG IFEVKATAGD THLGGEDFDN RLVNHFVAEF

251 RRKHKKDIST NARALRRLRT ACERAKRTLS STSQTTIEID SLYEGIDFYS

301 TITR**ARFEEL** **NMDLFR**KCME PVEKCLRDSK IDKSQVDDIV LVGGSTRIPK

351 VQQLLQDFFN GKELCKSINP DEAVAYGAAV QAAILSGEGD QKVQELLLLD

401 VTPLSLGIET AGGVMTVLIP RNTTIPAKK**E** **QIFSTYSDNQ** **PGVLIQVYEG**

451 **ERAR**TKDNNL LGTFELKGIP PAPRGVPQIN VCFDIDANGI LNVSAEDKTA

501 GVKNKITITN DKGRLSKEDI ERMVQEAEKY KAEDEQVKKK VEAKNALENY

551 AYNMRNTVKD EKFAGKLDSA DKQKIEKAID ETIEWLDGNQ LAEVDEFEDK

601 LK**ELEGLCNP** **IVSK**MYQGGA GGDVPMGGGA KPGSGYGNAS SGGSGSGPKI

651 EEVD

Band No.: B16

NCBI accession No.: gi|225456951 Species: *Vitis vinifera*

Protein name：cell division cycle protein 48 homolog

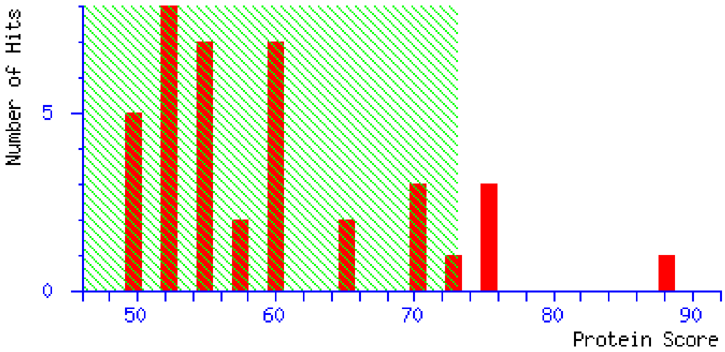
Mascot score: 88 Sequence coverage %: 33

Matched peptides No.: 27 Total peptides No.: 121

Calculated Mr: 91020 Calculated *p*I: 5.12

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold red

1 **MADPSSSGPS** **SSPEVKSVK**K **DFSTAILERK** KSPNRLVVDE AVNDDNSVVS

51 MNPATMEKLQ FFRGDTVLIK GKKR**KDTVCI** **VLVDEQCEEP** **K**IRMNKVVRA

101 NLR**VRLGDVV** **SVHQCPDVK**Y GKRVHILPID DTIEGVTGNL FDAYLKPYFL

151 ESYRPVR**KGD** **LFLVR**GGMRS VEFKVIETDP GEYCVVAPDT EIFCEGEPIK

201 REDEER**LNEV** **GYDDVGGVRK** **QMAQIRELVE** **LPLRHPQLFK** SIGVKPPK**GI**

251 **LLYGPPGSGK** TLIARAVANE TGAFFFLING PEIMSK**LAGE** **SESNLR**KAFE

301 EAEKNAPSII FIDELDSIAP KREKTHGEVE RRIVSQLLTL MDGLKTR**AHV**

351 **IVIGATNRPN** **SIDPALRRFG** **RFDR**EIDIGV PDEVGRLEVL RIHTKNMKLS

401 DDVDLERVAK DTHGYVGADL AALCTEAALQ CIREKMDVID LEDETIDAEV

451 LNSMAVTNEH FQTALGSSNP SALR**ETVVEV** **PNVSWEDIGG** **LDNVKRELQE**

501 **TVQYPVEHPE** **KFEK**FGMSPS KGVLFYGPPG CGKTLLAKAI ANECQANFIS

551 VK**GPELLTMW** **FGESEANVRE** **IFDKAR**QSAP CVLFFDELDS IATQR**GSSVG**

601 **DAGGAADR**VL NQLLTEMDGM TAKKTVFIIG ATNRPDIIDP ALLRPGR**LDQ**

651 **LIYIPLPDEA** **SRLQIFKACL** **RKSPVSR**DVD LVALARYTHG FSGADITEIC

701 QRSCKYAIRE NIEKDIERER KKTENPEAME EDDVDDVPEI KAAHFEESMK

751 FARRSVSDAD IR**KYQLFAQT** **LQQSR**GFGSE FRFPDQPNNA TAASTAADPF

801 SSAAAGDDD DLYS

Band No.: B17

NCBI accession No.: gi|66735596 Species: *Arachis hypogaea*

PFF score: [67] Protein name: phospholipase D alpha

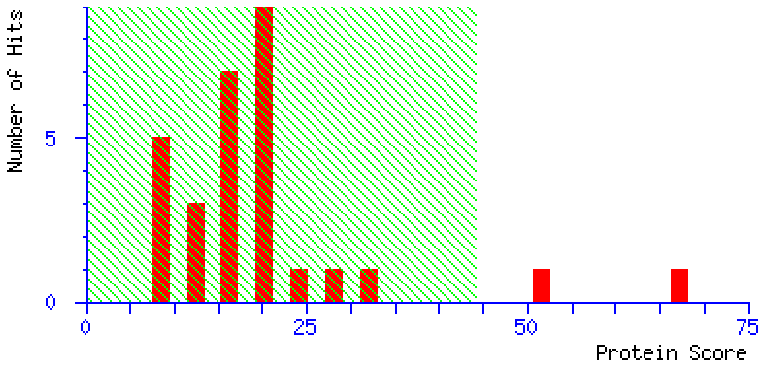
Matched peptides No.: [1] Sequence coverage %: [10]

Matched sequences: R.SIDGGAAFGFPETPEDAAR.A

Calculated Mr: 21036 Calculated *p*I: 5.22

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 HHDDFHQPNF AGASIMKGGP REPWHDIHSR LEGPIAWDVL FNFEQRWRKQ
51 GGKDLLIPLR ELEDVIIPPS PVTFAEDQET WNVQLFR**SID** **GGAAFGFPET**
101 **PEDAAR**AGLV SGKDNIIDRS IQDAYIHAIR RAKNFIYIEN QYFLGSCFGW
151 SPDDIKPEDI GALHLIPKEL SLKNVSKIEA GERFT

Band No.: B18

NCBI accession No.: gi|33326375 Species: *Hevea brasiliensis*

Protein name： heat shock protein

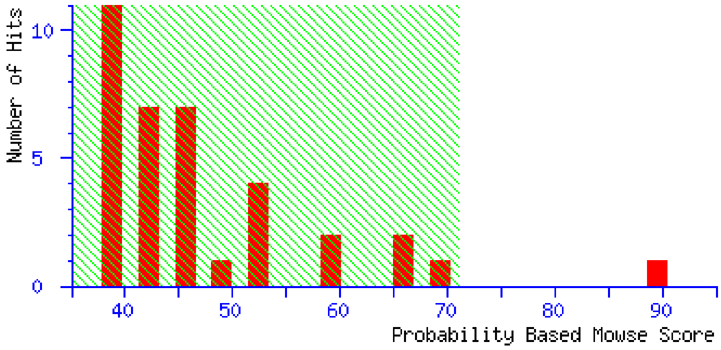
Mascot score: 90 Sequence coverage %: 28

Matched peptides No.:17 Total peptides No.: 52

Calculated Mr: 80380 Calculated *p*I: 5.02

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold red

1 MADAETFAFQ AEINQLLSLI INTFYSNKEI FLREIISNAS DALDKIRFES
51 LTDKSK**LDAQ** **PELFIR**LVPD KANKTLSIID SGIGMTK**ADL** **VNNLGTIARS**
101 GTKEFMEALQ AGADVSMIGQ FGVGFYSAYL VAEKVIVTTK **HNDDEQYIWE**
151 **SQAGGSFTVT** **R**DVNGDQLGR GTK**ITLFLKE** **DQLEYLEER**R IKDLVKKHSE
201 FISYPIYLWT EKTTEKEISD DEDDEPKKEE EGDVEDVDEE KETKSKKKK**I**
251 **KEVSHEWQLI** **NKQKPIWLRK** **PEEITKEEYA** **SFYKSLTNDW** **EDHLAVKHFS**
301 **VEGQLEFK**AI LFVPK**RAPFD** **LFDTR**KKMSN IKLYVR**RVFI** **MDNCEELIPE**
351 **YLGFVKGVVD** **SDDLPLNISR** EMLQQNKILK VIRKNLVKKC IEMFNEIAEN
401 KEDYNKFYEA FSKNLKLGIH EDSQNRAKLA DLLR**YHSTKS** **GDEMTSLK**DY
451 VTRMKEGQKD IYYITGESKK **AVENSPFLER** LKKKGYEVLF MVDAIDEYAV
501 GQLKEYDGKK LVSATKEGLK LDDETEEEKK KKEEKKKSFE NLCKTIKDIL
551 GDKVEKVVVS DRIVDSPCCL VTGEYGWTAN MERIMKAQAL RDSSMSSYMS
601 SKK**TMEINPD** **NVIVEELRK**R AEADKNDKSV KDLVLLLFET ALLTSGFSLD
651 DPNTFSARIH RMLKLGLSID DDETAGDDAD MPALEEDGAE ESKMEEVD

Band No.: B19

NCBI accession No.: gi|450880 Species: *Arabidopsis thaliana*

Protein name：heat shock cognate 70-1

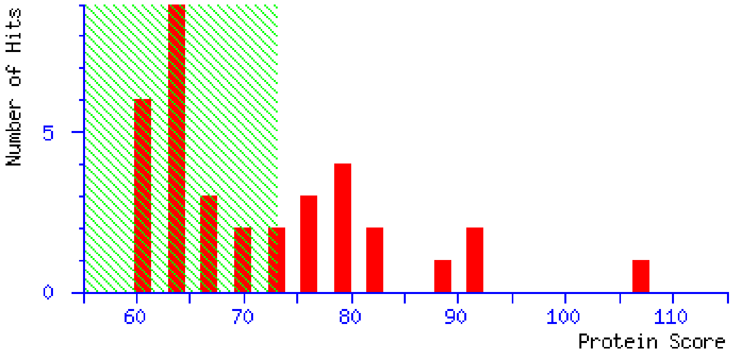
Mascot score: 107 Sequence coverage %: 47

Matched peptides No.: 28 Total peptides No.: 83

Calculated Mr: 70427 Calculated *p*I: 5.11

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 73 are significant ($p<0.05$).



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

1 GTTYSCVGVW QHDR**VEIIAN** **DQGNRTTPSY** **VAFTDSERLI** **GDAAKNQVAM**
51 **SPVNTVFDAK** RLIGRRFSDS SVQSDMKLWP FKIQAGPADK PMIYVEYKGE
101 EK**EFAAEEIS** **SMVLIK**MR**EI** **AEAYLGVTIK** **NAVVTVPAYF** **NDSQRQATKD**
151 **AGVIAGLNVM** **RIINEPTAAA** **IAYGLDKK**AT RVGEKNVLIF DLGGGTFDVS
201 LLTIEEGIFE VK**ATAGDTHL** **GGEDFDNRMV** **NHFVQEFK**RK SKKDITGNPR
251 ALRRLRTSCE RAKR**TLSSTA** **QTTIEIDSLY** **EGIDFYSTIT** **RARFEELNMD**
301 **LFR**KCMEPVE KCLRDAKMDK **STVHDVVLVG** **GSTR**IPK**VQQ** **LLQDFFNGKE**
351 **LCK**SINPVEA VVYGAAVQGA ILSGEGNEKV QDLLLLDVTP LSLGLETAGG
401 VMTTLIPRNT TIPTKK**EQVF** **STYSDNQPGV** **LIQVYEGER**A RTKDNNLLGK
451 FELSGIPPAP R**GVPQITVCF** **DIDANGILNV** **SAEDK**TTGQK NK**VTITNDKG**
501 **R**LSKDEIEK**M** **VQEAEKYK**SE DEEHKKKVEA K**NALENYAYN** **MR**NTIQDEKI
551 GEKLPAADKK KIEDSIEQAI QWLEGNQLAE ADEFEDK**MKE** **LESICNPIIA**
601 **K**MYQGAGGEA GGPGASGMDD DAPPASGGAG PKIEEVD

Band No.: B20

NCBI accession No.: gi|379068234

Species: *Rhododendron formosanum*

Protein name： nucleotide-binding site leucine-rich repeat protein

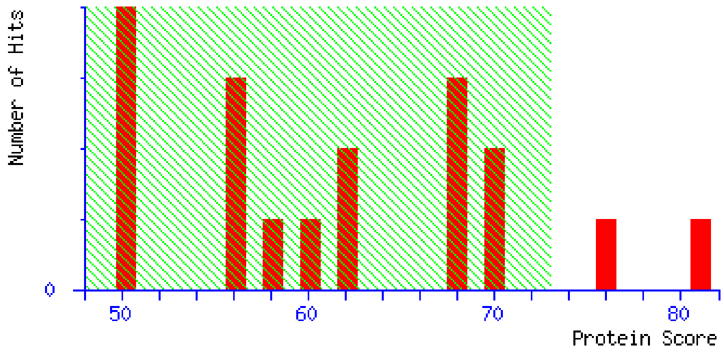
Mascot score: 81 Sequence coverage %: 56

Matched peptides No.:12 Total peptides No.: 60

Calculated Mr: 28360 Calculated *p*I: 7.01

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 73 are significant (p<0.05).



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

1 QVAKNTKEEK **LFDDVVMATV** **SQNLDARKIQ** **GEIADLLGFK** **FEQESDSGRA**
51 **DVLR**GHLKQK ARVLVILDDV WKR**FELNDIG** **IPFGEDHK**GC K**ILVTSRNEE**
101 **VCNDMGAQK**N FPVQILHKEE AWNLFKEMAG IPEDETNFRS TK**MAVANECG**
151 **GLPIALVTVA** **RALK**GKGK**SS** **WGSALEALRK** SIGKNVREVV DK**VFKSLELS**
201 **FNFLK**SKEAQ RCFLLCSLYS EDYDIPIEDL VR**YGYGQKLF** **GGIKSVGEAR**
251 A

Band No.: B21

NCBI accession No.: **gi|**14423688 Species: *Hevea brasiliensis*

Protein name：Enolase 1; 2-phosphoglycerate dehydratase 1

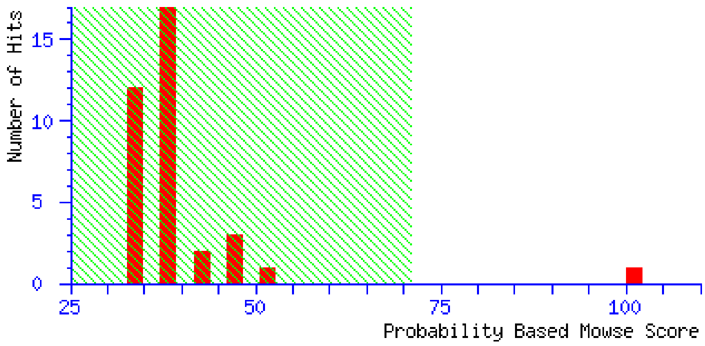
Mascot score: 101 Sequence coverage %: 35

Matched peptides No.: 10 Total peptides No.: 21

Calculated Mr: 48029 Calculated *p*I: 5.57

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold red

1 MAITIVSVRA R**QIFDSR**GNP TVEADVKLSD GYLAR**AAVPS** **GASTGIYEAL**

51 **ELRDGGSDYL** **GK**GVSKAVEN VNIIIGPALV GKDPTDQVGI DNFMVQQLDG

101 TVNEWGWCKQ KLGANAILAV SLAVCKAGAH VK**GIPLYEHI** **ANLAGNK**NLV

151 LPVPAFNVIN GGSHAGNKLA MQEFMILPVG ASSFKEAMKM GAEVYHHLKS

201 VIKKK**YGQDA** **TNVGDEGGFA** **PNIQENKEGL** **ELLK**TAIAKA GYTGKVVIGM

251 DVAASEFYGS DQTYDLNFKE ENNNGSQKIS GEALKDLYK**S** **FVAEYPIVSI**

301 **EDPFDQDDWA** **HYAKLTSEIG** **EKVQIVGDDL** **LVTNPK**RVEK AIKEKACNAL

351 LLKVNQIGSV TESIEAVKMS KR**AGWGVMAS** **HR**SGETEDTF IADLSVGLAT

401 GQIKTGAPCR SERLAK**YNQL** **LRIEEELGSE** **AVYAGANFR**K PVEPY

Band No.: B22

NCBI accession No.: **gi|3288200** Species: ***Hevea brasiliensis***

Protein name：latex allergen

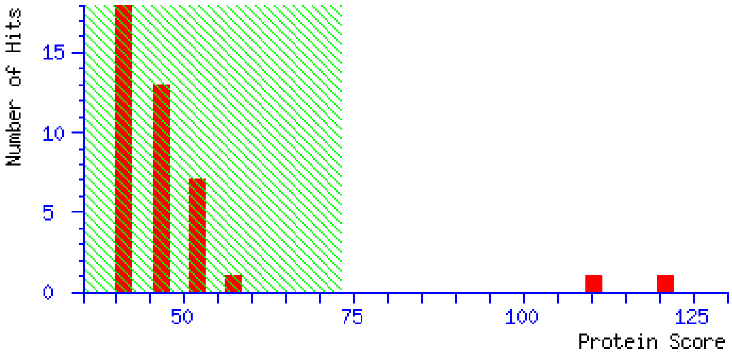
Mascot score: 121 Sequence coverage %: 47

Matched peptides No.: 16 Total peptides No.: 62

Calculated Mr: 43020 Calculated *p*I: 5.00

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold red

1 MATGSTTLTQ GK**KITVLSID** **GGGIRGIIPG** **IILASLESKL** **QDLDGPDAR**I
51 ADYFDIIAGT STGGLITTML TAPNEDKKPI YQAKDIKDFY LENCPK**IFPK**
101 **ESRDTYDPIH** **SIGPIYDGEY** **LR**ELCNNLLK DLTVK**DTLTD** **VIIPAFDIKL**
151 **LLPVIFSSDD** **AK**CNALKNAR LADVCISTSA APVLLPAHSF TTEDDKNIHT
201 FELIDGGVAA ANPTLLALTH IR**NEIIRQNP** **RFIGANLTES** **K**SRLVLSLGT
251 GKSEYKEKYN ADMTSKWRLY NWALYNGNSP AVDIFSNASS DMVDFHLSAL
301 FK**SLDCEDYY** **LRIQDDTLTG** **EESSGHIATE** **ENLQRLVEIG** **TELLEKQESR**
351 **INLDTGRLES** **IPGAPTNEAA** **IAK**FAK**LLSE** **ER**KLRQLK

Band No.: B23

NCBI accession No.: gi|113217 Species: *Daucus carota*

PFF score: [81] Protein name：Actin-1

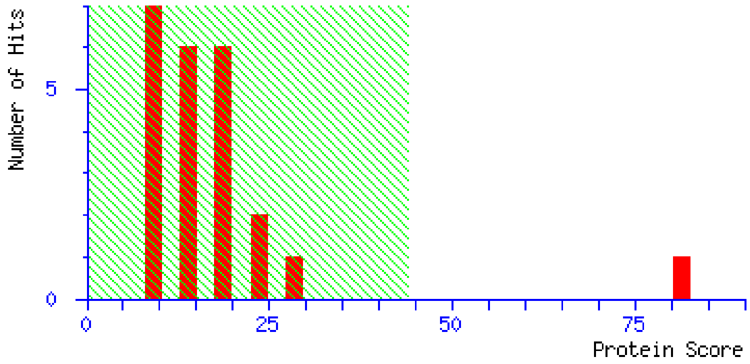
Matched peptides No.: [2] Sequence coverage %: [7]

Matched sequences: R.AVFPSIVGRPR.H；K.NYELPDGQVITIGAER.F

Calculated Mr: 42246 Calculated *p*I: 5.64

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MADGEDIQPL VCDNGTGMVK AGFAGDDAPR **AVFPSIVGRP** **R**HTGVMVGMG
51 QKDAYVGDEA QSKRGIITLK YPIEHGIVSN WDDMRIWHHT FYNELRASPE
101 EHPVLLTEAP LNPKANREKM TQIMIETFNV PAMYVAIQAV LSLYASGRTT
151 GIVLDSGDGV SHTVPIYEGY ALPHAILRLD LAGRDLTDGL MKILTEKSIC
201 HYTTAEREIV RDMKEKLAYV ALDYEQELET AKRRSAVEK**N** **YELPDGQVIT**
251 **IGAER**FRCPQ VLFQPSMIGM ESAGIHETTY NSIMKCDVDI RKDLYGNIVL
301 SGGSTMFPGI ADRMSKEITA LAPSSMKIKV VAPPERKYSD LWIGGSILAS
351 LSTFQQMWIS KGEYDESGPS IVHRKCLLAG

Band No.: B24

NCBI accession No.: gi|147835357 Species: *Vitis vinifera*

Protein name： hypothetical protein

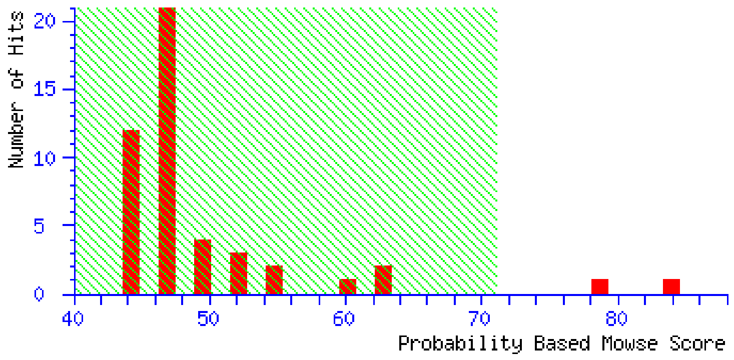
Mascot score: 84 Sequence coverage %: 34

Matched peptides No.: 25 Total peptides No.: 106

Calculated Mr: 97236 Calculated *p*I: 6.08

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 73 are significant (p<0.05).



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

1 MVDAVVTVFL EKLLNALEEE GR**VLFDFREQ** **FER**LRDELR**L** **MQSFLK**DAER
51 LKRK**NETLRT** **VMIGLR**ELIY EAEDILADCK VQSEGSQDIS GWYAVCFYPT
101 NLPFKYQTGK RLREINEKIT RIKQNIPSFL GVPILSQAEI ADSRNLPVDR
151 WSSSVFDHSQ VVGIEGDTRK VK**NWLLEAKD** **GILAIGVVGM** **GGVGKTTLAQ**
201 **VVFNDREMEA** **RFER**RMWVSV TGTPNEKRIL RSMLR**NLGDM** **NVGDDCGELL**
251 **RK**INQYLLGK R**FLLVMDDVG** **ENTNTWWRK**I SDGLPKGNGS SIIITTRTK**E**
301 **VATMMGVEEE** **RTHRPK**VLSK DDSWLLFRNV AFAANGGICT SSELENIGRE
351 IVXKCGGLPL AIK**AAGGMML** **YQQPYYHDWK** **RIADHFR**DEL AEEDGSVMAS
401 LELSYEELPS HLKSCFLCLS LYPEDCEITK EQLIHWWIAE GFVPLRRGRL
451 STEAGEDCFS GLTNR**CLIEV** **VEKSYTGAIQ** **TCK**IHDMVRD LVIKK**AEDDA**
501 **FSGPTTASCR** **HLGIEGDIDR** K**YDMPNQKLR** **ALLSTIKTGE** **VNKVASSNAK**
551 KFCDCRYLRV LDXSKTIFDK SLTGLLDHIG FLQHLTYLSL SNTHPLTEVP
601 PALEXLRNLQ VLDLSYCQNL KMLPSYVTTF EK**LTVLDVSH** **CGSLRYLPKG**
651 **LGSLSNLQVL** **LGFKPSK**SNQ LEGCR**IAELR** **SLTK**LRRLGL QLTQGDEIGD
701 NDDNVLVGLR GLQFLVISCF DSHGDDLIPK **LDKLSPPQQL** **HELSLR**FYPG
751 KMNPGWLNPF SLPILR**YLSI** **SSGNLTNMSQ** **R**FWGDGDNTW KIEGLMLESL
801 SDLGMEWSMV QQVMPRLRIV NVSWCPDLDS FPIEDVGFRG GVWKKGERPS

Band No.: B25

NCBI accession No.: **gi**|170525118 Species: *Physalis mendocina*

Protein name：geranylgeranyl reductase

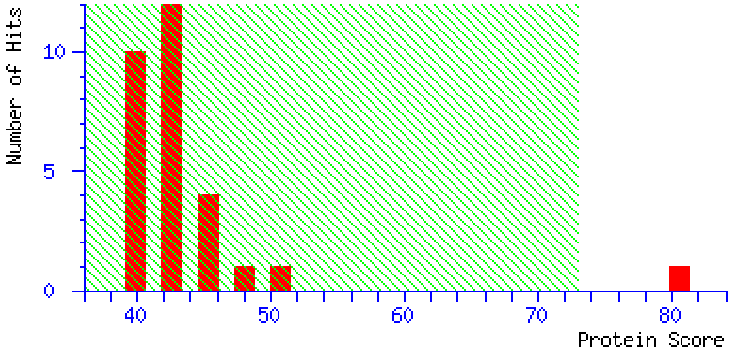
Mascot score: 81 Sequence coverage %: 76

Matched peptides No.: 7 Total peptides No.: 54

Calculated Mr: 5.67 Calculated *p*I: 11741

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold red:

1 **LKPHEYIGMV R**REVLDAYLR **DRAAEAGASV LNGLFLKMDM PKAPNAPYVL**
51 **HYSAYDSK**TN GAGEK**RTPEV DAVIGADGAN S**RVAK**SINAG DYEYAIAFQE**
101 **R**IRISDD

Band No.: B26

NCBI accession No.: gi|145346735

Species: *Ostreococcus lucimarinus CCE9901*

Protein name：predicted protein

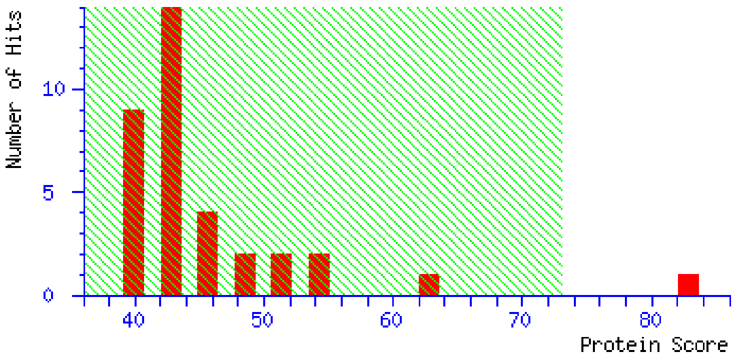
Mascot score: 83 Sequence coverage %: 22

Matched peptides No.: 9 Total peptides No.: 25

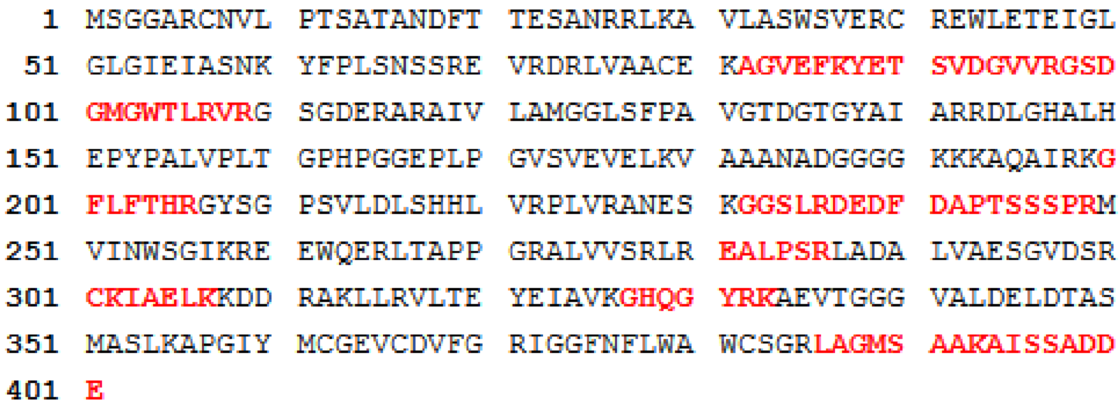
Calculated Mr: 43211 Calculated *p*I: 8.11

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold red:



1 MSGGARCNVL PTSATANDFT TESANRRLKA VLASWSVERC REWLETEIGL
51 GLGIEIASNK YFPLSNSSRE VRDRLVAACE K**AGVEFKYET** **SVDGVVRGSD**
101 **GMGWTLRVR**G SGDERARAIV LAMGGLSFPA VGTDGTGYAI ARRDLGHALH
151 EPYPALVPLT GPHPGGEPLP GVSVEVELKV AAANADGGGG KKKAQAIRK**G**
201 **FLFTHR**GYSG PSVLDLSHHL VRPLVRANES K**GGSLRDEDF** **DAPTSSSPR**M
251 VINWSGIKRE EWQERLTAPP GRALVVSRLR **EALPSR**LADA LVAESGVDSR
301 **CKIAELK**KDD RAKLLRVLTE YEIAVK**GHQG** **YRK**AEVTGGG VALDELDTAS
351 MASLKAPGIY MCGEVCDVFG RIGGFNFLWA WCSGR**LAGMS** **AAKAISSADD**
401 **E**

Band No.: B27

NCBI accession No.: gi| 37903393

Species: *Saccharum hybrid cultivar CP65-357*

PFF score: [101]   Protein name：14-3-3-like protein

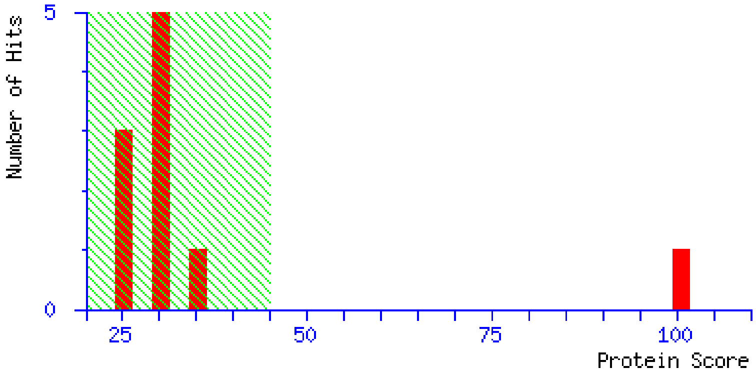
Matched peptides No.: [1]   Sequence coverage %: [4]

Matched sequences: K.TVDVEELTVEER.N

Calculated Mr: 28978   Calculated *p*I: 4.79

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MSREENVYMA KLAEQAERYE EMVEYMEKVA K**TVDVEELTV** **EER**NLLSVAY
51 KNVIGARRAS WRIVSSIEQK EESRKNEEHV NLIKEYRGKI EAELSNICDG
101 ILKLLDSHLV PSSTAAESKV FYLKMKGDYH RYLAEFKTGA ERKESAESTM
151 VAYKAAQDIA LAELAPTHPI RLGLALNFSV FYYEILNSPD KACNLAKQAF
201 DEAISELDTL GEESYKDSTL IMQLLRDNLT LWTSDLTEDG ADEGKEASKG
251 DAGEGQ

Band No.: B28

NCBI accession No.: gi|10946499 Species: *Hevea brasiliensis*

Protein name： beta-1,3-glucanase

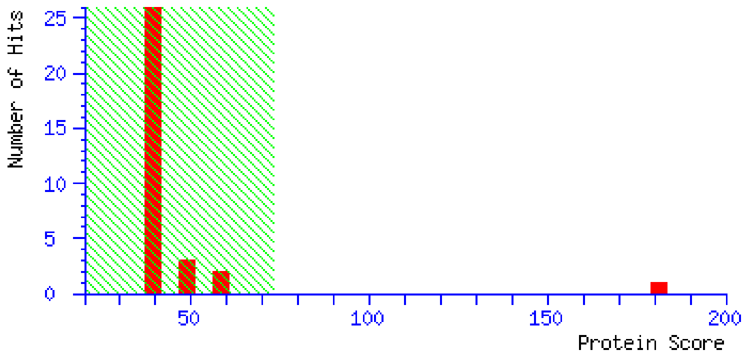
Mascot score: 181 Sequence coverage %: 66

Matched peptides No.:18 Total peptides No.:45

Calculated Mr: 35295 Calculated *p*I: 9.46

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold red:

1 QVGVCYGMQG NNLPPVSEVI ALYKKSNITR MR**IYDPNRAV** **LEALR**GSNIE
51 LILGVPNSDL QSLTNPSNAK SWVQKNVR**GF** **WSSVLFRYIA** **VGNEISPVNR**
101 **GTAWLAQFVL** **PAMRNIHDAI** **RSAGLQDQIK** **VSTAIDLTLV** **GNSYPPSAGA**
151 **FR**DDVR**SYLN** **PIIRFLSSIR** **SPLLANIYPY** **FTYAGNPRDI** **SLPYALFTSP**
201 **SVVVWDGQR**G YK**NLFDATLD** **VLYSALERAS** **GGSLEVVVSE** **SGWPSAGAFA**
251 **ATFDNGRTYL** **SNLIQHVK**RG TPKRPNR**AIE** **TYLFAMFDEN** **KK**QPEVEKQF
301 GLFFPDKWQK YNLNFG

Band No.: B29

NCBI accession No.: gi|124365253 Species: *Hevea brasiliensis*

Protein name： beta-1,3-glucanase

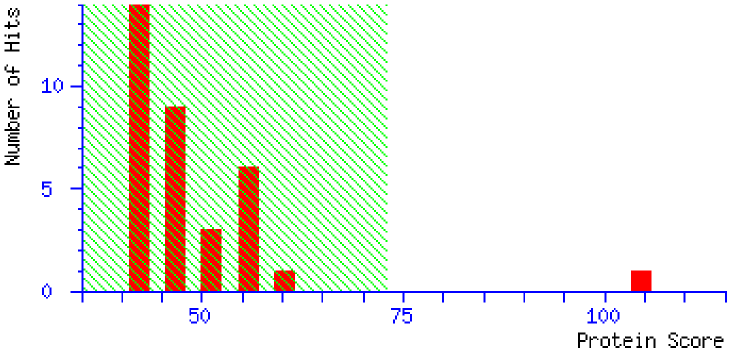
Mascot score: 105 Sequence coverage %: 38

Matched peptides No.: 10 Total peptides No.: 35

Calculated Mr: 41543 Calculated *p*I: 9.4

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold red:

1 MAISSSTSGT SSSLPSRTTV MLLLFFFTAS VGITDAQVGV CYGMQGNNLP

51 PVSEVIALYK KSNITRMR**IY** **DPNQAVLEAL** **R**GSNIELILG VPNSDLQSLT

101 NPSNAKSWVQ KNVRGFWSSV RFR**YIAVGNE** **ISPVNR**GTAW LAQFVLPAMR

151 **NIHDAIRSAG** **LQDQIKVSTA** **IDLTLVGNSY** **PPSAGAFR**DD VR**SYLNPIIR**

201 **FLSSIR**SPLL ANIYPYFTYA GNPR**DISLPY** **ALFTSPSVVV** **WDGQR**GYK**NL**

251 **FDATLDALYS** **ALERASGGSL** **EVVVSESGWP** **SAGAFAATFD** **NGR**TYLSNLI

301 QHVKRGTPKR PKRAIETYLF AMFDENKKQP EVEKHFGLFF PNKWQKYNLN

351 FSAEKNWDIS TEHNATILFL KSDM

Band No.: B30

NCBI accession No.: gi|14423933 Species: *Hevea brasiliensis*

Protein name：Small rubber particle protein; Short=SRPP; AltName: Full=22 kDa rubber particle protein; Short=22 kDa RPP; AltName: Full=27 kDa natural rubber allergen; AltName: Full=Latex allergen Hev b 3; AltName: Allergen=Hev b 3

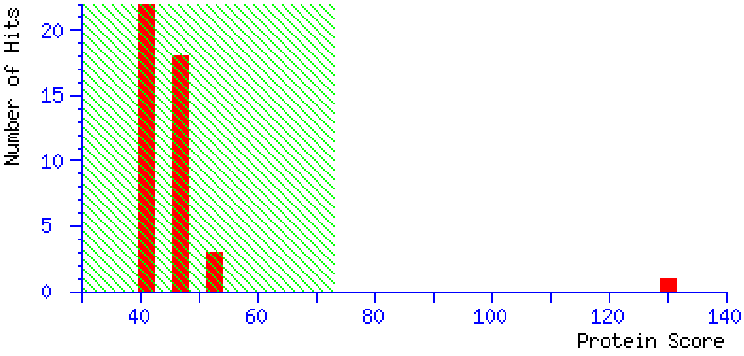
Mascot score: 130 Sequence coverage %: 51

Matched peptides No.:10 Total peptides No.: 26

Calculated Mr: 22331 Calculated *p*I: 4.80

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 73 are significant ($p<0.05$).



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

1 MAEEVEEERL K**YLDFVRAAG** **VYAVDSFSTL** **YLYAK**DISGP LKPGVDTIEN
51 VVK**TVVTPVY** **YIPLEAVK**FV DKTVDVSVTS LDGVVPPVIK **QVSAQTYSVA**
101 **QDAPRIVLDV** **ASSVFNTGVQ** **EGAKALYANL** **EPKAEQYAVI** **TWR**ALNKLPL
151 VPQVANVVVP TAVYFSEK**YN** **DVVRGTTEQG** **YR**VSSYLPLL PTEKITKVFG
201 DEAS

Band No.: B31

NCBI accession No.: gi|313586569 Species: *Hevea brasiliensis*

Protein name： hypothetical protein 19

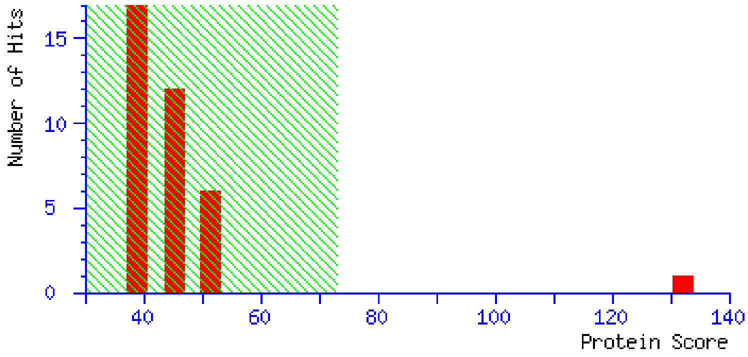
Mascot score: 132 Sequence coverage %: 48

Matched peptides No.: 12 Total peptides No.: 36

Calculated Mr: 20724 Calculated *p*I: 7.77

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold red:

1 MEELGSSHEK TESESSHCRK **PHLPSGSYLS** **KK**PSYKVYCK **ADPNFFLTIR**
51 **DGKVVLAPPD** **PSDEFQHWYK** **DEKFSTMVK**D EEGFPSFALV NKASGKALKH
101 SFGPTHPVLL TPYDPDDLEA SILWTESK**DL** **GDGYR**IVR**ML** **NNIRLNVEAL**
151 **RGDK**KSGGVS NGTK**VVLAYW** **NKGDHQKWR**I APL

Band No.: B32

NCBI accession No.: gi|327492451

Species: *Mesembryanthemum crystallinum*

Protein name： N-terminal end of polyubiquitin

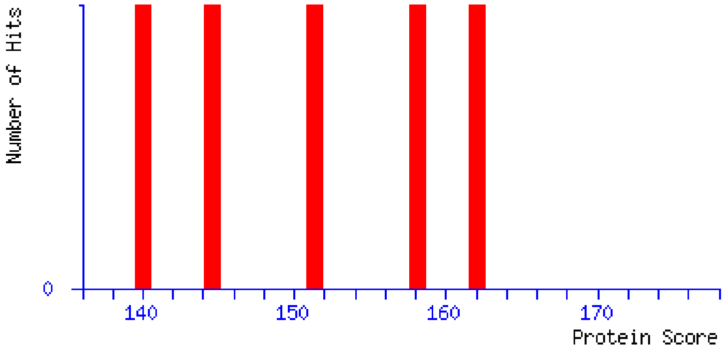
Mascot score: 162 Sequence coverage %: 96

Matched peptides No.: 12 Total peptides No.: 38

Calculated Mr: 8463 Calculated *p*I: 6.56

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold red:

1 **MQIFVKTLTG KTITLEVESS DTIDNVKAKI QDKEGIPPDQ QRLIFAGKQL**
51 **EDGRTLADYN IQKESTLHLV LR**LRG

Band No.: B33

NCBI accession No.: **gi**|27449246 Species: *Hevea brasiliensis*

Protein name：Cu/Zn superoxide dismutase

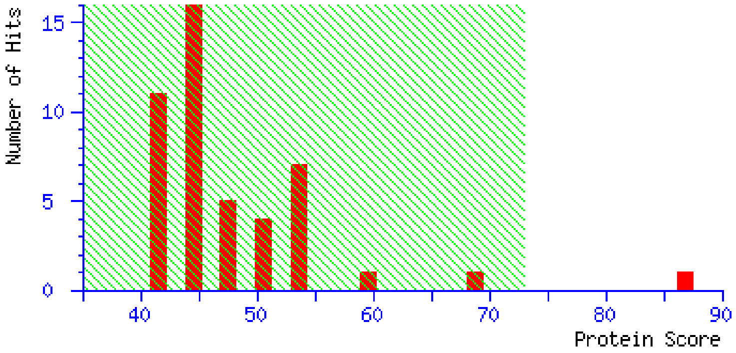
Mascot score: 87 Sequence coverage %: 38

Matched peptides No.: 6 Total peptides No.: 22

Calculated Mr: 15726 Calculated *p*I: 5.73

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold red:

1 MLKAVAVITS SEGISGKIFF TQEGDGPTTV TGSVSGLKPG LHGFHVHTFG
51 DTTNGCLSTG LHFNPASK**DH** **GGPEDENRHA** **GDLGNVNVGD** **DGTANFTIVD**
101 **KHIPLSGPHS** **IAGRSVVFHE** **GRDDLGK**GGH ELSKITGNAG DRIACGIIGL
151 QE

Band No.: B34

NCBI accession No.: gi| 29170601 Species: *Hevea brasiliensis*

Protein name： small rubber particle protein

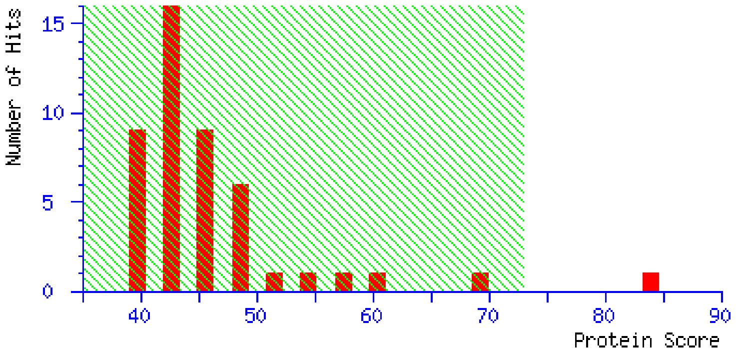
Mascot score: 84 Sequence coverage %: 61

Matched peptides No.: 7 Total peptides No.: 31

Calculated Mr: 12769 Calculated *p*I: 4.61

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 73 are significant ($p<0.05$).



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

1 MAEGK**ENENF** **QQEANEQEEK** **LK**YLEFVQAT TDNAVTALSN IYLYAK**DNSG**

51 **PLKPGVETIE** **GVAKTVVIPA** **SKIPTEAIKF** **ADRAVDASFT** **TLQNIVPSVL**

101 **K**QLPTQACDT SVKESAE

Spot No.: B35

NCBI accession No.: gi|242080683 Species: *Sorghum bicolor*

PFF score: [118]

Protein name：hypothetical protein SORBIDRAFT_07g004260

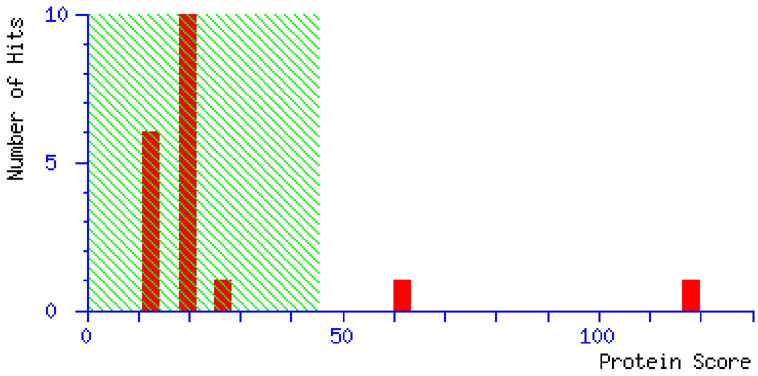
Matched peptides No.: [2] Sequence coverage %: [15]

Matched sequences: M.GLQEEFEEYAEK.A; M.GLQEEFEEYAEKAK.T

Calculated Mr: 10341 Calculated *p*I: 5.01

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 **MGLQEEFEEY** **AEKAK**TLPES TSNENKLILY GLYKQATVGN VNTDRPGIFY
51 QKDRAKWDAW KAVEGKPKEE AMNDYITKVK QLQEEAAAAT S

Supplementary Figure S2

Figure S2:

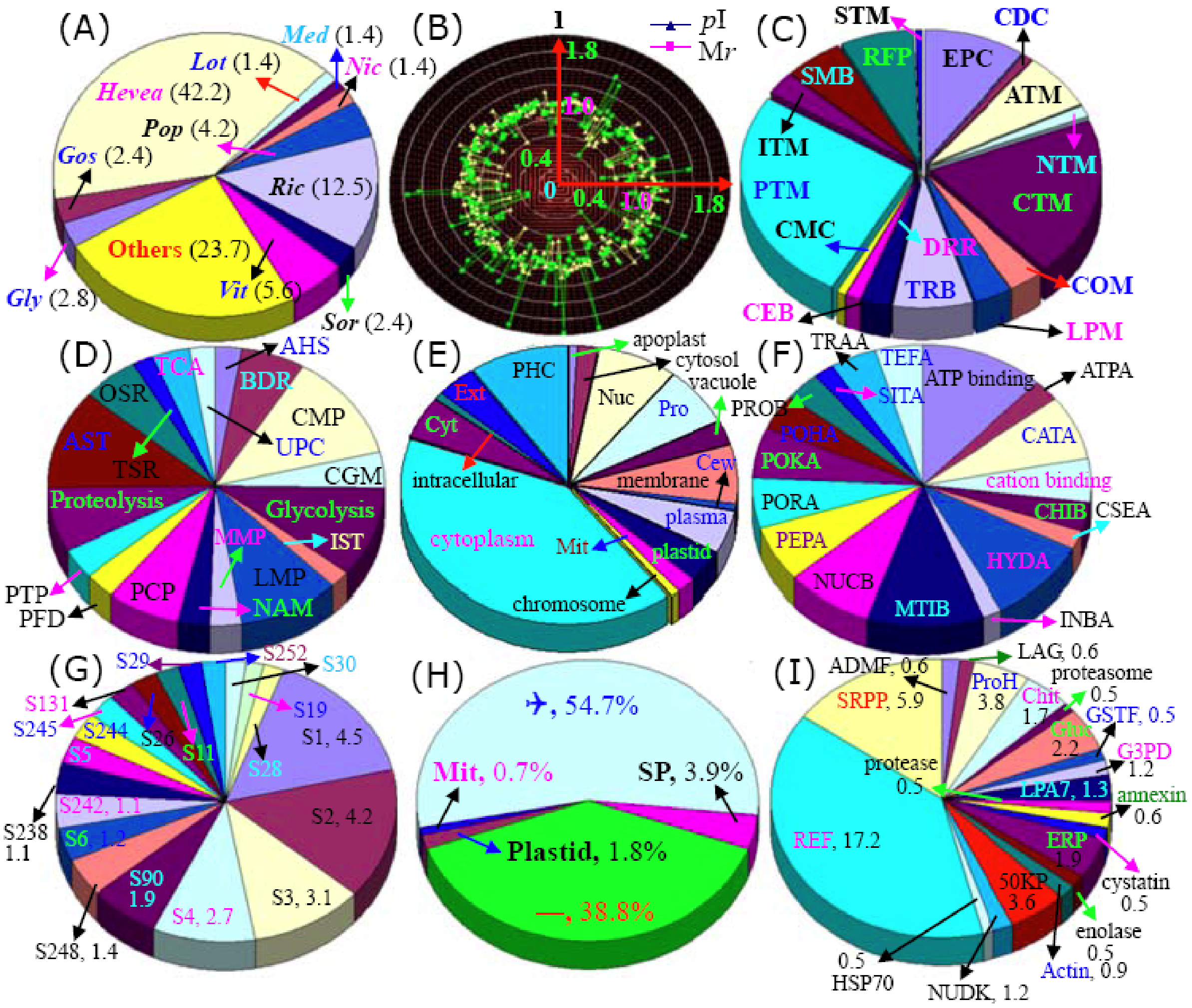


Figure S2: Classification and functional analysis of the identified main latex proteins. A total of 287 proteins including 184 unique proteins were positively identified from 252 spots and 35 bands by MS. The distributions of the identified proteins in different plant species were demonstrated (A). To evaluate the quality of identified proteins, the theoretical and experimental ratios of molecular mass (M*r*) and isoelectric point (*p*I) were calculated and presented in radial chart as radial and annular radar axis labels respectively (B). Then, each protein was functionally classified by COG and the proportion of each functional category was shown (C). The GO classification results including biological process (D), cellular component (E), and molecular function (F) were presented. The cellular locations of all the identified proteins were also determined by TargetP (H). To detect the protein expression abundance in rubber latex, the most abundant 20 protein spots (G) as well as the most abundant 20 kinds of proteins on the reference 2-DE gel were also determined. The spot number (S), protein name and the volume value (Vol%) in the reference 2-DE gel were presented.

The abbreviations used in this study were listed as the following.

The abbreviations for proteins:

ABAS, abscisic acid stress ripening-related protein; ACAT, Acetyl-CoA C-acetyltransferase; ACPX, ascorbate peroxidase; ADMF, actin depolymerizing factor; ADPF, actin-depolymerizing factor; APTS, asparaginyl-tRNA synthetase; ATPS, ATP synthase subunit beta; CAMT, caffeic acid 3-O-methyltransferase; CDCP, cell division cycle protein; CDPK, calcium-dependent protein kinase; Chit, chitinase; CIAD, cinnamyl alcohol dehydrogenase; CIBP, citrate-binding protein; CIPT, cis-prenyl transferase; CLBP, calcium lipid binding protein; COPC, COP9 signalosome complex subunit 1; COPT, copper transport protein; CVMP, coated vesicle membrane protein; CYAS, beta-cyanoalanine synthase; CYSP, cysteine protease; DMAPP, dimethylallyl diphosphate; ELRP, elicitor-responsive protein; ETEF, eukaryotic translation elongation factor; ETIF, eukaryotic translation initiation factor; ETHI, ethylene-inducible protein; ETHR, ethylene receptor; FADS, farnesyl diphosphate synthase; GLUD, glutaredoxin; GGCS, gamma-glutamylcysteine synthetase; GGDS, geranylgeranyl diphosphate synthase; Gluc, beta-1,3-glucanase; GLUR, glutathione reductase; GLUS, glutamine synthetase; GSGT, galactinol-sucrose galactosyltransferase; GSTF, glutathione-S-transferase; G3PD, glyceraldehyde 3-phosphate dehydrogenase; G6PD, glucose-6-phosphate dehydrogenase; G6PE, glucose-6-phosphate 1-epimerase; G6PI, glucose-6-phosphate isomerase; HMGR, hydroxymethylglutaryl coenzyme A reductase; HMGS, hHydroxymethylglutaryl coenzyme A synthase; HSP 70, heat shock protein 70; HYDL, hydroxynitrile lyase; LACG, latex cyanogenic beta glucosidase; LACT, latex cystatin; LAP, latex abundant protein; LAG, latex allergen; LPA7, latex protein allergen Hev b 7; MEVD, mevalonate disphosphate decarboxylase; MEVK, mevalonate kinase; MIPS, myo-inositol-1-phosphate synthase; NUDK, nucleoside diphosphate kinase; PDBP, pyridoxal biosynthesis protein; PHOK, phosphomevalonate kinase; PHOT, phosphoglyceride transfer family protei; PMPP, pyrophosphate-energized membrane proton pump; PPCI, peptidyl-prolyl cis-trans isomerase; ProH, prohevein; PROI, protease inhibitor protein; PseuH, pseudo-hevein; RAPK, receptor for activated protein kinase; REF, rubber elongation factor; RRMP, RNA recognition motif-containing protein; SOD, superoxide dismutase; SRPP, small rubber particle protein; SUCT, sucrose transporter; TMAP, translation machinery-associated protein; UBCE, ubiquitin-conjugating enzyme; UBPL, ubiquitin-protein ligase; VHAE, V-type proton ATPase subunit E; VHAF, V-type proton ATPase subunit; V-PPase, vacuolar-type inorganic pyrophosphatase; 50KP, 50 kDa protein.

The abbreviations for COG classification of each protein:

EPC, Energy production and conversion; CDC, Cell division and chromosome partitioning; ATM, Amino acid transport and metabolism; NTM, Nucleotide transport and metabolism; CTM, Carbohydrate transport and metabolism; COM, Coenzyme transport and metabolism; LPM, Lipid metabolism; TRB, Translation, ribosomal structure and biogenesis; DRR, DNA replication, recombination and repair; CMC, Cell envelope biogenesis, outer membrane/ G Carbohydrate transport and metabolism; PTM, Posttranslational modification, protein turnover, chaperones.

The abbreviations for GO-Biological process:

AHS, ATP hydrolysis and synthesis; BDR, biotic defense response; CMP, carbohydrate metabolic process; CGM, cellulose biosynthetic and glucose metabolic process; IST, intracellular signal transduction; LMP, lipid metabolic process; MMP, malate metabolic process; NAM, nuclear acid metabolic process; PCP, protein catabolic process; PFD, protein folding; PTP, protein transport; AST, abiotic stress response; OSR, oxidative stress response; TRR, translational regulation; TCA, tricarboxylic acid cycle; UPC, ubiquitin-dependent protein catabolic process.

The abbreviations for GO-Cellular component:

Nuc, nucleus; Pro, proteasome;Cew, cell wall;Mit, mitochondria; Cyt, cytoskeleton; Ext, extracellular region; PHC, phosphopyruvate hydratase complex.

The abbreviations for GO-Molecular function:

ATPA, ATPase activity; CATA, catalytic activity; CHIB, chitin binding; CSEA, cysteine synthase and endopeptidase activity; HYDA, hydrolase activity; INBA, inhibitor activity; MTIB, metal ion binding; NUCB, nucleotide binding; PEPA, peptidase activity; PORA, peroxidase and reductase activity; POKA, phosphate kinase activity; POHY, phosphopyruvate hydratase activity; PROB, protein binding; SITA, signal transducer activity;TRAA, transferase activity; TEFA, translation elongation factor activity.

The abbreviations for the cellular location in TargetP:

Mit, Mitochondrion, i.e. the sequence contains mTP, a mitochondrial targeting peptide; Plastid, Chloroplast or other plastids,, i.e. the sequence contains cTP, a chloroplast transit peptide; _, Any other location; Q , Don't know location, indicates that cutoff restrictions were set and the winning network output score was below the requested cutoff for that category; SP, Secretory pathway, i.e. the sequence contains SP, a signal peptide.

Supplementary Figure S3

Supplemental spectra and MALDI TOF/TOF MS /MS identification information for the ethylene responsive latex proteins

Annotated spectra 143 differential latex proteins on DIGE gels identified by PMF and the combination results of PMF and PFF.

CID: collision induced desorption;

MALDI TOF:

matrix assisted laser desorption/ionization time of flight;

MS: mass spectrometry;

PMF: peptide mass fingerprinting;

PFF: peptide fragment fingerprinting.

Spot No.: **D1**

NCBI accession No.: **gi|255545912**   Species: *Ricinus communis*

PFF score: [278]

Protein name: 14-3-3 protein, putative

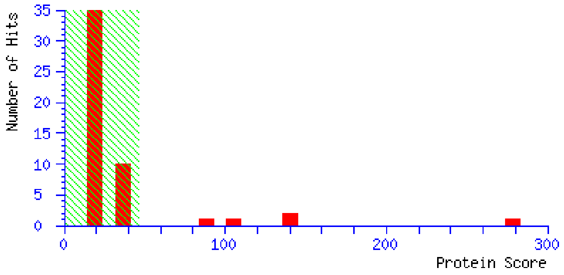
Matched peptides No.: [3]   Sequence coverage %: [17]

Matched sequences: R.IVSSIEQKEEGR.K;
K.LVLGSTPSGELTVEER.N;
K.AAQDIALADLAPTHPIR.L

Calculated Mr: **28647**   Calculated *p*I: **4.71**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAAAATVPDN LTRDQYVYLA KLAEQAERYE EMVQFMQK**LV** **LGSTPSGELT**
51 **VEER**NLLSVA YKNVIGSLRA AWR**IVSSIEQ** **KEEGR**KNEEH VVLVKEYRSK
101 VENELSDVCA SILSLLDSNL IPSASASESK VFYLKMKGDY HRYLAEFKAG
151 DERKTAAEDT MLAYK**AAQDI** **ALADLAPTHP** **IR**LGLALNFS VFYYEILNQS
201 DKACSMAKQA FEEAIAELDT LGEESYKDST LIMQLLRDNL TLWTSDVQDQ
251 LDEP

Spot No.: **D2**

NCBI accession No.: **gi| 37719658** Species: *Hevea brasiliensis*

Protein name: **50 kDa protein**

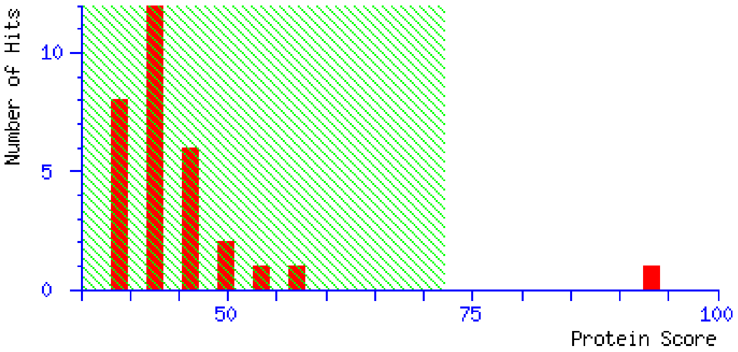
Mascot score: **93** Sequence coverage %: **31**

Matched peptides No.: **9** Total peptides No.: **33**

Calculated Mr: **41480** Calculated *p*I: **4.60**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MASLAYSLFI LSLFTFTLLN PVCSELDEYL FSFGDGLYDA GNAKFIYPDK
51 **YLPSYHHPYG TTFFDYPTGR** FSDGR**TVVDF VAENVSLPRI PPFK**NKEANF
101 TYGANFASEG ATASDSNPLI DFRSQIRDFG ELKLEWAVQL VNVTELARRL
151 KK**AVYLISFG ADDYLNYEIP SEASREQLES IVDVVLGNIS DRIKELYDFG**
201 **ARKFVVENVA PLGLIPFIK**Q TSDNSTLFYE LASLHAMKLP QILEKIQDGY
251 LFPEFNYTVF NYFGIIK**EII DAPGEHGFK**Y GDIACCGNST YRGQACGFLD
301 YEFCVCGNKT EYLFFDGTHN TDAANNLLAE LMWDKESGFI SPYGVKDFFP
351 SPTTIQTLLT EATALG

Spot No.: **D3**

NCBI accession No.: **gi| 37719658** Species: *Hevea brasiliensis*

Protein name： **50 kDa protein**

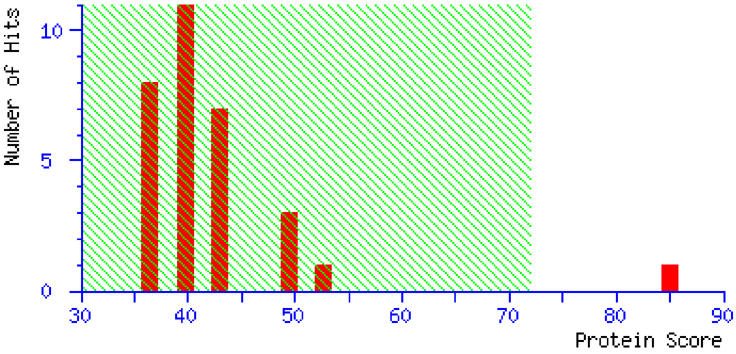
Mascot score: **93** Sequence coverage %: **36**

Matched peptides No.: **11** Total peptides No.: **44**

Calculated Mr: **41480** Calculated *p*I: **4.60**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MASLAYSLFI LSLFTFTLLN PVCSELDEYL FSFGDGLYDA GNAKFIYPDK
51 **YLPSYHHPYG TTFFDYPTGR FSDGRTVVDF VAENVSLPRI PPFK**NKEANF
101 TYGANFASEG ATASDSNPLI DFRSQIRDFG ELKLEWAVQL VNVTELARRL
151 KK**AVYLISFG ADDYLNYEIP SEASREQLES IVDVVLGNIS DRIKELYDFG**
201 **ARKFVVENVA PLGLIPFIK**Q TSDNSTLFYE LASLHAMKLP QILEKIQDGY
251 LFPEFNYTVF NYFGIIK**EII DAPGEHGFK**Y GDIACCGNST YRGQACGFLD
301 YEFCVCGNKT EYLFFDGTHN TDAANNLLAE LMWDK**ESGFI SPYGVK**DFFP
351 SPTTIQTLLT EATALG

Spot No.: **D4**

NCBI accession No.: **gi|147805616**   Species: *Vitis vinifera*

PFF score: [324]

Protein name: hypothetical protein VITISV_028800

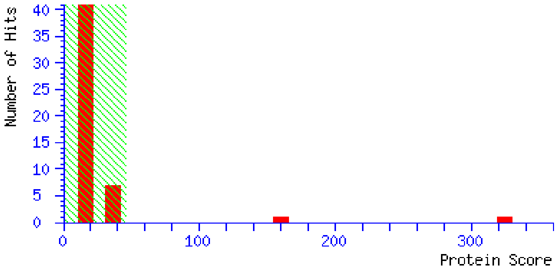
Matched peptides No.: [4]   Sequence coverage %: [14]

Matched sequences: R.GPYPADQVVR.D;
K.GCFFTTSGGLR.S;
R.DRGPYPADQVVR.D;
K.TANEVIIVIEAYR.T

Calculated Mr: **27385**   Calculated *p*I: **5.64**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MLAVFHKSIA EAPEGLRTPD SASLPALKDG FLPQFFASLH PSAVTVNLGS
51 SGAISYSVDK QNPLLPRLFA VVDDIFCLFQ GHIENVALLK QQYGLNK**TAN**
101 **EVIIVIEAYR** TLR**DRGPYPA** **DQVVR**DLHGK FAFVLYDSSN RTAFLAADAD
151 ESVPFFWGVD SEGHLVLSDD EETVKKGCGK SFAPFPK**GCF** **FTTSGGLR**SF
201 EHPLNELRAE PRVDSSGQVC GANFKVDVEA KKETGMPRVG SAANWSTHY

Spot No.: **D5**

NCBI accession No.: **gi|224137430**

Species: *Populus trichocarpa*

Protein name: predicted protein PFF score: [122]

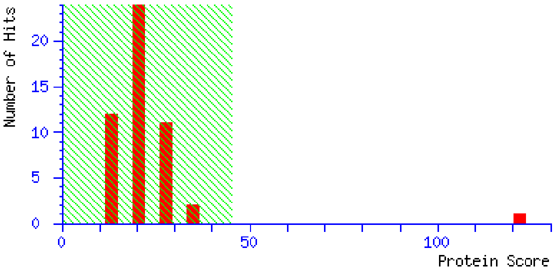
Matched peptides No.: [2] Sequence coverage %: [6]

Matched sequences: R.VYKDGTIER.L;
R.LLVIVAEKDILR.D

Calculated Mr: **35782** Calculated *p*I: **5.30**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MDQSKEIARD VFPFLR**VYKD** **GTIER**LAGTE VSHAGLDPET GVLSKDTVIV
51 PETGVSARLY RPNSAKGNRK LPLVIYYHGG GFFISSAADP KYHNSLNRLV
101 AEANIVLVSV DYRIAPENPL PAAYDDSWAA LQWVAAHAKE DGGSEAWLKD
151 YVDFGRVFLA GDSCGANVAH HFALKLKDCE LGHQINIQAI AMIFPYFWGK
201 DPIGVEVTDQ ARKSMVDNWW LLVCPSEKGC DDPLINPFAD GSPSLESLAC
251 KR**LLVIVAEK** **DILR**DRGRLY YEKMVNSEWQ GTAEFMEVQG EDHVFHIHNP
301 DCENAKSMFK GLASFINQA

Spot No.: D6

NCBI accession No.: **gi|14423688** Species: *Hevea brasiliensis*

PFF score: [229] Protein name: Enolase 1

Matched peptides No.: [3] Sequence coverage %: [10]

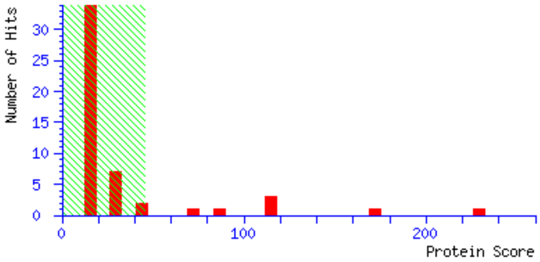
Matched sequences: R.AGWGVMASHR.S + Oxidation (M);

R.AAVPSGASTGIYEALELR.D;
R.IEEELGSEAVYAGANFR.K

Calculated Mr: **48029** Calculated *p*I: **5.57**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red

```
  1 MAITIVSVRA RQIFDSRGNP TVEADVKLSD GYLARAAVPS GASTGIYEAL
 51 ELRDGGSDYL GKGVSKAVEN VNIIIGPALV GKDPTDQVGI DNFMVQQLDG
101 TVNEWGWCKQ KLGANAILAV SLAVCKAGAH VKGIPLYEHI ANLAGNKNLV
151 LPVPAFNVIN GGSHAGNKLA MQEFMILPVG ASSFKEAMKM GAEVYHHLKS
201 VIKKKYGQDA TNVGDEGGFA PNIQENKEGL ELLKTAIAKA GYTGKVVIGM
251 DVAASEFYGS DQTYDLNFKE ENNNGSQKIS GEALKDLYKS FVAEYPIVSI
301 EDPFDQDDWA HYAKLTSEIG EKVQIVGDDL LVTNPKRVEK AIKEKACNAL
351 LLKVNQIGSV TESIEAVKMS KRAGWGVMAS HRSGETEDTF IADLSVGLAT
401 GQIKTGAPCR SERLAKYNQL LRIEEELGSE AVYAGANFRK PVEPY
```

Spot No.: **D7**

NCBI accession No.: **gi|37719658** Species: *Hevea brasiliensis*

Protein name： **50 kDa protein**

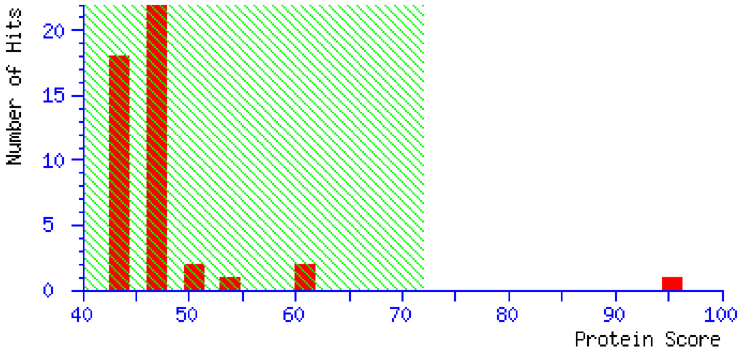
Mascot score: **95** Sequence coverage %: **42**

Matched peptides No.: **14** Total peptides No.: **66**

Calculated Mr: **41480** Calculated *p*I: **4.60**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MASLAYSLFI LSLFTFTLLN PVCSELDEYL FSFGDGLYDA GNAK**FIYPDK**
51 **YLPSYHHPYG TTFFDYPTGR FSDGRTVVDF VAENVSLPRI PPFK**NKEANF
101 TYGANFASEG ATASDSNPLI DFRSQIR**DFG ELK**LEWAVQL VNVTELARRL
151 KK**AVYLISFG ADDYLNYEIP SEASREQLES IVDVVLGNIS DRIKELYDFG**
201 **ARKFVVENVA PLGLIPFIK**Q TSDNSTLFYE LASLHAMK**LP QILEK**IQDGY
251 LFPEFNYTVF NYFGIIK**EII DAPGEHGFKY GDIACCGNST YR**GQACGFLD
301 YEFCVCGNKT EYLFFDGTHN TDAANNLLAE LMWDKESGFI SPYGVKDFFP
351 SPTTIQTLLT EATALG

Spot No.: **D8**

NCBI accession No.: **gi|255565836** Species: *Ricinus communis*

Protein name： eukaryotic translation elongation factor, putative

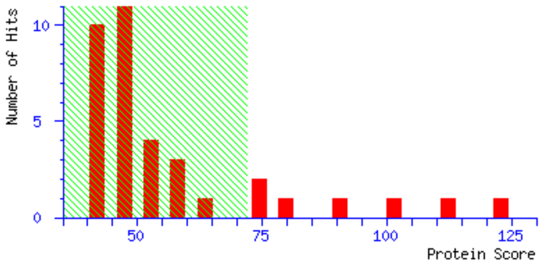
Mascot score: **123** Sequence coverage %: **30**

Matched peptides No.: **26** Total peptides No.: **56**

Calculated Mr: **94981** Calculated *p*I: **5.87**

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 MVK**FTAEELR** RIMDYKHNIR **NMSVIAHVDH** **GKSTLTDSLV** **AAAGIIAQEV**
51 **AGDVR**MTDTR QDEAERGITI KSTGISLYYE MTDEALKSFK GERQGNEYLI
101 NLIDSPGHVD FSSEVTAALR ITDGALVVVD CIEGVCVQTE TVLR**QALGER**
151 IRPVLTVNKM DRCFLELQVD GEEAYQTFSR VIENANVIMA TYEDPLLGDC
201 QVYPEKGTVA FSAGLHGWAF TLTNFAK**MYA** **SK**FGVDESKM MER**LWGENFF**
251 **DPATK**KWTSK **NTGSPTCKRG** **FVQFCYEPIK** QIINTCMNDQ KDKLWPMLQK
301 **LGVTMKSDEK** ELMGKALMKR VMQTWLPASS ALLEMMIFHL PSPAKAQR**YR**
351 **VENLYEGPLD** **DPYATAIRNC** **DPEGPLMLYV** **SK**MIPASDKG R**FFAFGR**VFA
401 GKVSTGLKVR **IMGPNYVPGE** **K**KDLYVK**SVQ** **RTVIWMGK**KQ ETVEDVPCGN
451 TVALVGLDQF ITKNATLTNE KEVDAHPIRA MK**FSVSPVVR** VAVQCKVASD
501 LPKLVEGLKR LAKSDPMVVC TIEESGEHII AGAGELHLEI CLK**DLQDDFM**
551 **GGAEIIK**SDP VVSFRETVLE KSCRVVMSKS PNKHNRLYME ARPMEEGLAE
601 AIDEGRIGPR DDPKARAK**IL** **SEEFGWDKDL** **AK**KIWCFGPE TTGPNMVVDM
651 CKGVQYLNEI K**DSVVAGFQW** **ASKEGALAEE** **NMR**GICFEVC DVVLHADAIH
701 R**GGGQVIPTA** **RRVIYASQLT** **AKPR**LLEPVY LVEIQAPEQA LGGIYSVLNQ
751 KR**GHVFEELQ** **RPGTPLYNIK** AYLPVIESFG FSGTLRAATS GQAFPQCVFD
801 HWDMMSSDPM EPGSQAANLV TEIRKRKGLK EQMTPLSEFE DKL

Spot No.: **D9**

NCBI accession No.: **gi|225428086** Species: *Vitis vinifera*

Protein name：PREDICTED: V-type proton ATPase subunit B 1

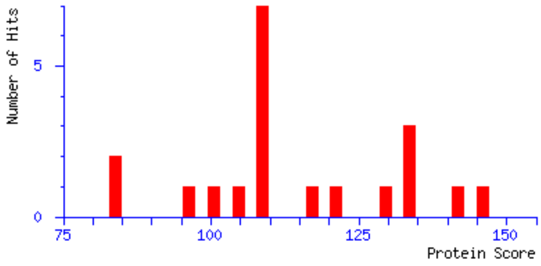
Mascot score: **146** Sequence coverage %: **52**

Matched peptides No.: 29 Total peptides No.: **52**

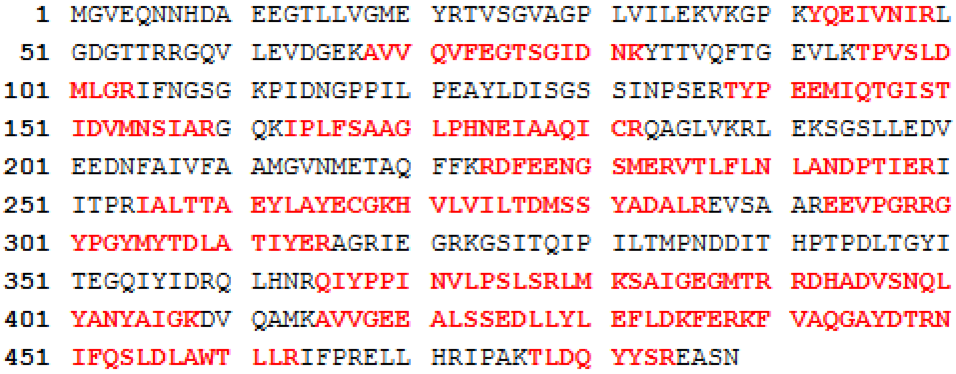
Calculated Mr: **54367** Calculated *p*I: **5.04**

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red


1 MGVEQNNHDA EEGTLLVGME YRTVSGVAGP LVILEKVKGP K**YQEIVNIR**L
51 GDGTTRRGQV LEVDGEK**AVV** **QVFEGTSGID** **NK**YTTVQFTG EVLK**TPVSLD**
101 **MLGR**IFNGSG KPIDNGPPIL PEAYLDISGS SINPSER**TYP** **EEMIQTGIST**
151 **IDVMNSIAR**G QK**IPLFSAAG** **LPHNEIAAQI** **CR**QAGLVKRL EKSGSLLEDV
201 EEDNFAIVFA AMGVNMETAQ FFK**RDFEENG** **SMERVTLFLN** **LANDPTIER**I
251 ITPR**IALTTA** **EYLAYECGKH** **VLVILTDMSS** **YADALR**EVSA AR**EEVPGRRG**
301 **YPGYMYTDLA** **TIYER**AGRIE GRKGSITQIP ILTMPNDDIT HPTPDLTGYI
351 TEGQIYIDRQ LHNR**QIYPPI** **NVLPSLSRLM** **KSAIGEGMTR** **RDHADVSNQL**
401 **YANYAIGK**DV QAMK**AVVGEE** **ALSSEDLLYL** **EFLDKFERKF** **VAQGAYDTRN**
451 **IFQSLDLAWT** **LLR**IFPRELL HRIPAK**TLDQ** **YYSR**EASN

Spot No.: **D10**

NCBI accession No.: **gi| 2832430**   Species: *Hevea brasiliensis*

PFF score: [446]

Protein name: Pro-hevein

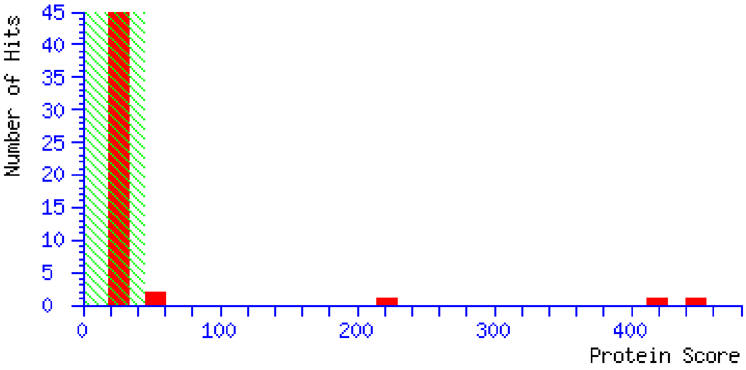
Matched peptides No.: [4]   Sequence coverage %: [32]

Matched sequences: K.YGWTAFCGPVGAHGQPSCGK.C; K.CLSVTNTGTGAK.A; R.IVDQCSNGGLDLDVNVFR.Q; R.QLDTDGKGYER.G

Calculated Mr: **20852**   Calculated *p*I: **5.65**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

```
  1 EQCGRQAGGK LCPNNLCCSQ WGWCGSTDEY CSPDHNCQSN CKDSGEGVGG
 51 GSASNVLATY HLYNSQDHGW DLNAASAYCS TWDANKPYSW RSKYGWTAFC
101 GPVGAHGQPS CGKCLSVTNT GTGAKATVRI VDQCSNGGLD LDVNVFRQLD
151 TDGKGYERGH LTVNYQFVDC GDSFNPLFSV MKSSVIN
```

Spot No.: **D11**

NCBI accession No.: **gi|123062** Species: *Hevea brasiliensis*

PFF score: [158]

Protein name: Pro-hevein

Matched peptides No.: [2] Sequence coverage %: [11]

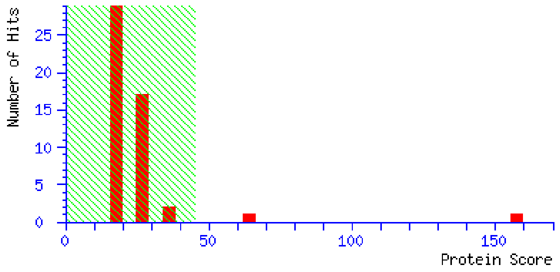
Matched sequences: K.CLSVTNTGTGAK.T;

R.QLDTDGKGYER.G

Calculated Mr: **22700** Calculated *p*I: **5.63**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MNIFIVVLLC LTGVAIAEQC GRQAGGKLCP NNLCCSQWGW CGSTDEYCSP
51 DHNCQSNCKD SGEGVGGGSA SNVLATYHLY NSQDHGWDLN AASAYCSTWD
101 ANKPYSWRSK YGWTAFCGPV GAHGQSSCGK **CLSVTNTGTG** **AK**TTVRIVDQ
151 CSNGGLDLDV NVFR**QLDTDG** **KGYER**GHITV NYQFVDCGDS FNPLFSVMKS
201 SVIN

Spot No.: **D12**

NCBI accession No.: **gi|15237159**   Species: *Arabidopsis thaliana*

PFF score: [77]

Protein name: regulatory particle triple-A ATPase 3

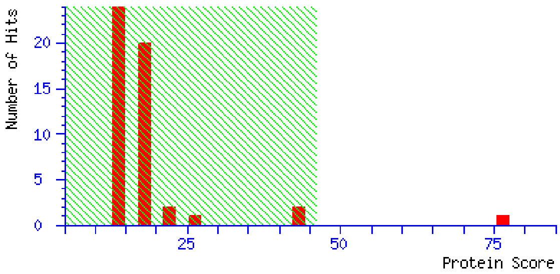
Matched peptides No.: [4]   Sequence coverage %: [13]

Matched sequences: K.AVANHTTAAFIR.V;
K.KPDTDFEFYK.-;
R.EAVELPLTHHELYK.Q;
K.ENAPAIIFIDEVDAIATAR.F

Calculated Mr: **45894**   Calculated *p*I: **5.42**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MASAAVASMV LDPKASPALM DLSTADEEDL YGRLKSLERQ LEFTDIQEEY
51 VKDEQKNLKR ELLRAQEEVK RIQSVPLVIG QFMEMVDQNN GIVGSTTGSN
101 YYVRILSTIN RELLKPSASV ALHRHSNALV DVLPPEADSS ISLLSQSEKP
151 DVSYNDIGGC DIQKQEIR**EA** **VELPLTHHEL** **YK**QIGIDPPR GVLLYGPPGT
201 GKTMLAK**AVA** **NHTTAAFIR**V VGSEFVQKYL GEGPRMVRDV FRLAK**ENAPA**
251 **IIFIDEVDAI** **ATAR**FDAQTG ADREVQRILM ELLNQMDGFD QTVNVKVIMA
301 TNRADTLDPA LLRPGRLDRK IEFPLPDRRQ KRLVFQVCTS KMNLSDEVDL
351 EDYVSRPDKI SAAEIAAICQ EAGMHAVRKN RYVILPKDFE KGYRANVK**KP**
401 **DTDFEFYK**

Spot No.: **D13**

NCBI accession No.: **gi|123062**   Species: *Hevea brasiliensis*

PFF score: [129]   Protein name: Pro-hevein

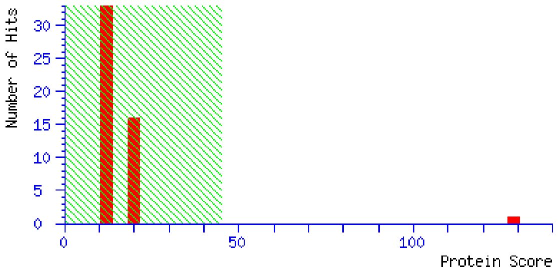
Matched peptides No.: [1]   Sequence coverage %: [8]

Matched sequences: R.IVDQCSNGGLDLDVNVFR.Q

Calculated Mr: **22700**   Calculated *p*I: **5.63**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MNIFIVVLLC LTGVAIAEQC GRQAGGKLCP NNLCCSQWGW CGSTDEYCSP
51 DHNCQSNCKD SGEGVGGGSA SNVLATYHLY NSQDHGWDLN AASAYCSTWD
101 ANKPYSWRSK YGWTAFCGPV GAHGQSSCGK CLSVTNTGTG AKTTVR**IVDQ**
151 **CSNGGLDLDV** **NVFR**QLDTDG KGYERGHITV NYQFVDCGDS FNPLFSVMKS
201 SVIN

Spot No.: **D14**

NCBI accession No.: **gi|225446010** Species: *Vitis vinifera*

PFF score: [196]

Protein name: putative glucose-6-phosphate 1-epimerase

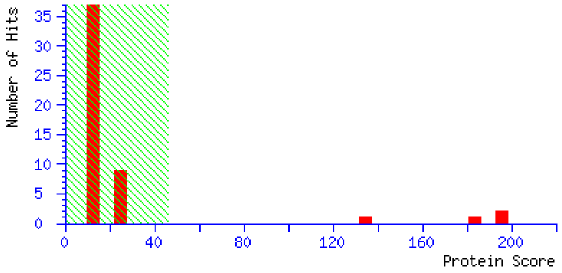
Matched peptides No.: [4] Sequence coverage %: [14]

Matched sequences: R.VALGPGGDLMLTSR.I;
R.VALGPGGDLMLTSR.I + Oxidation (M);
K.DGLPDAVVWNPWDKK.A;
R.VEGLETLDYLDNLQNK.E

Calculated Mr: **35638** Calculated *p*I: **5.75**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MSSERVPVEL CKGINGLEKV VLREVRGSSA EVYLYGGQVT SWKNDHGEEL
51 LFVSSKAIFK PPKAIRGGIP ICFPQFGNHG SLEQHGFARN RVWSIDVDPP
101 PFPTNTSSRA FIDLILKPSE EDMKIWPHSY EFRLR**VALGP** **GGDLMLTSR**I
151 RNTSTEGKPL TFTFAYHTYF SVSDISEVR**V** **EGLETLDYLD** **NLQNK**ERFTE
201 QGDAITFESE VDKIYVSTPT KIAILDHEKK RTFVIRK**DGL** **PDAVVWNPWD**
251 **KK**AKAMADFG DDEYKHMLCV EAAAVEKPIT LKPGEEWRGR QELSAVPSSY
301 CSGQLDPQKV LQCS

Spot No.: **D15**

NCBI accession No.: **gi|1143427** Species: *Cucumis sativus*

PFF score: [338] Protein name: heat shock protein 70

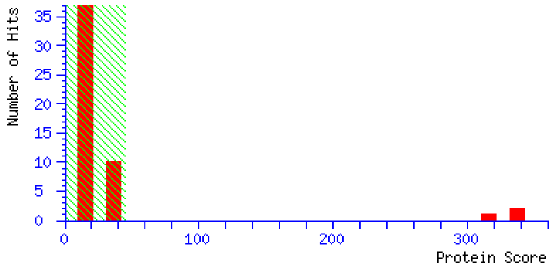
Matched peptides No.: [5] Sequence coverage %: [8]

Matched sequences: K.DIDEVILVGGSTR.I;
K.QFAAEEISAQVLR.K;
K.AVVTVPAYFNDSQR.T;
K.LSFKDIDEVILVGGSTR.I;
K.KQDITITGASTLPSDEVER.M

Calculated Mr: **75480** Calculated *p*I: **5.15**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MGASTAQIHG LGAPSFAAAS MRKSNNVSSR SVFFGQKLGN SSAFPAAAFL
51 NLRSNTSRRN SSVRPLRIVN EKVVGIDLGT TNSAVAAMEG GKPTIVTNAE
101 GQRTTPSVVA YTKNGDRLVG QIAKRQAVVN PENTFFSVKR FIGRKMSEVD
151 EESKQVSYRV ERDENGNVKL ECPAIGK**QFA** **AEEISAQVLR** KLVDDASKFL
201 NDKVTK**AVVT** **VPAYFNDSQR** TATKDAGRIA GLEVLRIINE PTAASLAYGF
251 EKKSNETILV FDLGGGTFDV SVLEVGDGVF EVLSTSGDTH LGGDDFDKRI
301 VDWLAANFKR DEGIDLLKDK QALQRLTETA EKAKMELSSL TQANISLPFI
351 TATADGPKHI ETTITRAKFE ELCSDLLDRL KTPVENSLRD AK**LSFKDIDE**
401 **VILVGGSTR**I PAVQELVKKM TGKEPNVTVN PDEVVALGAA VQAGVLAGDV
451 SDIVLLDVSP LSLGLETLGG VMTKIIPRNT TLPTSKSEVF STAADGQTSV
501 EINVLQGERE FVRDNKSLGS FRLDGIPPAP RGVPQIEVKF DIDANGILSV
551 TAIDKGSGK**K** **QDITITGAST** **LPSDEVER**MV SEADKFAKED KEKRDAIDTK
601 NQADSVVYQT EKQLKELGDK VPGPVKEKVE SKLGELKEAI SGGSTEAIKE
651 AMAALNQEVM QLGQSLYNQP GAGAAPGPGA SSESGPSEST GKGPEGDVID
701 ADFSDSK

Spot No.: **D16**

NCBI accession No.: **gi|255558037** Species: *Ricinus communis*

PFF score: [198]

Protein name: nucleic acid binding protein, putative

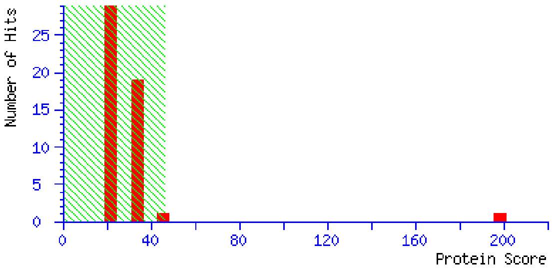
Matched peptides No.: [2] Sequence coverage %: [9]

Matched sequences: K.HQFTSTATSK.V;
R.YVLTGASWVTGAFNR.V

Calculated Mr: **67285** Calculated *p*I: **5.36**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAITTVKVSN VSLGATEQDI KEFFSFSGDI DYVELLGDNE RSQIAYVTFK
51 DQQGAETAVL LSGATIVDQS VTIELAPDYK LPAAASVPTT ATESSTASGA
101 ESAFQKAEDI VSSMLAKGFI LGKDAVNKAK AFDEK**HQFTS** **TATSK**VASLD
151 EKIGLTEKIS AGTTLVNDKV REVDEKFRVS ETTKSAFAAA EQTVSNAGSA
201 IMKNR**YVLTG** **ASWVTGAFNR** VAKAAGEVGQ KTKEKVLAEE EQNQVAEGYT
251 QIHGTDSPNM SEQMSKSSH

Spot No.: **D17**

NCBI accession No.: **gi|27449246** Species: *Hevea brasiliensis*

PFF score: [105] Protein name: heat shock protein 70

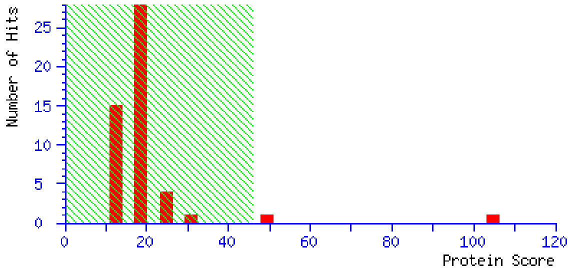
Matched peptides No.: [3] Sequence coverage %: [23]

Matched sequences: K.DHGGPEDENR.H;
K.HIPLSGPHSIAGR.S;
R.SVVFHEGRDDLGK.G

Calculated Mr: **15726** Calculated *p*I: **5.73**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MLKAVAVITS SEGISGKIFF TQEGDGPTTV TGSVSGLKPG LHGFHVHTFG
51 DTTNGCLSTG LHFNPASK**DH** **GGPEDENR**HA GDLGNVNVGD DGTANFTIVD
101 K**HIPLSGPHS** **IAGRSVVFHE** **GRDDLGK**GGH ELSKITGNAG DRIACGIIGL
151 QE

Spot No.: **D18**

NCBI accession No.: **gi|2832430** Species: *Hevea brasiliensis*

PFF score: [446] Protein name: prohevein

Matched peptides No.: [4] Sequence coverage %: [32]

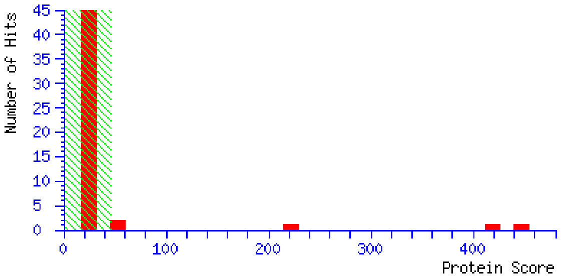
Matched sequences: K.CLSVTNTGTGAK.A;

R.QLDTDGKGYER.G;
R.IVDQCSNGGLDLDVNVFR.Q;
K.YGWTAFCGPVGAHGQPSCGK.C

Calculated Mr: **20852** Calculated *p*I: **5.64**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 EQCGRQAGGK LCPNNLCCSQ WGWCGSTDEY CSPDHNCQSN CKDSGEGVGG
51 GSASNVLATY HLYNSQDHGW DLNAASAYCS TWDANKPYSW RSK**YGWTAFC**
101 **GPVGAHGQPS** **CGKCLSVTNT** **GTGAK**ATVR**I** **VDQCSNGGLD** **LDVNVFRQLD**
151 **TDGKGYER**GH LTVNYQFVDC GDSFNPLFSV MKSSVIN

Spot No.: **D19**

NCBI accession No.: **gi|255551408** Species: *Ricinus communis*

PFF score: [301]

Protein name: chaperonin containing t-complex protein 1

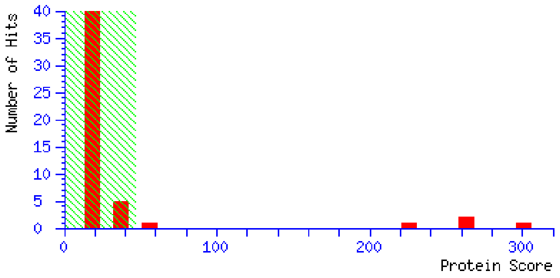
Matched peptides No.: [6] Sequence coverage %: [14]

Matched sequences: R.HKFDVDTR.L;
K.GPNDHTIAQIK.D;
K.GIDPPSLDLLAR.A;
R.LVEGLVLDHGSR.H;
K.SEINAGFFYSNAEQR.E;
K.NTIEDEAVVLGAGAFELAAR.K

Calculated Mr: **59556** Calculated *p*I: **6.08**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1	MSLRVLNPNA	EVLNKSAALH	MNINAAKGLQ	DVLKSNLGPK	GTIKMLVGGA
51	GDIKLTKDGN	TLLKEMQIQN	PTAIMIARTA	VAQDDISGDG	TTSTVIFIGE
101	LMKQSERYIG	EGMHPRVLVD	GFEIAKRATL	QFLEKFKTPV	VMGDEPDKEI
151	LKMVARTTLR	TKLYETLADQ	LTDIVVNAVL	CIRKPEEAID	LFMVEIMHMR
201	**HKFDVDTRLV**	**EGLVLDHGSR**	HPDMKRRAEN	CYILTCNVSL	EYDK**SEINAG**
251	**FFYSNAEQRE**	KMVAAERRQV	DERVEKIIEL	KNKVCSGNDN	NFVVINQK**GI**
301	**DPPSLDLLAR**	AGIIALRRAK	RRNMERLVLA	CGGEAVNSVD	DLTPDCLGWA
351	GLVYEHILGE	EKYTFVEHVK	NPHSCTILIK	**GPNDHTIAQI**	**K**DAVRDGLRA
401	VK**NTIEDEAV**	**VLGAGAFELA**	**AR**KYLISEVK	KTVKGRAQLG	IEAFADALLV
451	IPKTLAENSG	LDTQDEIVSL	TGEHDRENIV	GLNLQTGGPL	DPQMEGIFDN
501	YSVKRQLINS	GPVIASQLLL	VDEVIRAGRN	MRKPN	

Spot No.: **D20**

NCBI accession No.: **gi|225438145** Species: *Vitis vinifera*

PFF score: [75]

Protein name: PREDICTED: malate dehydrogenase, cytoplasmic

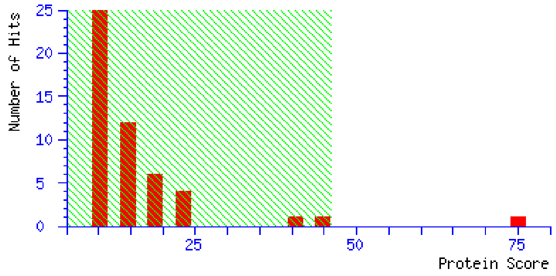
Matched peptides No.: [1] Sequence coverage %: [3]

Matched sequences: K.IVQGLHIDEFSR.K

Calculated Mr: **35881** Calculated *p*I: **6.18**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAKEPVRVLV TGAAGQIGYA LVPMIARGVM LGADQPVILH MLDIPPAAEA
51 LNGVKMELVD AAFPLLKGVV ATTDVVEACT GVNIAVMVGG FPRKEGMERK
101 DVMSKNVSIY KSQASALENH AAANCKVLVV ANPANTNALI LKEFAPSIPE
151 KNISCLTRLD HNRALGQVSE RLNVQVSDVK NVIIWGNHSS TQYPDVNHAT
201 VKTPAGEKPV RGLVGDDAWL NGEFITTVQQ RGAAIIKARK LSSALSAASA
251 ACDHIRDWVL GTPEGTWVSM GVYSDGSYNV PAGLIYSFPV TCCAGEWK**IV**
301 **QGLHIDEFSR** KKLDLTAQEL SEEKELAYSC LS

Spot No.: **D21**

NCBI accession No.: **gi|224056377** Species: *Ricinus communis*

PFF score: [116]

Protein name: Aspartic proteinase precursor

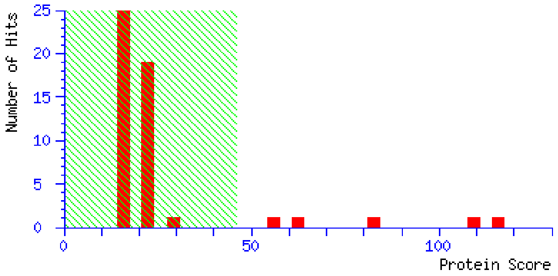
Matched peptides No.: [3] Sequence coverage %: [7]

Matched sequences: K.GEHTYVPVTQK.G;
K.EPVFSFWFNR.N;
K.NYMDAQYFGEIGIGTPPQK.F + Oxidation (M)

Calculated Mr: **56596** Calculated *p*I: **5.19**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

1 MGTIFKPALF FCLILLPLVC ATASSSNDGL VRIGLKKRKF DQNNRVAAQF
51 ESKEGEAFRA SIKKYHIRGN LGDAEDIDIV SLK**NYMDAQY** **FGEIGIGTPP**
101 **QK**FTVIFDTG SSNLWVPSSK CYFSVACYFH SKYKSGQSST YKKNGKSADI
151 HYGTGAISGF FSQDNVKVGE LVIKNQEFIE ATREPSITFL VAKFDGILGL
201 GFQEISVGNA VPVWYNMVNQ GLVK**EPVFSF** **WFNR**NADEDE GGEIVFGGMD
251 PNHYK**GEHTY** **VPVTQK**GYWQ FDMGDVLIDG KTTGICSSGC AAIADSGTSL
301 LAGPTTIITE VNHAIGATGV VSQECKAVVA QYGETIIAML LAKDQPQKIC
351 SQIGLCTFDG SRGVSMGIES VVNEKIQEVA GGLHDAMCST CEMAVVWMQN
401 QLKQNQTQEH ILNYVNELCE RLPSPMGESA VDCGSLSTMP NVSFTIGGRV
451 FDLAPEQYVL KVGDGEAAQC ISGFTALDVP PPRGPLWILG DVFMGPFHTV
501 FDYGNKRVGF AEVA

Spot No.: **D22**

NCBI accession No.: **gi|255554865** Species: *Ricinus communis*

PFF score: [145]

Protein name: lactoylglutathione lyase, putative

Matched peptides No.: [4] Sequence coverage %: [16]

Matched sequences: K.FYTECFGMK.L;
K.ITSFLDPDGWK.T;
K.DPDGYIFELIQR.G;
R.GPTPEPLCQVMLR.V + Oxidation (M)

Calculated Mr: **31641** Calculated *p*I: **7.63**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
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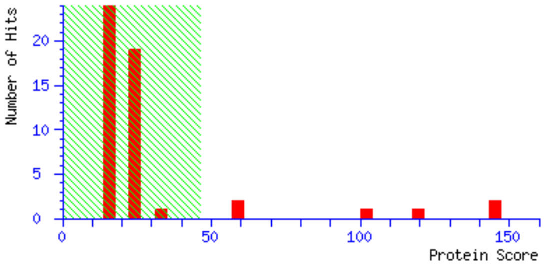

Matched peptide sequences: shown in Bold Red:

1 MAAEATAPNA DVLEWPKKDK RRLLHAVYRV GDLDRTIK**FY** **TECFGMK**LLR
51 KRDIPEEKYS NAFLGFGPEE TNFVVELTYN YGVTSYDIGT GFGHFAIATQ
101 DVYKLVEEVL AKGGAVTREP GPVKGGTTVI AFVK**DPDGYI** **FELIQRGPTP**
151 **EPLCQVMLR**V GDLDRSIRFY EKALGMKLLR KVDKPEYKYT LAMMGYADEY
201 ETTVLELTYN YGVTEYTKGN AYAQVAISTD DVYKSAEVVN LVTQELGGKI
251 TRQPGPIPGL NTK**ITSFLDP** **DGWK**TKRKRR

Spot No.: **D23**

NCBI accession No.: **gi|356517215** Species: *Glycine max*

PFF score: [466]

Protein name: uncharacterized protein LOC100817735

Matched peptides No.: [5] Sequence coverage %: [22]

Matched sequences: R.LGLSAVIMGSR.G;
K.IHIVKDHDMK.E + Oxidation (M);
K.IGVAVDLSDESAYAVR.W;
R.KIGVAVDLSDESAYAVR.W;
K.LGSVSDYCVHHCVCPVVVVR.Y

Calculated Mr: **27677** Calculated *p*I: **5.83**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
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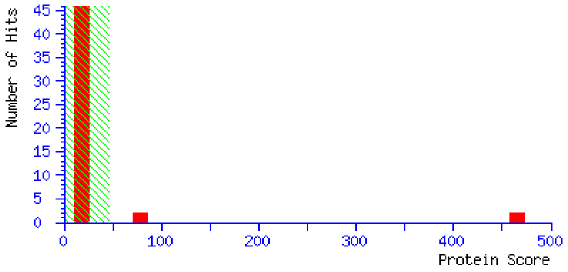


Matched peptide sequences: shown in **Bold Red:**

1 MQPHQNPPAL DSDPQLPQIK IHHPASPRHH HPSSAGAATP TPTAGARR**KI**
51 **GVAVDLSDES AYAVR**WAVQH YIRPGDAVIL LHVSATNVLF GADWGSIDLS
101 INTDPNSDED AVSAVNNSND HNSKRKLEDD FDAFTASKAA DLAKPLRELQ
151 IPFK**IHIVKD HDMK**ERLCLE VER**LGLSAVI MGSR**GFGAVR RGSDGK**LGSV**
201 **SDYCVHHCVC PVVVVR**YPDD KDAVAAATTA EPVVAVKDGD EGEAVVQPVP
251 HKKED

Spot No.: **D24**

NCBI accession No.: **gi|356569000**   Species: *Glycine max*

PFF score: [505]

Protein name: heat shock cognate 70 kDa protein-like

Matched peptides No.: [11]   Sequence coverage %: [19]

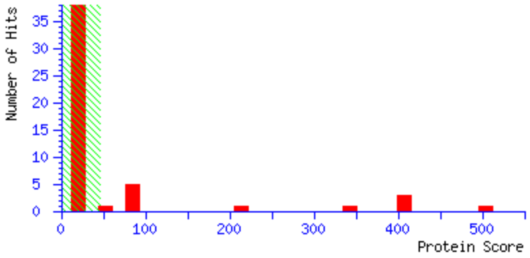
Matched sequences:

K.ITITNDKGR.L;K.DAGVIAGLNVMR.I;K.DAGVIAGLNVMR.I + Oxidation (M);R.MVNHFVQEFK.R + Oxidation (M);K.NALENYAYNMR.N;K.NALENYAYNMR.N (M);K.SSVHDVVLVGGSTR.I;R.TTPSYVAFTDTER.L;K.ATAGDTHLGGEDFDNR.M; R.IINEPTAAAIAYGLDKK.A;K.EQVFSTYSDNQPGVLIQVYEGER.T

Calculated Mr: **71194**   Calculated *p*I: **5.10**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MAGKGEGLAI GIDLGTTYSC VGVWQHDRVE IIANDQGNR**T TPSYVAFTDT**
51 **ER**LIGDAAKN QVAMNPINTV FDAKRLIGRR VSDPSVQSDM KLWPFKVTAG
101 AGEKPMIGVN YKGEEKQFAA EEISSMVLTK MREIAEAYLG STVKNAVVTV
151 PAYFNDSQRQ ATK**DAGVIAG LNVMRIINEP TAAAIAYGLD KK**ATSVGEKN
201 VLIFDLGGGT FDVSLLTIEE GIFEVK**ATAG DTHLGGEDFD NRMVNHFVQE**
251 **FK**RKNKKDIT GNPRALRRLR TSCERAKRTL SSTAQTTIEI DSLFEGIDFY
301 STITRARFEE LNMDLFRKCM EPVEKCLRDA KMDK**SSVHDV VLVGGSTR**IP
351 KVQQLLQDFF NGKDLCKSIN PDEAVAYGAA VQAAILSGEG NEKVQDLLLL
401 DVTPLSLGLE TAGGVMTVLI PRNTTIPTKK **EQVFSTYSDN QPGVLIQVYE**
451 **GER**TRTRDNN LLGKFELSGI PPAPRGVPQI TVCFDIDANG ILNVSAEDKT
501 TGQKNK**ITIT NDKGR**LSKEE IEKMVQEAEK YKSEDEEHKK KVEGK**NALEN**
551 **YAYNMR**NTIK DEKISSKLSS EDKTKIDNAI EQAIQWLDTN QLAEADEFED
601 KMKELEGICN PIIAKMYQGG AGTGGDVDDD APPAGGSGAG PKIEEVD

Spot No.: **D25**

NCBI accession No.: **gi|132270**   Species: *Hevea brasiliensis*

PFF score: [405]

Protein name: Rubber elongation factor protein

Matched peptides No.: [4]   Sequence coverage %: [38]

Matched sequences: K.NVAVPLYNR.F;
K.DASIQVVSAIR.A;
K.FVDSTVVASVTIIDR.S;
K.DKSGPLQPGVDIIEGPVK.N

Calculated Mr: **14713**   Calculated *p*I: **5.04**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
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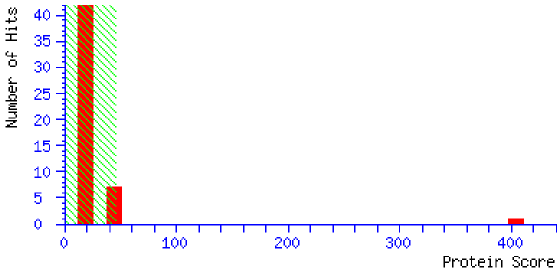


Matched peptide sequences: shown in Bold Red:

1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK **DKSGPLQPGV**
51 **DIIEGPVKNV** **AVPLYNR**FSY IPNGALK**FVD** **STVVASVTII** **DR**SLPPIVKD
101 **ASIQVVSAIR** AAPEAARSLA SSLPGQTKIL AKVFYGEN

Spot No.: **D26**

NCBI accession No.: **gi|6624721**   Species: *Pisum sativum*

PFF score: [79]

Protein name: putative cysteine protease

Matched peptides No.: [2]   Sequence coverage %: [7]

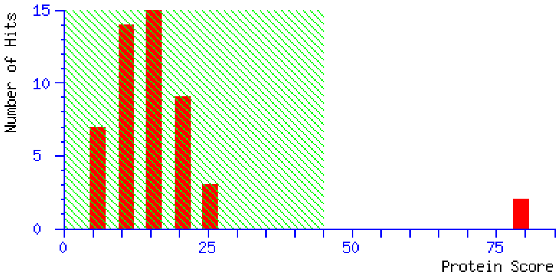
Matched sequences: R.SGQIDSNELR.D;

R.ALSSYNQSFSLR.T

Calculated Mr: **31321**   Calculated *p*I: **7.81**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 RFFLLLGKTL SPFNMSGYPN QSPNYGYGYN APPPTQSYGA PPPSQSYGAP
51 PPSQSYGAPP PSQYGAPPPG QSYSASPYGQ PSAPYAAPHQ KPPKEESHSS
101 GGGAYPPPAH GSPFASLLPS TFPPGTDPSI VACFQVADQD GSGLIDDKEL
151 QR**ALSSYNQS** **FSLR**TVHLLM YHFTNTSVKI GPKEFTSLFY SLQSWRGIFE
201 RFDKDR**SGQI** **DSNELR**DALL SLGYAVSPTV LDLLVSKFDK TGGKHKAVEY
251 DNFIECCLTV KGLTDKFKEK DTGILALQHF PMRRLC

Spot No.: **D27**

NCBI accession No.: **gi|132270** Species: *Hevea brasiliensis*

PFF score: [340]

Protein name: Rubber elongation factor protein

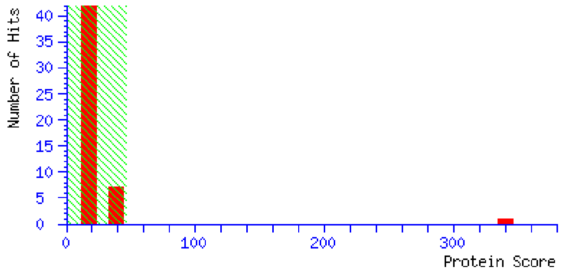
Matched peptides No.: [4] Sequence coverage %: [38]

Matched sequences: K.NVAVPLYNR.F;
K.DASIQVVSAIR.A;
K.FVDSTVVASVTIIDR.S;
K.DKSGPLQPGVDIIEGPVK.N

Calculated Mr: **14713** Calculated *p*I: **5.04**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK **DKSGPLQPGV**
51 **DIIEGPVKNV** **AVPLYNR**FSY IPNGALK**FVD** **STVVASVTII** **DR**SLPPIVK**D**
101 **ASIQVVSAIR** AAPEAARSLA SSLPGQTKIL AKVFYGEN

Spot No.: **D28**

NCBI accession No.: **gi|314991144**

Species: *Gossypium hirsutum*

PFF score: [115]

Protein name: mitogen-activated protein kinase

Matched peptides No.: [3]　　　Sequence coverage %: [9]

Matched sequences: K.YIHSANVLHR.D;

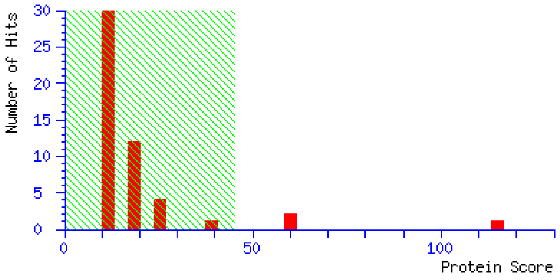
R.HMDHENVVAIR.D;

R.VTSESDFMTEYVVTR.W

Calculated Mr: **46237**　　　Calculated *p*I: **5.47**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



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

1 MEGGGPPQAA DTEMAEAAQQ QPQHHQQRPP QVAAGLENIP ATLSHGGRFI

51 QYNIFGNIFE VTAKYKPPIM PIGKGAYGIV CSALNSETNE HVALKKIANA

101 FDNKIDAKRT LREIKLLR**HM** **DHENVVAIR**D IIPPPQRECF NDVYIAYELM

151 DTDLHQIIRS NQALSEEHCQ YFPYQILRGL K**YIHSANVLH** **R**DLKPSNLLL

201 NANCDLKICD FGLAR**VTSES** **DFMTEYVVTR** WYRPPELLLN SSDYTAAIDV

251 WSVGCIFMEL MDRKPLFPGR DHVHQLRLLM ELIGTPSEAE LEFLNENAKR

301 YIRQLPLYRR QSFTEKFPNV PPLAIDLVEK MLTFDPRQRI TVEDALAHPY

351 LTSLHDISDE PVCMTPFSFD FEQHALTEEQ MKELIYREAL AFNPEYLQQ

Spot No.: **D29**

NCBI accession No.: **gi|118485535**

Species: *Populus trichocarpa*

PFF score: [82] Protein name: unknown

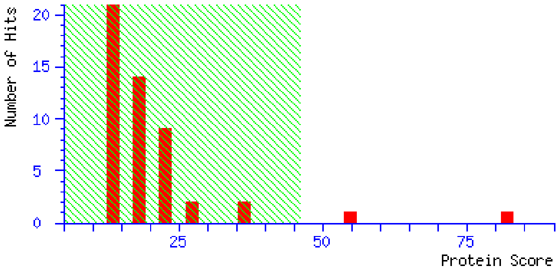
Matched peptides No.: [1] Sequence coverage %: [8]

Matched sequences: K.VATPAQAQEVHLELR.K

Calculated Mr: **18429** Calculated *p*I: **5.59**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



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

```
  1 MLVNLGIPWV ILGHSERRSL LNESNEFVGD KVAYALSLGL KVIACVGETL
 51 QQRESGSTMA VVAAQTKAIA ANVSYWDNVV MAYEPVWAIG TGKVATPAQA
101 QEVHLELRKW FHDNVGAEVA ASTRIIYGGS VNGANCKELA GQPDVDGFLV
151 GGASLKPEFI DIIKSATVKS QL
```

Spot No.: **D30**

NCBI accession No.: **gi|132270** Species: *Hevea brasiliensis*

PFF score: [470]

Protein name: Rubber elongation factor protein

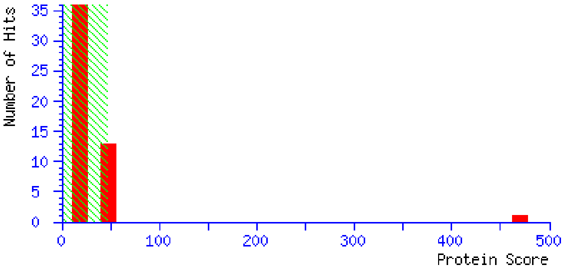
Matched peptides No.: [4] Sequence coverage %: [27]

Matched sequences: K.NVAVPLYNR.F;
K.DASIQVVSAIR.A;
K.SGPLQPGVDIIEGPVK.N;
K.DKSGPLQPGVDIIEGPVK.N

Calculated Mr: **14713** Calculated *p*I: **5.04**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK **DKSGPLQPGV**
51 **DIIEGPVKNV** **AVPLYNR**FSY IPNGALKFVD STVVASVTII DRSLPPIVK**D**
101 **ASIQVVSAIR** AAPEAARSLA SSLPGQTKIL AKVFYGEN

Spot No.: **D31**

NCBI accession No.: **gi|470127750**

Species: *Fragaria vesca subsp. Vesca* PFF score: [80]

Protein name: uncharacterized protein LOC101300446

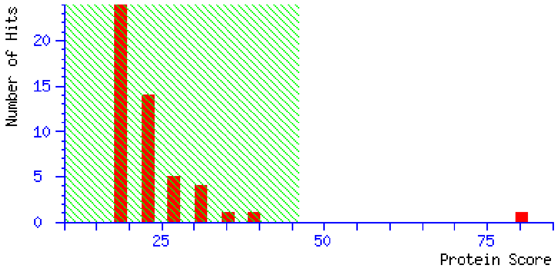
Matched peptides No.: [1] Sequence coverage %: [3]

Matched sequences: K.KLDLVITSPLLR.T

Calculated Mr: **36660** Calculated *p*I: **6.43**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MTVSISSIYT PHISLIPLSV PTSTSPSSKF PKSKHHSILL CFSSPPDMDA
51 AGATSLYPLH RSKTIHLVRH AQGIHNVEGE KDHLAYMSHD LFDAHLTPLG
101 WKQVDNLHKH VQACGLTK**KL** **DLVITSPLLR** TMQTAVGVFG GEAYTDGIDV
151 PPLMVENAGN SLHAAISSLN CPPFVAVELC REHLGVHPCD KRRSISEYRP
201 LFPAIDFSLI ENDDDILWTP DIREKNEEVA ARGLKFLNWL WTREEKNIAI
251 VTHSGFLYHT LSAFGNDCHS SIKNEISTHF ANCELRSMVI VDRGLIGSNS
301 TSATNYPGKN PQGLDLPSDL ADKKNPVSK

Spot No.: **D32**

NCBI accession No.: **gi|132270**   Species: *Hevea brasiliensis*

PFF score: [398]

Protein name: Rubber elongation factor protein

Matched peptides No.: [4]   Sequence coverage %: [38]

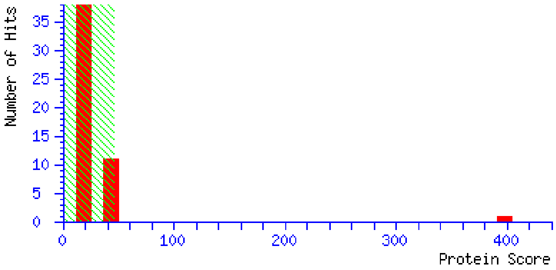
Matched sequences: K.NVAVPLYNR.F;

K.DASIQVVSAIR.A;
K.FVDSTVVASVTIIDR.S;
K.DKSGPLQPGVDIIEGPVK.N

Calculated Mr: **14713**   Calculated *p*I: **5.04**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK **DKSGPLQPGV**
51 **DIIEGPVKNV** **AVPLYNR**FSY IPNGALK**FVD** **STVVASVTII** **DR**SLPPIVK**D**
101 **ASIQVVSAIR** AAPEAARSLA SSLPGQTKIL AKVFYGEN

Spot No.: **D33**

NCBI accession No.: **gi|351724891** Species: *Glycine max*

PFF score: [106] Protein name: enolase

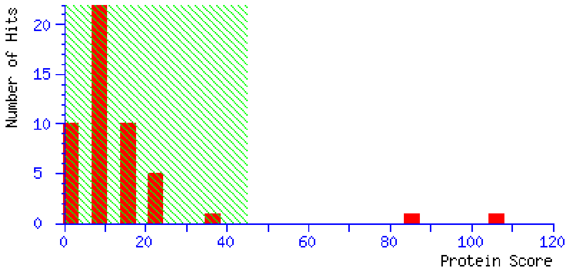
Matched peptides No.: [2] Sequence coverage %: [7]

Matched sequences: R.AAVPSGASTGIYEALELR.D;
R.IEEELGAEAVYAGANFR.T

Calculated Mr: **47975** Calculated *p*I: **5.31**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

1 MATIVSINAR QIFDSRGNPT VEVDLTCSDG TFAR**AAVPSG** **ASTGIYEALE**
51 **LR**DGGSDYLG KGVSKAVDNV NTVIGPALIG KDPTEQTAID NLMVQQLDGT
101 VNEWGWCKQK LGANAILAVF LAVCKAGASV LKIPLYKHIA NIAGNKKLVL
151 PVPAFNVING GSHAGNKLAM QEFMVLPVGA SSFKEAMKMG VEVYHNLKSV
201 IKKKYGQDAI NVGDEGGFAP NIQENKEGLE LLKTAIAKAG YTGKVVIGMD
251 VAASEFYKED KTYDLNFKED NNDGSQRISG DALKDLYKSF VSEYPIVSIE
301 DPFDQDDWEH YAKLTAEVGA NVQIVGDDLL VTNPKRVQKA IDTKACNALL
351 LKVNQIGSVT ESIEAVRMSK KAGWGVMASH RSGETEDTFI ADLSVGLATG
401 QIKTGAPCRS ERLAKYNQLL **RIEEELGAEA** **VYAGANFR**TP VEPY

Spot No.: **D34**

NCBI accession No.: **gi|255578278**   Species: *Ricinus communis*

PFF score: [154]

Protein name: hypothetical protein RCOM_0537780

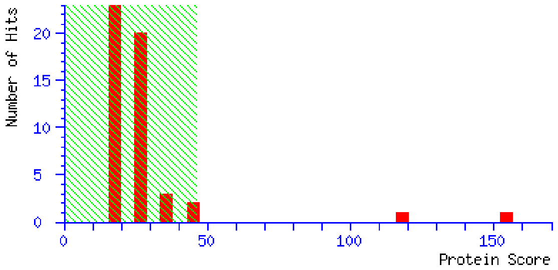
Matched peptides No.: [2]   Sequence coverage %: [6]

Matched sequences: K.QESEYGSGGYGR.R;
R.KPSYGEEGGYGER.T

Calculated Mr: **41389**   Calculated *p*I: **4.65**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MPYYTRSEDD VNDFDEFDPT PYGGGYDLAL TYGRPLPPSD ETCYQNSAIA
51 DDDVDYDRPN FTSYAEPSAY NDDILQEEYN SYSRPKPRPG FIPGGGIGGD
101 PYSRPHAAPG FQPGSGGYGG VSEYEKPSGY GRRPDSEYGS GGYGGGTEYE
151 RPSGEDYGSG HGRKQDSEYG SGGYGRRPES EYGSGGGYER PSSEEYGSGY
201 GRK**QESEYGS** **GGYGR**RPEAE YGSGYGGRPE TEYGGGGGSE YGGGYGR**KPS**
251 **YGEEGGYGER** TEYERPSYGD DPPRRPGYGR QDDEYERPSY ERKSDDDNDG
301 SRRKYGGDDD EKGYQKKYGG YGDDDDEEGS RRKYGYGGEE ESYGRKKYGD
351 DGSDDDEKKH HRHKHHQHKH SDDE

Spot No.: **D35**

NCBI accession No.: **gi|1143427** Species: *Cucumis sativus*

PFF score: [378] Protein name: heat shock protein 70

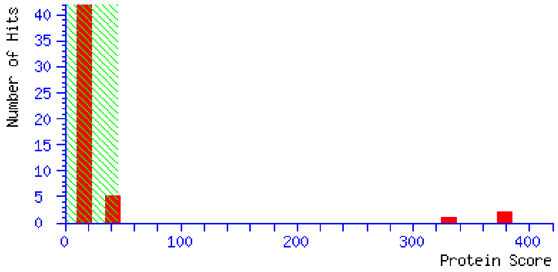
Matched peptides No.: [5] Sequence coverage %: [8]

Matched sequences: K.DIDEVILVGGSTR.I;
K.QFAAEEISAQVLR.K;
K.AVVTVPAYFNDSQR.T;
K.LSFKDIDEVILVGGSTR.I;
K.KQDITITGASTLPSDEVER.M

Calculated Mr: **75480** Calculated *p*I: **5.15**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MGASTAQIHG LGAPSFAAAS MRKSNNVSSR SVFFGQKLGN SSAFPAAAFL
51 NLRSNTSRRN SSVRPLRIVN EKVVGIDLGT TNSAVAAMEG GKPTIVTNAE
101 GQRTTPSVVA YTKNGDRLVG QIAKRQAVVN PENTFFSVKR FIGRKMSEVD
151 EESKQVSYRV ERDENGNVKL ECPAIGK**QFA** **AEEISAQVLR** KLVDDASKFL
201 NDKVTK**AVVT** **VPAYFNDSQR** TATKDAGRIA GLEVLRIINE PTAASLAYGF
251 EKKSNETILV FDLGGGTFDV SVLEVGDGVF EVLSTSGDTH LGGDDFDKRI
301 VDWLAANFKR DEGIDLLKDK QALQRLTETA EKAKMELSSL TQANISLPFI
351 TATADGPKHI ETTITRAKFE ELCSDLLDRL KTPVENSLRD AK**LSFKDIDE**
401 **VILVGGSTR**I PAVQELVKKM TGKEPNVTVN PDEVVALGAA VQAGVLAGDV
451 SDIVLLDVSP LSLGLETLGG VMTKIIPRNT TLPTSKSEVF STAADGQTSV
501 EINVLQGERE FVRDNKSLGS FRLDGIPPAP RGVPQIEVKF DIDANGILSV
551 TAIDKGSGK**K** **QDITITGAST** **LPSDEVER**MV SEADKFAKED KEKRDAIDTK
601 NQADSVVYQT EKQLKELGDK VPGPVKEKVE SKLGELKEAI SGGSTEAIKE
651 AMAALNQEVM QLGQSLYNQP GAGAAPGPGA SSESGPSEST GKGPEGDVID
701 ADFSDSK

Spot No.: **D36**

NCBI accession No.: **gi|164604960** Species: *Hevea brasiliensis*

PFF score: [120] Protein name: acetyl-CoA C-acetyltransferase

Matched peptides No.: [2] Sequence coverage %: [5]

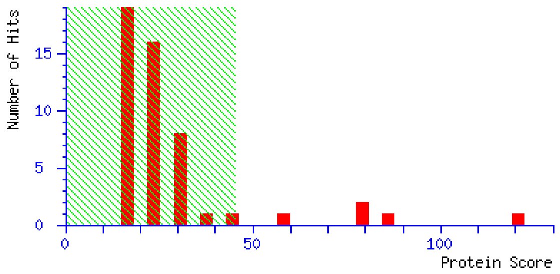
Matched sequences: R.ILVTLLGVLR.K;

M.APVAAAEIKPR.D

Calculated Mr: **41798** Calculated *p*I: **6.96**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 M**APVAAAEIK PR**DVCIVGVA RTPMGGFLGL LSTLPATKLG SIAIEAALKR
51 ASVDPSLVQE VFFGNVLSAN LGQAPARQAA LGAGIPNSVV CTTVNKVCAS
101 GMKATMLAAQ SIQLGINDVV VAGGMESMSN APKYLAEARK GSRLGHDSLV
151 DGMLKDGLWD VYNDVGMGSC AEICADNHSI TREDQDKFAI HSFERGIAAQ
201 ESGAFAWEIV PVEVSGGRGK PLTIVDKDEG LGKFDPVKLR KLRPSFKENG
251 GTVTAGNASS ISDGAAALIL VSGETALKLG LQVIAKIRGY ADAAQAPELF
301 TTAPALAIPK TIANAGLDAS QVDYYEINEA FAVVALANQK LLGLNPEKVN
351 VHGGAVSLGH PLGCSGAR**IL VTLLGVLR**KK NAKYGVGGVC NGGGGASALV
401 VELL

Spot No.: **D37**

NCBI accession No.: **gi|37622210** Species: *Hevea brasiliensis*

PFF score: [77] Protein name: small rubber particle protein

Matched peptides No.: [2] Sequence coverage %: [14]

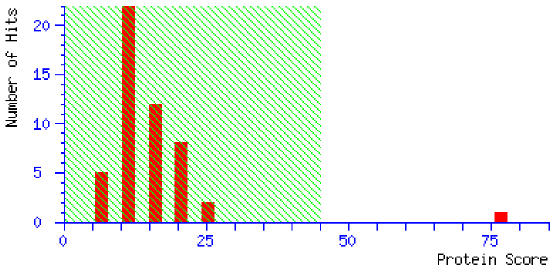
Matched sequences: R.AVASEVHQSGVK.E;

R.VSSYLPLVPTER.I

Calculated Mr: **18929** Calculated *p*I: **8.99**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 KFHDVPNEVL KFVDRKVDES VTSLDSRVPP VVKQVSAQAY SVAREAPVAA
51 **RAVASEVHQS** **GVK**ETASGLA KTLYTKYEPK AKELYSKYEP KAEQCAVTAW
101 RRLNQLPLFP QVAQVVVPTA AYCSEKYNQT VLSTFEKGYR **VSSYLPLVPT**
151 **ER**IAKVFSDD VAQSMPLVSS

Spot No.: **D38**

NCBI accession No.: **gi|255555641**   Species: *Ricinus communis*

PFF score: [109]

Protein name: 26S proteasome non-atpase regulatory subunit

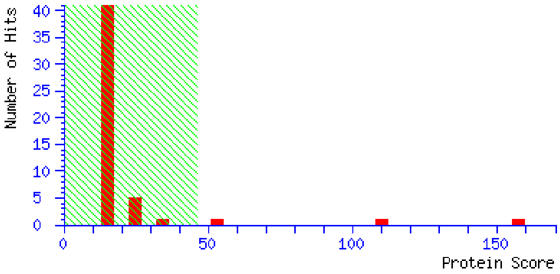
Matched peptides No.: [2]   Sequence coverage %: [12]

Matched sequences: K.HAVELEQSFMEGAYNR.V + Oxidation (M);
R.LPPSSQEYMILGLNLLR.L + Oxidation (M)

Calculated Mr: **30793**   Calculated *p*I: **4.87**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MDPKITEASQ LFERFKAACV REDVDACTKL LSSLKVMLTE FRSLPPLFED
51 TPNAIQELTL ARDIYEHAVL LNVKIGDQDA FERDFFQLKP YYTDASGR**LP**
101 **PSSQEYMILG** **LNLLR**LLVQN RIAEFHTELE LLSPAALENP AIK**HAVELEQ**
151 **SFMEGAYNR**V LSAKQTVPYK GYDYFMDLLA KTVRDEIAGC SEKAYDYLSI
201 NDARQMLLFS SDTELLQYIK EDHPEWEVKN GVVIFQKAKE SAPCKEIPSL
251 QLINQTLSYA RELERIV

Spot No.: **D39**

NCBI accession No.: **gi|255541320** Species: *Ricinus communis*

PFF score: [157]

Protein name: proteasome subunit beta type, putative

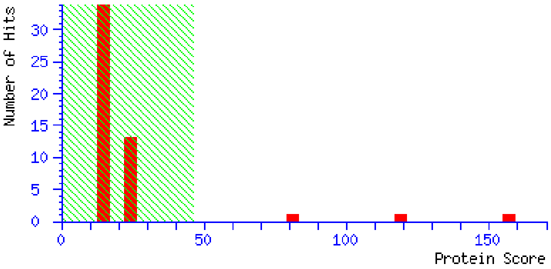
Matched peptides No.: [2] Sequence coverage %: [10]

Matched sequences: K.HLIYQHQHNK.Q;
K.GCVYTYDAVGSYER.V

Calculated Mr: **24880** Calculated *p*I: **6.08**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MTKQQANWSP YDNNGGSCVA IAGADYCVIA ADTRMSTGYN ILTRDYSKIC
51 QLAEKSVMAS SGFQADVQAL QKHLKAK**HLI** **YQHQHNK**QMS CPAMGQLLSN
101 TLYFKRFFPY YAFNVLGGLD SEGK**GCVYTY** **DAVGSYER**VG YSAQGSGSTL
151 IMPFLDNQLK SPSPLLLPAQ DAVTPLSEPE AVDLVKTVFA SATERDIYTG
201 DKVEIVVLNA DGIRREYMEL RKD

Spot No.: **D40**

NCBI accession No.: **gi|255570990** Species: *Ricinus communis*

PFF score: [459] Protein name: heat shock protein, putative

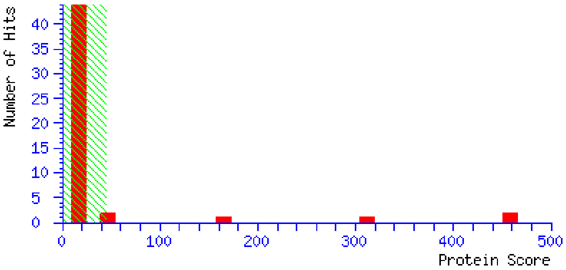
Matched peptides No.: [8] Sequence coverage %: [16]

Matched sequences: K.DIDEVILVGGSTR.I;K.QFAAEEISAQVLR.K;
K.AVVTVPAYFNDSQR.T;K.MSEVDEESKQVSYR.V + Oxidation (M);
R.QAVVNPENTFFSVKR.F;K.LSFKDIDEVILVGGSTR.I;
K.KQDITITGASTLPSDEVER.M;K.SEVFSTAADGQTSVEINVLQGER.E

Calculated Mr: **75431** Calculated *p*I: **5.35**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MASSTAQIHV LGGIGFPSSK SRKPSFSFPK KTVFLGSNLK SHQTAAFLRQ
51 SNTNARRKYG PLRVVNEKVV GIDLGTTNSA VAAMEGGKPT IVTNAEGQRT
101 TPSVVAYTKN GDRLVGQIAK R**QAVVNPENT** **FFSVKR**FIGR K**MSEVDEESK**
151 **QVSYR**VVRDE NGNVKLDCPA IGK**QFAAEEI** **SAQVLR**KLVD DASKFLNDKV
201 TK**AVVTVPAY** **FNDSQR**TATK DAGRIAGLEV LRIINEPTAA SLAYGFEKKN
251 NETILVFDLG GGTFDVSVLE VGDGVFEVLS TSGDTHLGGD DFDKRIVDWL
301 AGNFKRDEGI DLLKDKQALQ RLTETAEKAK MELSSLTQTN ISLPFITATA
351 DGPKHIETTI TRAKFEELCS DLLDRLKTPV ENSLRDAK**LS** **FKDIDEVILV**
401 **GGSTR**IPAVQ ELVKKMTGKD PNVTVNPDEV VALGAAVQAG VLSGDVSDIV
451 LLDVTPLSLG LETLGGVMTK IIPRNTTLPT SK**SEVFSTAA** **DGQTSVEINV**
501 **LQGER**EFVRD NKSLGSFRLD GIPPAPRGVP QIEVKFDIDA NGILSVTAID
551 KGTGK**KQDIT** **ITGASTLPSD** **EVER**MVSEAE RFAKEDKEKR DAIDTKNQAD
601 SVVYQTEKQL KELGDKVPAP VKEKVEAKLK ELKDAIEGGS TQGMKDAMAA
651 LNQEVMQLGQ SLYNQPGAGG AGPAPGGEAG PSSDSSSKGP EGDVIDADFT
701 DSK

Spot No.: **D41**

NCBI accession No.: **gi|351726646** Species: *Glycine max*

PFF score: [97]

Protein name: uncharacterized protein LOC100499738

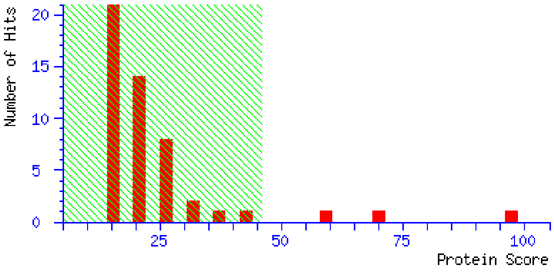
Matched peptides No.: [5] Sequence coverage %: [28]

Matched sequences: K.NVALYQFR.N;
K.LIAASGEPGDR.V;
K.SNEDKIMLLDSHK.L + Oxidation (M);
R.HYHSGMSVEEAIDLVDK.C;
K.LIAASGEPGDRVQFTEYIQK.N

Calculated Mr: **22699** Calculated *p*I: **5.86**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MECVFGLVGN GFAIVVADSS AVHSILVHK**S** **NEDKIMLLDS** **HKLIAASGEP**
51 **GDRVQFTEYI** **QKNVALYQFR** NGIPLTTAAA ANFTRGELAT ALRKNPYSVN
101 ILLAGYDKET GPELYYIDYI ATLHKLEKGA FGYGSYFSLS MMDR**HYHSGM**
151 **SVEEAIDLVD** **K**CIMEIRSRL VVAPPNFVIK IVDKDGAREY AWRESVKDTP
201 VPSA

Spot No.: **D42**

NCBI accession No.: **gi|166627** Species: *Arabidopsis thaliana*

PFF score: [111]

Protein name: nucleotide-binding subunit of vacuolar ATPase

Matched peptides No.: [3] Sequence coverage %: [7]

Matched sequences: K.YQEIVNIR.L;

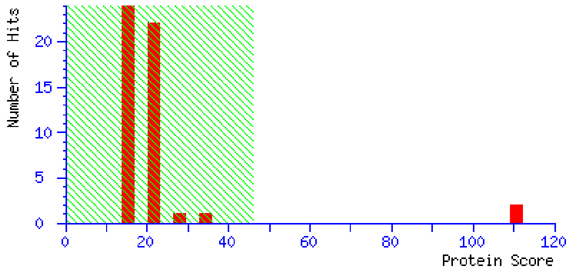
R.QIYPPINVLPSLSR.L;

R.GYPGYMYTDLATIYER.A + Oxidation (M)

Calculated Mr: **54819** Calculated *p*I: **4.98**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MSLSVNMGTN DLDIEEGTLE IGMEYRTVSG VAGPLVILDK VKGPK**YQEIV**
51 **NIR**LGDGSTR RGQVLEVDGE KAVVQVFEGT SGIDNKFTTV QFTGEVLKTP
101 VSLDMLGRIF NGSGKPIDNG PPILPEAYLD ISGSSINPSE RTYPEEMIQT
151 GISTIDVMNS IARGQKIPLF SAAGLPHNEI AAQICRQAGL VKRLEKTVDL
201 LEDHGEDNFA IVFAAMGVNM ETAQFFKRDF EENGSMERVT LFLNLANDPT
251 IERIITPRIA LTTAEYLAYE CGKHVLVILT DMSSYADALR EVSAAREEVP
301 GRR**GYPGYMY** **TDLATIYER**A GRIEGRKGSI TQIPILTMPN DDITHPTPDL
351 TGYITEGQIY IDRQLHNR**QI** **YPPINVLPSL** **SR**LMKSAIGE GMTRKDHSDV
401 SNQLYANYAI GKDVQAMKAV VGEEALSSED LLYLEFLDKF ERKFVMQGAY
451 DTRNIFQSLD LAWTLLRIFP RELLHRIPAK TLDQFYSRDS TS

Spot No.: **D43**

NCBI accession No.: **gi|132270** Species: *Hevea brasiliensis*

PFF score: [55]

Protein name: Rubber elongation factor protein

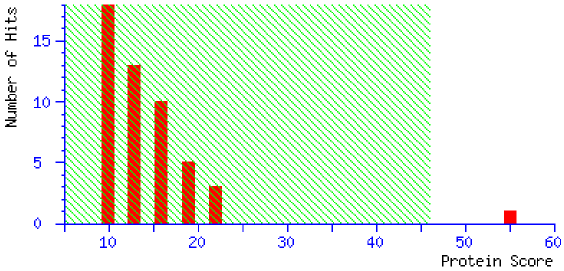
Matched peptides No.: [2] Sequence coverage %: [17]

Matched sequences: K.NVAVPLYNR.F;
K.FVDSTVVASVTIIDR.S

Calculated Mr: **14713** Calculated *p*I: **5.04**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK DKSGPLQPGV
51 DIIEGPVK**NV** **AVPLYNR**FSY IPNGALK**FVD** **STVVASVTII** **DR**SLPPIVKD
101 ASIQVVSAIR AAPEAARSLA SSLPGQTKIL AKVFYGEN

Spot No.: **D44**

NCBI accession No.: **gi|255583952** Species: *Ricinus communis*

PFF score: [366]

Protein name: proteasome subunit alpha type, putative

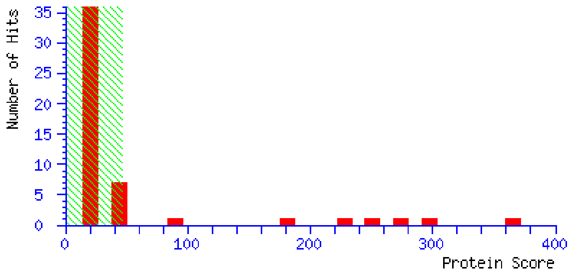
Matched peptides No.: [6] Sequence coverage %: [26]

Matched sequences: K.ATEIEVGVVR.T;R.HITIFSPEGR.L;
K.EQEAINFLEK.K;K.YGYEMPVDVLAK.W + Oxidation (M);
K.LLDHTSVTHLFPITK.Y;K.ATSAGLKEQEAINFLEK.K

Calculated Mr: **27504** Calculated *p*I: **5.84**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MSRGSGGGYD R**HITIFSPEG** **R**LFQVEYAFK AVKASGVTSI GVCGKDSVCV
51 VTQKKVPDK**L** **LDHTSVTHLF** **PITK**YLGLLA TGMTADARTL VQQARNEAAE
101 FRFK**YGYEMP** **VDVLAK**WIAD KSQIYTQHAY MRPLGVVAMV LGIDDEYGPR
151 LYKCDPAGHF FGHK**ATSAGL** **KEQEAINFLE** **K**KMKNDPAFT YEETVQTAIS
201 ALQSVLQEDF K**ATEIEVGVV** **R**TENPVFRVL STEEIDEHLT AISERD

Spot No.: **D45**

NCBI accession No.: **gi|356547978** Species: *Glycine max*

PFF score: [189]

Protein name: eukaryotic translation initiation factor 3 subunit K-like

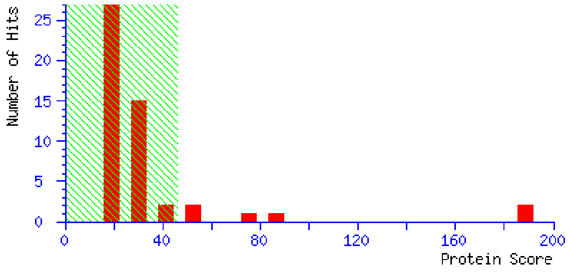
Matched peptides No.: [3] Sequence coverage %: [11]

Matched sequences: K.NAADSVPLEHITR.I;
K.TLIVLSHYLETGR.F;
K.KNAADSVPLEHITR.I

Calculated Mr: **26266** Calculated *p*I: **5.48**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MGREKETTKV AYAVEQLVAF NRYNPDILPD LENYVNDQVS SQTYSLDANL
51 CLLRLYQFEP EKMSSQIVAR ILVKALMAMP APDFSLCLFL IPERVQMEEQ
101 FK**TLIVLSHY** **LETGR**FRQFW DEAAKSRHIV EAVPGFEQAI QGYAIHVLSL
151 TYQRIPRTVL AEAINIEGLS LDKFLENQVA NNGWVIEKSQ GRAQLIVLPR
201 NEFNDPALK**K** **NAADSVPLEH** **ITR**IFPILS

Spot No.: **D46**

NCBI accession No.: **gi|310772392** Species: *Malpighia glabra*

PFF score: [78]

Protein name: dehydroascorbate reductase

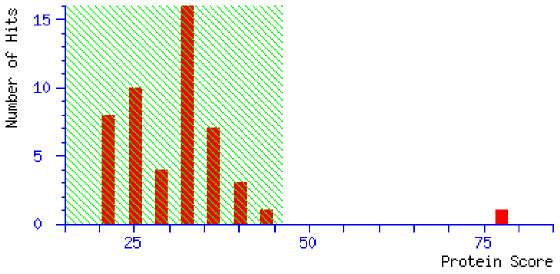
Matched peptides No.: [1] Sequence coverage %: [4]

Matched sequences: K.EHVIAGWEPK.V

Calculated Mr: **23725** Calculated *p*I: **6.40**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

```
  1 MALEICVKAA VGAPNVLGDC PFSQRALLTL EEKKLSYKRH LFDLSNKPQW
 51 FLEISPEGKV PVLKLDDKWV ADSDVIVGLL EEKYPEPSLK TPPEFSSVGS
101 NIFSSFVKFL KSKDANDGTE KALLEELVAL DDHLKAHGPF VAGERVTAVD
151 LSLAPKLYHL EIALGHFKKW TVPESLSHVR NYMKALFARE SFEKTKAAKE
201 HVIAGWEPKV NA
```

Spot No.: **D47**

NCBI accession No.: **gi|255547584**   Species: *Ricinus communis*

PFF score: [370]

Protein name: Regulator of ribonuclease activity A, putative

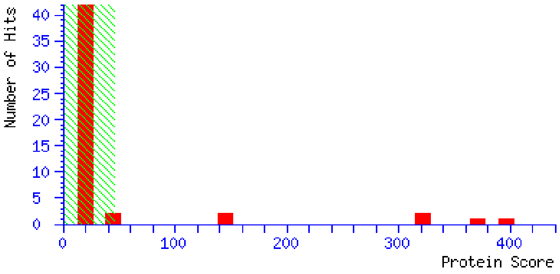
Matched peptides No.: [5]   Sequence coverage %: [33]

Matched sequences: R.VLVVDGGGSLR.C;
K.VFEDNVLIR.E;
R.ALQPIFQIYGR.R;
R.RQVFSGPVVTLK.V;
R.DVDEINGCDIGVR.A

Calculated Mr: **17958**   Calculated *p*I: **5.39**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MALVTTAEVC DANPQLIVSG ELR**ALQPIFQ** **IYGRRQVFSG** **PVVTLKVFED**
51 **NVLIR**EFLEE KGNGR**VLVVD** **GGGSLR**CAIL GGNPVVQAQN NGWAGILVNG
101 CIR**DVDEING** **CDIGVR**ALAS HPMKANKKGI GEKHVPITIG GTRISDGEFL
151 YADTDGILIS RNELSV

Spot No.: **D48**

NCBI accession No.: **gi|255568992** Species: *Ricinus communis*

PFF score: [128]

Protein name: conserved hypothetical protein

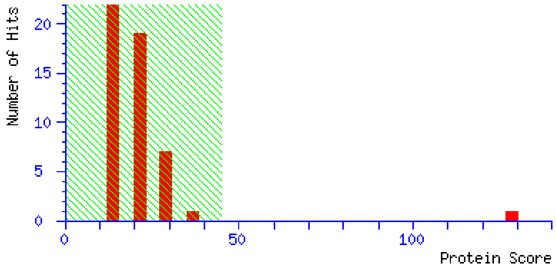
Matched peptides No.: [2] Sequence coverage %: [8]

Matched sequences: K.WNKGDNQR.W;
R.MVNNIHLNVDAFHGDKK.S

Calculated Mr: **35473** Calculated *p*I: **6.29**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MEFPFGHQSH THHHHQRNNA DDDDESRQFY PPPASAPPPP YTRDNEFAPP
51 PPYFQEPDFP PSPTRPYYRE NEYAPPPPPP PVQQAHVYHS SHNQELDSDY
101 YPPRPPTQVT HVSHERIGTE TQTHHSFQPH FPSFLQHHTH QSGSASGLDL
151 SNKPTYKVYS KAEPNFHLTI RDGKVVLAPS DPSDEFQNWY KDERYSTRVK
201 DEEGFPCFAL VNKASGQAMK HSIGGTHPVQ LIPYNPNVLD ESILWTESKD
251 LGDGYRAVR**M** **VNNIHLNVDA** **FHGDKK**SGGV HNGTTIVLWK **WNKGDNQR**WR
301 ITPHCKSLN

Spot No.: **D49**

NCBI accession No.: **gi|356522666** Species: *Glycine max*

PFF score: [206]

Protein name: ubiquitin carboxyl-terminal hydrolase 6-like

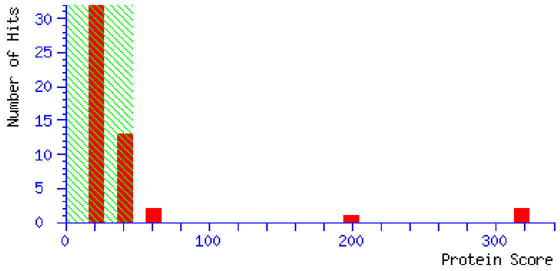
Matched peptides No.: [3] Sequence coverage %: [7]

Matched sequences: R.YLTVQFVR.F;
K.CQLYDLTGVPPER.Q;
K.CHISQEVNHLHEGIK.H

Calculated Mr: **54602** Calculated *p*I: **5.78**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



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

1 MITVSVRWQK EIFKDVELDT TQSPYVFK**CQ** **LYDLTGVPPE** **R**QKIMVKGGL
51 LKDDADWSTV GVKEGQKLMM MGTADEVVKT PEKGTVFVED LPEEEQVVAV
101 GHTAGLFNLG NTCYMNSTLQ CLHSVPELKS ALTNYSHSGR NNDVDQSSHL
151 LTIATRDLFS ELDKSVKPVA PMQFWMVLRK KYPQFGQLHN GVFMQQDAEE
201 CWTQLLYTLS QSLRSPGSSE NPDAVKALFG IELISRIHCQ ESKEESSEAE
251 SVYSLK**CHIS** **QEVNHLHEGI** **K**HGLKSELEK ASLVLGRSAI HLKESRINAL
301 PR**YLTVQFVR** FFWKRESNQK AKILRKVDYP LELDVYDFCS DELRKKLEAP
351 RQILRNEEGK KLGLKVNEKS SVQKENDVKM SDAEGATSGG GEPSVVPMEE
401 GEKETQMTGI YDLVAVLTHK GRSADSGHYV GWVKQENGKW IEFDDDNPKP
451 KLEEDITRLS GGGDWHMAYI IMYKARVVSV

Spot No.: **D50**

NCBI accession No.: **gi|224099853**

Species: *Populus trichocarpa* PFF score: [120]

Protein name: conserved hypothetical protein

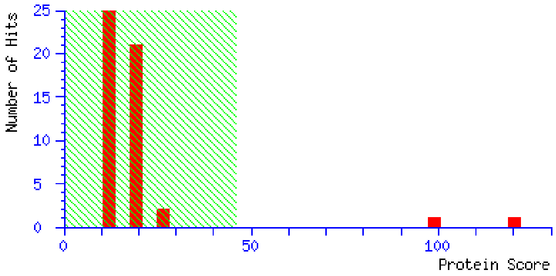
Matched peptides No.: [2] Sequence coverage %: [9]

Matched sequences: K.GCFFTTSGGLR.S;
R.SFEHPLNELKPVPR.V

Calculated Mr: **27448** Calculated *p*I: **5.84**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MLAVFDNTVA KCPDALQSPH SAPASSALKD GFLANHFASQ HPGSVTVNLG
51 TSGLISHSVE KQNPFLPRLF AVVDDIFCLF QGHIDNVAVL KQQYGLNKTA
101 NEVIVVIEAY RTLRDRGPYP ADQVVKDIQG KFAFILYDST SKATFFAADA
151 DGSVPFFWGA DSEGNLVLSD DVQIVQKGCG KSFAPFPK**GC** **FFTTSGGLRS**
201 **FEHPLNELKP** **VPR**VDSSGQV CGATFKVDAE TKKESVGMPR VDSSYNWSSN
251 Y

Spot No.: **D51**

NCBI accession No.: **gi|255568794**

Species: *Ricinus communis*

Protein name: nucleoredoxin, putative PFF score: [380]

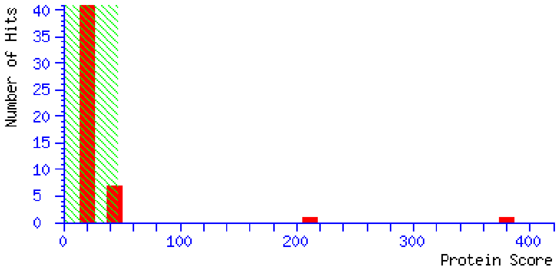
Matched peptides No.: [6] Sequence coverage %: [9]

Matched sequences: K.LIEAYHEIK.A;K.KCDFDLHPK.C;
K.LVELAEIEKAR.L;K.NQTLSSILVSSSR.D;
K.KNQTLSSILVSSSR.D;R.VEYFRQEEENAK.K

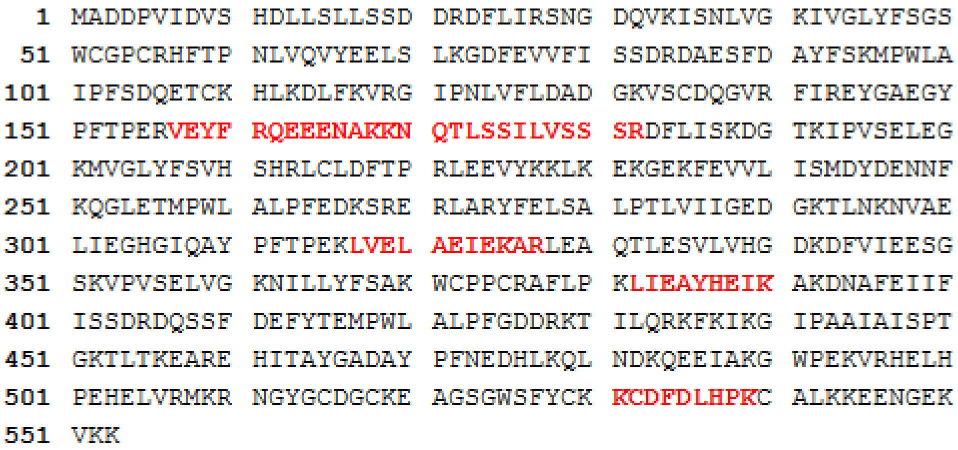
Calculated Mr: **63728** Calculated *p*I: **5.46**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:



```
  1 MADDPVIDVS HDLLSLLSSD DRDFLIRSNG DQVKISNLVG KIVGLYFSGS
 51 WCGPCRHFTP NLVQVYEELS LKGDFEVVFI SSDRDAESFD AYFSKMPWLA
101 IPFSDQETCK HLKDLFKVRG IPNLVFLDAD GKVSCDQGVR FIREYGAEGY
151 PFTPERVEYF RQEEENAKKN QTLSSILVSS SRDFLISKDG TKIPVSELEG
201 KMVGLYFSVH SHRLCLDFTP RLEEVYKKLK EKGEKFEVVL ISMDYDENNF
251 KQGLETMPWL ALPFEDKSRE RLARYFELSA LPTLVIIGED GKTLNKNVAE
301 LIEGHGIQAY PFTPEKLVEL AEIEKARLEA QTLESVLVHG DKDFVIEESG
351 SKVPVSELVG KNILLYFSAK WCPPCRAFLP KLIEAYHEIK AKDNAFEIIF
401 ISSDRDQSSF DEFYTEMPWL ALPFGDDRKT ILQRKFKIKG IPAAIAISPT
451 GKTLTKEARE HITAYGADAY PFNEDHLKQL NDKQEEIAKG WPEKVRHELH
501 PEHELVRMKR NGYGCDGCKE AGSGWSFYCK KCDFDLHPKC ALKKEENGEK
551 VKK
```

Spot No.: **D52**

NCBI accession No.: **gi|14423933** Species: *Hevea brasiliensis*

Protein name: Small rubber particle protein PFF score: [137]

Matched peptides No.: [2] Sequence coverage %: [16]

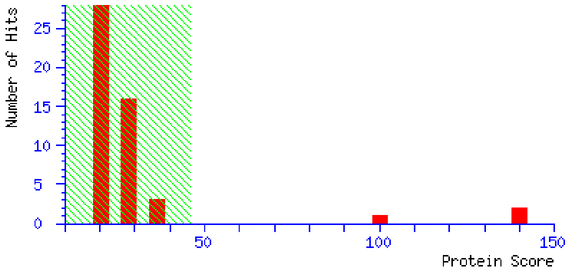
Matched sequences: K.QVSAQTYSVAQDAPR.I;

K.DISGPLKPGVDTIENVVK.T

Calculated Mr: **22331** Calculated *p*I: **4.80**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

```
  1 MAEEVEEERL KYLDFVRAAG VYAVDSFSTL YLYAKDISGP LKPGVDTIEN
 51 VVKTVVTPVY YIPLEAVKFV DKTVDVSVTS LDGVVPPVIK QVSAQTYSVA
101 QDAPRIVLDV ASSVFNTGVQ EGAKALYANL EPKAEQYAVI TWRALNKLPL
151 VPQVANVVVP TAVYFSEKYN DVVRGTTEQG YRVSSYLPLL PTEKITKVFG
201 DEAS
```

Spot No.: **D53**

NCBI accession No.: **gi|333690873** Species: *Hevea brasiliensis*

PFF score: [132]

Protein name: Small rubber particle protein

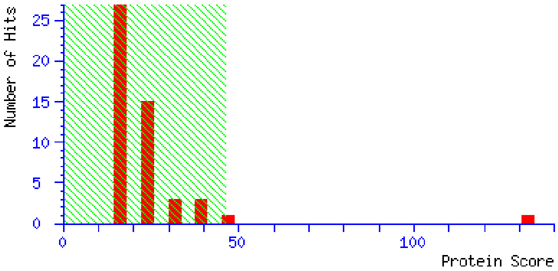
Matched peptides No.: [4] Sequence coverage %: [18]

Matched sequences: R.FWADFIDKK.I;
K.YEYREEDLR.N;
K.SPFLPSDPYQR.A;
K.SPLLLQMNPVHK.K + Oxidation (M)

Calculated Mr: **25595** Calculated *p*I: **5.48**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEEVILLDF WPSPFGMRVR IALAEKGVK**Y** **EYREEDLR**NK **SPLLLQMNPV**
51 **HK**KIPVLIHN GKPICESLIA VQYVDEVWKD K**SPFLPSDPY** **QR**AQAR**FWAD**
101 **FIDKK**IYDIG RKIWTTKGDE QEAAKKEFIE ALKLLEGELG NKPYFGGESM
151 GYVDVALIPF YSWFYAYETC GNFSIEPECP VLIAWAKRCL QKESVSESVP
201 DPEKVYEFVL VLKKKFGIE

Spot No.: **D54**

NCBI accession No.: **gi|356543702** Species: *Glycine max*

PFF score: [105]

Protein name: PREDICTED: (+)-pulegone reductase-like

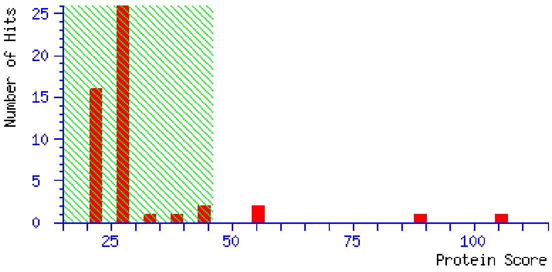
Matched peptides No.: [1] Sequence coverage %: [4]

Matched sequences: K.YFPDGIDVYLDNVGGK.M

Calculated Mr: **38361** Calculated *p*I: **5.71**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

```
  1 MGSVVESREW YLAAYSPHGV PNSDNLKLRT VALSLSSDSI PDGHVSLQIL
 51 FLSVDPYLRT RLTGTLDGLY IQQYPLNEVI TAYGVGRVIG SKDSKYTEGD
101 LILTPSAPVA EYCILPSSRV IRKIDAASGI SLPDYLSALG VPGFAAWVGI
151 VVLGDPKPGS NVFISAASGA VGMSAGQLAK IRGCRVIGST GSDEKVKLIK
201 EEFGYDDGFN YNKESDFDAA LSKYFPDGID VYLDNVGGKM LESVLNHVNK
251 YARIPLCGMI SQYNKVWTER EGVRNLLNMV GKEVRMEGFM LESYWHRFED
301 FAKEMEGYIK EGKVTSKNKI NIGIESFLDS LASLFSSSNI GKVVVQVNKA
```

Spot No.: **D55**

NCBI accession No.: **gi|351721881** Species: *Glycine max*

PFF score: [56]

Protein name: 18.5 kDa class I heat shock protein

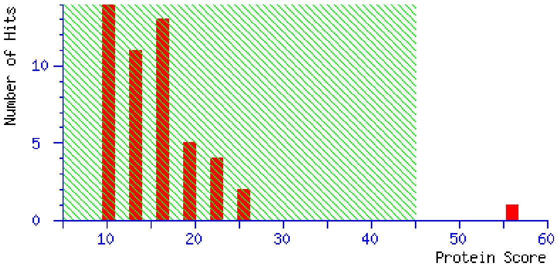
Matched peptides No.: [3] Sequence coverage %: [16]

Matched sequences: R.ENSAFVSTR.V;
K.ETPEAHVFK.A;
K.EDKNDTWHR.V

Calculated Mr: **18491** Calculated *p*I: **5.82**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MSLIPNFFGG RRNNVFDPFS LDVWDPFKDF PFPNTLSSAS FPEFSR**ENSA**
51 **FVSTR**VDWK**E** **TPEAHVFK**AD IPGLKKEEVK VQIEDDKVLQ ISGERNVEK**E**
101 **DKNDTWHR**VE RSSGKFMRRF RLPENAKVEQ VKASMENGVL TVTVPKEEVK
151 KPDVKAIEIS G

Spot No.: **D56**

NCBI accession No.: **gi|462406561** Species: *Prunus persica*

PFF score: [96]

Protein name: hypothetical protein PRUPE_ppa020028mg, partial

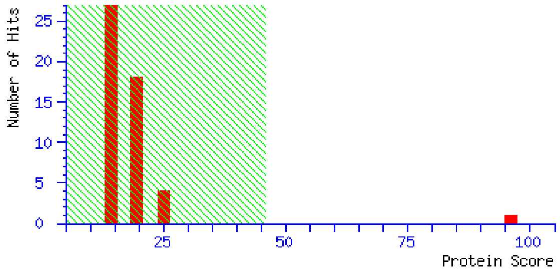
Matched peptides No.: [2] Sequence coverage %: [5]

Matched sequences: R.VDYQGYIFPR.R;
K.QEQAAFIEEISR.T

Calculated Mr: **48394** Calculated *p*I: **5.02**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MEGLIKGLID VALGHDENRN EDPGPRDRQE QSRSTWAQVV SGEEQDENDS
51 DRPHGSKQSH WNRQEQSHLG RAEWDNVDSE PSRRPHKAAH EGYERNDDGG
101 RHGYNQNYSR RKDEEENKDG WETVGKRPPR QQPHKIQMGQ WNGYKRPSTE
151 QEYSDEAEVG AKIEPSEEEL SDLSQACSKI WELDLNRLVP GKDYEIDCGG
201 GKKVYQKEDL AEGSLFTWLS EDIFRRPTFS RFCSLLDNYN PNEGCKEVIT
251 SEEK**QEQAAF** **IEEISR**TAPI KYLHKYLSRK GILSESYQDF KRTLTTLWFD
301 LYGRGGASAS SSAFEHVFVG EIKQRGEEEV SGFHNWLQFY LEEAKGR**VDY**
351 **QGYIFPR**RRG QTPDSETQLL TIQFEWNGVL KAVSSTLVGV SPEFEIALYT
401 LCFFMGGEDN HIELGPYQ

Spot No.: **D57**

NCBI accession No.: **gi|255570177** Species: *Ricinus communis*

PFF score: [56]

Protein name: proteasome subunit beta type 7,10, putative

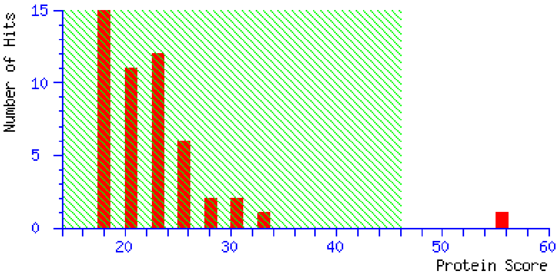
Matched peptides No.: [1] Sequence coverage %: [3]

Matched sequences: R.EGLNRDEGIK.L

Calculated Mr: **30600** Calculated *p*I: **7.60**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MSKSAIDVPP KGGFSFDLCK RNEMLAKKGV NLPSSYRKTG TTIVGLIFQD
51 GVILGADTRA TEGPIVCDKN CEKIHYMAPN IYCCGAGTAA DTEAVTDMVS
101 SQLQLHRYHT GRESRVITAL TLLKKHLFNY QGYVQAALVL GGVDCTGPHL
151 HTIYPHGSTD TLPFATMGSG SLAAMAIFES KYR**EGLNRDE** **GIK**LVTEAIC
201 SGVFNDLGSG SNVDVCVITK GHKEYLRNHL LPNPRTYINP KGYVFSKKTE
251 VLLTKITPLK EPSKEKEGVS EGGEAMEE

Spot No.: **D58**

NCBI accession No.: **gi|3834310** Species: *Arabidopsis thaliana*

PFF score: [197]

Protein name: Similar to Ubiquitin-conjugating enzyme E2-17 KD gb|D83004 from Homo sapiens

Matched peptides No.: [3] Sequence coverage %: [24]

Matched sequences: K.DKWSPALQIR.T;

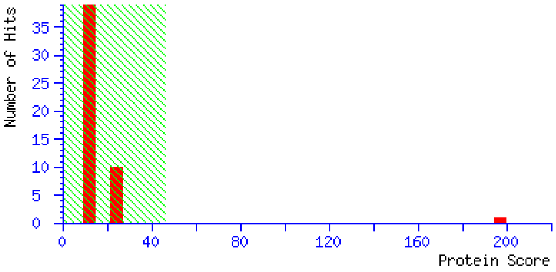
K.IYHPNIDKLGR.I;

R.LLSEPAPGISASPSEDNMR.Y + Oxidation (M)

Calculated Mr: **18339** Calculated *p*I: **5.93**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MANSNLPRRI IKETQR**LLSE** **PAPGISASPS** **EDNMR**YFNVM ILGPTQSPYE
51 GGVFKLELFL PEEYPMAAPK VRFLTK**IYHP** **NIDKLGR**ICL DILK**DKWSPA**
101 **LQIR**TVLLRS IQALLSAPNP DDPLSENIAK HWKSNEAEAV DTGDLRNGPV
151 FMQAAHDKLE GEN

Spot No.: **D59**

NCBI accession No.: **gi|315937232** Species: *Jatropha curcas*

PFF score: [256]

Protein name: ubiquitin-conjugating family protein

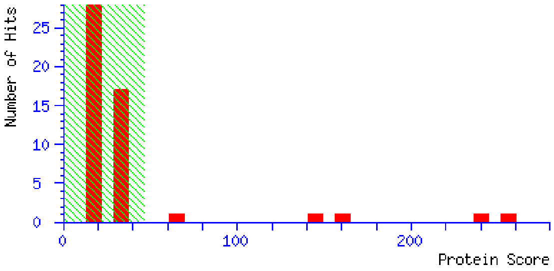
Matched peptides No.: [6] Sequence coverage %: [48]

Matched sequences: K.KEMAAPHNR.K + Oxidation (M);
K.FGLLANWQR.E;
M.TLGSGGSSVVVPR.N;
R.KLVQPPEGTYF.-;
R.EYTMEDILTQLK.K + Oxidation (M);
R.SWTGTIIGPHNTVHEGR.I

Calculated Mr: **16706** Calculated *p*I: **6.20**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 M**TLGSGGSSV** **VVPR**NFRLLE ELERGEKGIG DGTVSYGMDD GDDIYMR**SWT**
51 **GTIIGPHNTV** **HEGR**IYQLKL FCDKDYPEKP PSVRFHSRIN MTCVNHETGV
101 VEPKK**FGLLA** **NWQREYTMED** **ILTQLKKEMA** **APHNRKLVQP** **PEGTYF**

Spot No.: **D60**

NCBI accession No.: **gi|226531470**   Species: *Zea mays*

PFF score: [271]

Protein name: vacuolar ATP synthase subunit B

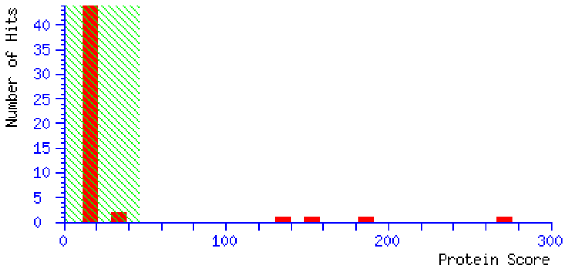
Matched peptides No.: [8]   Sequence coverage %: [20]

Matched sequences: K.YQEIVNIR.L;
K.TLDQYYSR.D;
K.FVTQGAYDTR.N;
R.RGQVLEVDGEK.A;
R.QIYPPINVLPSLSR.L;
R.VTLFLNLANDPTIER.I;
R.GYPGYMYTDLATIYER.A + Oxidation (M);
K.IPLFSAAGLPHNEIAAQICR.Q

Calculated Mr: **54142**   Calculated *p*I: **5.07**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MGLVKEGVDM EEGTLEIGME YRTVSGVAGP LVILDKVKGP K**YQEIVNIR**L
51 GDGTTR**RGQV** **LEVDGEK**AVV QVFEGTSGID NKYTTVQFTG EVLKTPVSLD
101 MLGRIFNGSG KPIDNGPPIL PEAYLDISGS SINPSERTYP EEMIQTGIST
151 IDVMNSIARG QK**IPLFSAAG** **LPHNEIAAQI** **CR**QAGLVKTL EKGKHAEGGE
201 DDNFAIVFAA MGVNMETAQF FKRDFEENGS MER**VTLFLNL** **ANDPTIER**II
251 TPRIALTTAE YLAYECGKHV LVILTDMSSY ADALREVSAA REEVPGRR**GY**
301 **PGYMYTDLAT** **IYER**AGRIEG RTGSITQIPI LTMPNDDITH PTPDLTGYIT
351 EGQIYIDRQL HNR**QIYPPIN** **VLPSLSR**LMK SAIGEGMTRR DHSDVSNQLY
401 ANYAIGKDVQ AMKAVVGEEA LSSEDLLYLE FLDKFERK**FV** **TQGAYDTR**NI
451 FQSLDLAWTL LRIFPRELLH RIPAK**TLDQY** **YSR**DASH

Spot No.: **D61**

NCBI accession No.: **gi|2832430** Species: *Hevea brasiliensis*

PFF score: [175] Protein name: prohevein

Matched peptides No.: [3] Sequence coverage %: [22]

Matched sequences: K.CLSVTNTGTGAK.A;

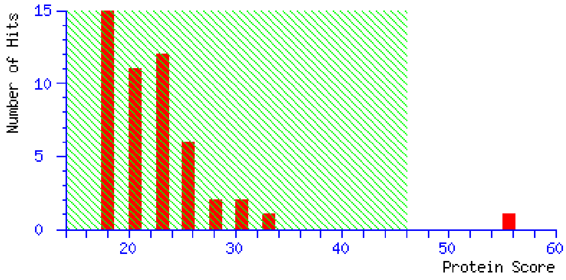
R.QLDTDGKGYER.G;

K.YGWTAFCGPVGAHGQPSCGK.C

Calculated Mr: **20852** Calculated *p*I: **5.64**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

1 MSKSAIDVPP KGGFSFDLCK RNEMLAKKGV NLPSSYRKTG TTIVGLIFQD

51 GVILGADTRA TEGPIVCDKN CEKIHYMAPN IYCCGAGTAA DTEAVTDMVS

101 SQLQLHRYHT GRESRVITAL TLLKKHLFNY QGYVQAALVL GGVDCTGPHL

151 HTIYPHGSTD TLPFATMGSG SLAAMAIFES KYR**EGLNRDE** **GIK**LVTEAIC

201 SGVFNDLGSG SNVDVCVITK GHKEYLRNHL LPNPRTYINP KGYVFSKKTE

251 VLLTKITPLK EPSKEKEGVS EGGEAMEE

Spot No.: **D62**

NCBI accession No.: **gi|114199044** Species: *Malus x domestica*

PFF score: [195]

Protein name: caffeic acid O-methyltransferase

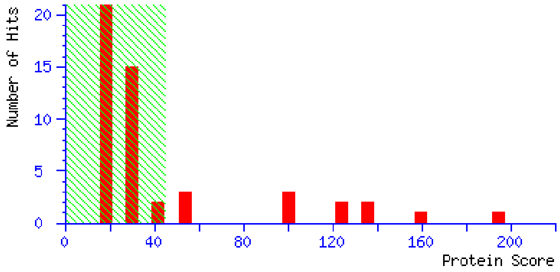
Matched peptides No.: [4] Sequence coverage %: [12]

Matched sequences: R.TLPDGKVER.L;
R.TEKEFEALAK.G;
R.VLASYSILTYSLR.T;
K.AYGMTAFEYHGTDPR.F + Oxidation (M)

Calculated Mr: **40047** Calculated *p*I: **5.54**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MGSTPETQMT PTQVSDEEAN LFAMQLASAS VLPMVLKAAI ELDLLEIMAK
51 AGPGAFVSPA DLSSQLPTKN PDAPVMLDRM LR**VLASYSIL** **TYSLRTLPDG**
101 **KVER**LYGLGP VCKFLTKSVD GASIGSLCLM NQDKVLMESW YNLKDAVLEG
151 GIPFNK**AYGM** **TAFEYHGTDP** **R**FNRVFNKGM ADHSTITMKK LLENYNGFEG
201 LTSIVDVGGG TGAVLNMIVS KYPSIKGINF DLPHVIEDAP QYPGVEHVGG
251 DMFVSVPKGD AIFMKWICHD WSDEHCLKFL KNCYAALPDN GKVIVAECIL
301 PVAPDSSLAT KGVVHIDAIM LAHNPGGKER **TEKEFEALAK** GSGFQGFRVV
351 CSAFNTYAIE FLKKN

Spot No.: **D63**

NCBI accession No.: **gi|255538084** Species: *Ricinus communis*

PFF score: [77]

Protein name: Adenine phosphoribosyltransferase, putative

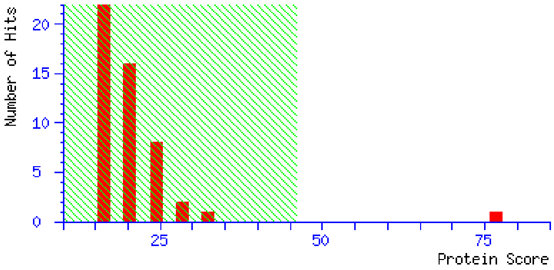
Matched peptides No.: [1] Sequence coverage %: [7]

Matched sequences: R.ALVIDDLIATGGTLCAAIR.L

Calculated Mr: **27683** Calculated *p*I: **8.33**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MLKSIHLRAP NSILPSRQLS PPSPNKQLSA RIVIAAPSTG QQAPSISLRN
51 YPPARPSLRC SAGGSDSQNQ KMAAQDDKDN RIERISSSIR VIPDFPKPGI
101 LFQDITTLLL DTKAFKDTID LFVERYKERD ISVVAGIEAR GFIFGPPIAL
151 AIGAKFVPMR KPNKLPGEVV SEEYSLEYGT DKMEMHVGAV QAGER**ALVID**
201 **DLIATGGTLC** **AAIR**LLERVG VEVVECACVI ELPELKGRER LGQTPLFVLV
251 SSA

Spot No.: **D64**

NCBI accession No.: **gi|255546213** Species: *Ricinus communis*

PFF score: [94]

Protein name: o-methyltransferase, putative

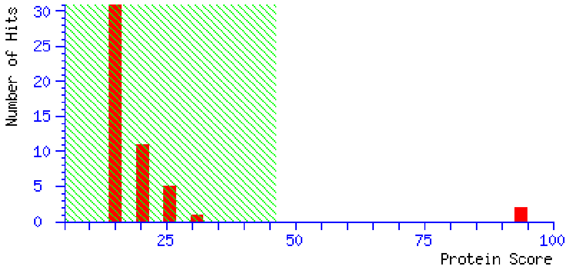
Matched peptides No.: [1] Sequence coverage %: [7]

Matched sequences: R.VQISHASLGDGITICR.R

Calculated Mr: **25951** Calculated *p*I: **5.55**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MQKGLLKSEE LYQYVLETSV FPREPEPLRE LRNITANHPW AKMATSPDAG
51 QFMAMLLQLV NAKKTIEVGV FTGYSLLLTA LSIPEDGKIV AIDVDREAYE
101 IGLPIIRKAG VEHKIDFMES EALPVLDKLL KEHGNESSFD FAFVDADKIN
151 YWNYHERLLK LVKVGGIVIY DNSLWRGSVA VPEEEAPEHL RFCRQLTIEH
201 NKFLAADSR**V** **QISHASLGDG** **ITICR**RIC

Spot No.: **D65 (S3)**

NCBI accession No.: **gi|132270** Species: *Hevea brasiliensis*

Protein name：Rubber elongation factor protein; Short=REF;

AltName: Allergen=Hev b 1

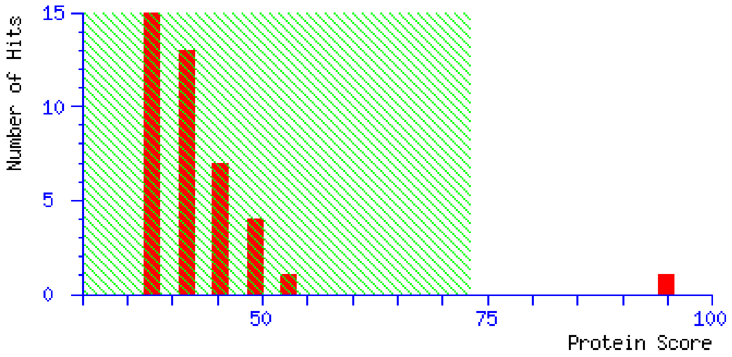
Mascot score: **95** Sequence coverage %: **56**

Matched peptides No.: **8** Total peptides No.: **42**

Calculated Mr: **14713** Calculated *p*I: **5.04**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK **DKSGPLQPGV**
51 **DIIEGPVKNV** **AVPLYNR**FSY IPNGALK**FVD** **STVVASVTII** **DRSLPPIVKD**
101 **ASIQVVSAIR** **AAPEAARSLA** **SSLPGQTK**IL AKVFYGEN

Spot No.: **D66 (S5)**

NCBI accession No.: **gi|14423933** Species: *Hevea brasiliensis*

Protein name：Small rubber particle protein; Short=SRPP; AltName: Full=22 kDa rubber particle protein; Short=22 kDa RPP; AltName: Full=27 kDa natural rubber allergen; AltName: Full=Latex allergen Hev b 3

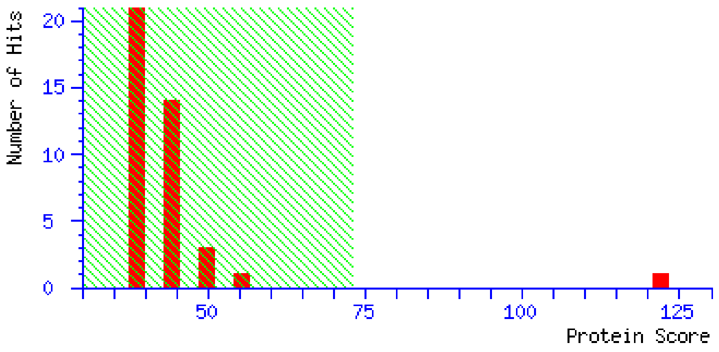
Mascot score: **122** Sequence coverage %: **85**

Matched peptides No.: **13** Total peptides No.: **55**

Calculated Mr: **22331** Calculated *p*I: **4.80**

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red:

1 MAEEVEEERL K**YLDFVRAAG VYAVDSFSTL YLYAKDISGP LKPGVDTIEN**
51 **VVKTVVTPVY YIPLEAVK**FV DK**TVDVSVTS LDGVVPPVIK QVSAQTYSVA**
101 **QDAPRIVLDV ASSVFNTGVQ EGAKALYANL EPKAEQYAVI TWR**ALNK**LPL**
151 **VPQVANVVVP TAVYFSEKYN DVVRGTTEQG YRVSSYLPLL PTEK**ITKVFG
201 DEAS

Spot No.: **D67 (S6)**

NCBI accession No.: **gi|14423933** Species: *Hevea brasiliensis*

Protein name：Small rubber particle protein; Short=SRPP; AltName: Full=22 kDa rubber particle protein; Short=22 kDa RPP; AltName: Full=27 kDa natural rubber allergen; AltName: Full=Latex allergen Hev b 3

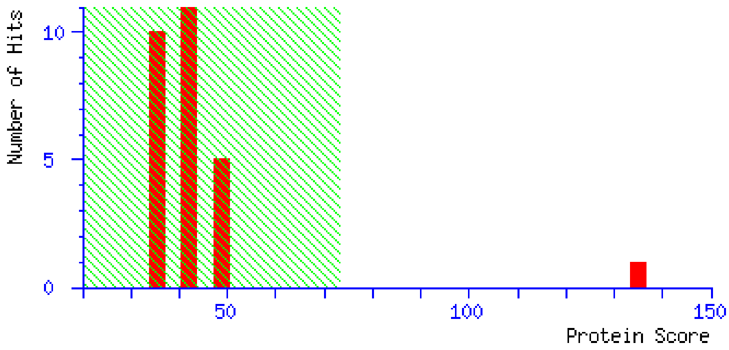
Mascot score: **135** Sequence coverage %: **75**

Matched peptides No.: **12** Total peptides No.: **31**

Calculated Mr: **22331** Calculated *p*I: **4.80**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

```
  1 MAEEVEEERL KYLDFVRAAG VYAVDSFSTL YLYAKDISGP LKPGVDTIEN
 51 VVKTVVTPVY YIPLEAVKFV DKTVDVSVTS LDGVVPPVIK QVSAQTYSVA
101 QDAPRIVLDV ASSVFNTGVQ EGAKALYANL EPKAEQYAVI TWRALNKLPL
151 VPQVANVVVP TAVYFSEKYN DVVRGTTEQG YRVSSYLPLL PTEKITKVFG
201 DEAS
```

Spot No.: **D68 (S9)**

NCBI accession No.: **gi|388503664** Species: *Lotus japonicus*

Protein name： **unknown**

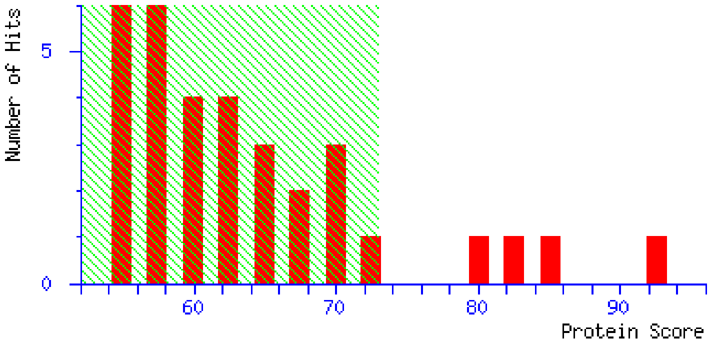
Mascot score: **93** Sequence coverage %: **45**

Matched peptides No.: **13** Total peptides No.: **48**

Calculated Mr: **29537** Calculated *p*I: **4.79**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MASSK**DRGTF** **VYVAKLAEQA** **ER**YEEMVDSM KKVANLDVEL TVEER**NLLSV**
51 **GYKNVIGAR**R ASWR**ILSSIE** **QK**EETKGNDV NAKR**IKEYR**Q KVESELADIC
101 NDVMRVIDEH LIPSATAGES TVFYYKMK**GD** **YYRYLAEFK**S GNEK**KEAADQ**
151 **SMKAYESATT** **AAEAELPPTH** **PIRLGLALNF** **SVFYYEILNS** **PERACHLAK**Q
201 AFDEAISELD TLNEESYK**DS** **TLIMQLLR**DN LTLWTSDIPE EGEDSLKAND
251 TAKVGGGEDA E

Spot No.: Spot No.: **D69 (S13)**

NCBI accession No.: **gi|4235430** Species: *Hevea brasiliensis*

Protein name: **latex-abundant protein**

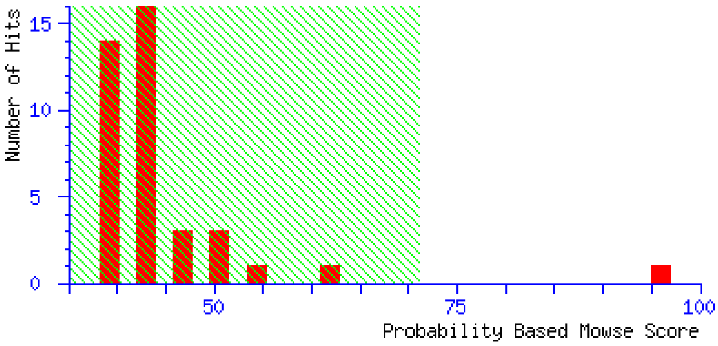
Mascot score: **96** Sequence coverage %: **54**

Matched peptides No.: **15** Total peptides No.: **37**

Calculated Mr: **46443** Calculated *p*I: **5.01**

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red:

1 MAKKAVLIGI NYPGTKAELK GCINDVKRMY RCLVDR**YGFS** **EEDITVLIDI**
51 **DESYIQPTGK** NIR**RVLTDLV** **RSAEPGDLLF** **VHYSGHGTRL** **PAETGEDDDT**
101 **GFDECIVPCD** **MNLITDDDFR** **EFVDQVPHGC** **RITVVSDSCH** **SGGLIDEAK**E
151 QIGESTKRKE EESESGFGFK SFLK**QTIQDA** **FESRGVHLPS** **DLHHHHGHRD**
201 **EEDFDNRVVE** **EDYGDSGYVK** SK**SLPLSTLI** **EILK**QKTGKD DIDVGK**LRPT**
251 **LFDMFGDDAS** **PK**VKKFMKVI LNKLRHGDGE SGGGGFLGMV GSLAQEFLK**H**
301 **KLDENDESYV** **KPALETEVDS** **K**QEVYAGKTK RSLPDGGILI SGCQTDQTSA
351 DASPSGKSSE AYGALSNAIQ TIIAETDGAV TNQELVLKAR KMLK**KQGFTQ**
401 **KPGLYCSDDH** **VEASFVC**

Spot No.: **D70 (S20)**

NCBI accession No.: **gi|30575570** Species: *Citrus x paradisi*

PFF score: **[86]** Protein name：HSP19 class II, partial

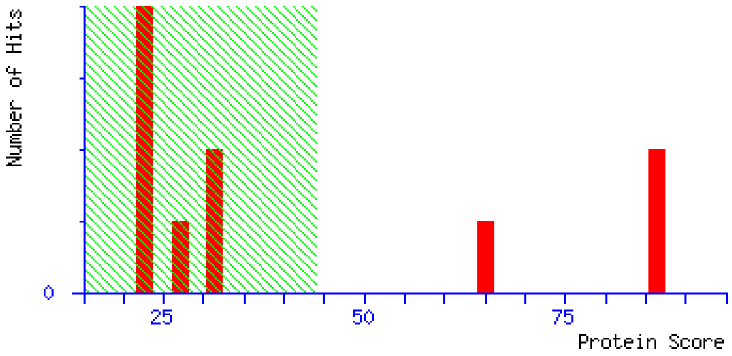
Matched peptides No.: [1] Sequence coverage %: [15]

Matched sequences: K.VQVEDDNVLLISGER.K;

Calculated Mr: **11191** Calculated *p*I: **8.01**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red：

1 YVFIVDMPGL KSGDIK**VQVE** **DDNVLLISGE** **R**KREEEKDGA KYVRMERRVG
51 KFMRKFVLPE NANVEAISAV CQDGVLTVTV DKLPPPEPKK PKTIEVKIA

Spot No.: **D71 (S22)**

NCBI accession No.: **gi|37806305**

Species: *Oryza sativa Japonica Group*

PFF score: **[60]** Protein name：hypothetical protein

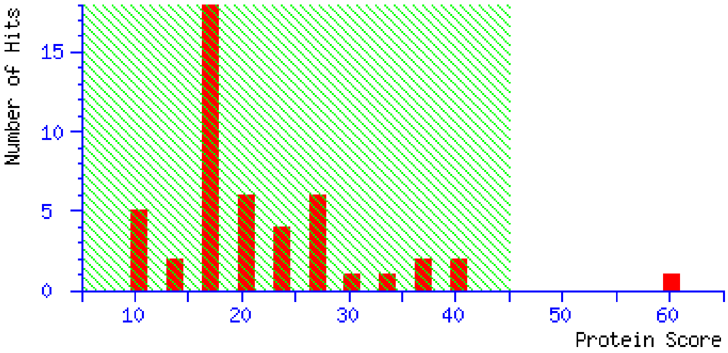
Matched peptides No.: [2] Sequence coverage %: [3]

Matched sequences: K.LGTLVLGDRPR.L ; K.LGTLVLGDRPR.L

Calculated Mr: **35105** Calculated *p*I: **8.29**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red：

```
  1 MEVFQGVQFA RLRNWWEETY VTADEDGRSV YHYAPDRHRP AHEAIWAVQM
 51 VLAGAPPTQY VLLRGAYGRY LGAPDAVVRR WPLSCCWPAP VVGQRDFDQP
101 EVDAIMWRAV RRADHVLCLH DKSGRYLRGK LGTLVLGDRP RLTVGDGRLN
151 DDEKALRWEV LPVLPNPGRP ELPISIVPEA DLVGRLVKAC FLPLQREIQF
201 VEADDDGNIG EGQEVWDSFQ YEGRSVQLLR NELEDRVGYA ITVCVRAGRH
251 GQHSPLLINL PHSRETLHIV VLRRNSEADN QLTFPDPKAS SRRRYRHRRR
301 AIIQ
```

Spot No.: **D72 (S26)**

NCBI accession No.: **gi|3451147** Species: *Hevea brasiliensis*

PFF score: [56] Protein name： chitinase

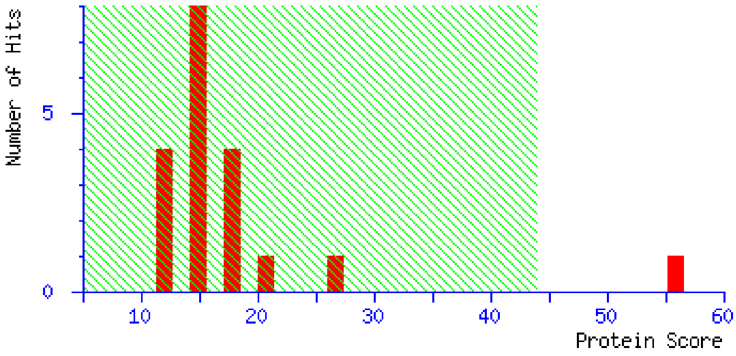
Matched peptides No.: [1] Sequence coverage %: [4]

Matched sequences: K.VYLTAAPQCPFPDR.Y

Calculated Mr: **34138** Calculated *p*I: **8.72**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red：

1 MAKRTQAILL LLLAISLIMS SSHVDGGGIA IYWGQNGNEG TLTQTCSTRK
51 YSYVNIAFLN KFGNGQTPQI NLAGHCNPAA GGCTIVSNGI RSCQIQGIKV
101 MLSLGGGIGS YTLASQADAK NVADYLWNNF LGGKSSSRPL GDAVLDGIDF
151 DIEHGSTLYW DDLARYLSAY SKQGKK**VYLT** **AAPQCPFPDR** YLGTALNTGL
201 FDYVWVQFYN NPPCQYSSGN INNIINSWNR WTTSINAGKI FLGLPAAPEA
251 AGSGYVPPDV LISRILPEIK KSPKYGGVML WSKFYDDKNG YSSSIRDSVL
301 FLHSEKCMTV L

Spot No.: **D73 (S30)**

NCBI accession No.: **gi|255540341** Species: *Ricinus communis*

Protein name: **glyceraldehyde 3-phosphate dehydrogenase, putative**

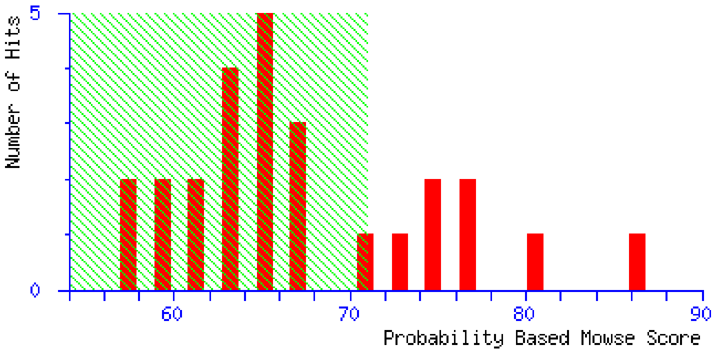
Mascot score: **86** Sequence coverage %:**42**

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

Calculated Mr: **36930** Calculated *p*I: **7.10**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MAKIK**IGING** **FGR**IGRLVAR **VALQR**DDVEL VAVNDPFIST EYMTYMFK**YD**
51 **TVHGQWK**HHE LKIKDDKTLL FGEKPVTVFG VR**NPEEIPWA** **ETGAEYIVES**
101 **TGVFTDKDK**A AAHLKGGAKK VIISAPSK**DA** **PMFVVGVNEK** EYTPDLHIIS
151 NASCTTNCLA PLAKVINDRF GIVEGLMTTV HSITATQK**TV** **DGPSMK**DWRG
201 GR**AASFNIIP** **SSTGAAKAVG** **K**VLPSLNGK**L** **TGMSFRVPTV** **DVSVVDLTVR**
251 LEKSATYEQI KAAIK**EESEG** **KLK**GILGYTE DDVVSTDFIG DKRSSIFDAK
301 **AGIALNDKFV** **KLVSWYDNEW** **GYSTR**VVDLI VHVASVH

Spot No.: **D74 (S35)**

NCBI accession No.: **gi|3288200** Species: *Hevea brasiliensis*

PFF score: [81]

Protein name：**latex allergen**

Matched peptides No.: [2] Sequence coverage %: [4]

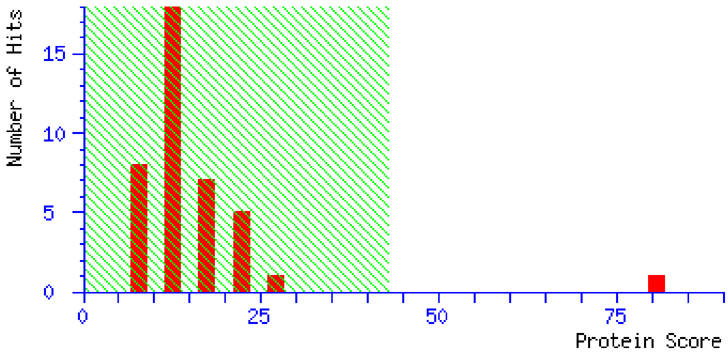
Matched sequences: R.DTYDPIHSIGPIYDGEYLR.E；

R.DTYDPIHSIGPIYDGEYLR.E

Calculated Mr: **43020** Calculated *p*I: **5.00**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 43 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MATGSTTLTQ GKKITVLSID GGGIRGIIPG IILASLESKL QDLDGPDARI
51 ADYFDIIAGT STGGLITTML TAPNEDKKPI YQAKDIKDFY LENCPKIFPK
101 ESR**DTYDPIH** **SIGPIYDGEY** **LR**ELCNNLLK DLTVKDTLTD VIIPAFDIKL
151 LLPVIFSSDD AKCNALKNAR LADVCISTSA APVLLPAHSF TTEDDKNIHT
201 FELIDGGVAA ANPTLLALTH IRNEIIRQNP RFIGANLTES KSRLVLSLGT
251 GKSEYKEKYN ADMTSKWRLY NWALYNGNSP AVDIFSNASS DMVDFHLSAL
301 FKSLDCEDYY LRIQDDTLTG EESSGHIATE ENLQRLVEIG TELLEKQESR
351 INLDTGRLES IPGAPTNEAA IAKFAKLLSE ERKLRQLK

Spot No.: **D75 (S36)**

NCBI accession No.: **gi|1916805** Species: *Hevea brasiliensis*

PFF score: [138]

Protein name: **latex patatin homolog**

Matched peptides No.: [2] Sequence coverage %: [8]

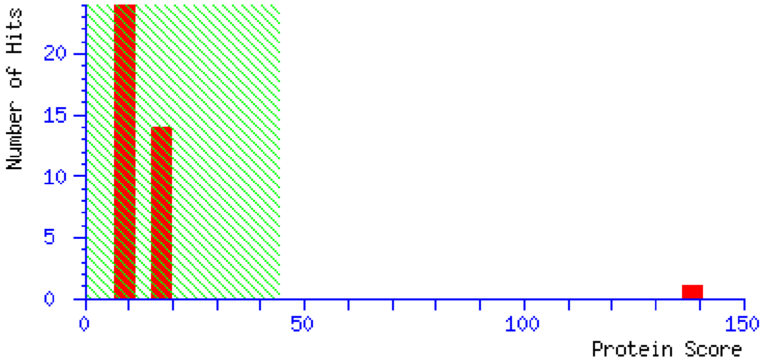
Matched sequences: K.SLDCEDYYLR.I;

R.IQDDTLTGEESSGHIATEENLQR.L

Calculated Mr: **43035** Calculated *p*I: **5.00**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MATGSTTLTQ GKKITVLSID GGGIRGIIPG IILASLESKL QDLDGPDARI
51 ADYFDIIAGT STGGLITTML TAPNEDKKPM YQAKDIKDFY LENCPKIFPK
101 ESRDNYDPIH SIGPIYDGEY LRELCNNLLK DLTVKDTSTD VIIPTFDIKL
151 LLPVIFPSDD AKCNALKNAR LADVCISTSA APVLLPAHSF TTEDDKNIHT
201 FELIDGGVAA TNPTLLALTH IRNEIIRQNP RFIGANLTES KSRLVLSLGT
251 GKSEYKEKYN ADMTSKWRLY NWALYNGNSP AVDIFSNASS DMVDSHLSAL
301 FK**SLDCEDYY** **LRIQDDTLTG** **EESSGHIATE** **ENLQR**LVEIG TELLEKQESR
351 INLDTGRLES IPGAPTNEAA IAKFAKLLSE ERKLRQLK

Spot No.: **D76 (S37)**

NCBI accession No.: **gi|41581137**   Species: *Hevea brasiliensis*

Protein name: **putative latex allergen hev b 7.02**

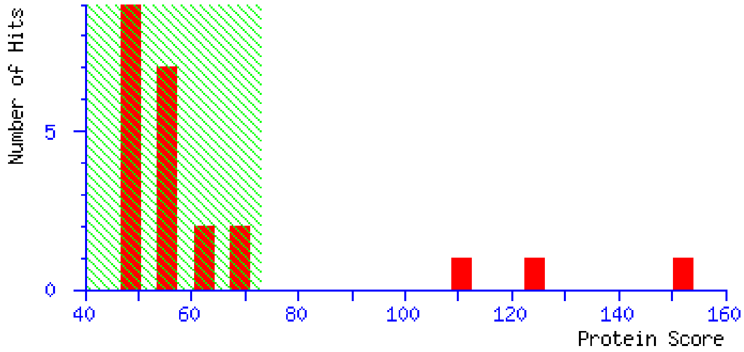
PMF score: **152**   Sequence coverage %: **44**

Matched peptides No.: **16**   Total peptides No.: **39**

Calculated Mr: **43027**   Calculated *p*I: **5.12**

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 73 are significant ($p<0.05$).



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

1 ATGSTTLTQG KK**ITVLSIDG** **GGIRGIIPGI** **ILASLESKLQ** **DLDGPDAR**IA

51 DYFDIIAGTS TGGLITTMLT APNEDK**KPMY** **QAK**DIK**DFYL** **ENCPK**IFPKE

101 SR**DNYDPIHS** **IGPIYDGEYL** **RELCNNLLK**D LTVK**DTLTDV** **IIPTFDIKLL**

151 **LPVIFSSDDA** **K**CNALKNARL ADVCISTSAA PVLLPAHSFT TEDDKNIHTF

201 ELIDGGVAAT NPTLLALTHI R**NEIIR**QNPR **FIGANLTESK** SRLVLSLGTG

251 KSEYKEKYNA DMTSKWRLYN WALYNGNSPA VDIFSNASSD MVDFHLSALF

301 K**SLDCEDYYL** **RIQDDTLTGE** **ESSGHIATEE** **NLQRLVEIGT** **R**LLEKQESR**I**

351 **NLDTGR**LESI PGASTNEAAI TKFAK**LLSEE** **R**KLRQLK

Spot No.: **D77 (S38)**

NCBI accession No.: **gi|41581137** Species: *Hevea brasiliensis*

Protein name： **putative latex allergen hev b 7.02**

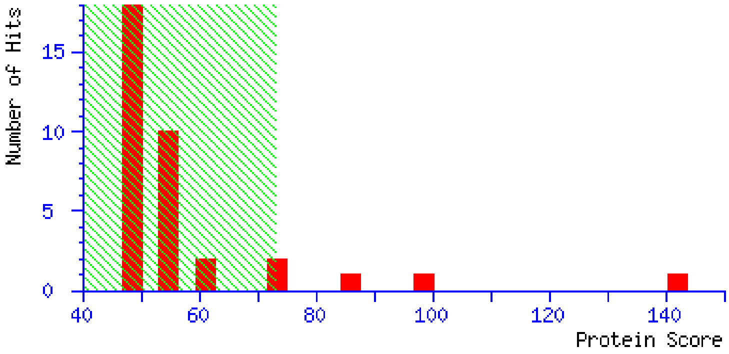
PMF score: **142** Sequence coverage %: **42**

Matched peptides No.: **15** Total peptides No.: **51**

Calculated Mr: **43027** Calculated *p*I: **5.12**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 ATGSTTLTQG KK**ITVLSIDG** **GGIRGIIPGI** **ILASLESKLQ** **DLDGPDARIA**
51 DYFDIIAGTS TGGLITTMLT APNEDKKPMY QAKDIK**DFYL** **ENCPK**IFPKE
101 SR**DNYDPIHS** **IGPIYDGEYL** **R**ELCNNLLK**D** **LTVKDTLTDV** **IIPTFDIKLL**
151 **LPVIFSSDDA** **K**CNALKNARL ADVCISTSAA PVLLPAHSFT TEDDKNIHTF
201 ELIDGGVAAT NPTLLALTHI R**NEIIR**QNPR **FIGANLTESK** SRLVLSLGTG
251 KSEYKEKYNA DMTSKWRLYN WALYNGNSPA VDIFSNASSD MVDFHLSALF
301 K**SLDCEDYYL** **RIQDDTLTGE** **ESSGHIATEE** **NLQRLVEIGT** **R**LLEKQESR**I**
351 **NLDTGR**LESI PGASTNEAAI TKFAK**LLSEE** **R**KLRQLK

Spot No.: **D78 (S46)**

NCBI accession No.: gi|4469175 Species: *Hevea brasiliensis*

Protein name： beta-1,3-glucanase

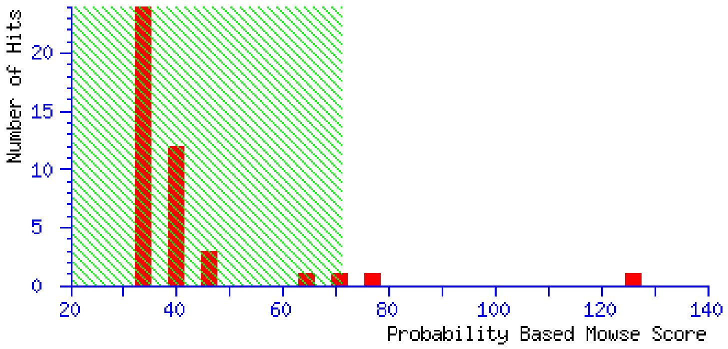
PMF score: **126** Sequence coverage %: **55**

Matched peptides No.: **19** Total peptides No.: **37**

Calculated Mr: **38930** Calculated *p*I: **9.45**

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 73 are significant ($p<0.05$).



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

1 **MAISSSTSGT** **SSSLPSR**TTV MLLLFFFAAS VGITDAQVGV CYGMQGNNLP
51 PVSEVIALYK KSNITRMR**IY** **DPNRAVLEAL** **R**GSNIELILG VPNSDLQSLT
101 NPSNAKSWVQ KNVR**GFWSSV** **LFRYIAVGNE** **ISPVNR**GTAW LAQFVLPAMR
151 **NIHDAIRSAG** **LQDQIKVSTA** **IDLTLVGNSY** **PPSAGAFRDD** **VRSYLNPIIR**
201 **FLSSIRSPLL** **ANIYPYFTYA** **GNPRDISLPY** **ALFTSPSVVV** **WDGQR**GYK**NL**
251 **FDATLDVLYS** **ALER**ASGGSL EVVVSESGWP SAGAFAATFD NGR**TYLSNLI**
301 **QHVK**R**GTPKR** **PNRAIETYLF** **AMFDENKK**QP EVEKQFGLFF PDKWQKYNLN
351 FG

Spot No.: **D79 (S54)**

NCBI accession No.: **gi|34538473** Species: *Hordeum vulgare*

Protein name： **caleosin 1**

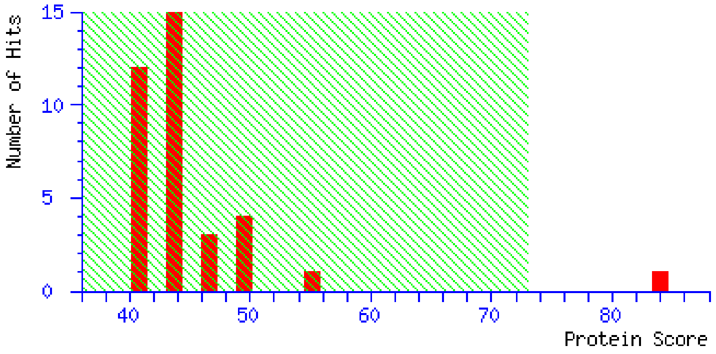
PMF score: **84** Sequence coverage %: **19**

Matched peptides No.: **10** Total peptides No.: **37**

Calculated Mr: **34330** Calculated *p*I: **6.11**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 **MATKAR**KVEV R**DASRAEGKG** **DAADVHVLRE** **AMRADGK**GDH DTAGGANRAD
51 GHGDAGGRVG DSRGVDGKDS LKMVALQAPV TVERPVRGDL EEHVPKPYLA
101 RALAAPDMYH PEGTTTDDHQ HHNMSVLQQH VAFFDRDNNG IIYPWETYDG
151 CRAVGFNVFM SAFIAFLVNL VMSYPTLPGW LPNPLFPIYV HNIHKSK**HGS**
201 **DSGTYDK**EGR FMPVNFENIF SKYARTYPDR LSYR**EMWR**MT EGCREVFDFF
251 GWVAMKLEWS ILYALARDDE GYLSR**EAIRR** MYDGSLFEYM ERQR**MEHVKM**
301 **S**

Spot No.: **D80 (S61)**

NCBI accession No.: **gi|255560725** Species: *Ricinus communis*

Protein name: dead box ATP-dependent RNA helicase, putative

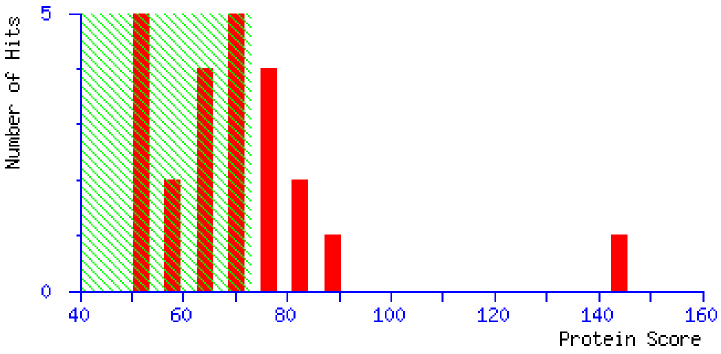
Mascot score: **144** Sequence coverage %: **68**

Matched peptides No.: **25** Total peptides No.: **91**

Calculated Mr: **47097** Calculated *p*I: **5.49**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

```
  1  MAGLAPEGSQ  FDAKQYDAKM  SELLSTEGQE  FFTTYDEVYD  SFDAMGLQEN
 51  LLRGIYAYGF  EKPSAIQQRG  IVPFCKGLDV  IQQAQSGTGK  TATFCSGILQ
101  QLDYGLVQCQ  ALVLAPTREL  AQQIEKVMRA  LGDYLGVKVH  ACVGGTSVRE
151  DQRILQAGVH  VVVGTPGRVF  DMLRRQSLRP  DYIKMFVLDE  ADEMLSRGFK
201  DQIYDIFQLL  PAKVQVGVFS  ATMPPEALEI  TRKFMNKPVR  ILVKRDELTL
251  EGIKQFYVNV  EKEEWKLETL  CDLYETLAIT  QSVIFVNTRR  KVDWLTDKMR
301  SRDHTVSATH  GDMDQNTRDI  IMREFRSGSS  RVLITTDLLA  RGIDVQQVSL
351  VINYDLPTQP  ENYLHRIGRG  GRFGRKGVAI  NFVTRDDERM  LFDIQKFYNV
401  VIEELPSNVA  DLL
```

Spot No.: **D81 (S63)**

NCBI accession No.: **gi|255578278** Species: *Ricinus communis*

PFF score: [76]

Protein name:hypothetical protein RCOM_0537780

Matched peptides No.: [3] Sequence coverage %: [6]

Matched sequences: K.QESEYGSGGYGR.R;

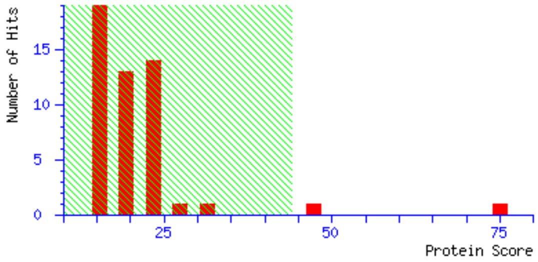
R.KPSYGEEGGYGER.T ;
R.KPSYGEEGGYGER.T

Calculated Mr: **41389** Calculated *p*I: **4.65**

Probability Based Mowse Score:

Mascot Score Histogram

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MPYYTRSEDD VNDFDEFDPT PYGGGYDLAL TYGRPLPPSD ETCYQNSAIA
51 DDDVDYDRPN FTSYAEPSAY NDDILQEEYN SYSRPKPRPG FIPGGGIGGD
101 PYSRPHAAPG FQPGSGGYGG VSEYEKPSGY GRRPDSEYGS GGYGGGTEYE
151 RPSGEDYGSG HGRKQDSEYG SGGYGRRPES EYGSGGGYER PSSEEYGSGY
201 GRK**QESEYGS** **GGYGR**RPEAE YGSGYGGRPE TEYGGGGGSE YGGGYGR**KPS**
251 **YGEEGGYGER** TEYERPSYGD DPPRRPGYGR QDDEYERPSY ERKSDDDNDG
301 SRRKYGGDDD EKGYQKKYGG YGDDDDEEGS RRKYGYGGEE ESYGRKKYGD
351 DGSDDDEKKH HRHKHHQHKH SDDE

Spot No.: **D82 (S69)**

NCBI accession No.: **gi|2501850**   Species: *Nicotiana tabacum*

Protein name：GDP dissociation inhibitor

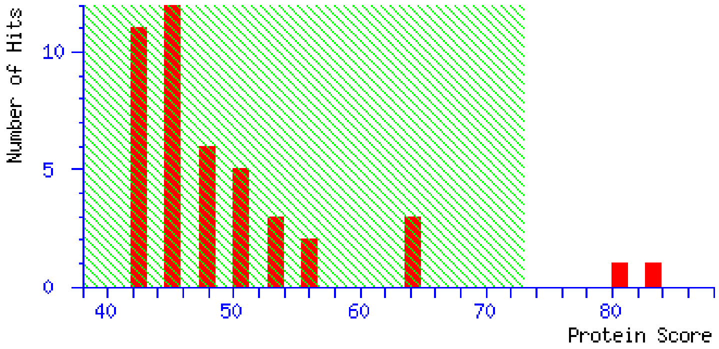
PMF score: **83**   Sequence coverage %: **34**

Matched peptides No.: **16**   Total peptides No.: **62**

Calculated Mr: **50127**   Calculated *p*I: **5.44**

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 73 are significant ($p<0.05$).



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

1 MDEEYDVIVL GTGLK**ECILS** **GLLSVDGLK**V LHMDRNDYYG GESTSLNLVQ
51 LWKRFR**GSDK** **PPAELGSSR**D FNVDMIPKFI MANGALVR**VL** **IHTDVTKYLY**
101 **FKAVDGSFVY** **NK**GKVHK**VPA** **TDMEALKSPL** **MGIFEK**RRAR KFFIYVQDYN
151 ESDPK**THEGM** **DLTR**VTTREL IAKYGLDDNT VDFIGHALAL HRDDR**YLDEP**
201 **AQDTVKR**MK**L** **YAESLARFQG** **GSPYIYPLYG** **LGELPQAFAR** **LSAVYGGTYM**
251 **LNKPECK**VEF DEEGKVCGVT SEGETAKCK**K** **VVCDPSYLPN** **K**VRKVGKVAR
301 AIAIMSHPIP NTNDSHSVQI ILPQKQLGRK SDMYLFCCSY THNVAPKGKF
351 IAFVSTEAET DNPESELKQG VNLLGPVDEI FYETYDRSEP VNEPSLDNCF
401 ISTSYDATTH FESTVDDVLN LYTKITGKVL DLNVDLSAAS AAEE

Spot No.: **D83 (S75)**

NCBI accession No.: **gi|3264769** Species: *Prunus armeniaca*

PFF score: [74] Protein name:late embryogenesis-like protein

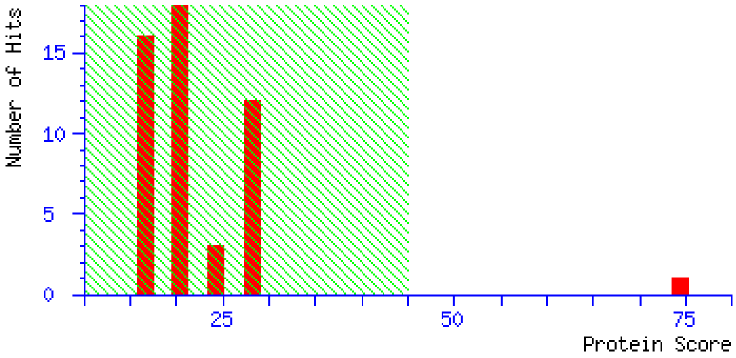
Matched peptides No.: [1] Sequence coverage %: [8]

Matched sequences: K.LVSGLIPDAGTIHAHGEETVK.V

Calculated Mr: **28937** Calculated *p*I: **4.72**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 DVTAIHIPSI NLEKAEIVVD VLIKNPNPVP IPLIDINYLI ESDGRK**LVSG**
51 **LIPDAGTIHA HGEETVK**VPV HLVYDDIKNT YDDIKPGSII PYRFKVDLIV
101 DVPVLGRLTL PLEKTGEIPI PYKPDVDVEK IKFQAFSFEE TVAVLHVKLE
151 NMNDFDLGLN ALDYEIWLSE VNIGGAQLSQ SANLAKKGVT FIELPITFRP
201 KDFGSALWDM IRGKGTGYTI KGNINVDTPF GAMKLPIVKE GGTTRLRKNK
251 EDGGDDDDED ED

Spot No.: **D84 (S85)**

NCBI accession No.: **gi|224099853** Species: ***Populus trichocarpa***

PFF score: [69] Protein name: **putative protein**

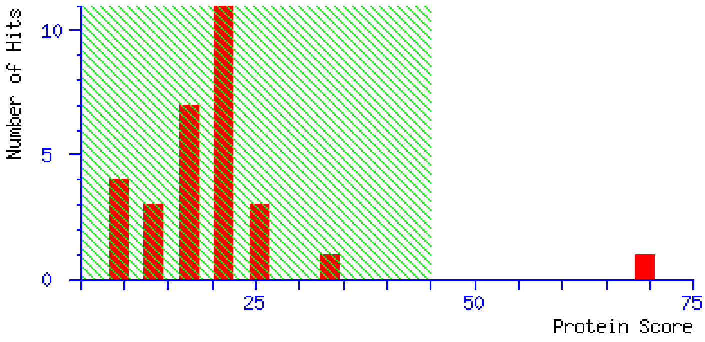
Matched peptides No.: [2] Sequence coverage %: [5]

Matched sequences: S FEHPLNELKP VPR

Calculated Mr: **27448** Calculated *p*I: **5.84**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red

1 MLAVFDNTVA KCPDALQSPH SAPASSALKD GFLANHFASQ HPGSVTVNLG
51 TSGLISHSVE KQNPFLPRLF AVVDDIFCLF QGHIDNVAVL KQQYGLNKTA
101 NEVIVVIEAY RTLRDRGPYP ADQVVKDIQG KFAFILYDST SKATFFAADA
151 DGSVPFFWGA DSEGNLVLSD DVQIVQKGCG KSFAPFPKGC FFTTSGGLR**S**
201 **FEHPLNELKP** **VPR**VDSSGQV CGATFKVDAE TKKESVGMPR VDSSYNWSSN
251 Y

Spot No.: **D85 (S86)**

NCBI accession No.: **gi|38122474** Species: *Hevea brasiliensis*

PFF score: [410] Protein name： rubber elongation factor

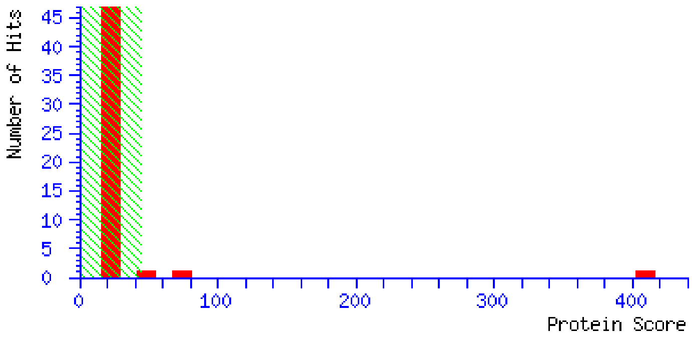
Matched peptides No.: [4] Sequence coverage %: [26]

Matched sequences: YLDFVQAATVYAR ;
SGPFKPGVNTVESR;
SVVRPVYNK ;
RVDAYVTVLDR

Calculated Mr: **19570** Calculated *p*I: **5.06**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red

1 MAEGEEEVNI QEEANKGEEN PQEEANIQEE TNKGEENIQE EANIEEEANK
51 EEESLK**YLDF** **VQAATVYAR**A SFSKLYLFAK DK**SGPFKPGV** **NTVESR**FK**SV**
101 **VRPVYNK**FQP VPNKVLKFAD R**RVDAYVTVL** **DR**IVPPIVKR ASIQAYSVAP
151 GAALAVASYL PLHTKRLSKV LYGDG

Spot No.: **D86 (S87)**

NCBI accession No.: **gi|38122474** Species: *Hevea brasiliensis*

PFF score: [226] Protein name： rubber elongation factor

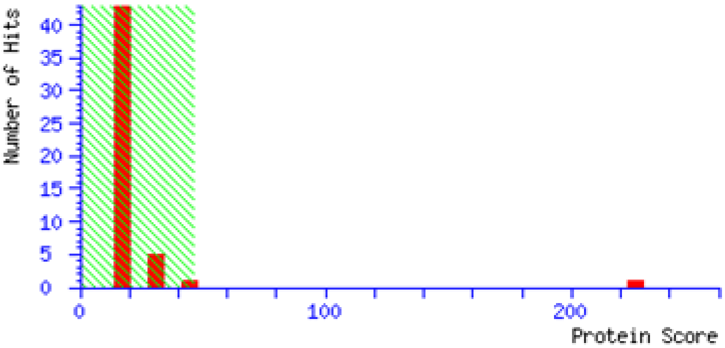
Matched peptides No.: [4] Sequence coverage %: [26]

Matched sequences: YLDFVQAATVYAR ;
SGPFKPGVNTVESR;
SVVRPVYNK ;
RVDAYVTVLDR

Calculated Mr: **19570** Calculated *p*I: **5.06**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MAEGEEEVNI QEEANKGEEN PQEEANIQEE TNKGEENIQE EANIEEEANK
51 EEESLK**YLDF** **VQAATVYAR**A SFSKLYLFAK DK**SGPFKPGV** **NTVESR**FK**SV**
101 **VRPVYNK**FQP VPNKVLKFAD R**RVDAYVTVL** **DR**IVPPIVKR ASIQAYSVAP
151 GAALAVASYL PLHTKRLSKV LYGDG

Spot No.: **D87 (S90)**

NCBI accession No.: **gi|334854634** Species: *Hevea brasiliensis*

PFF score: [490] Protein name： elicitor-responsive protein

Matched peptides No.: [3] Sequence coverage %: [59]

Matched sequences: PLGTVEVLLVGAKGLENTDFLNGVDPYVVLACR;

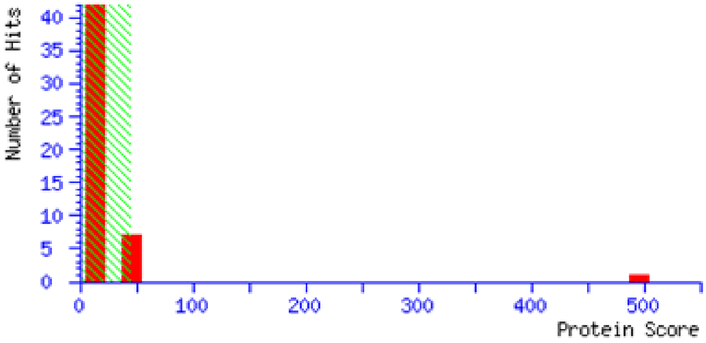
GSEP EWNEKFSFEVSDGDTELTLK;

GEITVGLTFTPEVEMDNVGVDGYDFRL

Calculated Mr: **15249** Calculated *p*I: **4.06**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

```
  1 MPLGTVEVLL VGAKGLENTD FLNGVDPYVV LACRTQEQKS SVASGKGSEP
 51 EWNEKFSFEV SDGDTELTLK IMDSDVGAAD DFVGEATIPL EPLFLEGNLP
101 STAYKVVKEQ EYKGEITVGL TFTPEVEMDN VGVDGYDFRL
```

Spot No.: **D88 (S92)**

NCBI accession No.: **gi|224144943** Species: *Populus trichocarpa*

PFF score: [180] Protein name: predicted protein

Matched peptides No.: [2] Sequence coverage %: [28]

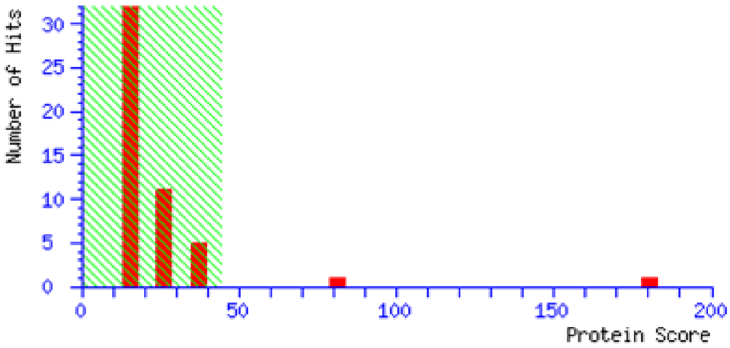
Matched sequences: VFEDNVLIRVLVVDGGGSLR;

HVPITIG GTRISDGEWLYADTDGILISR

Calculated Mr: **17971** Calculated *p*I: **5.39**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red

1 MALVTTAEVC DANPQLIVSG ELRALQPIFQ IYGRRQVFSG PVVTLK**VFED**
51 **NVLIR**EFLEE KGNGR**VLVVD** **GGGSLR**CAIL GGNPVVQAQN NGWAGIVVNG
101 CIRDVDEIMG CDIGVRALAS HPMKANKKGI GEK**HVPITIG** **GTRISDGEWL**
151 **YADTDGILIS** **R**TELAV

Spot No.: **D89 (S94)**

NCBI accession No.: gi|123062 Species: *Hevea brasiliensis*

PFF score: [96]

Protein name: prohevein

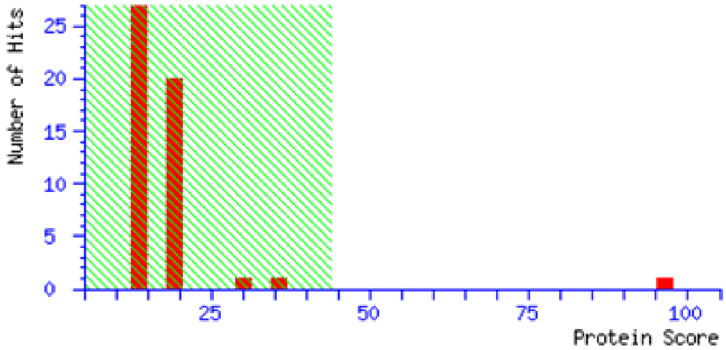
Matched peptides No.: [1] Sequence coverage %: [8]

Matched sequences: IVDQ CSNGGLDLDV NVFR

Calculated Mr: 22700 Calculated *p*I: 5.63

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MNIFIVVLLC LTGVAIAEQC GRQAGGKLCP NNLCCSQWGW CGSTDEYCSP
51 DHNCQSNCKD SGEGVGGGSA SNVLATYHLY NSQDHGWDLN AASAYCSTWD
101 ANKPYSWRSK YGWTAFCGPV GAHGQSSCGK CLSVTNTGTG AKTTVR**IVDQ**
151 **CSNGGLDLDV** **NVFR**QLDTDG KGYERGHITV NYQFVDCGDS FNPLFSVMKS
201 SVIN

Spot No.: **D90 (S98)**

NCBI accession No.: gi|38122474 Species: *Hevea brasiliensis*

Protein name: rubber elongation factor

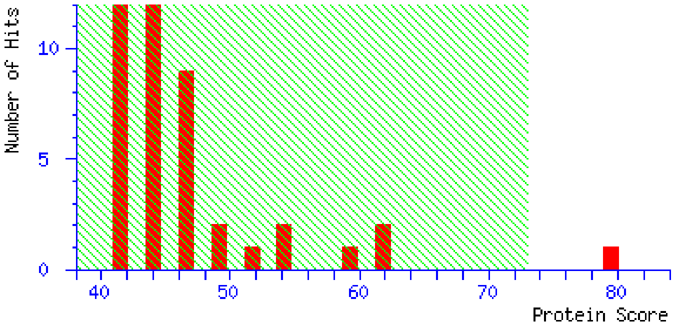
PMF score: 99 Sequence coverage %: 45

Matched peptides No.: 8 Total peptides No.: 39

Calculated Mr: 19570 Calculated *p*I: 5.06

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold red:

1 MAEGEEEVNI QEEANKGEEN PQEEANIQEE TNK**GEENIQE** **EANIEEEANK**
51 **EEESLKYLDF** **VQAATVYAR**A SFSK**LYLFAK** DK**SGPFKPGV** **NTVESRFKSV**
101 **VRPVYNK**FQP VPNKVLK**FAD** **RRVDAYVTVL** **DR**IVPPIVKR ASIQAYSVAP
151 GAALAVASYL PLHTKRLSKV LYGDG

Spot No.: **D91 (S100)**

NCBI accession No.: **gi|1709761** Species: *Spinacia oleracea*

PFF score: [49]

Protein name: Proteasome subunit alpha type-4

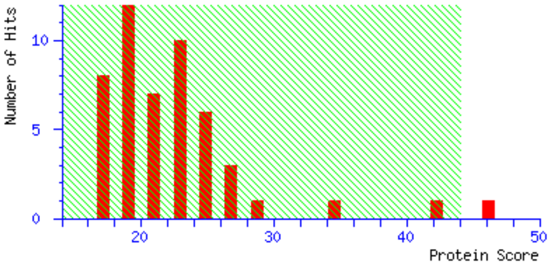
Matched peptides No.: [1] Sequence coverage %: [3]

Matched sequences: R.TTIFSPEGR.L

Calculated Mr: **27545** Calculated *p*I: **6.17**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MSRRYDSR**TT** **IFSPEGR**LYQ VEYAMEAIGN AGSAIGILAK DGVVLIGEKK
51 VTSKLLQTST STEKMYKIDD HVACAVAGIM SDANILINTA RVQAQRYTFS
101 YQEPMPVEQL VQSLCDTKQG YTQFGGLRPF GVSFLFAGWD KNYGFQLYMS
151 DPSGNYGGWK ATAIGANNQA AQSMLKQDYK DDVTREDAVK LALKALSKTM
201 DSTSLTSEKL ELAEVYLLPS GKVKYQVHSP ESLNRLLTES GLTQPAAETS

Spot No.: **D92 (S103)**

NCBI accession No.: gi|38122474 Species: ***Hevea Brasiliensis***

Protein name： rubber elongation factor

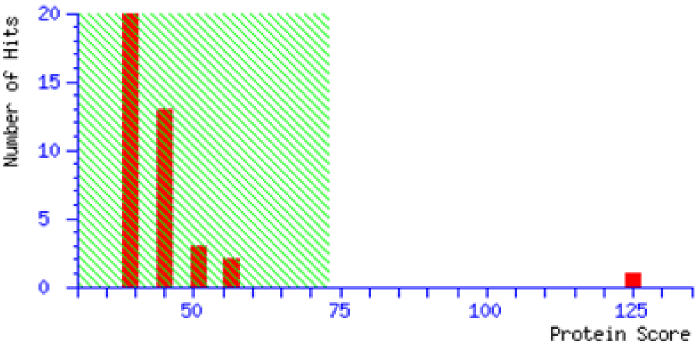
PMF score: **125** Sequence coverage %: **68**

Matched peptides No.: **11** Total peptides No.: **50**

Calculated Mr: **19570** Calculated *p*I: **5.06**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 M**AEGEEEVNI** **QEEANKGEEN** **PQEEANIQEE** **TNKGEENIQE** **EANIEEEANK**

51 **EEESLKYLDF** **VQAATVYAR**A SFSK**LYLFAK** DK**SGPFKPGV** **NTVESRFKSV**

101 **VRPVYNKFQP** **VPNK**VLK**FAD** **RRVDAYVTVL** **DR**IVPPIVKR ASIQAYSVAP

151 GAALAVASYL PLHTKRLSKV LYGDG

Spot No.: **D93 (S105)**

NCBI accession No.: gi|157831407 Species: *Hevea brasiliensis*

Protein name：Chain A, Crystal Structures Of Hevamine

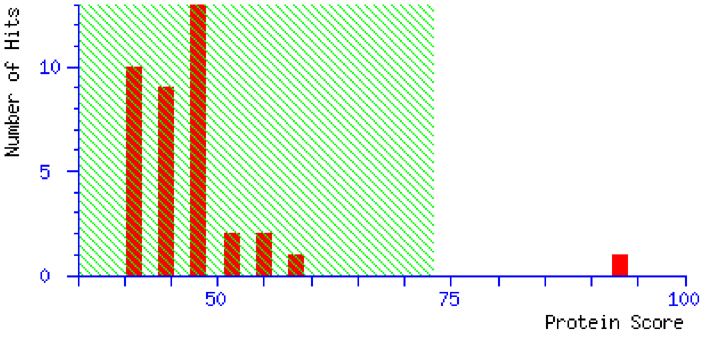
PMF score: 93 Sequence coverage %:51

Matched peptides No.: 13 Total peptides No.: 76

Calculated Mr: 29874 Calculated *p*I: 8.44

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold red:

1 GGIAIYWGQN GNEGTLTQTC STR**KYSYVNI** **AFLNK**FGNGQ TPQINLAGHC
51 NPAAGGCTIV SNGIR**SCQIQ** **GIKVMLSLGG** **GIGSYTLASQ** **ADAKNVADYL**
101 **WNNFLGGKSS** **SRPLGDAVLD** **GIDFDIEHGS** **TLYWDDLAR**Y LSAYSKQGK**K**
151 **VYLTAAPQCP** **FPDR**YLGTAL NTGLFDYVWV QFYNNPPCQY SSGNINNIIN
201 SWNRWTTSIN AGK**IFLGLPA** **APEAAGSGYV** **PPDVLISR**IL PEIKKSPK**YG**
251 **GVMLWSKFYD** **DK**NGYSSSIL DSV

Spot No.: **D94 (S108)**

NCBI accession No.: **gi|2493895** Species: *Citrullus lanatus*

PFF score: [89]

Protein name: cysteine synthase

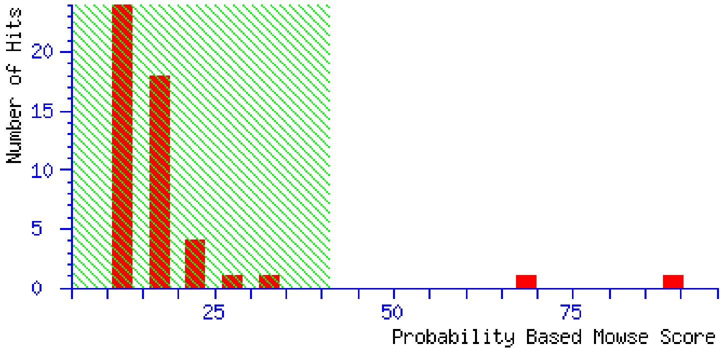
Matched peptides No.: [1] Sequence coverage %: [ ]

Matched sequences: K.EGLLVGISSGAAAAAAIR.I

Calculated Mr: **34495** Calculated *p*I: **6.26**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 41 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

```
  1 MADAKSTIAK DVTELIGNTP LVYLNRVVDG CVARVAAKLE MMEPCSSVKD RIGYSMISDA
 61 ENKGLITPGE SVLIEPTSGN TGIGLAFIAA AKGYRLIICM PASMSLERRT ILRAFGAELV
121 LTDPARGMKG AVQKAEEIKA KTPNSYILQQ FENPANPKIH YETTGPEIWR GSGGKIDALV
181 SGIGTGGTVT GAGKYLKEQN PNIKLYGVEP VESAILSGGK PGPHKIQGIG AGFIPGVLDV
241 NLLDEVIQVS SEESIETAKL LALKEGLLVG ISSGAAAAAA IRIAKRPENA GKLIVAVFPS
301 FGERYLSTVL FESVKRETEN MVFEP
```

Spot No.: **D95 (S117)**

NCBI accession No.: **gi|51315784** Species: *Hevea brasiliensis*

PFF score: [59]

Protein name: Esterase

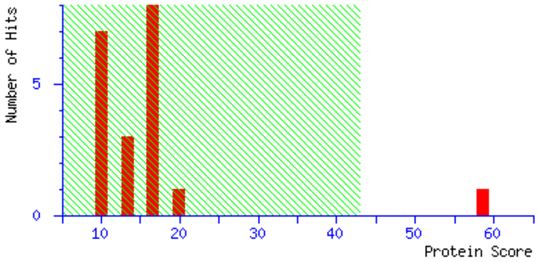
Matched peptides No.: [1] Sequence coverage %: [4]

Matched sequences: K.AAAFYPLNPPYGETFFHR.S

Calculated Mr: **43871** Calculated *p*I: **5.00**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 43 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MEFPETNNNP IITLSFLLCM LSLAYASETC DFPAIFNFGD SNSDTGGK**AA**
51 **AFYPLNPPYG** **ETFFHR**STGR YSDGRLIIDF IAESFNLPYL SPYLSSLGSN
101 FKHGADFATA GSTIKLPTTI IPAHGGFSPF YLDVQYSQFR QFIPRSQFIR
151 ETGGIFAELV PEEYYFEKAL YTFDIGQNDL TEGFLNLTVE EVNATVPDLV
201 NSFSANVKKI YDLGARTFWI HNTGPIGCLS FILTYFPWAE KDSAGCAKAY
251 NEVAQHFNHK LKEIVAQLRK DLPLATFVHV DIYSVKYSLF SEPEKHGFEF
301 PLITCCGYGG KYNFSVTAPC GDTVTADDGT KIVVGSCACP SVRVNWDGAH
351 YTEAANEYFF DQISTGAFSD PPVPLNMACH KTESLRTLAS V

Spot No.: **D96 (S118)**

NCBI accession No.: **gi|38122474** Species: *Hevea brasiliensis*

Protein name： rubber elongation factor

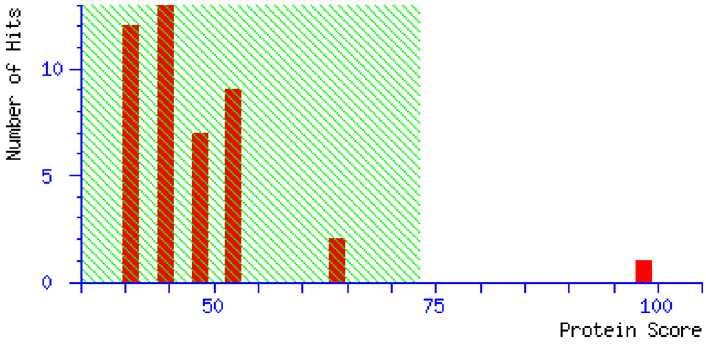
PMF score: **98** Sequence coverage %: **57**

Matched peptides No.: **9** Total peptides No.: **44**

Calculated Mr: **19570** Calculated *p*I: **5.06**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 M**AEGEEEVNI QEEANKGEEN PQEEANIQEE TNKGEENIQE EANIEEEANK**
51 **EEESLKYLDF VQAATVYAR**A SFSK**LYLFAK** DKSGPFKPGV NTVESRFK**SV**
101 **VRPVYNKFQP VPNK**VLKFAD R**RVDAYVTVL DR**IVPPIVKR ASIQAYSVAP
151 GAALAVASYL PLHTKRLSKV LYGDG

Spot No.: **D97 (S121)**

NCBI accession No.: **gi| 255554865** Species: *Ricinus communis*

PFF score: [55]

Protein name: lactoylglutathione lyase, putative

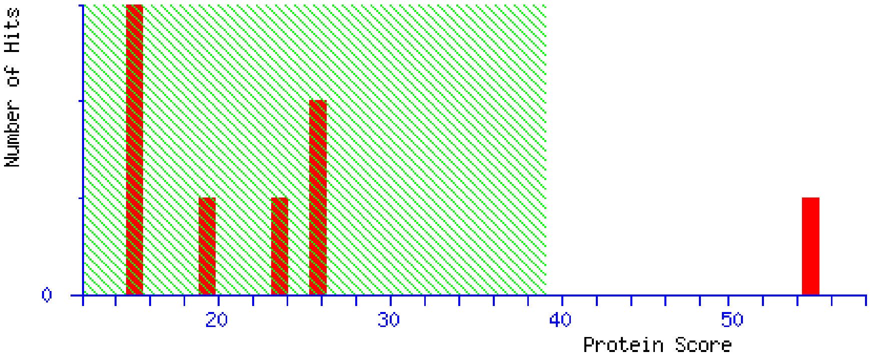
Matched peptides No.: [1] Sequence coverage %: [3]

Matched sequences: K.FYTECFGMK.L

Calculated Mr: **31641** Calculated *p*I: **7.63**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 40 indicate peptides with significant homology.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MAAEATAPNA DVLEWPKKDK RRLLHAVYRV GDLDRTIK**FY** **TECFGMK**LLR

51 KRDIPEEKYS NAFLGFGPEE TNFVVELTYN YGVTSYDIGT GFGHFAIATQ

101 DVYKLVEEVL AKGGAVTREP GPVKGGTTVI AFVKDPDGYI FELIQRGPTP

151 EPLCQVMLRV GDLDRSIRFY EKALGMKLLR KVDKPEYKYT LAMMGYADEY

201 ETTVLELTYN YGVTEYTKGN AYAQVAISTD DVYKSAEVVN LVTQELGGKI

251 TRQPGPIPGL NTKITSFLDP DGWKTKRKRR

Spot No.: **D98 (S123)**

NCBI accession No.: **gi|15225839** Species: *Arabidopsis thaliana*

Protein name: endopeptidase/ peptidase/ threonine-type endopeptidase

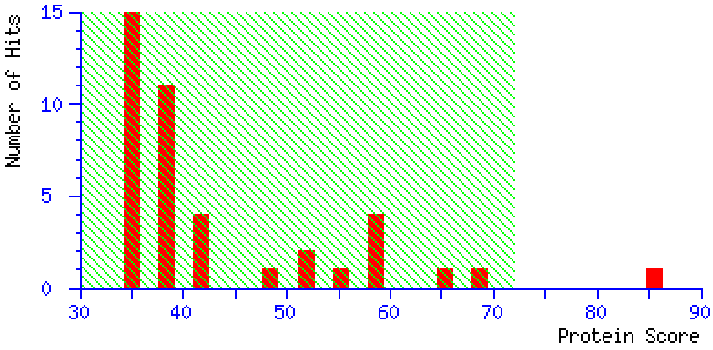
PMF Mascot score: **86** Sequence coverage %: **40**

Matched peptides No.: **14** Total peptides No.: **56**

Calculated Mr: **27645** Calculated *p*I: **5.93**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MSSIGTGYDL SVTTFSPDGR **VFQIEYAAK**A VDNSGTVVGI KCKDGIVMGV
51 EKLIASK**MML** **PGSNRRIHSV** **HRHAGMAVAG** **LAADGRQIVA** **RAKSEARSYE**
101 **SVYGDAVPVK** ELSERVASYV HLCTLYWWLR PFGCGVILGG YDR**DGPQLYM**
151 **IEPSGISYRY** **FGAAIGK**GKQ AAKTEIEKLN LSEMTCKEGV IEVAKIIYKL
201 HDEAK**DKAFE** **LEMSWICEES** **K**REHQKVPDD LLEEAKTAAK TALEEMDAD

Spot No.: **D99 (S126)**

NCBI accession No.: **gi|29170601** Species: *Hevea brasiliensis*

PFF score: [97]

Protein name: small rubber particle protein

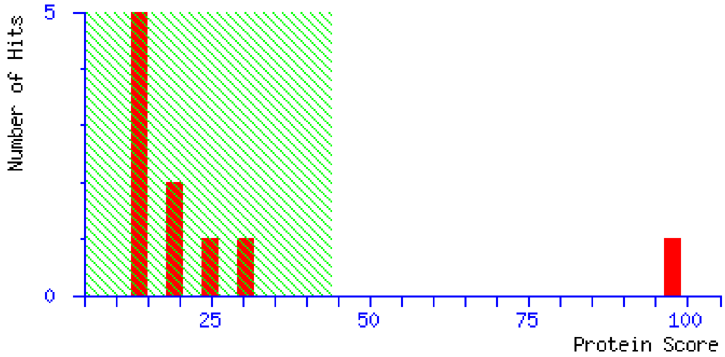
Matched peptides No.: [1] Sequence coverage %: [12]

Matched sequences: K.ENENFQQEANEQEEK.L

Calculated Mr: **12769** Calculated *p*I: **4.61**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

```
  1 MAEGKENENF QQEANEQEEK LKYLEFVQAT TDNAVTALSN IYLYAKDNSG
 51 PLKPGVETIE GVAKTVVIPA SKIPTEAIKF ADRAVDASFT TLQNIVPSVL
101 KQLPTQACDT SVKESAE
```

Spot No.: **D100 (S127)**

NCBI accession No.: **gi|2832430** Species: *Hevea brasiliensis*

PFF score: [84] Protein name: prohevein

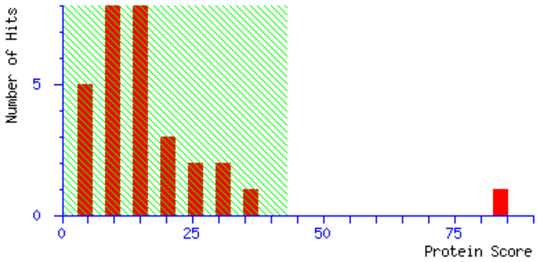
Matched peptides No.: [1] Sequence coverage %: [10]

Matched sequences: K.YGWTAFCGPVGAHGQPSCGK.C

Calculated Mr: **20852** Calculated *p*I: **5.64**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 43 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 EQCGRQAGGK LCPNNLCCSQ WGWCGSTDEY CSPDHNCQSN CKDSGEGVGG
51 GSASNVLATY HLYNSQDHGW DLNAASAYCS TWDANKPYSW RSK**YGWTAFC**
101 **GPVGAHGQPS** **CGK**CLSVTNT GTGAKATVRI VDQCSNGGLD LDVNVFRQLD
151 TDGKGYERGH LTVNYQFVDC GDSFNPLFSV MKSSVIN

Spot No.: **D101 (S128)**

NCBI accession No.: **gi|224054224** Species: *Populus trichocarpa*

PFF score: [68] Protein name: predicted protein

Matched peptides No.: [2] Sequence coverage %: [12]

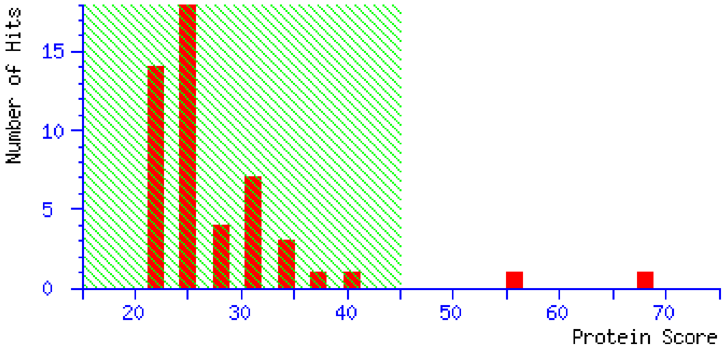
Matched sequences: R.AYVGDRPTWR.N;

R.NPQHPWR.V

Calculated Mr: **15003** Calculated *p*I: **6.82**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

```
  1 MTVKLVDATI SSFGSVFEKF KAEAPKNKVN LILFLADNDP STNLSWCPDC
 51 VRAEPVILKK LEALPDDVAL LRAYVGDRPT WRNPQHPWRV DSRFKLKGVP
101 TLISWENDAV KGRLEDYEAH LEHKINALVS GN
```

Spot No.: **D102 (S130)**

NCBI accession No.: **gi|268321205**

Plantspecies: ***Hevea brasiliensis*** Protein name：**latex cystatin**

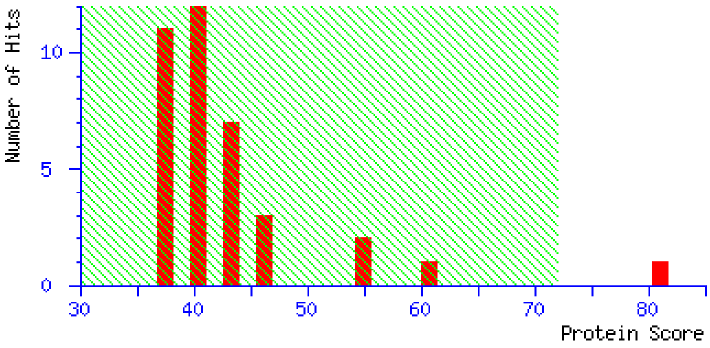
PMF score: **81** Sequence coverage %: **48**

Matched peptides No.: **6** Total peptides No.:**42**

Calculated Mr: **11248** Calculated *p*I: **5.45**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 MAKLGGVK**EV EGSANSVEIN SLARYAVDDY NQKQNALLEF K**KVVNAKQQV
51 VAGTIYYITL EVIDGGQKKV YEAK**VWEKPW LNFKEVQEFK** LIGDAPSDST
101 A

Spot No.: **D103 (S133)**

NCBI accession No.: **gi|242083244**

Plantspecies: ***Sorghum bicolor***

Protein name：**hypothetical protein SORBIDRAFT_08g008236**

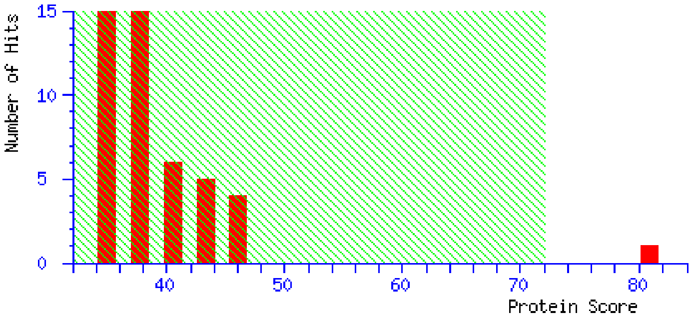
PMF score: **81** Sequence coverage %: **89**

Matched peptides No.: **7** Total peptides No.:**33**

Calculated Mr: **8620** Calculated *p*I: **6.4**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

1 **CVENIILSVL FWSKVQLCLR ASQPLLVALR IVDGDETPID PKIMVAMDVA**
51 **K**AIIKESLK**D KPILLNEVLK YYDNR**

Spot No.: **D104 (S134)**

NCBI accession No.: **gi|29170601** Species: *Hevea brasiliensis*

PFF score: [85]

Protein name: small rubber particle protein

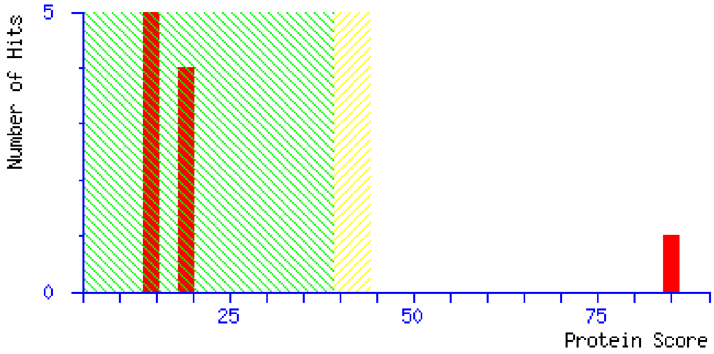
Matched peptides No.: [1] Sequence coverage %: [15]

Matched sequences: R.AVDASFTTLQNIVPSVLK.Q

Calculated Mr: **12769** Calculated *p*I: **4.61**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 39 indicate peptides with significant homology.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

```
  1 MAEGKENENF QQEANEQEEK LKYLEFVQAT TDNAVTALSN IYLYAKDNSG
 51 PLKPGVETIE GVAKTVVIPA SKIPTEAIKF ADRAVDASFT TLQNIVPSVL
101 KQLPTQACDT SVKESAE
```

Spot No.: **D105 (S136)**

NCBI accession No.: **gi|354318** Species: *Triticum aestivum*

PFF score: [128] Protein name: calmodulin

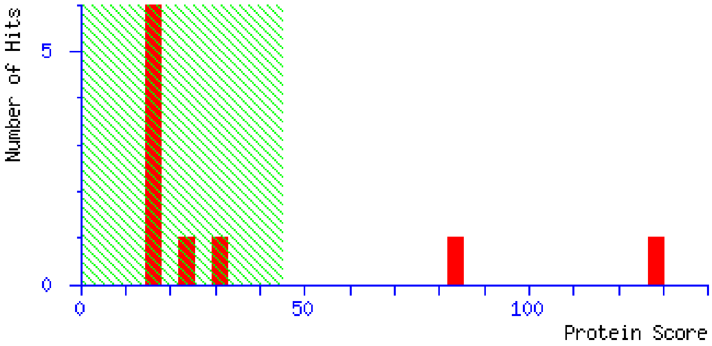
Matched peptides No.: [1] Sequence coverage %: [10]

Matched sequences: R.VFDKDQDGFISAAELR.H

Calculated Mr: **16876** Calculated *p*I: **4.10**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 ADQLTDEQNI AEFKEAFSLF DKDGDGCITT KELGTVMRSL GQNPTEAELQ
51 DMINEVDADG NGTIDFPEFL NLMARKMKDT DSEEELKEAF R**VFDKDQDGF**
101 **ISAAELR**HVM TNLGEKLTDE EVDEMIREAD VDGDGQINYE EFVKVMMAK

Spot No.: **D106 (S137)**

NCBI accession No.: gi|14423933   Species: *Hevea brasiliensis*

Protein name：Small rubber particle protein

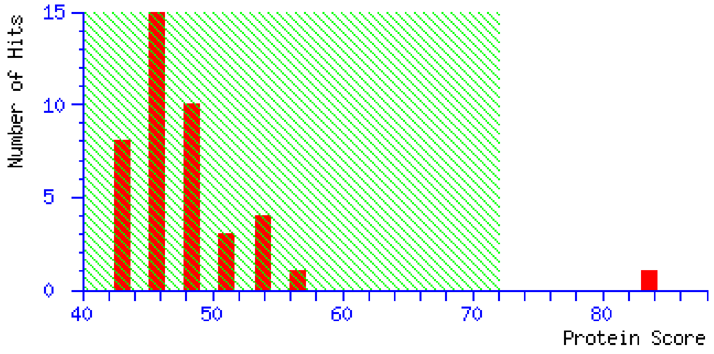
PMF score: **84**   Sequence coverage %: **65**

Matched peptides No.: **9**   Total peptides No.:**43**

Calculated Mr: **22331**   Calculated *p*I: **4.80**

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 73 are significant ($p<0.05$).



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

1 MAEEVEEERL K**YLDFVRAAG** **VYAVDSFSTL** **YLYAKDISGP** **LKPGVDTIEN**

51 **VVKTVVTPVY** **YIPLEAVK**FV DKTVDVSVTS LDGVVPPVIK **QVSAQTYSVA**

101 **QDAPRIVLDV** **ASSVFNTGVQ** **EGAK**ALYANL EPK**AEQYAVI** **TWR**ALNK**LPL**

151 **VPQVANVVVP** **TAVYFSEK**YN DVVRGTTEQG YR**VSSYLPLL** **PTEK**ITKVFG

201 DEAS

Spot No.: **D107 (S138)**

NCBI accession No.: gi|14423933 Species: *Hevea brasiliensis*

Protein name： Small rubber particle protein

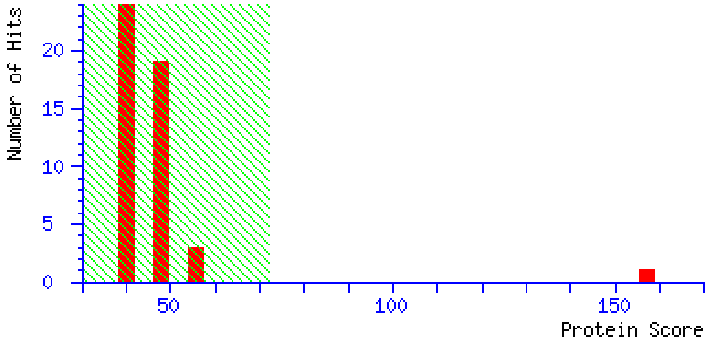
PMF score: **162** Sequence coverage %: **85**

Matched peptides No.: **13** Total peptides No.:**43**

Calculated Mr: **22331** Calculated *p*I: **4.80**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red

```
  1 MAEEVEEERL KYLDFVRAAG VYAVDSFSTL YLYAKDISGP LKPGVDTIEN
 51 VVKTVVTPVY YIPLEAVKFV DKTVDVSVTS LDGVVPPVIK QVSAQTYSVA
101 QDAPRIVLDV ASSVFNTGVQ EGAKALYANL EPKAEQYAVI TWRALNKLPL
151 VPQVANVVVP TAVYFSEKYN DVVRGTTEQG YRVSSYLPLL PTEKITKVFG
201 DEAS
```

Spot No.: **D108 (S139)**

NCBI accession No.: gi|14423688 Species: *Hevea brasiliensis*

Protein name： **Enolase 1**

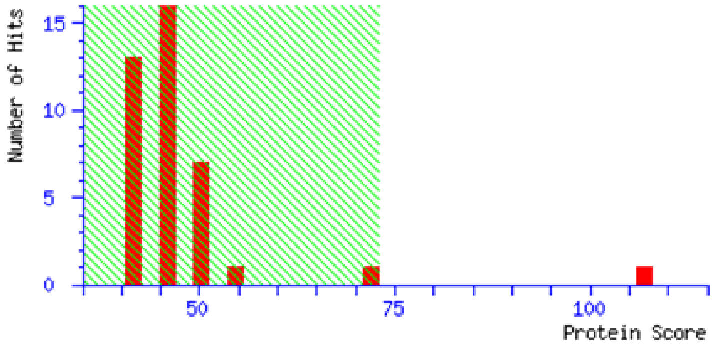
PMF score: 107 Sequence coverage %: 44

Matched peptides No.:14 Total peptides No.:47

Calculated Mr: 48029 Calculated *p*I:5.57

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold red:

1 M**AITIVSVRA** **RQIFDSR**GNP TVEADVK**LSD** **GYLARAAVPS** **GASTGIYEAL**
51 **ELR**DGGSDYL GKGVSK**AVEN** **VNIIIGPALV** **GK**DPTDQVGI DNFMVQQLDG
101 TVNEWGWCKQ KLGANAILAV SLAVCKAGAH VKGIPLYEHI ANLAGNKNLV
151 LPVPAFNVIN GGSHAGNK**LA** **MQEFMILPVG** **ASSFK**EAMKM GAEVYHHLKS
201 VIKKK**YGQDA** **TNVGDEGGFA** **PNIQENK**EGL ELLKTAIAKA GYTGKVVIGM
251 DVAASEFYGS DQTYDLNFKE ENNNGSQKIS GEALKDLYK**S** **FVAEYPIVSI**
301 **EDPFDQDDWA** **HYAK**LTSEIG EKVQIVGDDL LVTNPKRVEK AIKEKACNAL
351 LLK**VNQIGSV** **TESIEAVK**MS KR**AGWGVMAS** **HRSGETEDTF** **IADLSVGLAT**
401 **GQIK**TGAPCR SERLAK**YNQL** **LRIEEELGSE** **AVYAGANFRK** **PVEPY**

Spot No.: **D109 (S143)**

NCBI accession No.: **gi|333690873** Species: *Hevea brasiliensis*

PFF score: [52]

Protein name: glutathione-S-transferase tau 1

Matched peptides No.: [2] Sequence coverage %: [10]

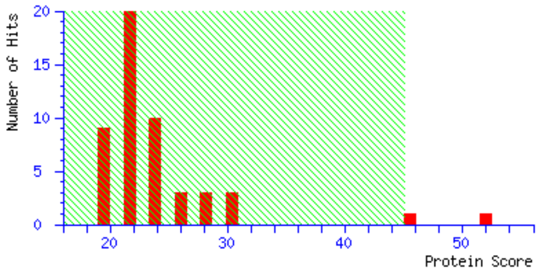
Matched sequences: K.YEYREEDLR.N;

K.DKSPFLPSDPYQR.A

Calculated Mr: 25595 Calculated *p*I: **5.48**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEEVILLDF WPSPFGMRVR IALAEKGVK**Y** **EYREEDLR**NK SPLLLQMNPV
51 HKKIPVLIHN GKPICESLIA VQYVDEVWK**D** **KSPFLPSDPY** **QR**AQARFWAD
101 FIDKKIYDIG RKIWTTKGDE QEAAKKEFIE ALKLLEGELG NKPYFGGESM
151 GYVDVALIPF YSWFYAYETC GNFSIEPECP VLIAWAKRCL QKESVSESVP
201 DPEKVYEFVL VLKKKFGIE

Spot No.: **D110 (S145)**

NCBI accession No.: **gi|30575570** Species: *Citrus x paradisi*

PFF score: [87]

Protein name: HSP19 class II

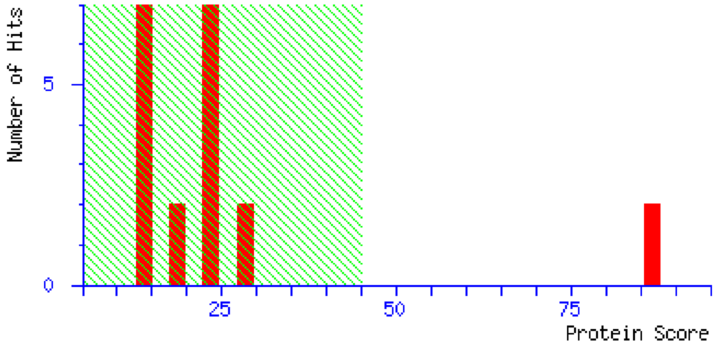
Matched peptides No.: [1] Sequence coverage %: [15]

Matched sequences: K.VQVEDDNVLLISGER.K

Calculated Mr: **11191** Calculated *p*I: **8.01**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

```
 1  YVFIVDMPGL KSGDIKVQVE DDNVLLISGE RKREEEKDGA KYVRMERRVG
51  KFMRKFVLPE NANVEAISAV CQDGVLTVTV DKLPPPEPKK PKTIEVKIA
```

Spot No.: **D111 (S146)**

NCBI accession No.: **gi|37901124** Species: *Hevea brasiliensis*

PFF score: [88]

Protein name: latex abundant protein 1

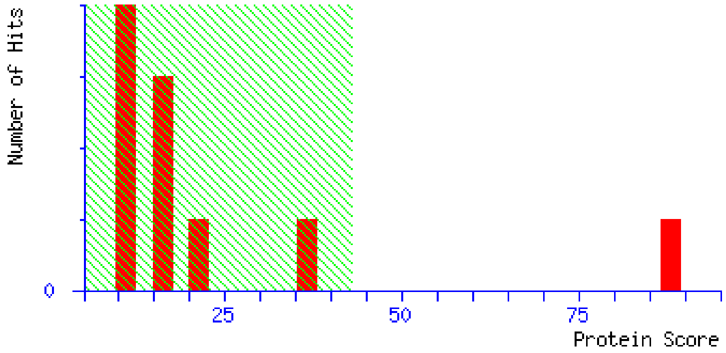
Matched peptides No.: [1] Sequence coverage %: [11]

Matched sequences: R.NKDDINCFNEYNPR.P

Calculated Mr: **14618** Calculated *p*I: **5.01**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 43 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

```
  1 MPYYTRNKDD INCFNEYNPR PYIGGYDMAL TYGRPISACE ETCYPRSSSA
 51 NEIDYDYPDF TWYVEPSAYN DDHLQEEYTS YARPKPRPAP NSLGSCPILG
101 GNDEEKKHHH CHHQHEKHCD DE
```

Spot No.: **D112 (S147)**

NCBI accession No.: **gi|359806300** Species: *Glycine max*

PFF score: [173]

Protein name: uncharacterized protein LOC100784610

Matched peptides No.: [3] Sequence coverage %: [9]

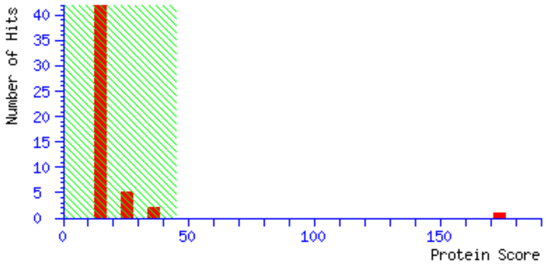
Matched sequences: K.NTALHYAAGYGR.K;

R.YWNNEEVLQK.L;
R.TALHFACGYGEVK.C

Calculated Mr: **38027** Calculated *p*I: **4.53**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MASDSKKDFP ADDKAGTEES KTSKDETSSK DSPAEQRATA TFGPRPGPAG
51 HPGNPFDLSA MSGLLNDPSI KELAEQIAKD PSFNQMAEQL QKTFQGAPQD
101 AIPSFDNQQY FSTMQQVMQN PNFMTMAERL GNALMQDPSM SAMLESFSNP
151 SNKDQLEERM ARIKEDPSLK HILEEIETGG PAAMMR**YWNN** **EEVLQK**LGQA
201 MGLANSGDAG ASAENSGADE TEDLGNEDES IVHHTASVGD VEGLKNALAS
251 GADKDEEDSE GR**TALHFACG** **YGEVK**CAQVL LEAGAKVDAL DKNK**NTALHY**
301 **AAGYGR**KECV ALLENGAAV TLQNMDGKTP IDVAKLNNQN EVLKLLEKDA
351 FL

Spot No.: **D113 (S148)**

NCBI accession No.: **gi|37625031**   Species: *Vitis aestivalis*

PFF score: [166]

Protein name: putative ankyrin-repeat protein

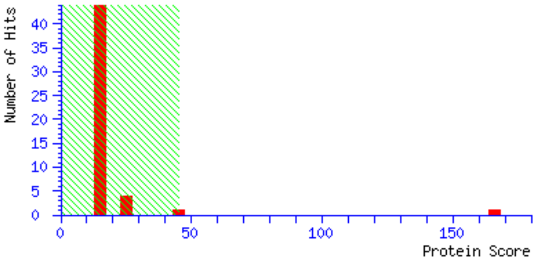
Matched peptides No.: [3]   Sequence coverage %: [9]

Matched sequences: K.LNNQHEVLK.L;
K.NTALHYAAGYGR.K;
R.TALHFACGYGEVK.C

Calculated Mr: **38089**   Calculated *p*I: **4.53**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MASNSDKDTP AGSAENSKSD SSSGESHSEQ RRAAAAASVP GAGLPTNPFD
51 FSAMTGLLND PSIKELAEQI AKDPAFNQMA EQLQKTFHGA AVEESIPQFD
101 TQQYYSTMQQ VMQNPQFMTM AERLGNALMQ DPSMSSMLEN LANPTHKDQL
151 EERMARIKED PSLKPILDEI ETGGPAAMMR YWNDKDVLQK LGEAMGLAVS
201 GDAAASADNS GLDEAEELAN EDESIAHHHS ESIVHDTASV GDVEGLKNAL
251 ASGADKDEED SEGR**TALHFA** **CGYGEVK**CAQ ILVEAGATVD ALDKNK**NTAL**
301 **HYAAGYGR**KE CVALLLENGA AVTLQNMDGK TPIDVAK**LNN** **QHEVLK**LLEK
351 DAFL

Spot No.: **D114 (S149)**

NCBI accession No.: **gi|13310811**   Species: *Nicotiana tabacum*

PFF score: [71]

Protein name: putative ankyrin-repeat protein

Matched peptides No.: [2]   Sequence coverage %: [7]

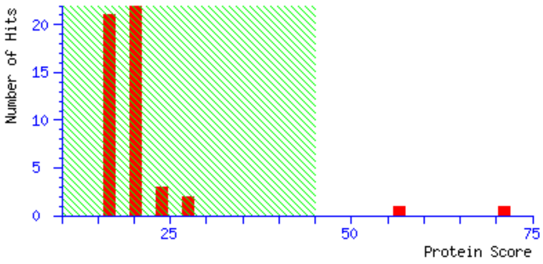
Matched sequences: K.NTALHYAAGYGR.K;

R.TALHFACGYGEVK.C

Calculated Mr: **37522**   Calculated *p*I: **4.45**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MSEGEKVLPT ASADEKSGAS ENKKSSESSS TEAPSGEART TSTAAAGAGL
51 QNPFDFSAMS GLLNDPSIKE LAEQIAKDPA FNQMAEQLQK TFQGAAVEES
101 VPNFDSQQYY STMQQVMQNP QFMTMAERLG NALMQDPSMS GMLESLSNPA
151 QKEQIEERMA RIKEDPSLKP ILEEIESGGP AAMMRYWNDQ ETLKKIGEAM
201 GFAAGGEGAT SSAIPGTDET EEANEDESVV HQCASVGDAE GLKAALTAGA
251 DKDEEDSEGR **TALHFACGYG** **EVK**CAQILLE AGAKVDALDK NK**NTALHYAA**
301 **GYGR**KECVAL LLENGAAVTL QNLDGKTPID VAKLNNQQEV LKLLEKDVFL

Spot No.: **D115 (S151)**

NCBI accession No.: **gi|378464888**

Species: *Ammopiptanthus mongolicus*

PFF score: [117]

Protein name: translation elongation factor

Matched peptides No.: [2]   Sequence coverage %: [11]

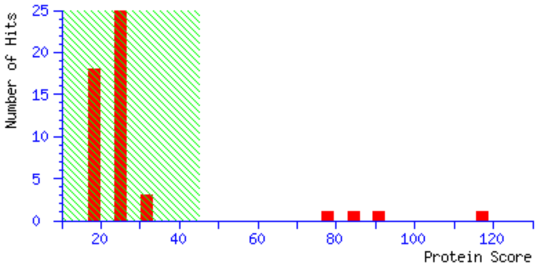
Matched sequences: R.WFNHIDALLR.I;

K.SSVLLDVKPWDDETDMK.K

Calculated Mr: **25300**   Calculated *p*I: **4.50**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MVLTLYNLSS EPGLKKLDEY LLSRSYITGY QASKDDLTVY AALPEVPSDK
51 YVNVSR**WFNH** **IDALLR**ISGV SGEGSGVTVE GSAPVAEETI ATPPAADTKA
101 TAAEDDDDDV DLFGEETEEE KKAAEERAAS VKASVKKKES GK**SSVLLDVK**
151 **PWDDETDMK**K LKEAVRSVSM EGLHWGASKL VPVGYGIKKL QIMLTIVDDL
201 VSVDNLIEEQ LQVEPINEYV QSCDIVAFNK I

Spot No.: **D116 (S153)**

NCBI accession No.: **gi|22261807** Species: *Solanum tuberosum*

PFF score: [132]

Protein name: Light-induced protein, chloroplastic

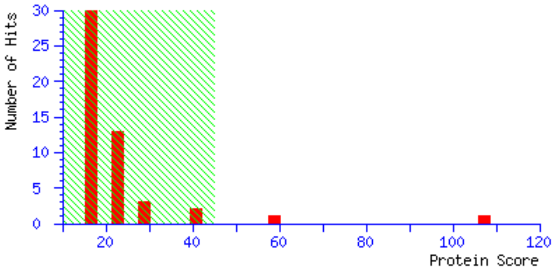
Matched peptides No.: [1] Sequence coverage %: [8]

Matched sequences: K.FEEGIIGTPQLTDSIVLPENVEFLGQK.I

Calculated Mr: **35671** Calculated *p*I: **5.26**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MAVTFYGVNS GSGLKKLDEY LLTRSYISGY QASKDDITVH AALSK**APSSE**
51 **YVNVSR**WYNH IESLLRISGV SGEGCGVTIE GFAPVDAVAT PPAEDTKATA
101 AEDDDDDDVD LFGEETEEEK KAAEARAAAV KASGKKKESG **KSSVLLDVKP**
151 **WDDETDMK**KL EEAVR**SIKME** **GLLWGASK**LV PVGYGIKKLQ IMLTIVDDLV
201 SVDDLIEEQL TVEPTNEYVQ SCDIVAFNKI

Spot No.: **D117 (S161)**

NCBI accession No.: **gi|147805616** Species: *Vitis vinifera*

PFF score: [136]

Protein name: hypothetical protein VITISV_028800

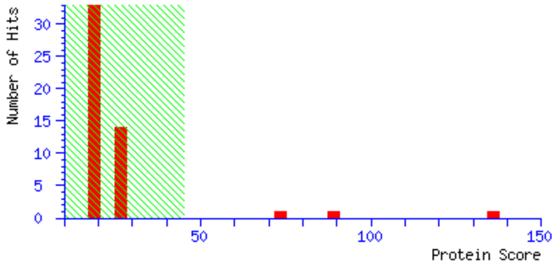
Matched peptides No.: [3] Sequence coverage %: [10]

Matched sequences: R.GPYPADQVVR.D;
R.DRGPYPADQVVR.D;
K.TANEVIIVIEAYR.T

Calculated Mr: 27385 Calculated *p*I: **5.64**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MLAVFHKSIA EAPEGLRTPD SASLPALKDG FLPQFFASLH PSAVTVNLGS
51 SGAISYSVDK QNPLLPRLFA VVDDIFCLFQ GHIENVALLK QQYGLNK**TAN**
101 **EVIIVIEAYR** TLR**DRGPYPA** **DQVVR**DLHGK FAFVLYDSSN RTAFLAADAD
151 ESVPFFWGVD SEGHLVLSDD EETVKKGCGK SFAPFPKGCF FTTSGGLRSF
201 EHPLNELRAE PRVDSSGQVC GANFKVDVEA KKETGMPRVG SAANWSTHY

Spot No.: **D118 (S164)**

NCBI accession No.: **gi|225428086** Species: *Vitis vinifera*

PFF score: [377]

Protein name： V-type proton ATPase subunit B 1

Matched peptides No.: [10] Sequence coverage %: [23]

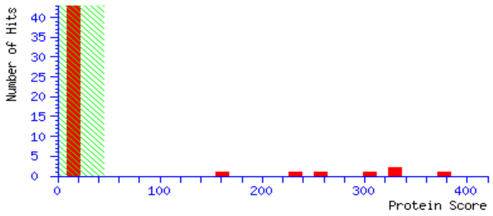
Matched sequences: K.YQEIVNIR.L;K.FVAQGAYDTR.N;
R.DFEENGSMER.V;R.RGQVLEVDGEK.A;
R.KFVAQGAYDTR.N;K.YTTVQFTGEVLK.T;
R.QIYPPINVLPSLSR.L;R.VTLFLNLANDPTIER.I;
R.GYPGYMYTDLATIYER.A;
R.RDHADVSNQLYANYAIGK.D

Calculated Mr: **54367** Calculated *p*I: **5.04**

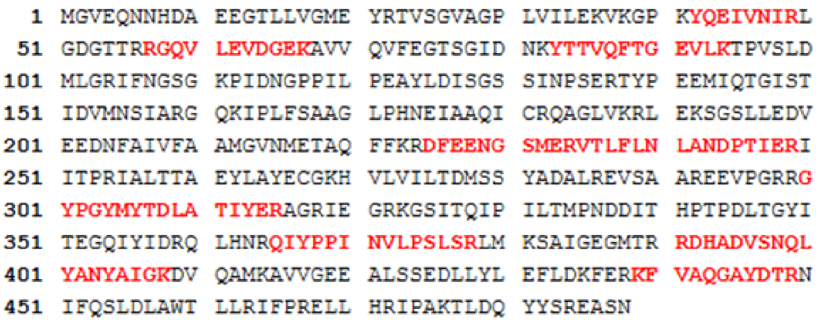
Probability Based Mowse Score:

Mascot Score Histogram

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:



```
  1 MGVEQNNHDA EEGTLLVGME YRTVSGVAGP LVILEKVKGP KYQEIVNIRL
 51 GDGTTRRGQV LEVDGEKAVV QVFEGTSGID NKYTTVQFTG EVLKTPVSLD
101 MLGRIFNGSG KPIDNGPPIL PEAYLDISGS SINPSERTYP EEMIQTGIST
151 IDVMNSIARG QKIPLFSAAG LPHNEIAAQI CRQAGLVKRL EKSGSLLEDV
201 EEDNFAIVFA AMGVNMETAQ FFKRDFEENG SMERVTLFLN LANDPTIERI
251 ITPRIALTTA EYLAYECGKH VLVILTDMSS YADALREVSA AREEVPGRRG
301 YPGYMYTDLA TIYERAGRIE GRKGSITQIP ILTMPNDDIT HPTPDLTGYI
351 TEGQIYIDRQ LHNRQIYPPI NVLPSLSRLM KSAIGEGMTR RDHADVSNQL
401 YANYAIGKDV QAMKAVVGEE ALSSEDLLYL EFLDKFERKF VAQGAYDTRN
451 IFQSLDLAWT LLRIFPRELL HRIPAKTLDQ YYSREASN
```

Spot No.: **D119 (S165)**

NCBI accession No.: **gi|224071449** Species: *Populus trichocarpa*

PFF score: [59]

Protein name: predicted protein

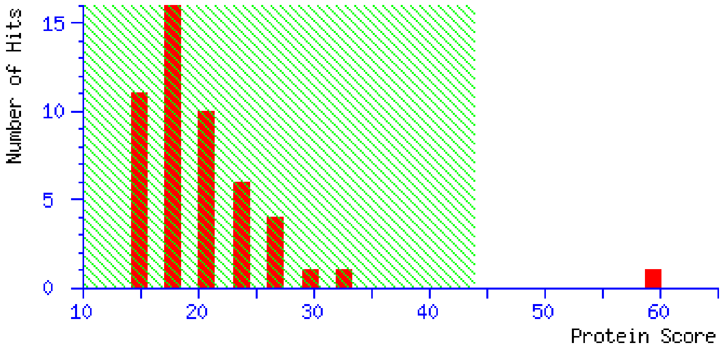
Matched peptides No.: [1] Sequence coverage %: [2]

Matched sequences: K.IDVIPHYPGR.L

Calculated Mr: **47121** Calculated *p*I: **5.28**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MDGTSEATWP EILGSRNWDN LLDPLDLSLR KLILRCGDFC QATYDAFNND
51 QNSRYCGTSR YGKRNFFHKV MLDNPENYQV SSFLYATARV SLPEAFLLHS
101 LSRDSWDRET NWIGYIAVTS DEQTKTLGRR EIYIAFRGTT RNYEWVDILG
151 AKLKSAKPLL RGATSTTHDQ ESSSSSDDDD DKVPKVMLGW LTMYISDDPN
201 SPFTKLSARA QLLAHIKELR ERYKDDDLSI IFTGHSLGAS LSILSAFDLV
251 ENGITDIPVS AFVFGSPQVG NKEFNERFNK YPNLKVLHIK NK**IDVIPHYP**
301 **GR**LMGYVYTG IEFEIDTRKS PSLKDSKNPS DWHNLQAMLH IVAGWNGEEQ
351 EFELKVKRSL ALVNKSSEFL KDECLVPGIW WVEKNKGMVR NEDGEWVLAP
401 PDEEDLPVPE C

Spot No.: **D120 (S166)**

NCBI accession No.: **gi|116789736** Species: *Picea sitchensis*

Protein name: unknown

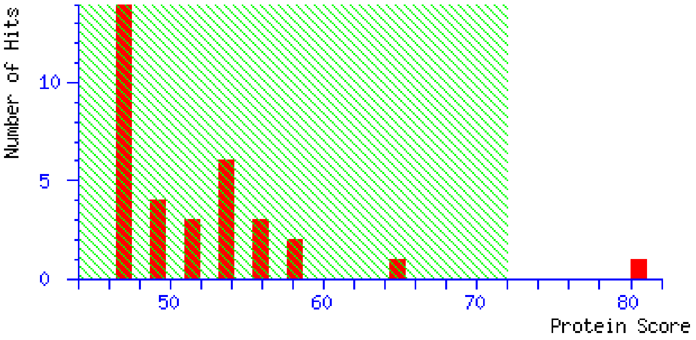
PMF Mascot score: **81** Sequence coverage %: **60**

Matched peptides No.: **6** Total peptides No.: **48**

Calculated Mr: **13436** Calculated *p*I: **5.91**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 **MPSHSLIGTT TTNRRGSMED YPNPFNPETI HELFKLVWSQ TNK**AR**AQKEG**
51 **GETELEVGAA ASK**K**TRTTTA NSNALK**LSCE FLRLFVTEAV QRAAIVAEVE
101 GSTQIEGTHL ERILPQLLLD F

Spot No.: **D121 (S167)**

NCBI accession No.: **gi|115392253**

Species: *Cercocarpus betuloides*

PFF score: [51] Protein name: polyphenol oxidase

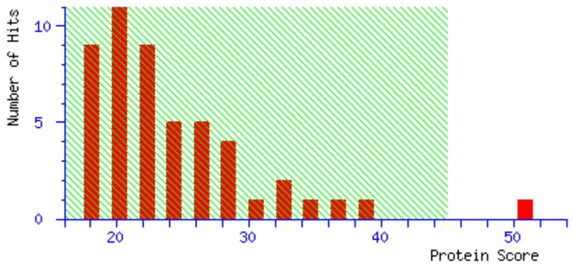
Matched peptides No.: [1] Sequence coverage %: [3]

Matched sequences: K.EKEQEEEILVIEGIEFDR.D

Calculated Mr: **51023** Calculated *p*I: **5.98**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

```
  1 PFAFAKPVAP PDVSKCGAAD LPTGAQPTNC CPPVASKIID FKLPSPTPLR VRPAAHAVDK
 61 AYIEKYSKAI ELMKALPDDD PRSFKQQANV HCAYCDGAYD QAGFPDLELQ IHNSWLFFPF
121 HRYYLYFHEK ILGSLIGDPT FALPFWNWDA PAGMPLPAIY ANPKSPLYDK FRAANHQPPT
181 LVDLDFNGTE DAASNETQIN ANLKIMYRQM VSNAKTPQLF FGNPYRAGDE PDPGGGSIEG
241 TPHGPVHLWT GDNTQPNFED MGNFYSAGRD PIFFAHHSNV DRLWSIWKTL GGKRTDITDT
301 DWLDSGFLFY DENAQMVRVK VRDCLESKNL GYVYQDANIP WLESKPTPRR VKAALGKIAK
361 KLHVAHAADN SSASKVVARA AFPIAKLDTK MSTVVARPKQ KKRSKKEKEQ EEEILVIEGI
421 EFDRDVAVKF DVYVNDEDDL PSGPDKSEFA GSFVS
```

Spot No.: **D122 (S168)**

NCBI accession No.: **gi|225430941**   Species: *Vitis vinifera*

PFF score: [210]

Protein name: regulator of ribonuclease-like protein 2

Matched peptides No.: [3]   Sequence coverage %: [24]

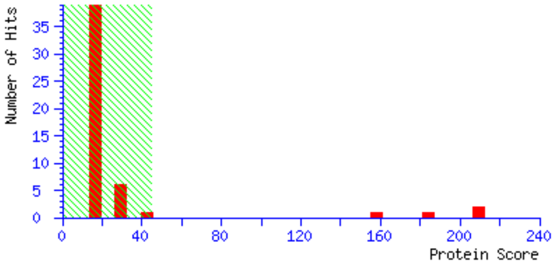
Matched sequences: K.VFEDNVLIR.E;

R.DVDEINGCDIGVR.A;
R.ISDGEWLYADTDGILISR.T

Calculated Mr: **17984**   Calculated *p*I: **5.39**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MALVTTAEVC DANPQLIVSG ELRALQPVFQ IYGRRPVFSG PIVTLK**VFED**
51 **NVLIR**EFLEE KGNGRVLVVD GGGSMRCAIL GGNPVVQAQN NGWAGIVVNG
101 CIR**DVDEING** **CDIGVR**ALNS HPMKANKKGI GEKHVPIAIA GTR**ISDGEWL**
151 **YADTDGILIS** **R**TELSV

Spot No.: **D123 (S171)**

NCBI accession No.: **gi|115392253**

Species: *Cercocarpus betuloides*

PFF score: [104] Protein name: actin depolymerizing factor

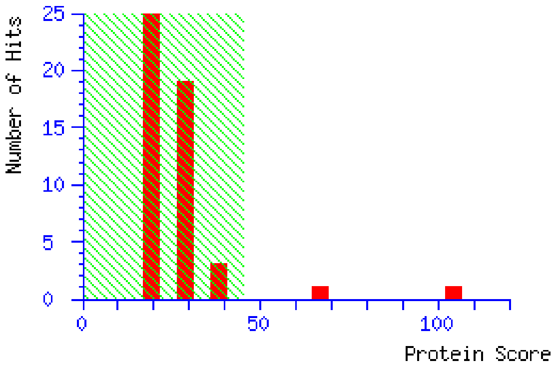
Matched peptides No.: [1] Sequence coverage %: [4]

Matched sequences: K.EKEQEEEILVIEGIEFDR.D

Calculated Mr: **58369** Calculated *p*I: **9.23**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 40 indicate peptides with significant homology.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 PFAFAKPVAP PDVSKCGAAD LPTGAQPTNC CPPVASKIID FKLPSPTPLR VRPAAHAVDK

61 AYIEKYSKAI ELMKALPDDD PRSFKQQANV HCAYCDGAYD QAGFPDLELQ IHNSWLFFPF

121 HRYYLYFHEK ILGSLIGDPT FALPFWNWDA PAGMPLPAIY ANPKSPLYDK FRAANHQPPT

181 LVDLDFNGTE DAASNETQIN ANLKIMYRQM VSNAKTPQLF FGNPYRAGDE PDPGGGSIEG

241 TPHGPVHLWT GDNTQPNFED MGNFYSAGRD PIFFAHHSNV DRLWSIWKTL GGKRTDITDT

301 DWLDSGFLFY DENAQMVRVK VRDCLESKNL GYVYQDANIP WLESKPTPRR VKAALGKIAK

361 KLHVAHAADN SSASKVVARA AFPIAKLDTK MSTVVARPKQ KKRSKK**EKEQ** **EEEILVIEGI**

421 **EFDR**DVAVKF DVYVNDEDDL PSGPDKSEFA GSFVS

Spot No.: **D124 (S177)**

NCBI accession No.: **gi|357480975** Species: *Medicago truncatula*

PFF score: [369]

Protein name: Proteasome subunit beta type

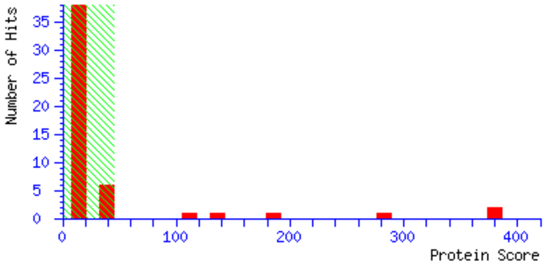
Matched peptides No.: [7] Sequence coverage %: [42]

Matched sequences: K.NVALYQFR.N;
R.VQFTEYIQK.N;
R.LVVAPPNFVIK.I;
R.NGIPLTTAAAANFTR.G;
K.GAFGYGSYFSLSMMDR.H;
K.ETGPSLYYIDYIATLHK.L;
K.LIAASGEPGDRVQFTEYIQK.N

Calculated Mr: **22572** Calculated *p*I: **6.06**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MECVFGLVGN GFAIVVADTS AVHSILVHKS NEDKIMFLDS HK**LIAASGEP**
51 **GDRVQFTEYI QKNVALYQFR NGIPLTTAAA ANFTR**GELAT ALRKNPYSVN
101 ILLAGYDK**ET GPSLYYIDYI ATLHK**LEK**GA FGYGSYFSLS MMDR**HFHSGM
151 NVEEAIDLVD KCILEIRSR**L VVAPPNFVIK** IVDKDGAREY AWRESVKDTP
201 ASA

Spot No.: **D125 (S187)**

NCBI accession No.: **gi|380468126** Species: *Hevea brasiliensis*

PFF score: [123]

Protein name: caffeic acid 3-O-methyltransferase

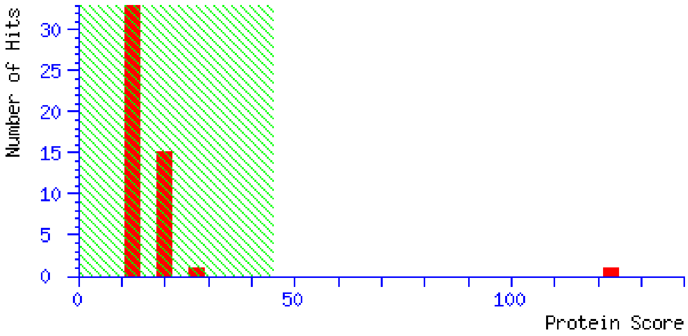
Matched peptides No.: [3] Sequence coverage %: [11]

Matched sequences: K.NPEAPVLLDR.M;
K.SWYHLNEAILEGGTPFNR.A;
R.AYGMNQFEYPGTDQR.F + Oxidation (M)

Calculated Mr: **40957** Calculated *p*I: **5.54**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MTGSEQSNSA SIMSGRSDEE TWNLAIDLAN TVILPMVLKS ALELNVIDII
51 STAGNSGASL SAPEIAQRIP EAK**NPEAPVL** **LDR**MLRLLAT YDIVKCSSNT
101 KENGEVERLY APGPICKFLT KNKNGSGSAA PLLLLHHDEV FMK**SWYHLNE**
151 **AILEGGTPFN** **RAYGMNQFEY** **PGTDQR**FNRV FNDAMSSYTT YLVKKILDAY
201 KGFDGLKSLV DVGGNSGVTL NSITSKYPHI KGINYDLPHV LADAPSYPGV
251 EHVAGDMFKS VPKGDAIILK WVLHDWNDDL CLKLLKNCWE ALPSNGKVIV
301 VESILPTVPE NNVTSQVLHK EDLMLLSFNV GGKERTRQEF EALASKSGFS
351 SCEFICCAYN SWVIEFHK

Spot No.: **D126 (S188)**

NCBI accession No.: **gi|380468126** Species: *Hevea brasiliensis*

PFF score: [117]

Protein name: caffeic acid 3-O-methyltransferase

Matched peptides No.: [2] Sequence coverage %: [8]

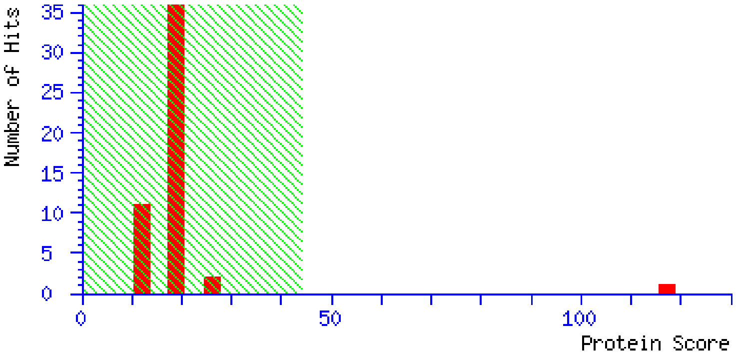
Matched sequences: K.SWYHLNEAILEGGTPFNR.A;

R.AYGMNQFEYPGTDQR.F + Oxidation (M)

Calculated Mr: **40957** Calculated *p*I: **5.54**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MTGSEQSNSA SIMSGRSDEE TWNLAIDLAN TVILPMVLKS ALELNVIDII
51 STAGNSGASL SAPEIAQRIP EAKNPEAPVL LDRMLRLLAT YDIVKCSSNT
101 KENGEVERLY APGPICKFLT KNKNGSGSAA PLLLLHHDEV FMK**SWYHLNE**
151 **AILEGGTPFN** **RAYGMNQFEY** **PGTDQR**FNRV FNDAMSSYTT YLVKKILDAY
201 KGFDGLKSLV DVGGNSGVTL NSITSKYPHI KGINYDLPHV LADAPSYPGV
251 EHVAGDMFKS VPKGDAIILK WVLHDWNDDL CLKLLKNCWE ALPSNGKVIV
301 VESILPTVPE NNVTSQVLHK EDLMLLSFNV GGKERTRQEF EALASKSGFS
351 SCEFICCAYN SWVIEFHK

Spot No.: **D127 (S189)**

NCBI accession No.: **gi|284433794** Species: *Jatropha curcas*

PFF score: [159]

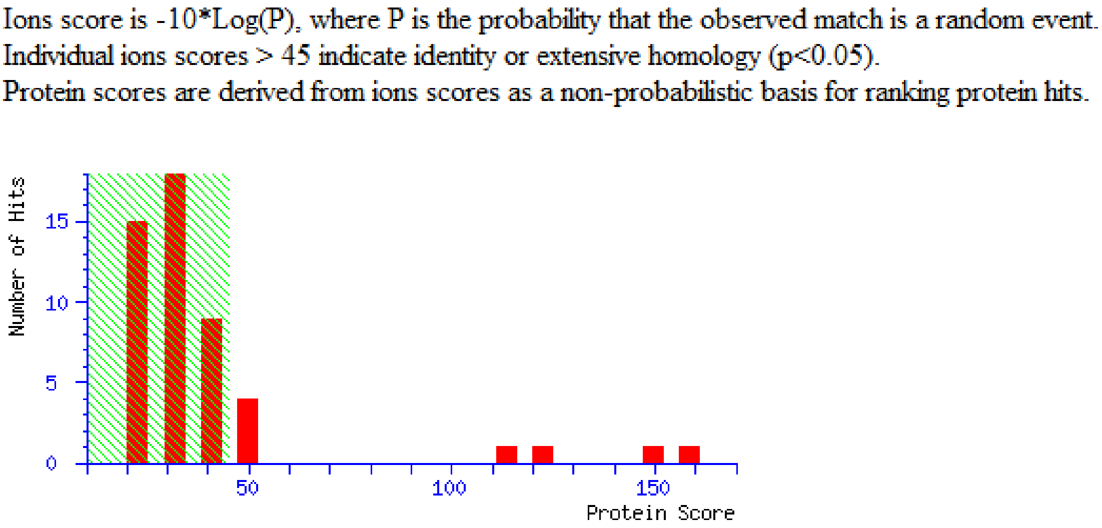
Protein name: glutathione S-transferase omega

Matched peptides No.: [3] Sequence coverage %: [10]

Matched sequences: K.IIGESLDLIK.Y;
K.YDITAGRPK.L;
K.ELVEFYK.K

Calculated Mr: **27480** Calculated *p*I: **5.41**

Probability Based Mowse Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Matched peptide sequences: shown in Bold Red:

1 MAATALDKSL PEKLPPILDA TAEQPPLFDG TIRLYTSYAC PFAQRVWITR
51 NYKGLQDKIK LVPLNLQNRP SWYGEKVYPA NKVPALEHNG **KIIGESLDLI**
101 **K**YIDANFEGP SLLPDDPAKK EFAEELFSYT DTFTKTVFTS FKGDAVKDAS
151 PAFDYLENAL HKFEDGPFLL GQFSLVDIAY IPFVERFQIF FSEVFK**YDIT**
201 **AGRPK**LAAWI EEMNKIEAYK QTKTDPK**ELV** **EFYK**KRLLAQ

Spot No.: **D128 (S190)**

NCBI accession No.: **gi|255567721**   Species: *Ricinus communis*

PFF score: [52]

Protein name: carboxymethylenebutenolidase, putative

Matched peptides No.: [1]   Sequence coverage %: [6]

Matched sequences: K.SMGMPDEDEAAVELAWSR.F + 2 Oxidation (M)

Calculated Mr: 30833   Calculated *p*I: **6.09**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
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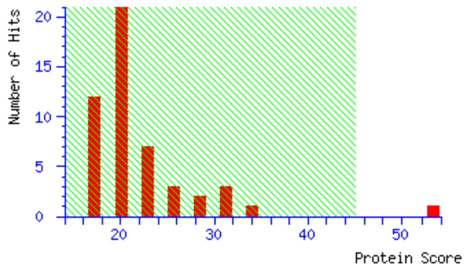


Matched peptide sequences: shown in Bold Red:

1 MLAAAIRSLS PSSTSSIFNK SALPPLLRSL SPSLSNSRFQ IRSMADSASS
51 PFKKVQIHRD NTTFDAYVIG KDDAPGIVVV QEWWGVDFEI KNHAEKISQL
101 EPGFKALIPD LYRGKVGLDV AEAQHLMDGL DWQGAVKDIG ASVNWLKANG
151 SKKAGVTGFC MGGALAIASS VLVPEVDAVV AFYGVPPSEL ADATQAKAPI
201 QAHFGELDNF VGFADITAAK ALEEKLKASG VPSEVHIYPG NAHAFMNRSA
251 EGVKRRK**SMG** **MPDEDEAAVE** **LAWSR**FRSWM NQYLSA

Spot No.: **D192 (S129)**

NCBI accession No.: **gi|255542380** Species: *Ricinus communis*

Protein name: cysteine synthase, putative

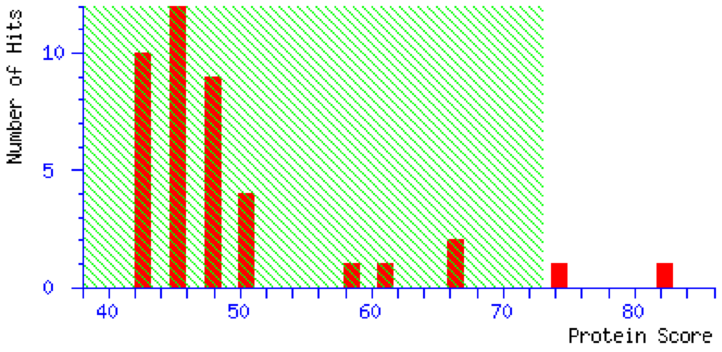
PMF Mascot score: **82** Sequence coverage %: **37**

Matched peptides No.: **13** Total peptides No.: **59**

Calculated Mr: **34435** Calculated *p*I: **5.50**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MVEEKSAIAK DVTELVGK**TP** **LVYLNHVVDG** **CVAR**IAAK**LE** **MMEPCSSVK**D

51 RIGYSMITDA EEK**GLIKPGE** **SVLIEPTSGN** **TGIGLAFMAA** **AK**GYK**LIITM**

101 **PASMSLERRM** **VLRAFGAELV** **LTDPAR**GMKG AVQKAEEILA KTPNSYILQQ

151 FENPANPKIH YETTGPEIWK GSGGKVDFFV SGIGTGGTVT GAGGYLREQN

201 PDIKLIGVEP VESAVLSGGK PGPHKIQGIG AGFIPGVLDV SLLDEVVQIS

251 SEEAIETAKL LALK**EGLLVG** **ISSGAAAAAA** **IK**IARR**PENA** **GK**LIVVIFPS

301 FGER**YLSSVL** **FESVKR**EAES MVFEP

Spot No.: **D130 (S197)**

NCBI accession No.: **gi|351727028** Species: *Glycine max*

Protein name: cell division cycle protein 48 homolog

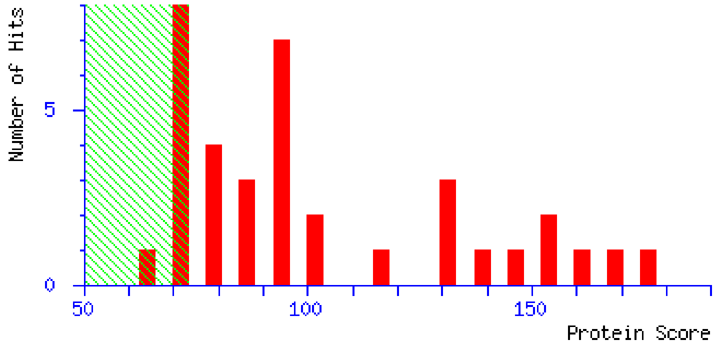
PMF Mascot score: **174** Sequence coverage %: **42**

Matched peptides No.: **37** Total peptides No.: **90**

Calculated Mr: **90512** Calculated *p*I: **5.18**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MSQQGESSDP KSGKK**DFSTA** **ILER**KKSPNR LVVDEAVNDD NSVVTMHPQT
51 MEK**LQLFR**GD TILIKGKKRK DTICIALADE NCEEPKIRMN KVVRSNLRVR
101 **LGDVVSVHQC** **PDVK**YGKRVH ILPIDDTIEG VTGNLFDAFL KPYFLEAYRP
151 VR**KGDLFLVR** GGMRSVEFKV VETDPGEYCV VAPDTEIFCE GEPLKREDEE
201 RLDEVGYDDV GGVR**KQMAQI** **RELVELPLRH** **PQLFK**SIGVK PPK**GILLYGP**
251 **PGSGK**TLIAR AVANETGAFF FCINGPEIMS K**LAGESESNL** **R**KAFEEAEKN
301 APSIIFIDEI DSIAPKREK**T** **HGEVERRIVS** **QLLTLMDGLK** **SRAHVIVIGA**
351 **TNRPNSIDPA** **LRRFGRFDRE** **IDIGVPDEVG** **RLEVLR**IHTK NMKLSDDVDL
401 ERIAK**DTHGY** **VGADLAALCT** **EAALQCIR**EK MDVIDLEDET IDAEVLNSMA
451 VTNEHFQTAL GTSNPSALR**E** **TVVEVPNVSW** **EDIGGLENVK** **RELQETVQYP**
501 **VEHPEKFEK**F GMSPSK**GVLF** **YGPPGCGK**TL LAK**AIANECQ** **ANFISVKGPE**
551 **LLTMWFGESE** **ANVR**EIFDKA R**QSAPCVLFF** **DELDSIATQR** **GSSVGDAGGA**
601 **ADRVLNQLLT** **EMDGMSAK**KT VFIIGATNRP DIIDPALLRP GR**LDQLIYIP**
651 **LPDEDSRHQI** **FK**ACLRKSPI AKNVDLRALA RHTQGFSGAD ITEICQRACK
701 YAIRENIEKD IERERKSREN PEAMDEDTVD DEVAEIKAAH FEESMKFARR
751 **SVSDADIRKY** **QAFAQTLQQS** **R**GFGSEFRFP ESGDRTTTGS DPFAASAGGA
801 DEDDLYS

Spot No.: **D131 (S218)**

NCBI accession No.: gi|14916100   Species: *Hevea brasiliensis*

PFF score: [802]

Protein name：hydroxymethylglutaryl coenzyme A

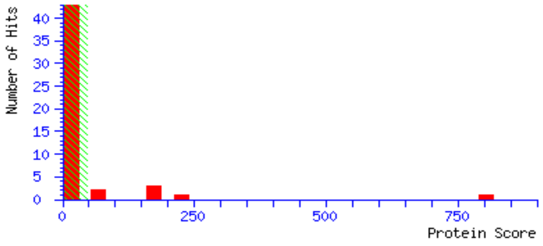
Matched peptides No.: [10]   Sequence coverage %: [35]

Matched sequences: R.LVFNDFVR.N;K.ARHELPPEK.F;
K.TFLMQIFEK.F + Oxidation (M);
K.VSQQVAKPLYDAK.V;K.LAPFSNLSGDESYQNR.D;
R.YGLVVCTDSAVYAEGPAR.P;
K.QFSISDAEYFVFHSPYNK.L;
K.DCSLLASGTYYLTEVDSLYR.R;
R.GSHMSHAYDFYKPNLASEYPVVDGK.L + Oxidation (M);
K.NVGILAVDIYFPPTFVQQEALEAHDGASK.G

Calculated Mr: **51761**   Calculated *p*I: **6.86**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAK**NVGILAV** **DIYFPPTFVQ** **QEALEAHDGA** **SK**GKYTIGLG QDCMAFCTEV
51 EDVISMSLTA VTSLLDKYNI DPKQIGRLEV GSETVIDKSK SIK**TFLMQIF**
101 **EK**FGNTDIEG VDSTNACYGG TAALFNCVNW VESSSWDGR**Y** **GLVVCTDSAV**
151 **YAEGPAR**PTG GAAAIAILVG PDAPIAFESK FR**GSHMSHAY** **DFYKPNLASE**
201 **YPVVDGK**LSQ TCYLMALDSC YKHFCAKYEK FEGK**QFSISD** **AEYFVFHSPY**
251 **NK**LVQKSFAR **LVFNDFVR**NA RSIDETAKEK **LAPFSNLSGD** **ESYQNR**DLEK
301 **VSQQVAKPLY** **DAK**VKPTTLI PKQVGNMYTA SLYAAFASLL HSKHTELAGK
351 RVTLFSYGSG LTATMFSLRL HEGQHPFSLS NIASVMNVAG KLK**ARHELPP**
401 **EK**FVNIMKLM EHRYGAKDFV RSK**DCSLLAS** **GTYYLTEVDS** **LYR**RFYAQKA
451 VGNTVENGLL ANGH

Spot No.: **D132 (S221)**

NCBI accession No.: **gi|357514973** Species: *Medicago truncatula*

PFF score: [99]

Protein name: **Annexin D4**

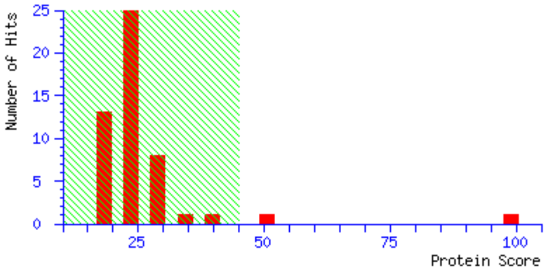
Matched peptides No.: [2] Sequence coverage %: [3]

Matched sequences: K.LLVALVSAYR.Y;
R.KLLVALVSAYR.Y

Calculated Mr: **36283** Calculated *p*I: **8.64**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

```
  1 MAFNQELEAI TQAFSGHGVD EKSLIAVLGK WDPLERETYR KKTSHFFIED
 51 HERQFQRWND HCVRLLKHEF VRFKNAVVLW SMHPWERDAR LAKEALKKGS
101 ISYGVLIEIA CTRSSEELLG ARKAYHSLFD HSIEEDVASH IHGNDRKLLV
151 ALVSAYRYEG TKVKDDTAKS EAKTLSNAIK NAQNKPIVED DEVIRILATR
201 SKLHLQAVYK HYKEISGKNL EEDLNDLRFK ETVQCLCTPQ VYFSKVLDAA
251 LKNDVNKNIK KSLTRVIVTR ADIDMKEIKA EYNNLYGVSL PQKIEETAKG
301 NYKDFLLTLI ARGG
```

Spot No.: **D133 (S222)**

NCBI accession No.: gi|21536853 Species: *Arabidopsis thaliana*

PFF score: [314]

Protein name： phosphoglycerate kinase, putative

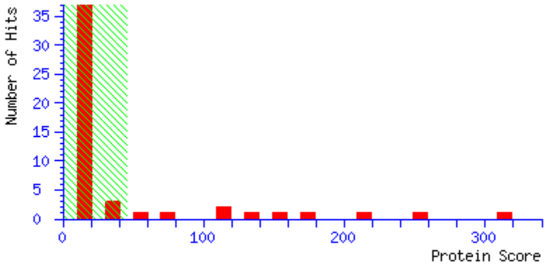
Matched peptides No.: [6] Sequence coverage %: [17]

Matched sequences: K.YSLKPLVPR.L;
K.ELDYLVGAVANPK.K;
K.YLKPSVAGFLMQK.E + Oxidation (M);
K.GVSLLLPTDVVIADK.F;
K.LAALADVYVNDAFGTAHR.A;
K.KLAALADVYVNDAFGTAHR.A

Calculated Mr: **42178** Calculated *p*I: **5.49**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

```
  1 MATKRSVGTL KEADLKGKSV FVRVDLNVPL DDNSNITDDT RIRAAVPTIK
 51 YLMGNGSRVV LCSHLGRPKG VTPKYSLKPL VPRLSELLGV EVVMANDSIG
101 EEVQKLVAGL PEGGVLLLEN VRFYAEEEKN DPEFAKKLAA LADVYVNDAF
151 GTAHRAHAST EGVAKYLKPS VAGFLMQKEL DYLVGAVANP KKPFAAIVGG
201 SKVSTKIGVI ESLLNTVDIL LLGGGMIFTF YKAQGLSVGS SLVEEDKLDL
251 AKSLMEKAKA KGVSLLLPTD VVIADKFAPD ANSKIVPATA IPDGWMGLDI
301 GPDSIKTFSE ALDTTKTIIW NGPMGVFEFD KFAAGTEAVA KQLAELSGKG
351 VTTIIGGGDS VAAVEKVGLA DKMSHISTGG GASLELIEGK PLPGVLALDE
401 A
```

Spot No.: **D134 (S223)**

NCBI accession No.: gi|255547137   Species: *Ricinus communis*

PFF score: [77]

Protein name：Alpha-1,4-glucan-protein synthase

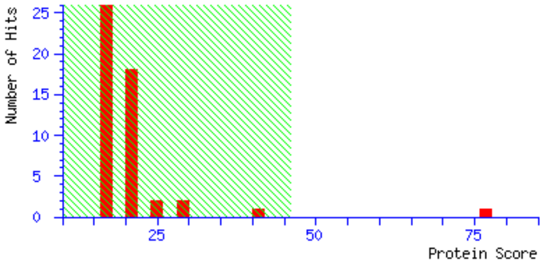
Matched peptides No.: [2]   Sequence coverage %: [5]

Matched sequences: K.DINALEQHIK.N;
K.VICDHLGFGVK.T

Calculated Mr: **41557**   Calculated *p*I: **5.82**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MADFAAISPT PLLKDELDIV IPTIRNLDFL EMWRPFFQPY HLIIVQDGDP
51 SKIIKVPEGF DYELYNRNDI NRILGPKASC ISFKDSACRC FGYMVSKKKY
101 IYTIDDDCFV AKDPSGK**DIN** **ALEQHIK**NLL CPSTPFFFNT LYDPYRTGAD
151 FVRGYPFSLR EGVPTAVSHG LWLNIPDYDA PTQLVKPLER NTRYVDAVMT
201 IPKGTLFPMC GMNLAFNREL IGPAMYFGLM GDGQPIGRYD DMWAGWCTK**V**
251 **ICDHLGFGVK** TGLPYIYHSK ASNPFVNLKK EYKGIYWQEE LIPFFQSAVL
301 PKECTTVQKC YIELSKQVRA KLGKIDEYFV KLADAMVTWV EAWDELNPSG
351 NSGELPNGAA K

Spot No.: **D135 (S227)**

NCBI accession No.: gi|333690873 Species: *Hevea brasiliensis*

PFF score: [386]

Protein name：glutathione-S-transferase tau 1

Matched peptides No.: [8] Sequence coverage %: [29]

Matched sequences: R.FWADFIDK.K;

K.VYEFVLVLK.K;
R.FWADFIDKK.I;
K.YEYREEDLR.N;
K.SPFLPSDPYQR.A;
K.SPLLLQMNPVHK.K + Oxidation (M);
K.DKSPFLPSDPYQR.A;
K.ESVSESVPDPEKVYEFVLVLK.K

Calculated Mr: **25595** Calculated *p*I: **5.48**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
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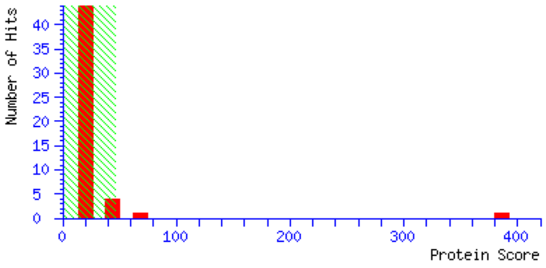


Matched peptide sequences: shown in Bold Red:

1 MAEEVILLDF WPSPFGMRVR IALAEKGVK**Y** **EYREEDLR**NK **SPLLLQMNPV**
51 **HK**KIPVLIHN GKPICESLIA VQYVDEVWK**D** **KSPFLPSDPY** **QR**AQAR**FWAD**
101 **FIDKK**IYDIG RKIWTTKGDE QEAAKKEFIE ALKLLEGELG NKPYFGGESM
151 GYVDVALIPF YSWFYAYETC GNFSIEPECP VLIAWAKRCL QK**ESVSESVP**
201 **DPEKVYEFVL** **VLK**KKFGIE

Spot No.: **D136 (S230)**

NCBI accession No.: gi|2970051   Species: *Vigna radiata*

PFF score: [104]

Protein name： ARG10

Matched peptides No.: [2]   Sequence coverage %: [12]

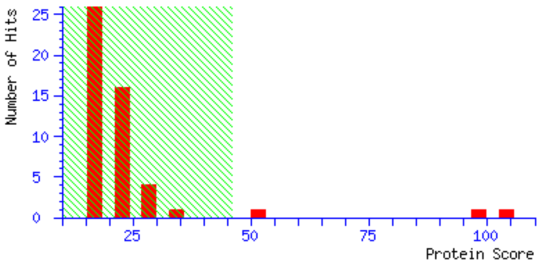
Matched sequences: K.SANEVILVIEAYK.A;

K.ITAVPAEEEEIWGATFK.V

Calculated Mr: **25750**   Calculated *p*I: **5.62**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MLGIFSSSVV SPPEELVAAG SRTPSPKTTA GKLLTRFVES KASAVSLQVG
51 EHVQLAYTHH SESPWYPRSF AVKDEIFCLF EGALDNLGSL RQQYGLAK**SA**
101 **NEVILVIEAY** **K**ALRDRAPYP ANRVVCHLSG SFAFIVFDKS TSTVFVASDQ
151 AGKVPLYWGI TADGYVAFAD DADLLKGSCG KSLASFPQGC FYSTAVGGLR
201 CYENPKNK**IT** **AVPAEEEEIW** **GATFK**VEGSA VLAATEY

Spot No.: **D137 (S231)**

NCBI accession No.: gi|2832430 Species: *Hevea brasiliensis*

PFF score: [217]

Protein name： prohevein

Matched peptides No.: [2] Sequence coverage %: [20]

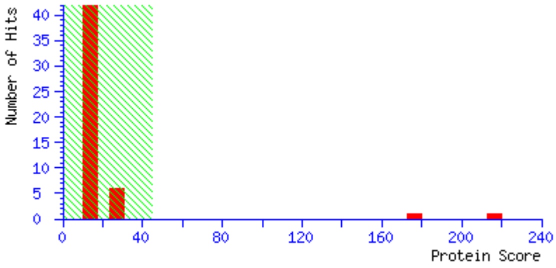
Matched sequences: R.IVDQCSNGGLDLDVNVFR.Q;

K.YGWTAFCGPVGAHGQPSCGK.C

Calculated Mr: **20852** Calculated *p*I: **5.64**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 EQCGRQAGGK LCPNNLCCSQ WGWCGSTDEY CSPDHNCQSN CKDSGEGVGG
51 GSASNVLATY HLYNSQDHGW DLNAASAYCS TWDANKPYSW RSK**YGWTAFC**
101 **GPVGAHGQPS** **CGK**CLSVTNT GTGAKATVR**I** **VDQCSNGGLD** **LDVNVFR**QLD
151 TDGKGYERGH LTVNYQFVDC GDSFNPLFSV MKSSVIN

Spot No.: **D138 (S233)**

NCBI accession No.: gi|14423933 Species: *Hevea brasiliensis*

PFF score: [384]

Protein name：Small rubber particle protein

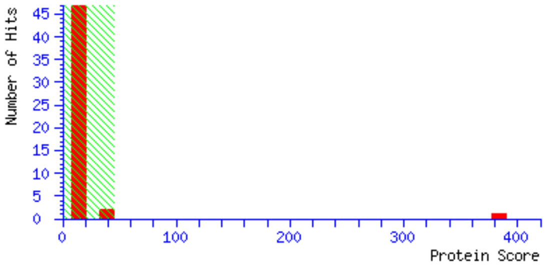
Matched peptides No.: [5] Sequence coverage %: [36]

Matched sequences: K.AEQYAVITWR.A;
R.VSSYLPLLPTEK.I;
K.QVSAQTYSVAQDAPR.I;
K.DISGPLKPGVDTIENVVK.T;
R.IVLDVASSVFNTGVQEGAK.A

Calculated Mr: **22331** Calculated *p*I: **4.80**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEEVEEERL KYLDFVRAAG VYAVDSFSTL YLYAK**DISGP** **LKPGVDTIEN**
51 **VVK**TVVTPVY YIPLEAVKFV DKTVDVSVTS LDGVVPPVIK **QVSAQTYSVA**
101 **QDAPRIVLDV** **ASSVFNTGVQ** **EGAK**ALYANL EPK**AEQYAVI** **TWR**ALNKLPL
151 VPQVANVVVP TAVYFSEKYN DVVRGTTEQG YR**VSSYLPLL** **PTEK**ITKVFG
201 DEAS

Spot No.: **D139 (S234)**

NCBI accession No.: gi|132270 Species: *Hevea brasiliensis*

PFF score: [379]

Protein name： Rubber elongation factor protein

Matched peptides No.: [4] Sequence coverage %: [38]

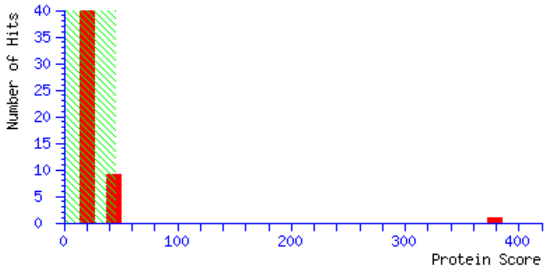
Matched sequences: K.NVAVPLYNR.F;

K.DASIQVVSAIR.A;
K.FVDSTVVASVTIIDR.S;
K.DKSGPLQPGVDIIEGPVK.N

Calculated Mr: **14713** Calculated *p*I: **5.04**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK **DKSGPLQPGV**
51 **DIIEGPVKNV** **AVPLYNR**FSY IPNGALK**FVD** **STVVASVTII** **DR**SLPPIVK**D**
101 **ASIQVVSAIR** AAPEAARSLA SSLPGQTKIL AKVFYGEN

Spot No.: **D140 (S238)**

NCBI accession No.: gi|2832430 Species: *Hevea brasiliensis*

PFF score: [344]

Protein name： prohevein

Matched peptides No.: [3] Sequence coverage %: [26]

Matched sequences: R.QLDTDGKGYER.G;

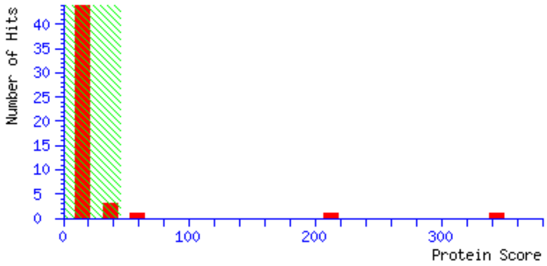
R.IVDQCSNGGLDLDVNVFR.Q;

K.YGWTAFCGPVGAHGQPSCGK.C

Calculated Mr: **20852** Calculated *p*I: **5.64**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 EQCGRQAGGK LCPNNLCCSQ WGWCGSTDEY CSPDHNCQSN CKDSGEGVGG

51 GSASNVLATY HLYNSQDHGW DLNAASAYCS TWDANKPYSW RSK**YGWTAFC**

101 **GPVGAHGQPS** **CGK**CLSVTNT GTGAKATVR**I** **VDQCSNGGLD** **LDVNVFRQLD**

151 **TDGKGYER**GH LTVNYQFVDC GDSFNPLFSV MKSSVIN

Spot No.: **D141 (S247)**

NCBI accession No.: **gi|123062** Species: *Hevea brasiliensis*

PFF score: [158]

Protein name: Pro-hevein

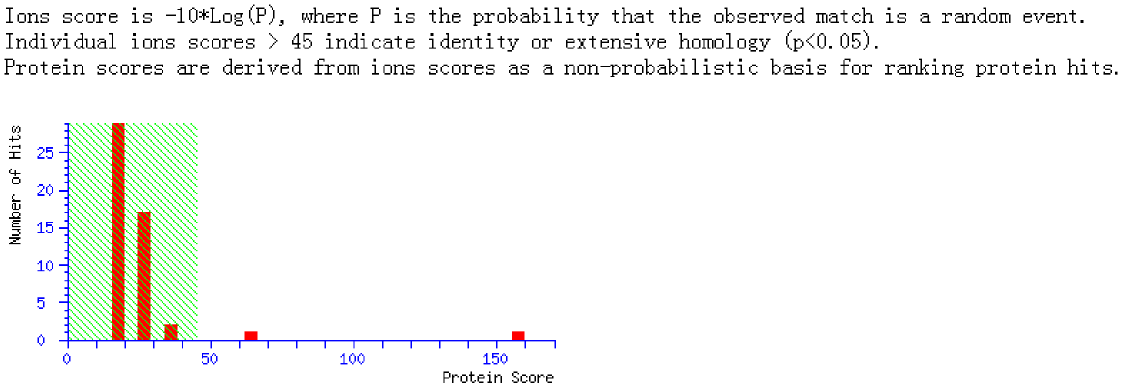
Matched peptides No.: [2] Sequence coverage %: [11]

Matched sequences: K.CLSVTNTGTGAK.T;

R.QLDTDGKGYER.G

Calculated Mr: **22700** Calculated *p*I: **5.63**

Probability Based Mowse Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Matched peptide sequences: shown in Bold Red:

1 MNIFIVVLLC LTGVAIAEQC GRQAGGKLCP NNLCCSQWGW CGSTDEYCSP
51 DHNCQSNCKD SGEGVGGGSA SNVLATYHLY NSQDHGWDLN AASAYCSTWD
101 ANKPYSWRSK YGWTAFCGPV GAHGQSSCGK **CLSVTNTGTG AK**TTVRIVDQ
151 CSNGGLDLDV NVFR**QLDTDG KGYER**GHITV NYQFVDCGDS FNPLFSVMKS
201 SVIN

Spot No.: **D142 (S249)**

NCBI accession No.: **gi|132270**   Species: *Hevea brasiliensis*

PFF score: [405]

Protein name: Rubber elongation factor protein

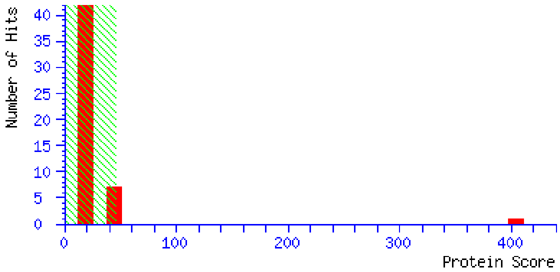
Matched peptides No.: [4]   Sequence coverage %: [38]

Matched sequences: K.NVAVPLYNR.F;
K.DASIQVVSAIR.A;
K.FVDSTVVASVTIIDR.S;
K.DKSGPLQPGVDIIEGPVK.N

Calculated Mr: **14713**   Calculated *p*I: **5.04**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK **DKSGPLQPGV**
51 **DIIEGPVKNV** **AVPLYNR**FSY IPNGALK**FVD** **STVVASVTII** **DR**SLPPIVK**D**
101 **ASIQVVSAIR** AAPEAARSLA SSLPGQTKIL AKVFYGEN

Spot No.: **D143 (S251)**

NCBI accession No.: **gi|132270**   Species: *Hevea brasiliensis*

PFF score: [470]

Protein name: Rubber elongation factor protein

Matched peptides No.: [4]   Sequence coverage %: [27]

Matched sequences: K.NVAVPLYNR.F;
K.DASIQVVSAIR.A;
K.SGPLQPGVDIIEGPVK.N;
K.DKSGPLQPGVDIIEGPVK.N

Calculated Mr: **14713**   Calculated *p*I: **5.04**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
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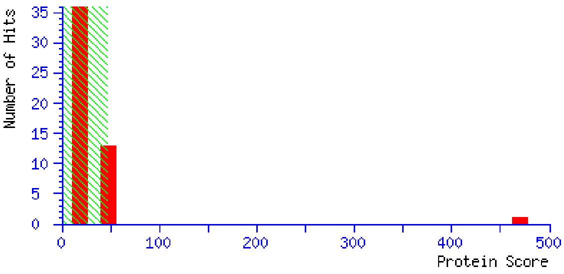


Matched peptide sequences: shown in Bold Red:

1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK **DKSGPLQPGV**
51 **DIIEGPVKNV** **AVPLYNR**FSY IPNGALKFVD STVVASVTII DRSLPPIVK**D**
101 **ASIQVVSAIR** AAPEAARSLA SSLPGQTKIL AKVFYGEN

Supplementary Figure S4

Identification of ethylene responsive latex proteins by iTRAQ

1. Labeled samples:

117:	**E3TL (total latex)**
116:	**E5TL**
115:	**D3TL**
114:	**D5TL**

Needed values: **117: 115= E3TL: D3TL**

116: 114= E5TL: D5TL

2.

14. Details of All Protein Summary for Rubber Latex _iTRAQ 4 plex

The 405 different proteins identified by ITRAQ.

Protein No.: I-2

Protein name and Species:

Beta-1,3-glucanase form 'RRII Gln 2' OS=Hevea brasiliensis PE=3 SV=1

Accession: Tr|D1M8S7|D1M8S7_HEVBR

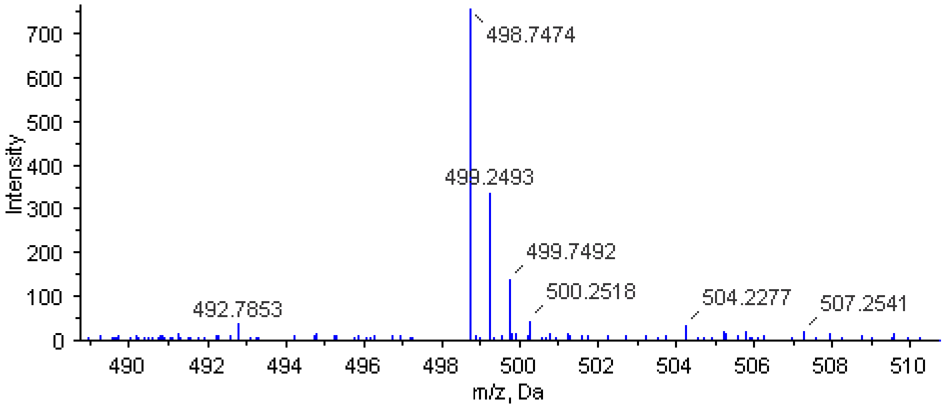
Unused ProtScore: 66.5 **Seq Cov %: 67.1**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.38

116: 114=E5TL: D5TL=0.57

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAICSSTSGTSSSLPSRTTVMLLLFFFTASVG**ITDAQVGVCYGMQGNNLPPVSEVIALYK**KSNIT**RMRI**
YDPNQAVLEALRGSNIELILGVPNSDLQSLTNPSNAKSWVQKNVRGFWSSVRFRYIAVGNEISPVNRGT
AWLAQFVLPAMRNIHDAIRSAGLQDQIKVSTAIDLTLVGNSYPPSAGAFRDDVR**SYLNPIIRFLSSIRS**
PLLANIYPYFTYAGNPRDISLPYALFTSPSVVVWDGQRGYK**NLFDATLDALYSALER**ASGGSLEVVVSE
SGWPSAGAF**AATFDNGRTYLSNLIQHVKR**GTPKRPKR**AIETYLFAMFDENKKQPEVEKHFGLFFPNK**WQ
K**YNLNFSAEK**NWDISTEHNAT**ILFLK**SDM

Protein No.: I-5

Protein name and Species:

Major latex allergen Hev b 5 OS=Hevea brasiliensis PE=1 SV=3

Accession:

sp|Q39967|ALL5_HEVBR

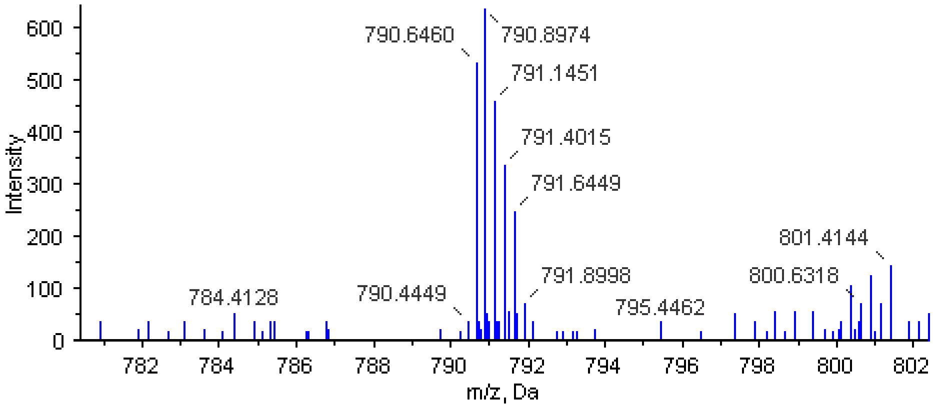
Unused ProtScore: 58.21 **Seq Cov %: 95.4**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=3.25

116: 114=E5TL: D5TL=1.54

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

M**ASVEVESAATALPKNETPEVTKAEETKTEEPAAPPASEQETADATPEKEEPTAAPAEPEAPAPETEKA**
EEVEKIEK**TEEPAPEADQTTPEEKPAEPEPVAEEEPKHETKETETEAPAAPAEGEKPAEEEKPITEAAE**
TATTEVPVEKTEE

Protein No.: I-7

Protein name and Species:

Latex allergen hev b 7.02 (Fragment) OS=Hevea brasiliensis PE=2 SV=1

Accession: tr|Q706V4|Q706V4_HEVBR

Unused ProtScore: 54.77

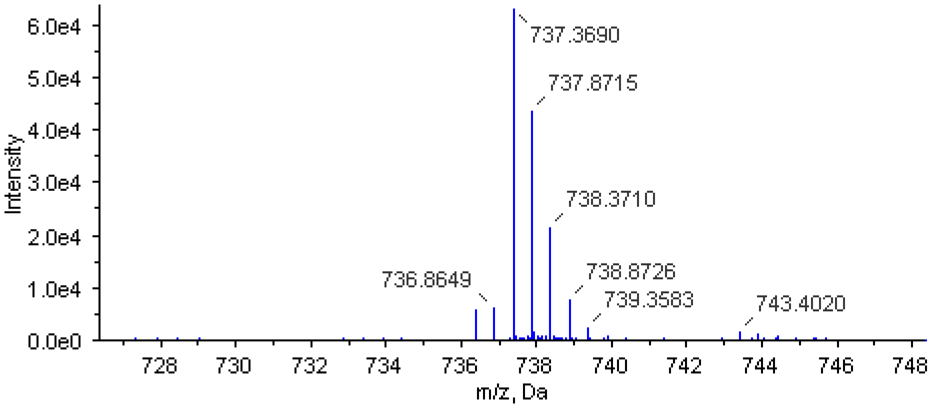
Seq Cov %: 71.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.33

116: 114=E5TL: D5TL=0.30

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

ATGSTTLTQGKKITVLSIDGGGIRGIIPGIILASLESKLQDLDGPDARIADYFDIIAGTSTGGLITTML
TAPNEDKKPMYQAKDIKDFYLENCPKIFPKESR**DNYDPIHSIGPIYDGEYLRELCNNLLK**DLTV**KDTLT**
DVIIPTFDIKLLLPVIFSSDDAKCNALKNAR**LADVCISTSAAPVLLPAHSFTTEDDK**NIH**TFELIDGGV**
AATNPTLLALTHIRNEIIRQNPR**FIGANLTESK**SR**LVLSLGTGK**SEYKEK**YNADMTSK**WRLYNWALYNG
NSPAVDIFSNASSDMVDFHLSALFK**SLDCEDYYLRIQDDTLTGEESSGHIATEENLQRLVEIGTR**LLEK
QESR**INLDTGRLESIPGASTNEAAITK**FAKLLSEERKLRQLK

Protein No.: I-10

Protein name and Species:

Actin OS=Morus alba PE=3 SV=2

Accession:

tr|E5FR85|E5FR85_MORAL

Unused ProtScore: **44.55**

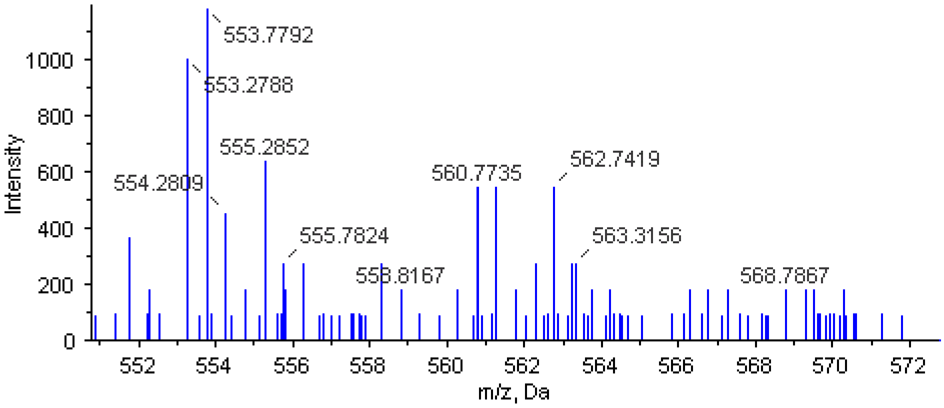
Seq Cov %: **56.2**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.39

116: 114=E5TL: D5TL=0.75

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MADAEDIQPLVCDNGTGMVK**AGFAGDDAPRAVFPSIVGRPRHTGVMVGMGQKDAYVGDEAQSK**RGILTL
K**YPIEHGIVSNWDDMEK**IWHHTFYNELR**VAPEEHPVLLTEAPLNPK**ANREKMTQIMFETFNVPAMYVAI
QAVLSLYASGR**TTGIVLDSGDGVSHTVPIYEGYALPHAILR**LDLAGR**DLTDALMK**ILTER**GYMFTTTAE**
REIVRDMKGK**LAYVALDYEQELETAK**SGSSVEK**NYELPDGQVITIGAER**YRCPQVLFQPSLIGMEAAGI
HETTYNSIMKC**DVDIR**K**DLYGNIVLSGGSTMFPGIADR**MSK**EITALAPSSMKIKVVAPPERK**YSVWIGG
SILASLSTFQQMWISK**GEYDESGPSIVHR**KCF

Protein No.: I-11

Protein name and Species:

Heat shock protein OS=Hevea brasiliensis PE=2 SV=1

Accession: tr|Q71EE1|Q71EE1_HEVBR

Unused ProtScore: 43.62

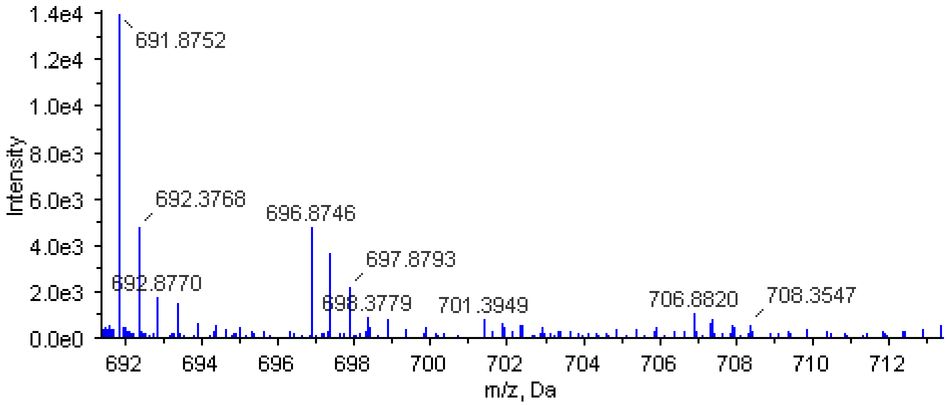
Seq Cov %: 38.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.58

116: 114=E5TL: D5TL=1.42

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MADAETFAFQAEINQLLSLIINTFYSNKEIFLR**EIISNASDALDKIR**FESLTDK**SKLDAQPELFIR**LVPDKANK**TLSIIDSGIGMTKADLVNNLGTIAR**SGTKEFMEALQAGADVSMIGQFGVGFYSAYLVAEKVIVTTKHNDDEQYIWESQAGGSFTVTRDVNGDQLGRGTK**ITLFLKEDQLEYLEER**RIKDLVKKHSEFISYPIYLWTEKTTEKEISDDEDDEPKKEEEGDVEDVDEEKETKSKKKKIKEVSHEWQLINKQKPIWLRKPEEITKEEYASFYKSLTNDWEDHLAVKHFSVEGQLEFKAILFVPK**RAPFDLFDTR**KKMSNIKLYVRR**VFIMDNCEELIPEYLGFVKGVVDSDDLPLNISR**EMLQQNKILKVIRKNLVKK**CIEMFNEIAENK**EDYNK**FYEAFSK**NLK**LGIHEDSQNR**AK**LADLLR**YHSTK**SGDEMTSLKDYVTR**MKEGQK**DIYYITGESK**K**AVENSPFLER**LKKKGYEVLF**MVDAIDEYAVGQLK**EYDGKKLVSATKEGLK**LDDETEEEK**KKKEEKKK**SFENLCK**TIK**DILGDK**VEK**VVVSDRIVDSPCCLVTGEYGWTANMER**IMKAQALRDSSMSSYMSSKK**TMEINPDNVIVEELR**KRAEADKNDKSVKDLVLLLFETALLTSGFSLDDPNTFSARIHRMLK**LGLSIDDDETAGDDADMPALEEDGAEESK**MEEVD

Protein No.: I-12

Protein name and Species:

50 kDa protein; Major latex allergen Hev b 4 OS=Hevea brasiliensis PE=2 SV=1

Accession: tr|Q5VLJ6|Q5VLJ6_HEVBR

Unused ProtScore: 42.03

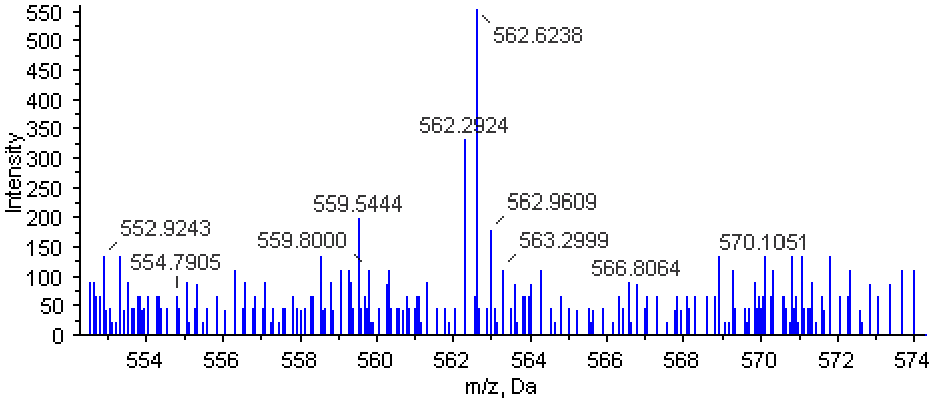
Seq Cov %: 35.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.46

116: 114=E5TL: D5TL=0.56

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAGKGEGPAIGIDLGTTYSCVGVWQHDR**VEIIANDQGNR**TTPSYVGFTDTER**LIGDAAKNQVAMNPINT**
VFDAKRLIGRR**FTDASVQSDIK**LWPFKVFSGPGDKPMIQVNYKGEDK**QFSAEEISSMVLMK**MR**EIAEAY**
LGTTVKNAVVTVPAYFNDSQRQATK**DAGVIAGLNVMRIINEPTAAAIAYGLDKK**ATSVGEKNVLIFDLG
GGTFDVSLLTIEEGIFEVK**ATAGDTHLGGEDFDNRMVNHFVQEFK**RKNKKDISGNPRALRRLRTACERA
KRTLSSTAQTTIEIDSLYEGIDFYSTITR**ARFEELNMDLFR**KCMEPVEKCLRDAKMDKRTVHDVVLVGG
STRIPK**VQQLLQDFFNGK**ELCK**SINPDEAVAYGAAVQAAILSGEGNEK**VQDLLLLDVTPL**SLGLETAGG**
VMTVLIPRNTTIPTKK**EQVFSTYSDNQPGVLIQVYEGER**TRTR**DNNLLGKFELSGIPPAPRG**VPQITVC
FDIDANGILNVSAEDKTTGQKNK**ITITNDK**GR**LSKEEIEKMVQEAEK**YKSEDEEHKKKVEAK**NALENYA**
YNMRNTVKDEKIGGKLDPADKKIEDAVEQTIQWLDSNQLGEADEFEDKMK**ELESICNPIIAK**MYQGGA
GPDMGGGMDDDVPAGGSGAGPKIEEVD

Protein No.: I-13

Protein name and Species:

Acetyl-CoA C-acetyltransferase OS=Hevea brasiliensis GN=HbAACT PE=2 SV=1

Accession: tr|A9ZMZ4|A9ZMZ4_HEVBR

Unused ProtScore: 41.88

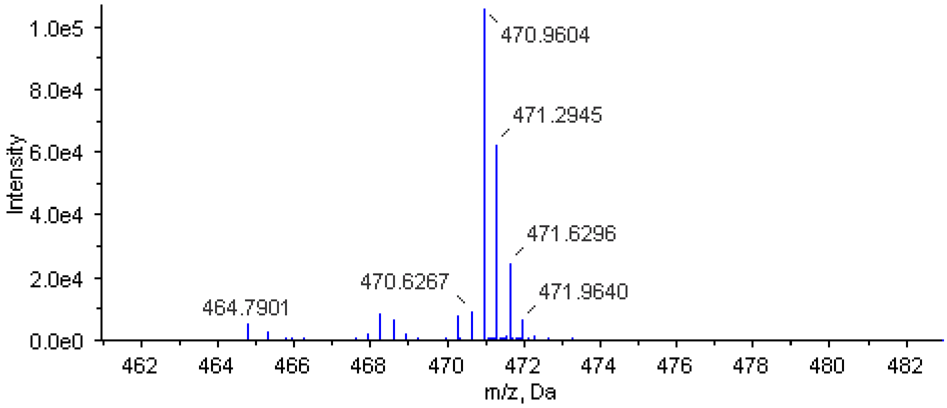
Seq Cov %: 76

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.65

116: 114=E5TL: D5TL=0.45

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

M**APVAAAEIKPRDVCIVGVARTPMGGFLGLLSTLPATKLGSIAIEAALK**R**ASVDPSLVQEVFFGNVLSA**
NLGQAPARQAALGAGIPNSVVCTTVNKVCASGMKATMLAAQSIQLGINDVVVAGGMESMSNAPKYLAEA
RKGSR**LGHDSLVDGMLK**DGLWDVYNDVGM**GSCAEICADNHSITREDQDKFAIHSFERGIAAQESGAFAW**
EIVPVEVSGGRGKPLTIVDKDEGLGKFDPVKLRKLRPSFK**ENGGTVTAGNASSISDGAAALILVSGETA**
LKLGLQVIAKIR**GYADAAQAPELFTTAPALAIPK**TIANAGLDASQVDYYEINEAFAVVALANQK**LLGLN**
PEKVNVHGGAVSLGHPLGCSGARILVTLLGVLRKKNAKYGVGGVCNGGGGASALVVELL

Protein No.: I-15

Protein name and Species:

Enolase 1 OS=Hevea brasiliensis GN=ENO1 PE=1 SV=1

Accession: sp|Q9LEJ0|ENO1_HEVBR

Unused ProtScore: 39.75

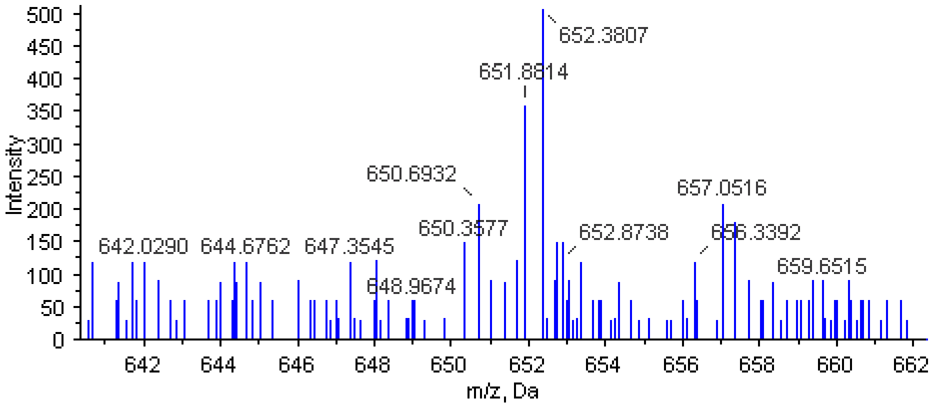
Seq Cov %: 45.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.30

116: 114=E5TL: D5TL=0.37

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

M**AITIVSVR**ARQIFDSR**GNPTVEADVKLSDGYLARAAVPSGASTGIYEALELRDGGSDYLGK**GVSK**AVE**
NVNIIIGPALVGKDPTDQVGIDNFMVQQLDGTVNEWGWCKQKLGANAILAVSLAVCK**AGAHVK**GIPLYE
HIANLAGNKNLVLPVPAFNVINGGSHAGNKLAMQEFMILPVGASSFKEAMK**MGAEVYHHLK**SVIKK**KYG**
QDATNVGDEGGFAPNIQENKEGLELLKTAIAKAGYTGKVVIGMDVAASEFYGSDQ**TYDLNFKEENNNGS**
QKISGEALKDLYKSFVAEYPIVSIEDPFDQDDWAHYAK**LTSEIGEKVQIVGDDLLVTNPK**RVEKAIKEK
ACNALLLKVNQIGSVTESIEAVKMSKR**AGWGVMASHR**SGETEDTFIADLSVGLATGQIKTGAPCRSERL
AKYNQLLR**IEEELGSEAVYAGANFR**KPVEPY

Protein No.: I-17

Protein name and Species:

Latex-abundant protein；caspase；type II metacaspase [Hevea brasiliensis] OS=Hevea brasiliensis GN=LAR PE=2 SV=1

Accession: tr|Q9ZSP8|Q9ZSP8_HEVBR

Unused ProtScore: 37.25

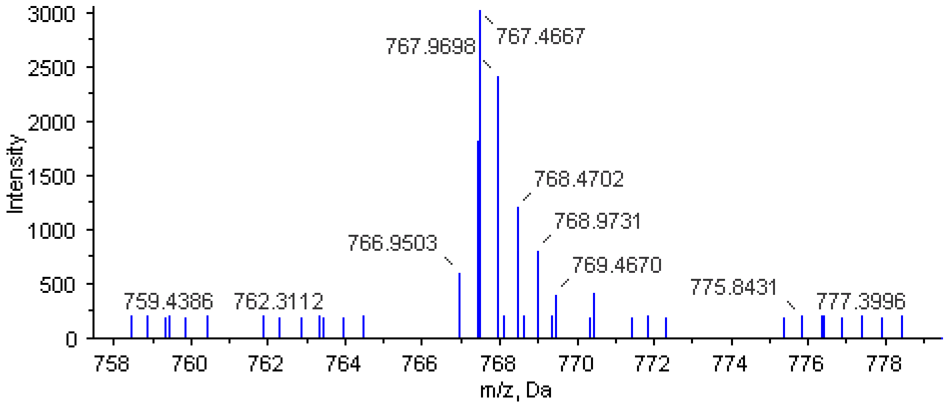
Seq Cov %: 65.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.52

116: 114=E5TL: D5TL=0.30

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAKK**AVLIGINYPGTK**AELK**GCINDVK**RMYRCLVDR**YGFSEEDITVLIDIDESYIQPTGK**NIRR**VLTDL**
VRSAEPGDLLFVHYSGHGTRLPAETGEDDDTGFDECIVPCDMNLITDDDFREFVDQVPHGCRITVVSDS
CHSGGLIDEAKEQIGESTKRK**EEESESGFGFK**SFLK**QTIQDAFESR**GVHLPSDLHHHHGHR**DEEDFDNR**
VVEEDYGDSGYVKSK**SLPLSTLIEILK**QK**TGKDDIDVGKLRPTLFDMFGDDASPK**VKKFMKVILNKLRH
GDGESGGGGFLGMVGSLAQEFLK**HKLDENDESYVKPALETEVDSKQEVYAGK**TKR**SLPDGGILISGCQT**
DQTSADASPSGKSSEAYGALSNAIQTIIAETDGAVTNQELVLKARKMLKKQGFTQKPGLYCSDDHVEAS
FVC

Protein No.: I-18

Protein name and Species:

Mevalonate disphosphate decarboxylase OS=Hevea brasiliensis PE=2 SV=1

Accession: tr|Q944G0|Q944G0_HEVBR

Unused ProtScore: 34.69

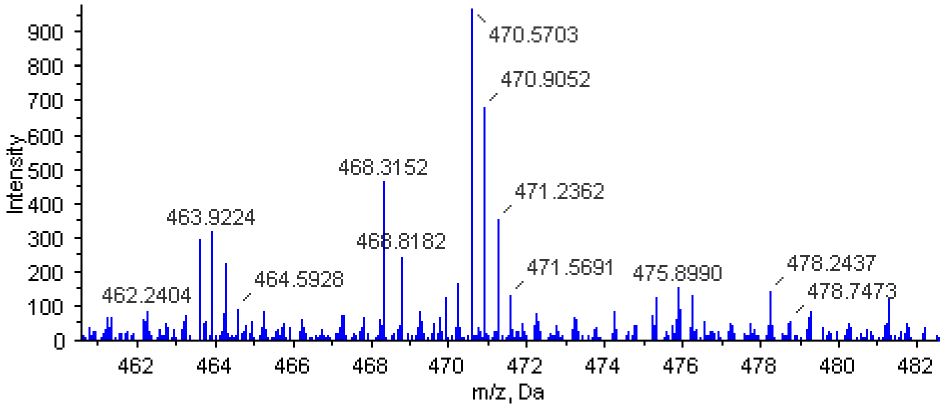
Seq Cov %: 43.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.49

116: 114=E5TL: D5TL=0.35

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAESWVI**MVTAQTPTNIAVIK**YWGKRDEKLILPVNDSISVTLDPAHLCTTTTVAVSPSFAQDRMWLNGK
EISLSGGRYQNCLREIRAR**ACDVEDKER**GIKISKKDWEKLYVHIASYNNFPTAAGLASSAAGFACLVFA
LAKLMNAK**EDNSELSAIAR**QGSGSACR**SLFGGFVK**WKMGK**VEDGSDSLAVQVVDEK**HWDDLVIIIAVVS
SRQKETSSTTGMR**ETVETSLLLQHR**AKEIVPKR**IVQMEESIK**NRNFASFAHLTCADSNQFHAVCMDTCP
PIFYMNDTSHR**IISCVEK**WNR**SVGTPQVAYTFDAGPNAVLIAHNR**KAAAQLLQK**LLFYFPPNSDTELNS**
YVLGDKSILK**DAGIEDLKDVEALPPPPEIK**DAPR**YKGDVSYFICTRPGQGPVLLSDESQALLSPETGLP**
K

Protein No.: I-19

Protein name and Species:

glyceraldehyde-3-phosphate dehydrogenase， NADP-dependent OS=Pisum sativum GN=GAPN PE=1 SV=1

Accession: sp|P81406|GAPN_PEA

Unused ProtScore: 32.73

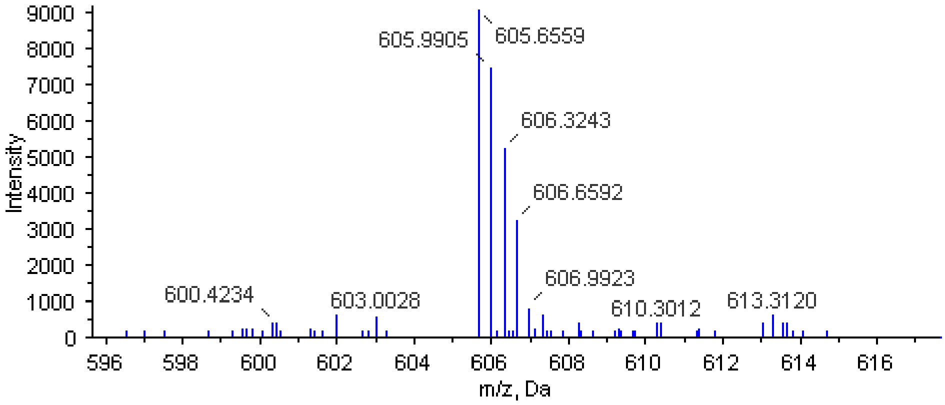
Seq Cov %: 46.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.50

116: 114=E5TL: D5TL=0.77

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAATGVLAEIIDGDVYKYYADGEWKKSTSGK**SVAIINPTTR**KPQYK**VQACSQEEVNK**VMDSAKSAQKSW
AKTPLWKR**AELLHK**AAAILKEHKAAIAECLVKEIAKPAK**DAVTEVVRSGDLVSYCAEEGVR**ILGEGK**FL**
VSDSFPGNERTKYCLTSK**IPLGVILAIPPFNYPVNLAVSK**IAPALIAGNSIVLKPPTQGAVAALHMVHC
FHLAGFPK**GLISCVTGKGSEIGDFLTMHPGVNCISFTGGDTGIAISKKSGMIPLQMELGGKDACIVLED**
ADLDLVAANIIKGGFSYSGQRCTAVK**VVLVMESVADALVEK**VKVKVAKLSVGPPEDDSDITPVVSESSA
NFIEGLVNDAKEK**GATFCQEYKR**EGNLIWPLLLDNVRPDMR**IAWEEPFGPVLPVIRINSVEEGIHHCNA**
SNFGLQGCVFTKDINKAIMISDAMESGTVQINSAPAR**GPDHFPFQGIKDSGIGSQGITNSINMMTK**VKT
TVINLPSPSYTMG

Protein No.: I-22

Protein name and Species:

Hydroxymethylglutaryl coenzyme A synthase OS=Hevea brasiliensis PE=2 SV=1

Accession: tr|Q944F8|Q944F8_HEVBR

Unused ProtScore: 31.1

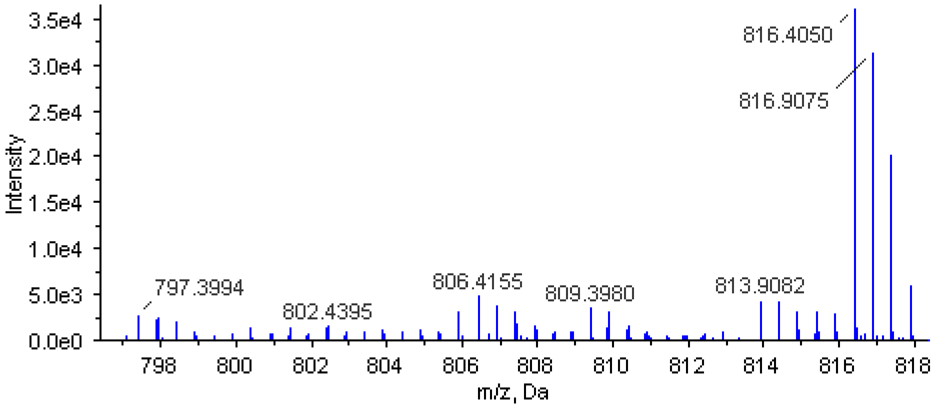
Seq Cov %: 42.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.19

116: 114=E5TL: D5TL=0.44

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAKNVGILAVDIYFPPTFVQQEALEAHDGASKGKYTIGLGQDCMAFCTEVEDVISMSLTAVTSLLDKYN
IDPKQIGR**LEVGSETVIDK**SKSIK**TFLMQIFEK**FGNTDIEGVDSTNACYGGTAALFNCVNWVESSSWDG
R**YGLVVCTDSAVYAEGPARPTGGAAAIAILVGPDAPIAFESK**FRGSHMSHAYDFYK**PNLASEYPVVDGK**
LSQTCYLMALDSCYKHFCAKYEKFEGKQFSISDAEYFVFHSPYNKLVQKSFAR**LVFNDFVRNASSIDET**
AKEK**LAPFSNLSGDESYQNRDLEKVSQQVAKPLYDAKVKPTTLIPK**QVGNMYTASLYAAFASLLHSKHT
ELAGKRVTLFSYGSGLTATMFSLR**LHEGQHPFSLSNIASVMNVAGK**LKARHELPPEKFVDIMKLMEHRY
GAKDFVTSK**DCSLLASGTYYLTEVDSLYR**RFYAQK**AVGNTVENGLLANGH**

Protein No.: I-23

Protein name and Species:

Methyl transferase; 5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase, putative OS=Ricinus communis GN=RCOM_1321820 PE=3 SV=1

Accession: tr|B9SI90|B9SI90_RICCO

Unused ProtScore: 30.18

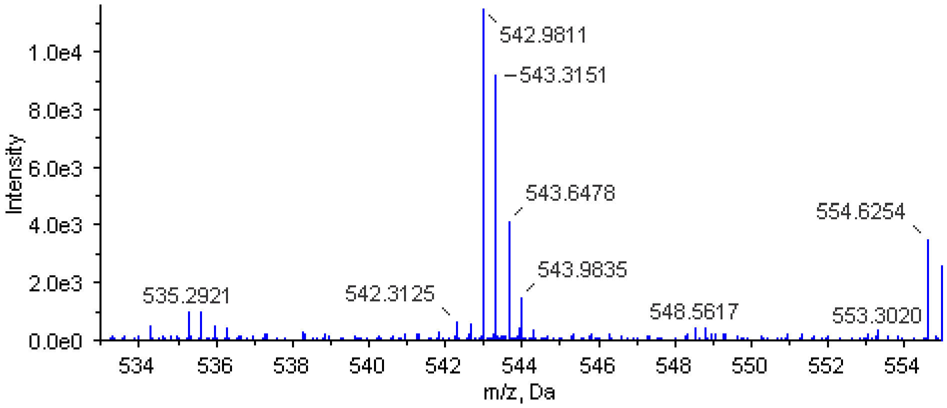
Seq Cov %: 25.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2.17

116: 114=E5TL: D5TL=1.57

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

M**ASHIVGYPR**MGPKRELK**FALESFWDGKSSAQDLEK**VASDLRESIWKQMAAAGIKHIPSNTFSYYDQVLDTTAMLGAVPPRYGWNGGEIGFDTYFSMAR**GNASVPAMEMTK**WFDTNYHFIVPELGPDVNFSYASHKAVTEYKEAKAHGVDTVPVLVGPVSYLLLSKPAKGVEK**TFSLLSLLGK**ILPVYKEVISELKAAGASWIQFDEPTLVLDLDSHKLQAFTDAYSELESTLSGLNVLIETYFADIPAEAFKTLTSLK**GVTAYGFDLVR**GTKTLDLIKSEFPKGK**YLFAGVVDGR**NIWANDLAASLTILHELEGIVGKDKLVVSTSSSLLHTAVDLVNETKLDKELK**SWLAFAAQK**IVEVNALAK**ALAGEKDEAFFSANAAAQASR**KSSPRVTNEAVQKAAAALKGSDHRRATNVSARLDAQQK**KLNLPILPTTTIGSFPQTIELR**RVRREYKAKKVSEDDYVKAIKEEISKVVKLQEELDIDVLVHGEPERNDMVEYFGEQLSGFAFTVNGWVQSYGSR**CVKPPIIYGDVSRPNPM**TVFWSSTAQSMTARPMK**GMLTGPVTILNWSFVR**NDQPRFETCYQIALAIKDE**VEDLEKAGINVIQIDEAALR**EGLPLRKSEQAFYLDWAVHSFRITNVGVQDTTQIHTHMCYSNFNDIIHSIIDMDADVITIENSRSDEKLLSVFREGVK**YGAGIGPGVYDIHSPRIPSTEEIADR**INKMLAVLEM**NILWVNPDCGLK**TRK**YSEVKPALSNMVAAAK**LLRTQLASAK

Protein No.: I-24

Protein name and Species:

ATP-citrate synthase, putative OS=Ricinus communis GN=RCOM_1000580 PE=4 SV=1

Accession: tr|B9RZR0|B9RZR0_RICCO

Unused ProtScore: 30.15

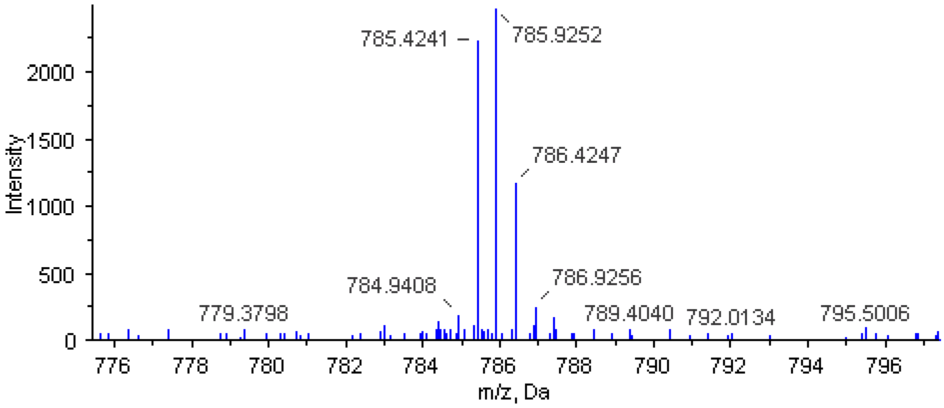
Seq Cov %: 42

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.31

116: 114=E5TL: D5TL=0.59

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MATGQLFSR**TTQALFYNYK**QLPIQR**MLDFDFLCGRETPSVAGIINPGSEGFQK**LFFGQEEIAIPVHSAI
EAACAAHPTADVFINFASFR**SAAASSMAALKQPTIRVVAIIAEGVPESDTK**QLIAYARANNK**VVIGPAT**
VGGIQAGAFKIGDTAGTIDNIIACKLYRPGSVGFVSKSGGMSNELYNTIARVTDGIYEGIAIGGDVFPG
STLSDHVLRFNNIPQVKMIVVLGELGGR**DEYSLVEALK**QGKVNKPVVAWVSGTCARLFK**SEVQFGHAGA**
KSGGEMESAQAKNQALK**DAGAVVPTSYEAFETAIK**ETFQKLVEEGKITPVK**EVKPPQIPEDLNTAIK**SG
KVR**APTHIISTISDDR**GEEPCYAGVPMSSIVEQGYGVGDVISLLWFKRSLPRYCTHFIEICIMLCADHG
PCVSGAHNTIVTARAGK**DLVSSLVSGLLTIGPRFGGAIDDAAR**YFKDAYDRGLAPYEFVESMKKKGIRV
PGIGHRIKRGDNRDKRVELLQRFARTHFPSVK**YMEYAVEVETYTLSK**ANNLVLNVDGAIGSLFLDLLAG
SGMFTKQEIDEIVEIGYLNGLFVLARSIGLIGNRSE

Protein No.: I-25

Protein name and Species:

Phosphofructokinase, putative OS=Ricinus communis GN=RCOM_1602260 PE=4 SV=1

Accession: tr|B9R8U5|B9R8U5_RICCO

Unused ProtScore: 29.94

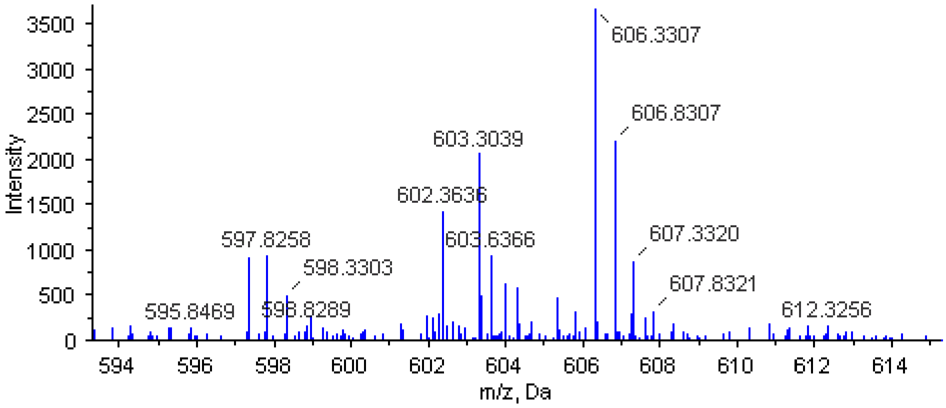
Seq Cov %: 42.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.34

116: 114=E5TL: D5TL=0.36

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDSDFGIPRELSDLQKLR**SLYQPELPPCLQGTTVR**VELGDGTTAADEAGAHTISR**SFPHTYGQPLAHFL**
RATAKVADAHIISEHPAMRVGVVFCGRQSPGGHNVVWGLHNALKIHNPN**STLLGFLGGSEGLFAQKTLE**
VTDDILSTYKNQGGYDLLGRTKDQIR**TTEQVHAALTTCK**NLK**LDGLVIIGGVTSNTDAAQLAETFAEAK**
CPTK**VVGVPVTLNGDLKNQFVETNVGFDTICKVNSQLISNVCTDALSAEK**YYYFIRLMGRK**ASHVALEC**
TLQSHPNMVILGEEVAASKLTLFDLTKQVCDAVQARAEQDKYHGVILLPEGLIESIPEVYALLK**EIHGL**
LRQGVSPNNISSQLSPWASALFEFLPPFIKK**QLLLYPESDDSAQLSQIETEKLLAHLVEAEMNK**RLKEG
TYKGKK**FNAICHFFGYQAR**GSLPSKFDCDYAYVLGHICYHVLAAGLNGYMATATNLKNPVNKWRCGAAP
IAAMMTVKRWAQNPGATSIGK**PAIHPAAVDLK**GKAYELLRLNAVK**FLMDDLYRNPGPLQFEGPGADAKP**
ITLCVEDQDYMGRIKKLQEYLDKVR**TIVKPGCSQEVLK**AALSVMASVTDVLLTMSSTSLDGQRPL

Protein No.: I-27

Protein name and Species:

14-3-3 protein 2 OS=Hevea brasiliensis PE=2 SV=1

Accession: tr|F2YZ43|F2YZ43_HEVBR

Unused ProtScore: 27.55

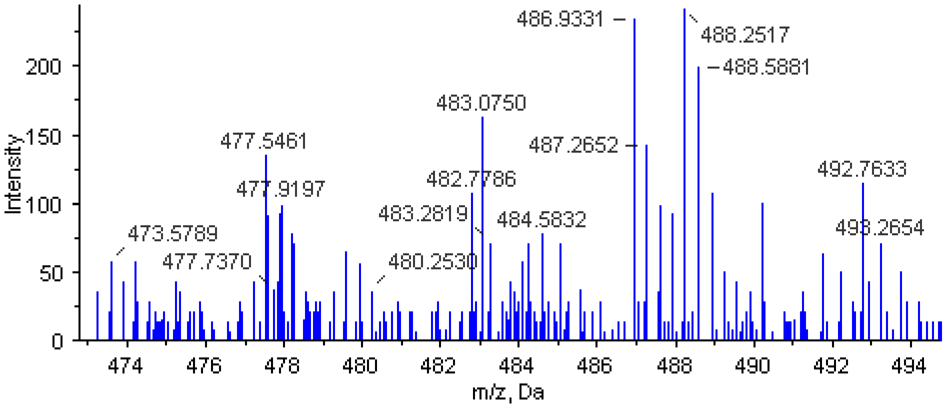
Seq Cov %: 51.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.53

116: 114=E5TL: D5TL=0.86

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSPTESSREENVYMAKLAEQAERYEEMVEFMEKVAKTVDVEELTVEERNLLSVAYKNVIGARRASWRII
SSIEQKEESRGNEDHVTIIKEYRGKIESELSKICDGILSLLESHLIPSASSAESKVFYLKMKGDYHRYL
AEFKTAGERKEAAESTLLAYKSAQDIALADLAPTHPIRLGLALNFSVFYYEILNSPDRACNLAKQAFDE
AISELDTLGEESYKDSTLIMQLLRDNLTLWTSDITDEAGDEIKEASKRESGEGQPQQ

Protein No.: I-28

Protein name and Species:

RAB2A OS=Lotus japonicus GN=rab2A PE=2 SV=1

Accession: tr|Q40208|Q40208_LOTJA

Unused ProtScore: 27.3

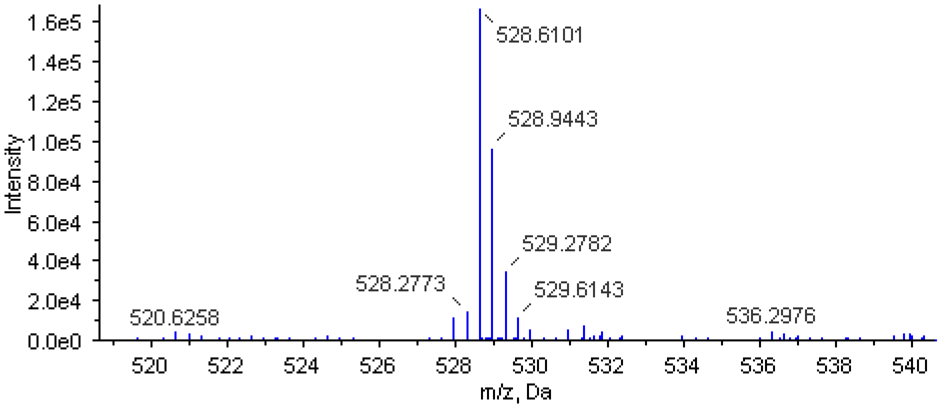
Seq Cov %: 65.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.38

116: 114=E5TL: D5TL=0.39

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSYAYLFK**YIIIGDTGVGKSCLLLQFTDKR**FQPVHDLTIGVEFGAR**MITIDNKPIKLQIWDTAGQESFR**
SITRSYY**RGAAGALLVYDITRRETFNHLASWLEDAR**QHANANMTIMLIGNKCDLAHRR**AVSTEEGEQFA**
KEHGLIFMEASAKTAQNVEEAFIKTAATIYKK**IQDGVFDVSNESYGIKVGYGGIPGPSGGR**DGPSASAG
GCCS

Protein No.: I-30

Protein name and Species:

Elicitor-responsive protein OS=Hevea brasiliensis GN=ERP PE=2 SV=1

Accession: tr|F8SKC5|F8SKC5_HEVBR

Unused ProtScore: 27.13

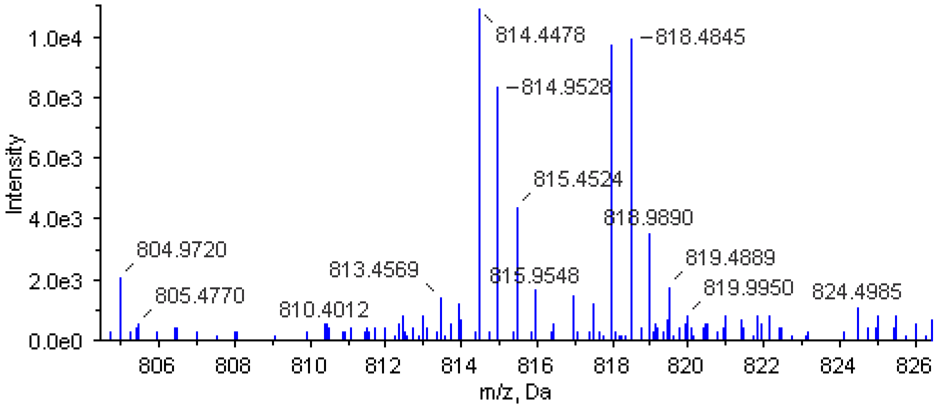
Seq Cov %: 90

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.33

116: 114=E5TL: D5TL=0.40

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MPLGTVEVLLVGAKGLENTDFLNGVDPYVVLACRTQEQKSSVASGKGSEPEWNEKFSFEVSDGDTELTL
KIMDSDVGAADDFVGEATIPLEPLFLEGNLPSTAYKVVKEQEYKGEITVGLTFTPEVEMDNVGVDGYDF
RL

Protein No.: I-31

Protein name and Species:

phospholipase D alpha 1-like [Glycine max] OS=Glycine max PE=2 SV=1

Accession:

tr|C6TEK4|C6TEK4_SOYBN

Unused ProtScore: 27.02

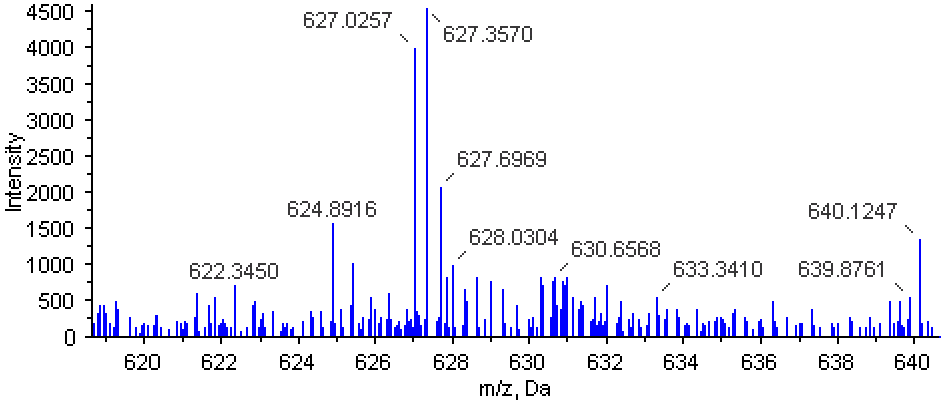
Seq Cov %: 37.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.60

116: 114=E5TL: D5TL=1.32

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MATEHEDDFKDEK**NPRPLDEDDIALLK**TYGLGPYSTSIKKAEKEIKEMAKK**VNDLCGIK**ESDTGLAAPS
QWDLVSDK**QMMQEEQPLQVAR**CTKIINPNSEDAKYVINVKQIAK**FVVGLGDK**VSPTDIEEGMRVGVDRN
KYQIQIPLPPK**IDPSVTMMTVEEKPDVTYNDVGGCK**EQIEKMR**EVVELPMLHPEK**FVKLGIDPPK**GVLC**
YGPPGTGKTLLARAVANR**TDACFIRVIGSELVQK**YVGEGARMVRELFQMARSKK**ACIVFFDEVDAIGGA**
RFDDGVGGDNEVQRTMLEIVNQLDGFDARGNIK**VLMATNR**PDTLDPALLRPGRLDR**KVEFGLPDLESR**T
QIFKIHTRTMNCERDIRFKLLARLCPNSTGADIR**SVCTEAGMYAIR**ARRKTVTEKDFLDAVNKVIKGYQ
KFSATPKYMVYN

Protein No.: I-32

Protein name and Species:

Phospholipase D OS=Ricinus communis GN=RCOM_0899520 PE=3 SV=1

Accession: tr|B9RV56|B9RV56_RICCO

Unused ProtScore: 27.02

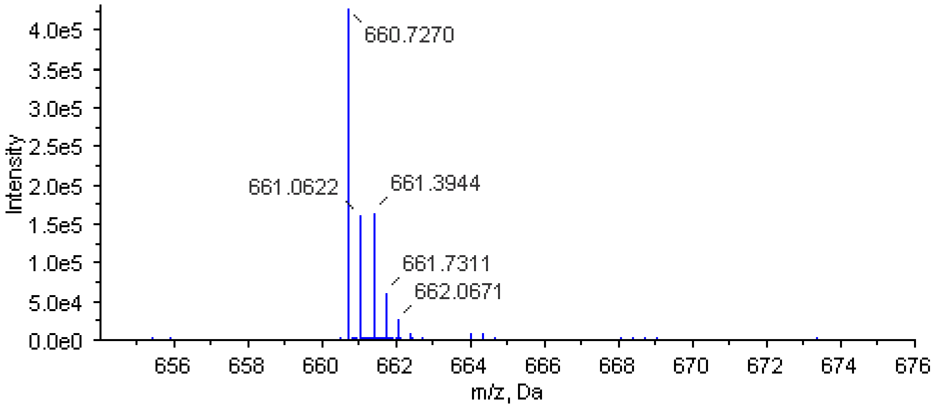
Seq Cov %: 22.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.63

116: 114=E5TL: D5TL=0.55

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAQISLHGTLHVTIYEVDKLHSGGGPHFFRKLVENIEETVGFGKGVSK**LYATIDLEK**ARVGRTRILENEQSNPRWYESFHVYCAHQASNVIFTVKDD**NPIGATLIGRAYVPVEELLDGEEIDR**WVEILDEDKNPVHSGSKIHVKLQYFEVTKDRNWGQGIRSSKYPGVPYTYFSQRQGCKVSLYQDAHIPDKFVPQIPLAGGNYYEPHR**CWEDVFDAITNAK**HLIYITGWSVYTEISLIRDSRRPK**PGGDITLGELLK**KKASEGVR**VLMLVWDDRTSVGLLK**KDGLMATHDEETEHFFQN**TDVHCVLCPR**NPDDGGSFVQDLQISTMFTHHQK**IVVVDSAMPNGDSQR**RR**IVSFVGGLDLCDGRYDSPFHSLFRTLDSAHHDDFHQPNFAGASIEK**GGPREPWHDIHSRLEGPIAWDVLFNFEQRWRKQGGKDLLIQLRELEDVIIPPSPVMYPDDFEAWNVQLFR**SIDGGAAFGFPETPEDAAR**AGLVSGKDNIIDR**SIQDAYIHAIR**RAKNFIYIENQYFLGSSFGWSPDGIKPEDINALHLIPKELSLKILSKIAAGERFTVYIVVPMWPEGIPESASVQAILDWQKRTMEMMYKDIVQALKANGIIEDPR**NYLTFFCLGNR**EVKKSGEYEPAEKPEPDTDYIRAQEARRFMIYVHTK**MMIVDDEYIIIGSANINQR**SMDGARDSEIAMGAYQPHHLSTRQPARGQIHGFRMSLWYEHLGMLDESFLNPESEECVRKVNQMAEKYWDLYSSETLEHDLPGHLLR**YPIGVASEGDVTELPGTEFFPDTK**ARVLGAKSDYLPPILTT

Protein No.: I-33

Protein name and Species:

Peptidyl-prolyl cis-trans isomerase OS=Hevea brasiliensis PE=2 SV=1

Accession: tr|B3FNQ1|B3FNQ1_HEVBR

Unused ProtScore: 26.07

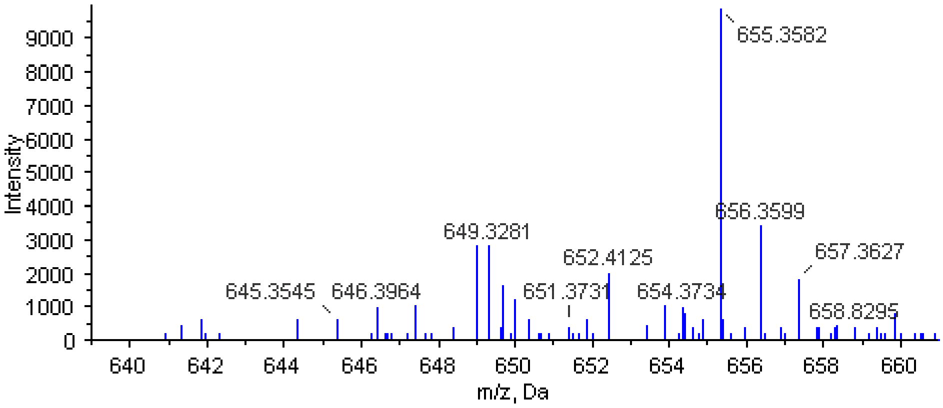
Seq Cov %: 64.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.06

116: 114=E5TL: D5TL=0.28

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MANPKVFFDMTIGGAPAGRIVMELFADTTPRTAENFRALCTGEKGIGRSRKPLHYKGSSFHRVIPGFMC
QGGDFTAGNGTGGESIYGAKFADENFIKKHTGPGILSMANAGPGTNGSQFFICTAKTEWLDGKHVVFGR
VVEGMDVVKTIEKVGSSSGRTSKPVVIADCGQLA

Protein No.: I-39

Protein name and Species:

Small rubber particle protein; REF-like stress related protein 2 OS=Hevea brasiliensis GN=SRPP PE=4 SV=1

Accession: tr|Q84T88|Q84T88_HEVBR

Unused ProtScore: 24.89

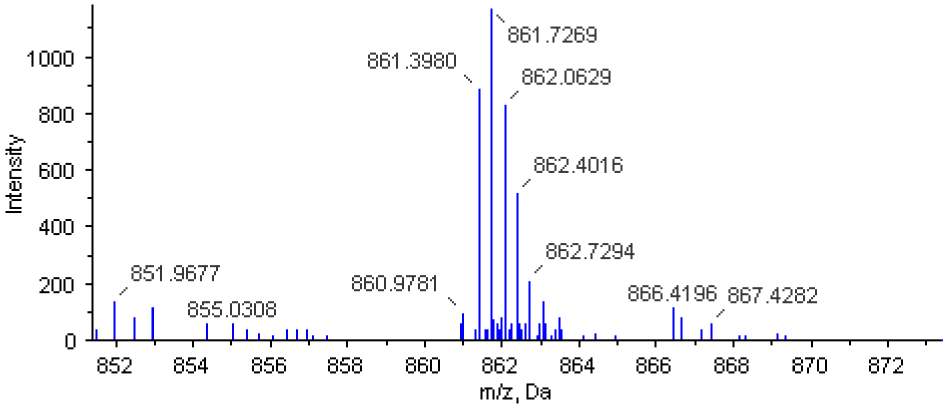
Seq Cov %: 97.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.39

116: 114=E5TL: D5TL=0.61

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

`MAEGKENENFQQEANEQEEKLKYLEFVQATTDNAVTALSNIYLYAKDNSGPLKPGVETIEGVAKTVVIP`
`ASKIPTEAIKFADRAVDASFTTLQNIVPSVLKQLPTQACDTSVKESAE`

Protein No.: I-40

Protein name and Species:

eukaryotic translation elongation factor 1-alpha OS=Bruguiera sexangula GN=bsef-1A PE=2 SV=1

Accession: tr|Q8H9B1|Q8H9B1_9ROSI

Unused ProtScore: 24.28

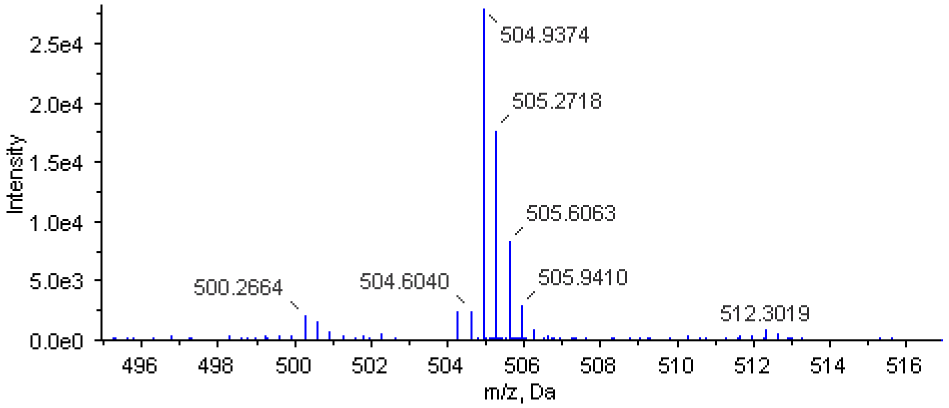
Seq Cov %: 45.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2.07

116: 114=E5TL: D5TL=1.56

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGKEKIHIN**IVVIGHVDSGKSTTTGHLIYK**LGGIDKRVIER**FEKEAAEMNK**RSFKYAWVLDKLKAERER
GITIDIALWKFETTK**YYCTVIDAPGHR**DFIK**NMITGTSQADCAVLIIDSTTGGFEAGISK**DGQTREHAL
LAFTLGVKQMICCCNKMDATTSKYSKARYDEIVKEVSSYLKK**VGYNPEKIPFVPISGFEGDNMIERSTN**
LDWYKGPTLLEALDMIQEPKRPSDKPLR**LPLQDVYKIGGIGTVPVGRVETGVLKPGMVVTFGPSGLTTE**
VKSVEMHHEALQEALPGDNVGFNVKNVSVKDLKRGYVASNSKDDPAKEASSFTSQVIIMNHPGQIGNGY
APVLDCHTSHIAVKFSEILTKIDRRSGKELEKEPKFLKNGDAGFVK**MIPTKPMVVETFSEYPPLGR**FAV
RDMR**QTVAVGVIKSVEK**KEPSGAKVTKSAAKKGGK

Protein No.: I-42

Protein name and Species:

Phosphoglucomutase, putative OS=Ricinus communis GN=RCOM_0628900 PE=3 SV=1

Accession: tr|B9SP64|B9SP64_RICCO

Unused ProtScore: 24.12

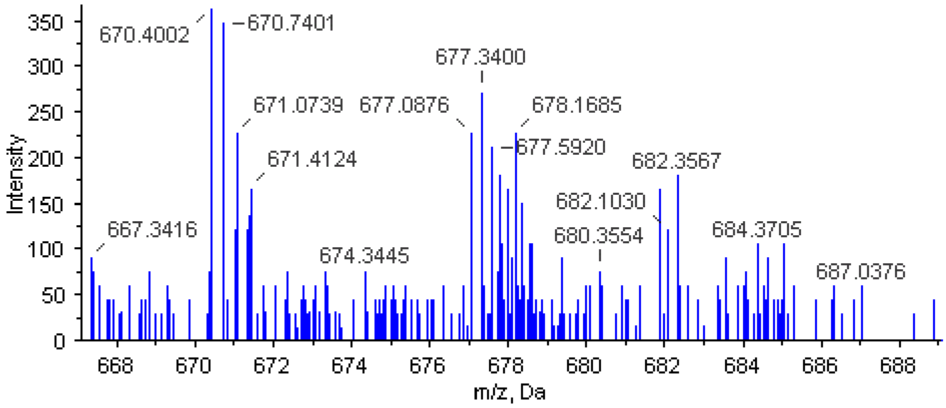
Seq Cov %: 36.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.87

116: 114=E5TL: D5TL=1.11

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MVFEVSRVSTTPFDGQKPGTSGLRKKVKVFTQPN**YLHNFVQSTFDALTAEK**VR**GATLVVSGDGR**YFSKD
AIQIIIKMSAANGVRR**VWVGQNGLLSTPAVSAVIR**ERVGLDGSK**ATGAFILTASHNPGGPHEDFGIKYN**
MENGGPAPEGITDKIYENTKTIKEYLISDLPDVDISAIGVTNFSGPEGQFDVDVFDSADDYVKLMKSIF
DFESIKKLISSPN**FTFCYDALHGVAGAYAK**RIFVEELCAQESSLLNCVPK**EDFGGGHPDPNLTYAK**ELV
ARMGLGK**SNSEVEPPEFGAAADGDADR**NMILGKRFFVTPSDSVAIIAANAVEAIPYFSAGLKGVARSMP
TSAALDIVAKHLNLKFFEVPTGWKFFGNLMDAGLCSVCGEESFGTGSDHIREKDGIWAVLAWLSILAYK
NKENLNGGKLVSVEDIVRNHWATYGRHYYTR**YDYENVDAGAAKELMAHLVKLQSSLGEVNEIVK**GIRSD
VAKVVHGDEFEYKDPVDGSISSHQGIRYLFEDGSRLVFR**LSGTGSEGATIRLYIEQYEK**DSSKTGR**DSQ**
EALAPLVEVALKLSK**MQEFTGR**SAPTVIT

Protein No.: I-43

Protein name and Species:

Trehalose-6-phosphate synthase, putative OS=Ricinus communis GN=RCOM_1251280 PE=4 SV=1

Accession: tr|B9S8D6|B9S8D6_RICCO

Unused ProtScore: 23.88

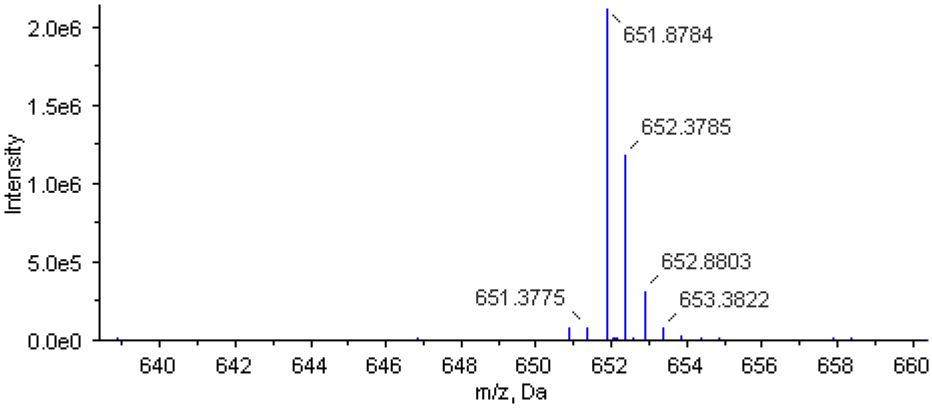
Seq Cov %: 22.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.59

116: 114=E5TL: D5TL=0.70

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MMSR**SYTNLLDLASGNFPVMGQPR**EKKRLPRVMTVPGVISELDDDQANSVASDVPSSLVQDR**IIIVANQ**
LPVKAKRRPDNKGWSFSWDDDSLLLQLK**DGLPEDMEVIYVGSLRVEVDMSEQDDVSQLLLDR**FK**CVPAF**
LPPDILSKFYHGFCKQHLWPLFHYMLPFSANHGGRFDR**SLWEAYVAANK**IFSQRVIEVINPEDDYVWIH
DYHLMVLPTFLRRRFNRLRMGFFLHSPFPSSEIYR**TLPVREEILK**ALLNSDLIGFHTFDYARHFLSCCS
R**MLGLEYQSK**R**GYIGLEYYGR**TVGIKIMPVGIHMGQIQSVLKLADKEWRVGELKQQFEGK**TVLLGVDDM**
DIFKGVNLK**LLAMEQMLK**QHPKWQGR**AVLVQIANPAR**GKGKDLLEIQAEIQASCKRINESFGQPGYEPI
VFIDRPVSLSERAAYYTIAECVVVAAVR**DGMNLTPYEYIVCR**QGVSGSESSSESNGPKK**SMLVVSEFIG**
CSPSLSGAIRVNPWNIEATAEAMNEAISMSDSEKQLRHEKHYRYVSTHDVAYWARSFFQDMERTCRDHF
RRRCWGIGLSFGFR**VVALDPNFR**KLSIDAIVSAYLRSKNRAILLDYDGTVMPQTSINKSPSQEVISIID
TLCSDAKNTVFVVSGRGRDSLGKWFSPCRK**LGIAAEHGYFMR**WSADRQWETCGQTTDFGWIQMAEPVMK
LYTESTDGSSIETKESALVWHHR**DADPGFGASQAKEMLDHLESVLANEPVAVK**SGQFIVEVKPQGISKG
FVAEKIFTSMAENGRQADFVLCIGDDRSDEDMFEIIGNAISSGVLSSSTSVFACTVGQKPSKAKYYVDD
TGEVINMLEALAEASSPSPSPPNSP

Protein No.: I-49

Protein name and Species: Exportin-1 OS=Populus trichocarpa GN=POPTRDRAFT_774005 PE=4 SV=1

Accession: tr|B9I8G4|B9I8G4_POPTR

Unused ProtScore: 22.33

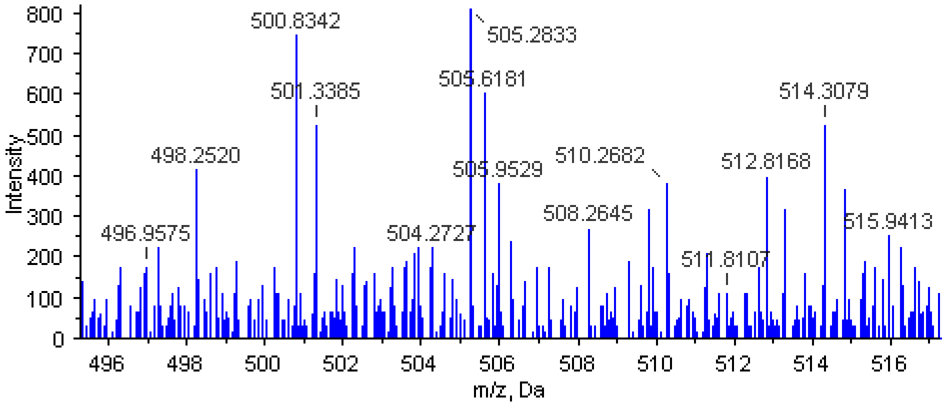
Seq Cov %: 12.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.84

116: 114=E5TL: D5TL=2.19

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAAEKFRDLSQAIDVPLLDATVAAFYGTGSKEERVAADRILQDLQNNPDMWLQVVHILQNTKNLNTKFF
ALQVLEGVIKYRWNALPVEQRDGMKNYISEVIVQLSSNEASFRMERLYVNKLNVTLVQILKHEWPARWR
SFIPDLVAAAKTSETICENCMVILKLLSEEVFDFSRGEMTQQKIKELKQSLNSEFQLIHELCLYVLSAS
QRTELIRATLSTLHAFLSWIPLGYIFESPLLETLLKFFPMPSYRNLTLQCLTEVAALNFGDFYNIQYVK
MYNFFMVQLQAILPLTTNIPEAYANGSSEEQAFIQNLALFFTSFYKSHIQVLESTQENITALLMGLEYL
INICYVDDTEVFKVCLDYWNSLVLELFEARHNLDNPAVAVNMMGLQMPLLHGMVDGLGSQILQRRQLYA
TPMSKLRMLMICR**MAKPEEVLIVEDENGNIVR**ETMK**DNDVLVQYK**IMRETLIYLSHLDHEDTEKQMLKK
LSKQLSGEDWNWNNLNTLCWAIGSISGSMMEEQENRFLVMVIR**DLLNLCEITK**GKDNK**AVIASNIMYVV**
GQYPRFLRAHWKFLKTVVNKLFEFMHETHPGVQDMACDTFLKIVQKCKRKFVIVQVGESEPFVSELLAG
LPTTVADLEPHQIHTFYESVGHMIQAESDPQKRDEYLQR**LMDLPNQK**WAEIIGQAR**QSVDFLK**DQDVIR
TVLNIMQTNTSVASALGTYFLSQISLIFLDMLNVYR**MYSELISSSIAEGGPYASK**TSYVKLLRSVKRET
LK**LIETFLDK**AEDQTQIGK**QFVPPMMDPVLGDYAR**NLPDARESEVLSLFATIINKYKAAMIEDVPRIFE
AVFQCTLEMITKNFEDYPEHRLKFFSLLR**AIATHCFPALIR**LSSEQLKLVMDSIIWAFRHTERNIAETG
LNLLVEMLK**NFQASEFCNQFYR**SYFLTIEQEIFAVLTDTFHKPGFKLHVLVLQHLFCLVESGALTEPLW
DAATISYSYPNNAMFVREYTIKLLGTSFPNMTASEVTQFVNGLFESRNDLSAFKNHIRDFLVQSK**EFSA**
QDNKDLYAEEAAAQRERERQRMLSIPGLIAPNEIQDEMLDS

Protein No.: I-50

Protein name and Species:

Invertase 2 OS=Hevea brasiliensis GN=NIN2 PE=2 SV=1

Accession: tr|E9KF95|E9KF95_HEVBR

Unused ProtScore: 22.29

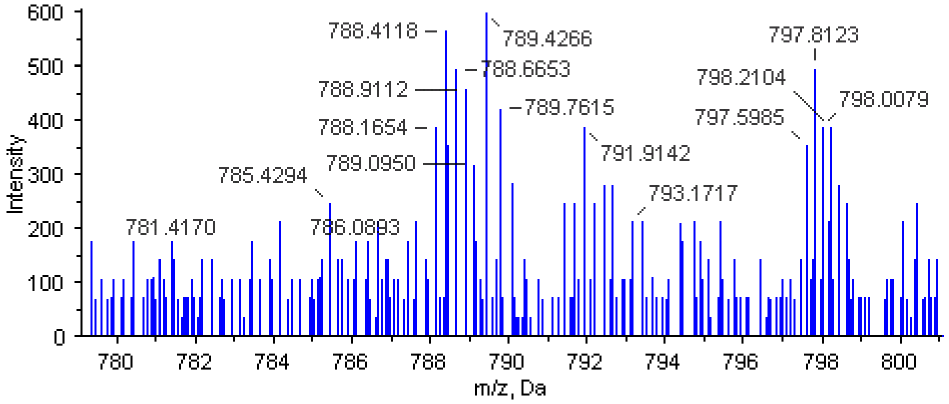
Seq Cov %: 26

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.51

116: 114=E5TL: D5TL=2.20

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDGTKEVGLR**NVSSTCSISEMDDFDLSR**LLDKPRLNIERQRSFDER**SLSELSIGLTRGGLDYCEITYSP**
GGRSGLDTPVSSARNSFEPHPMVADAWEALRR**SIVYFR**GQPVGTIAAIDHASEEVLNYDQVFVR**DFVPS**
ALAFLMNGEPEIVKNFLLKTLHLQGWEKRIDRFKLGEGVMPASFK**VLHDPVR****KTDTLMADFGESAIGR**V
APVDSGFWW**IILLR**AYTK**STGDLSLAETPECQK**GMRLILTLCLSEGFDTFPTLLCADGCSMIDRRMGIY
GYPIEIQALFFMALR**CALSMLK**HDTEGKECIERIVKRLHALSYHIRSYFWLDFQQLNDIYRYK**TEEYSH**
TAVNKFNVIPDSIPDWVFDFMPTR**GGYFIGNISPAR**MDFRWFALGNCVAILSSLATPEQSMAIMDLIES
RWEELVGEMPLK**IAYPAIESHDWR**IVTGCDPKNTRWSYHNGGSWPVLLWLLTAACIKTGRPQIARRAID
LAETRLLKDSWPEYYDGKLGKFIGKQARKYQTW**SIAGYLVAKMMLEDPSHLGMISLEEDK**QMKPVIKRS
SSWTC

Protein No.: I-53

Protein name and Species:

Sucrose synthase OS=Manihot esculenta PE=2 SV=1

Accession: tr|A9NIV2|A9NIV2_MANES

Unused ProtScore: 21.98

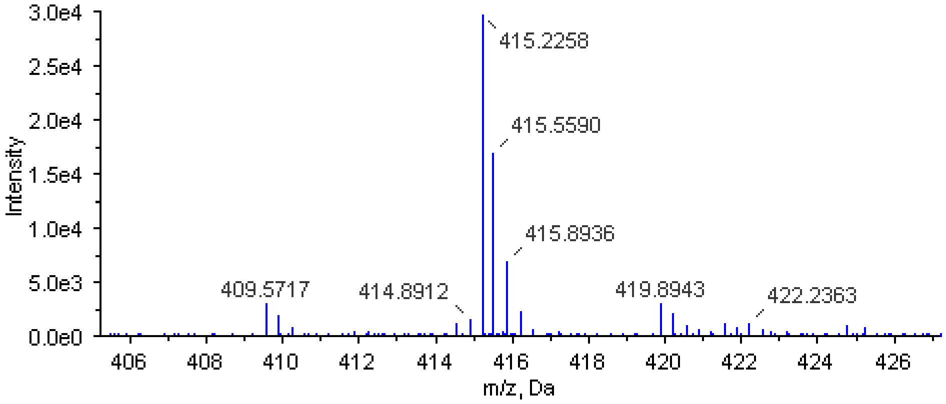
Seq Cov %: 15.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.57

116: 114=E5TL: D5TL=0.62

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAERVITRVQSIRER**LDETLSAHRNEIVALLSR**IEGKGKGILQHHQIIAEFEEIPEENRKK**LLESVFGE**
VLRSAQEAIVLPPWVALAVRPRPGVWEYIR**VNVHALVVEELR**VAEYLHFKEELVDGSVNGNFVLELDFE
PFNASFPRPTLSK**YIGNGVEFLNR**HLSAKLFHDK**ESLHPLLEFLK**VHCHKGKNMMLNDR**IHNLDSLQYV**
LRKAEEYLTALAPETPYSQFEHK**FQEIGLER**GWGDTAERVLEMIRLLLDLLEAPDPCTLETFLGRIPMV
FNVVIMSPHGYFAQDNVLGYPDTGGQVVYILDQVR**ALETEMLHR**IKQQGLDITPRILIITR**LLPDAVGT**
TCGQRLEK**VFGTEHSDILR**IPFKTEKGIVRKWISRFEVWPYLETYTEDVATEIGKEFQGKPDLIFGNYS
DGNIVASLLAHK**LGVTECTIAHALEK**TKYPESDIYWKKFDEKYHFSCQFTADLIAMNHTDFIITSTFQE
IAGSKDTVGQYESHTALTLPGLYR**VVHGIDVFDPK**FNIVSPGADETIYFSYTEEKRRLTSFHPEIEELL
YSPVENEEHLCVLKDRSKPIIFTMARLDRVKNLTGLVEWYGKNAKLRELANLVVVGGDRRKESK**DLEEQ**
AEMKKMHSLIEK**YNLNGHFR**WISSQMNRVRNGELYRYICDTKGVFVQPAIYEAFGLTVVEAM**TCGLPTF**
ATCNGGPAEIIVHGKSGFNIDPYHGDQAAELLVQFFEKCKADPSHWIKISEGAMQRIQEKYTWQIYSQR
LLTLTGVYGFWKHVSKLDRRESRR**YLEMFYALK**YRKLAESVPLTVED

Protein No.: I-54

Protein name and Species:

Malate dehydrogenase OS=Populus trichocarpa GN=POPTRDRAFT_747123 PE=3 SV=1

Accession: tr|B9NBW3|B9NBW3_POPTR

Unused ProtScore: 21.97

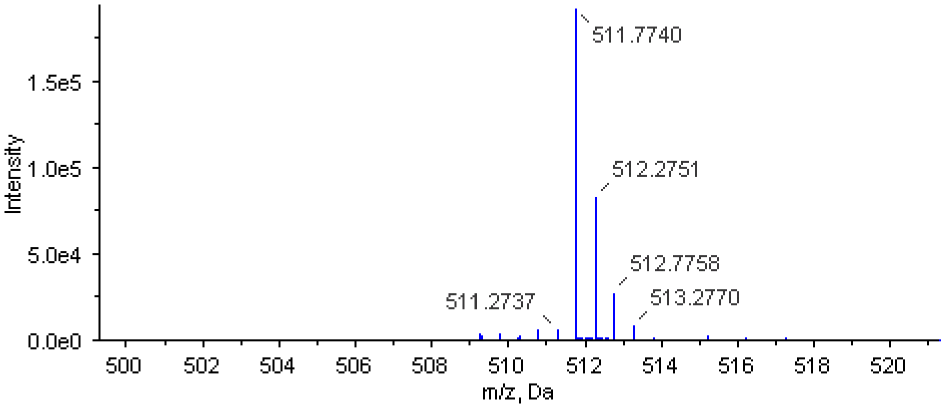
Seq Cov %: 32.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.31

116: 114=E5TL: D5TL=0.92

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAKEPAR**VLVTGAAGQIGYALVPMIAR**GVMLGPDQPVILH**MLDIPPAAEALNGVKMELVDAAFPLLK**GV
VATTDVVEACTGVNIAVM**VGGFPR**KEGMERKDVMSKNVSIYKSQASALEK**HAAANCKVLVVANPANTNA**
LILKEFAPSIPEKNITCLTRLDHNR**ALGQISERLNVQVSDVKNVIIWGNHSSTQYPDVNHATVK**TPAGE
KPVRELVKDDAWLNAEFITTVQQRGAAIIKARKLSSALSAASSACDHIHDWVLGTPEGTWVSMGVYSDG
SYNVPAGLIYSFPVTCQNGEWKIVQGLS**IDEFSR**K**KLDLTADELSEEK**ALAYSCLT

Protein No.: I-55

Protein name and Species:

Chaperonin containing t-complex protein 1, zeta subunit, tcpz, putative OS=Ricinus communis GN=RCOM_1727810 PE=3 SV=1

Accession: tr|B9RSN1|B9RSN1_RICCO

Unused ProtScore: 21.39

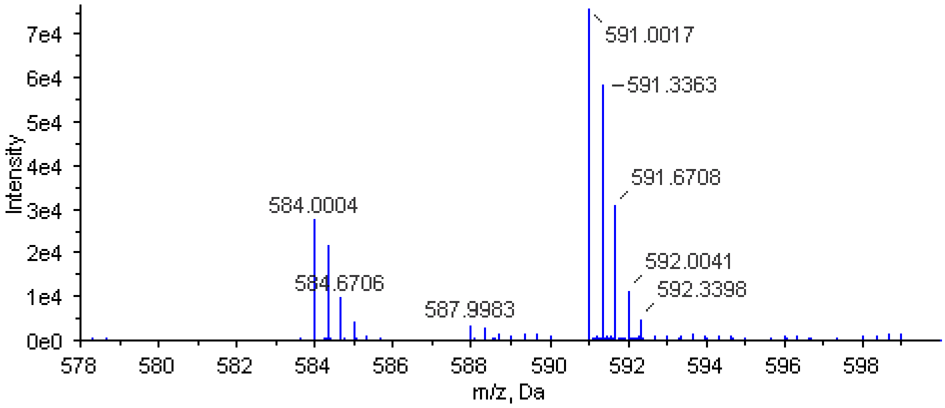
Seq Cov %: 30.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.51

116: 114=E5TL: D5TL=1.63

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSLR**VLNPNAEVLNKSAALHMNINAAK**GLQDVLKSNLGPKGTIK**MLVGGAGDIK**LTKDGNTLLK**EMQIQ**
NPTAIMIARTAVAQDDISGDGTTSTVIFIGELMKQSERYIGEGMHPR**VLVDGFEIAK**R**ATLQFLEK**FK**T**
PVVMGDEPDKEILKMVARTTLRTKLYETLADQLTDIVVNAVLCIRKPEEAIDLFMVEIMHMRHKFDVDT
R**LVEGLVLDHGSR**HPDMKRRAENCYILTCNVSLEYDK**SEINAGFFYSNAEQR**EKMVAAERRQVDERVEK
IIELKNK**VCSGNDNNFVVINQKGIDPPSLDLLAR**AG**IIALR**RAKRRNMERLVLACGGEAVNSVDDLTPD
CLGWAGLVYEHILGEEKYTFVEHVK**NPHSCTILIK****GPNDHTIAQIK**DAVRDGLRAVK**NTIEDEAVVLGA**
GAFELAARKYLISEVKKTVKGRAQLGIEAFADALLVIPK**TLAENSGLDTQDEIVSLTGEHDR**ENIVGLN
LQTGGPLDPQMEGIFDNYSVKRQLINSGPVIASQLLLVDEVIRAGRNMRKPN

Protein No.: I-57

Protein name and Species: **Luminal binding protein (BiP), Nucleotide-Binding Domain of the sugar kinase/HSP70/actin superfamily OS=Thellungiella halophila PE=2 SV=1**

Accession: **tr|E4MXI2|E4MXI2_THEHA**

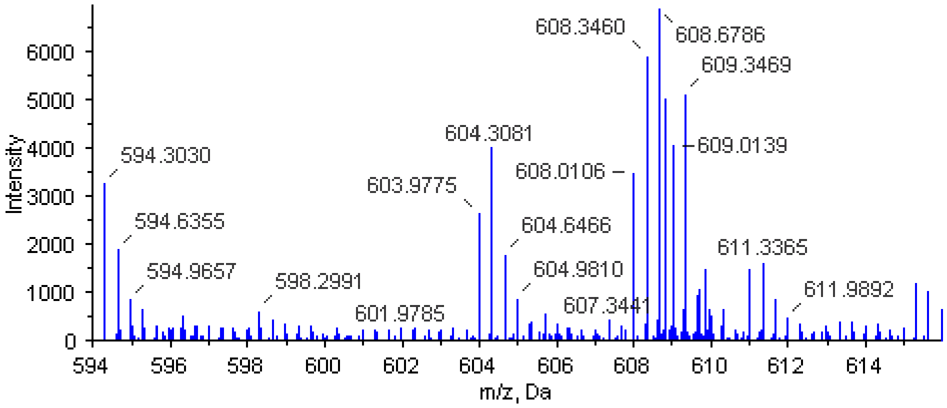
Unused ProtScore: **21.05** **Seq Cov %:** **24.2**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=3.50

116: 114=E5TL: D5TL=2.24

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MARSFGANGTVVLAIIFFGCLFAFSTAKEEATKLGTVIGIDLGTTYSCVGVYK**NGHVEIIANDQGNR**IT
PSWVGFTDSERLIGEAAKNQAAVNPER**TIFDVK**RLIGRKFEDKEVQKDKKLVPYQIVNKDGKPYIQVKI
KDGETKVFSPEEISAMILTKMKETAEAYLGKK**IKDAVVTVPAYFNDAQR**QATKDAGVIAGLNVAR**IINE**
PTAAAIAYGLDKKGGEKNILVFDLGGGTFDVSVLTIDNGVFEVL**STNGDTHLGGEDFDHR**IMDYFIKLI
KKKHQKDISKDNKALGKLRRECERAKRALSSQHQVR**VEIESLFDGVDFSEPLTR**AR**FEELNNDLFR**KTM
GPVKKAMDDAGLQKS**QIDEIVLVGGSTR**IPK**VQQLLK**DFFEGKEPNK**GVNPDEAVAYGAAVQGGILSGE**
GGDETKDILLLDVAPLTLGIETVGGVMTKLIPRNTVIPTKKSQVFTTYQDQQTTVSIQVFEGERSLTKD
CRLLGK**FDLTGIPPAPR**GTPQIEVTFEVDANGILNVKAEDKASGKSEKITITNEKGR**LSQEEIER**MVK**E**
AEEFAEEDKKVKERIDAR**NSLETYVYNMK**NQVSDKDKLADKLEADEKDKIEAATKEALEWLDENQNSEK
EDYEEKLK**EVEAVCNPIITAVYQR**SGGAPGAAGGDSATDEEDESHDEL

Protein No.: I-58

Protein name and Species: **Glucosamine-fructose-6-phosphate aminotransferase, putative OS=Ricinus communis GN=RCOM_1077800 PE=4 SV=1**

Accession: **tr|B9RM60|B9RM60_RICCO**

Unused ProtScore: **21.05**

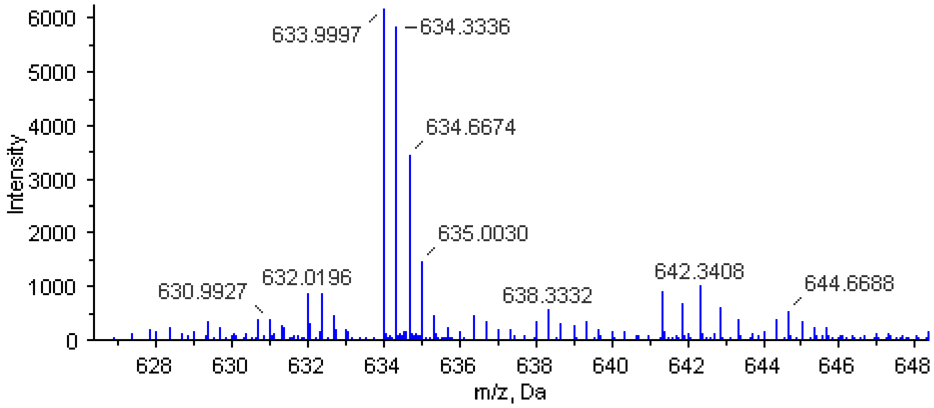
Seq Cov %: **22.7**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.36

116: 114=E5TL: D5TL=0.70

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MCGIFAYLNYNVNRERRYILQVLFNGLRRLEYRGYDSAGISIENSIPSESSDPIPSSSSHSPSPLVFR**Q**
EGNIESLVKSVYQDVATIDLNLEESFSVHAGIAHTR**WATHGEPAPR**NSHPQTSGAGNEFLVVHNGVITN
YEVLKETLVRHGFTFESETDTEVIPKLAKYVFDKANEGEGAQPVTFSQVVLEVMRHLEGAYALIFKSRH
YPNELIACKR**GSPLLLGVKELNEDMNSGSAFHDAK**SLSKDGHAK**ELFLSSDANAIIEHTK**RVLMIEDGE
VVHLKDGSVSILKFENAKGRHGGALSRPASVQR**ALSVLEMEVEQINK**GNYEHYMQK**EIHEQPESLTTTM**
RGRLIRGGSCKAK**TVLLGGLK**DHLKTIRRSRR**IVFVGCGTSYNAALAAR**PILEELSGVPVTMEIASDLV
DRQGPIYREDTAVFVSQSGETADTLHALEYALENGALCVGITNTVGSAIARNTHCGIHINAGAEIGVAS
TKAYTSQIVVMAMLALAIGGDAISSQAKR**EAIIDGLFDLPNR**VREVLKLDQEMKDLAELLMAEQSLLVF
GR**GYNYATALEGALK**VK**EVALMHSEGMLAGEMK**HGPLALVDENLPIIVIATRDACFRK**QQSVIQQLHAR**
KGRLIVMCSKGDAASVCPGESCRVIEVPQVEDCLQPVVNIVPLQLLAYHLTVLR**GYNVDQPR**NLAKSVT
TQ

Protein No.: I-60

Protein name and Species:

Leucine aminopeptidase, putative OS=Ricinus communis GN=RCOM_0623200 PE=3 SV=1

Accession: tr|B9STR1|B9STR1_RICCO

Unused ProtScore: 20.86

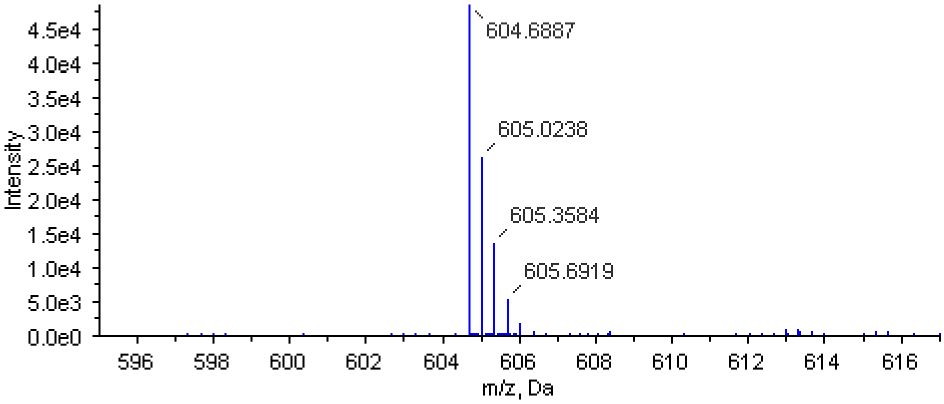
Seq Cov %: 29.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.29

116: 114=E5TL: D5TL=0.40

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAARVVSLAASISSFAVPFSSTSSSLFLTRLRSPSVLRFSFAVAPLSYRSRGGGGGGGGKLMAHSLAR**A**
TLGLTQPANVDVPKISFSAKEIDVVEWK**GDILAVGVTEK**DMTKDKSTKFDNSLLKK**LDTHLGGLLSEAS**
SEEDFTGKAGQSMVLRLPGLGSKRIGLIGLGQSASTTFAFRNFGETIAATAKAAQASNVAIVLASAESI
SNELKLNTASAIASGTVLGTYEDARFKSESKKPVLKSVDILGFGTGPDLAKKLK**YAEDVSSAVIFGKEL**
VNSPANVLTPAVLAEEASKIASTYSDVLSANILSAEQCKELKMGSYLGVAAASANPPHFIHLHYKPPGG
TVKAK**LALVGKGLTFDSGGYNIKTGPGCSIELMKFDMGGSAAVLGAAK**AIGQIKPPGVEVHFIVAACEN
MISGTGMR**PGDIVTASNGKTIEVNNTDAEGRLTLADALVYACNQGVDK**IVDLATLTGACVVALGPSIAG
VFTPSDDLANEVFTAAEASGEKLWRMPLEESYWENMK**SGVADMVNTGGRQGGAITAALFLK**QFINEKVQ
WMHIDMAGPVWNEKKRTATGFGISTLVEWILHNSS

Protein No.: I-61

Protein name and Species:

Rab GDP dissociation inhibitor OS=Ricinus communis GN=RCOM_1750690 PE=4 SV=1

Accession: tr|B9RIY3|B9RIY3_RICCO

Unused ProtScore: 20.57

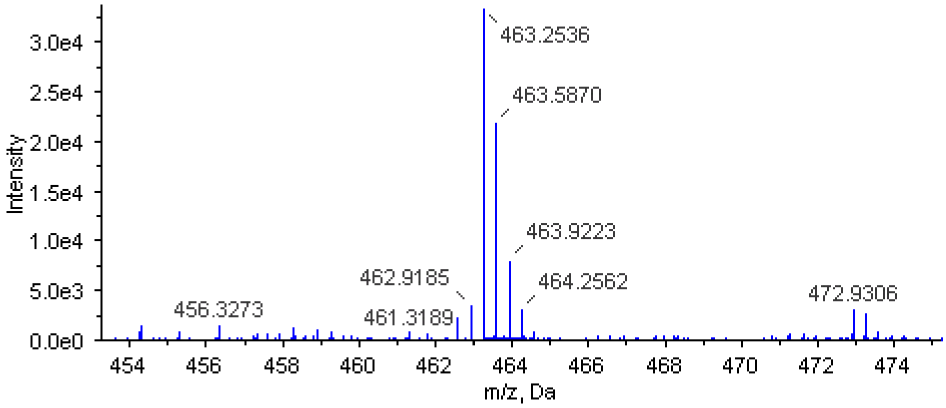
Seq Cov %: 41.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.63

116: 114=E5TL: D5TL=0.39

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDEEYDVIVLGTGLK**ECILSGLLSVDGLK**VLHMDKNDYYGGESASLNLNQLWKRFR**GSDKPPAHLGSSR**
DYNVDMIPKFMMANGNLVRVLIHTDVTKYLYFKAVDGSFVYNKGKVHK**VPATDMEALKSPLMGIFEK**RR
ARK**FFIYVQDYNESDPKTHEGMDLTR**VTTRELIAK**YGLDDNTMDFIGHALALHRDDRYLDEPALDTVMR**
MK**LYAESLAR**FQGGSPY**IYPLYGLGELPQAFARLSAVYGGTYMLNKPECKVEFDEEGKVVGVTSEGETA**
KCK**KVVCDPSYLPNK**ARKVSRVAR**AIAIMSHPIPNTNDSHSAQVILPQK**QLGRRSDMYLFCCSYSHNVA
PKGKYIAFVSSEAETDNPEVELKPGIDLLGPVDEIFFEVYDRYEPVNEPSLDNCFISTSYDATTHFEST
VTDVLNMYSMITGKVLDLSVDLSAASAAEE

Protein No.: I-64

Protein name and Species:

Alpha-1,4-glucan-protein synthase [UDP-forming], putative OS=Ricinus communis GN=RCOM_1468610 PE=4 SV=1

Accession: tr|B9RLK7|B9RLK7_RICCO

Unused ProtScore: 19.65

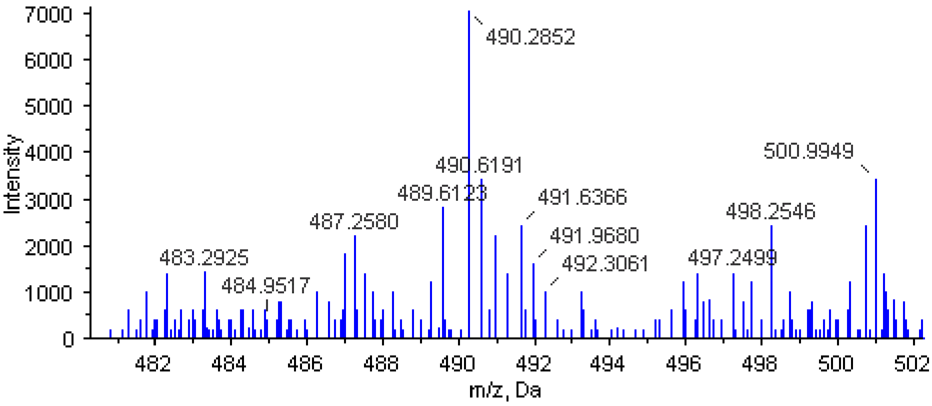
Seq Cov %: 36.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.60

116: 114=E5TL: D5TL=0.44

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MADFAAISPTPLLKDELDIVIPTIRNLDFLEMWRPFFQPYHLIIVQDGDPSKIIKVPEGFDYELYNRND
INRILGPKASCISFKDSACRCFGYMVSKKKYIYTIDDDCFVAKDPSGKDINALEQHIKNLLCPSTPFFF
NTLYDPYRTGADFVRGYPFSLREGVPTAVSHGLWLNIPDYDAPTQLVKPLERNTRYVDAVMTIPKGTLF
PMCGMNLAFNRELIGPAMYFGLMGDGQPIGRYDDMWAGWCTKVICDHLGFGVKTGLPYIYHSKASNPFV
NLKKEYKGIYWQEELIPFFQSAVLPKECTTVQKCYIELSKQVRAKLGKIDEYFVKLADAMVTWVEAWDE
LNPSGNSGELPNGAAK

Protein No.: I-69

Protein name and Species:

Heat shock protein 70 (HSP70)-interacting protein, putative OS=Ricinus communis GN=RCOM_1679700 PE=4 SV=1

Accession: tr|B9RBP6|B9RBP6_RICCO

Unused ProtScore: 18.74

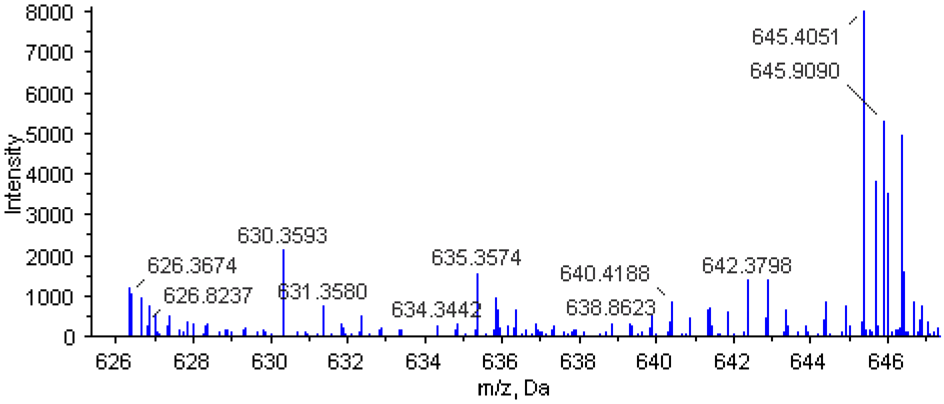
Seq Cov %: 19.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.58

116: 114=E5TL: D5TL=0.57

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAEEAKAKGNAAFSAGDFTTAVKHFTEAISIAPSNHVLYSNR**SAALASLHNYADALTDAK**KTVELKPDW
SKGYSRLGAAYLGLNQTQDAISAYKKGLDIDPSNEALKSGLADAQARFSAPPPPPSPFGDAFNGPEMWA
KLTADPSTRMYLQQPDFVKMMQEIQK**NPNNLNLYLK**DQRVMQALGVLLNLKFRAPNAGAEDMEVPQEDD
HSSSPPPQAEQPAKKAPQPEPEPEPMDVITEEDKEAKERKAQAVKEK**ELGNAAYK**QKDFETAISHYTTA
LELDDEDISYLTNR**AAVYLEMGK**YEDCIKDCDKAVERGRELRSDFKMIARALTRKGTALVKMAKSSKDY
DSAIETFQKALTEHRNPETLKKLNEAERAKK**ELEQQEYFDPK**LADEEREK**GNEYFK**QQK**YPEAVK**HYTE
SLRRNPEDPRAYSNRAACYTK**LGALPEGLK**DAEKCIELDPTFTKGYTRKGAVQFFMKEYDK**ALETYQEG**
LKHDPQNQELLDGVRRCVEQLNKASR**GDLSPEELKERQAKAMQDPEIQNILSDPVMRQVLVDFQENPK**S
AQDHMKNPMVMNKIQK**LVNAGIVQIR**

Protein No.: I-70

Protein name and Species:

DnaJ protein OS=Hevea brasiliensis PE=2 SV=1

Accession: tr|Q9ZSZ6|Q9ZSZ6_HEVBR

Unused ProtScore: 18.66

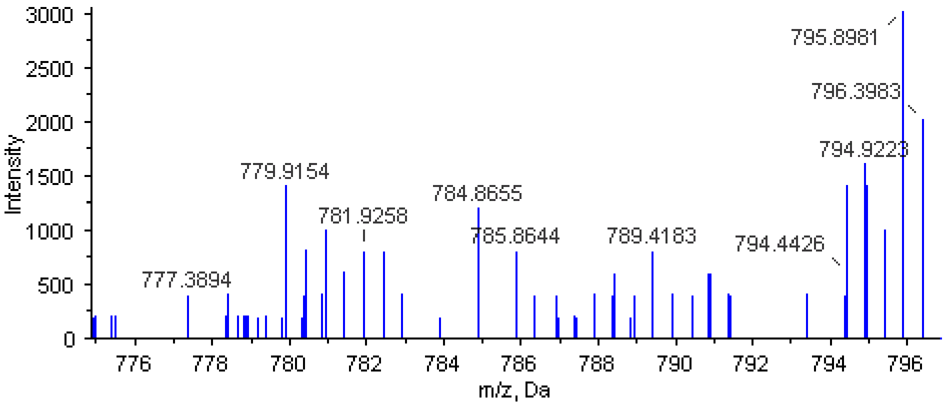
Seq Cov %: 38.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.52

116: 114=E5TL: D5TL=0.45

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MFGRAPKKSDNTK**YYEILGVSK**NASQDDLKKAYRKAAIKNHPDKGGDPEKFK**ELAQAYEVLSDPEKREI**
YDQYGEDALKEGMGSGGGAHDPFDIFQSFFGGNPFGGGGSSRGRRKE**GEDVIHPLK****VSLEDLYNGTSK**K
LSLSRNVICSKCKGKGSKSGASMKCSGCQGSGMKVSIR**QLGPSMIQQMQHPCNECKGTGETINDKDR**CP
QCKGEKVVQEKK**VLEVIVEK**GMQNGQRITFPGEADEAPDTITGDIVFVLQQKEHPKFKRKGDDLIVDHT
LSLTEALCASQFILTHLDGDLLIK**SQPGEVVKPDQFKAINDEGMPMYQR**PFMRGKLYIHFSVDFPDSLP
PDQCK**ALEAVLPSR****TSVQLSDMELDECEETTLHDVNFDEEMR**RK**QQQAQEAYDEDDDMHGGGQR**VQCAQ
Q

Protein No.: I-71

Protein name and Species:

Phosphoglycerate kinase OS=Ricinus communis GN=RCOM_1574570 PE=3 SV=1

Accession: tr|B9RHY3|B9RHY3_RICCO

Unused ProtScore: 18.31

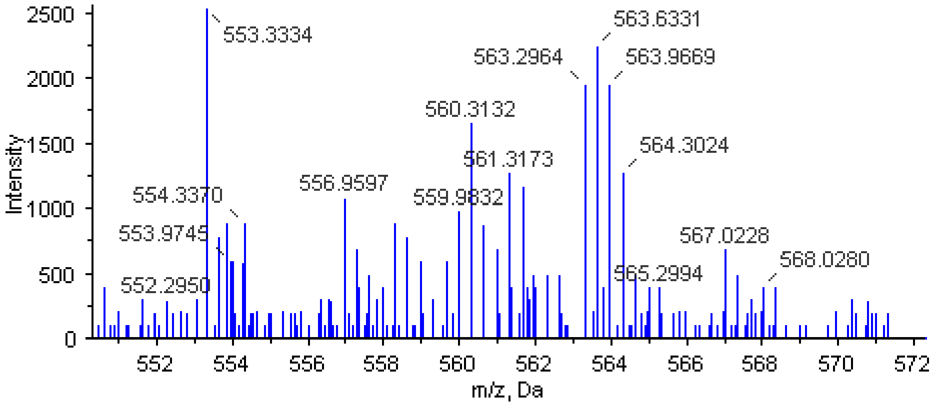
Seq Cov %: 33.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.54

116: 114=E5TL: D5TL=0.63

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MATKK**SVSSLKEADLK**GKRVFVRVDLNVPLDDNLNITDDTRIR**AAVPTIK**YLMDHGAR**VILCTHLGR**PK
GVTPK**YSLKPLVPRLSELLGVEVK**MASDCIGEEVEK**LVAEIPEGGVLLLENVR**FHKEEEKNEPEFAKKL
AGLADVYVNDAFGTAHR**AHASTEGVAKYLKPSVAGFLMQKELDYLVGAVANPKKPFAAIVGGSK**VSTK**I**
GVIESLLEKVDILILGGGMIFTFYKAQGHSVGSSLVEGDKLDLASSLIEKAKAKGVDLLLPTDVVIADK
FAADANSK**VVPASSIPDGWMGLDVGPDAIK**TFCEALDTTQTIIWNGPM**GVFEFDKFAVGTEAIAK**K**LAE**
LSGKGVTTIIGGGDSVAAVEKVGLADKMSHISTGGGASLELLEGKPLPGVLALDDA

Protein No.: I-73

Protein name and Species:

Alanyl-tRNA synthetase, putative OS=Ricinus communis GN=RCOM_0036070 PE=3 SV=1

Accession: tr|B9SYR5|B9SYR5_RICCO

Unused ProtScore: 18.11

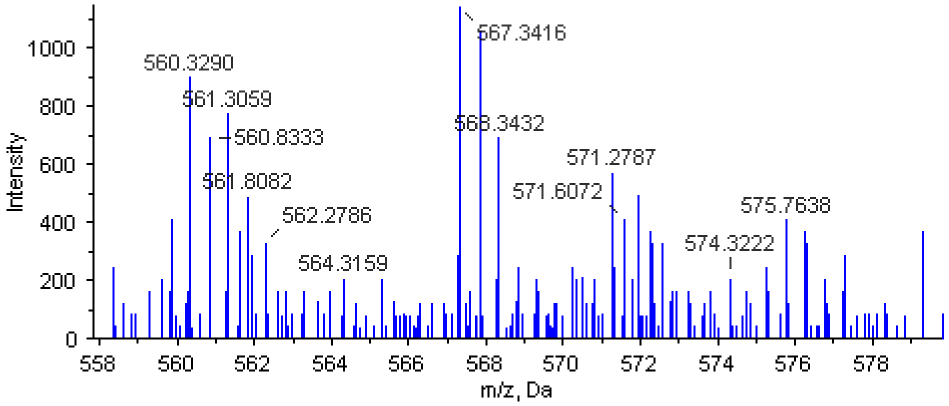
Seq Cov %: 13.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.63

116: 114=E5TL: D5TL=0.52

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MKRITSTAAAAAASSSLSVTLHRTALHSPHLLAAIVVAAARVSLLHPSRATLFASFSSSSSSPLLSHIA
AMPGVDPQEMEWPAKKVRDTFIS**FFEDK**KHVHWKSSPVVPVNDPTLLFANAGMNQFK**PIFLGTADPNTA**
LSKLSRACNTQKCIRAGGK**HNDLDDVGK**DTYHHTFFEMLGNWSFGDYFKREAIGWAWELLTKIYKLPAD
RIYATYFGGDEKAGLAPDAEARDFWLQFLPPERVLPFGCKDNFWEMGDTGPCGPCTEIHYDRVGNRDAS
QLVNNDDPTCIEIWNLVFIQFNRESDGSLKPLPAK**HVDTGMGFERLTSVLQNK**MSNYDTDVFLPIFDAI
QQATGARPYSGKVGSDDVDRVDMAYRVVADHIR**TLSFAIADGSCPGNEGR**EYVLRRILRRAVRYGSEVL
KAQEGFFNGLVNIVVKVMGDVFPELIQNEVRIREIIKEEEASFGKTLLKGIEKFKKAAQEVQGKVSCLQ
DAFVLWDTYGFPLDLTQLMAEERGLW**VDVEGFNNAMDEAR**ERSRNAQNKQAGGDIIMDADATSALHKKG
VSVTDDSYKFIWFQDHESVIKAIYTGTEFLGSTTSSNEVGIVLESTSFYAEQGGQIFDTGSLEGTFGSF
QVSNVQIFGGFVVHIGSLTRAAPRLSVGDKVICKVDYDRRT**LIAPNHTCTHMLNFALREVLGNHVDQK**G
SIVLPEKLRFDFSHGKPVDPALLR**KIESIVNEQIK****AELEVSAK**EATLSEAKRINGLR**AVFGEVYPDPVR**
VVAIGRKVEDLLADPENKEWSSISAELCGGTHISNTKEAK**AFALLSEEGIAK**GVRRITAVTTDGAFKAM
ELASLLEQEADEISKTEGSLLEKKVASLKSRVDSAPIPAAKKFDIRTKISALQDEVRKAQKKISEENMQ
KAVKIATEMAEVAASEGKQFCISR**VDVGLDAAAVR**EAVSKVLQKKGLSAMVFSIDETTNK**VVVCAGVAE**
KGDKSKQLEVSEWLTAALKPLNGRCGKGKGGLATGQGTEGVHLDAAMNLAAEFAQMKLR

Protein No.: I-76

Protein name and Species:

T-complex protein 1 subunit theta-like OS=Populus trichocarpa GN=POPTRDRAFT_823706 PE=3 SV=1

Accession: tr|B9I5Y4|B9I5Y4_POPTR

Unused ProtScore: 17.33

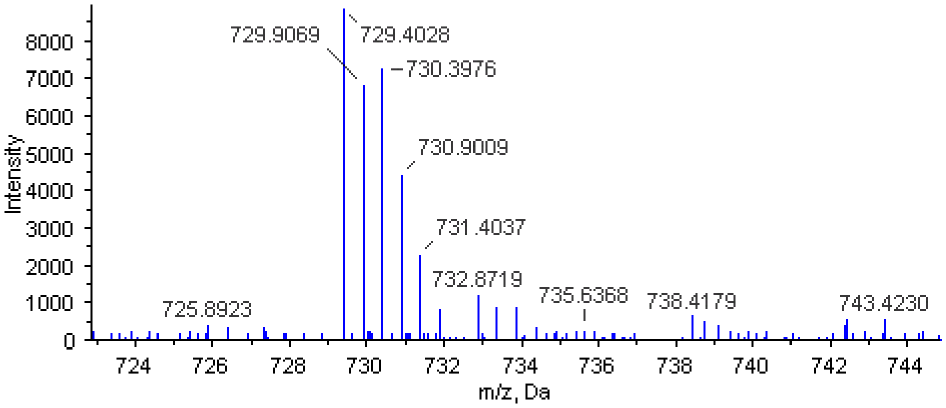
Seq Cov %: 21.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.72

116: 114=E5TL: D5TL=1.29

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGFSMQPYGMQSMLKEGHK**HLSGLDEAVLK**NIDACKQLSAITR**TSLGPNGMNK**MVINHLDK**LFVTNDAA**
TIVNELEVQHPAAK**ILVLAGK**AQQEEIGDGANLTISFAGEMLQN**ADELIR**MGLHPSEIISGYNKAINKA
IEILSELVEPGSENMDVRNKEQVICRMKAAVASKQFGQEDILCNLIADACIQVCPKNPVNFNVDNVRVA
KLVGGGLINSSIVRGMVLKGDTVGTIKRVEKAK**VAVFAGGVDTSATETKGTVLIHSAEQLENYAK**TEEA
K**VEELIK**AVAETGAKVIVSGAAVGEMALHFCERYK**LMVLK**ISSKFELRRFCRTTGAVAILKLSPPSPDD
LGCVDSISVEEIGGARVTIVR**NEEGGNSVCTVVLRGSTDSILDDLER****AVDDGVNTYK**AMCRDSRIIPGG
AATEIELAKRLREFSFK**ETGLDQYAIAK**FAESFEMIPKTLAENAGLNAMEIISSLYAEHASGNTKVGID
LEEGVFKDVSTTNIWDLYVTKFFALK**YAADAACTVLR**VDQIIMAKPAGGPRRDAAPGGMDED

Protein No.: I-77

Protein name and Species:

Cis-prenyl transferase II (Rubber transferase) OS=Hevea brasiliensis GN=Hpt3 PE=2 SV=1

Accession: tr|Q8L3U6|Q8L3U6_HEVBR

Unused ProtScore: 17.27

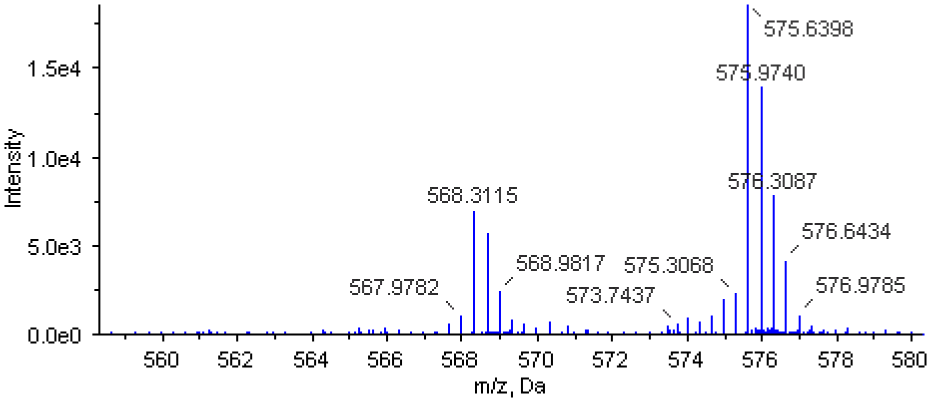
Seq Cov %: 42.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2.23

116: 114=E5TL: D5TL=1.96

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MEIYTGQRPSVFRIFGKYMRK**GLYSILTQGPIPTHLAF**IMDGNRRFAKKHK**MKEAEGYKAGYLALLR**TL
TYCYELGVRYVTIY**AFSIDNFR**RQPR**EVQCVMNLMMEK**IEEIIVEESIMNAYDVGVR**IVGNLNLLDEPI**
RIAAEKIMRATANNSRFVLLIAVAYSSTDEIVHAVEESSKDK**LNSNEVCNNGIEAEQEFKEANGTGNSV**
IPVQKTESYSGINLADLEKNTYVNPHPDVLIRTSGLSRLSNYLLWQTSNCILYSPFALWPEIGLR**HLVW**
TVMNFQRHHSYLEKHKEYLK

Protein No.: I-80

Protein name and Species:

GTP-binding protein ras-like protein OS=Ricinus communis GN=RCOM_1012250 PE=3 SV=1

Accession: tr|B9S943|B9S943_RICCO

Unused ProtScore: 16.77

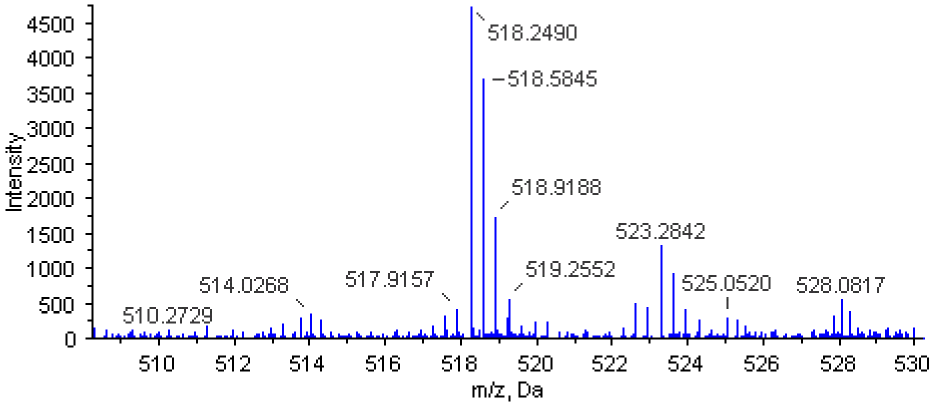
Seq Cov %: 39.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.47

116: 114=E5TL: D5TL=0.72

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGAYR**ADDDYDYLFKVVLIGDSGVGKSNLLSR**FTR**NEFSLESKSTIGVEFATR**SIHVDDKVVK**AQIWDT**
AGQERYR**AITSAYYRGAVGALLVYDVTRHVTFENVER**WLKELRDHTDANIVIMLVGNKADLRHLRAITI
EDATAFAQRQNTFFMETSALESMNVENAFTEVLTQIYRVVSR**KALDIGDDPAALPR**GQTINVGSRDDVS
AVKKAGCCSS

Protein No.: I-83

Protein name and Species: cullin-associated NEDD8-dissociated protein 1-like [Vitis vinifera] OS=Vitis vinifera GN=VIT_12s0035g01840 PE=4 SV=1

Accession: tr|F6HJZ9|F6HJZ9_VITVI

Unused ProtScore: 16.69

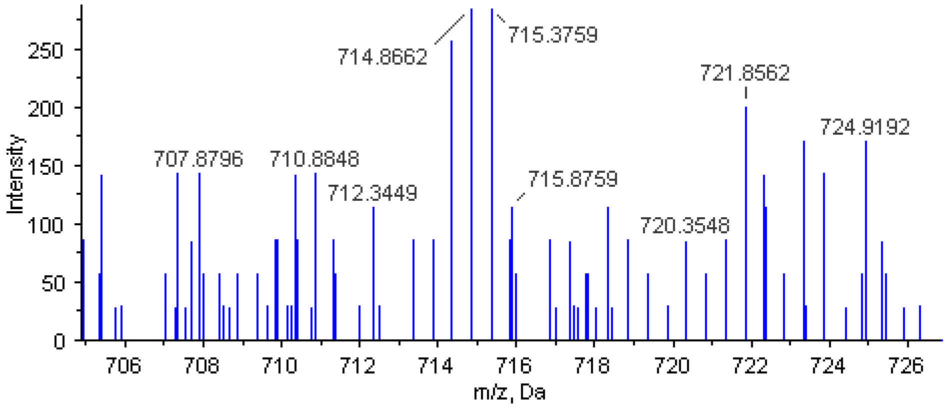
Seq Cov %: 7.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.23

116: 114=E5TL: D5TL=0.66

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MANLAITSILEKMTGKDKDYRYMATSDLLNELNKEGFRADADLEIKLSNIVLQQLDDAAGDVSGLAVKC
LAPLVKKVSETRLVEMTNKLCDKLLNGKDQHR**DIASIALK**TIVSEVTTSAVAQCVLVSLSPQLIKGITS
PGMTTEMKCECLDILCDVLHKFGNLMATDHELLLGALLSQLSSNQASVRKKTVSCIASLASSLSDDLLA
KATVEVVRNLRSKGVKPEMTRTNIQMIGALSRAVGYRFGSHLGDTVPVLINYCTSASENDEELREYSLQ
ALESFLLRCPRDISSYCDEILHLTLEYLSYDPNFTDNMEEDTDDENHEEEEDDESATEYTDDEDVSWKV
RRAAAKCLAALIVSRPEMLSKLYEEACPKLIDRFKEREENVKMDVFNTF**IELLR**QTGNVTKGQTDMNEL
SPRWLLKQEVPKIVKSINRQLREKTIKTK**VGAFSVLK**ELVVVLPDCLADHIGSLISGIEKALSDKSSTS
NLKIEALIFTRLVLASHSPSVFHPYIKALSSPVLSAVGERYYKVTAEALR**VCGELVR**VVRPNIEGYGFD
FKPYVHPIYNAIMTRLTNQDQDQEVKECAISCMGLLVSTFGDNLR**AELPACLPVLVDR**MGNEITRLTAV
KAFAVIATSPLNIDLSCVLEHVIAELTAFLRKANRALRQATLGTLNSLIVAYGDKIGSSAYEVIIVELS
SLISDSDLHMTALALELCCTLMADKRASPNVGLAVRNKVLPQALTLIKSSLLQGQALMALQNFFATLVY
SANTSFDALLDSLLSSAKPSPQSGGVAKQALCSIAQCVAVLCLAAGDQKCSTTVKMLTDILRDDSSSNS
AK**QHLALLCLGEIGR**RKDLSSHAHIENIVIESFQSPFEEIK**SAASYALGNIAVGNLSK**YLPFILDQIDN
QQKKQYLLLHSLKEVIVRQSVDK**AEFQDSSVEK**ILK**LLFNHCESEEEGVR**NVVAECLGKIALIEPAKLV
PALKVRTASPAAFTRATVVIAVKYSIVERPEKIDEIIYPEISSFLMLIKDHDRHVRRAAVLALSTAAHN
KPNLIKGLLPELLPLLYDQTIVKQELIRTVDLGPFKHIVDDGLELRKAAFECVDTLLDSCLDQVNPSSF
IVPYLKSGLDDHYDVKMPCHLILSKLADKCPSAVLAVLDSLVDPLLKTINFKPKQDAVK**QEVDRNEDMI**
RSALRAIASLNRISGGDCSLKFKHLMNEISKSSTLWEKYHSIRNE

Protein No.: I-85

Protein name and Species:

Proteasome subunit alpha type OS=Ricinus communis GN=RCOM_0711430 PE=3 SV=1

Accession: tr|B9RR89|B9RR89_RICCO

Unused ProtScore: 16.45

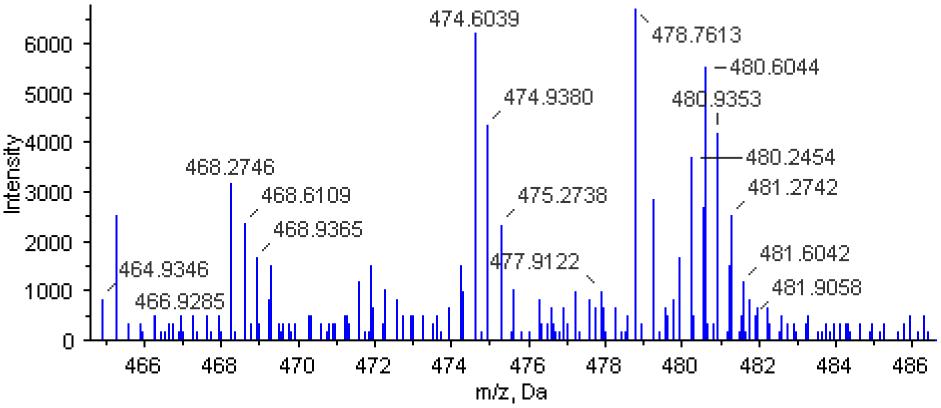
Seq Cov %: 40.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.71

116: 114=E5TL: D5TL=1.12

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSRGSGGGYDR**HITIFSPEGR**LFQVEYAFKAVK**AAAVTSIGVRGKDSVCVVTQK**KVPDK**LLDQTSVTHL**
FPITKYLGLLATGMTADARTLVQQAR**NEAAEFR**FRYGYEMPVDVLARWIADK**SQVYTQHAYMR**PLGVIA
MVLGIDEENGPQLYKCDPAGHFFGHKATSAGLK**EQEAINFLEK**KMKNDRAFTYEETVQTAISALQSVLQ
EDFK**ATEIEVGVVR**ADDRVFR**VLSTEEIDEHLTAISERD**

Protein No.: I-86

Protein name and Species:

Proteasome subunit alpha type OS=Glycine max PE=2 SV=1

Accession: tr|C6TKI4|C6TKI4_SOYBN

Unused ProtScore: 16.41

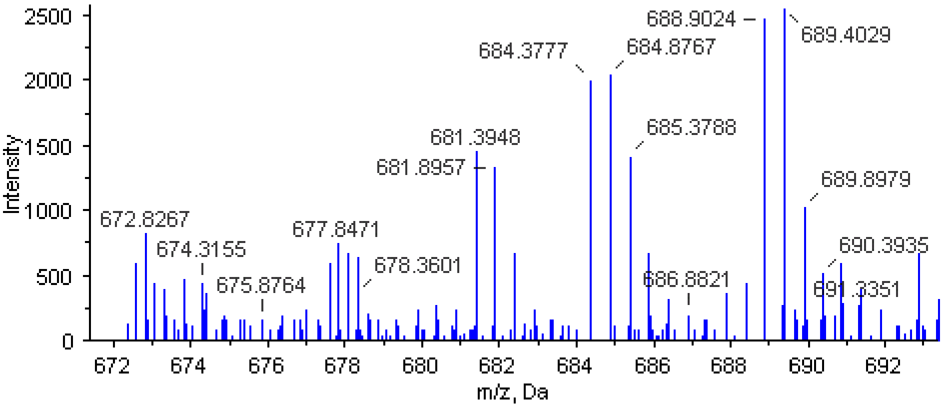
Seq Cov %: 37.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2.07

116: 114=E5TL: D5TL=1.87

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGDSQYSFSLTTFSPSGKLVQIEH**ALTAVGSGQTSLGIKAANGVVIATEKKLPSILVDETSVQK**IQLST
PN**IGVVYSGMGPDFR**VLVRKSRKQAEQYHR**LYKEPIPVTQLVR**EVAAVMQEFTQSGGVRPFGVSLLVAG
FDDN**GPQLYQVDPSGSYFSWK**ASAMGKNVSNAKTFLEKRYTDDMELDDAVHTSILTLK**EGFEGQISGKN**
IEIGIIGADKKFRVLTPAEIDDYLAEVE

Protein No.: I-87

Protein name and Species:

Glucose-6-phosphate isomerase OS=Ricinus communis GN=RCOM_1594100 PE=3 SV=1

Accession: tr|B9R7S8|B9R7S8_RICCO

Unused ProtScore: 16.33

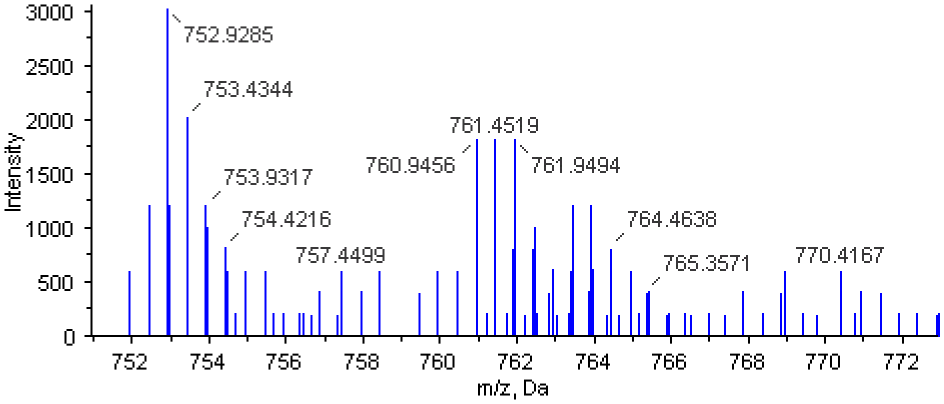
Seq Cov %: 16.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.41

116: 114=E5TL: D5TL=0.26

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MALSALICDTQPWKDLKAHVEDIKKTHLRNLLGDTERCKSMLVEFDGIMLDYSRQTATIDTLDK**LYNLA**
EAAHLKEKIHRMFNGERINSTENR**SVLHVALR**APRDAIVNSDGK**NVVPDVWNVLDK**IKEFSERVRNGSW
VGATGKPLTDVIAIGIGGSFLGPLFVHTALQTDPEASKSAKGRQLRFLANVDPIDVARNIAGLSPETTL
VVVVSK**TFTTAETMLNAR**TLRAWISR**ELGPSAVAK**HMVAVSTNLTLVEKFGIDPNNAFAFWDWVGGRYS
VCSAVGVLPLSLQYGFSIVEKFLKGASSIDQHFSSAPFEKNIPVLLGLLSVWNVSVLGYPAR**AILPYSQ**
ALEKLAPHIQQVSMESNGKGVSMDGVPLPFETGEIDFGEPGTNGQHSFYQLIHQGR**VIPCDFIGVVK**SQ
QPVYLEGEVVNNHDELMSNFFAQPDALAYGKTAEQLQKENVPQHLIPHKTFSGNRPSVSILLSSLDAYK
IGQLLAIYEHRVAVQGFVWGINSFDQWGVELGKSLATQVRKQLNASR**TKGEPVEGFNFSTTTMLTR**YLE
ETSEVPAKPQTLLPRI

Protein No.: I-89

Protein name and Species:

26S proteasome regulatory subunit S3, putative OS=Ricinus communis GN=RCOM_0977830 PE=4 SV=1

Accession: tr|B9S5K6|B9S5K6_RICCO

Unused ProtScore: 16.31

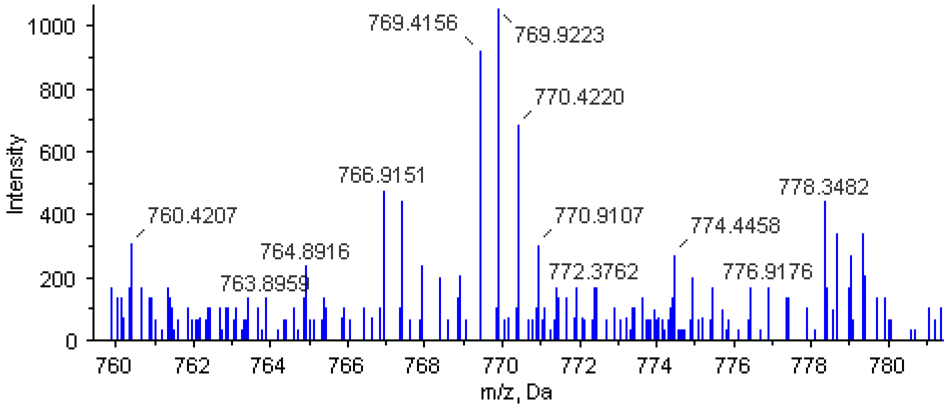
Seq Cov %: 19.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2.11

116: 114=E5TL: D5TL=1.37

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MTQDVEMKEVPAAAAAPSNSTTSSSPSTLQHLK**EIASLIETGAYAR**EVRRIVRAVRLTMALRRKLKAQL
LSAFLNSILTPGSDPYTRLSSFLPKEDDHEMEVDTATSVTQAPAKHPLPELEMYCYLLVLIYLIDQKKY
NEAKACSTACIARLKNLNRRTVDVLASRLYFYYSLSYELTGDLAEIRGNLLALHRIATLRHDELGQETL
LNLLLR**NYLHYNLYDQAEK**LRSKAPR**FEAHSNQQFCR**YLFYLGKIR**TIQLEYTDAK**ESLLQAARKSPVA
ALGFRVQCNKWAIIVRLLLGEIPERTVFMQKGMEKALRPYFELTNAVR**IGDLELFK**SVAEKFSTIFSAD
RTHNLIVRLRHNVIRTGLR**NISISYSRISLADVAK**KLR**LDSANPVADAESIVAK**AIRDGAIDATLDHAN
GWMVSK**ETGDIYSTNEPQIAFNSR**IAFCLNMHNEAVRALRFPPNSHKEKESAEKRRERQQQEQELAK**HI**
AEEDDDEF

Protein No.: I-95

Protein name and Species:

UDP-D-glucose pyrophosphorylase OS=Gossypium hirsutum PE=2 SV=1

Accession: tr|D2D2Z1|D2D2Z1_GOSHI

Unused ProtScore: 16.17

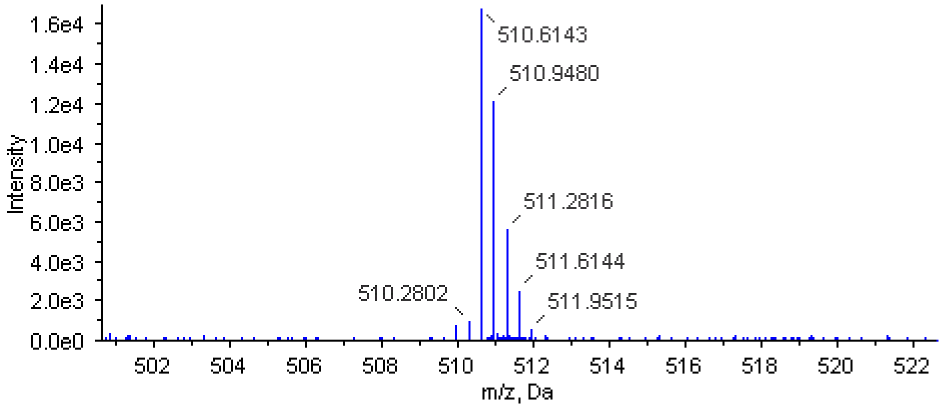
Seq Cov %: 27.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.47

116: 114=E5TL: D5TL=0.74

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MEKLEHLKSAVAALSEISENEKNGFINLVSRYLSGEAQHIEWSK**IQTPTDEVVVPYDTLSPSPDDPAET**
KKLLDKLVVLK**LNGGLGTTMGCTGPKSVIEVR**NGLTFLDLIVIQIENLNSKYGCNVPLVLMNSFNTHDD
TLKIVDKYSNSNIEIHTFNQSQYPR**LVVEDFAPLPSK**GQHGKDGWYPPGHGDVFPSLMNSGKLDAFLSQ
GKEYVFVANSDNLGAIVDMKILNHLVQNK**NEYCMEVTPK**TLADVK**GGTLISYEGK**VQLLEIAQVPDEHV
NEFKSIEKFKIFNTNNLWVNLNAIKR**LVEADALKMEIIPNPK**EVNGIK**VLQLETAAGAAIRFFDHAIGI**
NVPRSRFLPVKATSDLLLVQSDLYTLVDGFVIRNKDRANPTN**PSIELGPEFK**KVGNFLSRFK**SIPSIIE**
LDSLKVTGDVWFGAGIVLKGK**VSIAAKPGVK**LEIPDGAVIEKKEINVPEDI

Protein No.: I-98

Protein name and Species:

Eukaryotic translation initiation factor 2c, putative OS=Ricinus communis GN=RCOM_0605410 PE=4 SV=1

Accession: tr|B9SJV6|B9SJV6_RICCO

Unused ProtScore: 15.62

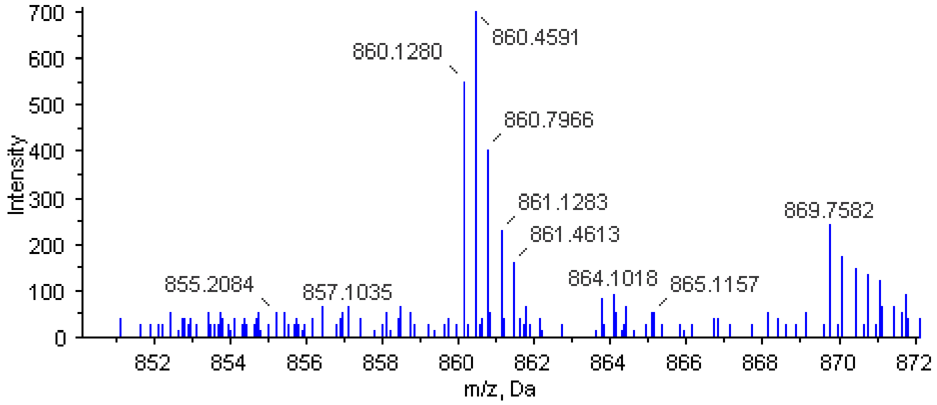
Seq Cov %: 14.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.61

116: 114=E5TL: D5TL=0.59

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MVRKRRTEAPASGGESSEPHEAASGGSQRPYERNAPPQQGPGGPYQGGRSWGPQSQQGGRGGGGRGRSG
GMSQQQQYGGGPEYQGRGRGPPQQGGRGGYGGGRSSSNRGGPPSVGPSRPPVPELHQATLAPYQAGVSP
QLMPSEGSSSSGPPEPSPVVVAQQMQELSIQQEVSSSQPIQAPPPSSKSMRFPLRPGKGSTGIRCIVKA
NHFFAELPDKDLHQYDVTITPEVTSRGVNRAVMEQLVKLYRESHLGK**RLPAYDGR**K**SLYTAGPLPFISK**
EFKITLIDEDDGSGGQRREREFRVVIKLAARADLHHLGLFLQGR**QADAPQEALQVLDIVLR**ELPTTRYC
PVGR**SFYSPDLGR**RQPLGEGLESWRGFYQSIRPTQMGLSLNIDMSSTAFIEPLPVIDFVNQLLNR**DVSS**
RPLSDADRVKIKKALRGVKVEVTHRGNMRRKYRISGLTSQATR**ELTFPVDER**GTMKSVVEYFYETYGFV
IQHTQWPCLQVGNQQRPN**YLPMEVCK**VVEGQRYSKRLNERQITALLKVTCQRPQERERDIMQTVHHNAY
GNDPYAKEFGIKISEKLASVEARILPAPWLKYHDTGREKDCLPQVGQWNMMNKKMVNGGTVNNWICINF
SRNVQDSVARGFCYELAQMCY**ISGMAFNPEPVLPPVSARPEQVEK**VLKTRYHDAMTKLQQGKELDLLIV
ILPDNNGSLYGELKR**ICETDLGLVSQCCLTK**HVFRMNKQYLANVALKINVKVGGRNTVLVDALSRRIPL
VSDRPTIIFGADVTHPHPGEDSSPSIAAVVASQDWPEVTK**YAGLVCAQAHRQELIQDLFK**EWQDPVRGR
VTGGMIK**ELLISFR**RATGQKPQRIIFYRDGVSEGQFYQVLLYELDAIRK**ACASLEPNYQPPVTFVVVQK**
RHHTRLFANNHNDRNAVDKSGNILPGTVVDSKICHPTEFDFYLCSHAGIQGTSRPAHYHVLWDENKFTA
DGLQSLTNNLCYTYARCTR**SVSIVPPAYYAH****LAAFR**ARFYMEPETSDSGSMTSGPVGGRGGMGGGAGAR
STRGP**AASAAVRPLPALK**ENVKRVMFYC

Protein No.: I-99

Protein name and Species:

Coatomer subunit beta OS=Vitis vinifera GN=VIT_04s0008g02320 PE=3 SV=1

Accession: tr|A5AHP0|A5AHP0_VITVI

Unused ProtScore: 15.49

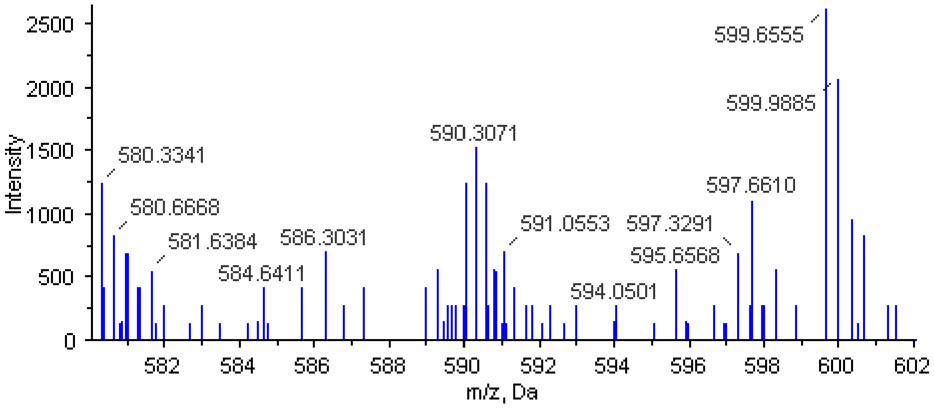
Seq Cov %: 11.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.80

116: 114=E5TL: D5TL=1.49

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MEKSCSLLIYFDK**GTPAIANEIK**EALEGNDDYAKIEAMKKAIMLLLNGETLPQLFITIVRYVLPSEDHT
VQKLLLLYLEIIEKTDAKGKVMPEMILICQNLR**NNLQHPNEYIR**GVTLRFLCRLNEAEIIEPLIPSVLQ
NLEHRHPFIRRNAILAVMSIYK**LPQGEQLLVDAPEMIEK**VLSTEQDPSAKR**NAFLMLFTCAQDRAINYL**
LTHVDRVPEWGELLQMVV**LELIR**KVCRTNRGEKGKYIKIIISLLNAPSTAVIYECAGTLVSLSSAPTAI
R**AAANTYCQLLLSQSDNNVK**LIVLDRLNELKSSHREIMVDMIMDVLRALSSPNLDIRRKTLDIVLELIT
PRNINEVVLTLKKEVVKTQSGELEKNGEYRQMLIQAIHSCAIKFPEVASTVVHLLMDFLGDSNVASAID
VVVFVREIIETNPKLRVSIITR**LLDTFYQIR**AARVCSCALWIIGEYCLSLSEVESGITTIKQCLGDLPF
FSVSEEGEASDSSKKVQQVNATTVSSRRPAVLADGTYATQSAASETAFSPPTLVQGSLSSGNLRSLLLT
GDFFLGAVVACTLTKLVLRLEEVQPSKAEVNKVSSQALLIMVSMLQLGQSSVLPHPIDNDSYDRIVLCI
RLLCNTGDDIRKIWLQSCRQSYVKMLADKQLRETEEIKAKAQISYAQPDDLIDFYHLKSRK**GMSQLELE**
DEVQDDLKRATGEFIKDGDDANKLNRILQLTGFSDPVYAEAYVTVHHYDIVLDVTVINRTKETLQNLCL
ELATMGDLK**LVDRPQNYTLAPESSK**QIKANIKVSSTETGVIFGNIVYETSNVHERMVVVLNDIHIDIMD
YISPAVCTDVAFRTMWAEFEWENKVAVNTVLQNEKEFLEHIIKSTNMKCLTASSALDGDCGFLAANLYA
KSVFGEDALVNISIEKQADGKLSGYIRIRSK**TQGIALSLGDK**ITLKQKGGS

Protein No.: I-102

Protein name and Species:

Nucleoredoxin, putative OS=Ricinus communis GN=RCOM_0528050 PE=4 SV=1

Accession: tr|B9SH99|B9SH99_RICCO

Unused ProtScore: 15.18

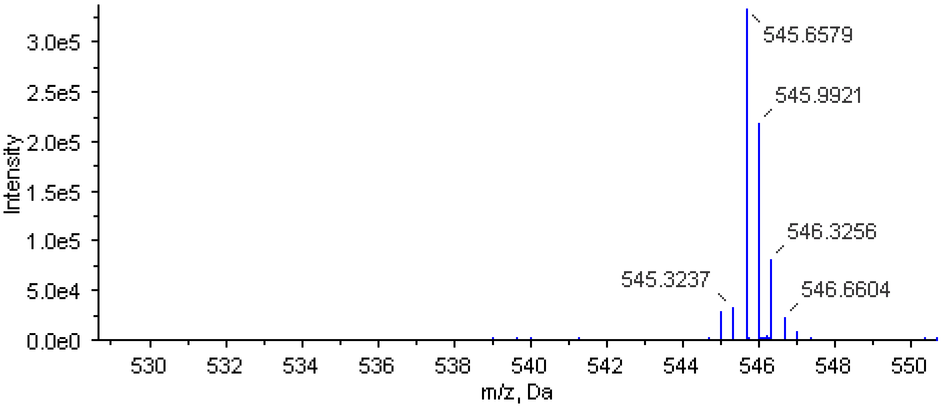
Seq Cov %: 18.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.42

116: 114=E5TL: D5TL=0.59

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MADDPVIDVSHDLLSLLSSDDRDFLIRSNGDQVKISNLVGKIVGLYFSGSWCGPCRHFTPNLVQVYEEL
SLKGDFEVVFISSDRDAESFDAYFSKMPWLAIPFSDQETCKHLKDLFKVRGIPNLVFLDADGKVSCDQG
VRFIR**EYGAEGYPFTPER**VEYFRQEEENAK**KNQTLSSILVSSSR**DFLISKDGTK**IPVSELEGK**MVGLYF
SVHSHRLCLDFTPRLEEVYKKLKEKGEKFEVVLISMDYDENNFKQGLETMPWLALPFEDKSRERLARYF
ELS**ALPTLVIIGEDGK**TLNKNVAELIEGHGIQAYPFTPEK**LVELAEIEK**AR**LEAQTLESVLVHGDK**DFV
IEESGSKVPVSELVGK**NILLYFSAK**WCPPCRAFLPK**LIEAYHEIK**AKDNAFEIIFISSDRDQSSFDEFY
TEMPWLALPFGDDRKTILQRKFKIK**GIPAAIAISPT**GKTLTKEAREHITAYGADAYPFNEDHLKQLNDK
QEEIAKGWPEKVRHELHPEHELVRMKRNGYGCDGCKEAGSGWSFYCKKCDFDLHPKCALKKEENGEKVK
K

Protein No.: I-106

Protein name and Species:

L-lactate dehydrogenase OS=Ricinus communis GN=RCOM_0540790 PE=3 SV=1

Accession: tr|B9SIT3|B9SIT3_RICCO

Unused ProtScore: 14.96

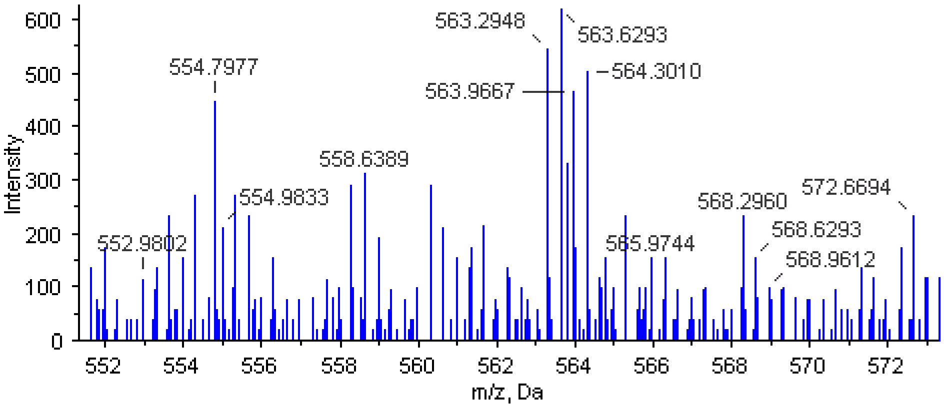
Seq Cov %: 32.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.44

116: 114=E5TL: D5TL=0.76

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MQQSSSAASLGPGGLDLSQVFFKPIHNTSPPSPTKRHTKISVIGTGNVGMAIAQTILTQDLADELALVD
VNPNKLR**GEMLDLQHAAAFLPR**TKILASPDYSVTIGSDLCIVTAGARQIPGESR**LNLLQR**NVTLFKNII
PPLAKYSPDSILMIVSNPVDILTFIAWK**LSGFPSNR**VVGSGTNLDSSRFRFLIADHLDVNAQDVQAYIV
GEHGDSSVALWSSISVGGVPILSFLEKQDIAYEK**ETLENIHKAVVDSAYEVISLKGYTSWAIGYSAANL
AR**SLLRDQRK**IHPVSVLAKGFYGIDGGDVFLSLPAQLGRGGVLGVTNVHLTEEEAQR**LRDSAKTLLEVQ
SQLGI

Protein No.: I-108

Protein name and Species:

26S proteasome regulatory subunit 4 homolog A [Vitis vinifera] OS=Vitis vinifera GN=VIT_07s0005g05160 PE=3 SV=1

Accession: tr|A5BEF3|A5BEF3_VITVI

Unused ProtScore: 14.87

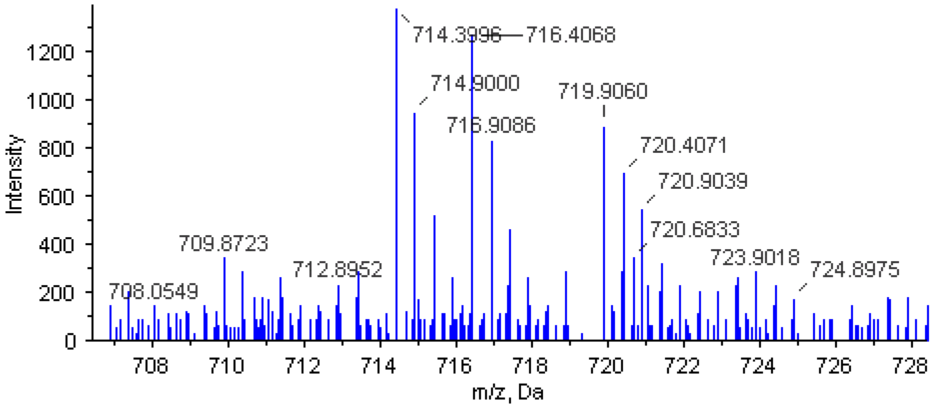
Seq Cov %: 27.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.51

116: 114=E5TL: D5TL=1.47

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGQGASGGLNRQGLPGDRKNDGDKKEK**KFEPAAPPAR**VGRKQRKQKGPEAAARLPTVTPLSKCKLRLLK
LERIKDYLLMEEEFVSNQERLKPQEEKTEEDRSKVDDLRGSPMSVGNLEELIDENHAIVSSSVGPEYYV
GILS**FVDK**DQLEPGCAILMHNKVLSVVGLLQDEVDPMVSVMKVEK**APLESYADIGGLDAQIQEIK**EAVE
LPLTHPELYEDIGIKPPK**GVILYGEPGTGK**TLLAK**AVANSTSATFLRVVGSELIQK**YLGDGPKLVRELF
R**VADDLSPSIVFIDEIDAVGTK**RYDAHSGGEREIQR**TMLELLNQLDGFDSR**GDVKVILATNR**IESLDPA**
LLRPGRIDRKIEFPLPDIKTRRR**IFQIHTSRMTLADDVNLEEFVMTKDEFSGADIKAICTEAGLLALR**E
RRMKVTHVDFKKAKEKVMFKK**KEGVPEGLYM**

Protein No.: I-109

Protein name and Species:

Chaperonin containing t-complex protein 1, eta subunit, tcph, putative OS=Ricinus communis GN=RCOM_0395630 PE=3 SV=1

Accession: tr|B9SS36|B9SS36_RICCO

Unused ProtScore: 14.75

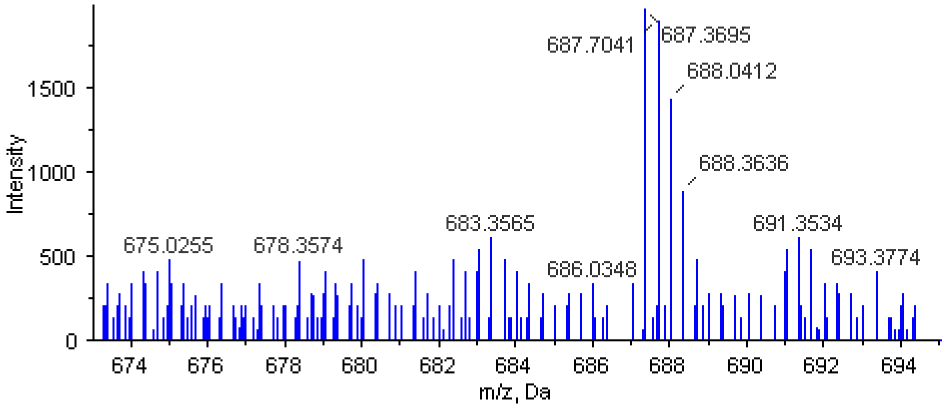
Seq Cov %: 17.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.55

116: 114=E5TL: D5TL=0.72

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAAMLQPQIILLKEGTDTSQGK**AQLVSNINACTAVADVVR**TTLGPRGMDKLIHDDKGNVTISNDGATIM
K**LLDIVHPAAK**ILVDIAKSQDSEVGDGTTTVVLLAAEFLKEAKPFIEDGVHSQNLIRSYRTACNLALEK
IRELAFSIEGKSIEEKKSLLAKCASTTLSSKLIGGEKEFFAQMVVDAVIAIGNEDR**LNMIGIK**KVPGGN
MR**DSFLVNGVAFK**K**TFSYAGFEQQPK**KFVNPKLLLLNIELELKSEKENAEIRLSDPSEYQSIVDAEWNI
IYDKLDKCVQSGAKVVLSR**LAIGDLATQYFADR**DIFCAGR**VAEEDLQR**VAAATGGTVQTTVNNIIDEVL
GTCEIFEEKQVGNERFNIFSGCPSGKTATIVLR**GGADQFIEEAERSLHDAIMIVR**RAMK**NSTVVAGGGA**
IDMEISRFLRQHARTIAGK**SQLFINSYAK**ALEVIPRQLCDNAGFDATDVLNKLRQKHALPSGEGAPFGV
DINTGGIADSFANFVWEPAVVKINAINAATEAACLILSVDETVKNPK**SESAQGEAAAGAMGGRGRGGAA**
FRGRGRGMRRR

Protein No.: I-112

Protein name and Species:

Lactoylglutathione lyase, putative OS=Ricinus communis GN=RCOM_0904280 PE=4 SV=1

Accession: tr|B9RXK1|B9RXK1_RICCO

Unused ProtScore: 14.47

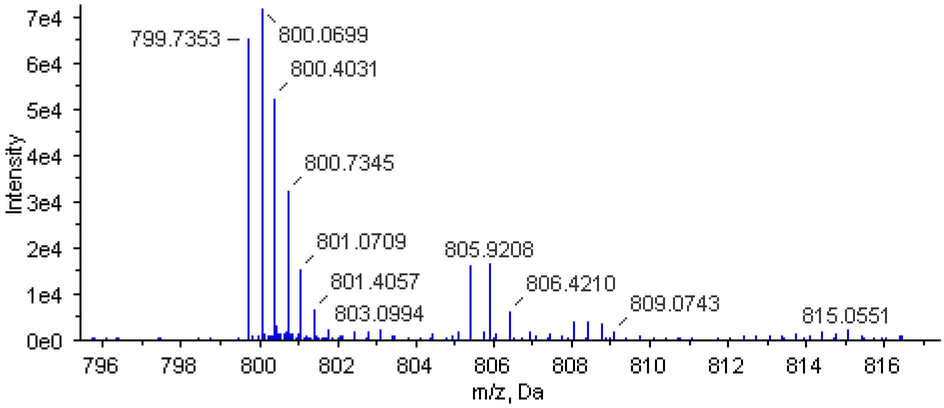
Seq Cov %: 30

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.08

116: 114=E5TL: D5TL=0.10

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAAEATAPNADVLEWPKKDKRRLLHAVYR**VGDLDR**TIK**FYTECFGMK**LLRKRDIPEEKYSNAFLGFGPE
ETNFVVELTYNYGVTSYDIGTGFGHFAIATQDVYKLVEEVLAKGGAVTREPGPVK**GGTTVIAFVKDPDG**
YIFELIQRGPTPEPLCQVMLRVGDLDRSIRFYEKALGMKLLRKVDKPEYKYTLAMMGYADEYETTVLEL
TYNYGVTEYTK**GNAYAQVAISTDDVYKSAEVVNLVTQELGGKITRQPGPIPGLNTKITSFLDPDGWK**TK
RKRR

Protein No.: I-115

Protein name and Species:

Glucose 4-6-dehydratase, putative OS=Ricinus communis GN=RCOM_1185970 PE=4 SV=1

Accession: tr|B9SN65|B9SN65_RICCO

Unused ProtScore: 14.31

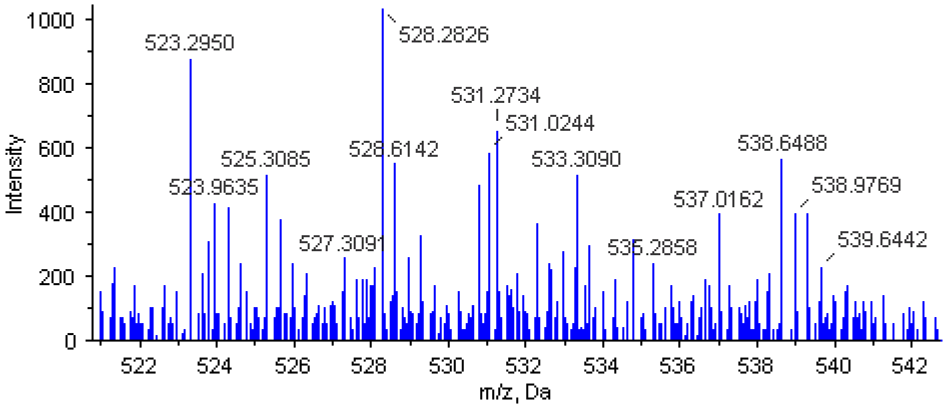
Seq Cov %: 28.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=3.10

116: 114=E5TL: D5TL=1.52

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MANR**VDLDGR**PIKEMTIC**MIGAGGFIGSHLCEK**ILNETPHK**ILALDVYNDK**IKHLLEPDSLPWAGRIQF
HRINIKHDSR**LEGLIK****MADLTINLAAICTPADYNTR**PLDTIYSNFIDALPVVKYCSENNKRLIHFSTXX
SYFSWDPAYYILKEDESPCIFGSIEKQRWSYACAKQLIERLIYAEGAENGLEFTIVRPFNWIGPR**MDFI
PGIDGPSEGVPR**VLACFSNALLRGEPLKLVDGGQSQRTFVYIK**DAIEAVLLMIENPARANGHIFNVGNP
HNEVTVK**QLAEMMTEVYSKVSGEPVLEVPTVDISSK**EFYGEGYDDSDKR****IPDMTIINR**QLGWNPKTSLW
DLLESTLTYQHRTYAEAIKKVLAKPTSS

Protein No.: I-117

Protein name and Species:

Regulator of ribonuclease activity A OS=Populus trichocarpa GN=POPTRDRAFT_738638 PE=2 SV=1

Accession: tr|A9PFQ6|A9PFQ6_POPTR

Unused ProtScore: 14.13

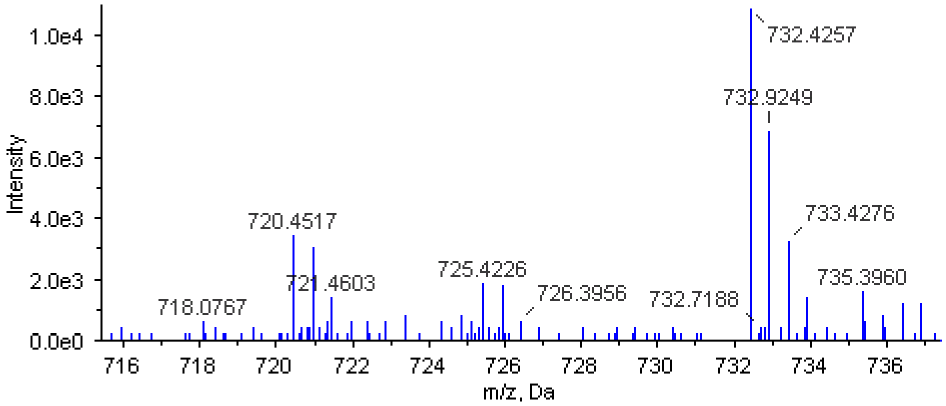
Seq Cov %: 42.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.30

116: 114=E5TL: D5TL=0.37

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MALVTTAEVCDANPQLIVSGELR**ALQPIFQIYGRRQVFSGPVVTLKVFEDNVLIR**EFLEEKGNGR**VLVVDGGGSLR**CAILGGNPVVQAQNNGWAGIVVNGCIRDVDEIMGCDIGVRALASHPMKANKKGIGEK**HVPITIGGTRISDGEWLYADTDGILISR**TELAV

Protein No.: I-119

Protein name and Species:

Hydroxymethylglutaryl coenzyme A reductase OS=Hevea brasiliensis PE=2 SV=1

Accession: tr|Q547W6|Q547W6_HEVBR

Unused ProtScore: 14.02

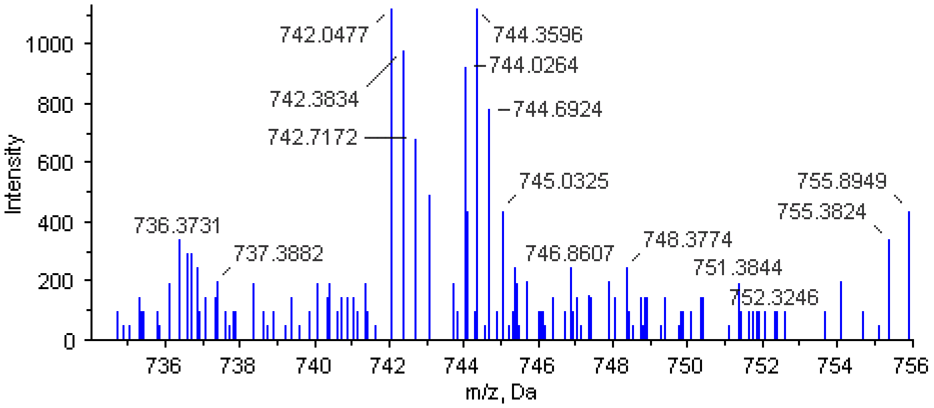
Seq Cov %: 22.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.22

116: 114=E5TL: D5TL=0.28

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDTTGRLHHRKHATPVEDRSPTTPKASDALPLPLYLTNAVFFTLFFSVAYYLLHRWRDKIRNSTPLHIV

TLSEIVAIVSLIASFIYLLGFFGIDFVQSFIARASHDVWDLEDTDPNYLIDEDHR**LVTCPPANISTKTT**

IIAAPTKLPTSEPLIAPLVSEEDEMIVNSVVDGKIPSYSLESKLGDCKRAAAIRREALQRMTRRSLEGL

PVEGFDYESILGQCCEMPVGYVQIPVGIAGPLLLNGR**EYSVPMATTEGCLVASTNR**GCK**AIYLSGGATS**

VLLKDGMTRAPVVRFASATRAAELKFFLEDPDNFDTLAVVFNKSSRFARLQGIKCSIAGKNLYIR**FSCS**

TGDAMGMNMVSKGVQNVLEFLQSDFSDMDVIGISGNFCSDKKPAAVNWIEGRGKSVVCEAIIKEEVVKK

VLK**TNVASLVELNMLKNLAGSAVAGALGGFNAH**AGNIVSAIFIATGQDPAQNVESSHCITMMEAVNDGK

DLHISVTMPSIEVGTVGGGTQLASQSACLNLLGVKGANKESPGSNSRLLAAIVAGSVLAGELSLMSAIA

AGQLVKSHMKYNRSSKDMSKAAS

Protein No.: I-122

Protein name and Species:

villin-2 OS=Populus trichocarpa GN=POPTRDRAFT_576360 PE=4 SV=1

Accession: tr|B9II82|B9II82_POPTR

Unused ProtScore: 13.95

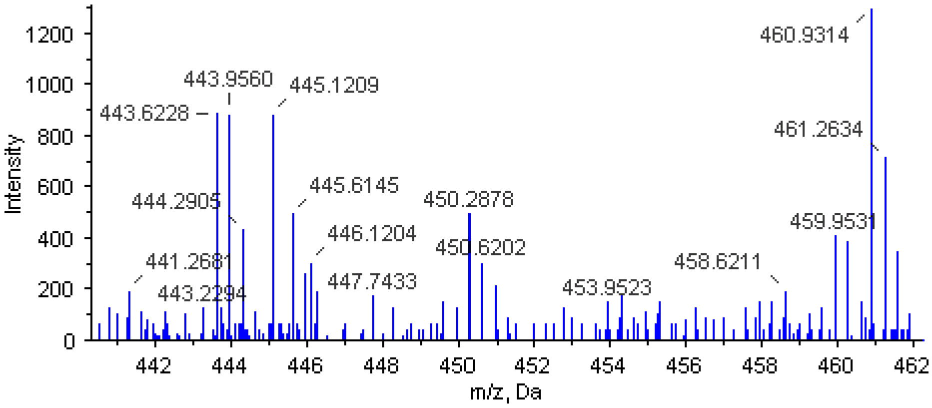
Seq Cov %: 13.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.58

116: 114=E5TL: D5TL=1.19

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSSSAKALDPAFQGVGQRPGTEIWRIENFQPVPLPKSDHGK**FYMGDSYIVLQTTTGK**GGAYLYDIHFWI
GK**DTSQDEAGTAAIKTVELDAVLGGR**AVQHR**ELQGHESDK**FLSYFKPCIIPLEGGVATGFKKVEEEAFE
IRLYVCRGKRVVRLKQVPFARSSLNHDDVFILDTEKK**IYQFNGANSNIQER**GK**ALEVIQFLK**EK**YHEGT**
CDVAIVDDGKLDTESDSGEFWVLFGGFAPIGKKVANEDDIIPETTPAK**LYSITDGEVK**IVEGELSKGLL
ENNKCYLLDCGAEIFVWVGRVTQVEERKAASQAAEEFVASQNRPKTTQLTRLIQGYETRSFKTNFDSWP
AGSAAPGAEEGRGKVAALLKQQGVGLKGMTK**SAPVNEEVPPLLEGGGK**MEVWCINGSSKTPLPKEDVGK
FYSGDCYIILYTYHSGDRKEDYLLCCWFGNDSSEIHGHPIQEDQKMAARLANTMSNSLKGRPVQGRIFQ
GKEPPQFVALFQPIVILKGGLSSGYKKSIAEK**GLSDETYTADSVALFR**ISGTSVHNDKAVQVDAVATSL
NSAECFLLQSGSSIFTWHGNQSTFEQQQLAAK**IAEFLKPGVALK**HAKEGTESSAFWFALGGKQSYTSKK
FSPETVR**DPHLFTFSFNK**GKFQVEEVYNFSQDDLLTEDILILDTHAEVFVWVGQYVDPKEKQNVFDIGQ
KYIEMAVSLDGLSPNVPLYKVTEGNEPSFFTTYFSWDLTKATVQGNSFQKKAALLFGLGHHVVEERSNG
NQGGPTQR**ASALAALSSAFNPSSGK**SSLLDRSNGSNQGGTTQRASALAALSSAFNSSPGSKTTASRPSG
TGQGSQRRAAVAALSSVLTAEKKQTPETSPSRSPPSETNLPEGSEGVAEVKEMEETASVSESNGGEDSE
RKQDTEHGESDDGNGQSTFCYDQLKAHSDNPVKGIDFKRREAYLSDEEFQTIFGVTKEAFYKMPKWKQD
MQKKKFDLF

Protein No.: I-125

Protein name and Species:

Cysteine synthase OS=Vitis vinifera GN=VIT_14s0030g01560 PE=3 SV=1

Accession: tr|F6HTU8|F6HTU8_VITVI

Unused ProtScore: 13.43

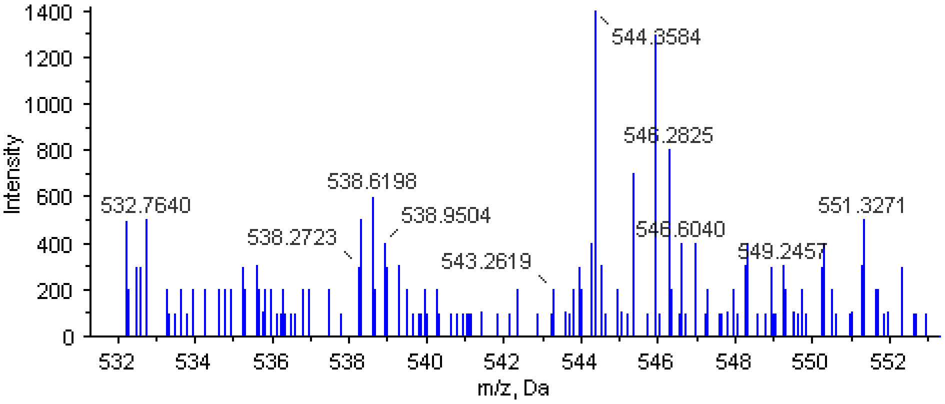
Seq Cov %: 11.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.17

116: 114=E5TL: D5TL=0.40

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MIQKKSELILIYNIKLGNLILNLILFVRFIQEKQFAILPSLFIKVVSVETVGDVQKPQNRKKKQRIRKG
DLVVGISGDLCEMAEEKCFIAK**DVTELIGK**TPLVYLNNVVDGCVARIAAK**LEMMEPCSSVK**DRIGYSMI
TDAEEKGLITPGESVLIEPTSGNTGIGLAFMAAAKGYK**LIITMPASMSLER**RIILRAFGAELVLTDPAK
GMKGAVQK**AEEILAKTPNSYILQQFENPANPK**IHYETTGPEIWRGTGGKVDAFVSGIGTGGTITGAGKF
LKEQNSDIK**LYGVEPVESAVLSGGKPGPHK**IQGIGAGFIPGVLDVNLLDEVVQVSSEEAIETAK**LLALK**
EGLLVGISSGGAAAAAIKLAK**RPENAGKLIVVVFPSFGER**YLSSVLFDSVKREAENMLKKKHGGQMLDC
KRCYRTSIAVKLEAMEPCSSVKDRIALSMIKDVEDKGLIQLGKTVLIEPTSGNSGIELAYIAAVKGYKL
ILAMPASMSRERRIVLRAFGDELHLTDPVKGIKGIHEKAELLEKTPYGYMLKQFANPANPKIHYETTGT
EIWRGCGGKVDVFVSGVGTGGTVTGVGRFLKEKNPDIKVYGVEPAESAVLNGGEPGLHKIQGIDPGFIT
PILDVSILDEVVPISSEEAIETAK**LLALK**EGLLVGKPSGVAAAAAIKIAK**RPENAGKLIVVVFPSFGER**
YLSTVLFDSIR

Protein No.: I-129

Protein name and Species:

Proteasome subunit alpha type OS=Glycine max PE=2 SV=1

Accession: tr|C6TGU2|C6TGU2_SOYBN

Unused ProtScore: 13.13

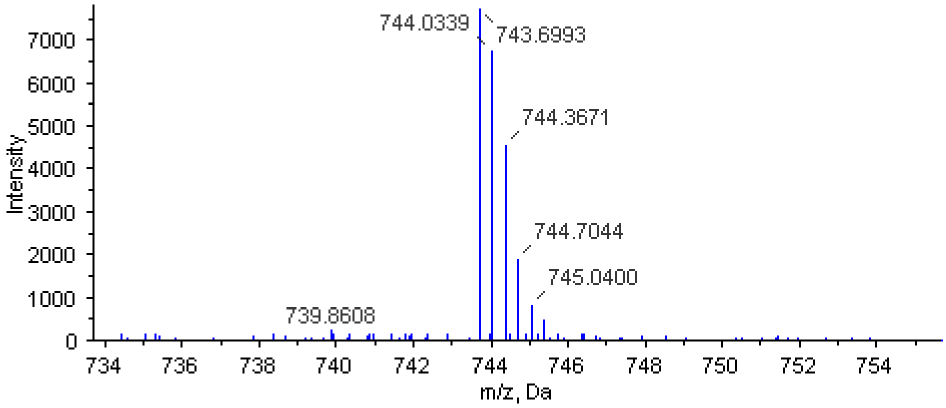
Seq Cov %: 39.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.52

116: 114=E5TL: D5TL=0.66

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MFLTRTEYDR**GVNTFSPEGRLFQVEYAIEAIK**LGSTAIGLKTKEGVVLAVEK**RITSPLLEPSSVEK**IME
IDEHIGCAMSGLIADARTLVEHARVETQNHR**FSYGEPMTVESTTQALCDLALR**FGEGDEESMSRPFGVS
LLIAGHDENGPSLYYTDPSGTFWQCNGK**AIGSGSEGADSSLQEQYNKDLTLQEAETIALSILK**QVMEEK
VTPNNVDIAKVAPTYHLYTPSEVEAVISRL

Protein No.: I-131

Protein name and Species:

40S ribosomal protein SA OS=Glycine max PE=2 SV=1

Accession: sp|O22518|RSSA_SOYBN

Unused ProtScore: 12.95

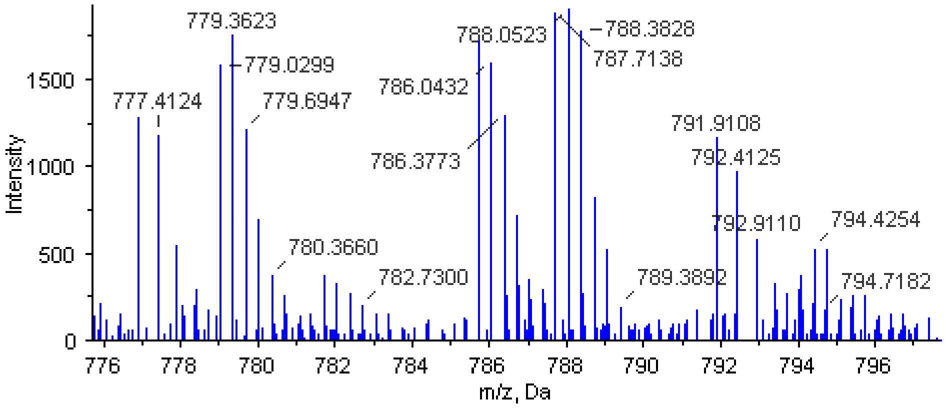
Seq Cov %: 31.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2.47

116: 114=E5TL: D5TL=1.62

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MATATNAAAAPPRQLSQKEADIQMMLAADVHLGTKNCDFQMERYIFKRRNDGIYIINLGKTWEKLQLAA
RVIVAIENPQDIIVQSARPYGQRAVLKFAQYTGAHAIAGRHTPGTFTNQLQTSFSEPRLLILTDPRTDH
QPIKEAALGNIPTIAFCDTDSPMRYVDIGIPANNKGKHSIGCLFWLLARMVLQMRGTIRPGLKWDVMVD
LFFYREPEEAKQQEEEEAPAVDYAITDFNAGAIAADGQWPGTIDQSWSDAVPQPIPAVPGVNWGAPAEA
PAAAGGDWGEAVPPPQQIPVPPSGIDTVQPSGWD

Protein No.: I-132

Protein name and Species:

UDP-D-glucose dehydrogenase OS=Gossypium hirsutum PE=2 SV=1

Accession: **tr|D2D2Z2|D2D2Z2_GOSHI**

Unused ProtScore: **12.91**

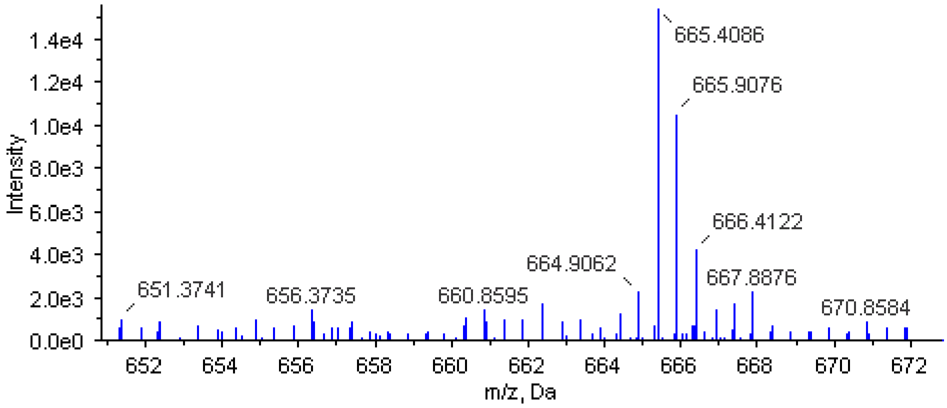
Seq Cov %: **19.8**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2.27

116: 114=E5TL: D5TL=1.66

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MK**ICCIGAGYVGGPTMAVIALK**CPDIEVAVVDISVPRIAAWNSDQLPIYEPGLDGVVKECRGRNLFFST
DVEKHVREADIVFVSVNTPTKTRGLGAGKAADLTYWESAARMIADVSKSDKIVVEKSTVPVKTAEAIEK
ILTHNSKGIKFQILSNPEFLAEGTAIQDLFNPDRVLIGGRETPEGNKAVQALKEVYAHWVPEER**ILTTN**
LWSAELSKLAANAFLAQRISSVNAM**SALCEATGADVTQVSYAVGK**DTRIGPKFLNASVGFGGSCFQKDI
LNLVYICECNGLPEVAEYWKQVIKINDYQKNRFVNR**VVSSMFNTVSNK**K**IAILGFAFK**KDTGDTR**ETPA**
IDVCKGLLGDKAR**LSIYDPQVTEDQVQR**DLSMNKFDWDHPLHLQPMSPTTVKQVSWVWDAYEATKDAHG
ICILTEWDEFKKLDFKR**IYDNMQKPAFVFDGR**NIVNADELREIGFIVYSIGKPLDPWLKDMPAVA

Protein No.: I-133

Protein name and Species:

Farnesyl diphosphate synthase OS=Hevea brasiliensis GN=FDP PE=2 SV=1

Accession: **tr|Q8L7F4|Q8L7F4_HEVBR**

Unused ProtScore: **12.91**

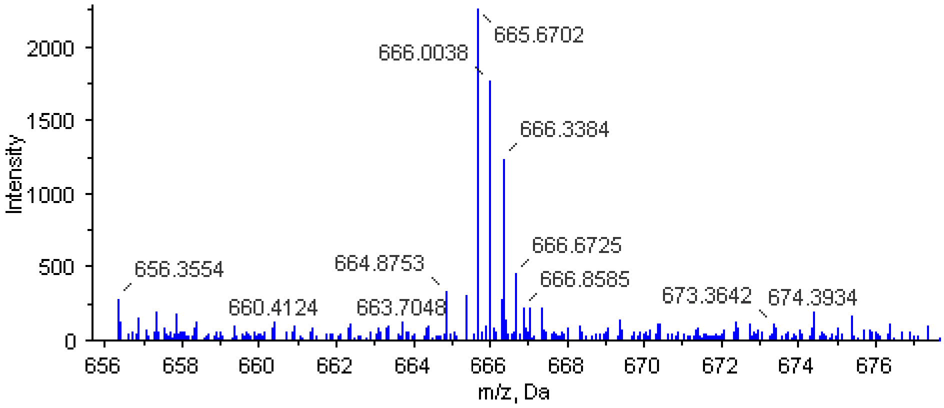
Seq Cov %: **25.4**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.56

116: 114=E5TL: D5TL=0.73

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MADLKSTFLK**VYSVLKQELLEDPAFEWTPDSR**QWVER**MLDYNVPGGK**LNR**GLSVIDSYK**LLKEGQELTE
EEIFLASALGWCIEWLQAYFLVLDDIMDSSHTRR**GQPCWFR**VPK**VGLIAANDGILLR**NHIPRILKKHFR
GKAYYVDLLDLFNEVEFQTASGQMIDLITTLEGEKDLSKYTLSLHRRIVQYKTAYYSFYLPVACALLIA
GENLDNHIVVKDILVQMGIYFQVQDDYLDCFGDPETIGK**IGTDIEDFK**CSWLVVK**ALELCNEEQK**K**VLY**
EHYGKADPASVAKVK**VLYNELKLQGVFTEYENESYK**KLVTSIEAHPSKPVQAVLKSFLAKIYKRQK

Protein No.: I-134

Protein name and Species:

Serine/threonine-protein phosphatase OS=Vitis vinifera GN=VIT_13s0156g00060 PE=3 SV=1

Accession: tr|F6HPS0|F6HPS0_VITVI

Unused ProtScore: 12.79

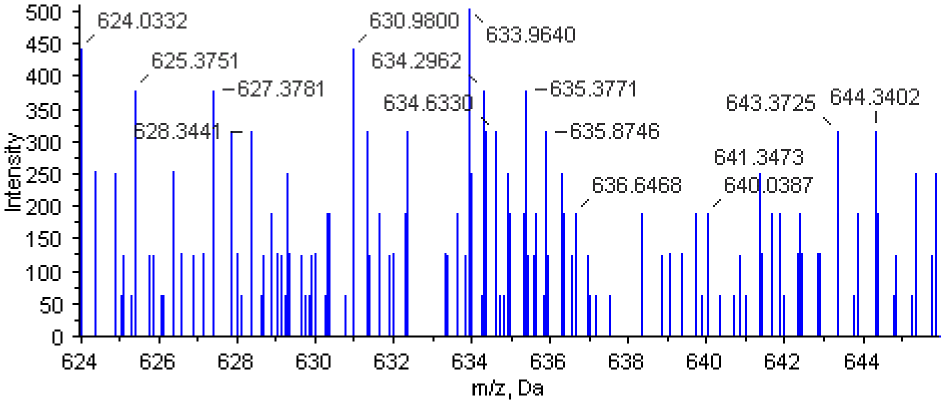
Seq Cov %: 27.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.21

116: 114=E5TL: D5TL=0.77

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDLISSDSHGNLDAQISQLMQCK**PLSEQEVR**TLCEKAK**EILMEESNVQPVK**SPVTICGDIHGQFHD**LAELFR**IGGK**CPDTNYLFMGDYVDR**GYYSVETVTMFVKSNKQDRVSKSPTKFEYRTMSLACSKIIWLRGLLAELDFSETDPTPLHADNTSANQITTNPVYHERTKHIEVDCHSIRAAFEARLLVALKVRYPQR**ITILR**GNHESR**QITQVYGFYDECLR**KYGNANVWKIFTDLFDYFPLTALVESEIFCLHGGLSPSIETLDNIRNFDRVQEVPHEGPMCDLLWSDPDDRCGWGISPR**GAGYTFGQDISEQFNHTNNLK**LIARAHQLVMEGFNWGHEQK**VVTIFSAPNYCYRCGNMASILEVDDCKGHTFIQFEPAPR**RGEPDVTRRTPDYFL

Protein No.: I-135

Protein name and Species:

Calcium-dependent protein kinase, putative OS=Ricinus communis GN=RCOM_1689450 PE=4 SV=1

Accession: tr|B9RCK2|B9RCK2_RICCO

Unused ProtScore: 12.78

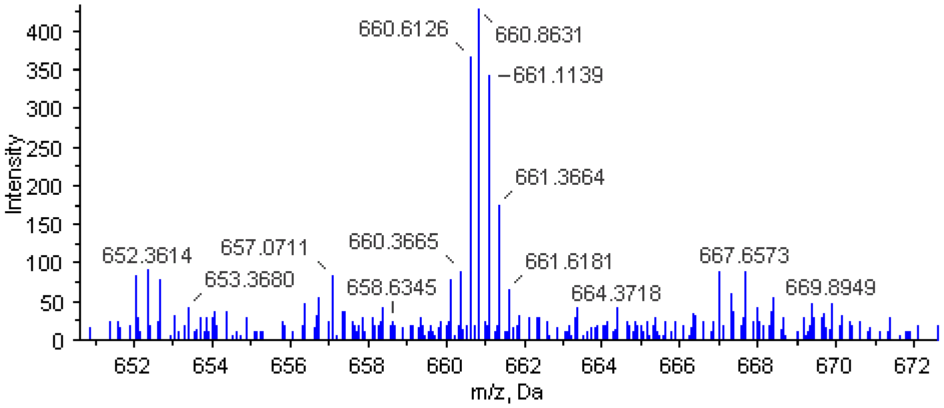
Seq Cov %: 18.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.63

116: 114=E5TL: D5TL=1.20

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGNCSSNLPSTSTFTADRPPPPPPSHGITVHPPTASPPPRPPPPHSLQPTSNNRPSAAPAAVGR**VLGRP**
MEDVRSIYAFGRELGR**GQFGVTYLVTHK**ETKQQFACKSIATRKLINRDDIEDVRREVQIMHHLTGHRNI
VELKGAYEDRHSVNLVMELCAGGELFDRIIAKGHYSERAAANLCRQIVTVVHDCHSMGVIHR**DLKPENF**
LFLSTDENSPLKATDFGLSVFFKPGDTFK**DLVGSAYYVAPEVLR**RNYGPAIDIWSAGVILYILLSGVPP
FWGETEQAIFDTVLRGHIDFSSDPWPSISSSAKDLVKKMLTADAKDRISAAEVLNHPWMR**VDGDASDKP**
LDIAVLTRMKQFRAMNKLKKVALK**VIAENLSEEEIMGLK**EMFKSMDTDNNGTITYEELKAGLPKLGTKL
SESEVKQLMEAADVDGNGTIDYIEFITATMHMNRMEREDHLYKAFEYFDKDK**SGYITMEELEHALK**EYN
MGDARTIKEIIAEVDTDHDGR**INYEEFVAMMR**KGNPELVTNRRRK

Protein No.: I-136

Protein name and Species:

obg-like ATPase 1 [Vitis vinifera] OS=Vitis vinifera GN=VIT_10s0003g05020 PE=4 SV=1

Accession: tr|D7TKK5|D7TKK5_VITVI

Unused ProtScore: 12.7

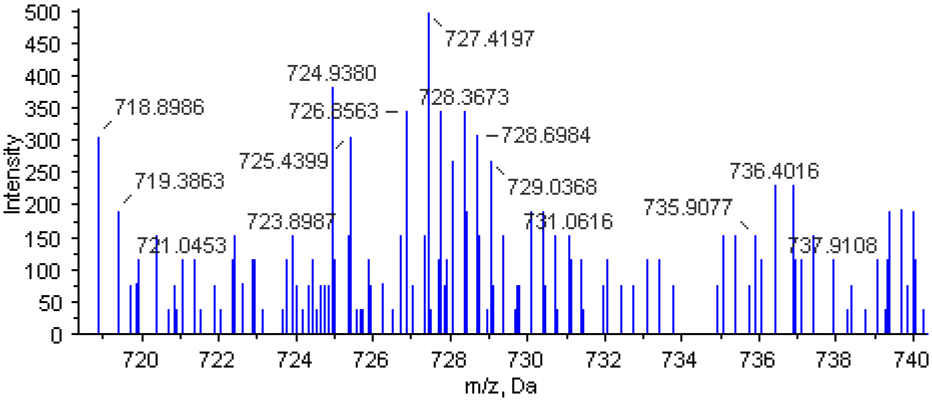
Seq Cov %: 18.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.64

116: 114=E5TL: D5TL=0.79

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MPPKSSKSK**EAPAERPILGR**FSSHLK**IGIVGLPNVGK****STLFNTLTK**LAIPAENFPFCTIEPNEARVNIP
DERFEWLCQLYKPKSEVSAFLEIHDIAGLVRGAHQGQGLGNSFLSHIR**AVDGIFHVLRAFEDPDIIHVD**
DSVDPVRDLEVISEELRLKDIEFIEKRIEDVEKSMKRSNDKQLKIELELCLKVKAFLEDGKDIRLGDWK
AADVEILNTFQLLTAK**PVVYLVNMNEK**DYQRKKNKFLPKIHAWVQDHGGETIIPFSCALERNLADMPED
EAAKYCEENKVQSALPKIIKTGFSAINLIYFFTAGPDEVKCWQIRRQTK**APQAAGTIHSDFERGFICAE**
VMKFDDLKELGSEGAVKAAGKYRQEGKTYVVQDADIIFFKFNVSGGGKK

Protein No.: I-138

Protein name and Species:

GTP-binding nuclear protein Ran-3-like [Vitis vinifera] OS=Vitis vinifera GN=VIT_04s0008g05030 PE=4 SV=1

Accession: tr|D7SUQ2|D7SUQ2_VITVI

Unused ProtScore: 12.64

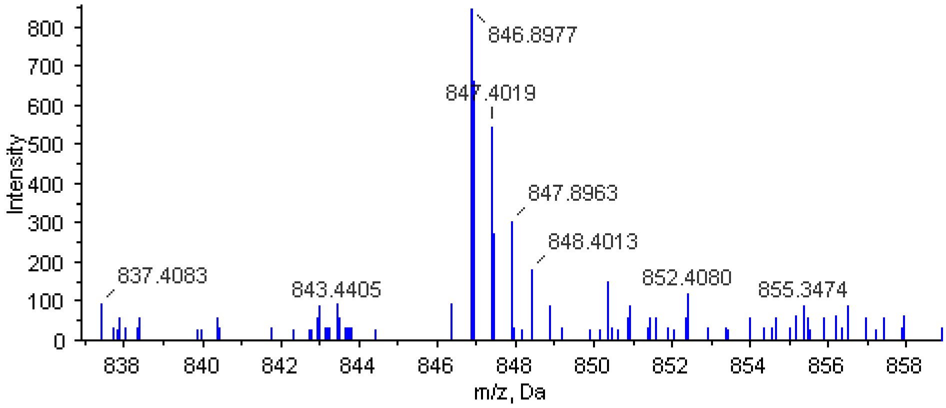
Seq Cov %: 19.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.46

116: 114=E5TL: D5TL=0.69

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MPFCYNNNYCYFIKSKKIVITKLFRDLIQRLREIASIKGYNENTRRLLIYIRLKLLLPPHSKLKPSFQS
APWRLPYEKLTLTLQMALPNQQTVDYPSFK**LVIVGDGGTGK**TTFVKRHLTGEFEKKYEPTIGVEVHPLD
FFTNCGKIR**FYCWDTAGQEK**FGGLRDGYYIHGQCAIIMFDVTARLTYKNVPTWHRDLCR**VCENIPIVLC**
GNKVDVKNRQVKAKQVTFHRKK**NLQYYEISAKSNYNFEKPFLYLAR**KLAGDVNLHFVESPALAPPEVQI
DMAAQAHHEAELAAAAAQPLPDDDDDTFE

Protein No.: I-141

Protein name and Species:

Aspartate aminotransferase OS=Vitis vinifera GN=VIT_04s0008g03770 PE=3 SV=1

Accession: tr|D7SUD7|D7SUD7_VITVI

Unused ProtScore: 12.36

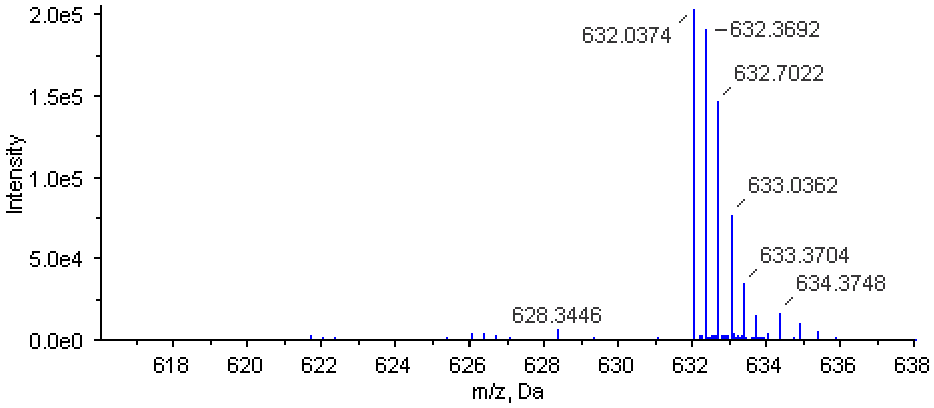
Seq Cov %: 27

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.55

116: 114=E5TL: D5TL=0.47

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDPNHTISASATSGSDFGGSVFDHVVQ**APEDPILGVTVAYNK**DPSPVK**LNLGVGAYRTEEGKPLVLNVV**
RRAEQLLVNDRSRVK**EYLPIVGLAEFNK**LSAKLMFGADSPAIQVKR**VTTVQCLSGTGSLR**VGAEFLARH
HHQRTIYIPQPTWGNHGKIFTLAGLSVKTYRYYDPATRGLNFQGLLEDLSLAPSGAIVLLHACAHNPTG
VDPTLQQWEQIRQLIRLK**GLLPFFDSAYQGFASGSLDADAQSVR**MFVADGGECLAAQSYAKNMGLYGER
VGALSIVCKTADVASRVESQVKLVIRPMFSNPPIHGASIVAIILKNRDMYNEWTVELKAMADRIISMRQ
QLFDALRARGTPGDWNHILKQIGMFTFTGLNTAQVAFMTKEYHVYMTSDGR**ISMAGLSSKTVPHLADAI**
HAAVTRAI

Protein No.: I-145

Protein name and Species:

Citrate-binding protein OS=Hevea brasiliensis GN=CBP PE=1 SV=1

Accession: sp|Q39962|CBPR_HEVBR

Unused ProtScore: 12.21

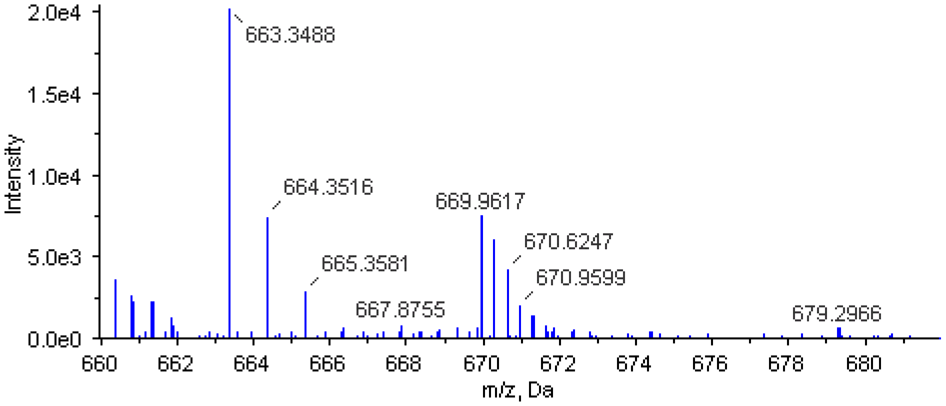
Seq Cov %:34.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.29

116: 114=E5TL: D5TL=0.38

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MKMKRSPYCFCCSFALLLLVSFLKDRHFCSA**DPTDGFTEVPLTEDNFVIQKPY**DKPLNDRYSYKNGIRR
LWVYENDKPFKVGSPTRPRTEIRIKGHDYSSGVWQFEGQVHVPEGTSGVTVMQVFGAVNK**ATALQLRVY**
NGDLKSYK**SNSVATDIYNK**WLR**VNVIHK**VGK**GEITVFINGQQKLVVNDDGPAEHYFKCGVYAAPDGSSN**
YMESRWKNIKLYKSDNKLEGCNNNHGTWLVQ

Protein No.: I-148

Protein name and Species:

Acetyl-CoA C-acetyltransferase OS=Hevea brasiliensis GN=HbAACT PE=2 SV=1

Accession: tr|A9ZMZ5|A9ZMZ5_HEVBR

Unused ProtScore: 12

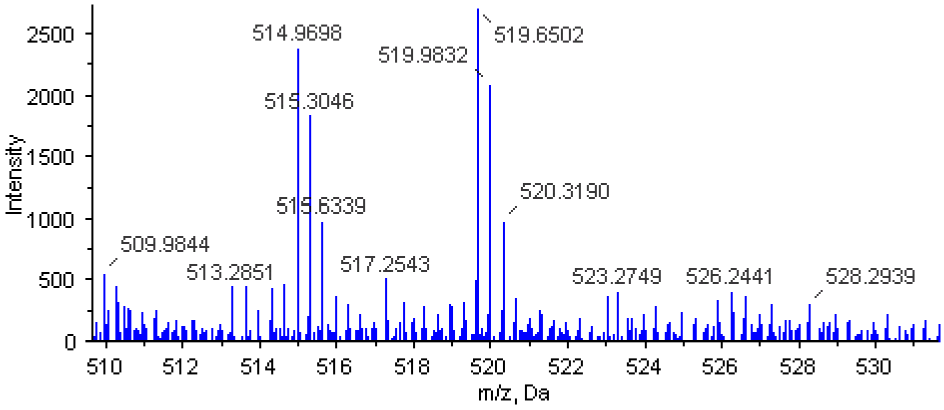
Seq Cov %: 61.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.55

116: 114=E5TL: D5TL=0.66

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

M**APAAATAVAAEIKPRDVCIVGVARTPMGGFLGSLCTLSATKLGSIAIEAALK**R**ANVDPSLVQEVFFGN**
VLSANLGQAPARQAALGAGIPNSVVCTTVNKVCASGMKATMLAAQSIQLGINDVVVAGGMESMSNAPKY
LAEARKGSR**LGHDSLVDGMLK**DGLWDVYNDVGM**GSCAEICADNHSITREDQDKFAIHSFERGIAAQESG**
AFAWEIVPVEVSGGRGKPSTIVDKDEGLGKFDPVKLRKLRPSFK**ENGGTVTAGNASSISDGAAAVILVS**
GETALKLGLQVIAKIGGYADAAQAPELFTTSPALAIPKTIANGGLDASQVDYYEINEAFAVVALANQK**L**
LGLNPEKI**NVHGGAVSLGHPLGCSGARILVTLLGVLR**QKNGKYGVGGVCNGGGGASALVVELL

Protein No.: I-150

Protein name and Species:

Pyridoxal biosynthesis protein PDX1 OS=Hevea brasiliensis GN=PDX1 PE=2 SV=1

Accession: **sp|Q39963|PDX1_HEVBR**

Unused ProtScore: **11.87**

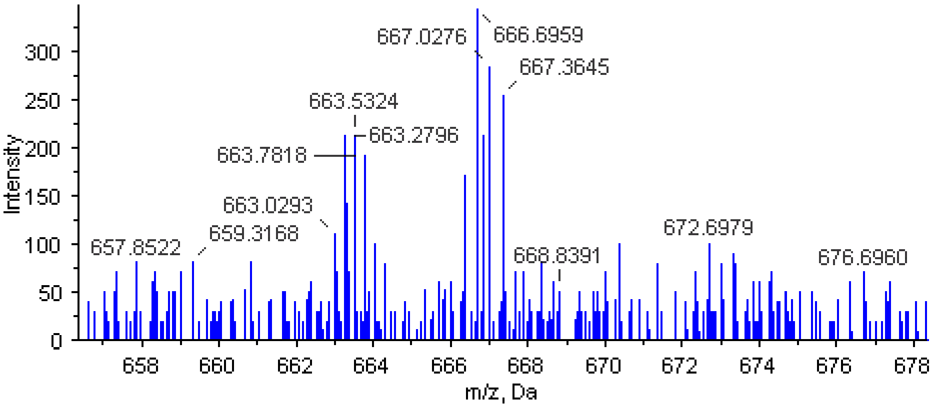
Seq Cov %: **29.8**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2.40

116: 114=E5TL: D5TL=1.42

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

M**AGTGVVAVYGNGAITETK**KSPFSVK**VGLAQMLRGGVIMDVVNPEQARIAEEAGACAVMALER**VPADIR
AQGGVAR**MSDPQLIK**EIK**QSVTIPVMAK**ARIGHFVEAQILEAIGIDYVDESEVLTPADEENHINKHNFR
IPFVCGCRNLGEALRRIREGAAMIR**TKGEAGTGNVIEAVR**HVRSVMGDIRLLRNMDDDEVFTFAKK**IAA**
PYDLVMQTKQLGRLPVVQFAAGGVATPADAALMMQLGCDGVFVGSGVFKSGDPARRARAIVQAVTHYSD
PDMLAEVSCGLGEAMVGINLNDKKVERFANRSE

Protein No.: I-151

Protein name and Species:

NAD dependent epimerase/dehydratase, putative OS=Ricinus communis GN=RCOM_1683000 PE=4 SV=1

Accession: tr|B9RC03|B9RC03_RICCO

Unused ProtScore: 11.81

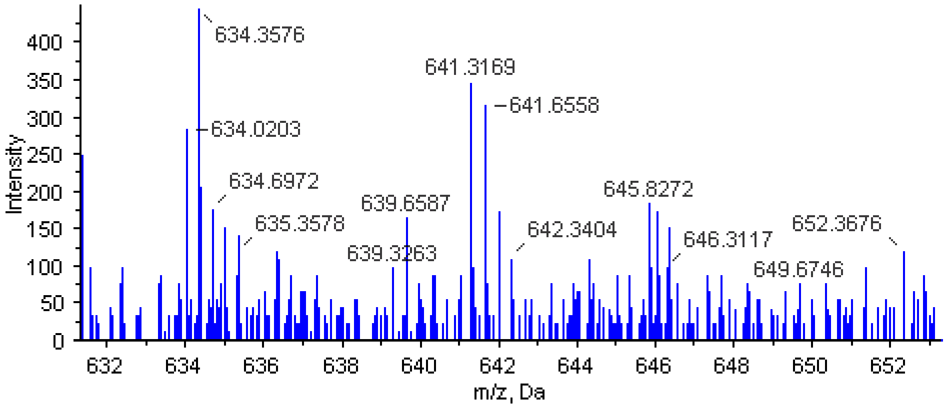
Seq Cov %: 27.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.75

116: 114=E5TL: D5TL=1.51

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGFQSNGATDNKKPYKFLIYGR**TGWIGGLLGKLCESQGIDYTYGNGR**LENRVSLENDIASIN**PTHVFNAAGVTGR**PNVDWCESHKVETIR**TNVAGTLTLADVCR**EKGLVLINYATGCIFEYDDKHPLGSGIGFK**EEDTPNFIGSFYSK**TK**AMVEELLK**NYENVCTLRVRMPISSDLANPRNFITKITRYEKVVDIPNSMTILDELLPISIEMAKRNLTGIWNFTNPGVVSHNEILEMYRDYVDPNFTWKNFTLEEQAKVIVAPRSNNELDATKLSK**EFPEMLPIK**ESLIKYVFKPNQKTAAA

Protein No.: I-152

Protein name and Species:

Calmodulin OS=Clematoclethra scandens subsp. tomentella GN=CaM PE=4 SV=1

Accession: tr|B1NDK1|B1NDK1_9ERIC

Unused ProtScore: 11.77

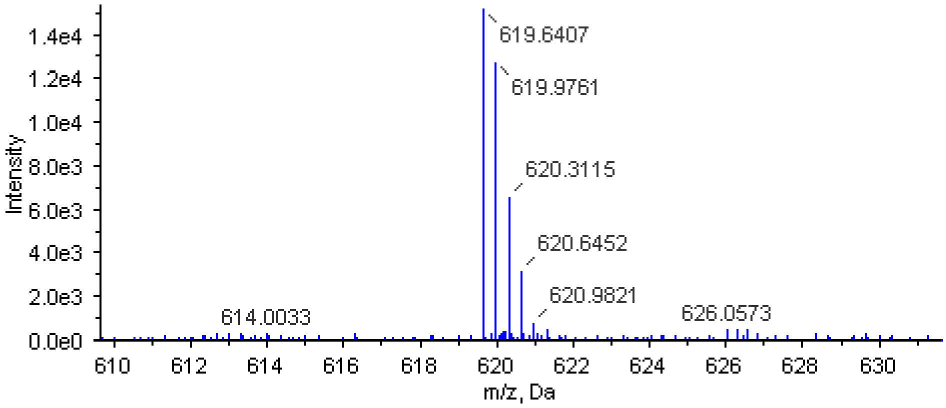
Seq Cov %: 50

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.61

116: 114=E5TL: D5TL=0.63

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MADPLTDDQISEFK**EAFSLFDKDGDGCITTK**ELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDFPEF
LNLMARKMK**DTDSEEELKEAFRVFDKDQNGFISAAELR**HVMANLGEK**LTDEEVDEMIREADVDGDGQIN**
YEEFVKVMMA

Protein No.: I-160

Protein name and Species:

26S proteasome non-atpase regulatory subunit, putative OS=Ricinus communis GN=RCOM_1507340 PE=4 SV=1

Accession: tr|B9RAM4|B9RAM4_RICCO

Unused ProtScore: 11.38

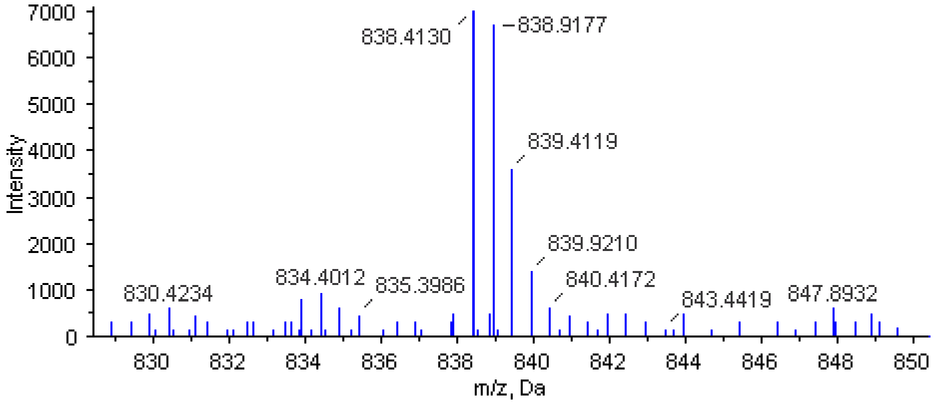
Seq Cov %: 20.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.44

116: 114=E5TL: D5TL=0.62

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MEGQEGTQQPHLILAHKR**FLLTHPDVQDIEK**VRLKEEVFAAVKSDDMAPLYETLITEGLLEKDQSILDL
MRAKNEDELKKIDEK**IADAEENLGESEVR**EAHLAKSLFYIRIGDKEKALEQLKVTESKTVAVGQKMDLV
FYTLQLGFFYMDFDLISKSIDKAK**NLFEEGGDWER**KNRLK**VYEGLYCMSTR**NFTKAATLFLDSISTFTT
YELFPYDTFIFYTVLTSIITLDRVSLKQK**VVDAPEILTVIGK**IPYLSEFLNSLYFCQYKSFFSAFAGIA
EQIKLDRYLHPHFRYYMREVR**TVVYSQFLESYK**SVTIEAMAKAFGVTVEFIDLELSRFIAAGKLHCKID
K**VAGVLETNRPDAKNALYQATIKQGDFLLNR**IQKLSRVIDL

Protein No.: I-161

Protein name and Species:

Abscisic acid stress ripening-related protein 1 OS=Hevea brasiliensis GN=ASRLP1 PE=4 SV=1

Accession: tr|Q6XNP8|Q6XNP8_HEVBR

Unused ProtScore: 11.37

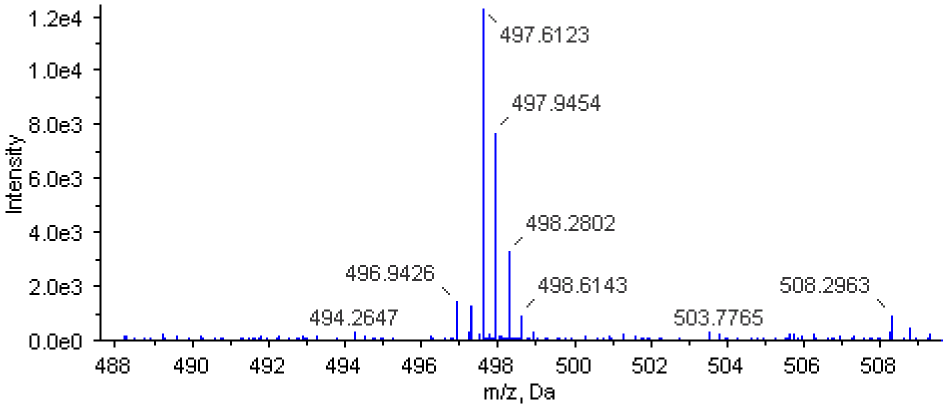
Seq Cov %: 21.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.31

116: 114=E5TL: D5TL=0.42

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAEEKHHHLFHHHK**EGQEAVDCR**KEEKHHKHLCQLGK**LGAAAAGTYALHEK**HAAKKDPEHAHGHKIKEE
VAAAAAIGAGGFAFHEHHEKKEAKKK**NEEGHGK**KHHHPF

Protein No.: I-167

Protein name and Species:

Myo-inositol-1-phosphate synthase OS=Ricinus communis GN=MIPS PE=2 SV=1

Accession: tr|C7B9C0|C7B9C0_RICCO

Unused ProtScore: 11.12

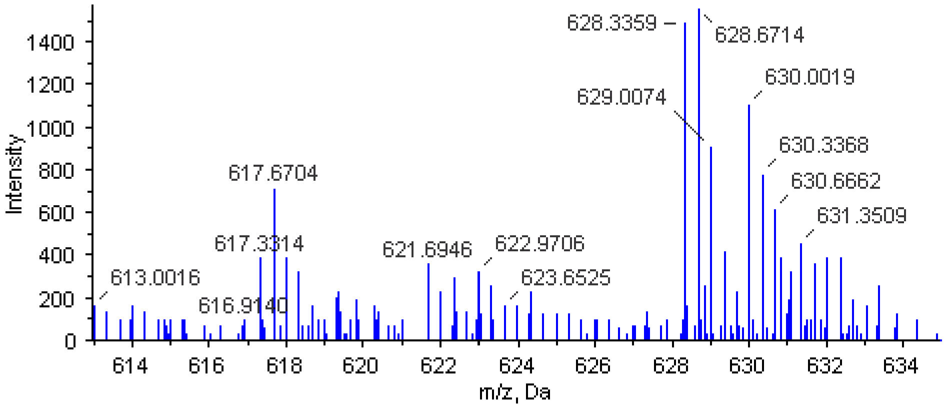
Seq Cov %: 18

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=10.47

116: 114=E5TL: D5TL=2.51

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MFIEKFQVESPNVKYSEDEIH**SVYNYETTELVHENR**NGTYQWIVKPKTVQYEFKTDVHVPKLGVMLVGW
GGNNGSTLTGGVIANREGISWATKDK**VQQANYFGSLTQASSIRVGSFNGEEIYAPFK**SLLPMVNPDDIV
FGGWDISDMNLADAMARAKVLDIDLQKQLRPYMESMVPLPGIYDPDFIAANQGSRANNVIKGTKKEQME
QIVKDIREFKEKTKVDKVVVLWTANTERYSNVVVGLNDTMESLLASLERNEAEISPSTLYALACIFENV
PFINGSPQNTFVPGVIDLAIKGNSLIGGDDFKSGQTKMKSVLVDFLVGAGIKPTSIVSYNHLGNNDGMN
LSAPQTFRSKEISKSNVVDDMVSSNGILYEPGEHPDHVVVIK**YVPYVGDSK**R**AMDEYTSEIFMGGK**STI
VLHNTCEDSLLAAPIILDLVLLAELSTRIQLKAEGEGKFHSFHPVATILSYLTK**APLVPPGTPVVNALS**
KQR**AMLENILR**A**CVGLAPENNMILEYK**

Protein No.: I-168

Protein name and Species:

Catalytic, putative OS=Ricinus communis GN=RCOM_0291690 PE=4 SV=1

Accession: tr|B9SZU0|B9SZU0_RICCO

Unused ProtScore: 10.98

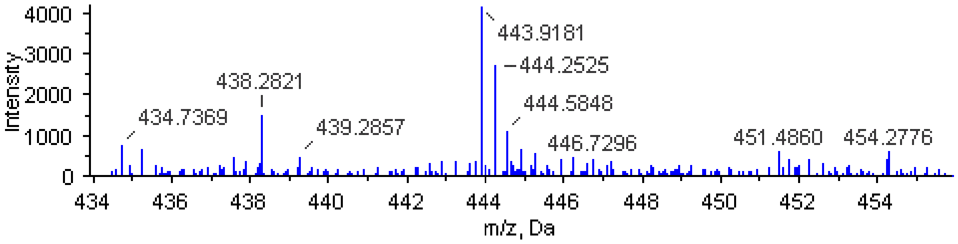
Seq Cov %: 22.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.45

116: 114=E5TL: D5TL= 0.64

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MVPITVLLSSFLLLFTVSHGFAPPRSFLQSLSGSNTYLTTKELWFNQILDHYSPYDHRRFQQRYYEYLD
YFRAPGGPIFLK**ICGESSCNGIANDYISVLAK**K**FGAAVVSLEHR**YYGKSTPFKSSETKNLRYLSSK**QAL**
FDLAVFRQHYQEALNLKLNRTNVENPWIVFGISYSGALSAWYRLKFPHLTCGSVASSAVVLAVYNFTEF
DQQIGESAGAECKAALQETTQLVDERLASNRKAVKTLFNAAELEIDGDFLYFLADAAVIAFQYGNPDK**L**
CSPLVEAKK**AGEDLVEAYAK**YVKEYYVGSFGVSVETYNQKHLKDTAINENSSDRLWWFQVCTEVAYFQV
APSNDSIRSSKVNTR**YHLDLCKNVFGEGIYPEVDTTNIYYGGTK**IAGSKIVFTNGSQDPWRHASK**QISS**
PDTPSYIITCHNCGHGTDMRGCPQSPLSLEGNAQNCSSPDAVQKVRQQVIEHIDLWLSECEASGRSYI

Protein No.: I-169

Protein name and Species:

Proliferation-associated 2g4, putative OS=Ricinus communis GN=RCOM_0489730 PE=4 SV=1

Accession: tr|B9SWY5|B9SWY5_RICCO

Unused ProtScore: 10.97

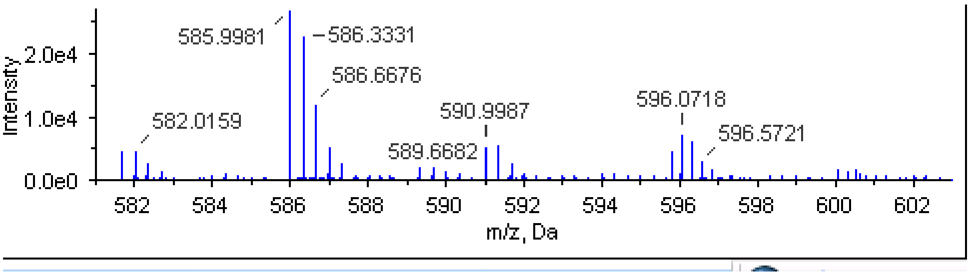
Seq Cov %: 15.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 1.53

116: 114=E5TL: D5TL= 1.66

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSDDEREEK**ELDLTSPEVVTK**YK**SAAEIVNK**ALQLVISECKPKAK**IVDLCEK**GDAFIREQTGNMYKNVK
KKIERGVAFPTCVSVNNTVCHCSPLASDETLLEEGDVVKIDMGCHIDGFIAVVGHTHVLQAGPVTGR**AA**
DVIAAANTAAEVALRLVRPGKKNKDVTEAIQK**VAAAYDCK****IVEGVLSHQLKQFVIDGNK**VILSVSNPET
RVDDAEFEENEVYAIDIVTTTGEGKPKLLDEKHTTIYKRAVDKNYHLKMKASR**FIFSEISQK**FPIMPFT
ARALEEKRARLGLVECVNHDLLQPYPVLHEKPGDIVAHIK**FTVLLMPNGSDR**ITSHSLQELQPTKTIDD
PEIKAWLALGTKTKKKGGGKKKKAKKGDKAEESTEAEPMDATNGAETQE

Protein No.: I-170

Protein name and Species:

Aspartic proteinase, putative OS=Ricinus communis GN=RCOM_1303660 PE=3 SV=1

Accession: tr|B9SVA7|B9SVA7_RICCO

Unused ProtScore: 10.95

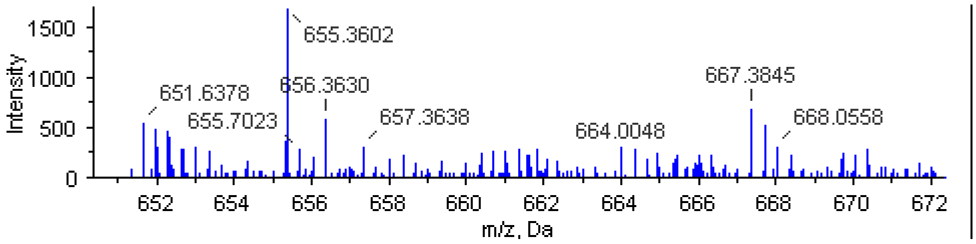
Seq Cov %: 26.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.30

116: 114=E5TL: D5TL= 0.52

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGTIFKPALFFCLILLPLVCATASSSNDGLVRIGLKKRKFDQNNRVAAQFESKEGEAFRASIKKYHIRG
NLGDAEDIDIVSLK**NYMDAQYFGEIGIGTPPQK**FTVIFDTGSSNLWVPSSK**CYFSVACYFHSK**YKSGQS
STYKKNGKSADIHYGTGAISGFFSQDNVKVGELVIKNQEFIEATR**EPSITFLVAK**FDGILGLGFQEISV
GN**AVPVWYNMVNQGLVK**EPVFSFWFNR**NADEDEGGEIVFGGMDPN**HYK**GEHTYVPVTQK**GYWQFDMGDV
LIDGKTTGICSSGCAAIADSGTSLLAGPTTIITEVNHAIGATGVVSQECK**AVVAQYGETIIAMLLAK**DQ
PQKICSQIGLCTFDGSRGVSMGIESVVNEKIQEVAGGLHDAMCSTCEMAVVWMQNQLKQNQTQEHILNY
VNELCERLPSPMGESAVDCGSLSTMPNVSFTIGGRVFDLAPEQYVLK**VGDGEAAQCISGFTALDVPPPR**
GPLWILGDVFMGP**FHTVFDYGNK**RVGFAEVA

Protein No.: I-175

Protein name and Species:

Phosphoglyceride transfer family protein OS=Hevea brasiliensis PE=2 SV=1

Accession: tr|Q6J6I5|Q6J6I5_HEVBR

Unused ProtScore: 10.83

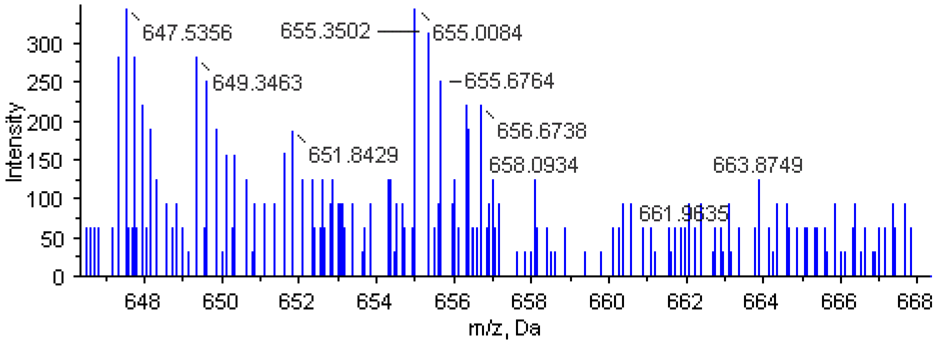
Seq Cov %: 33.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.08

116: 114=E5TL: D5TL= 0.59

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MLTGTLKWRATYKPEEIRWHEISHEVEKGKVFRANFHDRYGR**TVLIMRPEMQNTTSAVDNIR**HLAYVIE
NSILNLAEGQEQMSWLIDFTGLSLSNSMSIGTGVDIIK**ILQNHYPERLAVAFVYNPPR**IFEAFWKAVKC
VLNSKTSEKVK**FVYPNNK**ESEEVMR**HFFDVDNLPGEFGGK**ATMK**YDHEEFSRLMAQDDVK**TAKYWGFDE
KPTHIANAQLRPQLAPEPTPFAPPAS

Protein No.: I-181

Protein name and Species:

Polyadenylate-binding protein, putative OS=Ricinus communis GN=RCOM_0812530 PE=4 SV=1

Accession: tr|B9RYE9|B9RYE9_RICCO

Unused ProtScore: 10.63

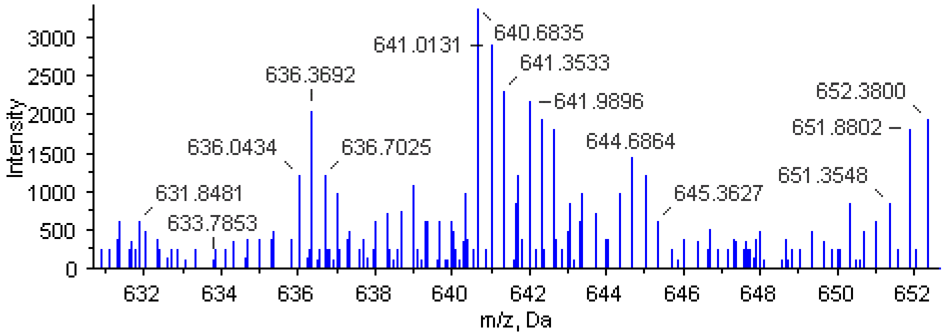
Seq Cov %: 15.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 1.75

116: 114=E5TL: D5TL= 1.24

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAQVQVPVQGQNVNGGANAPYVTTSLYVGDLEANVTDSHLYDLFNQVGQVVSVRVCRDLTTRR**SLGYGY**
VNYSSPQDAARALDMLNFTPLNGSPIRIMYSHRDPSVRK**SGSGNIFIK**NLDKGIDHKALHDTFSAFGNI
LSCKVATDSSGQSKGYGFVQFDNEESAQKAIEKLNGMLLNDK**QVYVGPFLR**KQERESAIDKTRFNNVYV
KNLSETTTEEDLKKAFGEYGTITSAVVMRDGDGKTKCFGFVNFENADDAATAVEALNGKKFDDKEWFVG
KAQKKNERENELKVR**FEQSMKEAADKFQGANLYIK****NLDDSIGDDRLK**QLFSPFGTITSCKVMRDPNGIS
RGSGFVAFSTPEEASKALMEMNGK**MVVSKPLYVALAQR**KEDRRARLQAQFSQIRPVAMAPSVAPRMPMY
PPGGPGLGQQIFYGQAPPAIIPPQPGFGYQQQLVPGMRPGGAPMPNFFVPMVQQGQQGQRPGGRRAGAA
QQSQQPVPLMQQQMVPRGRVYRYPPGRGIPDVPMTGVAGGMLSVPYDMSGMPMRDAALSQPIPIGALAS
ALANASPEQQR**TMLGENLYPLVEQLEPDAAAK**VTGMLLEMDQTEVLHLLESPEALKAK**VAEAMEVLR**SV
QQQQAGGAADQLASLSLNDNLVS

Protein No.: I-186

Protein name and Species:

Proteasome subunit beta type OS=Ricinus communis GN=RCOM_0205360 PE=3 SV=1

Accession: tr|B9SPS6|B9SPS6_RICCO

Unused ProtScore: 10.47

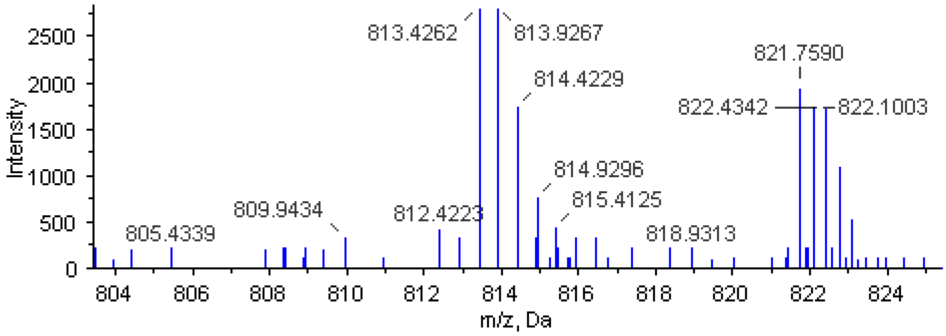
Seq Cov %: 29

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 1.60

116: 114=E5TL: D5TL= 1.41

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDLKAPHSMG**TTIIGVTYNGGVVLGADSRTSTGMYVANR**ASDK**ITQLTDNVYVCRSGSAADSQIVSDYV**
RYFLHQHTIQLGQPATVK**VAANLVRLISYNNKNMLETGLIVGGWDK**YDGGKIYGIPLGGTIIEQPFAIG
GSGSSYLYGFFDQAWKEGMTK**DEAEQLVVK**AVSLAMARDGASGGVVR**TVIINSEGVTR**NFYPGDSLPLW
HEELEPQNSLLDILNASSPEPMNI

Protein No.: I-187

Protein name and Species:

ras-related protein RABC1 isoform 1 OS=Populus trichocarpa GN=POPTRDRAFT_798654 PE=3 SV=1

Accession: tr|B9GTP5|B9GTP5_POPTR

Unused ProtScore: 10.45

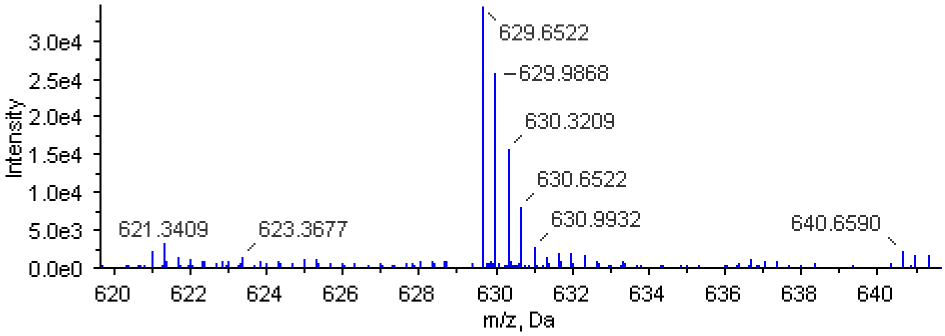
Seq Cov %: 42.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.52

116: 114=E5TL: D5TL= 0.70

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MEVPSTSQQEFE**YLFK****LLLIGDSGVGKSTLLLSFTSK**NFEDLSPTIGVDFKVKHV**TIGGK**KLKLAIWDT
AGQERFR**TLTSSYYR****GAQGIIMVYDVTR**RETFTNLSEIWAK**EIDLYSTNQDCIK**MLVGNKVDKESERVV
TKK**EGIDFAR****EYGCLFLECSAK**TR**VNVEQCFEELVLKILETPSLLAEGSSGVKK**NVFKQKPPEDVTTSS
CCSW

Protein No.: I-188

Protein name and Species:

ATP synthase subunit beta, mitochondrial OS=Hevea brasiliensis GN=ATPB PE=2 SV=1

Accession: sp|P29685|ATPBM_HEVBR

Unused ProtScore: 10.41

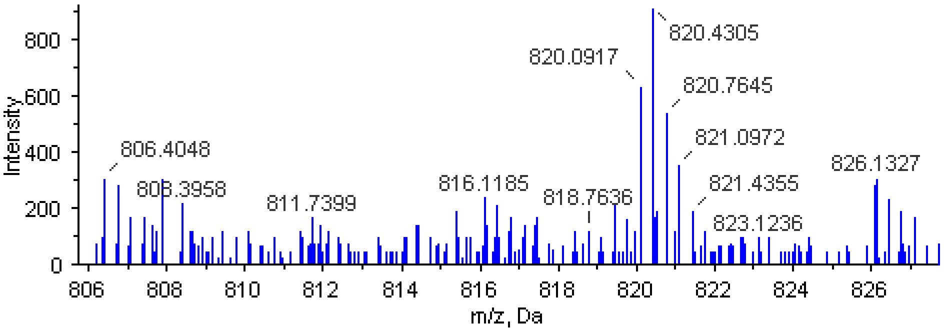
Seq Cov %: 17.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 7.52

116: 114=E5TL: D5TL= 1.63

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MASRRLLSSLLRSSSRRSVSKSPISNINPKLSSSSPSSKSRASPYGYLLTRAAEYATSAAAAAPPQPPP
AKPEGGKGGGK**ITDEFTGK**GAIGQVCQVIGAVVDVRFDEGLPPILTSLEVLDHSIRLVLEVAQHMGEGM
VRTIAMDGTEGLVRGQRVLNTGSPITVPVGRANPWTYHEVIGEPIDERGDIKTSHFLPIHR**EAPAFVDQ**
ATEQQILVTGIKVVDLLAPYQRGGKIGLFGGAGVGKTVLIMELINNVAKAHGGFSVFAGVGERTREGND
LYREMIESGVIKLGDKQADSKCALVYGQMNEPPGARAR**VGLTGLTVAEHFR**DAEGQDVLLFIDNIFR**FT**
QANSEVSALLGRIPSAVGYQPTLATDLGGLQERITTTKKGSITSVQAIYVPADDLTDPAPATTFAHLDA
TTVLSRQISELGIYPAVDPLDSTSRMLSPH**ILGEEHYNTAR**GVQKVLQNYKNLQDIIAILGMDELSEDD
KLTVARARKIQRFLSQPFHVAEVFTGAPGKYVELKESITSFQGVLDGKYDDLPEQSFYMVGGIDEVIAK
ADKIAKESAS

Protein No.: I-191

Protein name and Species:

Acid phosphatase, putative OS=Ricinus communis GN=RCOM_0854040 PE=4 SV=1

Accession: tr|B9RUL1|B9RUL1_RICCO

Unused ProtScore: 10.38

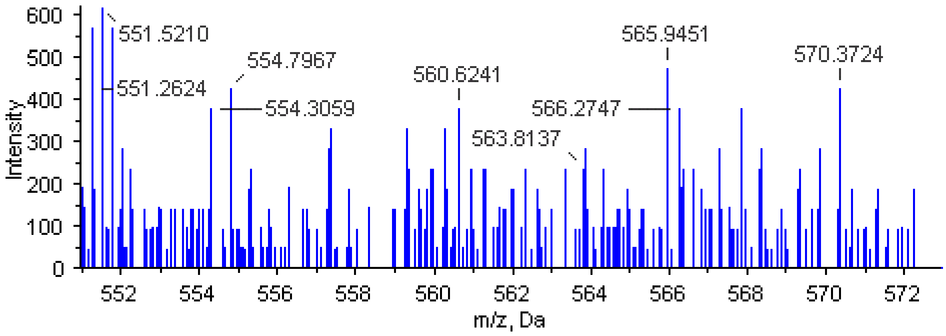
Seq Cov %: 7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.58

116: 114=E5TL: D5TL=0.60

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MEEEGGEMEKKIKIGVCVMEKKVLSAPMGQIMDRLQAFGEFEIIHFGDKVIAEDPIESWPICDCLIAFY
SSGYPLEK**AEAYAALR**KPFLVNELEPQHLLHDRRKVYQRLEMYGIPVPRYALVNREFPYQELDYFSEEE
DFVEVHGNRFWKPFVEKPIDGDNHSIMIYYPSSAGGGMKELFRKVGNRSSEFHPEVRRVRREGSYIYEE
FMPTGGTDVK**VYTVGPEYAHAEAR**KSPVVDGVVMRNPDGKEVRYPVLLTPNEKQMAREVCIAFRQAVCG
FDLLRCEGRSYVCDVNGWSFVKNSYKYYDDAACVLRKMFLDAKAPHLSSTIPPTLPWKINEPVQPSEGL
TRQGSGIIGTFGQSEELRCVITVMRHGDRTPKQKVKLKVTEEK**LLNLMLK**YNGGRPRSETKLK**SAIQLQ**
DLLDATRILVPRIRPGR**ESDSEAEDIEHAEK**LRQVK**AVLEEGGHFSGIYR**KVQLKPLKWVKIPKSTGEA
EEERPVEA**LMVLK**YGGVLTHAGRKQAEELGRYFRNNMYPGEGTGLLRLHSTYRHDLKIYSSDEGRVQMS
AAAFAKGLLDLEGQLTPILVSLVSKDSSMLDGLDNASSEMEEAKARLNEIITSSTKAANSNESPEFPWM
TDGAGLPPNASELLPELVKLTKKVTEQVRLLAKDEDEELTETSSYNVIPPYDQAKALGKINIDVDRIAA
GLPCGSEGFLLMYARWRKLERDLYNERKDR**FDITQIPDVYDSCK**YDLLHNAHLNLEGLDELFK**VAQLLA**
DGVIPNEYGINPKQKLKIGSKIARRLLGKILIDLRNTREEAISVAELKSNQDQHSTSTKNEKEDADYQS
KLFIKNEDTRRTSTSEISTDHDDDDDKETKYRLDPKYANVKTPERHVRTRLYFTSESHIHSLVNVLRYC
NLDESLQEEDSLVCHNALERLHKTKELDYMSYIVLRMFENTEVPLEDPKRYRIEMTYSRGADLSPLEKN
DSEANSLHQEHTLPIMGPERLQEVGSYLTLEKMETMIRPFAMPAEDFPPPSTPAGFSGYFSKSAAVLER
LVNLWPFHKHDKHASANGK

Protein No.: I-195

Protein name and Species:

Putative uncharacterized protein OS=Ricinus communis GN=RCOM_1341920 PE=4 SV=1

Accession: tr|B9RN01|B9RN01_RICCO

Unused ProtScore: 10.23

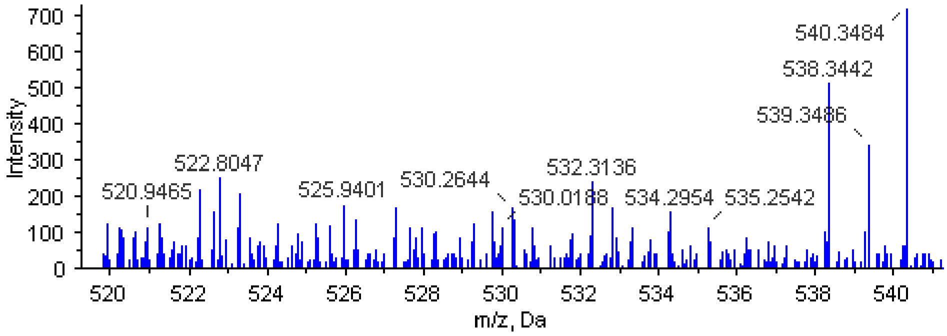
Seq Cov %: 4.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=5.50

116: 114=E5TL: D5TL= 2.29

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSIPKELEQVMKLRGGSVLGKKTILKSDHFPGCQNKRLTPQIDGAPNYRQADSLPVHGVAIPTTEGIRNVLKHIGAQKDGKRVQVIWFNLREEPVVYINGRPFVLR**DVERPFSNLEYTGINR**SRVEQMESRLKEDILMEAARYGNKILVTDELPDGQMVDQWEPVSRDSANEELQLEGYLFDYERVPVTDEKSPEEPDFDILVDKIYQADLNTEIIFNCQMGRGRTTTGMVIATLVYLNRIGASGIPRTNSIGRVFDTGPTVTDNLPNSEEAIRRGEYAVIRSLTR**VLEGGVEGK**RQVDKVIDKCASMQNLR**EAIANYR**NRILRQPDEMKREASLSFFVEYLERYYFLICFAVYIHSERDALRSSSFGHSSFADWMR**ARPELYSILR**RLLRRDPMGALGYASSKPSLMKIAESADGRPHEMGVVAALRNGEVLGSQTVLKSDHCPGCQIHTLPERVEGAPNFREVPGFPVYGVANPTIDGILSVIQRIGSSKGGRPIFWHNMREEPVIYINGKPFVLREVERPYKNMLEYSGIDRERVQGMEARLKEDILREAESYGGAIMVIHETDDGQIFDAWEHVNFDSVKTPLEVFKCLEVDGFPIKYARVPITDGKAPKSSDFDTLAVNIASASKDTAFVFNCQMGRGRTTTGTVIACLLKLRIDYGRPIRVLVDDMACEEADSGSSSGEETGGNAARSPPSNTRMRTGTEQARAFGIDDILLLWKITRLFDNGVECREALDAVIDRCSALQNIRQAVLHYRK**VVNQQHVEPR**VRRVALNRGAEYLERYFRLIAFAAYLGSEAFDGFCGQGESRMTFKTWLHQRPEVQAMKWSIRLRPGR**FFTIPEELRAPQESQHGDAVMEATIK**ARNGSVLGTGSILKMYFFPGQRTSSHLQIHGAPHVYKVDGYPVYSMATPTIAGAKEMLAYLGAKPNGEGSLAQKVILTDLREEAVVYINGTPFVLRELHKPVDTLKHVGITGPLVEHMEAR**LKEDIVSEVR**ESGGRMLLHREEYNPATNQSSVIGYWENIFANDVKTPAEVYAALKDEGYDMTYRRIPLTRERDALASDVDAIQYCKDDCAGSYLFVSHTGFGGIAYAMAIICLRLGAEATFTAEIPQTLVDTESFSVHEEILPSQLSEEETFRMGDYRDILSLTRVLMYGPKSKADVDIVIDKCVGAGHLRDDILYYSKELRKCPHHDDEQLAHLMDMGVKALRRYFFLITFRSYLYCAKPTETRFTSWMNARPELGHLCNNLRIDK

Protein No.: I-197

Protein name and Species:

chitinase Class I, putative OS=Ricinus communis GN=RCOM_0806420 PE=4 SV=1

Accession: tr|B9SIC4|B9SIC4_RICCO

Unused ProtScore: 10.18

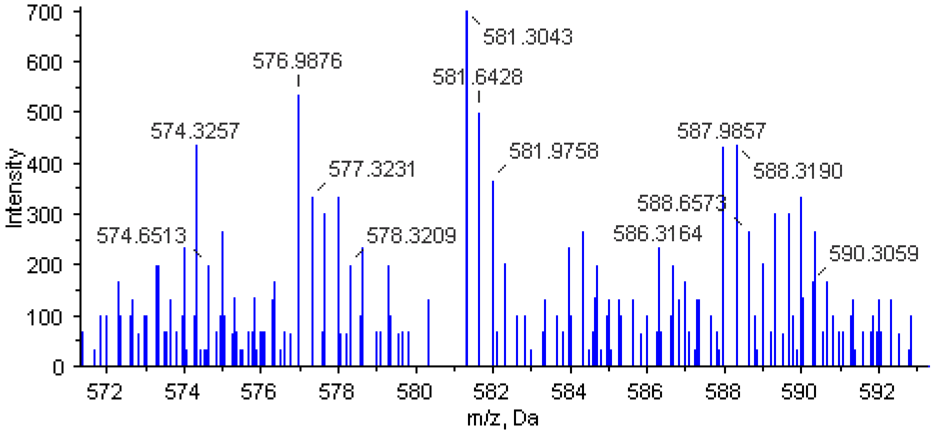
Seq Cov %: 24.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.55

116: 114=E5TL: D5TL= 0.59

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MLPKMEVYAFTVFYIFFSFLLGGLA**EQCGR**QADGALCPGGLCCSQYGWCGNTDPYCGGGCQSQCGGGG**G**
GGGGDLGSIISRSTFDQLLKHRNDGACPGK**GFYTYDAFISAAKDFPGFGTTGDVATR**KGEIAAFFGQTS
HETTGGWPSAPDGPYAWGYCFIR**EQNPGSYCSPSSTYPCAPNK**QYYGR**GPIQLTWNYNYGQCGR**AIGVD
LLNNPDLVATDPVISFKAAIWFWMTPQSPK**PSCHDVITGRWSPSAADR**SAGRLAGYGVLTNIINGALEC
GRGWDSRVDDR**IGFYK**RYCDLLGIGYGNNLDCYNQRSFGNGAFGLVDTM

Protein No.: I-198

Protein name and Species:

Stem-specific protein TSJT1, putative OS=Ricinus communis GN=RCOM_0910970 PE=4 SV=1

Accession: tr|B9RTJ4|B9RTJ4_RICCO

Unused ProtScore: 10.16

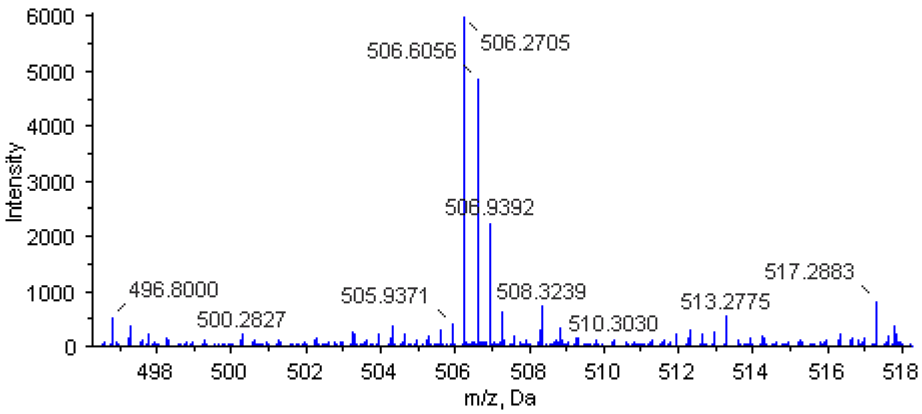
Seq Cov %: 20.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.52

116: 114=E5TL: D5TL= 0.31

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MLAVFDNTVAKCPDALQSPHSASSSALKDGFLAKHFGSIHPASVTVNLGTAGIIAYSLDK**QNPLLPR**LFAVVDDIFCLFQGHIENIAVLKQQYGLNKTANEVIIVIEAFRTLR**DRGPYPADQVVR**DIQGKFAFVLYDSTSKATFIAADADGSVPFFWGADSERHLVLSDDAQILQQACGK**SFAPFPKGCFFTTSGGLR**SYEHPLNELKPVPR**VDSSGQVCGATFK**VDAETKKEGGMPRVGSAYDWSSNY

Protein No.: I-204

Protein name and Species:

Pyruvate kinase OS=Populus trichocarpa GN=POPTRDRAFT_563414 PE=2 SV=1

Accession: tr|A9PFJ7|A9PFJ7_POPTR

Unused ProtScore: 9.98

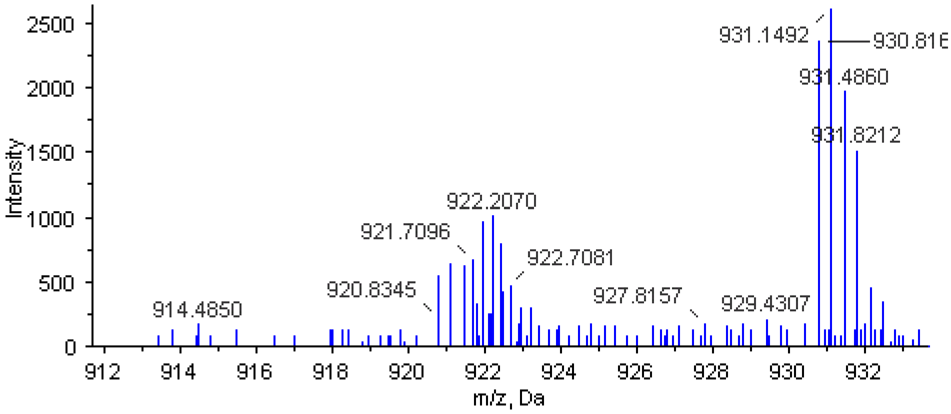
Seq Cov %: 21.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 1.85

116: 114=E5TL: D5TL= 1.56

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MANID**IEGLLK**EHQDDEEGRVPRTKIVCTLGPSSRSVPMLEKLLRAGMNVARFNFSHGTHEYHQETLNN
LRIAMQNTNILAAVMLDTKGPEIRTGFLKDGNPIQLKEGQEITITTDYSIK**GDTDMISMSYK**KLPVDIK
PRNTILCADGTITLTVLSCDPKAGTVRCRCENTAMLGERKNVNLPGVVVDLPTLTDKDKEDILGWGVPN
N**IDMIALSFVR**KGSDLVNVRKVLGPHAKHIQLMSK**VENQEGVVNFDEILR**ETDSFMVAR**GDLGMEIPVE**
KIFLAQKMMIYKCNIVGKPVVTATQMLESMIKSPRPTR**AEATDVANAVLDGTDCVMLSGESAAGAYPEL**
AVKTMRRICIEAESSLDYAAIFKEMIR**STPLPMSPLESLASSAVR**TANKARAKLIVVLTRGGTTAKLVA
KYRPAVPILSVVVPVLTTDSFDWTCSDETPARHSLIYR**GLIPLLAEGSAK**ATDAESTEVILEAALKSAT
KRGLCKPGDAVVALHRIGAASVIKICLVK

Protein No.: I-205

Protein name and Species:

Peptidyl-prolyl cis-trans isomerase OS=Hevea brasiliensis PE=2 SV=1

Accession: tr|F8RW92|F8RW92_HEVBR

Unused ProtScore: 9.88

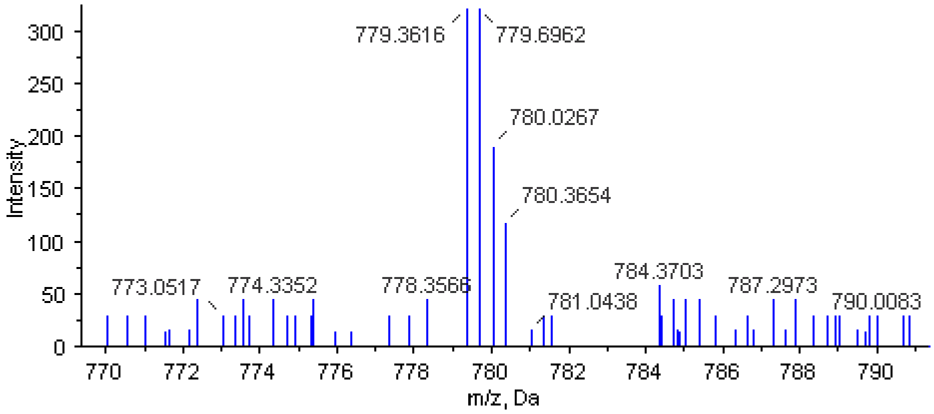
Seq Cov %: 66.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.66

116: 114=E5TL: D5TL= 0.75

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MANPKVFFDMSVGGHPAGKIVMELYADVVPRTAENFRALCTGEKGIGKSGKPLHYKGSSFHRVIPGFMC
QGGDFTAGNGTGGESIYGAKFADENFTKKHTGPGVLSMANAGPGTNGSQFFVCTAKTEWLDGKHVVFGQ
VVEGMDVVKAIEKVGSSSGRTSKPVVIADCGQLS

Protein No.: I-208

Protein name and Species:

Importin beta-3, putative OS=Ricinus communis GN=RCOM_1361100 PE=4 SV=1

Accession: tr|B9T1E9|B9T1E9_RICCO

Unused ProtScore: 9.79

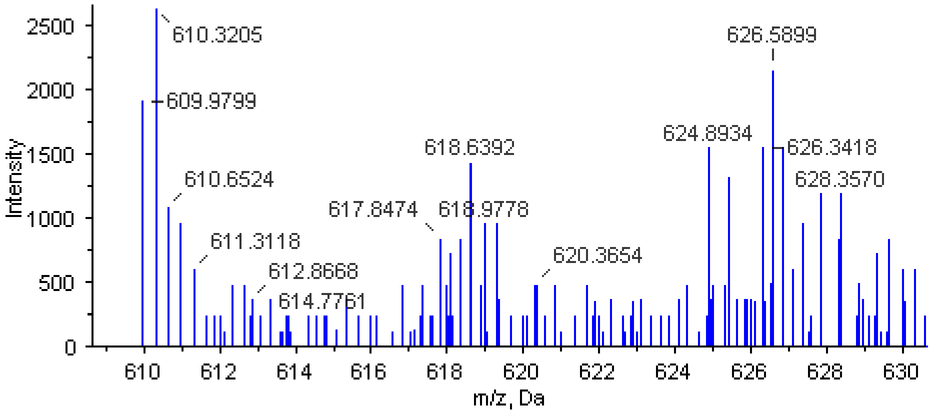
Seq Cov %: 6.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 3.31

116: 114=E5TL: D5TL= 2.11

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDESAQQLQLQQAQLAAILGQDSAPFETLISSLMSSSNEQRSQAEVLFNLCKQTDPNTLSLKLSHLLQF
SPHVDARAMSAVLLRKLLTRDNHVVVDTDSSSYLWPR**LSLATQSSIK**SILLTSIQHESTKSILKKLCDT
VSELAANILPDNGWPELLPFMFNCVSSDSAKLQESAFLIFAQLSQYIGESLIPFIKDLHTVFLQCLGSS
PSFDVKIAALNAVINFIQCLTSSADRDRFQDLLPAMMRTLTEALNNGNEATAQEALELLIELAGTEPRF
LRRQLVDVVGSMLQIAEAESLEEGTRHLAIEFVITLAEARERAPGMMRKLPQFISRLFAILMRMLLDIE
DDPAWHSAENEDEDAGETSNYSVGQECLDRLAISLGGNTIVPVASEQLPAYLAAPEWQKHHAALIALAQ
IAEGCSKVMIKNLEHVVSMVLNSFHDPHPRVRWAAINAIGQLSTDLGPDLQNQYHQRILPALASAMDDF
QNPRVQAHAASAVLNFSENCTPEILTPYLDGIVSKLLVLLQNGK**QMVQEGALTALASVADSSQEHFQKY**
YDAVMPYLKTILVNATDKSNRMLRAKSMECISLVGMAVGKDKFREDAKQVMEVLMSLQGSQMETDDPTT
SYMLQPDVTITSADSDNDIDDSDDESMETITLGDKRIGIKTSVLEEKATACNMLCCYADELKEGFFPWI
DQVAPTLVPLLKFYFHEEVRKAAVSAMPELLRSAKLAVEKGLSQGRNESYVKQLSDYIIPALVEALHKE
PDTEICANMLDALNECLQISGTLVDEGQVRSIVDEIKQVITASSSRKKERADRAKAEDFDAEEGELIKE
ENEQEEEVFDQVGEILGTLIKTFKASFLPFFDELSTYLTPMWGKDKTAEERR**IAICIFDDVAEQCR**ETA
LKYYDTYLPFLLEACNDENPDVRQAAVYGLGVCAEFGGSVFKPLVGEALSRLNVVIQHPNAKQSENVMA
YDNAVSALGKICQFHRESINSAQIVPAWLNCLPITGDLIEAK**VVHEQLCSMVER**SDSELLGPNNQYLPK
IVSVFAEVLCGKDLATEQTASRMVNLLRHLQQTLPPATLASTWSLLHPQQQMALQSILSS

Protein No.: I-210

Protein name and Species:

Profilin OS=Mangifera indica GN=Man i 3.01 PE=2 SV=1

Accession: tr|Q2XPH2|Q2XPH2_MANIN

Unused ProtScore: 9.66

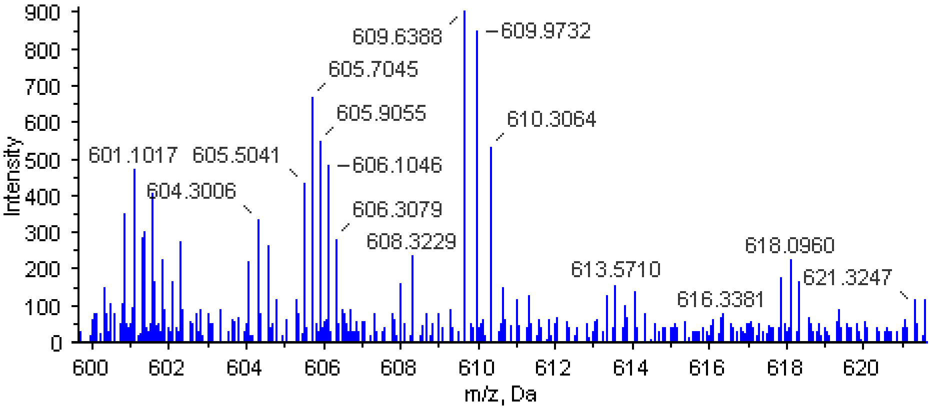
Seq Cov %: 31.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 1.67

116: 114=E5TL: D5TL= 1.53

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSWQAYVDEHLMCDIEGHHLTAAAIVGLDGSVWAQSANFPKLNPEEITAINK**DFDEPGSLAPTGLHLGG**
TKYMVIQGEPGAVIRGK**KGPGGVTVK**KTNMAFVIGIYDEPMTPGQCNMIVERLGDYLVEQGL

Protein No.: I-212

Protein name and Species:

Superoxide dismutase [Cu-Zn] OS=Hevea brasiliensis GN=Cu/Zn-SOD PE=2 SV=1

Accession: tr|Q8GZP2|Q8GZP2_HEVBR

Unused ProtScore: 9.6

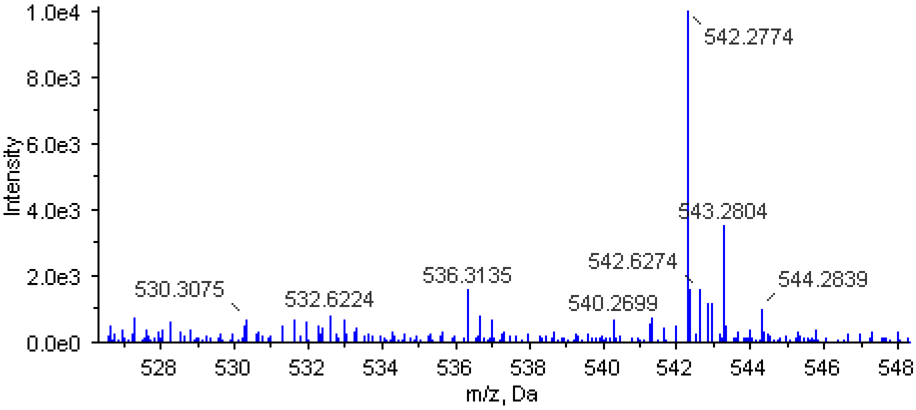
Seq Cov %: 37.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.35

116: 114=E5TL: D5TL= 0.72

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MLK**AVAVITSSEGISGK**IFFTQEGDGPTTVTGSVSGLKPGLHGFHVHTFGDTTNGCLSTGLHFNPASKD
HGGPEDENR**HAGDLGNVNVGDDGTANFTIVDKHIPLSGPHSIAGR**SVVFHEGRDDLGK**GGHELSK**ITGN
AGDRIACGIIGLQE

Protein No.: I-213

Protein name and Species:

Seryl-tRNA synthetase, putative OS=Ricinus communis GN=RCOM_1564380 PE=3 SV=1

Accession: tr|B9RKX9|B9RKX9_RICCO

Unused ProtScore: 9.57

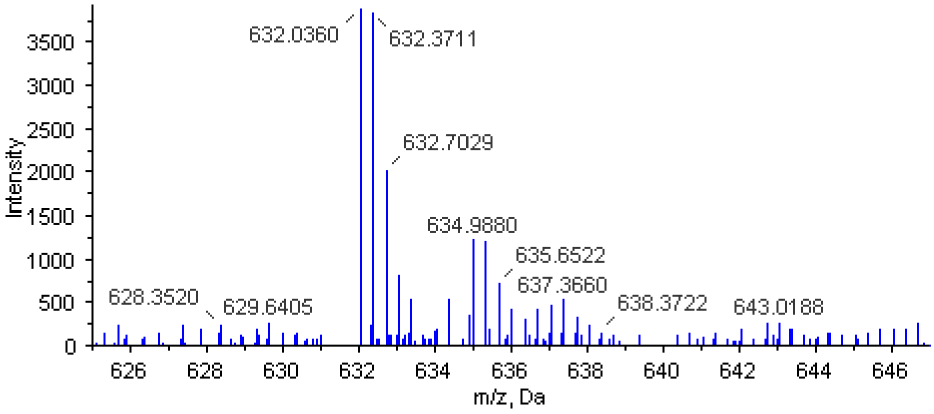
Seq Cov %: 13.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.66

116: 114=E5TL: D5TL= 0.53

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MLDINLFREDKGHNPQLIRESQRRRFANVNVVGEIILLDKEWRQRQYELDNLRKDFNKINKLVAKLKIA
GEDATEMIKDTNENKRLTAEKEAQVQEAALALNKKLEEVGNLVHDSVPVSNDEANNAVIRVWGEKRLEP
KLKNHVDLVELLGIADTKKGANVAGGRGFYLKGDGVRLNQALINVALDFLEKRGYTALQTPFFMRKDIM
AK**CAQLAQFDEELYK**VTGEGEDKYLIATAEQPLCAYHLDDWIHPSQLPIR**YAGYSSCFR**KEAGSHGRDT
LGIFRVHQFEKVEQFCITSPNGNDSWDMHEEMIKNSEDFYKMLNIPYQVVAIVSGALNDAAAKKYDLEA
WFPASNTYR**ELVSCSNCTDYQSR**KLEIRYGQKKNNEQAK**QYVHLLNSTLTATERTLCCILENYQK**ENGV
EIPEPLRGYMGGKSFLPFQNNPPTEGKGKKSKA

Protein No.: I-216

Protein name and Species:

Phospholipase D OS=Populus trichocarpa GN=POPTRDRAFT_829577 PE=3 SV=1

Accession: tr|B9GH43|B9GH43_POPTR

Unused ProtScore: 9.47

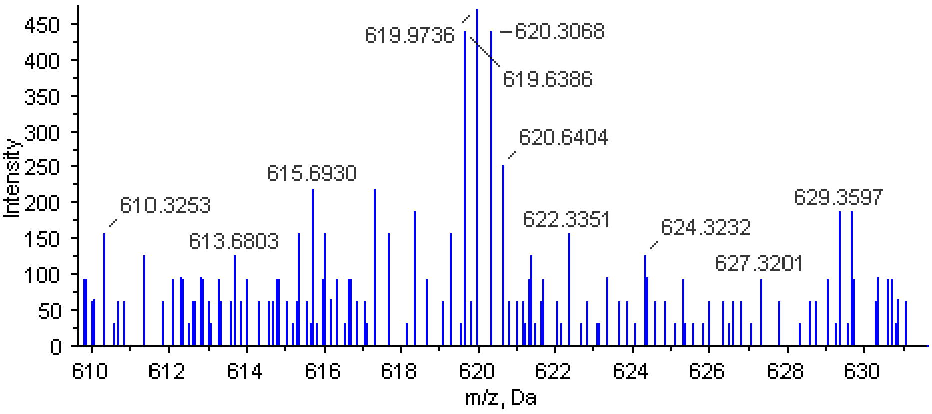
Seq Cov %: 18.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.36

116: 114=E5TL: D5TL= 0.77

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAQILLHGNLHVTIYEVDKIGEGGGHGFFHKLVGKVGEKVGIGNGISR**LYATIDLEK**ARVGRTRILENE
ATNPRWYESFHIYCAHMASNVIFTVK**DVNPIGATLIGR**AYIPVEEILDGEEIDRWVEILDGDKNPIRAG
SKIHVKLQYFDITNDHNWGRGIRGSK**YPGVPYTFYSQR**QGCRVSLYQDAHIPDKFIPKIPLASGEYYEP
HR**CWEDVFDAITNAK**HLIYITGWSVYTEISLVRDSRRPK**PGGDITLGELLK**KKASEGVRVLMLIWDDR**T**
SVGLLKRDGLMATHDEETEHYFQNTDVHCILCPRNPDDGGSIVQDLQISTMFTHHQK**IVVVDSAMPNGD**
SQRRRIVSYIGGIDLCDGR**YDTPFHSLFRTLDTAHHDDFHQPNFTGASIQK**GGPREPWHDIHSRLEGPI
AWDVLFNFEQRWKKQGGKDLLVQLRELEDVIIPPSPVTYPDDHETWNVQLFRSIDGGAAFGFPETPEDA
AKAGLVSGKDNIIDRSIQDAYINAIRRAKNFIYIENQYFLGSSFCWSADGIKPEDINALHLIPKELSLK
IVSK**IEAGER**FTVYVVVPMWPEGIPESASVQAILDWQRRTMDMMYKDVIQALRAKGLEEDPR**NYLTFFC**
LGNREVKK**SGEYEPSEKPEPDSDYIR**AQEARR**FMIYVHAK****MMIVDDEYIIIGSANINQR**SMDGARDSEI
AMGGYQPYHLATRQPARGQIHGFRLGLWYEHLGMLDDTFLKPENEDCIR**KVNQIADK**YWDLYSSETLEG
DLPGHLLRYPIGISSEGNVTELPGTEYFPDTKARVLGAKSDYMPPILTT

Protein No.: I-219

Protein name and Species:

14-3-3 protein 3 OS=Hevea brasiliensis PE=2 SV=1

Accession: tr|F2YZ44|F2YZ44_HEVBR

Unused ProtScore: 9.44

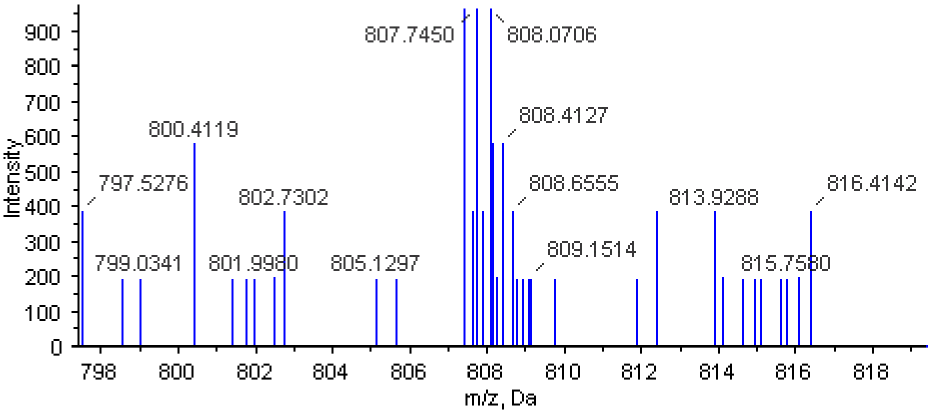
Seq Cov %: 47.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.65

116: 114=E5TL: D5TL= 0.66

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAVAPSSR**EESIYMAKLAEQAERYEEMVEFMEKVSASVEKEELTVEERNLLSVAYKNVIGAR**RASWR**IISSIEQKEESRGNENHVSMIR**DYRAK**IESELSSICDGILK**LLDTRLIPPASPGDSKVFYLKMKGDYHR**YLAEFK**TGAERK**EAAESTLTAYKSAQDIATAELAPTHPIR**LGLALNFSVFYYEILNSPDRACSLAK**QAFDEAIAELDTLGEESYKDSTLIMQLLRDNLTLWTSDIADEAGDEIK**EASKRESGEGQPQQ

Protein No.: I-220

Protein name and Species:

Caffeic acid O-methyltransferase OS=Boehmeria nivea GN=COMT PE=2 SV=1

Accession: tr|Q14VV8|Q14VV8_BOENI

Unused ProtScore: 9.44

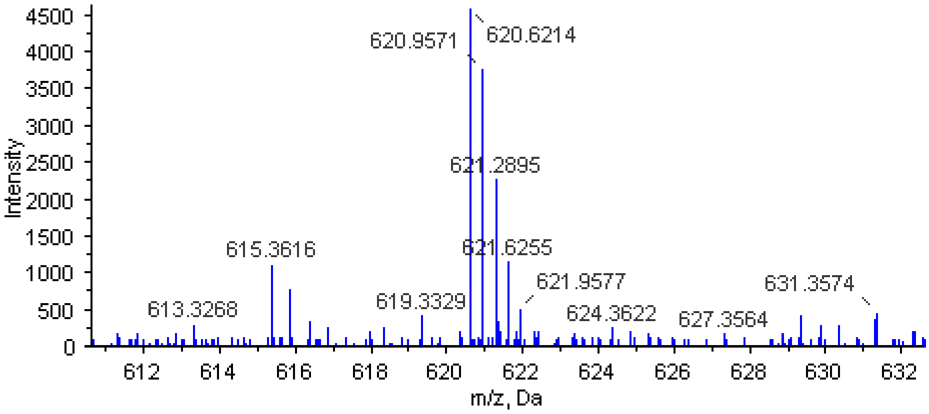
Seq Cov %: 19.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.61

116: 114=E5TL: D5TL= 0.63

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGSTGETQMTPTQVSDEEANLFAMQLASASVLPMVLKTAIELDLLEIIAKAGPGAWLSPAEIAAQLPTT
NPAAPVMLDRILRLLACYSVVACQLRTLPGGAAER**LYGLAPVCKFLTK**NNDGVSISPLCLMNQDKVLME
SWYYLK**DAVLEGGIPFNKAYGMTAFEYHGTDPR**FNKVFNR**GMSDHSTITMK**KLLETYKGFEGLNSVVDV
GGGTGAVLSMIVSNYPSIKGINFDLPHVIEDAPAYPGVEHVGGDMFVSVPK**GDAIFMK**WICHDWSDEHC
LKFLKSCYDALPNNGKVIVAECILPVAPDTSLATKGVAHIDVIMLAHNPGGKERAEKEFQALAK**GAGFQ**
GFRVVCSAFNTYVMEFLKKP

Protein No.: I-221

Protein name and Species:

Pathogenesis-related thaumatin (Fragment) OS=Populus deltoides GN=PR52-1 PE=4 SV=1

Accession: tr|D2JWP4|D2JWP4_POPDE

Unused ProtScore: 9.34

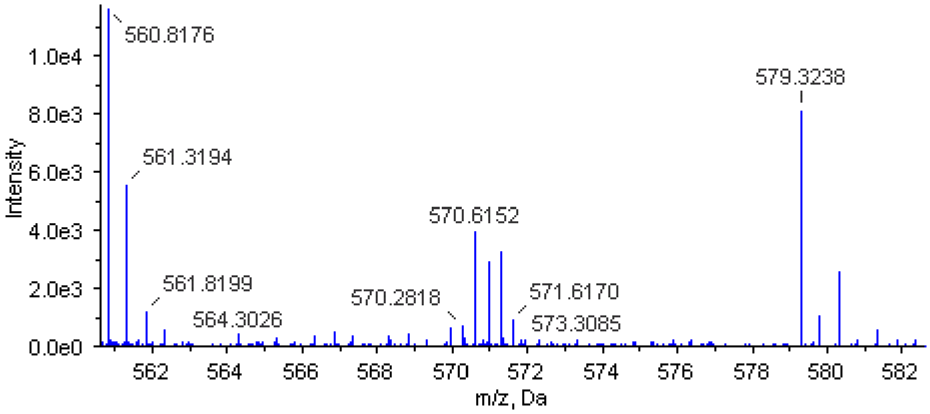
Seq Cov %: 35.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.28

116: 114=E5TL: D5TL= 0.53

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSHLTKFLTSSLLFSLLIISTNAATFEIR**NNCPYTVWAAASPGGGRRLDRGQTWYLNVPAGTSMAR**IWG
R**TNCNFDGSGR**GRCQTGDCTGGLECKGWGVPPNTLAEYALNQFGNLDFYDISLVDGFNIPMEFSPTSSG
GSGKCQALLCTADINGQCPNELR**APGGCNNPCTVFK**TNEYCCTNGQGSCGPTYFSRFFKDR**CPTSYSYP**
QDDPSSTFTCPGGTNYRVIFCPWGSPHFPLEMVE

Protein No.: I-224

Protein name and Species:

Glutathione transferase, Lambda class OS=Populus trichocarpa PE=2 SV=1

Accession: tr|D2WL72|D2WL72_POPTR

Unused ProtScore: 9.24

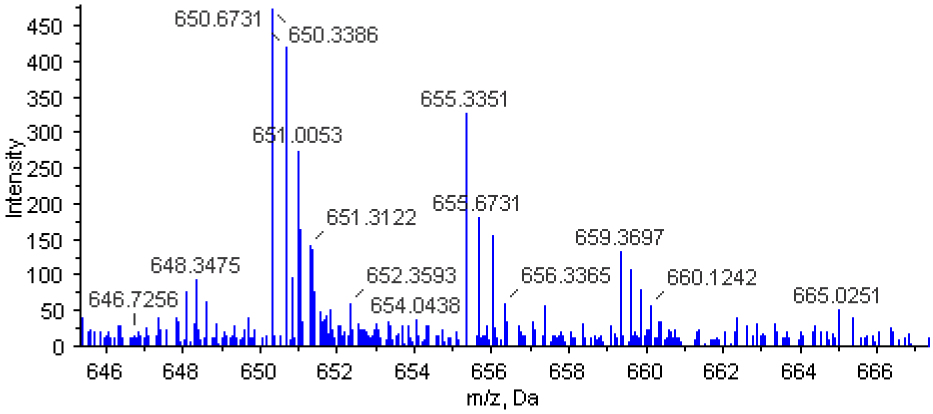
Seq Cov %: 32.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.52

116: 114=E5TL: D5TL= 0.61

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MELPRLYTCYTCPFAHRVWITRNFKG**LQDEIK**LVPLILQNRPAWYSEKVYPPNK**VPSLEHNGK**ITGESL
DLIKYLESNFQGPSLLPEDPAKK**EFAEELFSYTDTFNRTVFTSFK**GDPAK**EAGPAFDHLENALHK**FGDG
PFFLGQEF**SLVDIAYIPFVER**FCIFLSEVFK**YDITAGRPKLAAWIEELNK**IEAYKQTKTDPKEMVEVYK
KRFMA

Protein No.: I-226

Protein name and Species:

Latex cystatin OS=Hevea brasiliensis PE=4 SV=1

Accession: tr|E8Z9H3|E8Z9H3_HEVBR

Unused ProtScore: 9.2

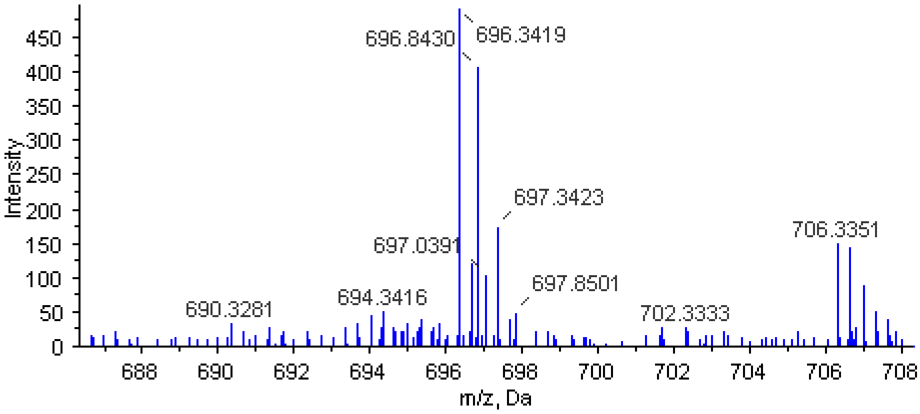
Seq Cov %: 32.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.57

116: 114=E5TL: D5TL= 0.52

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAKLGGVK**EVEGSANSVEINSLARYAVDDYNQKQNALLEFK**KVVNAKQQVVAGTIYYITLEVIDGGQKK
VYEAKVWEK**PWLNFKEVQEFKLIGDAPSDSTA**

Protein No.: I-227

Protein name and Species:

Rab4 OS=Hevea brasiliensis PE=2 SV=1

Accession: tr|F2VXU6|F2VXU6_HEVBR

Unused ProtScore: 9.17

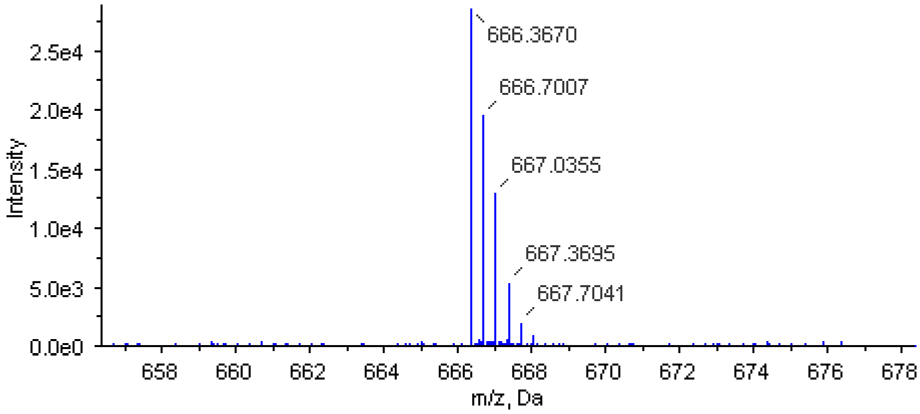
Seq Cov %: 40.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.17

116: 114=E5TL: D5TL=0.40

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSNEYDYLFK**LLLIGDSSVGKSCLLLRFADDSYVDSYISTIGVDFK**IR**TVELDGK**TIK**LQIWDTAGQER**
FR**TITSSYYR**GAHGIIIVYDVTEMESFNNVK**QWLNEIDRYANDSVCK**LLVGNKCDLVDNKVVDTQTAK**A**
FADELGIPFLETSAKDSINVEQAFLTMAGEIKKK**MGSQPAASK**STGTTVQMKGQPIQQKNNCCG

Protein No.: I-230

Protein name and Species:

6-phosphofructokinase 3 OS=Populus trichocarpa GN=POPTRDRAFT_866992 PE=4 SV=1

Accession: **tr|B9H8X6|B9H8X6_POPTR**

Unused ProtScore: **9.12**

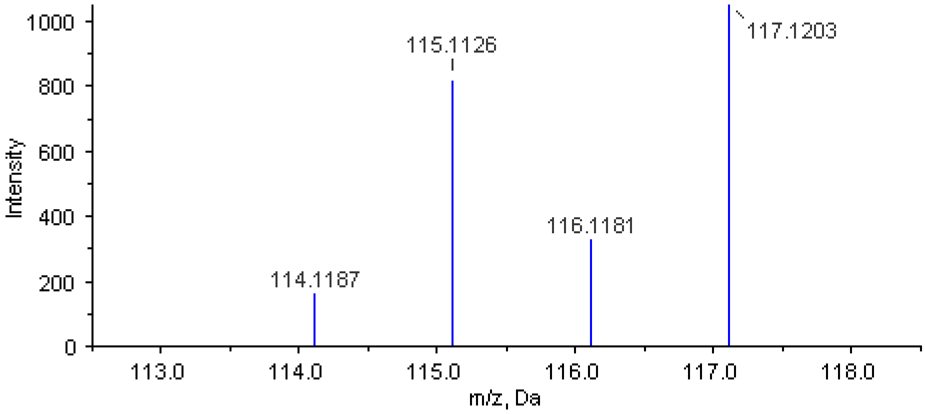
Seq Cov %: **14.9**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.54

116: 114=E5TL: D5TL= 0.62

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MASNDVSKPKIITGDFGYVLEDVPHFTDYIPDLSTYSNPLQDNPAFCVVK**QYFVHVDDSVPQK**IVVHKD
SPRGIHFRRAGPRQKVYFDSDEVHACIVTCGGLCPGLNTVIREIVYSLYHMYGVTT**VLGIDGGYR**GFYA
RNTIALTPKVVNDIHKRGGTILGTSRGGHDTSKIVDSIQDRGINQVYIIGGDGTQK**GASVIFEEIR**RRG
LKVVVAGIPK**TIDNDIPVIDKSFGFDTAVEEAQRAINAAHVEAESVENGIGLVK**LMGRYSGFIAMYATL
ASRDVDCCLIPESPFYLDGKGGLFEYIEKQLKENGHMVIVIAEGAGQELLSESMQSRNQQDASGNKLLQ
DVGLWISQGIKDYFSRQKTMAINLK**YIDPTYMIR**AVPSNASDNVYSTLLAQSAVHGAMAGYTGFTSGLV
NGRQTYIPFYRIIEKQNKVVITDRMWARLLSSTNQPSFMSDKDVIEDKTECISGEKKEEDPATQFLDNG
NRADGVLENKEVSSV

Protein No.: I-241

Protein name and Species:

Acyl-CoA-binding protein (Fragment) OS=Jatropha curcas PE=2 SV=1

Accession: tr|D6BR55|D6BR55_9ROSI

Unused ProtScore: 8.78

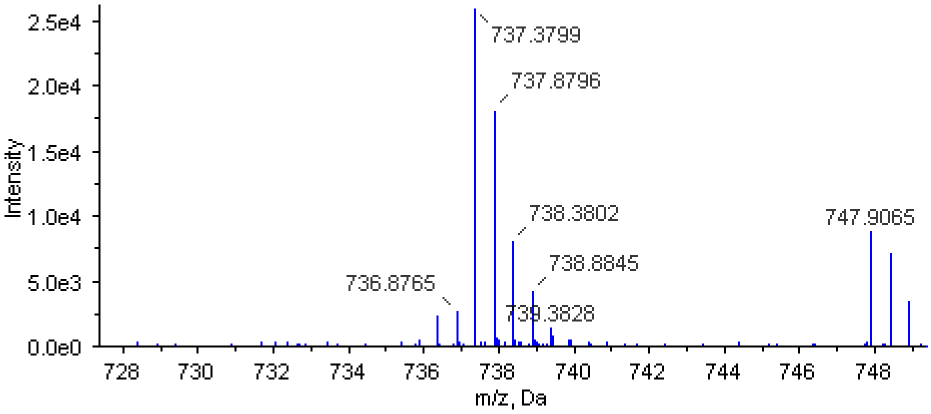
Seq Cov %: 35.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.40

116: 114=E5TL: D5TL= 0.58

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGLKEEFEEYAEKAKTLPENTTNENKLILYGLFKQATVGPVNTSRPGMFNMRDRAKWDAWKAVEGKSKE
EAMSDYITKVKLLLEEAAAAASA

Protein No.: I-242

Protein name and Species:

Actin-depolymerizing factor OS=Hevea brasiliensis GN=ADF PE=2 SV=1

Accession: tr|D9I9X9|D9I9X9_HEVBR

Unused ProtScore: 8.71

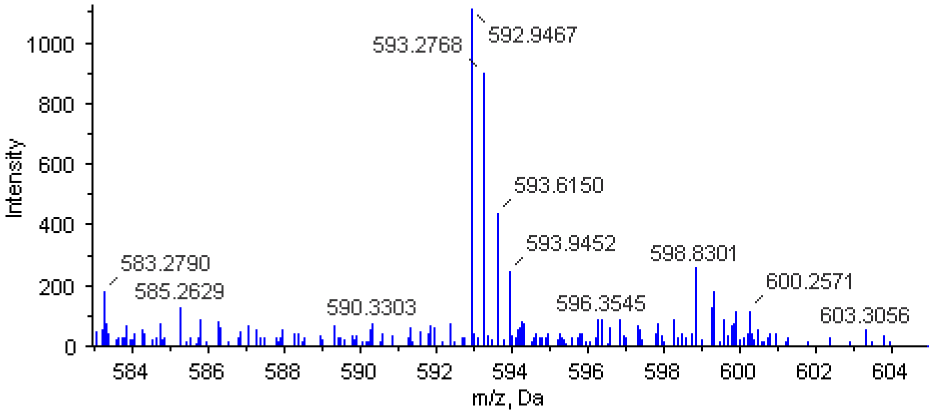
Seq Cov %: 61.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.58

116: 114=E5TL: D5TL= 0.58

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MANAASGMAVHDDCKLRFLELKAKRTYRYIVFKIEEKAKQVIVEKLGEPTQSYEDFTASLPADECRYAV
YDFDFVTEENCQKSRIFFIAWSPDTSRVRSKMIYASSKDRFKRELDGIQVELQATDPTEMGLDVFKSRA
S

Protein No.: I-244

Protein name and Species:

Proteasome subunit alpha type OS=Ricinus communis GN=RCOM_1595040 PE=3 SV=1

Accession: tr|B9R7X1|B9R7X1_RICCO

Unused ProtScore: 8.65

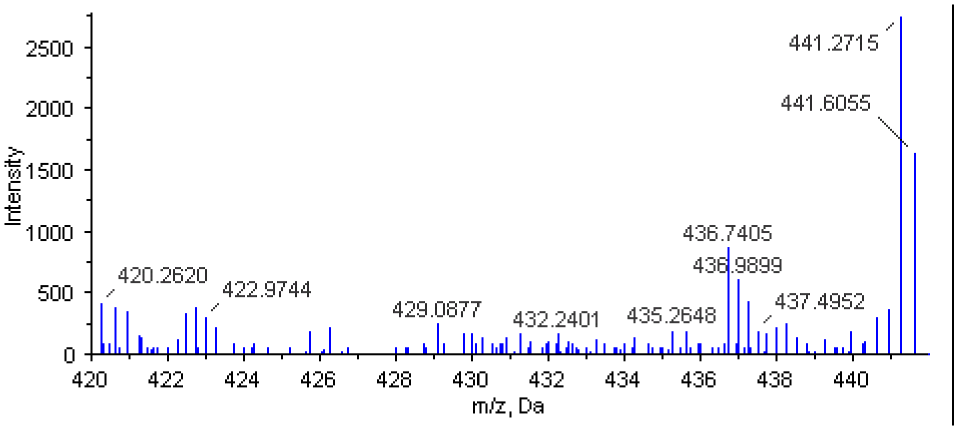
Seq Cov %: 23.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 1.61

116: 114=E5TL: D5TL=1.50

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MFR**NQYDTDVTTWSPAGRLFQVEYAMEAVKQGSAAIGLR**SK**THVVLACVNK**ANSELSSHQKKIFK**VDDHIGVAIAGLTADGR**VLSRYMR**SECINYSFTYESPLPVGRLVVQLADK**AQVCTQRSWKRPYGVGLLVAGLDESGAHLYYNCPSGNYFEYQAFAIGSRSQAAKTYMER**RFENFMDSSR**DDLIKDALIAVRETLQGETLKSSICTVAVVGVGEAFHVLDQETVQQLIDAFEIVGEPEAPAAEPDAAAEGGGGAAADQGGAAADQGGAAADEGVAPMDI

Protein No.: I-245

Protein name and Species:

ubiquitin-protein ligase 1 OS=Hevea brasiliensis PE=2 SV=1

Accession: tr|F8RWS9|F8RWS9_HEVBR

Unused ProtScore: 8.65

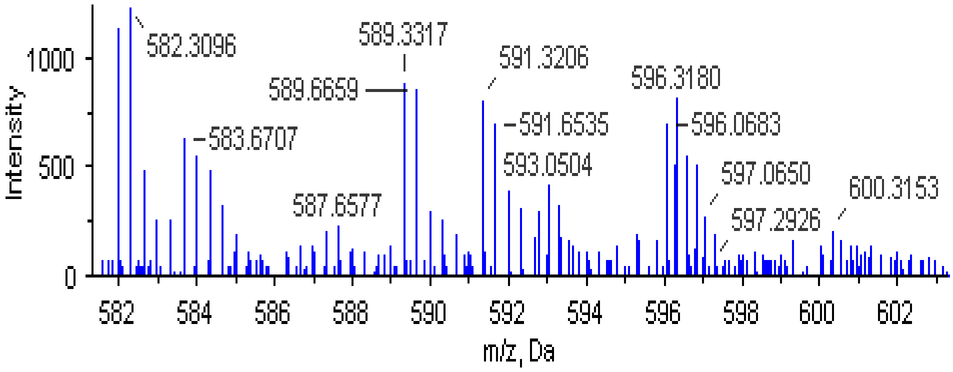
Seq Cov %: 41.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.65

116: 114=E5TL: D5TL=0.70

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

M**TLGSGGSSVVVPR**NFR**LLEELER**GEK**GIGDGTVSYGMDDGDDIYMR**SWTGTIIGPHNTVHEGRIYQLK
LFCDKDYPEKPPSVRFHSR**INMTCVNHETGVVEPK**KFGLLANWQR**EYTMEDILTQLK**KEMAAPHNRKLV
QPPEGTYF

Protein No.: I-246

Protein name and Species:

Plant synaptotagmin OS=Populus trichocarpa GN=NTMC2T1.2 PE=4 SV=1

Accession: **tr|B9HR67|B9HR67_POPTR**

Unused ProtScore: **8.6**

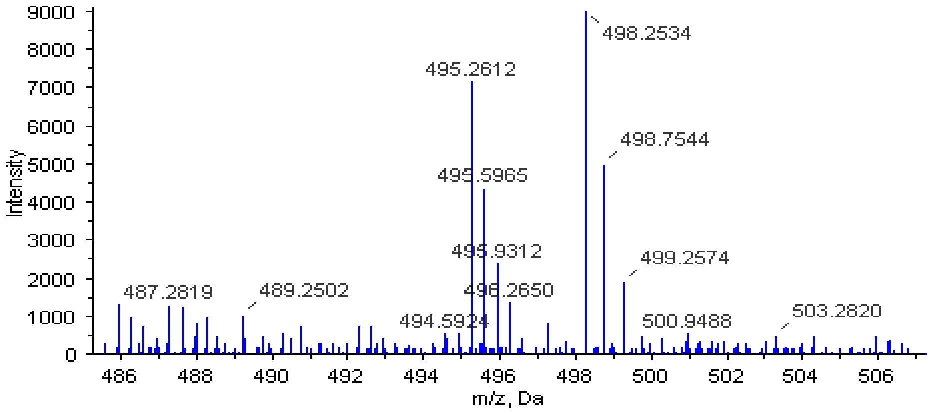
Seq Cov %: **12.1**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 1.79

116: 114=E5TL: D5TL= 0.69

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGFLSTISGFCGFGVGLSTGLTIGYYLFIYFQPTDVKDPEVR**PLAEQDSETLQR**ILPEIPLWVKNPDYD
RIDWLNRFIQLMWPYLDKAICKTVKNIAKPIIAEQIPKYKIDAVEFETLTLGTLPPTFHGMKVYVTDEK
ELIMEPCIK**WAGNPNVTVAVK**AFGLKATAQVVDLQVFASPRITLKPLVPSFPCFANIYVSLMEKPHVDF
GLK**LLGADLMSIPGLYR**V**VQEIIK**DQVANMYLWPKTLEVPILDPAKAMKLKKK**DLMGASDPYVK**IKLTE
DKLPAKKTTVKHKNLNPEWNEEFNLVVKDPESQALELRVYDWEQVGKHDR**MGMNVVPLK**DLTPEEPK**VM**
TLDLLKNMDLNDPQNEKSRGQLMVELTYKPFKEDDLNKSFKDEVEQKAPEGTPAGGGLLVVTIHEAQDV
EGKHHTNPYVRLLFRGEEMKTKRVKKNRDPRWEEEFQFTLEEPPVNAKLH**VEVVSTSSR**IGLLHPKESL
GYVEINLSDVVSNRRINERYHLIDSKNGKIQIELQWRPAS

Protein No.: I-247

Protein name and Species: **P5CS, Delta 1-pyrroline-5-carboxylate synthetase, putative OS=Ricinus communis GN=RCOM_1482350 PE=3 SV=1**

Accession: **tr|B9SE11|B9SE11_RICCO**

Unused ProtScore: **8.57**

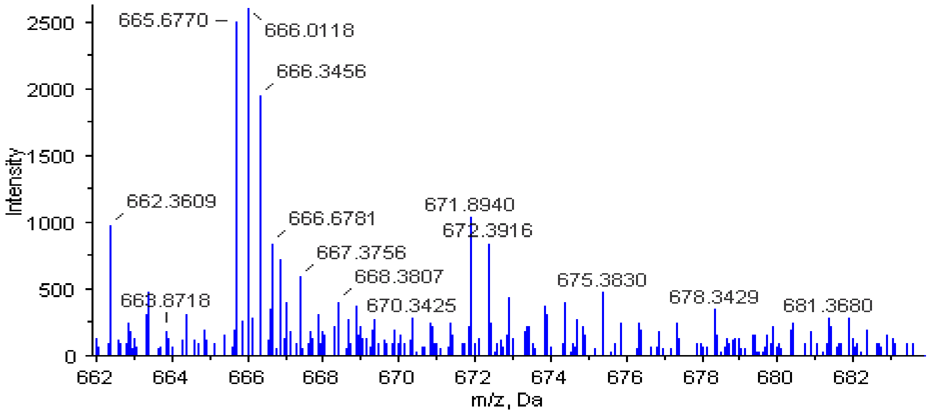
Seq Cov %: **6.7**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 2.03

116: 114=E5TL: D5TL= 1.66

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MNGGMDRSRAFVKDVKRLVIKVGTAVVTRGDGRLALGRLGAFCEQVKELNSQGYEVIVVSSGAVGLGRQ
RLRYRKLVNSSFADLQKPQVEIDGKASAAVGQSSLMALYDTMFSQLDVTSAQLLVTDNDFRDKDFRKQL
NETVESLLSLR**VIPIFNENDAVSTR**KAPYEDASGIFWDNDSLSALLALELKADLLVLLSDVDGLYSGPP
SDPRSKLIHTYIKEIHHGEITFGDKSRVGRGGMTAKVKAAVNAAYAGIPVIITSGFARENILKVLQGER
VGTLFHQDAHIWVPIKEVCGREMAVAARESSRRLQALSSQERKRILLDIADALEANEEQIKIENEADVA
AAQLAGLEKSLISRLALKSGKIKSLANSIRVLANMEDPIGCVLK**RTELADGLLLEK**TSSPLGVLLIIFE
SRPDALVQIASLAIRSGNGLLLKGGKEAKRSNEILHKIITAAIPETIGGK**LIGLVTSR**DEIPDLLK**LDD**
VIDLVIPRGSNKLVSQIKASTKIPVLGHADGICHVYVDKSANMEMAKRIVLDAKIDYPAACNAMETLLV
HK**DLVQTGGLNELTVDLR**TEGVNLYGGPRASKELNVPEVDSFHHEYNSMACTIEIVDDVYAAIEHIHEH
GSAHTDCIITEDHEVAEVFLC**QVDSAAVFHNASTR**FSDGARFGLGAEVGISTSRIHAR**GPVGVEGLLTT**
RWILRGNGQVVDGDKGVIYTHKDVTHIHSNGFVPASLTKEDN

Protein No.: I-248

Protein name and Species:

adenosine kinase 2 [Vitis vinifera] OS=Vitis vinifera GN=VIT_13s0019g04480 PE=4 SV=1

Accession: tr|F6HNF4|F6HNF4_VITVI

Unused ProtScore: 8.56

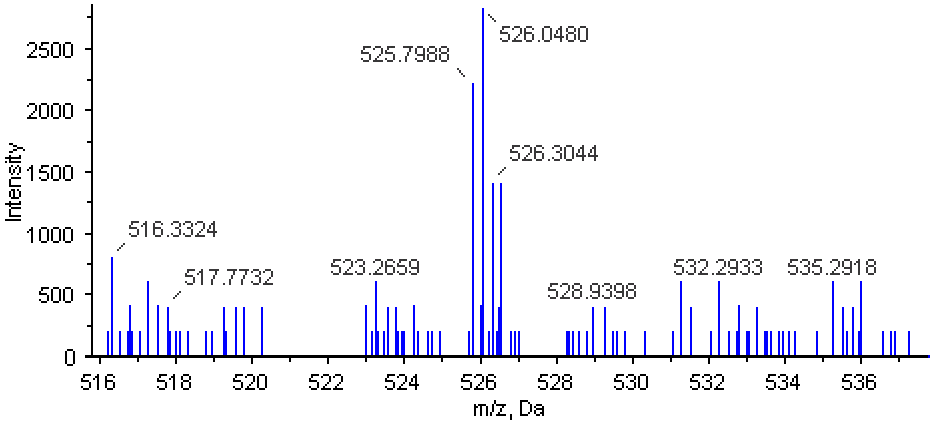
Seq Cov %: 16.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.34

116: 114=E5TL: D5TL= 0.50

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAYEGILLGMGNPLLDISSVVDEEFLQRYDIK**LNNAILAEDKHLPMYDEMASKYNVEYIAGGATQNSIR**
VCQWMLQIPGATSYMGCIGKDK**FGEEMK**KNSKLAGVNVHYREDETAPTGTCAVCVVGGER**SLIANLSAA**
NCYKSEHLKRPENWALVEKAKYFYIAGFFLTVSPESILLVAEHAAANNKVFMMNLSAPFICEFFKDQQE
KALPYMDYVFGNETEARTFSR**VHGWETDNVEEIAIK**ISQWPKASGTHKR**ITVITQGADPVVVAEDGK**VK
SFPVILLPKEKLVDTNGAGDAFVGGFLSQLVQEKPIEECVRAGCYASHVIIQR**SGCTYPEKPDFS**

Protein No.: I-256

Protein name and Species:

Fructose-bisphosphate aldolase OS=Populus trichocarpa GN=POPTRDRAFT_832739 PE=3 SV=1

Accession: tr|B9HJ73|B9HJ73_POPTR

Unused ProtScore: 8.36

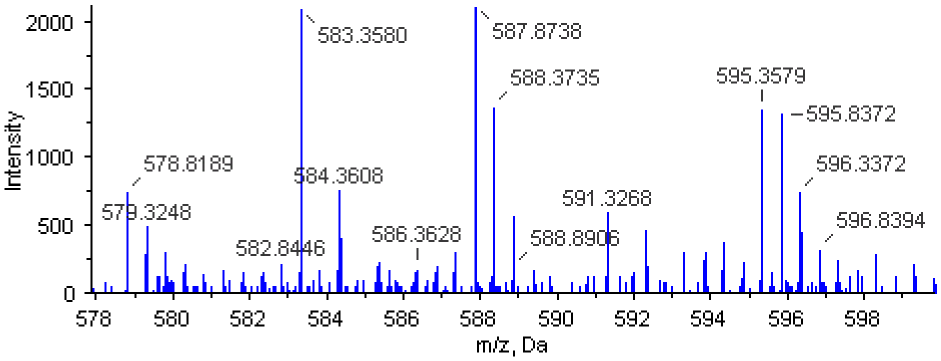
Seq Cov %: 19.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.66

116: 114=E5TL: D5TL= 0.75

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MACASFVKLNAASSSWTGQKSSFGKRSPGSSTRRVSFSIRASSYTDELVQTAKLIASPGR**GILAIDESNATCGK**RLASIGLDNTETNRQAYRQLLLTTPGLGEYISGAILFEETLYQSTTDGRK**FVDCLRDENIVPGIK**VDK**GLVPLPGSNNESWCQGLDGLASR**SAEYYKQGARFAKWR**TVVSIPCGPSALAVKEAAWGLAR**YAAISQDNGLVPIVEPEILLDGDHPIDRTLEVAEKVWAEVFYYLAENNVVFEGILLKPSMVTPGAEHKEKASPDTIAK**YTLTMLK**RRVPPAVPGIMFLSGGQSEVQATLNLNAMNQSPNPWHVSFSYAR**ALQNTVLK**TWQGRPENVEAAQKSLLVRAKANSLAQLGRYSAEGESEEAKKGMFVKGYTY

Protein No.: I-261

Protein name and Species:

Arginyl-tRNA synthetase, putative OS=Ricinus communis GN=RCOM_1049090 PE=3 SV=1

Accession: tr|B9RKG2|B9RKG2_RICCO

Unused ProtScore: 8.15

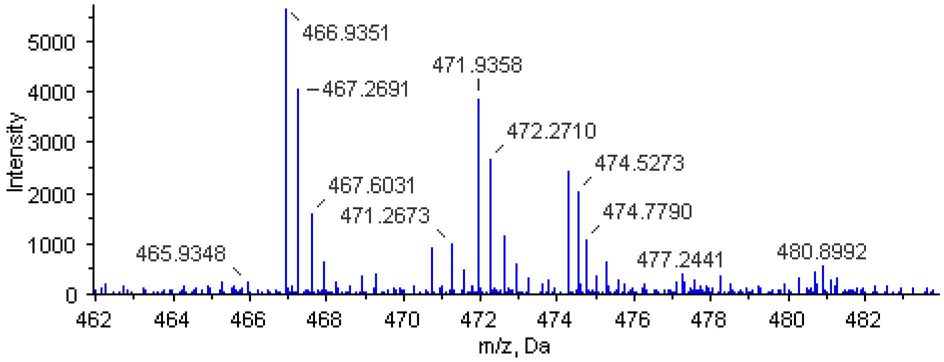
Seq Cov %: 14.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.53

116: 114=E5TL: D5TL= 0.96

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MATNAENEDNVGNLKKQIAK**LFEASLRETVPSEPDVEPLVAACTAK**FGDYQCNNAMSLWSKIKGKNTEF
K**GPPAVGQAIMKNLPPSEVIESCSVAGPGFVNVVLSK**KWMSKKIQKMLIDGIDSWAPKLLVKRAVVDFS
SPNIAKEMHVGHLRSTIIGDTLARMLEFSKVDVLRRNHVGDWGTQFGMLIEFLFEK**FPNFEDVNERAIG**
DLQAFYKASKQRFDADSEFKERAQKAVVRLQGGEPKYRQAWAQICDISRKEFDKVYQRLGVQLEEKGES
FYNPYIPGIIDALSNQGLVEESEGARVIFIEGVNIP**LIVVK**SDGGFNYASTDLTALWYRLNEEKAEWII
YVTDVGQQQHFDMVFKAAKRASWLPADDSMFPKASHVGFGLVLGDDGKRFRTRATEVVR**LVDLLDEAK**T
RSKAVLVERGKAEEWTEQELEQIAEAIGYGAVKYADLKNNRLTNYTFNYDQMLNDK**GNTAVYLLYAHAR**
ICSIIRKSGRDMEELKKMGSLVLDHPDERSLGLHLLQFAETVEEACTNLLPNVLCEYLYNLSEYFTKFY
SNCKVVESPEETSRLLLCEATAVVMRKCFFLLGIVPVYKI

Protein No.: I-262

Protein name and Species: Carotenoid cleavage dioxygenase 1 OS=Manihot esculenta GN=CCD1 PE=2 SV=1

Accession: tr|E2DQG6|E2DQG6_MANES

Unused ProtScore: 8.15

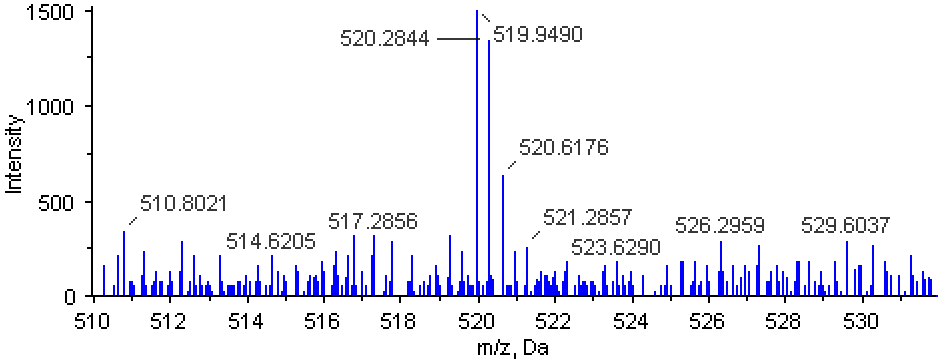
Seq Cov %: 10.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.20

116: 114=E5TL: D5TL= 0.65

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAEEKSEVEKKQGNSGGAGVPIVEVKPKPRKGLASKFVDLLEKLIVKLMFDASKPLHYLSGNFAPVTDE
TPPVRDLSVKGHLPDCLNGEFVRVGPNPKFAPVAGYHWFDGDGMIHGMRIKNGKATYVRRYVRTSR**IQQ**
EEFFGGSKIMKVGDLKGLFGLFMVNMQILRAKLKVLDMSYGNGTANTALIYHHGKLLALQEADKPYVVK
VLEDGDLQTVGMLDYDKRLKHSFTAHPKVDPNTGEMFTFGYAHEPPYITYRVISKDGVMHDPVPITISD
PIMMHDFAITENYAIFLDLPLYFRPKEMVKDKKLIFTFDATKKARFGVLPRYAKDDHQIRWFELPNCFI
FHNANAWEEEDEVVLITCRLENPDLDMVSGNVKEKLENFANELYEMRFNMKTGVASQKRLSAPAVDFPR
VNESYTGRKQR**YVYGTILDSIAK**VTGIIK**FDLHAEPQQGK**TKLEVGGNIKGIFDLGPGRFGSEAVFVPR
EPGTSSEEDDGYLIFFTHDENTGKSSVNVIDAK**TMSSDPVAVVELPHR**VPYGFHAFFVTEEQLQAQATL

Protein No.: I-264

Protein name and Species:

Glutaredoxin OS=Hevea brasiliensis PE=4 SV=1

Accession: tr|B3FNP8|B3FNP8_HEVBR

Unused ProtScore: 8.09

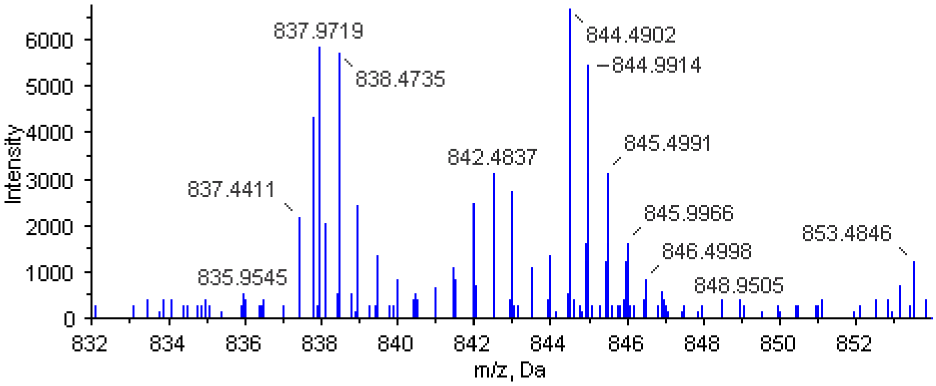
Seq Cov %: 43

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.28

116: 114=E5TL: D5TL= 0.31

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAMTKAK**ELVSSNSVVVFSKTYCPYCTSVK**K**LLDELGANYK**TVELDTEGDGSQVQSALAEWTGQR**SVPNVFISGK**HIGGCDTTTGMHK**EGK****LIPLLTEAGALAK**ASA

Protein No.: I-266

Protein name and Species:

ras-related protein RABA3 OS=Ricinus communis GN=RCOM_0143940 PE=3 SV=1

Accession: tr|B9T509|B9T509_RICCO

Unused ProtScore: 8.05

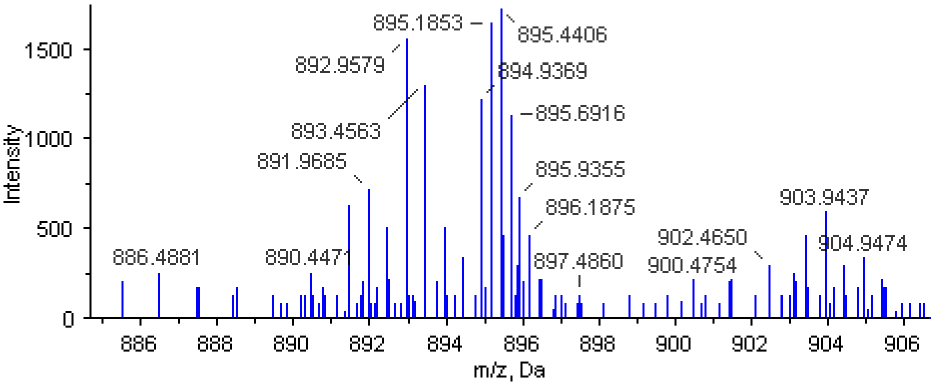
Seq Cov %: 42

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.46

116: 114=E5TL: D5TL= 0.58

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MNQEMNGDDQENLQEKIDYVFK**VVVIGDSAVGK**TQLLSRFTK**NEFCFDSK**STIGVEFQTRTVTIKGKVV
K**AQIWDTAGQER**YR**AVTSAYYRGALGAMLVYDITK**RATFDHVARWVEELRAHADNSIVITLIGNKADLV
DQR**AVPTEDAVEFAEDQGLFFSETSALSGDNVDR**AFFRLLEEIYGVISKKSLECGGHKTNGADSVMLRG
SK**IDVISGSDLEISEMK**KLSACSC

Protein No.: I-267

Protein name and Species:

Peroxiredoxin, putative OS=Ricinus communis GN=RCOM_1052060 PE=4 SV=1

Accession: tr|B9RKM9|B9RKM9_RICCO

Unused ProtScore: 8.02

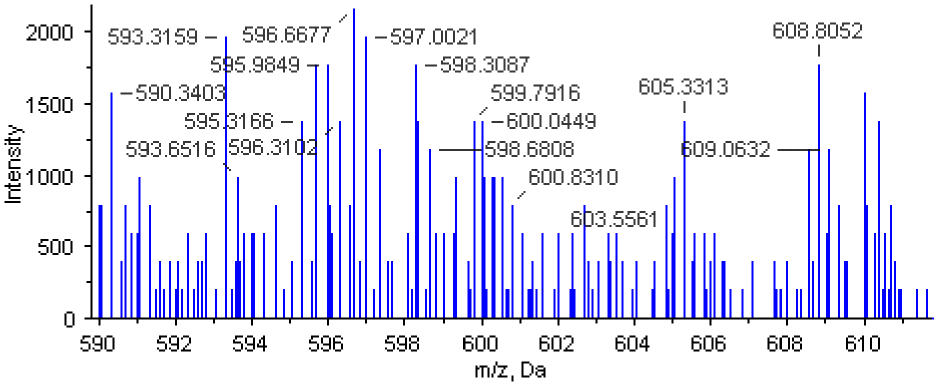
Seq Cov %: 29

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.39

116: 114=E5TL: D5TL= 0.12

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAPIAAGDTLPDGTLAYFDEQDQLQQVSIHSLAAGK**KVVIVGVPGAFTPTCSLK**HVP**GFIEK**AEELKSK

GVAEILCLSVNDPFVMKAWAKTYPENKHVKFLADGSATYTHALGLELDLKEKGLGTRSRR**FALLVDDLK**

VK**AANLEEGGEFTVSSVDEILK**AL

Protein No.: I-268

Protein name and Species:

Ubiquilin, putative OS=Ricinus communis GN=RCOM_0873810 PE=4 SV=1

Accession: tr|B9S6T7|B9S6T7_RICCO

Unused ProtScore: 8

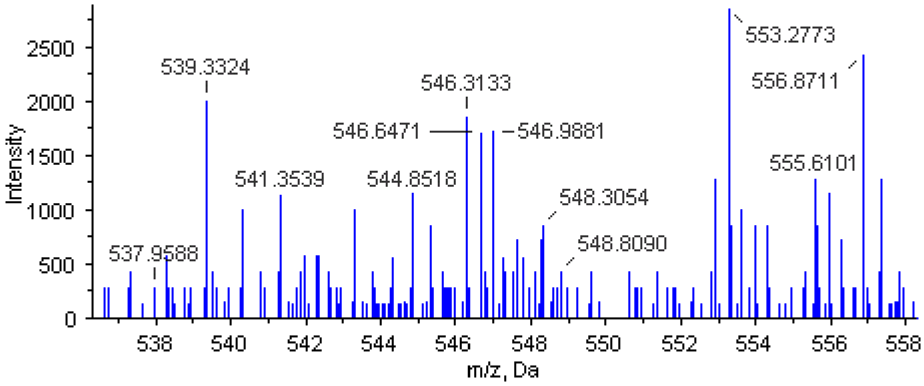
Seq Cov %: 9.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 1.53

116: 114=E5TL: D5TL= 1.67

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGGGNGASVDESSNGGDEVNVNIRCSNGSKFSVGISLSESVETFKTVLAGKCDVPADQQRLIYKGRILK

DDQTLQSYGLEADHTVHLVRGFAPAAAANTAPPSNTGGSNPASTNTRAVGSNEGGALGGSDLGLFPGMR

LNGLGGSAGLFGAGLPEFEQVQQQLTRNPNIMREIMNTPVVQNLMNNPEIMRNLIMNNPQMR**EIIDRNP**

ELAHILNDPSTLRQTLEAARNPELMREMMRNTDR**AMSNIESSPEGFNMLR**RMYETVQEPFLNATTMAGN

TGGDSANPFAALLGNQAGNQASDATTNPSIASSESTTGSPAPNTNPLPNPWTATGTGGALNNTARSSNT

GDARPQTPVGLGGLGLPEFDSMFGAMPDSNVMSQMLQNPAISQMMQSLLSNPQYMNQMLGSNPQFRSML

DSNSQFREMMQNPEFLRQLTSPETMQQLLTFQQALLSQFGRQQSNQEPGQTGAGTGTPNNMGLDMLMNM

FGGLGAGSLAVPNRSNVPPEELYATQLSQLQEMGFFDTQENIR**ALIATAGNVHAAVER**LLGNSGQ

Protein No.: I-269

Protein name and Species: **2,3-bisphosphoglycerate-independent phosphoglycerate mutase OS=Populus trichocarpa GN=POPTRDRAFT_825441 PE=4 SV=1**

Accession: **tr|B9IGY9|B9IGY9_POPTR**

Unused ProtScore: **7.99**

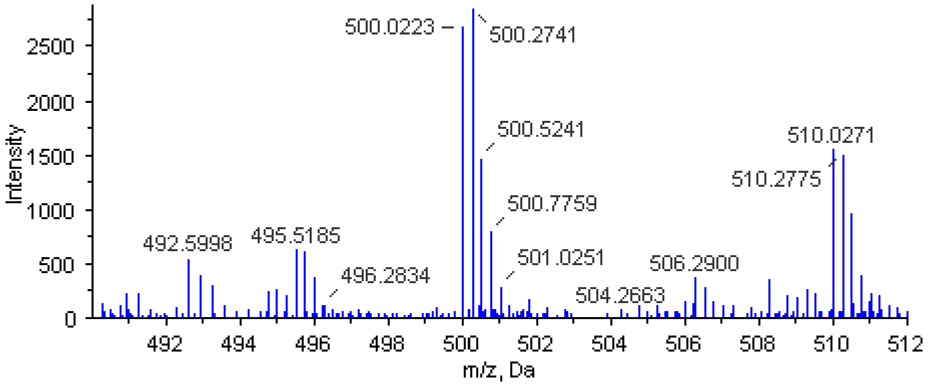
Seq Cov %: **7.5**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.61

116: 114=E5TL: D5TL= 0.57

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGSPGQNAWKLADHPKLPKGKTIAMVVLDGWGEAKPDQYNCIHVAHTPTMDSFKTTAPEKWRLIKAHGT
AVGLPSEDDMGNSEVGHNALGAGRIFAQGAK**LVDLALASGKIYDGEGFK**YIKECFDNGTLHLIGLLSDG
GVHSR**LDQLQLLLK**GAVENGAKRIRVHILTDGR**DVLDGSSIGFVETLEK**DLSNLREKGIDAQIASGGGR
MYVTMDRYENDWDVVKRGWDAQVLGEAPYKFRNAVEAVKKLREEPKANDQYLPPFVIVDESGNPVGPIK
DGDAVVTFNFRADRMAMLAK**ALEYEDFDKFDR**VRVPK**IHYAGMLQYDGELK**LPSHYLVSPPEIDR**TSGE**
YLVHNGIRTFACSETVKFGHVTFFWNGNRSGYFNQEMEEYVEIPSDV**GITFNVQPK**MK**AIEIAEK**ARDA
ILSGKFDQVR**VNLPNGDMVGHTGDIEATVVACK**VADDAVKMIIDAIEQVGGIFVITADHGNAEDMVKRD
KSGKPLLDKNGNLQILTSHTLQPVPIAIGGPGLAPGARFRNDVPTGGLANVAATVMNLHGFEAPSDYEP
TLIEVVDN

Protein No.: I-278

Protein name and Species:

26S proteasome non-atpase regulatory subunit, putative OS=Ricinus communis GN=RCOM_0974240 PE=4 SV=1

Accession: tr|B9SXW5|B9SXW5_RICCO

Unused ProtScore: 7.82

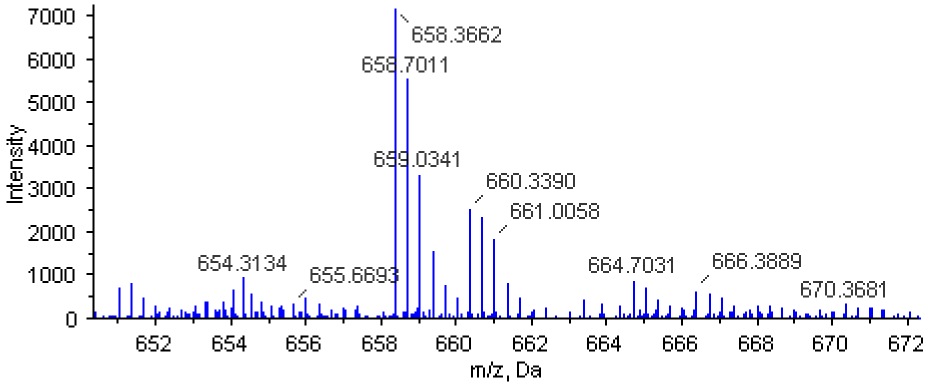
Seq Cov %: 20.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.58

116: 114=E5TL: D5TL= 0.62

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MVLEATMICIDNSEWMRNGDYNPSRFHAQADAVNLICGAK**TQSNPENTVGVLTMAGK**GVR**VLVTPTSDL
GK**ILACMHGLEIGGEMNLAAGIQVAQLALKHRQNKKQQQRIIVFAGSSIKHDKKALEMIGKKLKKNNVA
LDIVDFGEEDDEKAEKLEALLAAVNSNDTSHIVHVPPGPSALSDVLISTPVFTGDGEGGSGFAAAAAAA
AAGGVSGFEFGVDPNLDPELALALR**VSMEEER**ARQEAAAKKAAEEAAKQEK**GGEQPSSSQDATMTESAS
VTASEADNKR**HDLTNEENALLQQALAM**SMDDPASSQELR**DTDMSEAAADDPELALALQLSVQDSPKDSG
NPTDMSKLLADQSFVSSILASLPGVDPNDPSVK**DLLASMQSQSEPQEK**KDEDKPKEEK

Protein No.: I-279

Protein name and Species:

FAS-associated factor 2 OS=Populus trichocarpa GN=POPTRDRAFT_554543 PE=4 SV=1

Accession: tr|B9GXV5|B9GXV5_POPTR

Unused ProtScore: 7.78

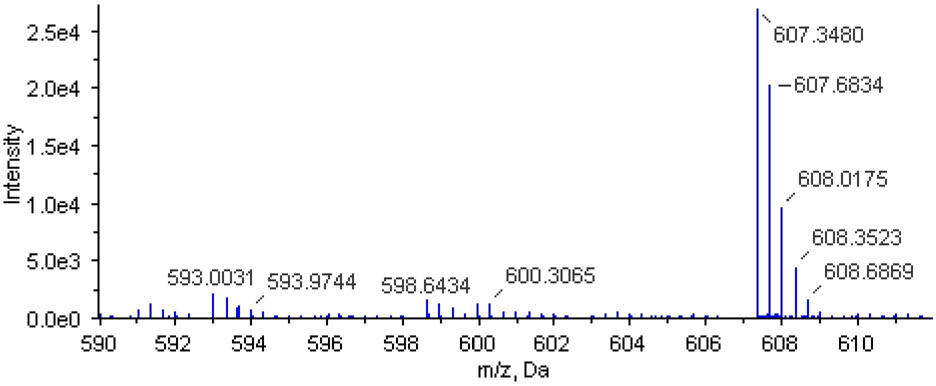
Seq Cov %: 14.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.47

116: 114=E5TL: D5TL= 0.67

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MVDVADKLAYFQAITGLEDPDLCTQILQAHNWDLELAISSFTSNHNNDPLSYSSSTATATTSTVVEPPI
SSIHRSDSTAIAPVAPPPPGLGWKIITLPISIVSGSLRLISGAVGFGFWAAGSIFSYSLGFIGFSSNSG
RGGDSSAQLVTVSAASREALEFIAQFERDYGGSGSSSRPNFVGEGFMDALTRSRNSFKLLFVYLHSPDH
PDTPAFCEGTLCSEVFSAFVNENFVAWGGSLRGSEGFKMSNSLKASR**FPFCAVVMPATNQRIALLQQVE**
GPKSPEEMLMTLQRVLEESAPVLVAARLEAEERTTNMR**LREEQDAAYR**AALEADQARERQLREEQERLE
REAAEAERKRKEEEEAQERATREAAEKEAALARMRQEK**ALSLGAEPEKGPNVTQVLVR**FPTGERKERRF
HSTATIQSLYDYVDSLGCLDVENYSLVSNFPRVVYGTDKVSLSLKEAGLHPQASLFVELN

Protein No.: I-280

Protein name and Species:

Putative uncharacterized protein OS=Ricinus communis GN=RCOM_0799000 PE=4 SV=1

Accession: tr|B9RRX1|B9RRX1_RICCO

Unused ProtScore: 7.72

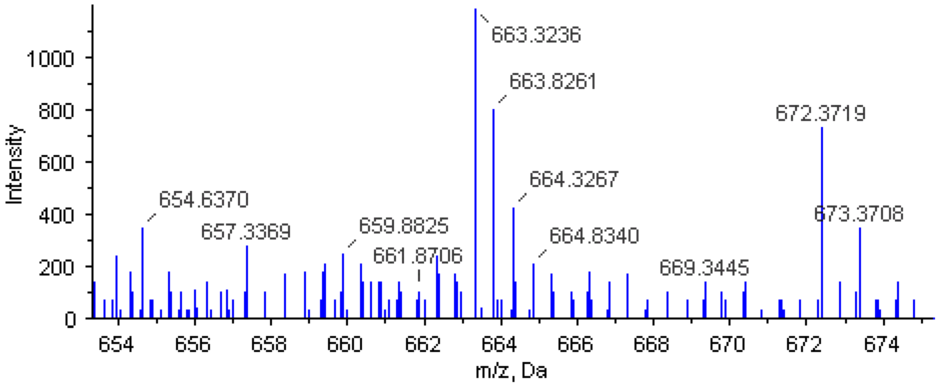
Seq Cov %: 3.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.34

116: 114=E5TL: D5TL= 0.50

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MARFYSSVTLFFNFAIIITTTLISNPNFVISSNNVHTSFSIIDYDSNLFHQDYSPPSPPPPPPHAPSVS
CTDDLGGIGSLDTTCRIISNVNLTRDVYIAGKGNFYIHPGVSFNCLSFGCSVTINITGNFTLSINASIV
TSSFELVAYNASFSNNSVVNTTGLAGNPPPQTSGTPQGIDGAGGGHGGR**GACCLVDDK**KLPEDVWGGDA
YSWSSLQIPNSYGSRGGSTSKEVNYGGGGGGKVKFTISEYLVVDGGILADGGDGGSKGGGGSGGSIFIK
AYKMTGSGR**ISACGGSGFAGGGGGRVSVDIFSR**HDDPQIFVHGGSSF**GCPENAGAAGTLYDAVPR**SLIV
SNHNMSTDTETLLLDFPYQPLWTNVYYVRNHARATVPLLWSRVQVQGQISLLCHGVLSFGLAHYASSEFE
LLAEELLMSDSVIKVYGALRMTVKIFLMWNSKMIVDGGEDTTVTTSWLEASNLIVLKESSVIQSNANLG
VHGQGLLNLSGPGDSIEAQRLVLSLFYSIHVGPGSVLRGPLQNATSDAVTPRLYCELQDCPIELLHPPE
DCNVNSSLSFTLQICRVEDITVEGLIKGSVVHFHRARTVSVLSSGRISASGMGCTGGVGRGHVLENGIG
SGGGHGGKGGLGCYNGSCIEGGMSYGNVELPCELGSGSGDESSAGSTAGGGIIVMGSLDHPLSSLSVEG
SVRADGESFQQTVKLGKLTVKNDTTGGPGGGSGGTILMFLHTLDLSESAVLSSGGGYGSQNGAGGGGGG
RIHFHWSDIPTGDVYQPIASVKGSILFGGGTGRDEGCAGENGTVTGKACPKGLFGVFCEECPAGTFKNV
TGSERSLCHPCPANELPHRAVYVAVRGGIAETPCPYKCISDRFHMPHCYTALEELIYTFGGPWLFCLLL
VALLILLALVLSVARMKFVGVDELPGPAPTQHGSQIDHSFPFLESLNEVLETNRAEESQNHVHRMYFMG
PNTFSEPWHLPHTPPEQIKEIVYESAYNSFVDEINAITAYQWWEGAMYSILSALLYPLAWSWQQWRRRI
KLQKLREFVRSEYDHACLRSCRSR**ALYEGLK**VAATPDLMLAYLDFFLGGDEKRTDLPPRLHQRFPMSII
FGGDGSYMAPFSIQSDNILTSLMSQTVPPTTWYRMVAGLNAQLRLVRRGRLRVTFRSVIKWLETHANPA
LRIHGIRVDLAWFQATACGYCQYGLLVYAIEEETGESIDGGKQTLQESRENYTRRKKSYWGSIDTNNLQ
MLEEKRDIFCLLSFIIHNTKPVGHQDLVGLVISMLLLGDFSLVLLTLLQLYSISLVDVLLVLLILPLGI
LLPFPAGINALFSHGPRRSAGLARIYALWNVMSLINVVVAFVCGYVHYHSQSSSSKKFPFQPWNISMDE
SEWWIFPAGLVLCKILQSQLVNWHVANLEIQDRSLYSSDFELFWQS

Protein No.: I-281

Protein name and Species:

Glutamate decarboxylase, putative OS=Ricinus communis GN=RCOM_0112580 PE=3 SV=1

Accession: tr|B9SR96|B9SR96_RICCO

Unused ProtScore: 7.7

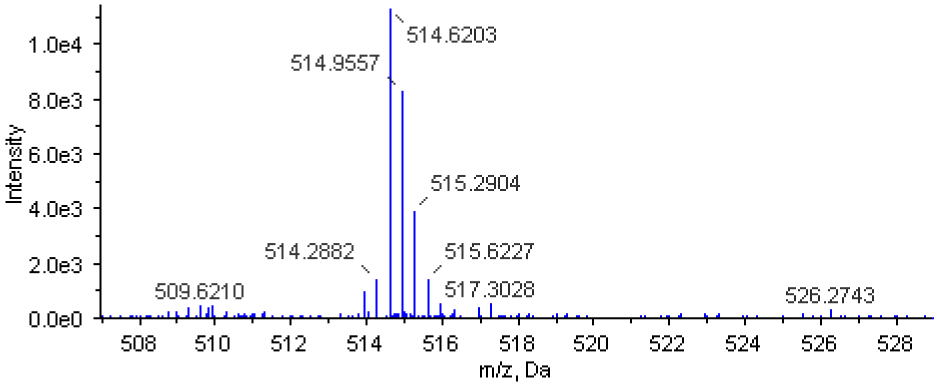
Seq Cov %: 12.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 3.25

116: 114=E5TL: D5TL= 0.90

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MVLSKTASESDVSVHSTFASRYVRASLPRFKMPESSIPK**EAAYQIINDELMLDGNPR**LNLASFVTTWME

PECDKLIMASINK**NYVDMDEYPVTTELQNR**CVNMIAHLFNAPLGDSETAVGVGTVGSSEAIMLAGLAFK

RKWQNKRKAEGKPYDKPNIVTGANVQVCWEKFARYFEVELKEVKLRDGYYVMDPVKAVEMVDENTICVA

AILGSTLNGEFEDVKLLNDLLTEKNKQTGWDTPIHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSGH

KYGLVYAGIGWVIWRNKDDLPDELIFHINYLGADQPTFTLNFSK**GSSQVIAQYYQLIR**LGYEGYRNIME

NCRDNMLVLKDGLEKTGRFTIVSK**DNGVPLVAFSLK**DNSSHNEFEISELLRRFGWIVPAYTMPPDAQHV

TVLRVVIREDFSRTFAER**LVLDIEK**VLHELDTLPSRLREKIAIVEEKEKNGTKAAKKSVIETQREITTI

WKKFVLEKKKMNGVC

Protein No.: I-284

Protein name and Species:

hydroxycinnamoyltransferase ; Quinate O-hydroxycinnamoyltransferase/shikimate O-hydroxycinnamoyltransferase OS=Populus trichocarpa PE=2 SV=1

Accession: tr|B2Z6Q5|B2Z6Q5_POPTR

Unused ProtScore: 7.66

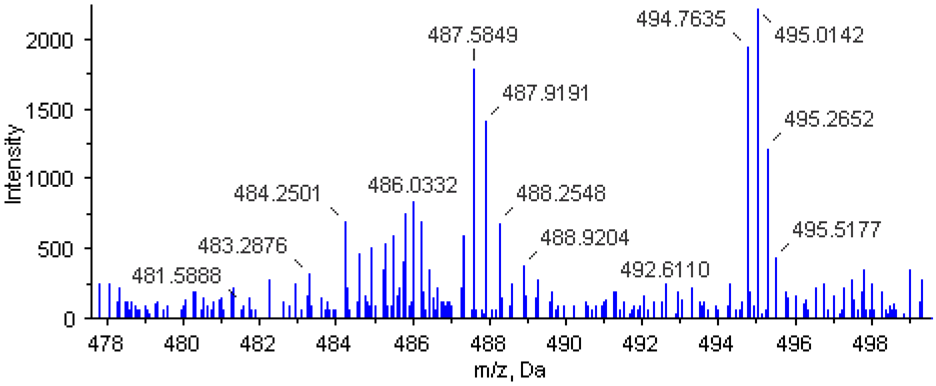
Seq Cov %: 15

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.38

116: 114=E5TL: D5TL= 1.00

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MIINVKESTMVQPAEETPRRGLWNSNVDLVVPR**FHTPSVYFYR**PTGASNFFDAKVLKEALSK**ALVPFYP**
MAGRLRRDDDGRIEIDCNAEGVLFVEAGTASVVADFGDFAPTLELKQLIPTVDYSGGISTYPLLVLQVT
YFKCGGVSLGVGMQHHAADGFSGLHFVNTWSDMAR**GLDLTIPPFIDR**TLLRAR**DPPQPAFHHVEYQPPP**
AMKTVLETSKPESTAVSIFKLTRDQLNTLKAKAKEGGNNIGYSSYEMLAGHVWRSACKARGLPDDQETK
LYIATDGRSRLRPTLPPGYFGNVIFTATPIAVAGEIQSKPTWYAAGKIHDSLVR**MDNDYLRSALDFLEL**
QPDLSALVRGAHTFR**CPNLGITSWVR**LPIHDADFGWGRPIFMGPGGIAYEGLSFIIPSSTNDGSLSVAI
SLQAEHMKLFEKFIYDIKE

Protein No.: I-289

Protein name and Species:

Eukaryotic translation initiation factor 2c, putative OS=Ricinus communis GN=RCOM_0476750 PE=4 SV=1

Accession: tr|B9SCN8|B9SCN8_RICCO

Unused ProtScore: 7.53

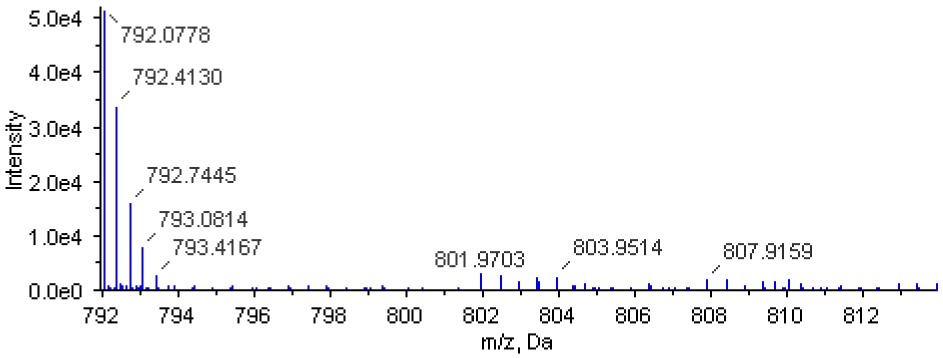
Seq Cov %: 7.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 1.50

116: 114=E5TL: D5TL= 1.39

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSHRGGGRRQESQRDRQSSATSPSFNRGGGGGRGGRGRGGAGSFYAQPAPPPAGSDFPSLSRPPTTSSR
AAAAPQAAPPSSSSRAPPAPAPAPAPPPAAAASTSTQIEKLTHGVEQLTTTAGAPTPSSSKEIRFPNRP
GYGSIGMKCVVKANHFLVDVADRDLRQYDVSITPELTSKKINRDVISQLIRMFRQSHLGNRRAAYDGRK
SLYTAGPLPFESKEFVVKLVESNKNAGSSVSSKKEREFKVAIKFASKPDIHHLKQFLIGRQMDCPQETI
QVLDIVLRETPSEKYTPVGRSFFSPDLGQKGELGDGIEYWRGYYQSLRPTQMGLSLNIDVSARSFYEPI
IVTDFVSKYLKLRDMSRPLSDQDRIKVKKALKSVKVQILHREYAKSYKVTGISNKPLNQIFFKLDDKST
DISVVQYFREKYNIGLKYTSLPALQAGSDAKPIYLPMELCKIVDGQRYSKKLNERQVTALLRATCQRPH
EREESIKQMVKRNSYNQDVLVRDEFGIQVK**EELTFVDAR**VLPAPMLNYHETGRESRVDPRCGQWNMINK
KMVNGGSVNFWTCVNFSLNINRDLPAEFCR**QLIQMCVSK**GMAFNPNPIIPISSAHPGQIGKTLNDIKRQ
CEAKLVKQLQLLIIILPDISGSYGIIKR**VCETELGIVSQCCQPR**QAAKLSKQYFENVALKINVKVGGRN
TVLNDAVQRRIPLVTDCPTIIFGADVTHPPPGEDSSPSIAAVVASMDWPEVTKYRGIVSAQAHR**EEIIQ**
DLYKSFQDPQGILKHSGMIRELFVAFRRETGMKPKRIIFYRDGVSEGQFSQVLLYEMDAIRKACASLEE
GYLPPVTFVVVQKRHHTRLFPVDRGQTDR**SGNILPGTVIDTK**ICHQREFDFYLNSHAGIQGTSRPTHYH
VLYDENHFTADNLQVLTNNLCYTFARCTR**SVSIVPPAYYAH**LAAFRARYYIEGEMSDGGSTSGKSTTGR
SKEVQPLPVIKDNVKDVMFYC

Protein No.: I-290

Protein name and Species:

Fructose-bisphosphate aldolase OS=Mesembryanthemum crystallinum PE=2 SV=1

Accession: tr|O04975|O04975_MESCR

Unused ProtScore: 7.51

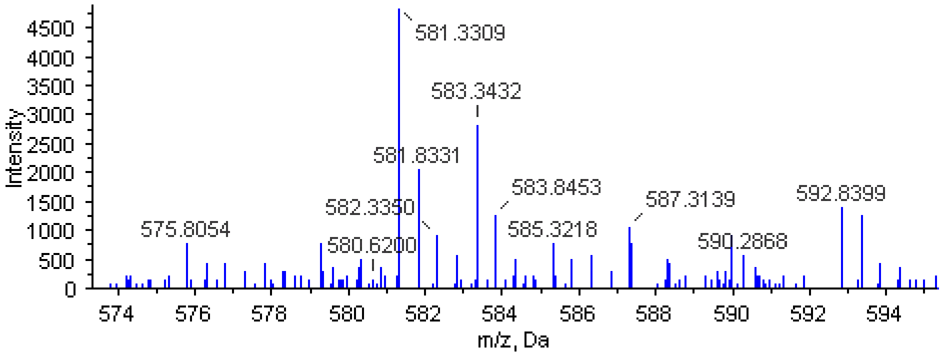
Seq Cov %: 21.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.66

116: 114=E5TL: D5TL= 1.37

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MTAYRGK**YADELIANAAYIGTPGKGILAADESTGTIGKR**FAGINVENVESNRRALRELLFTTPGAVQYL
SGVILFEETLYQKTAAGKPFVEVLKEGNVLPGIKVDKGVVELAGTNGETTTQGLDGLGARCAQYYAAGA
RFAKWRAVLKIGPTEPSPLAILENANGLARYAIICQENGLVPIVEPEILVDGPHDIDRCAEVTER**VLAA**
CYKALNDHHVLLEGTLLKPNMVTPGSESKKVAPEVIAEYTVRALQRTVPPAVPAVMFLSGGQSEEEATV
NLNAMNKLQGKKPWTLSFSYGRALQSSTLKAWSGKEENVEKAQAVFLARAKGNSEATLGKYQGGAGGAD
ASESLHVKDYKY

Protein No.: I-293

Protein name and Species:

Nuclear protein localization, putative OS=Ricinus communis GN=RCOM_0557110 PE=4 SV=1

Accession: tr|B9S3Y6|B9S3Y6_RICCO

Unused ProtScore: 7.44

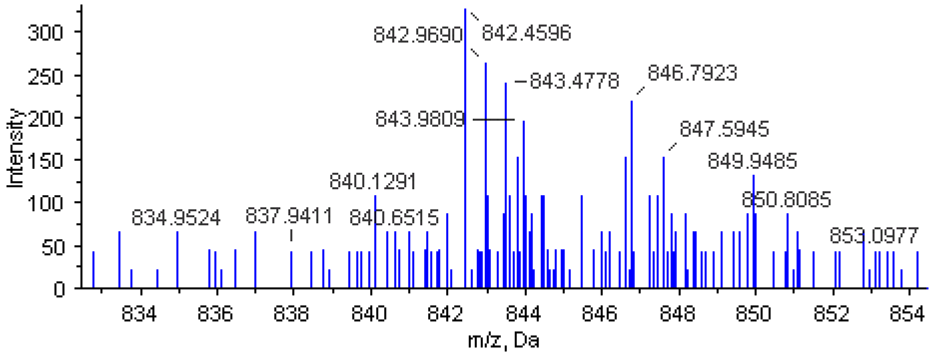
Seq Cov %: 18.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.11

116: 114=E5TL: D5TL= 0.68

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MMIRIRSRDGLER**VSVENPNITVSQLK**TLIQNQLNIPIQNQTLSTNQNLLLAKSPSDVLKFTDMSNPNT

PLSSLNITHGSILFLTYDGERTIAGPAVNPAGSFGRKMTMDDLIAKQMRITRQENPHCESVSFDRDCAN

AFQHIPMMVKLRFIIIYEPPQQGTEENLMLLRDPEEEKLVDAIAVGLGMRR**VGFIFTQTITQDK**KDYTL

SNR**EVLQAAELHAESELK**EWVTAIVKLEVNEDGGADVHFEAFQMSDMCIRLFKEDWFEKEIAEDSDPKL

SKMKKDVVVGGKDVR**EVDNDFFLVVVKILDHLGPLSSSFPIENR**INQVTKRALKSHLDRLKNLSFVKRI

SDFHLLLFLGRFLDVSDVPALAECVLTQTAVPEGYQLIIESVANS

Protein No.: I-297

Protein name and Species: **Nucleic acid binding protein, putative OS=Ricinus communis GN=RCOM_1326600 PE=4 SV=1**

Accession: **tr|B9S228|B9S228_RICCO**

Unused ProtScore: **7.32**

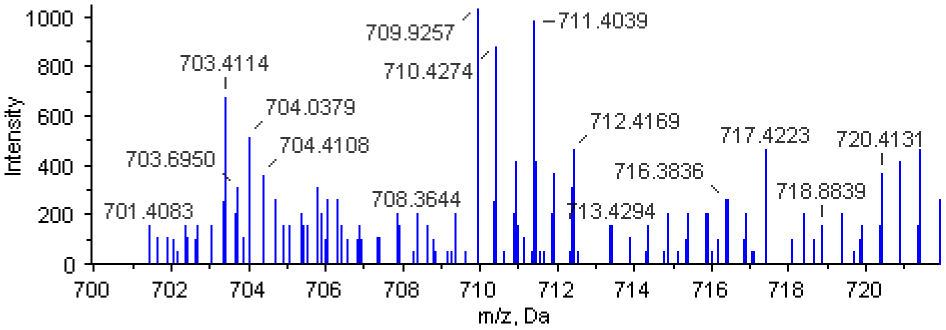
Seq Cov %: **21.9**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.50

116: 114=E5TL: D5TL= 0.64

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAITTVK**VSNVSLGATEQDIK**EFFSFSGDIDYVELLGDNERSQIAYVTFKDQQGAETAVLLSGATIVDQSVTIELAPDYKLPAAASVPTTATESSTASGAESAFQK**AEDIVSSMLAK**GFILGKDAVNKAKAFDEKHQFTSTATSKVASLDEKIGLTEK**ISAGTTLVNDK**VREVDEKFRVSETTK**SAFAAAEQTVSNAGSAIMK**NR**YVLTGASWVTGAFNR**VAKAAGEVGQKTKEKVLAEEEQNQVAEGYTQIHGTDSPNMSEQMSKSSH

Protein No.: I-299

Protein name and Species:

Proteasome subunit beta type OS=Populus trichocarpa GN=POPTRDRAFT_814139 PE=3 SV=1

Accession: tr|B9HUT6|B9HUT6_POPTR

Unused ProtScore: 7.28

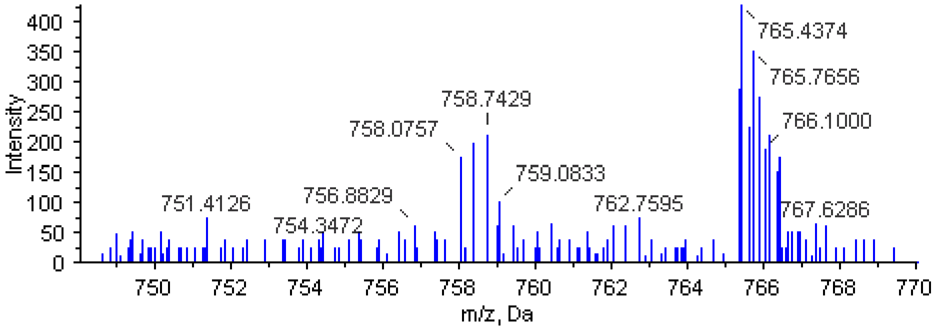
Seq Cov %: 28.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 1.57

116: 114=E5TL: D5TL= 0.84

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MECVFGLVGDGFVIVASDTSAVNSILVHKTNEDKIMKLDSHKLVAASGESGDR**VQFTEYIQKNVALYQF**

RNGIPLTTAAAANFTRGELATALRKNPYMVNILLAGYDK**ETGPSLYYIDYIATLHK**VDRGAFGYGSYFC

LSMMDRHYHSGMSVEEAVELVDKCITEIQSR**LVVAPPNFVIK**IVDRDGAREYAWRESVKDTPTAQPEAL

GV

Protein No.: I-306

Protein name and Species:

Ganglioside induced differentiation associated protein, putative OS=Populus trichocarpa GN=POPTRDRAFT_765804 PE=4 SV=1

Accession: tr|B9HIC5|B9HIC5_POPTR

Unused ProtScore: 7.1

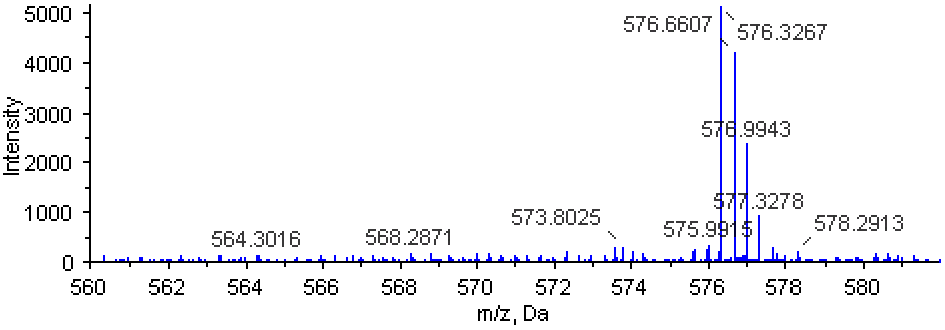
Seq Cov %: 12.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 2.78

116: 114=E5TL: D5TL= 1.59

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MYQRVPAAVTTR**GGSPTDNGDSVVTLDQVPR**WSDAESRSSFGYDNEDPSFTNPFFPDPLTSPSEGESSS
CGMVSR**FPVDHEINSK**IYLWRGNPWNLEVDAVVNSTNELLDEAHSSPGLHAAAGPGLAEECTTLGGCRT
GMAKVTNAYDLPARRVIHTVGPKYAMKYHTAAENALSHCYRSCLELLIENGLQSIAMGCIYTESKNYPR
EPAAHVAIRTVRRFLEKQKNKITAVVFCTTTSTDTEIYKRLLPLYFPREKHEEEVAIAK**LPADVGDENG**
ETIIDERKIRIKPLPKKNIPRPSQPLADLPVIDVGLVRRNSSYLDSYLDPAFMSVIKDPDQRRKEQWEK
TAQAQSGWNCAKIFGFGDLGGPTLSAAEEYSLHSRYLAK**ANSLNLSEIAEMK**IVYRGGVDSEGRPVMVV
VGAHFLLRCLDLERFVLHVVKEFEPLIQKPYTIVYFHSAASLQVQPDLGWIRRLQQILTRKHQRNLHAI
YVLHPNFHLKATIFALQV**FVDK**VTWKKVVYVDRLVQLFRYVPREQLTIPDFVFQHDLEVNGGKGLIVDP
RTKYVYHRP

Protein No.: I-310

Protein name and Species:

40S ribosomal protein S2, putative OS=Ricinus communis GN=RCOM_1577790 PE=3 SV=1

Accession: tr|B9RIC4|B9RIC4_RICCO

Unused ProtScore: 7.05

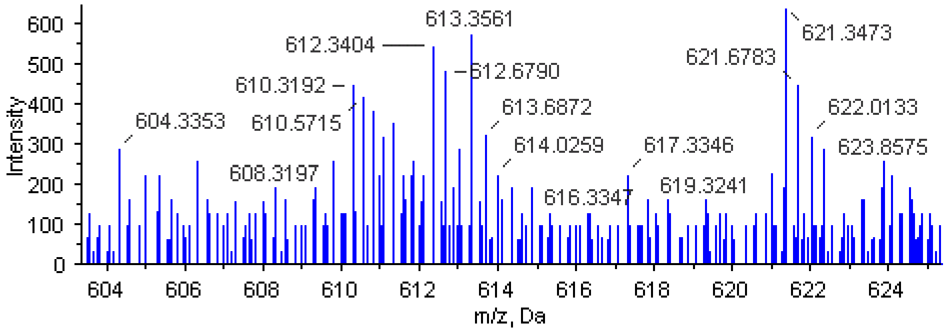
Seq Cov %: 18.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 1.51

116: 114=E5TL: D5TL= 1.12

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSERPGGGERGAFRRGFGGAGRGDRGGRGRRRPRREEEEKWVPVTKLGRLVKEGKIR**SLEQIYLHSLPI**
KEHQIIDTLVGPSLKDEVMKITPVQKQTRAGQRTRFKAFVVVGDGNGHVGLGVKCSKEVATAIRGAIIL
AKLSVIPVRRGYWGNKIGKPHTVPCKVTGKCGSVTVRMVPAPRGAGIVAARVPKK**VLQFAGIEDVFTSS**
RGSTK**TLGNFVK**ATFDCLLKTYGFLTPDFWRETHFTKSPFQEYTDLLGKPTKVLIEDVERVDA

Protein No.: I-314

Protein name and Species:

DNA damage-inducible protein OS=Populus trichocarpa GN=POPTRDRAFT_744891 PE=2 SV=1

Accession: tr|A9PEP6|A9PEP6_POPTR

Unused ProtScore: 6.98

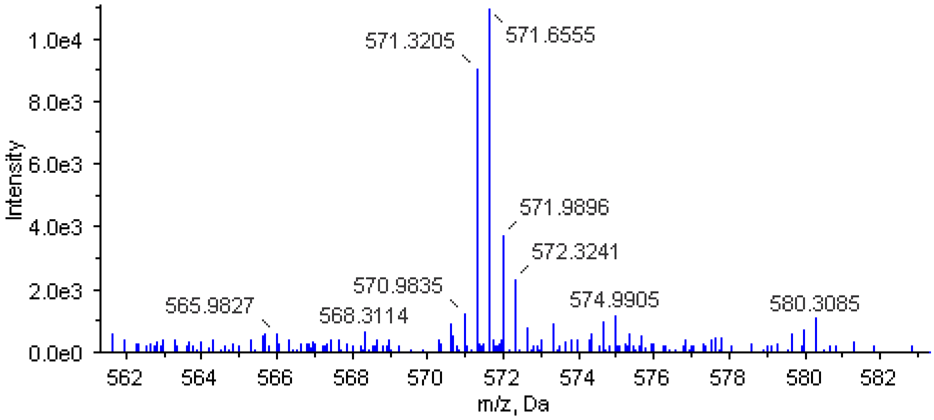
Seq Cov %: 13.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.47

116: 114=E5TL: D5TL= 0.52

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MRITVMTADEQIISLEVDPHESVENVK**ALLEVETQVPLQQQQLLYNGR**EMRNNEK**LSALGVK**DEDLVMM
VSNAAALSAPSNNLGLNPDGSAMNPGAFQQQLRNDSNTMAQLFQADPELAQVILGNDLNK**LQDLLR**QRH
RQRSELHRQQEEEFALLEADPFDVEAQKKIEAAIRQK**GIDENWAAALEYNPEAFAR**VIMLYVDMEVNGV
PLK**AFVDSGAQSTIISK**SCAERCGLLRLLDQRYKGIAHGVGQSEILGR**IHVAPIK**IGNIFYPCSFMVLD
SPNMEFLFGLDMLRKHQCIIDLKENVLR**VGGGEVSVPFLQEK**DIPPRFLDEERYSKEASSSGNPVTSGK
AEKKNDPPAMGQSSGVARSSVTQGPDFEAKVAK**LVELGFGR**EAVIQALKLFDGNEEQAAGFLFGG

Protein No.: I-315

Protein name and Species:

Putative uncharacterized protein OS=Vitis vinifera GN=VIT_18s0001g08370 PE=3 SV=1

Accession: tr|F6H158|F6H158_VITVI

Unused ProtScore: 6.98

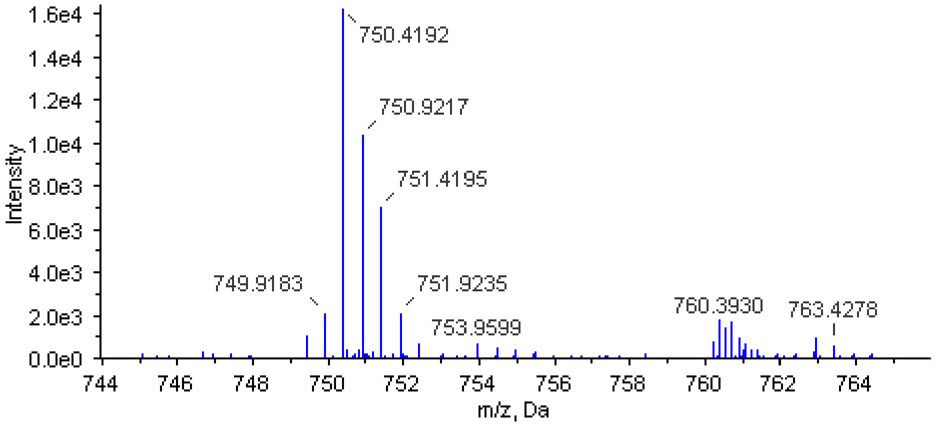
Seq Cov %: 5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.44

116: 114=E5TL: D5TL= 0.60

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MRRIWPCCFTRRVSNTHQKAEDIQRSIGTMENPKEGNADHGVSEKQNESTIKSRDSLSSNIILNHDFSR
GLHSWNLNCCNGSVVSAESGFLEGISVKSGGNYAVITNRKECWQGLEQDITSRVSLGSTYSVSACVGVS
GSLQGSAVVQATLKLEYQGSATSYLFIGRTSVSREQWKK**LEGTFSLSTMPDR**VVFYLEGPSPGLDLLIE
SVVIFCSSPTEEESSSTRCAAAGDENIILNPIFEDGVNNWSGRGCKILLHDSMGGGKIVPQSGKFFASA
TERTQSWNGIQQEITGRVQR**KLAYEVAAVVR**IFGNNVTSADVRVTLWVQTPNLREQYIGVANSQATDKD
WIQLQGKFLLNASPSRVVIYLEGPPPGTDILVNSLVVKHAEKIPPSPPPVIEDPAFGINTIQNSNLNDG
SNGWFPLGSCTLSVATGSPRILPPMARDSLGAHNPLSGHYILVTNRTQTWMGPAQMITDRVKLYLTYQV
SAWVRIGPGATAPQNVNVALGVDSQWVNGGQANVSDDRWYEIGGSFRIEKQPLKVMVYVQGPASGVDLM
VAGLQIFPVDRHARFRHLKKETDKIRKRDVILNFSGSGTGTSIGTFVKVRQTQNSFGFGSCVSRTNIDN
EDFVDFFVK**NFNWAVFGNELK**WYWTESQQGNFNYRDADELLDLCKSHNMETRGHCIFWEVEGTVQPWVK
SLNKNDLMTAVQNRLTGLLTRYKGKFRHYDVNNEMLHGSFYQDRLGKDIRANMFKTANQLDSSAALFVN
DYHVEDGCDTRSSPEKYIEQVIDLQKQGAPVGGIGIQGHIDSPVGPIVCSALDKLGVLGLPIWFTELDV
SSINECIRADDLEVMLREAFAHPAVDGIMLWGFWELFMSRNNAHLVNAEGEINETGWRYLALRKEWLSH
AHGHIDEQGEFMFRGFHGSYVVEIGTGSKKISKTFVVDNGESPLVVSIGL

Protein No.: I-321

Protein name and Species:

Ubiquitin-protein ligase, putative OS=Ricinus communis GN=RCOM_1154930 PE=4 SV=1

Accession: tr|B9SG36|B9SG36_RICCO

Unused ProtScore: 6.86

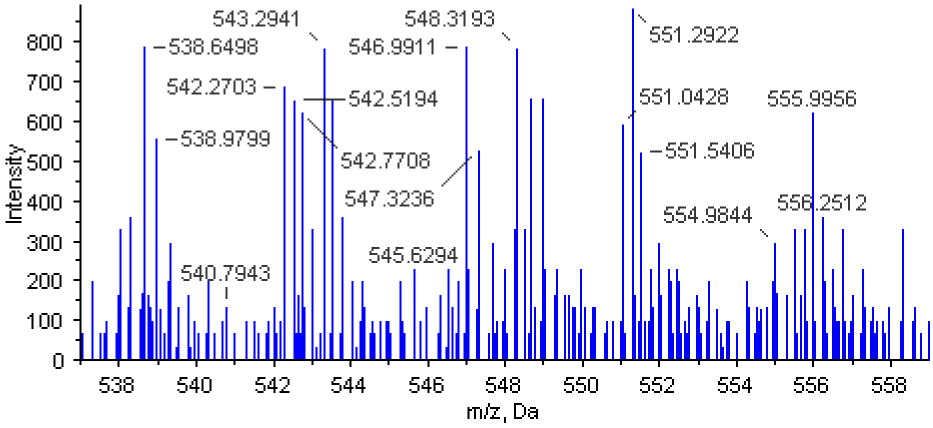
Seq Cov %: 6.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 1.80

116: 114=E5TL: D5TL= 1.08

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSVMGYNLAGDVTSANLFHKESSVMEISLLKALLSNISSFLHLSSIDNICSDLVQKCYQK**AEEILK**LLK
PILDAIVDSEIASDEVLTKAFDELGQSVDELRELFENWQPLSSKVFFVLQIESLISKIRTLGLDIFQLL
KSSHEHLPDELSTSSLEEILIEAVALEKLKENAEQAEKPREAELFDQMISLSQTCSHVPIPADFCCPLS
LELMTDPVIVGSGQTYERAFIKNWIELGLTVCPKTRQTLAHTNLIPNYTVKALIANWCESNNVKLPDPV
KSVSFNQPSALLIHAESGTPRGSHGFYSRGNQPMSPESTRSTDSPDRNWISSSVHRESTSPCHPRSTSD
SSLSGIVGNEQGLDMARISLASSEERSVNLEGRNRDSGVRHSVSPSRNEVSNAVRVGEPIAQSHSRNAS
ASSINASFSQGAQVDTNDSSEVLNHLTSYSSDNSGEVKAETQASTALNSPRPHREPEFAPRFIETRSRS
QTIWRRPSDRLIPRIVSSPAIETRADLSGVETQVRNLVEDLKSDSIDVQRAATAELRLLAKHNMDNRIV
IANCGAINILVNLLRSADAKIQENAVTALLNLSINDNNKTAIANADAIGPLIHVLETGSPEAKENSAAT
LFSLSVIEDNKVRIGRSGAVGPLVDLLGNGTPRGKKDAATALFNLSIFHENKARIVQAGAVK**HLVELMD**
PAAGMVDKAVAVLANLATIPEGRTAIGQEGGIPVLVEVVELGSARGKENAAAALLQLCTNSNRFCNTVL
QEGAVPPLVALSQSGTPRAKEKAQALLSFFRNQRHGNARG

Protein No.: I-322

Protein name and Species:

alanine aminotransferase OS=Populus trichocarpa GN=POPTRDRAFT_1073568 PE=4 SV=1

Accession: tr|B9GXZ6|B9GXZ6_POPTR

Unused ProtScore: 6.86

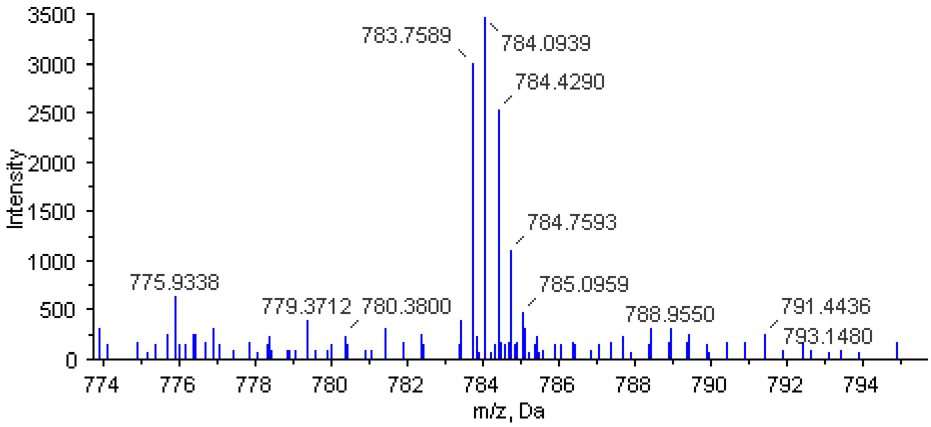
Seq Cov %: 20.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.44

116: 114=E5TL: D5TL= 2.25

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MPPVSLDNINPKVLKCEYAVRGEIVTLAQALQEELKSKPGSHPFDEILYCNIGNPQSLGQQPITFFREV
LALCDHPSILDR**SETQGLFSADAIER**AWQILDQIPGR**ATGAYSHSQGIK**GLRDTIAAGIEARDGFPADP
NDIFLTDGASPAVHMMMQLLIRSEKDGILCPIPQYPLYSASIALHGGALVPYYLDEATGWGLEVSELKK
QLADAKSKGITPR**ALVVINPGNPTGQVLAEDNQR**GIVEFCK**QEGLVLLADEVYQENVYVPEK**KFDSFKK
VARSMGYGEKDISLVSFQSVSKGYYGECGKRGGYMEVTGFGPEIREQIYKVASVNLCSNISGQILASLV
MSPPK**VGDESYESYSAEK**DGILSSLARRAKTLEDAFNNLEAVTCNKAEGAMYLFPCICLPEKAIKAAEA
AKTAPDNFYCRRLLNATGIVFVPGSGFGQLPGTWHFR**CTILPQEDKIPAVVSR**LTEFHKSFMDEFRD

Protein No.: I-324

Protein name and Species:

ATP-citrate synthase alpha chain OS=Vitis vinifera GN=VITISV_017316 PE=4 SV=1

Accession: tr|A5AQP2|A5AQP2_VITVI

Unused ProtScore: 6.85

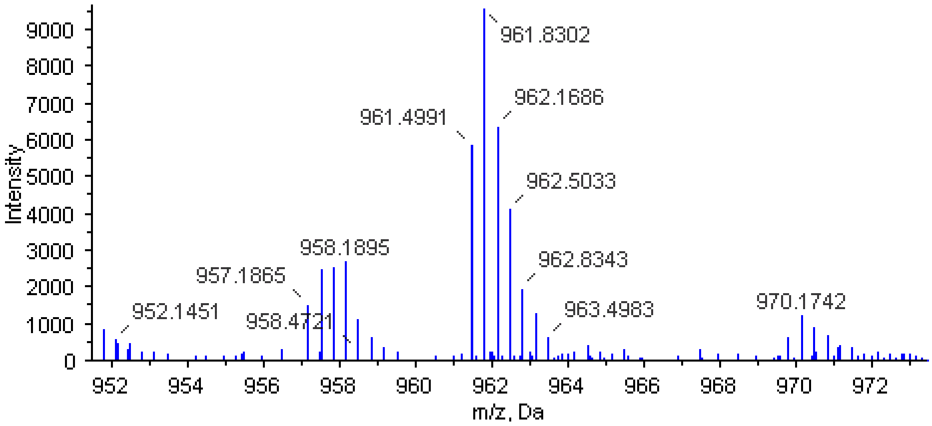
Seq Cov %: 19.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.51

116: 114=E5TL: D5TL= 0.71

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MARKKIREYDSKRLLKEHLKRLVGIDLQICSAQVTEATDFAELTNKEPWLSSTRLVVKPDMLFGKRGKS
GLVALNLDLAQVAEFVKARLGVEVEMGGCKAPITTFIVEPFVPHDQEYYLSIVSDRLGCTISFSECGGI
EIEENWDKVKTINLPTEKPMTPETCAPLIATLPLEVRGKIGDFIKGVFAVFQDLDFSFLEMNPFTLVNG
EPYPLDMRGELDDTAAFKNFKTWGNIEFPLPFGRVLSPTEGYIHLLDEKTSASLKFTVLNPKGRIWTMV
AGGGASVIYADTVGDLGYASELGNYAEYSGAPNEEEVLQYARVVLDCATADPDGRKRALLIGGGIANFT
DVAATFNGIIRALKEKESKLKASRMHIYVRRGGPNYQTGLARMRALGEELGIPLEVYGPEATMTGICKQ
AIDCIMSTA

Protein No.: I-327

Protein name and Species:

Heat shock protein 70 OS=Hevea brasiliensis GN=HSP70 PE=2 SV=1

Accession: tr|B2MW33|B2MW33_HEVBR

Unused ProtScore: 6.81

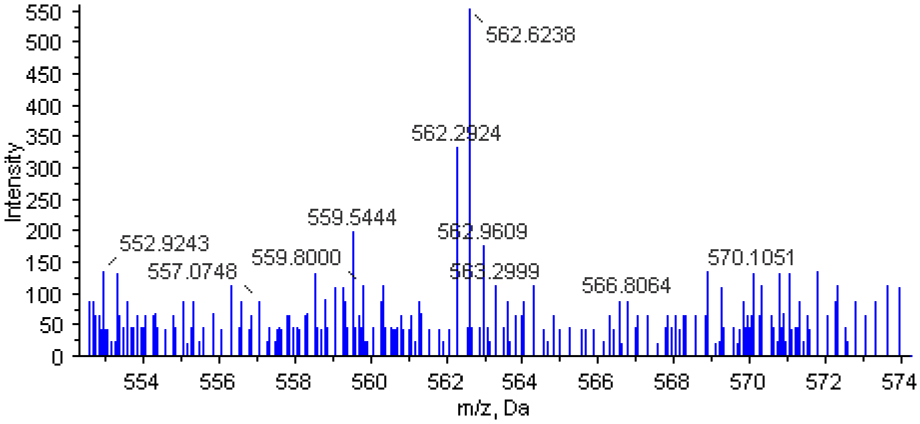
Seq Cov %: 33.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.65

116: 114=E5TL: D5TL=0.70

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAPKTEGKAIGIDLGTTYSCVGVWQNDR**VEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVAMNPQNT**
VFDAKRLIGRR**FSDPSVQSDMK**HWPFK**VISGPGDKPMIVVQYK**GEEK**QFAPEEISSMVLTK**MK**EIAEAY**
LGQTVKNAVITVPAYFNDSQRQATKDAGAIAGVNVMR**IINEPTAAAIAYGLDKK**GSSTGEKNVLIFDLG
GGTFDVSLLTIEEGIFEVK**ATAGDTHLGGEDFDNRLVNHFVAEFK**GKHKKDISTNARALRRLRTARERA
KRTLSSTSQTTIEIDSLYEGIDFYATITR**ARFEELNMDLFR**KCMEPVEKCLRDSKIDK**SQVHDVVLVGG**
STRIPK**VQQLLQDIFNGK**ELCK**SINPDEAVAYGAAVQAAILSGEGDEK**VQDLLLLDVTPL**SLGIETAGG**
VMTVLIPRNTTIPTKKEQIFSTYSDNQPGVLIQVYEGERARTK**DNNLLGKFELTGIPPAPR**GVPQINVC
FDIDANGIVNVSAEDKTAGVKNK**ITITNDK**GR**LSKEEIERMVQEAEK**YKAEDEEVKKKVEAKNS**LENYA**
YNMRNTVKDDKFAGKLAPADKGKIEKAIDETIEWLDRNQLAEVEEFEDKLKELEG**LCNPIIAK**MYQGGA
GGDVPVGGAEMPNSNYGKTSSGGSGAGPKIEEVD

Protein No.: I-328

Protein name and Species:

Esterase D, putative OS=Ricinus communis GN=RCOM_0893450 PE=4 SV=1

Accession: tr|B9SCD6|B9SCD6_RICCO

Unused ProtScore: 6.77

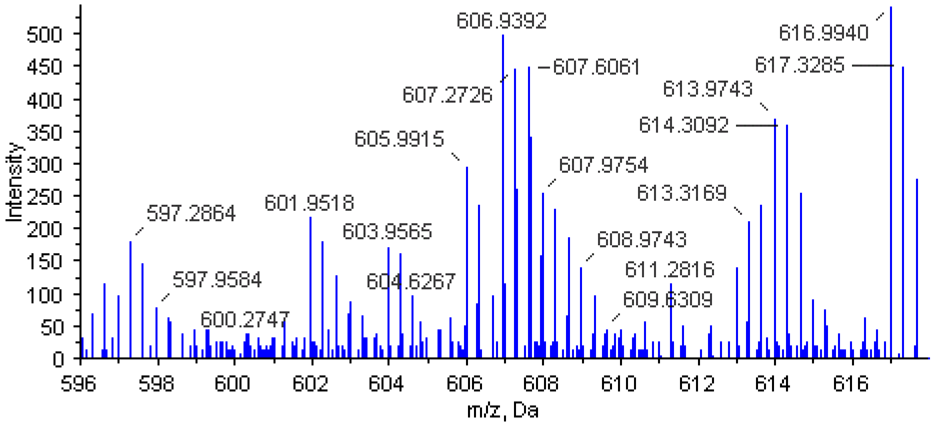
Seq Cov %: 17.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.32

116: 114=E5TL: D5TL= 2.32

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MKSVAQRCLEDTIKDTDISILYFLSGLTCTDENFIIKSGAQR**AASSEGVALIAPDTSPR**GLNVEGEADS
WDFGVGAGFYLNATQEKWKNWRMYDYVVK**ELPKLLSDNFPQLDTSR**ASLSGHSMGGHGALTIYLKNLDK
YKSVSAFAPISNPINCPWGQKAFTNYLGSSKGDWEEYDATSLVSKFHDVSATILIDQGEDDKFLHDKQL
LPQK**FEEACRSANVPLLLR**MQPGYDHSYFFISTFIDDHIRHHAQALNL

Protein No.: I-329

Protein name and Species:

Predicted protein OS=Populus trichocarpa GN=POPTRDRAFT_647799 PE=4 SV=1

Accession: tr|B9H2B8|B9H2B8_POPTR

Unused ProtScore: 6.77

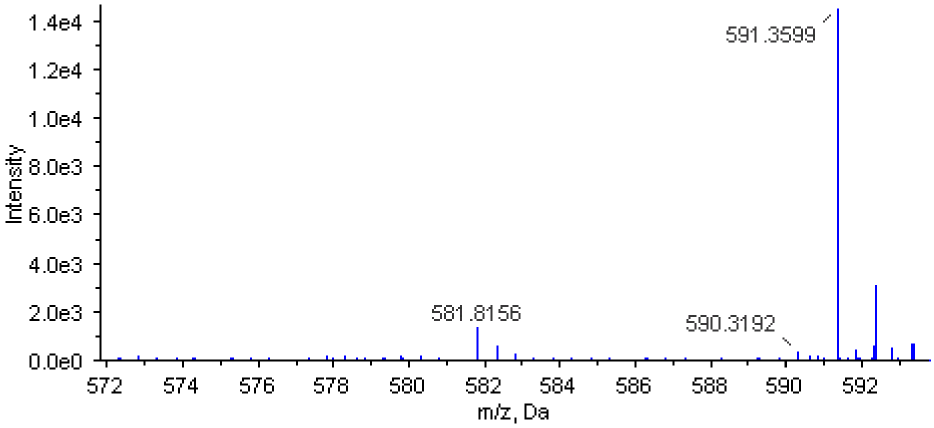
Seq Cov %: 30.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.23

116: 114=E5TL: D5TL= 0.75

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MTSQHIATHREKAEIHTGESLCKQKSLELLEEIH**LPMGLLPLDDIVEVGYNR**TTGFVWLKQKKRKDHRF
LKIGRQVSYDT**EVTAFVENR**RMRRLTGVKTKELLFWVSISDIYVDEKDLE**KITFGNPTGISRTFPVSAF**
ELEEEKK

Protein No.: I-335

Protein name and Species:

L-asparaginase, putative OS=Ricinus communis GN=RCOM_1467530 PE=4 SV=1

Accession: tr|B9RLJ0|B9RLJ0_RICCO

Unused ProtScore: 6.7

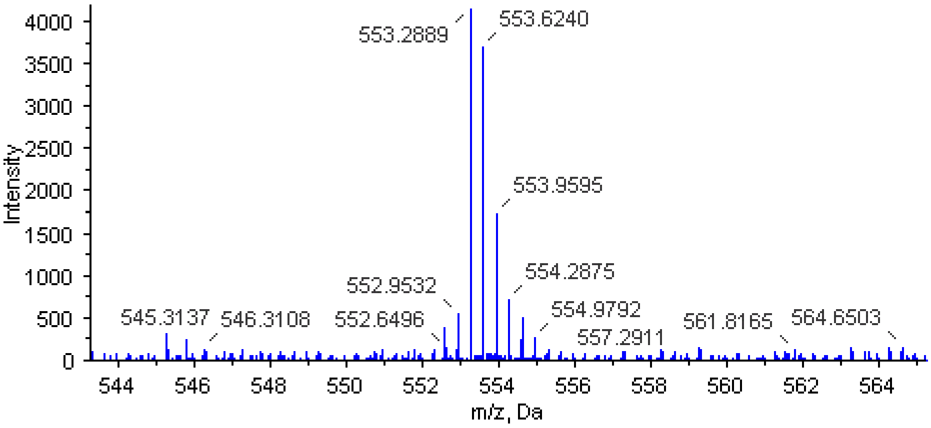
Seq Cov %: 24.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.37

116: 114=E5TL: D5TL= 0.53

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGWAIALHGGAGDIPLNLPPERRLPREAALRHCLEIGVAALQAQK**HPLDVVELVVRELENHPNFNAGK**G
SVLTTEGTVEMEACIMDGKTKKCGAVSGLTTVVNAISLARLVMEKTPHIYLAFDGAEAFAR**EQGVETVD**
SSQFVTPENVERLKQAKEANR**VQIDYTQPIQK**NEETQNPNADGDSQIG**TVGCVAVDTNGNLASATSTGG**
LVNKMVGR**IGDTPIIGAGTYANNLCAVSATGK**GEFIIRGTVARDVAALMEYKGLSLMEAAAYVVEQCVP
RATVGLVAVSATGEVTMPFNTTGMFRACATEDGYSEIAIWPPVQD

Protein No.: I-338

Protein name and Species:

Chorismate synthase OS=Populus trichocarpa GN=CS1 PE=3 SV=1

Accession: tr|B9HLM0|B9HLM0_POPTR

Unused ProtScore: 6.66

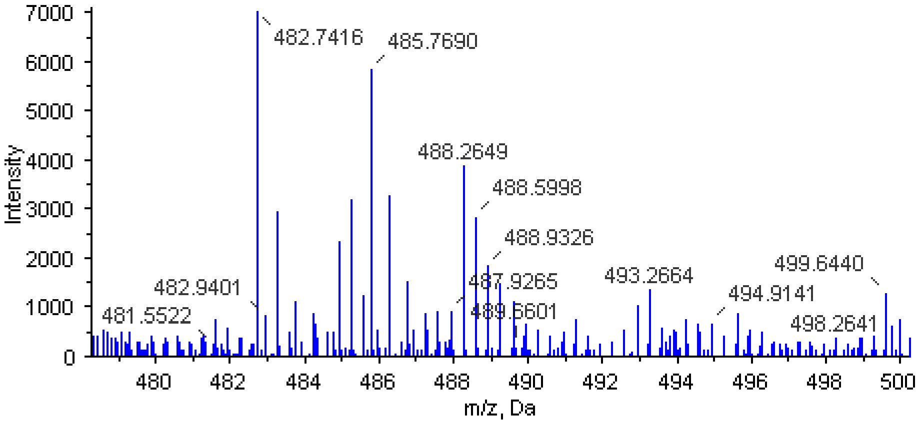
Seq Cov %: 12.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.61

116: 114=E5TL: D5TL= 1.26

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MASSTLTSKSFLDSSRIDTASLSSAHLRKLSFSSVQISSRSRLPKKLQINAAGSTFGNNFR**VTTFGESH**
GGGVGCIIDGCPPRIPLSESDMQFDLDRRRPGQSRITTPRKETDTCKISSGVSEGQTTGTPIHVFVPNT
DQRGFDYNEMSVAYRPSHADATYDMKYGVRSVQGGGRSSARETIGRVAAGAVAKKILKLYAGTEILAYV
SQVHKVVLPEGVVNHDSLSLDQIESNIVRCPDPEYAEKMIAAIDAVRVK**GDSVGGVVTCIVR**NAPRGLG
SPVFDK**LEAELAK**AAMSLPATKGFEFGSGFSGTFLSGSEHNDEFYTDEHGRIRTRTNRSGGIQGGISNG
EIINLR**IAFKPTSTIGR**KQHTVTRDKKEIELIARGRHDPCVVPRAVPMVEAMVALVLMDQLMAQFSQSY
LFPINPDLQEPLTMPRLEAANASV

Protein No.: I-343

Protein name and Species:

40S ribosomal protein S11, putative OS=Ricinus communis GN=RCOM_0658740 PE=3 SV=1

Accession: **tr|B9SKG4|B9SKG4_RICCO**

Unused ProtScore: **6.6**

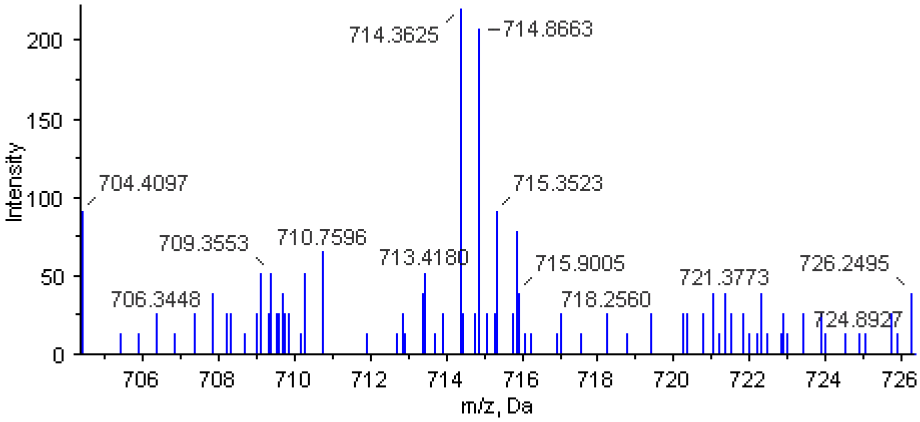
Seq Cov %: **17.6**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 2.09

116: 114=E5TL: D5TL= 0.82

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAEQTEKAFLKQPK**VFLSSK**KTGKGKRPGKGGNRFWK**SIGLGFK**TPR**EAIEGTYIDK**KCPFTGTVSIRG
R**ILAGTCHSAK**MNRTIIVRRNYLHFIKKYQRYEKRHSNIPAHISPCFRVK**EGDHVIIGQCR**PLSKTVRF
NVLKVIPAGSSGGAKKAFTAM

Protein No.: I-345

Protein name and Species:

JHL07K02.17 protein OS=Jatropha curcas GN=JHL07K02.17 PE=4 SV=1

Accession: **tr|E6NU17|E6NU17_9ROSI**

Unused ProtScore: **6.54**

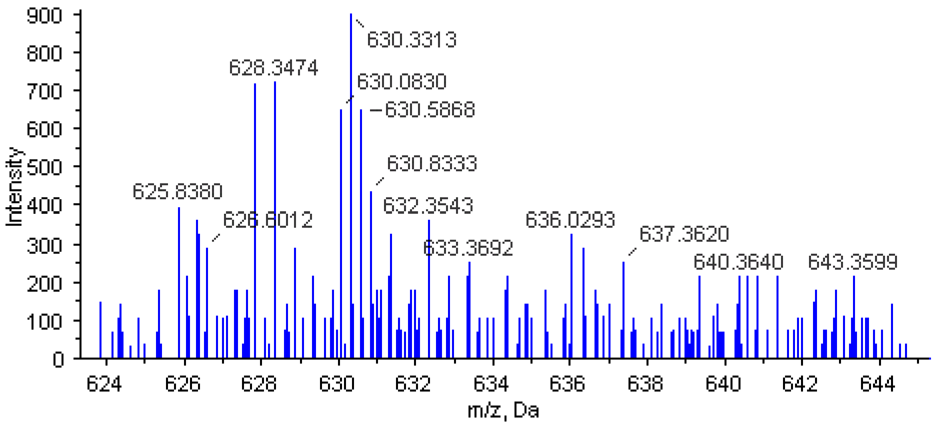
Seq Cov %: **6.8**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.33

116: 114=E5TL: D5TL= 1.27

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGNCCSDEAGGRAAVGGTGTASAGHTTTANDAIDYYLKSRGFRGMFFQIELSFSATNLRDRDVLSK**SDP**
MVVVYTKGRDEPPTEVFRTEVVLNSLNPTWITKYSITFQFEVVQTLQFHVYDVDTQFHNVDVKMLKLDE
QQFLGEASCVLSEIVTRPNRTLTLDLVHKDSTISSQPRCGQLVVHAEECISSKTTTQMTLRCSDLEHK**D**
LFSRINPFLVISKTVESGMPIPVCKTEVLKNDHSPVWKPVFLNIQQVGSKDSPLVIECYNFNSSGK**HDL**
IGEVRKSLADLEKLCSTGAGQNLFLQTAVGHDHSKALKSQLFVDNFSESIQYTFLDYLKGGCELNFMVA
IDFTASNGNPR**LPDSLHYIDPSGR**PNAYQQAILEVGEVLQFYDSDKRFPAWGFGARPIDGPVSHCFNLS
GSTNHCEVEGIQGIMTSYTSALFNVSLAGPTLFGPVISNAAHIAGQSIANGGKKYFVLLIITDGVVTDL
QETKDAIVKASDLPLSILIVGVGGADFKEMEILDADKGERLESSTGRVASR**DIVQFVPFR**SIQSQQISV
VQALLAELPTQFLTYMRSRNIQPNI

Protein No.: I-348

Protein name and Species:

Hydrolase, hydrolyzing O-glycosyl compounds, putative OS=Ricinus communis GN=RCOM_0750500 PE=4 SV=1

Accession: tr|B9SUE9|B9SUE9_RICCO

Unused ProtScore: 6.52

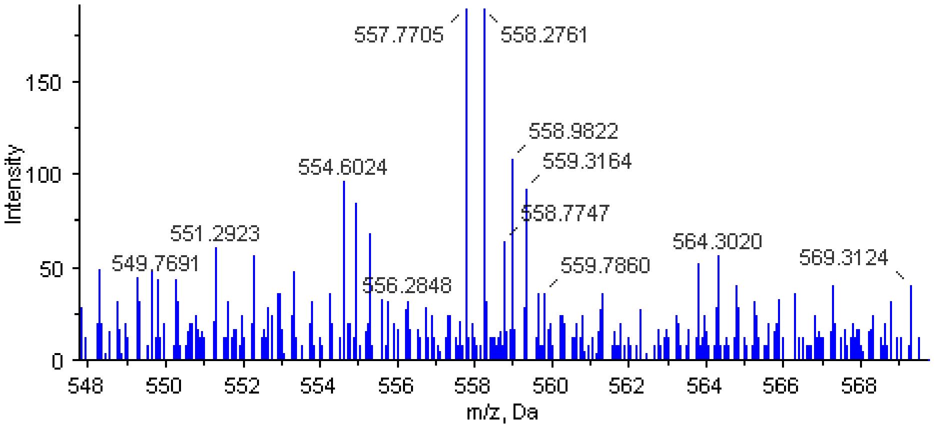
Seq Cov %: 7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 31.33

116: 114=E5TL: D5TL= 2.51

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MTVTPN**ISINDGNLVVHGK**TILTRVPDNIVLTPGSGVGLLAGAFIGASAADSKSLHVFPVGVLEGLRFM
CCFRFKLWWMTQRMGTCGKDIPLETQFMLVESKDGGEGVDQDDAQTIYTVFLPLLEGQFRAVLQGNEKS
EMEICLESGDTAVETNQGHYLVYMHAGTNPFEVINQAVKAVEKHMQTFLHREKKKVTISFFFFYIKNFY
HKHCEAESASISSFVLLVLCSCPLFLTGLAGLKHVVEDAKKHHNVKYVYAWHALAGYWGGVKPAAAGME
HYDTALAYPMSSPGVKGNQPDIVMDSLSVHGLGLVHPKKVFNFYNELHAYLASCGIDGVK**VDVQNIIET**
LGAGHGGRVSLTR**SYHQALEASIAR**NFPDNGCIACMCHNTDGLYSAKQTAVVR**ASDDFYPR**DPASHTIH
ISSVVYNSLFLGEFMQPDWDMFHSLHPAADYHGAARAIGGCPIYVSDKPGNHNFELLKKLVLPDGSVLR
AQLPGRPTRDCLFADPARDGTSLLKVWNMNKCTGVVGVFNCQGAGWCKIEKKTR**IHDASPGTLTASVR**A
SDVDCIAQVANADWNGETVVYAHRSADVIRLPKGASLPVTLKVLEYELFHFCPIKEIISNISFAPIGLL
DMFNSSGAVDQVEIRTASDGKPELFDGEVSSELTTSLSENRSPTATIEMRRPLKCLVGGAETDFNYDSD
SGLLTLTLPVPEEDMYRWPVEIHV

Protein No.: I-349

Protein name and Species:

60S ribosomal protein L12, putative OS=Ricinus communis GN=RCOM_0153900 PE=3 SV=1

Accession: **tr|B9SWB0|B9SWB0_RICCO**

Unused ProtScore: **6.51**

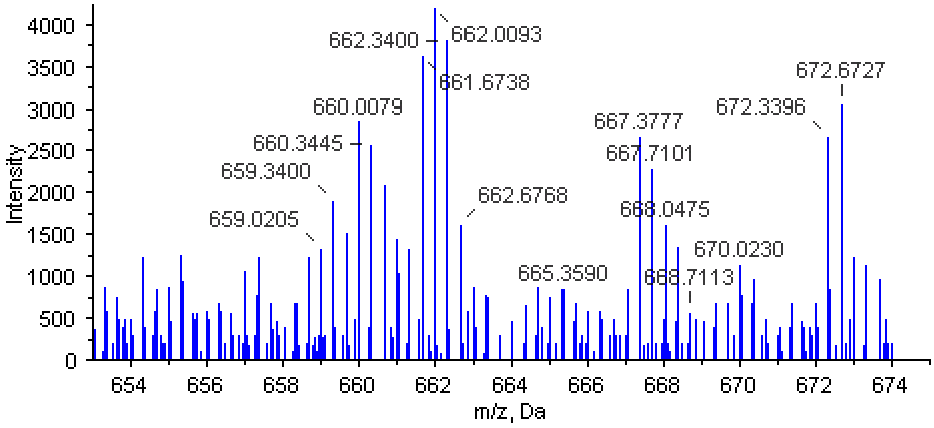
Seq Cov %: **31.9**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 2.42

116: 114=E5TL: D5TL= 1.28

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MPPKFDPSQVVDVFVR**VTGGEVGAASSLAPKIGPLGLSPK**KIGEDIAKETAKDWKGLRVTVKLTVQNRQAK**VTVVPSAAALVIK**ALKEPERDRKKTKNIKHSGNISLDDVIEIAKVMKPRSMAKDLSGTVK**EILGTCVSVGCTVDGK**DPKDLQQEITDGDVEVPLD

Protein No.: I-350

Protein name and Species:

developmentally-regulated GTP-binding protein OS=Populus trichocarpa GN=POPTRDRAFT_718912 PE=4 SV=1

Accession: tr|B9HG22|B9HG22_POPTR

Unused ProtScore: 6.49

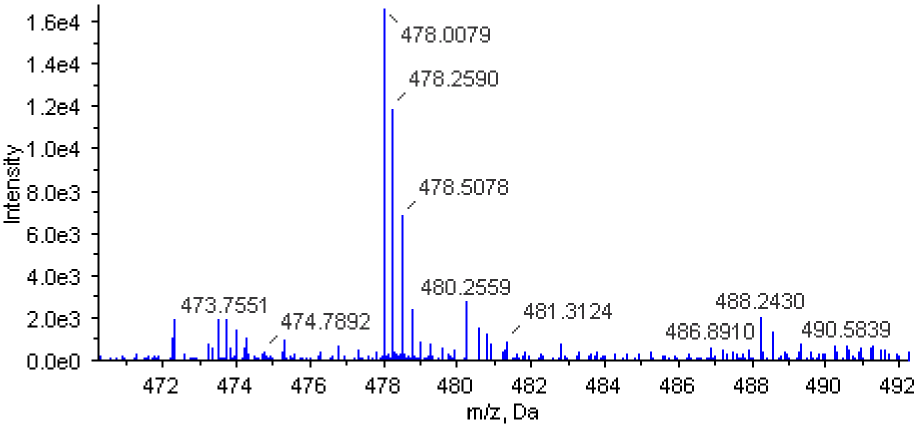
Seq Cov %: 14.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.48

116: 114=E5TL: D5TL= 0.84

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSTVMQKIKDIEDEMARTQKNKATAHHLGLLKAKLAKLRRELLEPSAK**GGGGAGQGFDVTK**SGDAR**VGL**
VGFPSVGKSTLLNKLTGTFSEVASYEFTTLTCIPGVIVYKGAKIQLLDLPGIIEGAKDGKGRGRQVIST
ARTCNCILIVLDAIKPITHKRLIEKELEGFGIRLNKEPPNLTFRKKDKGGINFTSTVANTHLDLDTVK**A**
ICSEYRMHNADITLR**YDATADDLIDVIEGSR**IYMPCIYVVNK**IDQITLEELEILDK**LPHYCPVSAHLEW
NLDGLLDKVWEYLNLTRIYTKPKGMNPDYEDPVILSSKKRTVEDFCERIHKDMLKQFKYALVWGSSAKH
KPQRVGKEHELEDEDVVQIIKKV

Protein No.: I-351

Protein name and Species:

Cis-prenyl transferase OS=Hevea brasiliensis GN=HbCPT PE=2 SV=1

Accession: tr|A9ZN23|A9ZN23_HEVBR

Unused ProtScore: 6.48

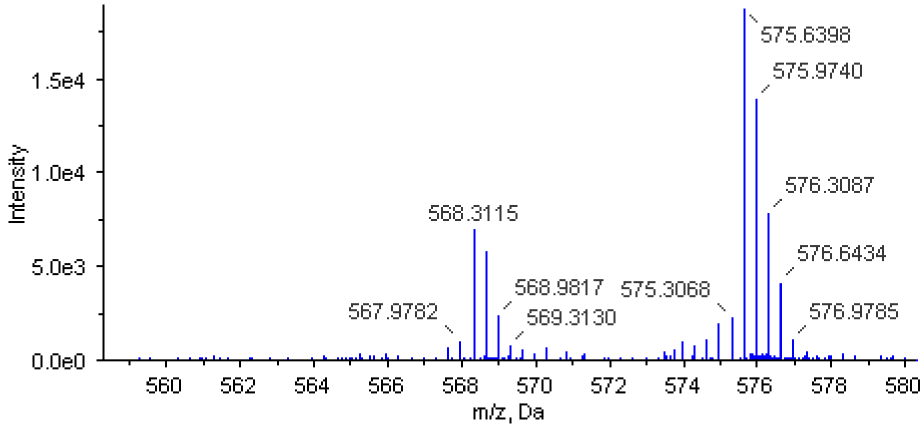
Seq Cov %: 37.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.39

116: 114=E5TL: D5TL= 0.72

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MELYNGERPSVFRLLGKYMRKGLYGILTQGPIPTHLAFILDGNRRFAKKHKLPEGGGHKAGFLALLNVL
TYCYELGVKYATIYAFSIDNFRRKPHEVQYVMDLMLEKIEGMIMEESIINAYDICVRFVGNLKLLSEPV
KTAADQSMRATANNSRFVLLIAVAYSSTDEIVHAVEESSKDKLNSNEVCNNGIEAEQEFKEANGTGNSV
IPVQKTESYSGIKLVDLEKNTYINPYPDVLIRTSGETRLSNYLLWQTTNCILYSPYALWPEIGLRHVVW
SVINFQRHYSYLEKHKEYLK

Protein No.: I-355

Protein name and Species:

40S ribosomal protein S14, putative OS=Ricinus communis GN=RCOM_0632900 PE=3 SV=1

Accession: tr|B9S120|B9S120_RICCO

Unused ProtScore: 6.46

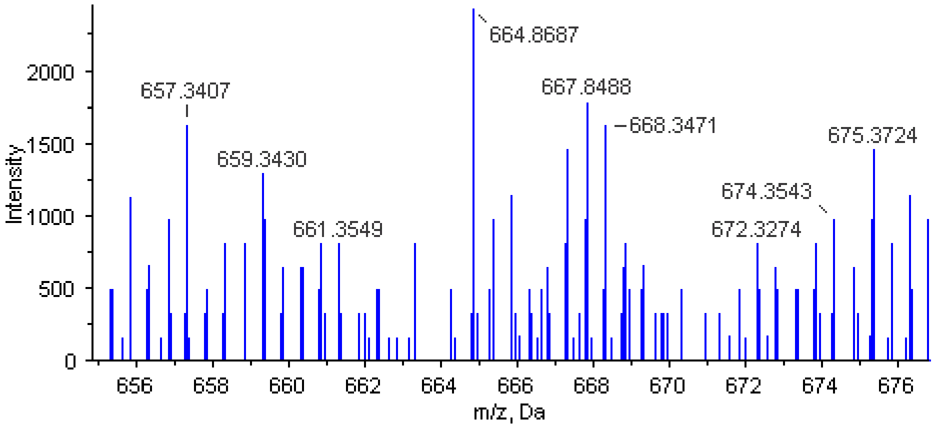
Seq Cov %: 22.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 2.27

116: 114=E5TL: D5TL= 0.86

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSKKKTR**EPK****EENVTLGPAVR**EGEHVFGVAHIFASFNDTFIHVTDLSGRETLVRITGGMKVK**ADRDESS**
PYAAMLAAQDVTQRCK**ELGITALHIK**LRATGGNKTK**TPGPGAQSALR**ALARSGMRIGR**IEDVTPIPTDS**
TRRKGGRRGRRL

Protein No.: I-357

Protein name and Species:

Rubber elongation factor OS=Hevea brasiliensis GN=REF PE=2 SV=1

Accession: **tr|Q6T708|Q6T708_HEVBR**

Unused ProtScore: **6.44**

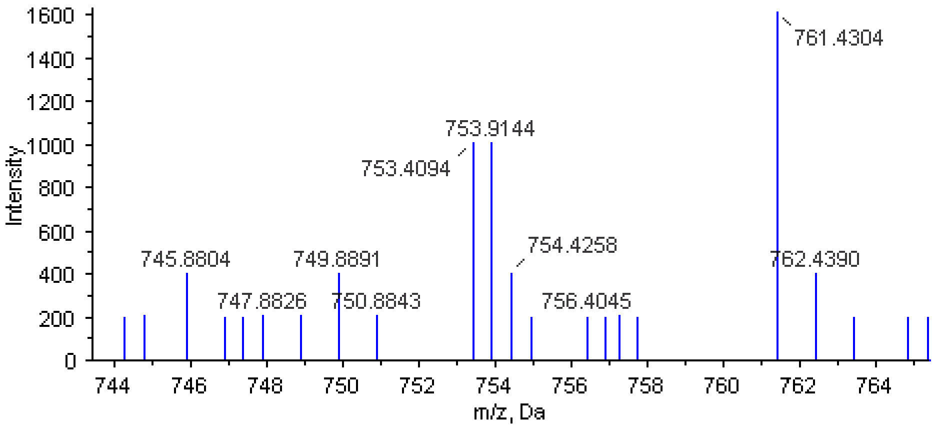
Seq Cov %: **64**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL= 0.51

116: 114=E5TL: D5TL= 1.17

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAEGEEEVNIQEEANK**GEENPQEEANIQEETNKGEENIQEEANIEEEANKEEESLKYLDFVQAATVYAR**ASFSKLYLFAKDK**SGPFKPGVNTVESR**FK**SVVRPVYNK**FQPVPNKVLKFADR**RVDAYVTVLDR**IVPPIVKR**ASIQAYSVAPGAALAVASYLPLHTK**RLSKVLYGDG

Protein No.: I-364

Protein name and Species:

chitinase，Class I (Fragment) OS=Gossypium hirsutum PE=2 SV=1

Accession: tr|Q9ZTT8|Q9ZTT8_GOSHI

Unused ProtScore: 6.34

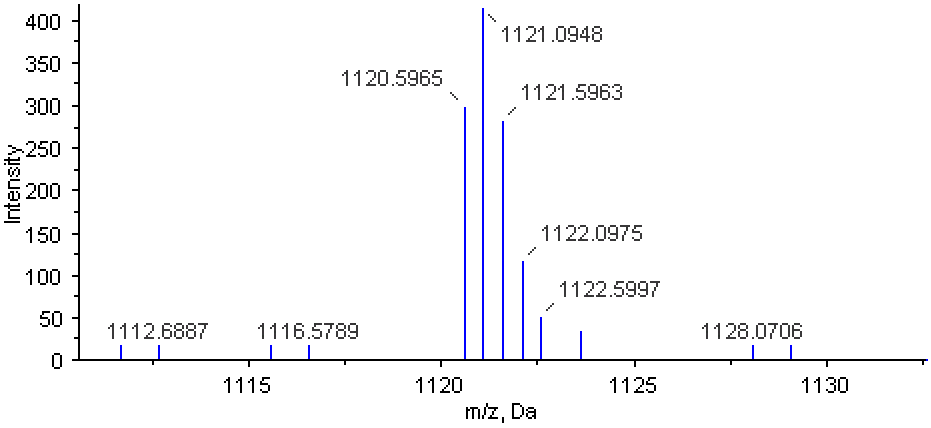
Seq Cov %: 13.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.60

116: 114=E5TL: D5TL=0.62

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

EQCGRQAGGALCPGGLCCSQFGWCGSTADYCTVPGCQSQCSGSGPAPGPGGLTNLISRETFNRMLLHRN
DGACPARGFYTYDAFIAAARSFPAFATTGDQATRKREIAAFLAQTSHETTGGAGWAAPDGPYAWGYCYN
RELNPPSSYCASGPNYPCSPGKQYFGRGPMQLSWNYNYGPCGRAIGVDLLNNPDLLSSDPTVSFKSAFW
FWMTPQSPKPSCHNVIIGAWSPSSSDRAAGR**ATGYGVITNIINGGLECGK**GWNAQVEDRIGFYKR**YCDI**
LGVSYGNNLDCYNQRPFGNGVSVDSM

Protein No.: I-366

Protein name and Species:

Protease inhibitor protein OS=Hevea brasiliensis PE=4 SV=1

Accession: tr|B3FNP9|B3FNP9_HEVBR

Unused ProtScore: 6.31

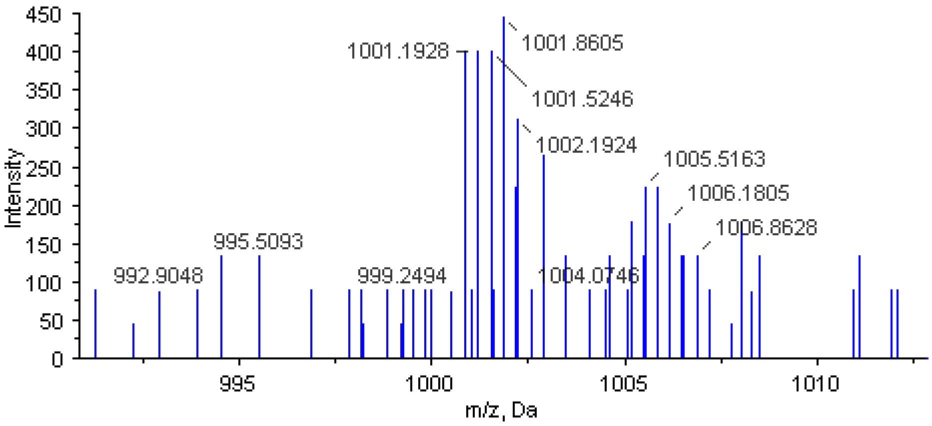
Seq Cov %: 67.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2.78

116: 114=E5TL: D5TL=1.56

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MASQCPVK**DAWPELIGTNGDIAAGIIETENANVK**AIVLKK**GSPMTMEYNLCRVLVFVDDNR**VVTQAPVI
G

Protein No.: I-369

Protein name and Species:

Ras-related protein RABB1b-like OS=Populus trichocarpa GN=POPTRDRAFT_648984 PE=2 SV=1

Accession: tr|A9P8X5|A9P8X5_POPTR

Unused ProtScore: 6.2

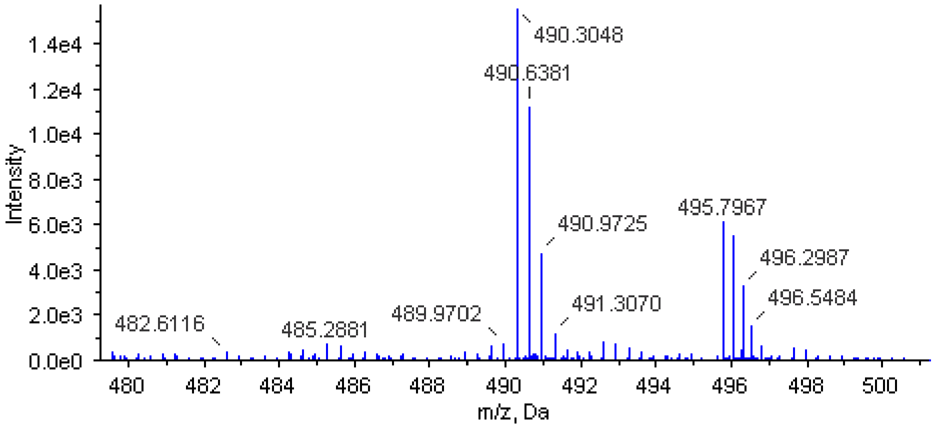
Seq Cov %: 51.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2.61

116: 114=E5TL: D5TL=1.12

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSYDYLFK**YIIIGDTGVGKSCLLLQFTDKR**FQPVHDLTIGVEFGARMVTIDARPIK**LQIWDTAGQESFR**
SITRSYY**RGAAGALLVYDITRRETFNHLASWLEDAR**QHANPNMSIMLIGNKCDLAHRRAVSKEEGEQFA
K**ENGLLFLEASAR**TAQNVEEAFIGTAGK**ILQNIQEGVFDVSNESSGIKVGYGRPQGASGAR**DGTVAQRG
GCCS

Protein No.: I-370

Protein name and Species:

Asparaginyl-tRNA synthetase, cytoplasmic 1-like [Vitis vinifera] OS=Vitis vinifera GN=VIT_11s0016g02680 PE=3 SV=1

Accession: tr|F6HGX0|F6HGX0_VITVI

Unused ProtScore: 6.18

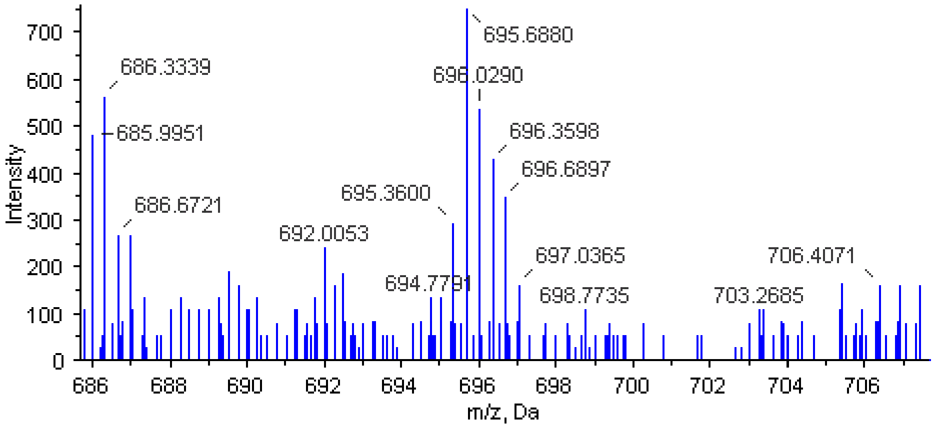
Seq Cov %: 11.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.64

116: 114=E5TL: D5TL=1.17

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAEDSVPPVDQMALATLNDDVSTPFVKAQFSDRHLIRTILSRPDGGAGLAGQTVKVGGWVKTGREQGKG
SFAFLELNDGSCPANLQVIVDAAVAPLGQLVQTGTCVHVEGLLKVPPEGTKQRVELRVEKVHHVGPVDP
AKYPLPKTR**LTLEFLR**DFVHFRPR**TNTISAVAR**IRNALAYATHTFFQNHGFLYIHTPIITTSDCEGAGE
MFQVTTLISDAEKVEK**ELIKNPPPSEADIEAAK**ALVKEKGEAVAQLKSAKASKGEITASVAELNKAKEN
LSRLEERSKLKPGIPQKDGKIDYSQDFFARQAFLTVSGQLQVETYACAVSSVYTFGPTFRAEHSHTSRH
LAEFWMVEPEIAFADLKDDMNCAEAYVKFLCQWLLDNCIDDMEFMAKNFDKGCIDRLRMVASTPFER**IS**
YTEAIKLLEEAVKKDKKFENKVEWGIDLASEHERFLTEVLFKKPVIVHDYPKGIKAFYMRLNDDMK**TVA**
AMDVLVPKVGELIGGSQREERYEVIEKRILEMGLPLEPYEWYLDLRRYGTVK**HCGFGLGFERMILFATG**
IDNIRDVIPFPRYPGRADL

Protein No.: I-371

Protein name and Species:

S-adenosyl-methionine-sterol-C-methyltransferase OS=Ricinus communis PE=2 SV=1

Accession: tr|O24328|O24328_RICCO

Unused ProtScore: 6.18

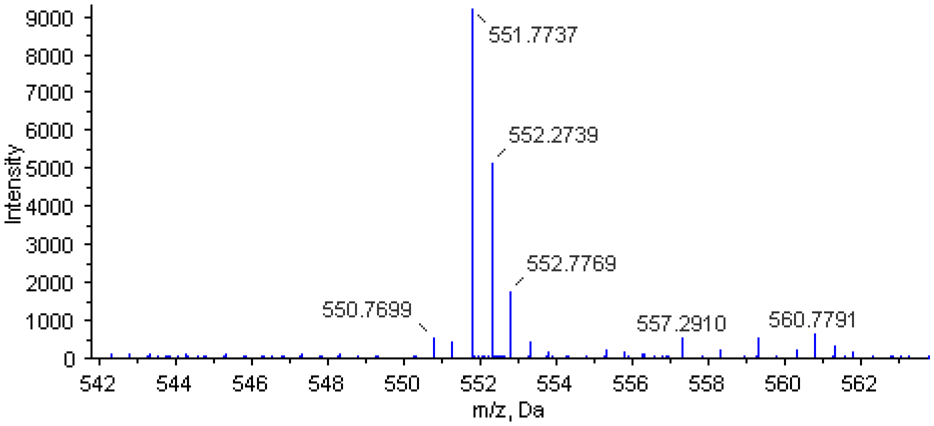
Seq Cov %: 17.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.63

116: 114=E5TL: D5TL=1.24

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSKAGALDLASGVGGKIDKNEVLSAVEKYEKYHVYYGGAEEERKANYTDMVNKYYDLVTSFYEFGWGES
FHFAHRFKGESLRESIKRHEHFLALQLGLKPEQK**VLDVGCGIGGPLR**EISR**FSLTSVTGLNNNEYQITR**
GKVLNRIAGVDKTCDFVKADFMKMPFPANSFDAVYAIEATCHAPDAYGCYSEIYRVLKPGQFFAAYEWC
MTDSFDPNNQEHQKIK**AEIEIGDGLPDIR**LTGQCIEALKKAGFDVIWSGDLTASSPVPWYLPLDKNQYS
LTGFRLTAIGRFFTRNMIKALEFAGLAPKGSQR**VQDFLEKAAEGLVEGGR**KEIFTPMFFFLAQKPHSEN
Q

Protein No.: I-372

Protein name and Species:

60S ribosomal protein L4 [Vitis vinifera] OS=Vitis vinifera GN=VIT_08s0040g03200 PE=4 SV=1

Accession: tr|F6HQV3|F6HQV3_VITVI

Unused ProtScore: 6.14

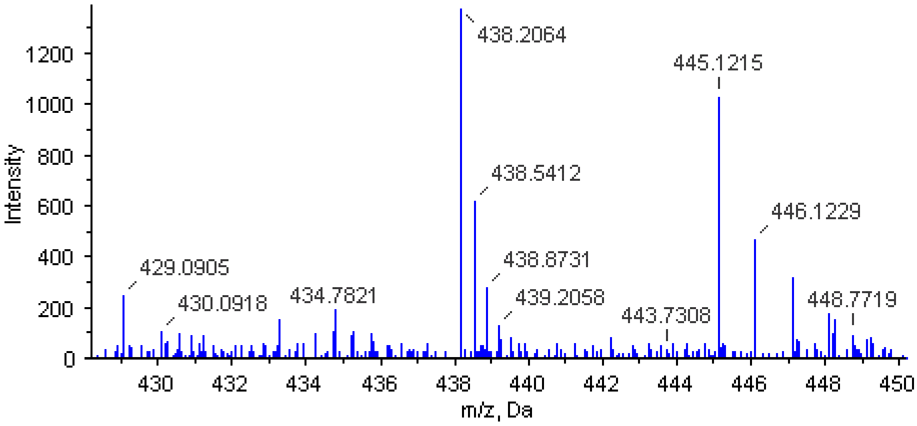
Seq Cov %: 8.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2.31

116: 114=E5TL: D5TL=2.14

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAAAAARPLVTVQVLKSDMATDGGNAVPLPDVMKASIRPDIVTFVHSNISKNSRQPYAVSRRAGHQTSA
ESWGTGRAVSRIPRVPGGGTHR**AGQGAFGNMCR**GGRMFAPTKIWRRWHRKINVNQKRYAVVSAIAASAI
PSLVMARGHRIESVPELPLVIGDSAESVEKTSAAIDILKQVGAYPDAEKAKDSHAIRPGKGKMRNRRYI
SRKGPLIVYGTEGAKLVKAFR**NIPGVEVANVDR**LNLLKLAPGGHLGRFVIWTKSAFEK**LDSIYGSFEK**T
SEKKNGYLLPRSKMVNADLARIINSDEVQSVVRPIKKEVKRAPMKKNPLKNLNTMLKLNPYAKTARRMA
LLAEAQRVKAKQEKLDKKRKQIPKEEVAAIKAAGKAWYQTMISDSDYTEFDNFSKWLGVSQ

Protein No.: I-373

Protein name and Species:

Malate dehydrogenase OS=Ricinus communis GN=RCOM_1520380 PE=3 SV=1

Accession: tr|B9SE47|B9SE47_RICCO

Unused ProtScore: 6.14

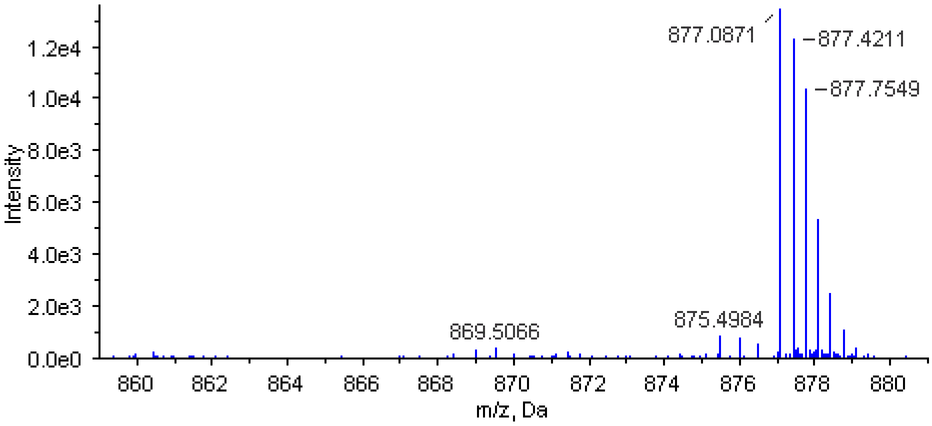
Seq Cov %: 13.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.28

116: 114=E5TL: D5TL=0.31

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MRSSLFRSVKALGSTSSSSHLLRRGYASEAVPDRK**VAVLGAAGGIGQPLALLMK**LNPLVSNLALYDIAN
TPGVAADVSHINTRSDVKGYVGEDQLGK**ALEGSDVVIIPAGVPR**KPGMTR**DDLFNINAGIVK**GLCEAIA
KYCPNALVNMISNPVNSTVPIAAEVFKKAGTYDEKRLFGVTTLDVVRAKTFYAGKAKVPVAEVNVPVVG
GHAGITILPLLSQATPKANLPDEEIVALTKRTQDGGTEVVEAKAGKGSATLSMAYAGAIFADACLKGLN
GVPDVVECSFVQSTVTELPFFASKVRLGK**NGVEEVLGLGPLSDYEK**EGLEKLKPELLSSIEKGINFANK

Protein No.: I-374

Protein name and Species:

Alcohol dehydrogenase, putative OS=Ricinus communis GN=RCOM_0605880 PE=4 SV=1

Accession: tr|B9SUZ4|B9SUZ4_RICCO

Unused ProtScore: 6.12

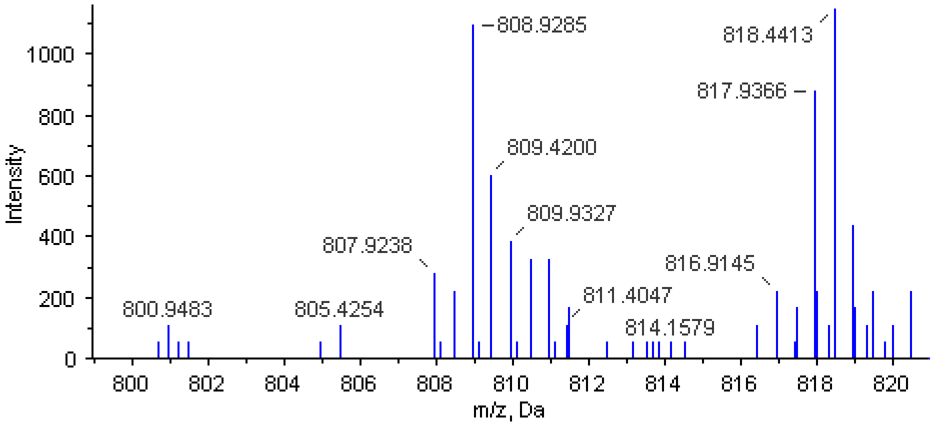
Seq Cov %: 18.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.09

116: 114=E5TL: D5TL=0.29

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MTSKESVHRNSRRKAIDYREMASEAEVVSNKQVIFKEYVSGFPKESDMYMTTSSVKLQVEEGSTSVLVK
NLYLSCDPYMRGRMRNTPSDDPEFSPLHPGSPVFGLGVAK**VVDSGHPGFK**KGDLVWGSTRWEEYTLITA
PEGLFKIHHTDIPLSYYTGLLGMPGITAYFGLNDICTPKKGER**VYVSAASGAVGQLVGQFAKLMGCYVV**
GSAGSKEKVDLLKNKFGFDEAFNYREEHDWNAALKR**YFPEGIDIYFENVGGKMLDAVLLNMR**THGRIAA
CGMISQYNLEHPDGVHNLIVVVHKRIRIQGFISFDYFGQYSK**FLDFVLPYIR**EGKITYVEDIAEGIESA
PAALVGLFSGRNVGK**QVVAVAHE**

Protein No.: I-375

Protein name and Species:

Methionine synthase OS=Camellia sinensis PE=2 SV=1

Accession: tr|G3G858|G3G858_CAMSI

Unused ProtScore: 6.11

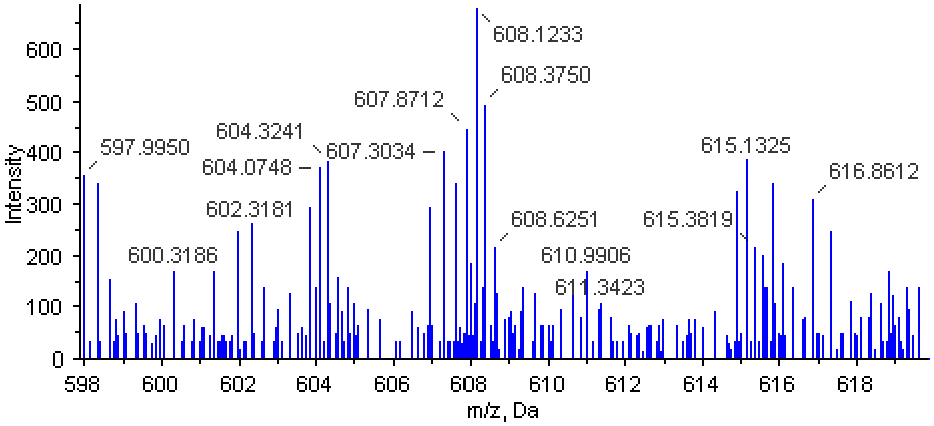
Seq Cov %: 17.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.39

116: 114=E5TL: D5TL=0.51

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

M**ASHIVGYPR**MGPKRELK**FALESFWDK**KSSAEDLKKVAADLRSSIWKQMASAGIKYIPSNTFSYYDQVL
DTTAMLGAVPPRYGWTGGEIGFDTYFSMARGNASVPAMEMAKWFDTNYHFIVPELGPEIKFSYASHKAV
DEYKEAK**ALGVDTVPVLVGPVSYLLLSK**PAKGVEK**SFSLLSLLDK**ILPIYKEVVAELKAAGASWIQFDE
PTLVKDLESHQLQAFTAAYSELESALSGLNVIVETYFADVPAEAFKTLTSLKCVTGFGFDLVRGAQTLD
LITSGFPSGE**YLFAGVVDGR**NIWANDLAASLSLLQTLEGIVGKDKLVVSTSCSLLHTAVDLVNETKFDK
ELK**SWLAFAAQK**VVEVNSLAKALAGHKDEAFFSENAAAQASRKSSPRVTNEAVQKAAAALRGSDHRRAT
NVSARLDAQQK**KLNLPILPTTTIGSFPQTIELR**RVRREYKAKKISEEEYVKAIKEEINKVVKLQEELDI
DVLVHGEPERNDMVEYFGEQLSGFAFSANGWVQSYGSRCVKPPIIFGDVSRPKAMTVFWSSMAQSMTTR
PMK**GMLTGPVTILNWSFVR**NDQPRFETCYQIALAIKDE**VEDLEK**AGINVIQMDEAALREGLPLRKSEQA
FYLDWAVHSFRITNCGVTDTTQIHTHMCYSNFNDIIHSIIDMDADVITIENSRSDEKLLSVFREGVK**YG**
AGIGPGVYDIHSPRIPSTEEIADRINKMLQVLET**NILWVNPDCGLK**TRKYHEVKPALLNMVAAAKQIRT
QLASAK

Protein No.: I-382

Protein name and Species:

Trafficking protein particle complex subunit, putative OS=Ricinus communis GN=RCOM_0183430 PE=4 SV=1

Accession: tr|B9SA27|B9SA27_RICCO

Unused ProtScore: 6.03

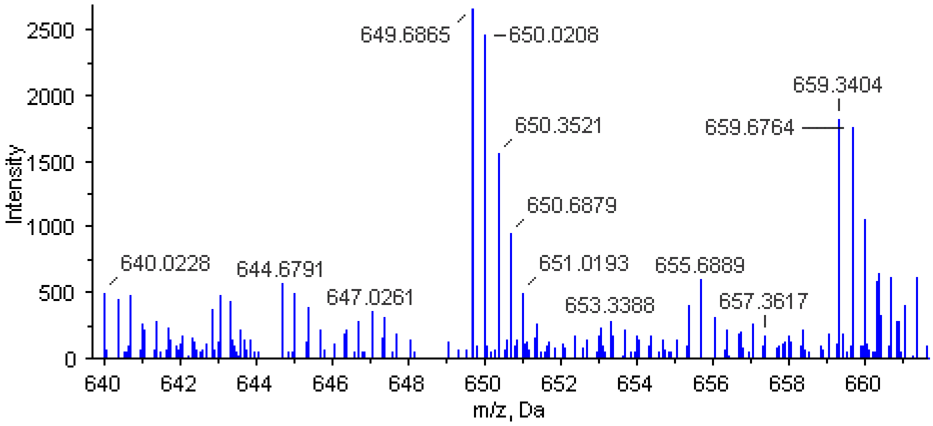
Seq Cov %: 24.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.71

116: 114=E5TL: D5TL=1.47

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAPVGPR**SGDAIFASVER**VNAELFTLTYGAIVR**QLLTDLEEVEEVNKQLDQMGYNIGIRLVDEFLAK**SN
VNRCVDFRETAEVIAKVGFKMFLGVSASVTNWDADGTCCSIILEDNPLVDFVELPDTCQGLYYCNILSG
VIRGALEMVSMKTEVTWARDMLRGDDAYELQVKLLK**QVPEEYPYKDDE**

Protein No.: I-383

Protein name and Species:

Sucrose phosphate phosphatase OS=Malus domestica PE=2 SV=1

Accession: tr|Q5J3P0|Q5J3P0_MALDO

Unused ProtScore: 6.02

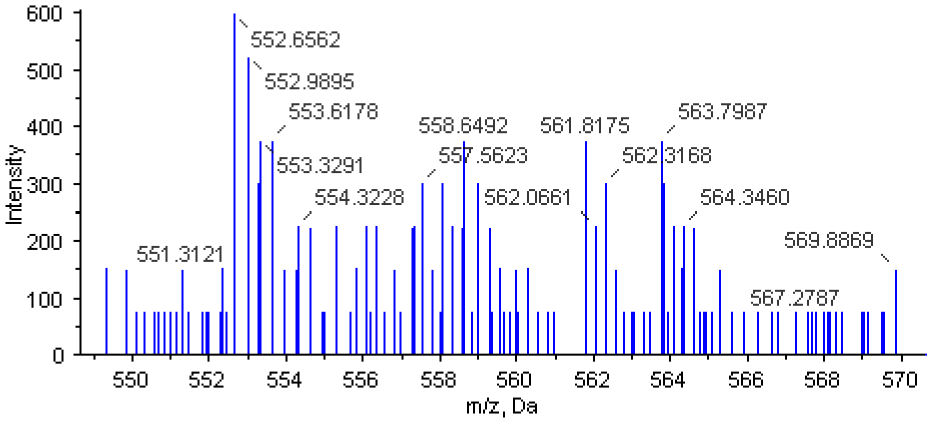
Seq Cov %: 9.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.50

116: 114=E5TL: D5TL=0.58

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDRLEAPARLMIVSDLDHTMVDHHDTENLSLLRFNSLWEANYC**HDSLLVFSTGR**SPTLYKELRKEKPML
TPDITIMSVGTEITYGNAMVPDDGWVEVLNQKWDRNIVKEEASKYSELKLQAETEQRPHKVSFYVEKAK
AQAVTKALSEVFEKRGLDVK**IIYSGGMDLDILPQGAGK**GQALAYLLKKFKSEGSSPVNTLVCGDSGNDA
ELFSIPEVYGVMVSNAQEELLQWHAENAKGNTRIIHATER**CAAGIIQAIGHFK**LGPSLPPRDIADFSDF
KLENPNPGHELVKFFLFYEKWRRAEVENSEIYLASLKADCSPSGTFVHPSGVEHSLSDSINALRNCYGD
KQGKQFRVWVDGVLATHVGSNTWLVKFDKWELSGEERYAIKGTAVISSKGSGVSDGFTWIRVHQTWYKG
YEAKDDSTWFF

Protein No.: I-386

Protein name and Species:

60S ribosomal protein L9, putative OS=Ricinus communis GN=RCOM_1315040 PE=4 SV=1

Accession: tr|B9RYZ1|B9RYZ1_RICCO

Unused ProtScore: 6

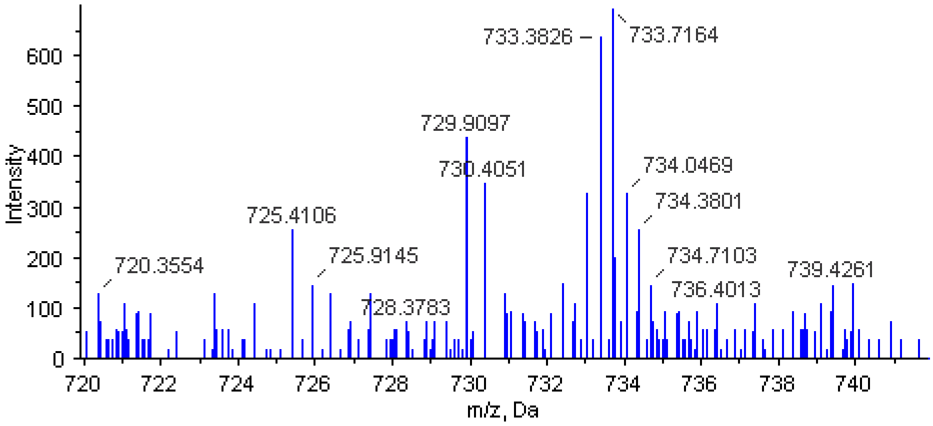
Seq Cov %: 19.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2.19

116: 114=E5TL: D5TL=1.74

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MKTILSSETMDIPDGVKIKVNAKIIEVEGPRGKLTRNFKHLNLDFQLIKDEETGKRKLKIEAWFGSRKT
SAAIR**TALSHVENLITGVTK**GYRYKMRFVYAHFPINASITNSNSAIEIRNFLGEKKVR**KVDMLEGVTVV**
RSEKVKDELVLDGNDIELVSRSAALINQKCHVKNKDIRK**FLDGIYVSEK**GTVAEQE

Protein No.: I-389

Protein name and Species:

Predicted protein OS=Populus trichocarpa GN=POPTRDRAFT_571988 PE=4 SV=1

Accession: tr|B9IBL7|B9IBL7_POPTR

Unused ProtScore: 6

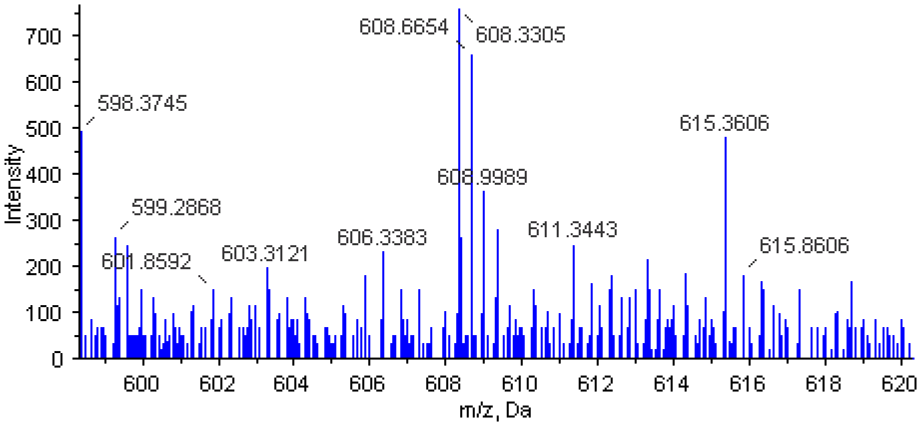
Seq Cov %: 6.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=6.19

116: 114=E5TL: D5TL=1.20

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSWLARSIANSLKFEDDDQQPDKNTTATTTSAPTTDNVNNNKDLSNSESDQQQSATPRGVKEDLTDLKK
TLTRQLWGVASFLAPPPEPPLTENRSHTSDPDGSNDDDDDAALIAGIR**SDFAEIGGR**FKSGITKLSSNK
TVSEFTKIASNLLQLGSESHEIGTTASAVGVTEEVVGFARDVAMHPETWLDFPLPDVQGFEDFDMSDAQ
QEHALAVEHLAPRLAALRIELCPGYMSEGCFWK**IYFVLLHPR**LSK**HDAELLSTPQIVEAR**AMLSHELQN
KAKAKSTPDWSGVDTSNVKADLPHEESLSVPSRAKSESVPIMTSGIEAVSPTLAAKTSDNEAAPSFVSV
ESETEKHPVESTQMQIIDKSVVEEGKVDQTKHQHSSSSSSSGILEEKFDDDGDDWLKDDSSEMIGVSGS
SMPLGNDEDVSFSDLEEDDGDEPASYKKVASGSDCATKGSQDWVQLSRSSADSVKDIKPVSIKNAGSEK
VSARNSENKESSDWLDVDDIDVI

Protein No.: I-390

Protein name and Species:

Putative uncharacterized protein OS=Vitis vinifera GN=VIT_19s0015g02610 PE=3 SV=1

Accession: tr|F6I510|F6I510_VITVI

Unused ProtScore: 5.99

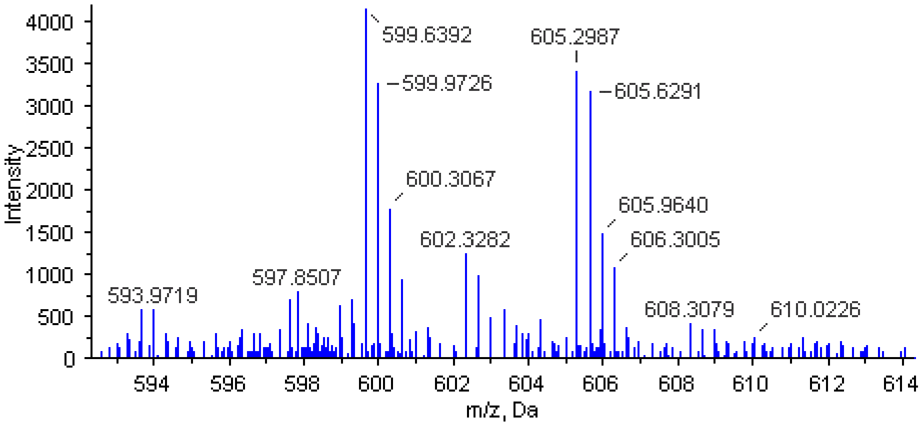
Seq Cov %: 18

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.39

116: 114=E5TL: D5TL=0.71

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MADEIILLDFWPSMFGMRVR**LALAEK**GLK**YEYRQEDLR**NK**SPLLLEMNPVHK**KIPVLIHNGKPICESLI
IVQYIDEVWK**DKSPLLPSDPYQR**AQARFWADYVDKKLYELGGKIWSTKGEEQETGKKEFIECLKLLEGE
LGEKPYFGGEKIGFVDVALVTFSCWFYAYETFGNFSIEAECPKLVAWTKRCMEKESVSSSLEDPHKVHG
FIMGMRKRFGIEVR**LALAEK**GLKYEYKEEDLRNK**SPLLLEMNPVHK**KIPVLIHNGKPICESLIIVQYID
EVWH**DKSPLLPSDPYQR**AQARFWADYVDKKGFVQNAGFFFTHSLPKAPSSS

Protein No.: I-391

Protein name and Species:

Carbonic anhydrase OS=Populus trichocarpa GN=POPTRDRAFT_666464 PE=3 SV=1

Accession: tr|B9IER7|B9IER7_POPTR

Unused ProtScore: 5.98

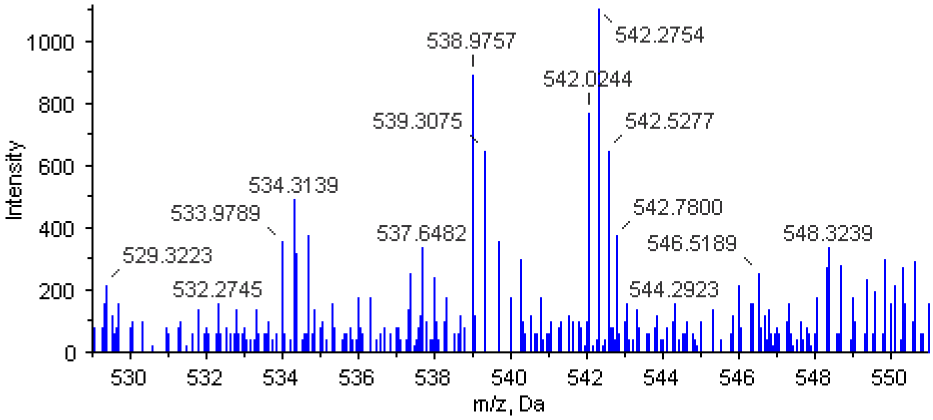
Seq Cov %: 11.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.54

116: 114=E5TL: D5TL=1.06

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSNLSHEGAIEGSKKLLIDNEKDDQLNKEVEAKIEKLIGELQGKRLPDHCDPVGRILEGFHRFKTTKFD
KYPELYRELAEGQSPKFLVFACSDSR**VSPSHVLDFQPGEAFMVRNIANLVPAFNQLR**YSGVGATIEYAV
ATLGVENILVIGHSRCGGIERLMTLPEDGSTANDFVDDWVK**IGLPAK**AKVEAEFGHLPLPEQIHKCEKE
AVNLSLINLQTYPYVQERMAEGALALRGGYYDFVKGCFELWEVKSTVTPPISTCCK

Protein No.: I-392

Protein name and Species:

Protein SEY1, putative; root hair defective 3 OS=Ricinus communis GN=RCOM_0312010 PE=4 SV=1

Accession: tr|B9SN36|B9SN36_RICCO

Unused ProtScore: 5.95

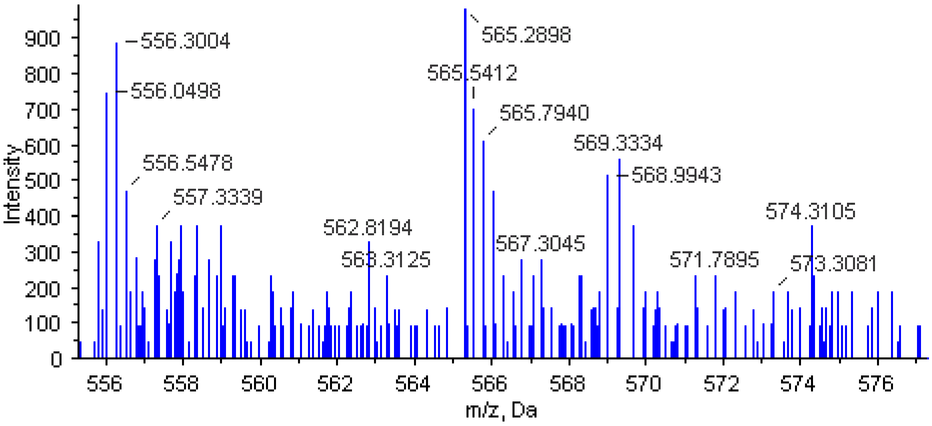
Seq Cov %: 7.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=5.06

116: 114=E5TL: D5TL=1.78

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MANSEESCSTQLIDGDGTFNAAGLEHFTKEVRLGECGLSYAVVSIMGPQSSGKSTLLNNLFGTNFREMD
AFRGRSQTTKGIWLAR**CAGIEPCTLVMDLEGTDGR**ERGEDDTAFEKQSALFALAVSDIVLINMWCHDIG
REQAANKPLLKTVFQVMMRLFSPRKTTLMFVIRDKTR**TPLENLEPVLR**EDIQKIWDAVPKPQEHKETPL
SEFFNVEVVALSSYEEKEEQFKEQVASLRQR**FFHSIAPGGLAGDR**RGVVPASGFSFSAQQMWKVIKENK
DLDLPAHKVMVATVRCEEIANEKYANFTTNEEWHQIEEAVQSGPVSGFGKKLSSTLSTSFSEYDAEAIY
FDEGVRSAKRKQLEEKLLQLVQPAHQSMLGHIRSGTLDKFKEAFDKALAAGEGFSSAAYSCTQYYMTVF
DEGCTDAIIEQASWDTSKVRDKLRRDIDAHVASVRAAK**LSELTSSFEAK**LNEALSGPVEALLDGATSET
WPAIRKLLQRESESAVSGLSSALAGFDMDKQSKDKMLSSLETYARGVVEAKAKEEAGRVLIRMKDRFSM
LFSHDSDSMPRVWTGKEDIRAITKTARSASLKLLSVMVAIRLDDEVDNVESTLSSVFLDTKNNAAVTER
SITKTDPLASSTWDEVPSSKTLITPVQCKSLWRQFK**AETEYSVTQAISAQEANK**RNNNWLPPPWAIVAL
VVLGFNEFMTLLRNPLYLGFIFVVFLLVKALWVQLDVSGEFRNGALPGLISLSTKFLPTIMNLIKKLAE
EGQKPATNDPQRNPALAAKSFRNGVGSSDDMSTASSGVTSTENGTEFSSASKDD

Protein No.: I-395

Protein name and Species:

Receptor for activated protein kinase C, putative OS=Ricinus communis GN=RCOM_0571360 PE=4 SV=1

Accession: tr|B9SU88|B9SU88_RICCO

Unused ProtScore: 5.85

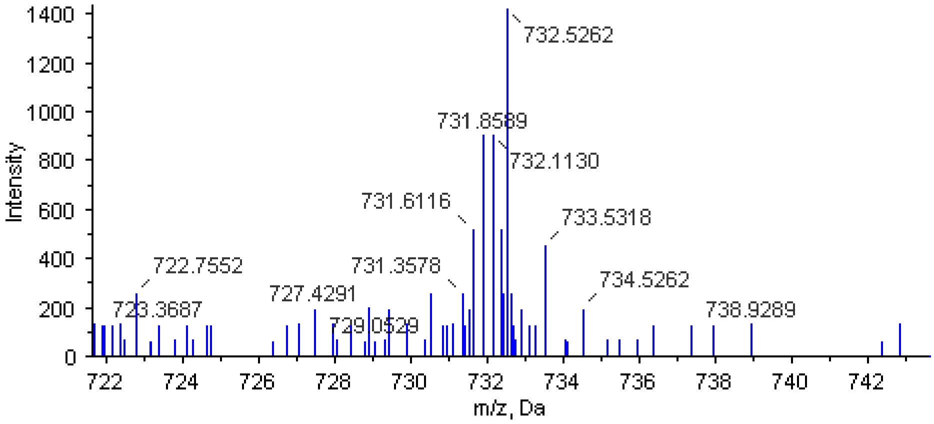
Seq Cov %: 17.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.75

116: 114=E5TL: D5TL=1.46

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAERLILLGTMRAHTDQVTAIATPIDNSDMIVTASRDKSIILWKLIKDEKTYGVAHRRLTGHSHFVQDV
VLSSDGQFALSGSWDGELRLWDLAAGVSARRFVGHTKDVLSVAFSIDNRQIVSASRDRTIKLWNTLGEC
KYTIQDGDAHNDWVSCVR**FSPNTLQPTIVSASWDR**TVKVWNLTNCKLR**CTLAGHGGYVNTVAVSPDGSL**
CASGGKDGVILLWDLAEGKRLYNLDAGAVIHALCFSPNRYWLCAATENSIKIWDLESK**SIVEDLK**VDLK
AEAEKSDGSTVASTGAKKKNIYCTSLSWNADGSTLFSGYTDGVIRVWGIGRF

Protein No.: I-401

Protein name and Species:

Fumarylacetoacetate hydrolase (Fragment) OS=Dimocarpus longan PE=2 SV=1

Accession: tr|G0YC94|G0YC94_9ROSI

Unused ProtScore: 5.79

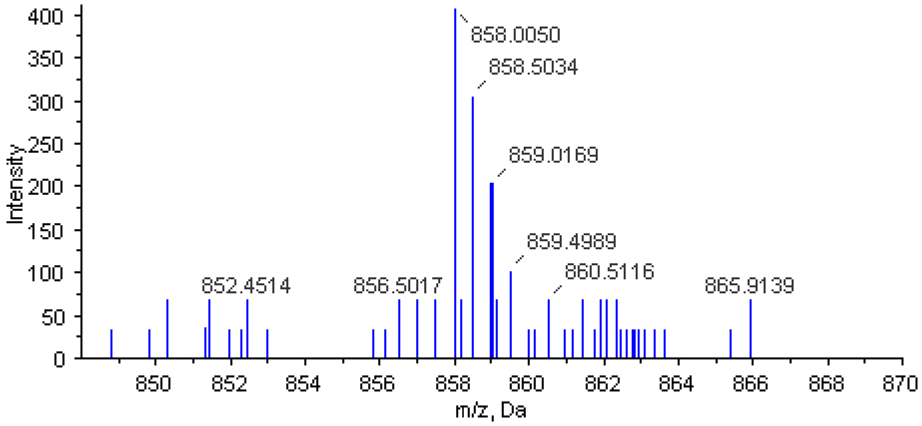
Seq Cov %: 22.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.61

116: 114=E5TL: D5TL=3.14

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAVLQSFVEVKPDSHFPIQNLPYGVFKPDPTSSPRPGIAIGDYVLDLSEIAKAGLFNGPTLS**GSDCFLQ**
PNLNKFLALGRPAWKEARATLQKLLSSSEAALRDNASLRQKSLVSMDKVEMVVPIAIGDYTDFFSSMHH
AK**NCGTIFR**GPQNPVPANWFHLPIAYHGR**ASSIVISGTDIVRPR**GQGVPSGNSPPPFGPSQK**LDFELEM**
AAVVGPGNELGKPVDVNEAADHIFGVVLMNDWSAR**DIQAWEYVPLGPFLGK**SFGTTISPWIVTL

Protein No.: I-408

Protein name and Species:

Protease inhibitor HPI OS=Hevea brasiliensis GN=PI1 PE=1 SV=2

Accession: sp|Q6XNP7|HPI_HEVBR

Unused ProtScore: 5.72

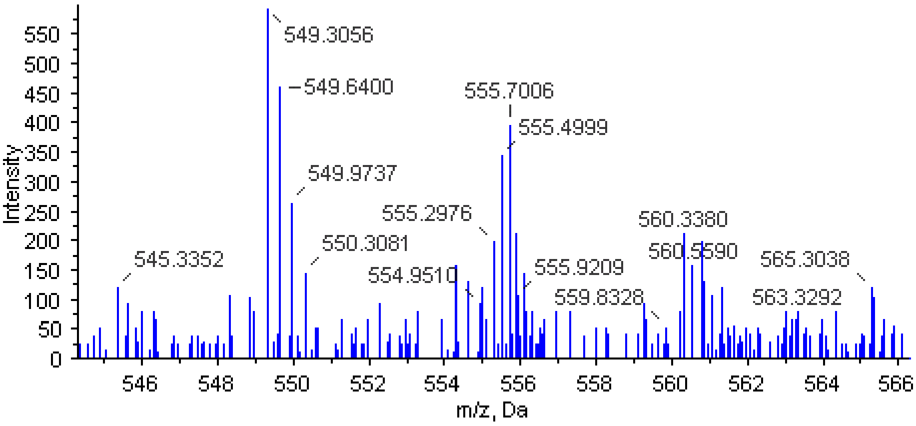
Seq Cov %: 65.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.51

116: 114=E5TL: D5TL=1.34

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MASQCPVK**NSWPELVGTNGDIAAGIIQTENANVK**AIVVK**EGLPITQDLNFNR**VR**VFVDENR**VVTQVPAIG

Protein No.: I-409

Protein name and Species:

1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase, putative OS=Ricinus communis GN=RCOM_0339640 PE=4 SV=1

Accession: tr|B9T5Y1|B9T5Y1_RICCO

Unused ProtScore: 5.7

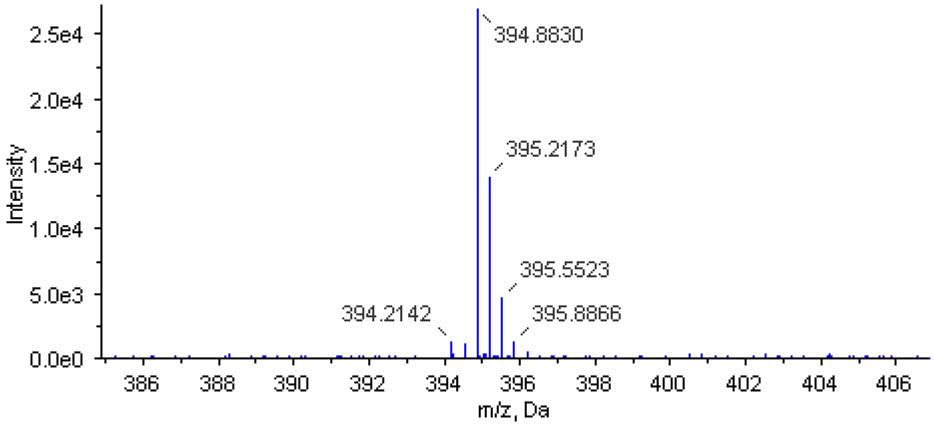
Seq Cov %: 13.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.58

116: 114=E5TL: D5TL=0.50

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSKQTYRVCFCFRRRFRLAVAEAPQEIKSLFDQYSDNNGLMSIDQLRRFLVEIQKQDNATTEDAQAIFN
NLHELKHLNIFHRKGLNLEAFFK**YLFGDINPPLDVK**RGVHHDMTCPLSHYFIYTGHNSYLTGNQLSSDC
SDVPIIQALQRGVRVIELDIWPNSTK**DNVEVLHGR**TLTTPVELIKCLRSIKEHAFRASDYPVVITLEDH
LTPDLQAK**VAEMITQTFGDILFTPGSECLKEFPSPESLK**KRIIVSTKPPKEYLEVREIREREGDSQSGK
PGSDEETWGKEIPDLKGHFRVDDKNELDEDNNDDEDAAPDGDNKSQQNIAPEYK**HLIAIHAGKPKGGIE**
ECLKVDPDKVRRLSLSEQQLEKAAETHGKEIVRFTQRNILRVYPKGIRVDSSNYNPLIGWMHGAQMVAF
NMQGHGRSLWLMQGMFR**ANGGCGYVK****KPDFLLK**SGPHGEVFDPRAKLPVKTTLKVKVYMGEGWYYDFDR
THFDAYSPPDFYARVGIAGVPADTIMKKTKTLEDNWIPVWNEEFE**FPLTVPELALLR**VEVHEYDMSEKD
DFGGQSCLPVSELRKGIRAIPLHDRKGVKYNSVKLLVRFDFV

Protein No.: I-410

Protein name and Species:

Protein disulfide isomerase, putative OS=Populus trichocarpa GN=POPTRDRAFT_643603 PE=3 SV=1

Accession: tr|B9GU26|B9GU26_POPTR

Unused ProtScore: 5.68

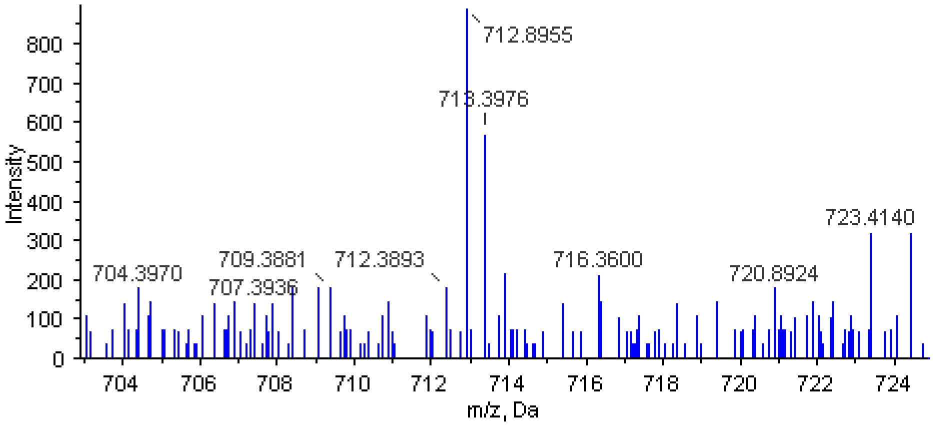
Seq Cov %: 8.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2.29

116: 114=E5TL: D5TL=2.13

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MASTVSFWSCIFLLSLIVALSAGEDESKEYVLTLDHSNFNETVSKHDFIVVEFYAPWCGHCKKLAPEYE
KAASILSSNDPQVVLAKVDANEDANKEIASQYDVKGFPTIVILRKGGKSVQEYKGPR**EADGIVEYLK**KQ
SGPASAELKSDDDATGFIGDKKVVIVGVFPK**FSGEEFENFLAVAEK**LR**SDYEFGHTLDAK**YLPRGESSV
SGPLVRLFKPFDELFVDSK**DFNVDALEK**FVEESSIPIVTLFNKDPSNHPFVVKYFDSPLAKAMLFMNFS
SENGDSIRTKYQEVAGLHKGDGLVFLLGDVEASQGALQYFGLKEDQVPLIVIQTTDGQKYLKPNLVSDQ
IAPWLKEYKEGKVPPFKKSEPIPEVNDEPVKVVVADSLDELVTKSGKNVFLEFYAPWCGHCQKLAPILE
EVAISFQSDADVVIAKLDATANDIPSDTYDVKGFPTIFFR**SATGKLVQYEGDR**TKQDIIDFIEKNRDKI
GQQEPAKEEEPAKEQETAKDEL

Protein No.: I-412

Protein name and Species:

DEAD-box ATP-dependent RNA helicase 37-like [Vitis vinifera]

OS=Vitis vinifera GN=VIT_08s0007g07070 PE=4 SV=1

Accession: tr|F6HLF4|F6HLF4_VITVI

Unused ProtScore: 5.65

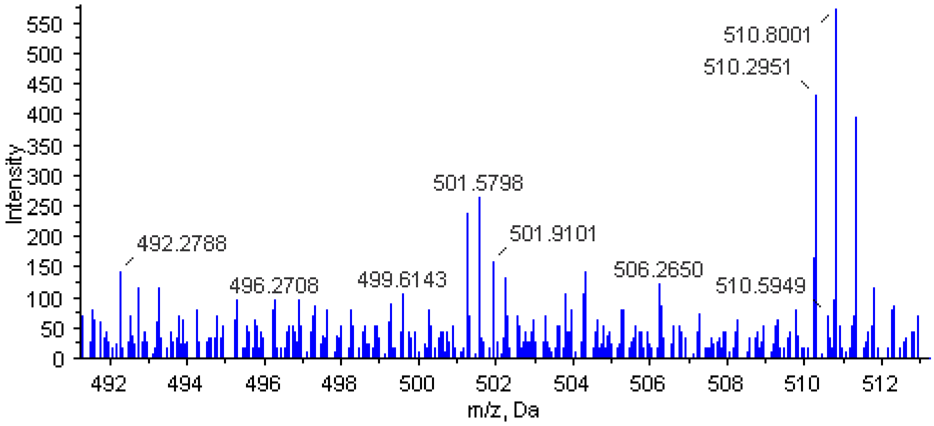
Seq Cov %: 8.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=3.16

116: 114=E5TL: D5TL=1.61

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MRTSWADSVANSTSDNLVSGSSDNSGFGAGAPSRSGRSSYVPPHLRNRPPSSDPPAPSYTSQASAGYGG
PPGGTRWGGGSRADFGR**SGVTTGVTSGGR**VGGSSGWNTRSGGWDRGRDREVNPFGDDDNAEPAFSEQEN
TGINFDAYEDIPVETSGDNVPPPVNTFAEIDLGEALNQNIRRCKYVKPTPVQRHAIPISLSGKDLMACA
QTGSGKTAAFCFPIISGIMTGQFAQRPRGAR**TVYPLALILSPTRELSCQIHDEAR**KFSYQTGVKVVVAY
GGAPINQQLRELERGVDILVATPGR**LVDLLER**ARVSLQMIRYLALDEADR**MLDMGFEPQIR**KIVEQMDM
PPPGVRQTMLFSATFPKEIQRLASDFLSSYIFLAVGRVGSSTDLIVQRVEFVHESDKRSHLMDLLHAQR
ANGAHGKQSLTLVFVETKKGADSLEHWLCMNGFPATTIHGDRTQQEREHALRSFK**SGNTPILVATDVAA**
RGLDIPHVAHVVNFDLPNDIDDYVHRIGRTGRAGK**TGLATAFFNENNSSLAR**PLADLMQEANQEVPAWL
TRYASRASYGGGKNRRSGGGRFGGRDFRKDTSFNRGGGATDYYGGNTSSGYGIPGSYGGGYGPGVTSAW
D

Protein No.: I-413

Protein name and Species:

Urease accessory protein ureG OS=Morus alba GN=ureG PE=2 SV=1

Accession: tr|B9A9C9|B9A9C9_MORAL

Unused ProtScore: 5.62

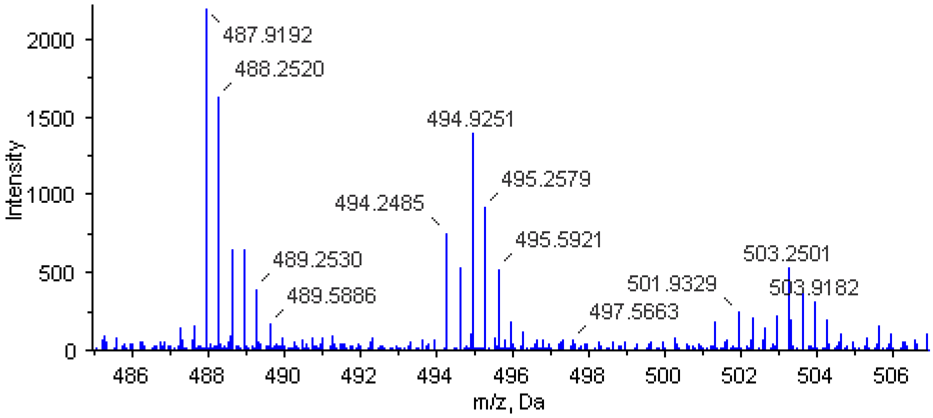
Seq Cov %: 15.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.64

116: 114=E5TL: D5TL=1.25

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MASDDHHHHHDHHHHHDHDHDHDHHGDSRTGAWVGPDGRVYHSHDGLAPHSHEPIYSPGSFSKRAPPLL
TRDFNERAFTIGIGGPVGTGKTALMLALCKFLRDK**YSLAAVTNDIFTK**EDGEFLVKNGALPEERIR**AVE**
TGGCPHAAIREDISINLGPLEELSNLFKADILLCESGGDNLAANFSRELADYIIYIIDVSAGDKIPRKG
GPGITQADLLVINK**TDLAPAVGADLAVMER**DALRMR**DGGPFVFAQVK**HGVGIEEIVNHVLQAWEAATGK
KRH

Protein No.: I-414

Protein name and Species:

Predicted protein OS=Populus trichocarpa GN=POPTRDRAFT_580946 PE=4 SV=1

Accession: tr|B9N3J3|B9N3J3_POPTR

Unused ProtScore: 5.61

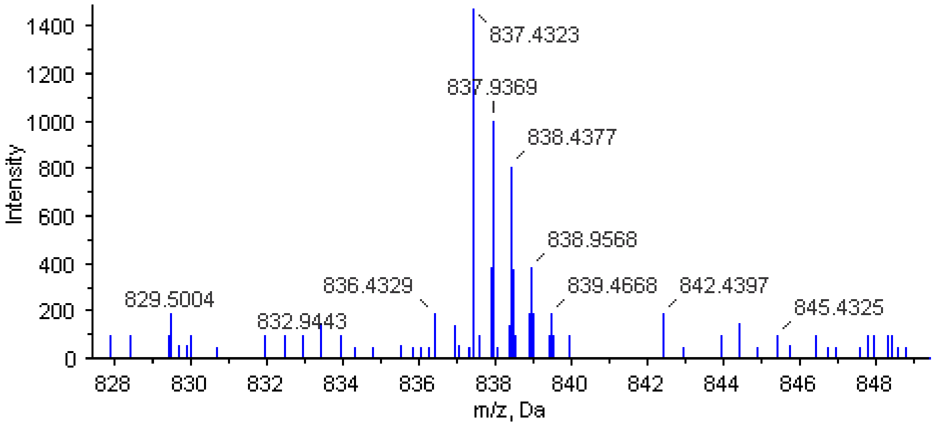
Seq Cov %: 7.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.41

116: 114=E5TL: D5TL=1.27

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGVDYYNTLKVDKNAKDEDLKKAYRKLAMKWHPDKNPNNKKEAEAKFK**QISEAYEVLSDPQKRAIYDQYGEEGLK**GQVPPPETGGPGGATFFSTGDGPATFRFNPRNADDIFAEFFGFSSPFGGMGGGGGGMRGGSRSFGGMFGDDIFSSFGEARPTNPAPRKAPPIENT**LPCSLEELYK**GTTKKMKISREIVDVSGKTLPVEEILTIDIKPGWKRGTKITFPEKGNEQPNVIPADLVFVIDEKPHSTFTREGNDLVVTKKIPLVEALTGC**TVHLTTLDGR**TLTIPVNNVIHPNYEEVVAKEGMPIPKDPSRRGNLRIKFDIKFPTRLSAEQKSGIKKLLNS

Protein No.: I-419

Protein name and Species:

Predicted protein OS=Populus trichocarpa GN=POPTRDRAFT_825512 PE=4 SV=1

Accession: tr|B9IJM2|B9IJM2_POPTR

Unused ProtScore: 5.57

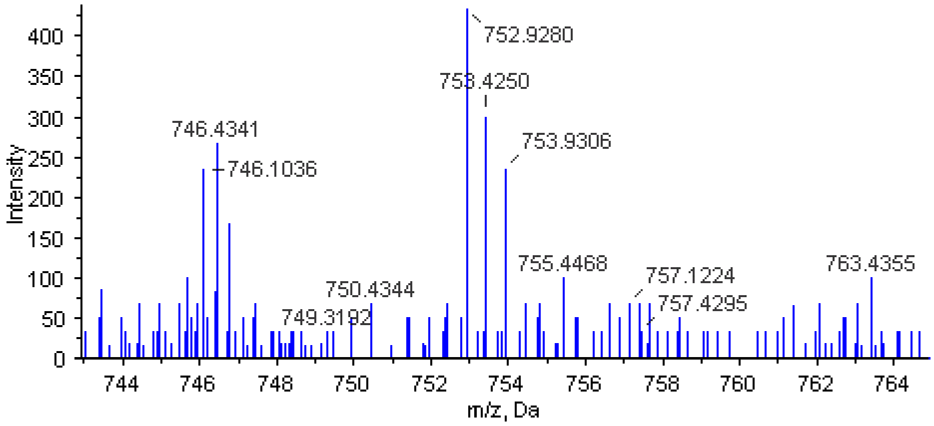
Seq Cov %: 11.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.41

116: 114=E5TL: D5TL=0.73

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MEGAEATRIMMGVNESTIKGYPHASISSR**GAFDWTLQK**IVRSNTSGFKLLFLHVQVPDEDGFDDMDSLYASPEDFKNMKHRDRTR**GLHLLEYFVNR**CHEIGVACEAWIKKGDPK**EVICHEVK**RVQPDLLVVGSR**GLGPFQRVFVGTVSEFCQKHAECPVISIK**R**RADETPQDPVDD**

Protein No.: I-422

Protein name and Species:

Aspartic protease (Fragment) OS=Manihot esculenta PE=2 SV=1

Accession: tr|Q94KV2|Q94KV2_MANES

Unused ProtScore: 5.53

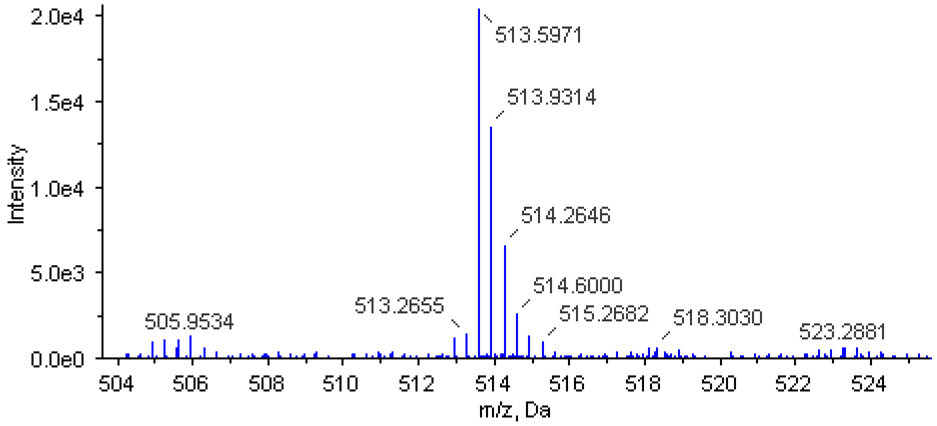
Seq Cov %: 43.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.25

116: 114=E5TL: D5TL=0.40

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

CTFDGSRGVSMTIESVVNENSQEVAGSLHDAMCSTCEMAVIWMQNQLKQNATLER**ILNYANELCER**LPS
PMGESAVDCGSLSTMPNVSFTIGGK**VFDLSPEQYVLKVGEGEAAQCISGFTALDVPPPRGPLWILGDVF**
MGRFHTVFDYGNLRVGFAEAA

Protein No.: I-424

Protein name and Species:

Vacuolar H+-ATPase catalytic subunit A; V-type proton ATPase catalytic subunit A-like OS=Populus trichocarpa

Accession: tr|B9HV14|B9HV14_POPTR

Unused ProtScore: 5.45

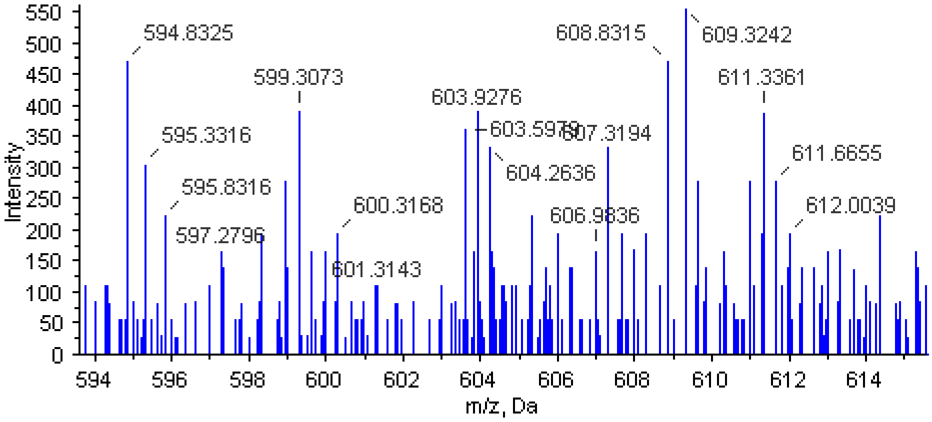
Seq Cov %: 43.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=3.02

116: 114=E5TL: D5TL=2.08

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MPSVYGAR**LTTFEDSEKESEYGYVR**K**VSGPVVVADGMAGAAMYELVRVGHDNLIGEIIR**LEGHSATIQV
YEETAGLMVNDPVLR**THKPLSVELGPGILGNIFDGIQRPLK**TIARI**SGDVYIPR**GVSVPALDKDTLWEF
QPKKIGEGDLVTGGDLYATVFENTLMQHHVALPPDAMGKITFIAPPGQYSLK**DTVLELEFQGVK**KQFTM
LQTWPVRSPRPVASK**LAADTPLLTGQRVLDALFPSVLGGTCAIPGAFGCGKTVISQALSKYSNSDTVVY**
VGCGERGNEMAEVLMDFPQLTMTLPDGREESVMKR**TTLVANTSNMPVAAR**EASIYTGITIAEYFR**DMGY**
NVSMMADSTSRWAEALREISGR**LAEMPADSGYPAYLAARLASFYER**AGKVKCLGSPERTGSVTIVGAVS
PPGGDFSDPVTSATLSIVQVFWGLDKKLAQRKHFPSVNWLISYSKYSGALESFYERFDPDFINIRTKAR
EVLQR**EDDLNEIVQLVGK**DALAETDKITLETAKLLR**EDYLAQNAFTPYDK**FCPFYKSVWMMRNIIHFCN
LANQAVERGAGMDGQKISYSLIKHR**LGDLFYR**LVSQKFEDPAEGEAVLVEKFSK**LHEDLTAGFRALEDE**
TR

Protein No.: I-426

Protein name and Species:

Enolase 2 OS=Hevea brasiliensis GN=ENO2 PE=1 SV=1

Accession: sp|Q9LEI9|ENO2_HEVBR

Unused ProtScore: 5.44

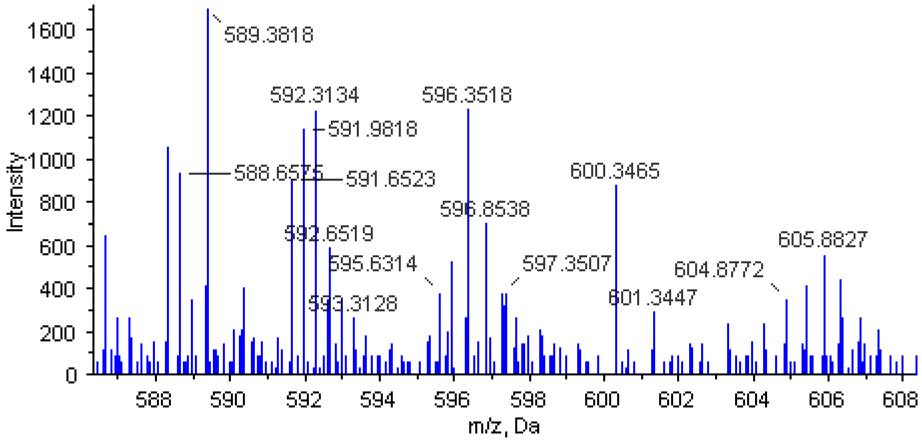
Seq Cov %: 42.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.41

116: 114=E5TL: D5TL=0.52

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

M**AITIVSVR**ARQIFDSR**GNPTVEADVKLSDGYLAR**AAVPRGASTGIYEALELR**DGGSDYLGK**GVSK**AVE**
NVNIIIGPALVGKDPTDQVGIDNFMVQQLDGTVNEWGWCKQKLGANAILAVSLAVCK**AGAHVKGIPLYK**
HVANLAGNK**NLVLPVPAFNVINGGSHAGNKLAMQEFMILPVGASSFK**EAMK**MGAEVYHHLK**SVIKK**KYG**
QDATNVGDEGGFAPNIQENKEGLELLKTAIAKAGYTGK**VVIGMDVAASEFYGSDKTYDLNFKEENNNGS**
QKISGDVLKDLYKSFVTEYPIVSIEDPFDQDDWEHYAK**LTSEIGVKVQIVGDDLLVTNPK**RVEKAIKEK
ACNALLLKVNQIGSVTESIEAVKMSKR**AGWGVMASHR**SGETEDTFIADLSVGLATGQIKTGAPCRSERL
AKYNQLLR**IEEELGAEAVYAGANFR**TPVEPY

Protein No.: I-429

Protein name and Species:

alpha-galactosidase-like isoform 1 [Glycine max] OS=Glycine max PE=2 SV=1

Accession: tr|C6TFR0|C6TFR0_SOYBN

Unused ProtScore: 5.42

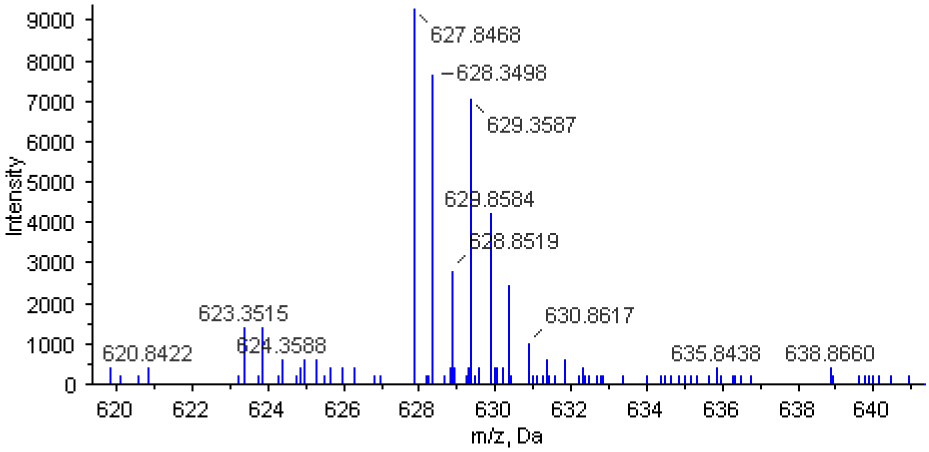
Seq Cov %: 8.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.43

116: 114=E5TL: D5TL=0.58

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MTKQKIRNALLVHLVILFFFSTSVVSARVVSLLQNYGNPIFRSNFHSIYDTSKYGVFQLSNGLGKTPQM
GWNSWNFFACNINEMVIKETADALVSTGLADLGYVYVNIDDCWSSVTRNLKGQLVPDHKTFPSGIK**ALA**
DYVHGKGLKLGIYSDAGVFTCQVRPGSIFHETDDADLFASWGVDYLK**YDNCYNLGIPPK**ERYPPMRDAL
NATGQKIFYSLCEWGVEDPALWADKVGNSWRTTGDINDSWASMTTIADLNDKWAAYAGPGGWNDPDMLE
VGNGGMTYQEYRAHFSIWALAK**APLLIGCDVR**NLTGETLEILSNKEVIAINQDSLGVQGRKVQVSGADG
CRQVWAGPLSGNRLAVALWNRCSKVATIT

Protein No.: I-436

Protein name and Species:

Betaine-aldehyde dehydrogenase OS=Gossypium hirsutum PE=2 SV=1

Accession: tr|Q6S9W9|Q6S9W9_GOSHI

Unused ProtScore: 5.37

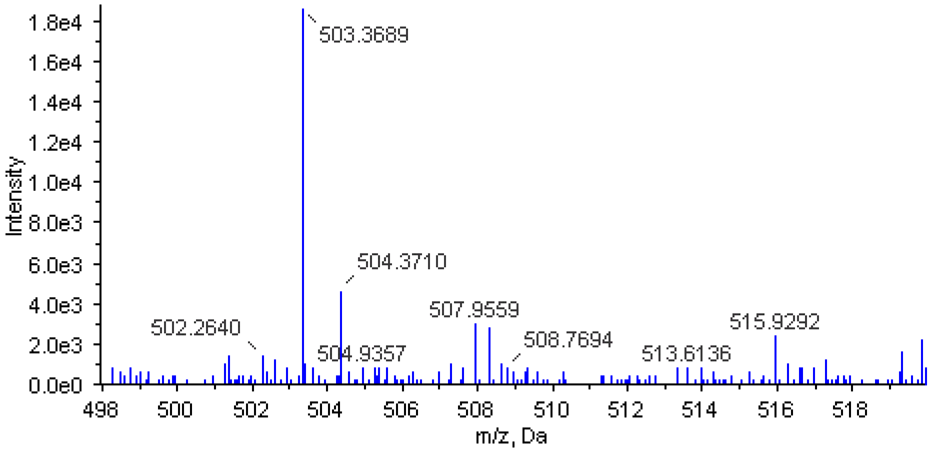
Seq Cov %: 7.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.65

116: 114=E5TL: D5TL=1.35

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAVQVPSRQLFIDGEWREPILKERLPTINPATEEIIGNIPAATAEDVELAVAAARRALSRNKGKDWATA
PGAVRAKYLRAIAAKVTERKTELAKLEAIDCGKPLDEAVWDIEDVAGCFEYYADLAEGLDARQKAPVSL
PMETFKSYVLKEPIGVVGLITPWNYPLLMATWKVAPSLAAGCAAILKPSELASITCLELAKVVKGSRLP
PGVLNILAGLGPEAGAPLASHPDVDKIAFTGSSATGSKIMAAAAQMVKPVSLELGGK**SPIIVFEDVDLD**
KAAEWTAFGCFWTNGQICSATSRLIVHENIAREFLDRLVKWTKNIKISDPFEEGCR**LGPVVSGGQYEK**V
LKFISTAKSEGATILSGGVRPEHLKKGFFVEPTIITDVTTSMQIWR**EEVFGPVLCVK**TFRTEEEALELA
NDTHYGLGAAVISNDLERCDRVSKNLQAGIVWVNCSQPCFCQAPWGGNKRSGFGRELGEWGLDNYLSVK
QVTQYVSDEPWGWYRSPSKL

Protein No.: I-437

Protein name and Species:

2-hydroxyphytanoyl-CoA lyase, putative OS=Ricinus communis GN=RCOM_0466960 PE=3 SV=1

Accession: tr|B9SPZ1|B9SPZ1_RICCO

Unused ProtScore: 5.35

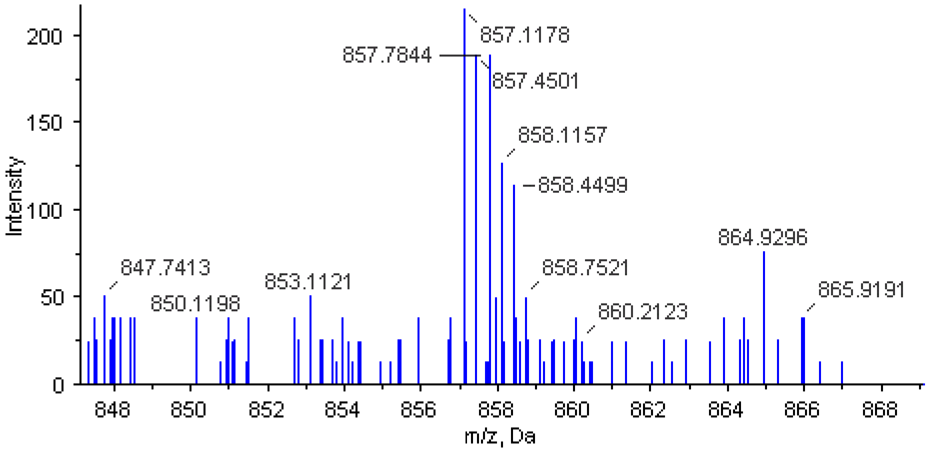
Seq Cov %: 12.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.45

116: 114=E5TL: D5TL=0.61

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MADSNPQNAPESRIDGNILAAKSLARYGVTHMFGVVGIPVTSLANR**AVSLGIR**FVAFHNEQSAGYAASA
YGYLTGKPGLLLTVSGPGCVHGLAGLSNAMVNTWPMVMISGSCDQNDVGKGDFQELDQIEAVKPFVKFS
VKVKDIK**EIPNCVFQVLDR**AVSGRPGGCYLDIPSDVLHQTVDESEAESLLSDAFKPKSIVNEFNTKSSD
FERAAELLRTAER**PLIVFGK**GAAYARAESELKKLVELTGIPFLPTPMGKGILPDNHELAASAARSLAIG
K**CDVALVVGAR**LNWLLHFGQPPKWSKDVKFILVDVCEDEIELRKPHLGLVGDAKK**VLEIINK**EIKDDPF
CLAKNHPWVEAISSKVKENVSRMESQLAK**NVVPFNFLTPMR**IIR**DAILGVGSPAPIVVSEGANTMDVGR**
AVLVQTEPRTRLDAGTWGTMGVGLGYCIAAAVAEPNRLVVAVEGDSGFGFSAMEVETLVRYKLPVVVIV
FNNGGVYGGDRRSPEEIAGPFKDDPAPTSFVPGAAYHILIKAFGGKGYLVATPDELK**SALSESFSAREP**
TVINVTIDPYAGAESGRLQHKN

Protein No.: I-439

Protein name and Species:

Calcium-dependent protein kinase 5; CDPK OS=Arabidopsis thaliana GN=CPK5 PE=1 SV=1

Accession: sp|Q38871|CDPK5_ARATH

Unused ProtScore: 5.34

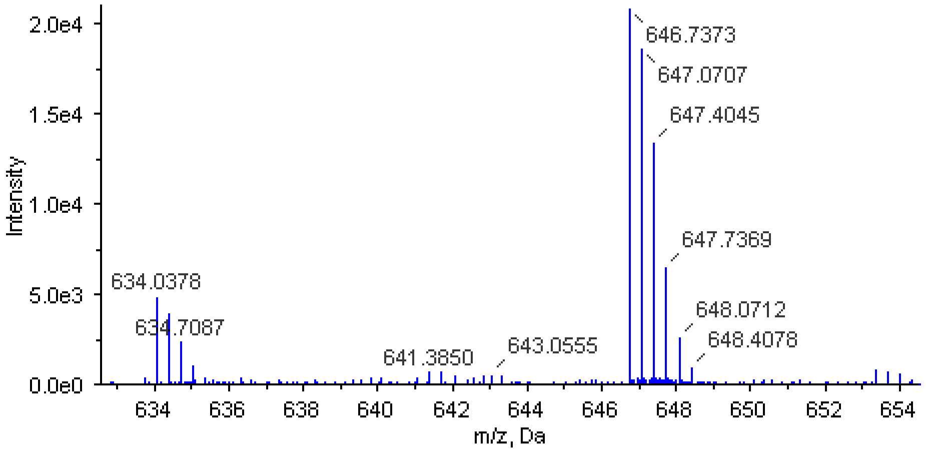
Seq Cov %: 9.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2.58

116: 114=E5TL: D5TL=2.14

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGNSCRGSFKDKLDEGDNNKPEDYSKTSTTNLSSNSDHSPNAADIIAQEFSKDNNSNNNSKDPALVIPL
REPIMRRNPDNQAYYVLGHKTPNIRDIYTLSRKLGQGQFGTTYLCTEIASGVDYACKSISKRKLISKED
VEDVRREIQIMHHLAGHGSIVTIKGAYEDSLYVHIVMELCAGGELFDRIIQRGHYSERKAAELTK**IIVG**
VVEACHSLGVMHRDLKPENFLLVNK**DDDFSLK**AIDFGLSVFFKPGQIFTDVVGSPYYVAPEVLLKRYGP
EADVWTAGVILYILLSGVPPFWAETQQGIFDAVLKGYIDFESDPWPVISDSAKDLIRRMLSSKPAERLT
AHEVLRHPWICENGVAPDRALDPAVLSRLKQFSAMNKLKKMALK**VIAESLSEEEIAGLREMFQAMDTDN**
SGAITFDELKAGLRKYGSTLKDTEIHDLMDAADVDNSGTIDYSEFIAATIHLNKLEREEHLVAAFQYFD
KDGSGFITIDELQQACVEHGMADVF**LEDIIK**EVDQNNDGKIDYGEFVEMMQKGNAGVGRRTMRNSLNIS
MRDA

Protein No.: I-441

Protein name and Species:

O-linked n-acetylglucosamine transferase, ogt, putative OS=Ricinus communis GN=RCOM_1259290 PE=4 SV=1

Accession: tr|B9SX16|B9SX16_RICCO

Unused ProtScore: 5.34

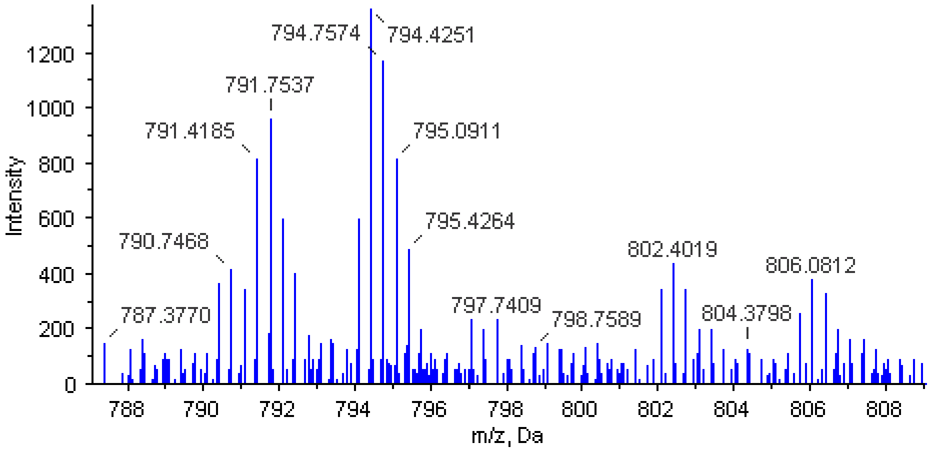
Seq Cov %: 8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.10

116: 114=E5TL: D5TL=0.39

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAWTEKNNGNGKEGGPIEDNGFLKGTQEPSPSASGSPVAVAAGLKGIEEKDSLSYANILRSRNK**FVDAL**
AIYESVLEKDSGNVEAYIGKGICLQMQNMGRLAFDSFAEAIK**LDPQNACALTHCGILYK**EEGRLVEAAE
SYQKALRADPLYKPAAECLSIVLTDLGTSLK**LSGNTQEGIQK**YYEALKIDPHYAPAYYNLGVVYSEMMQ
YDTALNCYEKAALERPMYAEAYCNMGVIYKNR**GDLESAIACYER**CLAVSPNFEIAKNNMAIALTDLGTK
VKLEGDINQGIAYYKKALYYNWHYADAMYNLGVAYGEMLKFDNAIVFYELAFHFNPHCAEACNNLGVIY
KDRDNLDKAVECYQTALSIKPNFSQSLNNLGVVYTVQGKMDAAASMIEK**AIMANPTYAEAYNNLGVLYR**
DAGNIPMAINAYEQCLKIDPDSRNAGQNRLLAMNYINEGHDEKLFEAHRDWGRRFMRLYPQYTMWDNPK
DLDRPLVIGYVSPDYFTHSVSYFIEAPLVYHDYANYKVVVYSAVVKADAKTIRFREKVLKQGGIWRDIY
GIDEKKVASMVREDNVDILVELTGHTANNKLGMMACRPAPIQVTWIGYPNTTGLPTIDYRITDSLADPR
DTKQKHVEELVRLPDCFLCYTPSPEAGPVCPTPALANGFITFGSFNNLAKITPKVLQVWARILCAVPNS
RLVVKCKPFCCDSVRQRFLTMLEELGLESLRVDLLPLILLNHDHMQAYSLMDISLDTFPYAGTTTTCES
LYMGVPCVTMAGAIHAHNVGVSLLSKVGLGHLVAQNEDNYVQLALQLASDIPALSNLRMSLRDLMSKSP
VCDGSKFTLGLESSYRDMWHRYCKGDVPSLKRMELLKQQKGSEAVPNENFEPTRNAFPVEGPPESVKLN
GYNIVSSSILNRSSEENVSQTQLNHTTNSDKPS

Protein No.: I-447

Protein name and Species:

Triosephosphate isomerase OS=Vitis vinifera GN=VIT_13s0019g01090 PE=3 SV=1

Accession: tr|D7TLU7|D7TLU7_VITVI

Unused ProtScore: 5.22

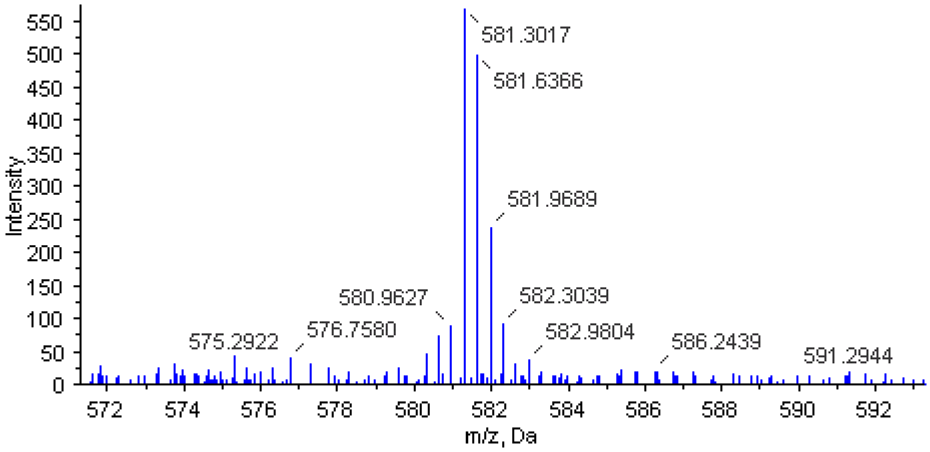
Seq Cov %: 16.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.21

116: 114=E5TL: D5TL=0.17

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGRKFFVGGNWKCNGTGEEVKKIVSTLNAGEVPSGDVVEVVVSPPFVFLPLVKSTLRPDFHVAAQNCWV
KKGGAFTGEISAEMLVNLGIPWVIIGHSERRLLLNESNEFVGEKVAYALSKGLK**VIACVGETLEQRESG**
STMEVVAAQTKAIADKVSNWANVVLAYEPVWAIGTGK**VATPAQAQEVHSELR**NWFQANASPEVAATIRI
IYGGSVSGANCKELAAKPDVDGFLVGGASLKPEFIDIIKSAEVKKNC

Protein No.: I-448

Protein name and Species:

Serine-threonine kinase receptor-associated protein, putative OS=Ricinus communis GN=RCOM_0897280 PE=4 SV=1

Accession: tr|B9RUZ3|B9RUZ3_RICCO

Unused ProtScore: 5.22

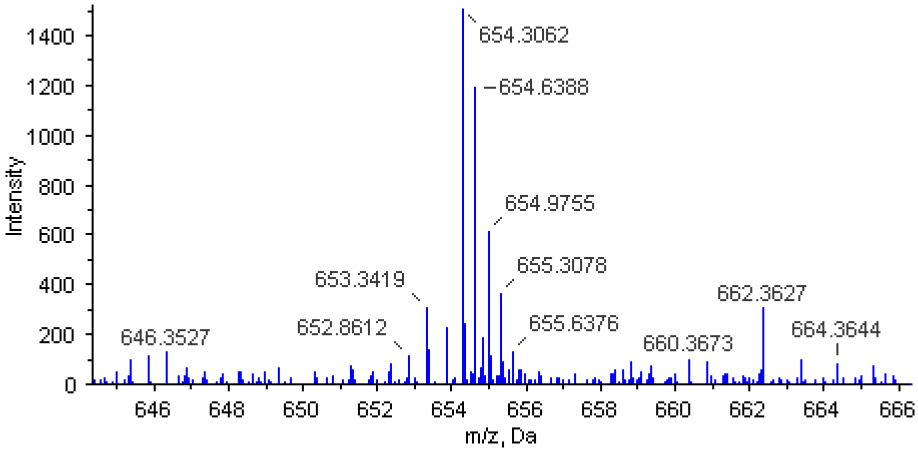
Seq Cov %: 17.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=9.73

116: 114=E5TL: D5TL=2.08

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDKKKVAVPLVCHGHSRPVVDLFYSPVTPDGFFLISASKDSSPMLRNGETGDWIGTFEGHKGAVWSCSL
DTKALRAASASADFTAKLWDALTGDELHSFEHRHIVRACAFSEDTHLLLTGGMEKILRLFDLNRPDAPP
REVNSSPGSIRTVAWLHSDQTILSSCTDMGGVRLWDIRSGKIVQTLETKSPVTSAEVSQDGRYITTADG
STVKFWDANHFGLVKSYNMPCNVESASLEPKLGNKFVAGGEDMWIHVFDFHTGEQIGCNKGHHGPVHCL
RFSPGGESYASGSEDGTIRIWQTGPQNHDENGPTGKAMASADDVTQKIKGKGGKTAGTDP

Protein No.: I-449

Protein name and Species:

40S ribosomal protein OS=Populus trichocarpa GN=POPTRDRAFT_814470 PE=2 SV=1

Accession: tr|A9PGL4|A9PGL4_POPTR

Unused ProtScore: 5.22

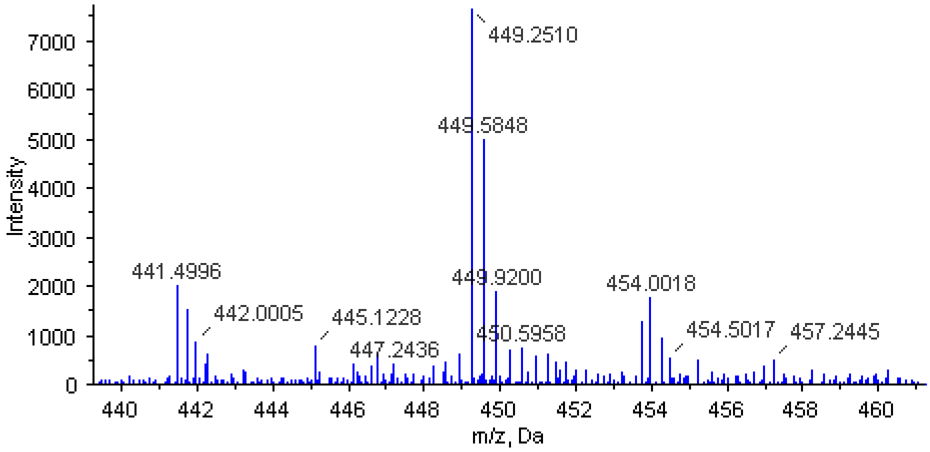
Seq Cov %: 21.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.56

116: 114=E5TL: D5TL=1.71

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MATAKSVK**DVSPHEFVK**AYSAHLKRSGKIELPLWTDIVKTGKFK**ELAPYDPDWYYVR**AASMARKIYIRG
GLGVGAFRRIYGGSKRNGSRPPHFCKSSGSIARHILQQLQNVNIIDIDPKGGRRITSSGQRDLDQVAGR
IVVAP

Protein No.: I-453

Protein name and Species:

quinone oxidoreductase, putative OS=Populus trichocarpa GN=POPTRDRAFT_826614 PE=4 SV=1

Accession: tr|B9MU39|B9MU39_POPTR

Unused ProtScore: 5.19

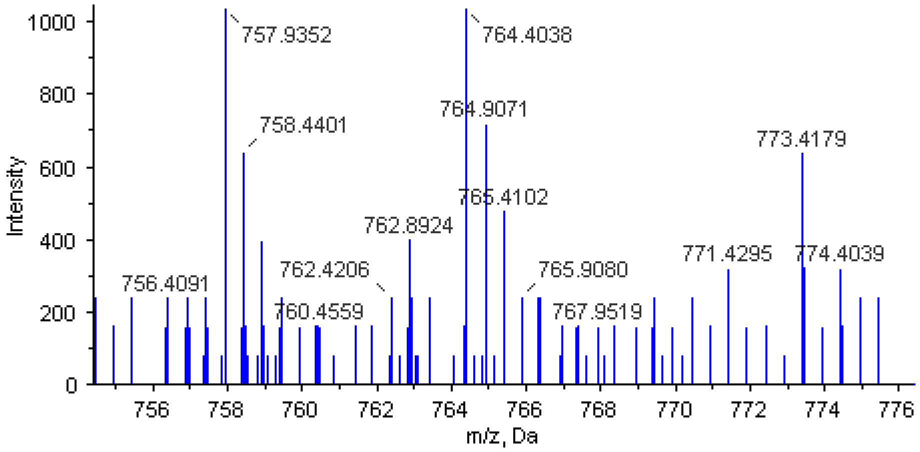
Seq Cov %: 20.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.38

116: 114=E5TL: D5TL=0.53

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MVKAIR**VHELGGPEVLK**WEDVEIGEPGEGEIRVKNKAIGLNFIDVYYRKGVYTASTMPFIPGREAVGEV
IAVGPGLTGRKVGDVVAYAGDPMGSYAEEQILPANKVVSVPESISPVIAASVMLKGMTTQFLLRRCFKV
EPGHTILVHAAAGGVGSLLCQWANALGATVIGTVSTKEKAAQAKEDGCQHVILYQEEDFVARVNEITSC
NGVDVVYDSVGK**DTFQGSLACLK**TR**GYMVSFGQSSGTPDPVPLSALAPK**SLFLTRPSMMHYNQTRDELL
GAAGELFSALASGVLRVR**VNHTYPLSQAAQAHADIESR**KTTGSVVLIP

Protein No.: I-456

Protein name and Species:

Beta-1,3-glucanase OS=Hevea brasiliensis GN=Glu I PE=4 SV=1

Accession: tr|Q7XJ83|Q7XJ83_HEVBR

Unused ProtScore: 5.16

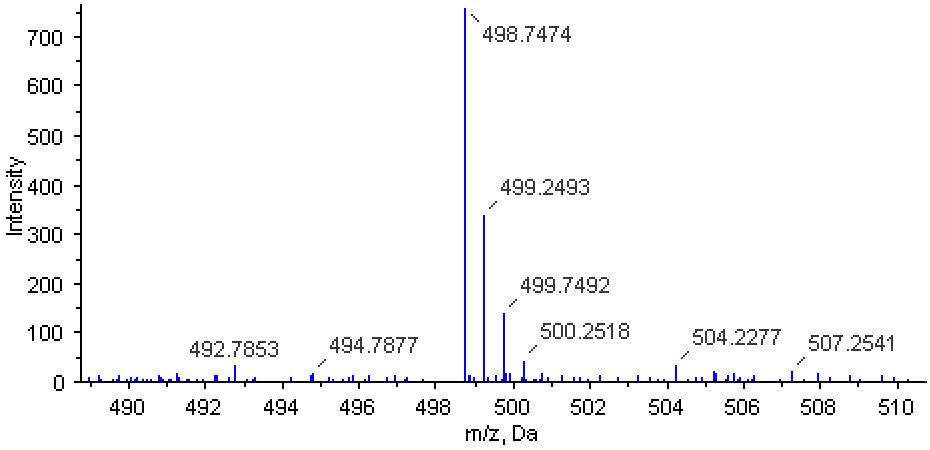
Seq Cov %: 59.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.13

116: 114=E5TL: D5TL=0.65

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAISSSTSGTSSSLPSRTTVMLLLIFFTASLG**ITDAQVGVCYGMQGNNLPPVSEVIALYK**QSNIKRMR**IYDPNRAVLEALRGSNIELILGVPNSDLQSLTNPSNANSWVQK**NVR**GFWSSVLFR**YIAVGNEISPVNG**GTAWLAQFVLPAMRNIHDAIRSAGLQDQIKVSTAIDLTLVGNSYPPSAGAFR**DDVR**SYLDPIIGFLSSIRSPLLANIYPYFTYAGNPRDISLPYALFTSPSVVVWDGQR**GYK**NLFDATLDALYSALER**ASGGSLEVVVSESGWPSAGAF**AATFDNGRTYLSNLIQHVKGG**TPKRPNR**AIETYLFAMFDENKKQPEVEKHFGLFFPDK**RPK**YNLNFGAEK**NWDISTEHNAT**ILFLK**SDM

Protein No.: I-459

Protein name and Species:

ATP-citrate synthase beta chain OS=Populus trichocarpa GN=POPTRDRAFT_656642 PE=4 SV=1

Accession: tr|B9HIN6|B9HIN6_POPTR

Unused ProtScore: 5.11

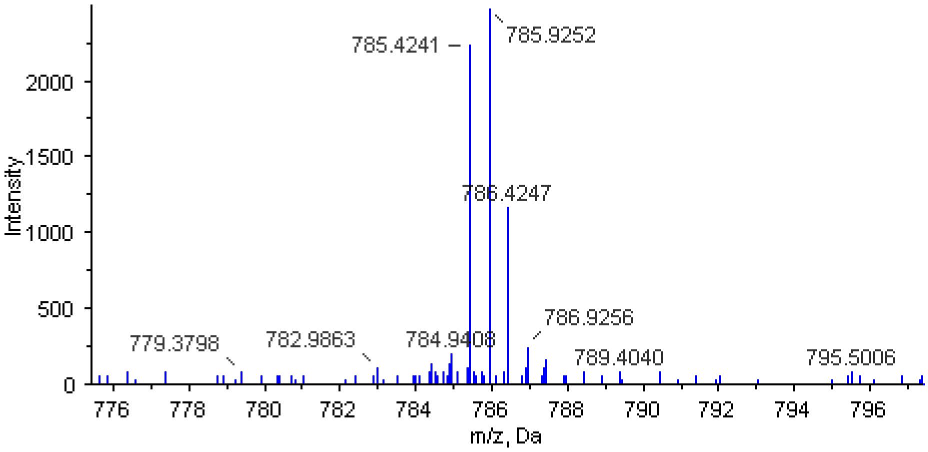
Seq Cov %: 38.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.47

116: 114=E5TL: D5TL=0.54

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MATGQLFSR**TTQALFYNYK**QLPIQR**MLDFDFLCGRELPSVAGIINPGAEGFQK**LFFGQEEIAIPVHSTI
EAACAAHPTADVFINFASFRSAAASSMSALKQPTVR**VVAIIAEGVPEADAK**QLIAYARANNK**VVIGPAT**
VGGIQAGAFKIGDTAGTIDNIIACKLYRPGSVGFVSKSGGMSNELYNSIARVTDGIYEGIAIGGDVFPG
STLSDHVLRFNNIPQVKMIVVLGELGGR**DEYSLVEALK**QGKVSKPVVAWVSGTCARLFK**SEVQFGHAGA**
KSGGEMESAQAKNQALK**DAGAVVPTSYEAFETAIK**ETFEKLVEEGKISSVKEFTPPQIPEDLNIAIKSG
KVR**APTHIISTISDDR**GEEPCYAGVPMSSIVEQGYGVGDVISLLWFKRSLPRYCTHFIEICIMLCADHG
PCVSGAHNTIVTARAGK**DLVSSLVSGLLTIGPRFGGAIDDAAR**YFKDAYDR**GLTPYEFVESMK**KKGIRV
PGIGHRIKRGDNRDK**RVELLQLFAR**THFPSVK**YMEYAVQVETYTLSK**ANNLVLNVDGAIGSLFLDLLAG
SGMFTKQEIDEIVGIGYLNGLFVLAR**SIGLIGHTFDQK**RLKQPLYRHPWEDVLYSK

Protein No.: I-467

Protein name and Species:

COP9 signalosome complex subunit 1 [Vitis vinifera] OS=Vitis vinifera GN=VIT_15s0048g01980 PE=4 SV=1

Accession: tr|D7U7I9|D7U7I9_VITVI

Unused ProtScore: 4.99

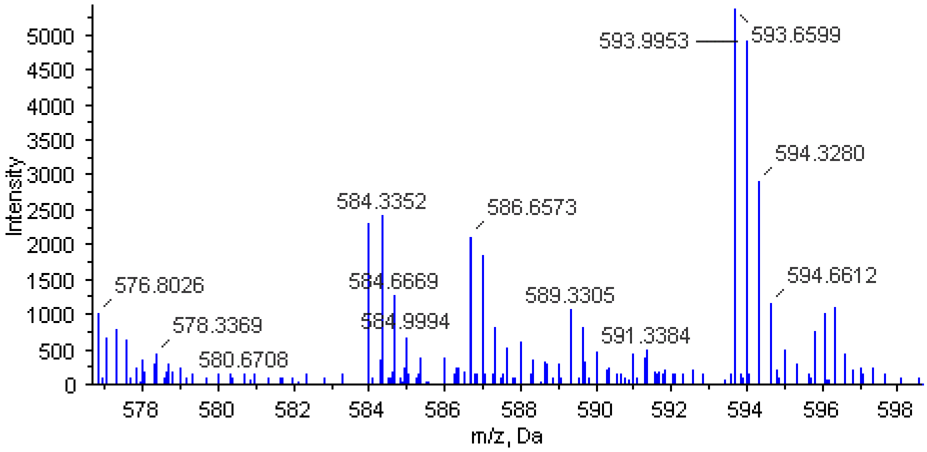
Seq Cov %: 7.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.59

116: 114=E5TL: D5TL=1.10

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MEGEEESSAGAMIDEIYSNGGDAKRNRPIISGEALDIEAYASLYSGRTKITRLLFIADRCENRQMQMEA
YRMAYDEIKKGENTQLYREVVQKIDGRLGPQYGLDLVWTESVERRADQRKEK**LENELNAYR**TNLIKESI
RMGYNDFGDFYYAHGLLADAFKNYVRTRDYCTTSKHIIHMCLNAILVSIEMGQFTHVTSYVSKAEQTPE
ALDPVTVAKLR**CAAGLAHLEAK**KYKLAARKFLETGAELGNNYTEVIAPQDVATYGGLCALASFDRTELK
NKVIDNLNFR**NFLELVPEVR**ELIHDFYSSHYASCLDYLGNLKTNLLLDIHLHDHVEMLYNQIRHKALIQ
YTHPFVSVDLRMMANAFKTSVAGLEK**ELEALITDNQIQAR**IDSHNKILYARHADQRNATFQRVLQTGNE
FDRDVRAMLLRANLLKHEYNLRASRKP

Protein No.: I-475

Protein name and Species:

Amidase, putative OS=Ricinus communis GN=RCOM_1431340 PE=4 SV=1

Accession: tr|B9RF45|B9RF45_RICCO

Unused ProtScore: 4.89

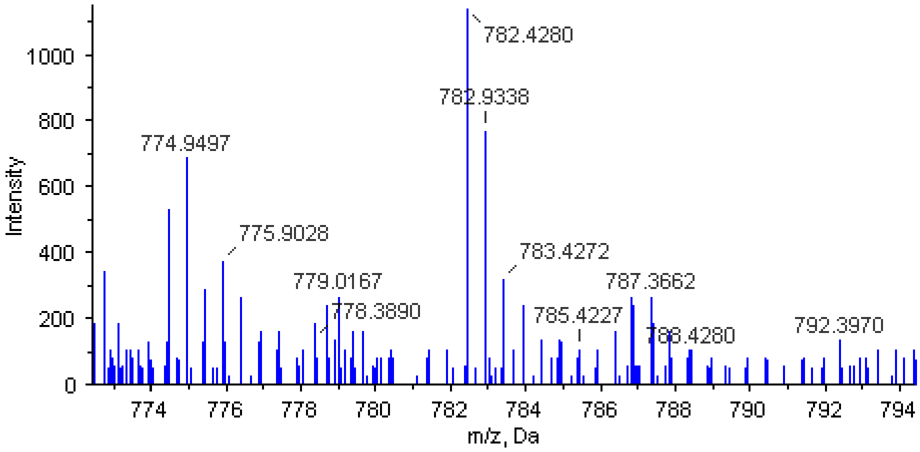
Seq Cov %: 5.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.60

116: 114=E5TL: D5TL=0.64

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MTHQFYELAITLCCSVLSDSNQSPACQWIKGWPTENDQIVLWKIGRPAKAACQIDRESWDRAQSLTVRA
VTDMAISPDYGAFMEKFVLKPSSSSDQLPLHSLTFAVKDIFDVDGYVTGFGNPDWARTHSAATATAPAV
LAVLRGGATCVGKVIMDEMAYSINGENAHYGTPTNPSAPDR**VPGGSSSGSAVAVGAK**LVDFSLGSDTGG
SVRVPASYCGILGFRPSHGVVSVSGVIPMAQSFDTVGWFSRNPVILKHVGRLLLQLPDVDRTKPNQIFI
AEDCFQLSSIPKK**RVSQVLVKSVEKLFGGDIVK**HVNLGDYVEDKVPSLRHFMSKEIKEQEYNIAPLAAL
SSAMRMLQRYEFKTNHGEWVTTVKPDFGPGLKERIWEAVRSTEENIDAFQSVRTELRAALTNLLEEFGI
IAIPTVPGVPPK**LNTDPTTLEIFR**AKAFSLLSITGVSGFCQVSIPLGMHDGLPVSISLLAKHGSDVFLL
NVVETLYDTLQEEVCNI

Protein No.: I-478

Protein name and Species:

Ligatin, putative OS=Ricinus communis GN=RCOM_1045170 PE=4 SV=1

Accession: tr|B9SBV7|B9SBV7_RICCO

Unused ProtScore: 4.86

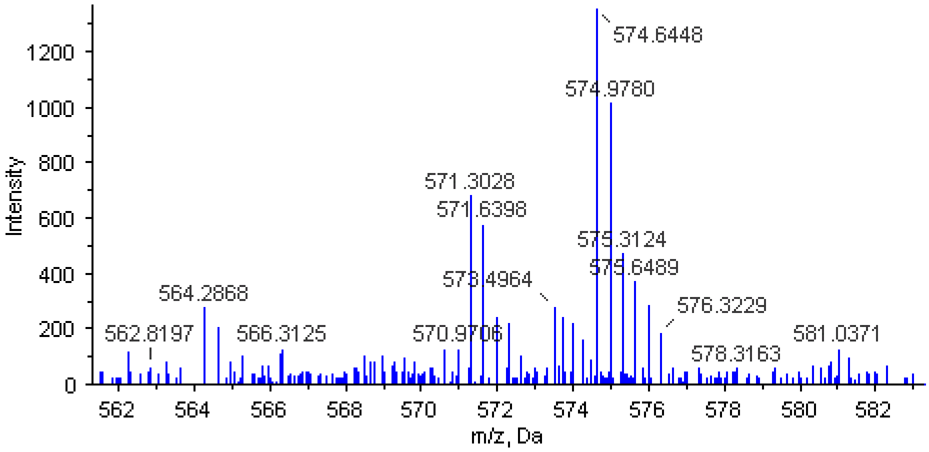
Seq Cov %: 5.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.52

116: 114=E5TL: D5TL=1.06

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MFKKAVEAKSHQRLSGADRKKLKRSIRDKFPRASDADIDTLLPPKADITVAKFQNRVHVYGVEGGFPMF

FDVDGRGTDIFPTVFALWNVPEFLPSFMLKGGEVSRYILGGADLMFPGISIPAEGLPSFSAGEPWAVKV

PGNPAPIAVGSTTMSSSEAIKAGLRGKALRITHYYRDLLWESVEGHYVPNAGFFEDVVFEDPAFTSSIQ

VSDSYETAYDVSNDQLNKVETDEIGESADVNDVISESHPSTITELDSKESKHDIIEQVTAVVSDMKVMD

NDTADESTIEEQHILSTGDVDAYLDKCLLQALHTTVKDKDLPMPGSTLWSNHVLPCRPPGVLLDIKKSS

HKKLSKWLQAKSSAGLISVKEDKYKKETVLISINRSHPDYLSFKPEKRQEQKIDQAGDRATSESQSKKM

LEVAEIYKPSVHVNPIFASVGADTGKLYTASEASDIVFNYIEKENLVKPTNKSFVVLDATLCDALFKGT

VKK**GSTYPTEIHK**KDLGSIFISR**MQAHYIVTR**GSDSAIRKGSLKTIQILTERRQGNKKVTKVSGLEQFL

MDAEALASELQKK**FACSTSVQELPGK**KGNEVLIQGGVIDDVAR**HLVEQYGVPK**R**YIEVLDK**TKK

Protein No.: I-481

Protein name and Species:

Steroid dehydrogenase, putative OS=Ricinus communis GN=RCOM_1082860 PE=3 SV=1

Accession: tr|B9RMR2|B9RMR2_RICCO

Unused ProtScore: 4.82

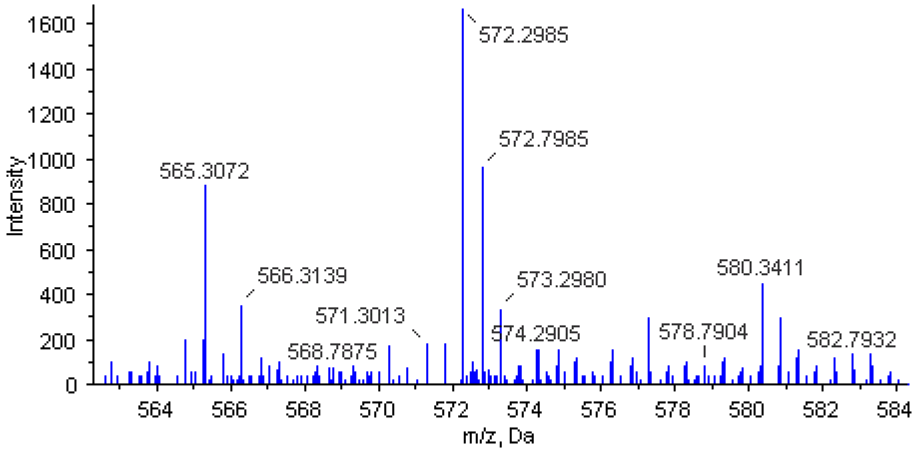
Seq Cov %: 5.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=3.40

116: 114=E5TL: D5TL=1.38

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MELCFVDKLKSQPLWFLVLFSLGSLSLLRCFFTILNWVYVNFLRPAKNLKKYGSWALVTGPTDGIGK**GF**
AFQLARKGLNLVLVARNPDKLKDVSDSILSKYGKVQIKTVVVDFSGDIDEGVKRIKDTVEGLDVGVLIN
NVGVSYPYAR**FFHEVDEELLK**NLIKVNVEGTTKVTHAVLPGMLKRKKGAIINIGSGAAIVIPSDPLYAV
YAATK**AYIDQFSR**CLYVEYKKSGIDVQCQVPLYVATKMASIRRSSFFVPSTDDYARAGLRWVGYEPRCT
PYWPHSLIWGLISIVPEFAVDAWRYKFNLGIRKRGQQKDARKKE

Protein No.: I-482

Protein name and Species:

Importin alpha-2 subunit, putative OS=Ricinus communis GN=RCOM_0819430 PE=4 SV=1

Accession: **tr|B9SGQ4|B9SGQ4_RICCO**

Unused ProtScore: **4.81**

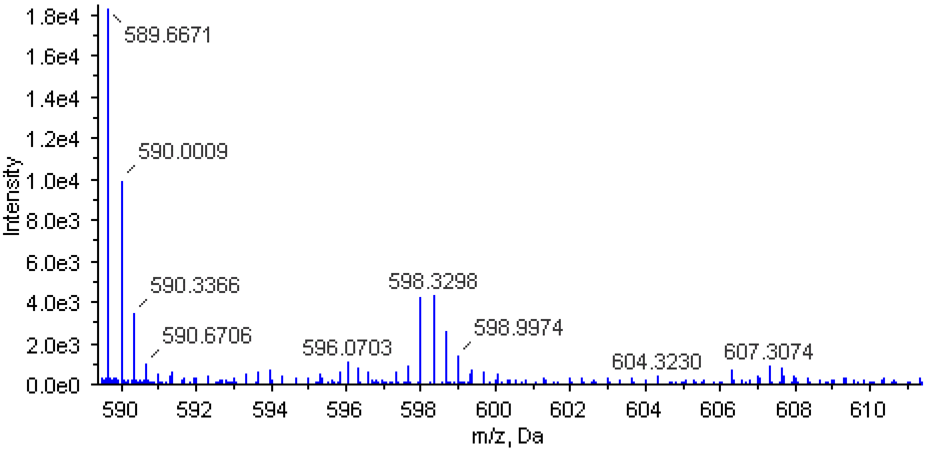
Seq Cov %: **11.6**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.61

116: 114=E5TL: D5TL=0.56

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAEEGLTSLKREPIKSSVGNVAAQKRKQNAVAVGKERRESLVRAKRLCRVGTSGDSDSEMIIDEEQSIL
DAQTSSAVEELKSAVAFQGKGAMQKKVGALRELRRLLSRSEFPPIEAAIKAGAIILLVQCLSFGSPDEQ
LLEAAWCLTNIAAGKPEETKALLPALPLLIAHLGERSSSPVAEQCAWALGNVAGEGEDLR**NVLLSQGAL**
PPLARMMLPNRGSTVR**TAAWALSNLIK**GPDPKAATELIRVDGVLDAIVRHLRKADEELATEVAWAVVYL
SALSNVATSMLVKSDVLQLLIQR**LATSNSLQLLIPVLR**SLGNLIAGDSHTISAVLLPGIEITDSIIAVL
VKCLKSEHRVLKKEAAWVLSNIAAGSVEHKQLIYCSEAVPLLLR**LLSTAPFDLR**KEVAYVLGNLCVAPA
EGTGKPDLILEHLVSLVSRGCLPGFIDLVRSVDTEAARLGLQFIELVLRGMPNGEGPKLVEQENGIEAM
ER**FQFHENEDLR**NMANGLVDRYFGEDYGLTELTD

Protein No.: I-485

Protein name and Species:

Adenylyl cyclase-associated protein OS=Populus trichocarpa GN=POPTRDRAFT_722043 PE=3 SV=1

Accession: tr|B9HRN7|B9HRN7_POPTR

Unused ProtScore: 4.79

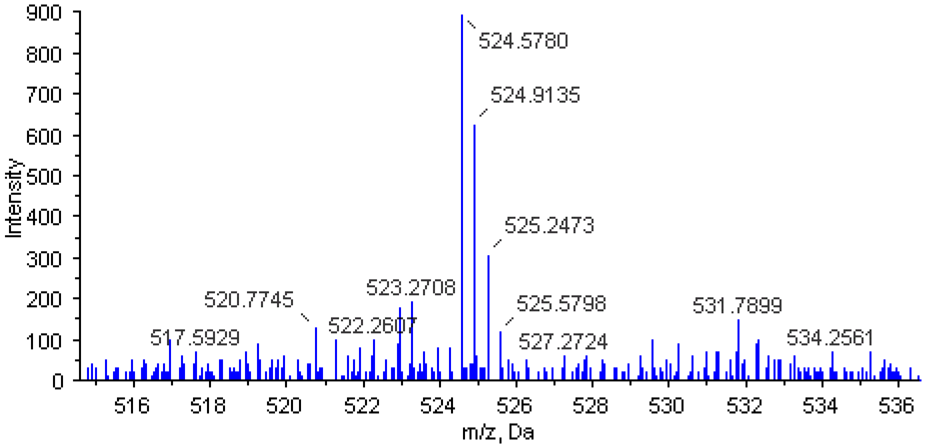
Seq Cov %: 8.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.58

116: 114=E5TL: D5TL=0.72

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MEEKLIERLESAVARLEALSLRSGGLALSGGDDSAATDPSIVAFDDFIGTFFVRVSSAAEKIGGQVLEV
TRILEQALNVQKELLIKIKQTRKPDLAGLAEFLKPLNEVIMK**ANAMTEGRR**SDFFNHLKAAADSLTALA
WIAYTGKDCGMSMPIAHVEESWQMAEFYSNK**ILVQYK**SKDPNHVEWAKALKDLYLPGLRDYVKSHYPLG
PVWSTTGKATASAPSKAPAPPPPPPASLFSSESSQPSSSKPKEGMAAVFQEISSGKSVTTGSLKKVTDD
MKTKNRADRTGVVAVTEKGGRASAPSFSKAGPPK**LELQMGR**KWVVENQIGKKNLVIDDCDAK**QSVYVFG**
CKDSVLQIQGKVNNITIDKCTKMGVVFTDVVAACEIVNCTGVEVQCQGSAPTISVDNTGGCQLYLSK**DS**
LGASITTAKSSEINVLVPGAEPGGDLAEHALPQQFIHAFK**DGQFETTPVSHSGG**

Protein No.: I-487

Protein name and Species:

Mevalonate kinase, putative OS=Ricinus communis GN=RCOM_1431350 PE=3 SV=1

Accession: tr|B9RF46|B9RF46_RICCO

Unused ProtScore: 4.74

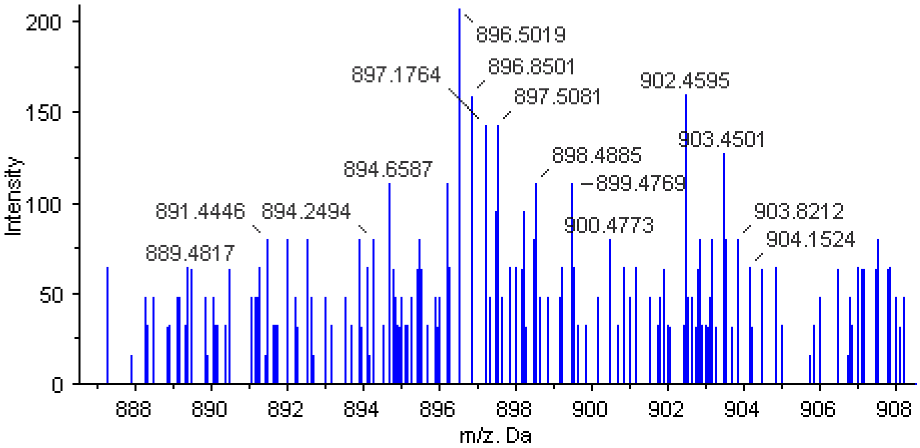
Seq Cov %: 10.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.66

116: 114=E5TL: D5TL=0.89

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MEVKARAPGKIILSGEHAVVHGSTAVAAALDLYTYVSISFPSSGNDGTLKLQLKDLALEFSWPVAKIREALPNLGVPSSSTPTSCSIESLKSISALVEEQDIPEAKIALASGVSAFLWLYTSIQGFEPATVVVTSDLPLGSGLGSSAAYCVSLSAALLAFSDSVDVDRGHQGWLKFGVPDLELLNKWAFEGEKIIHGK**PSGIDNTVSTYGNMIK**FRSGNLTRMKSNMPLKMLITNTRVGRNTK**ALVAGVSER**TFRHPNAMSFVFNAVDSISNELANIIQSPAPDELSITEKEEMLEELMEMNQGLLQCMGVSHASIETVLQTTLKYKLASK**LTGAGGGGCVLTLLPTLLSGTVVDK**VIAELESSGFQCLIAGIGGDGAEICFASSS

Protein No.: I-498

Protein name and Species:

Heat shock protein 90-2 OS=Glycine max PE=2 SV=1

Accession: tr|B6EBD6|B6EBD6_SOYBN

Unused ProtScore: 4.69

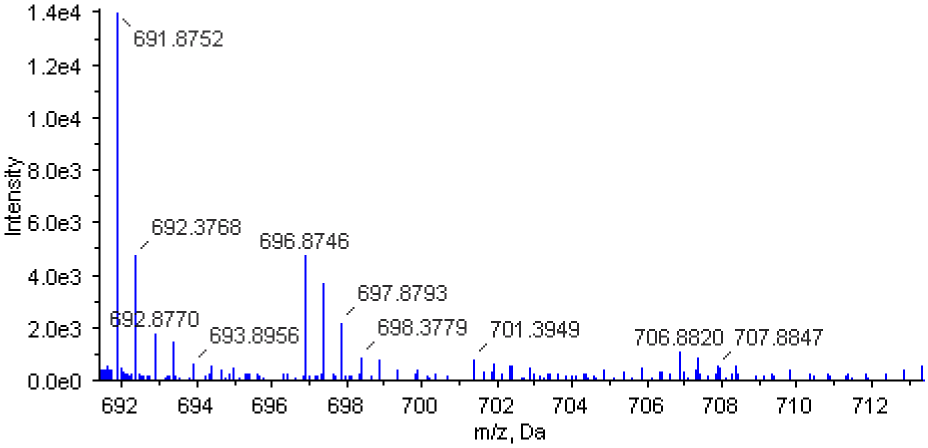
Seq Cov %: 30.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.10

116: 114=E5TL: D5TL=0.44

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MASETETFAFQAEINQLLSLIINTFYSNKEIFLR**ELISNASDALDKIRFESLTDK**SK**LDAQPELFIHII**
PDKTNNTLSIIDSGIGMTKADLVNNLGTIARSGTKEFMEALAAGADVSMIGQFGVGFYSAYLVADKVIV
TTKHNDDEQYVWESHAGGSFTVTRDTSGENLGRGTK**ITLFLKEDQLEYLEERRLKDLIK**KHSEFISYPI
SLWIEKTTEKEISDDEDEEEKKDEEGKVEDVDEDKEKEEKKKKTIKEVSHEWSLVNKQKPIWMRKPEEI
TK**EEYAAFYK**SLTNDWEEHLAVKHFSVEGQLEFKAVLFIPK**RAPFDLFDTK**KKPNNIKLYVRRVFIMDN
CEELMPEYLSFVK**GIVDSEDLPLNISR**EMLQQNKILKVIRKNLVKKCIEMFFEIAENKEDYNK**FYEAFS**
KNLK**LGIHEDSQNK**TK**LAELLR**YHSTK**SGDEMTSLKDYVTR**MK**EGQNDIYYITGESKKAVENSPFLEK**L
KKKGFEVLY**MVDAIDEYAVGQLK**EFEGKK**LVSATK**EGLKLDESEDEKKKKEELKEKFEGLCHVIKDVLG
DKVEK**VVVSDRVVDSPCCLVTGEYGWTANMER**IMKAQALRDSSMAGYMSSKKTMEINPENPIMEELRKR
ADADKNDKSVKDLVLLLFETALLTSGFSLDDPNTFGNRIHRMLK**LGLSIDEDAGEADADMPPLEDADAD**
AEGSKMEEVD

Protein No.: I-503

Protein name and Species:

isoflavone reductase related protein OS=Populus trichocarpa PE=2 SV=1

Accession: tr|A9PF66|A9PF66_POPTR

Unused ProtScore: 4.65

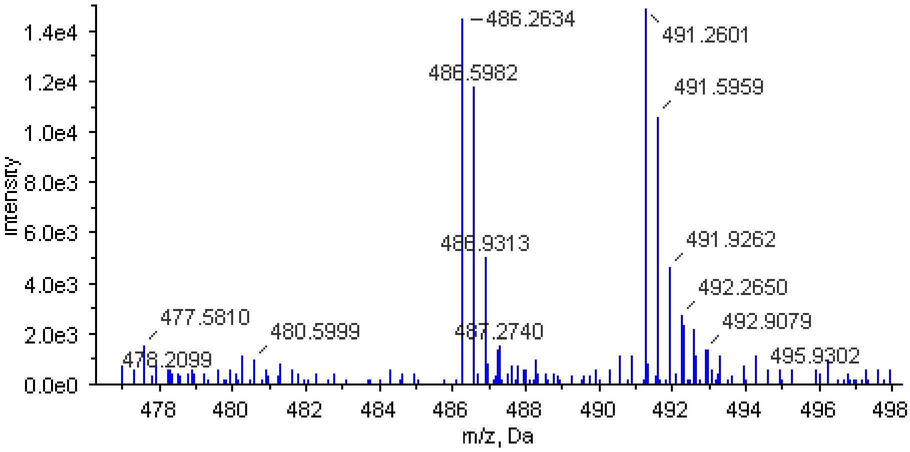
Seq Cov %: 4.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.60

116: 114=E5TL: D5TL=0.69

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MASKILFIGGTGYIGKFIVEASAKAGHPTFVLVRESTLSNPAKSVVIDNFKNLGVNFLIGDLFDHESLV
KAIKQVDVVISTVGHAQLVEQDRIIAAIKEAGNVKR**FFPSEFGNDVDRVNAVEPAK**SAFATKANVRRAI
EAEGIPYTYVSSNFFSGYFLLSFNQPGATAPPRDK**VVILGDGNPKAVFNKEDDIATYTIK**AVDDPRTLN
KILYIKPPANTISFNDLVSLWEKKIGKTLER**IYVPEEQLLK**NIQEASVPVNVVLSIGHSVFVKGDHTNF
EIEPSFGVEASELYPDVKYTTVDEYLKQFV

Protein No.: I-504

Protein name and Species:

Superoxide dismutase (Fragment) OS=Hevea brasiliensis GN=sod PE=2 SV=1

Accession: tr|Q9STB5|Q9STB5_HEVBR

Unused ProtScore: 4.65

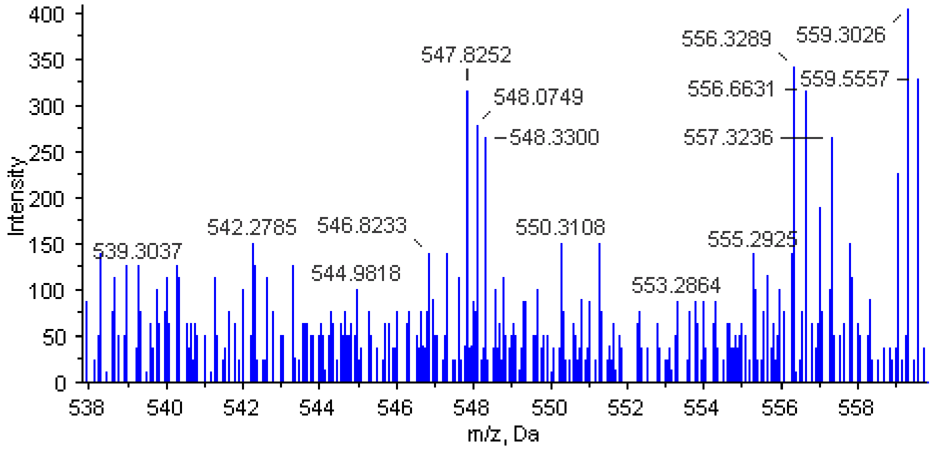
Seq Cov %: 13.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.44

116: 114=E5TL: D5TL=0.57

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

QTFSLPDLPYDYGALEPAISGEIMQLHHQKHHQTYITNYNK**ALEQLNDAIEK**GDSAAVVKLQSAIKFNG
GGHVNHSIFWKNLAPVREGGGELPHGSLGWAIDADFGSLEKLIQLMNAEGVALQGSGWVWLALDKELK**K**
LVVETTANQDPLVTKGPTLVPLLGIDVWEHAYYLQYKNVRPDYLKNIWKVMNWKYASEVYAKECPSS

Protein No.: I-506

Protein name and Species:

Cysteine synthase OS=Glycine max PE=2 SV=1

Accession: tr|C6TIP9|C6TIP9_SOYBN

Unused ProtScore: 4.63

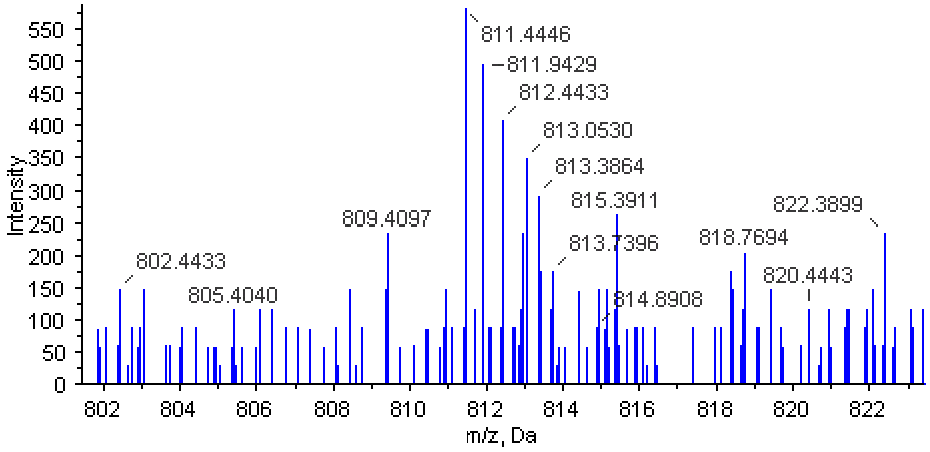
Seq Cov %: 16.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.63

116: 114=E5TL: D5TL=0.70

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAAEKSNIAK**DVTELIGK**TPLVYLNHIVDGCVAKVAAK**LEMMEPCSSVK**DRIGHSMIVDAEEKGLITPG
ESVLIEPTSGNTGIGLAFMAAAKGYK**LIITMPSSMSLER**RTILRAFGAELVLTDPAKGMKGAVQKAEEI
RDKTPNSYMLQQFENPTNPKVHYETTGPEIWKGSSGK**VDALVSGIGTGGTVTGAGKYLKEQNPDIK**LYG
IEPVESPILSGGKPGPHKIQGIGAGFIPGVLDVDLLDEVVQISSEEAIETAK**LLALK**EGLLVGISSGAA
AAAAVKIAK**RPENAGK**LVVAVFPSFGER**YLSSVLFESVK**REAESLVFEP

Protein No.: I-510

Protein name and Species:

Fimbrin, putative OS=Ricinus communis GN=RCOM_0549750 PE=4 SV=1

Accession: tr|B9T216|B9T216_RICCO

Unused ProtScore: 4.59

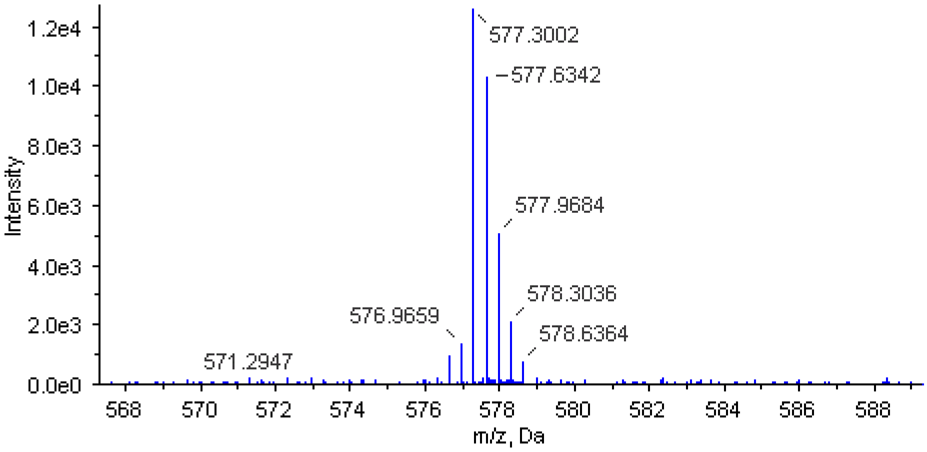
Seq Cov %: 15.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.54

116: 114=E5TL: D5TL=1.43

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSAGFVGVLVSDPWLQSQFTQVELRTLKAKYVSIRTEGGR**VTVGDLPPVFVK**LR**AFTEVFNEDEIK**AIL
KESYSKAEEELDFETFLR**AYLNVQAR**VPAKSGGKKLRYSSSFLKASTTTFRHNINESEKASYVSHINNH
LGEDSFLKTYLPIDPATNALFDLVKHGVLLCK**LINVAVPGTIDER**AINTKKEMNPWER**NENHTLCLNSA**
KAIGCTVVNIGTQDLAEARPHLVLGLISQIIKIQLLADLNLKK**TPQLVELVDDSK**DVEELMGLPPEKVL
LKWMNFHLKKAGYNK**EVTNFSSDVK**DGEAYVYLLNALAPELSTPDTKAASNPAER**AKVVLEQAEK**LDCK
RYLNANDIVEGSPNLNLAF**VAQIFQHR**NGLSTDTNKMPVAEMMEDDAETSREERCFRLWINSIGIVTYV
NNVFEDVRNGWVLLEVLDKVSPGSVNWKQATKPPIKMPFRKVENCNQAIKIGKELSFSLVNVAGNDIVQ
GNKKLLLAFLWQLMRFTMLQLLRNLRSHSSHSQGK**EITDADILKWANSK**VKKVGK**TSQMESFK**DKTLSN
GVFFLDLLGAVEPRVVNWSVVTKGESDEDKKLNSTYIISVARK**LGCSIFLLPEDIIEVNQK**MMLTLTAS
IMFWSLQHQAAEPESSAAEDNADASSTASMEGENEAALAGEVSDMTMDDAASDSAMSP

Protein No.: I-511

Protein name and Species:

Folylpolyglutamate synthase OS=Populus trichocarpa GN=FPGS2 PE=4 SV=1

Accession: tr|B9HMM6|B9HMM6_POPTR

Unused ProtScore: 4.59

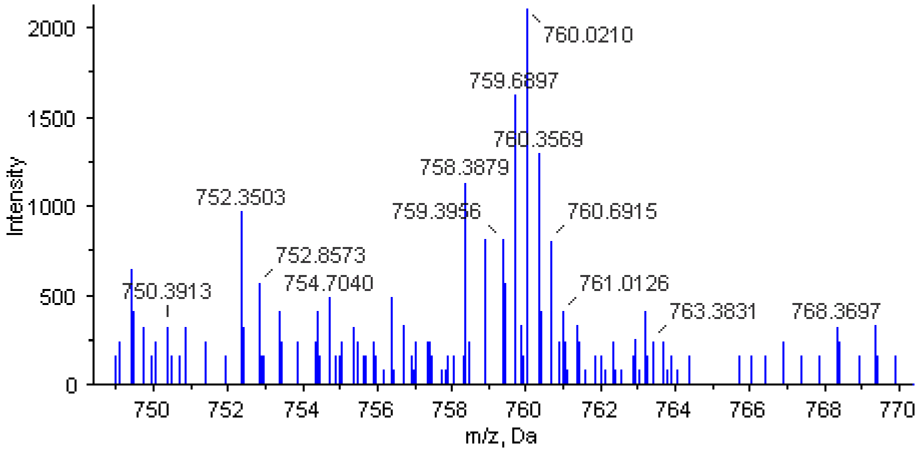
Seq Cov %: 5.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.26

116: 114=E5TL: D5TL=1.11

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAEGDNNGSSKPTVTPYEEALDALSSLITKRSRADKSNNGDRFDVLFDYLKLEEAISEMKIIHVAGTKG
K**GSTCTFTESILR**NCGFR**TGLFTSPHLIDVR**ERFRLDGKDICEEKFLAYFWWCYDRLKEKSTEDVPMPT
YFRFLA**LLAFK**IFSAEQVDVAILEVGLGGKFDATNVVQKPIVCGVASLGYDHMEILGNTLAQIAGEKAG
IFKDGIPAFTVPQPDEAMNVLEEKASELNVHLQVAEPLDAKLLNGLKLRLEGEHQYLNAGLAIALSFTW
LQRTGHHEFTHMEQASSLPEQFIKGLTTASLQGRAQIVTDQYINAESYGDLVFYLDGAHSPESMEMCAR
WFSLAIKEDSQKRTFNYPPQNNSESTIELVQEHHDERYGKSSMQILLFNCMSVRDPQLLLPPLMKACAS
HGVYFKKALFVANTSVYYKVGSHALPPTDSQFNLSWQFALQRVWENLIQSDKGGEVKHAVAVCEEGKED
AKMSGR**TCENSAVFPSLPLAIK**WLKESVQRNRSVHYQVLVTGSLHLVGDVLRLVKK

Protein No.: I-512

Protein name and Species:

Myosin XI, putative OS=Ricinus communis GN=RCOM_1724180 PE=4 SV=1

Accession: tr|B9S596|B9S596_RICCO

Unused ProtScore: 4.58

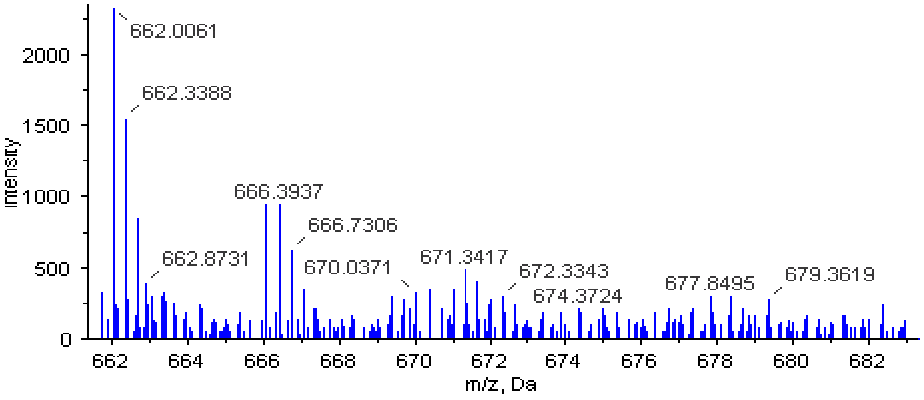
Seq Cov %: 5.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.61

116: 114=E5TL: D5TL=1.52

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MMKQAAAVTLVVGSLVWLEDPDVAWIDGEVVEMKGDNIKVLCTSGKTVVVKASNIYPK**DAEAPPCGVDD**
MTKLAYLHEPGVLQNLRSRYDMNEIYTYTGNILIAVNPFRKLPHLYDSHMMAQYKGAAFGELSPHPFAV
ADAAYRLMINEGI**SQSILVSGESGAGK**TESTKLLMRYLAYMGGRAVAEGR**TVEQQVLESNPVLEAFGNA**
KTVRNNNSSRFGKFVEIQFDQMGRISGAAIRTYLLERSR**VCQVSDPER**NYHCFYMLCAAPQEDVQRYKL
GNPRTFHYLNQSNCYELDGIDDSKEYIATRR**AMDIVGISSDEQDAIFR**VVAAVLHLGNIEFAKGKETDS
SMPKDEKSRFHLRTAAELLMCDVKALEDSLCKR**VIVTR**DETITKWLDPESAVLSRDALAKIVYSRLFDW
IVDKINNSIGQDPDSKSLIGVLDIYGFESFKTNSFEQFCINLTNEKLQQHFNQHVFKMEQEEYTKEEID
WSYIDFVDNQDVLDLIEKKPGGIIALLDEACMFPRSTHETFAQKLYQTFKNHKRFSKPKLARSDFTICH
YAGDVTYQTELFLDKNKDYVVAEHQALLSASTCSFVSGLFPLSAEESSKQSKFSSIGSRFKQQLQSLLE
TLSATEPHYIRCVKPNNLLKPAIFENKNILQQLRCGGVMEAIR**ISCAGYPTR**KPFDEFVDRFSILAPEV
LDGSSDEITACKRLLEKVGLEGYQIGKTKVFLRAGQMADLDTRRSEVLGRSASIIQRKVRSYLSRRSFI
MLRRAAIHIQASCRGQLARQVYENMLREAASLRIQTYLRMYVARKAYIELYCSAISIQTCMRGMAARDE
LRFRRRTRAAIVIQSHCRKYLARLHFMELKKATITAQCAWRGRVARKELRTLKMAARETGALQAAKNKL
EKQVEELTWRLQLEKRMRADLEEAKTQENSKLQSALQEMQLQFKETKEMLVKEREAAKTAKEIIPVIQE
VPVVDNAMLEKLTTENEKLKAMVSSLEKKIDETEKKFEETSKISEERLKQALEAESKIVELKTAMHRLE
EKFTDMETENQILRQQSLLQTPVKKTSDRPPIPAVPNLENGHHVNEEHRASEPQTPVKVFGTESDSKFR
RSHIERQHENIDALINCVMHNIGFSHGKPVAAFTIYKCLLHWKSFEAEKTSVFDRLIQMIGSAIENEDN
NDHMAYWLSNTSTLLFLLQKSLKAAGAGGATPNKKPSSAASLFGRMAMGFRSSPSSSNLAAALAVVRQV
EAKYPALLFKQQLAAYVEKIYGIIRDNLKKELSSLLSLCIQAPRTSKGSALRSGRSFGKDSPSSHWQSI
IDSLNILLSTLKQNFVPPVLIQKIYTQTFSYINVQLFNR

Protein No.: I-514

Protein name and Species:

Cinnamyl alcohol dehydrogenase 1-like [Vitis vinifera] OS=Vitis vinifera GN=VITISV_025556 PE=3 SV=1

Accession: tr|A5C5R6|A5C5R6_VITVI

Unused ProtScore: 4.58

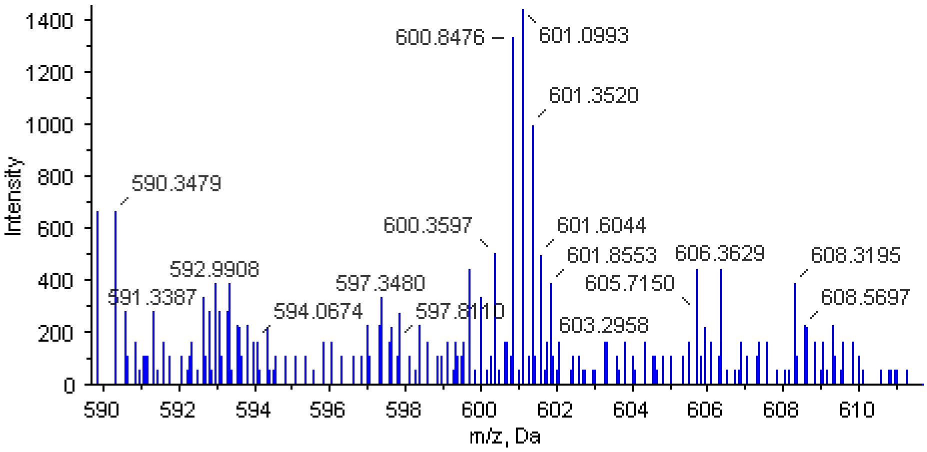
Seq Cov %: 4.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.29

116: 114=E5TL: D5TL=0.25

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDSVKEKTHGDTKSKKLAQQRSRLQTMSLNWVSCMSKPDMMNNNCLGWAARDESGVLSPYTFTRREVGD
EDVSLKITHCGICYADMLFTKNRLGDSR**YPLVPGHEIVGIVK**EVGSNVHHFKVGHRVGVGAYVNSCREC
ESCNQSLEVYCSKGSVYTSNGVDADGTITN**GGYSSFIVVHER**YCFRIPDEYPLALAAPLLCPGITAYSP
MVRHKMNQPGKSLEVIGLGGVGHLAVKFGKAFGLNVKLFSTSISKKEEALSLLGDDNFVVSSDEQQMKA
MANSLDFIIDTASGDHSLDHYMSCLKTAGVLALVGFPGMKTISGSLVGGVKETQEMLDFCAAHKIYPDI
EIVPIQYVNEAWERLTKGDVKYRVVGSDDVSLKITHCGICYADIIHTRNKFGNSKYPVVPGHDIVGIVK
EVGSNVGVFKVGDSVGVGTYVNSCRECENCEEGLEIHCSKGPVFTFGGVDVDGTITKGGYSSFIVVHQR
YCYRIADDYPLGLAAPLLCAGITVYTPMIRHKMNQPGK**SLGVIGLGGLGHMAVK**FGKAFRLNVTVFSTS
MSKKEEALTLLGADKFVLSSDEQDMKAMAKSLDFIINTASGDHPFDPYMSLLKTAGILEAQKTQEMLDF
CAAHKIYPEVEMVAIQNVNEALERVIKRDVKYRF**VIEIEK**SLK

Protein No.: I-516

Protein name and Species:

Acetylornithine deacetylase, putative OS=Ricinus communis GN=RCOM_0864770 PE=4 SV=1

Accession: tr|B9S1F8|B9S1F8_RICCO

Unused ProtScore: 4.57

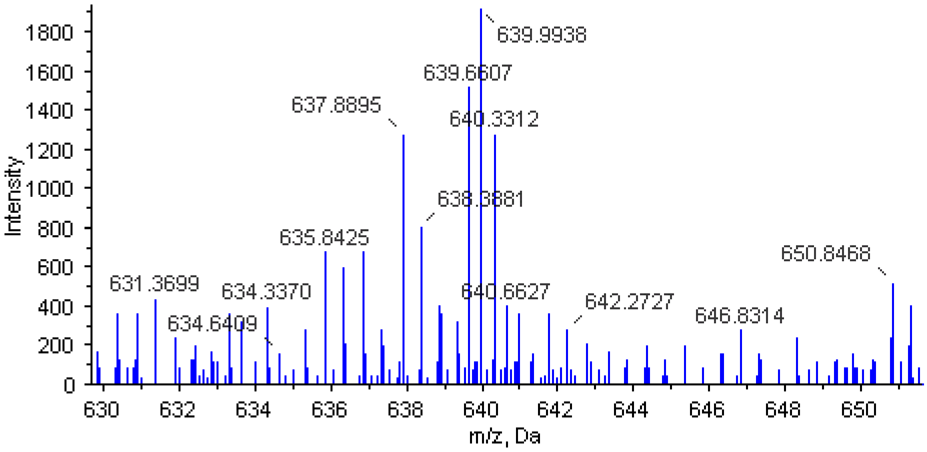
Seq Cov %: 12.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.14

116: 114=E5TL: D5TL=0.57

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MANVEEILGELDKESFVTLLRKIIGESK**HVQNNPPELIPEEDR**VVKHVLDSLLPYSTTSGGGPLIVNHV
SYFPGR**GNLIVEYPGTEPGK**ILSFVGMHMDVVTANPNDWEFDPFSLTINGDKLCGRGTTDCLGHVAVVT
ELMKMLAEKKPKLKSTVVAVFIANEENSAITGVGVDALVQDGLLDKLKGGPLFWIDTADKQPCIGTGGM
IPWKLHVTGKLFHSGLAHKAINALELAMDALQEMQSRFYKDFPPHPREQVYGFATASTMKPTQWSYPGG
GINQIPGECTISGDVR**LTPFYNLVDVK**NM**LQEYVDDINENIEK**LGTRGPVSKYVLPDENLRGSITLTFE
EAMSGVACNLDSRGFHVLCKATEKVVGHVKPY**SITGSLPLIR**ELQEEGFDVQTAGYGLMATYHAKNEYC
LLSDMCQGYRVFVSIISQLED

Protein No.: I-520

Protein name and Species:

Isoleucyl tRNA synthetase, putative OS=Ricinus communis GN=RCOM_0574620 PE=3 SV=1

Accession: tr|B9SUT5|B9SUT5_RICCO

Unused ProtScore: 4.51

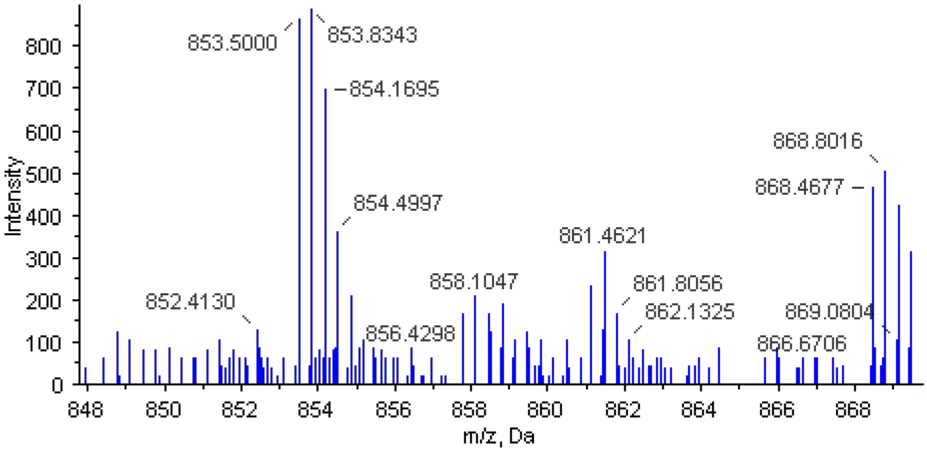
Seq Cov %: 5.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.38

116: 114=E5TL: D5TL=0.57

nnotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MEEVCEGKDFSFPNQEEKILSFWSEIK**AFETQLSR**TESLPEYIFYDGPPFATGLPHYGHILAGTIKDIV
TRYQTMRGHHVTRRFGWDCHGLPVENEIDRKLGIQRRDEVLKMGIDKYNEECRSIVTRYVGEWEKVITR
TGRWIDFKNDYKTMDLKFMESVWWVFYQLFDKGLVYKGFK**VMPYSTGCKTVLSNFEAGQNYK**DVPDPEI
MVAFPIVDDPHNAAFVAWTTTPWTLPSNLALCVNGNFDYVKVRNKYTGK**VYVVAESR**LSALPTEKPKSS
AVNGPAGGKTKGGKTENLMDSFELLEKVKGNELVKKKYVPLFNFFSDFSNTAFRVVADNYVTDDSGTGI
VHCAPAFGEDDYRVCIENQIINKGENLIVAVDDDGCFAERITEFSGRYVKDADKDIIEAVKAKGRLVKS
GTFTHSYPFCWRSDTPLIYRAVPSWFVRVEELKVQLLENNKQTYWVPDYVKEKRFHNWLENARDWAVSR
SRFWGTPLPVWISQDGEEVIVMDSVAKLEKLSGIK**VFDLHR**HHIDHITIPSSRGPEFGVLRRVDDVFDC
WFESGSMPYAYIHYPFENIELFEKSFPGQFIAEGLDQTRGWFYTLMVLSTALFGKPAFK**NLVCNGLVLA**
EDGKKMSKKLKNYPSPMEVIDDFGADALRLYLINSPVVRAETLRFKKEGVYSVVKDVFLPWYNAYRFLV
QNAKRLEVEGLAPFTPLDFGKLQNSSNVLDRWINSATQSLVHFVRQEMDGYRLYTVVPYLLKFLDNLTN
IYVRFNRKRLKGRIGEEDCR**TALSTLYSVLLTSCK**VMSPFTPFFTEVLYQNMRKVSSGAEESIHYCSFP
QEEGERDERIEQSVSR**MMTIIDLAR**NIRERHYKPLKSPLREMIVVHHDADFLDDIAGKLK**EYVLEELNV**
RSLIPCVDTLKYASLRAEPEFSLLGKRLGKAMGVVAKEIKAMSQKDILAFEEAGEVTIASHNLKLADIK
VVREFKRPDGLTEKEIDAAGDGDVLVIMDLRPDESLYEAGVAREVVNRIQKLRKK**VALEPTDVVDVYFE**
SLDDDKSKLGRVLNSQEQYIKDAIGSPLLSSTMMPPEAVVIGEESYHHIYELSFT**IYLAR**AALVFKSDA
ILTLYAGNTKFAKGLETYLLSRDHSNLRSEFQQRNGKITVDCIENQPAADVVLGEHLFLTVGDYFLRTR
SG

Protein No.: I-533

Protein name and Species:

3R-hydroxymyristoyl ACP dehydrase [Arabidopsis thaliana] OS=Arabidopsis lyrata subsp. lyrata GN=ARALYDRAFT_481086 PE=3 SV=1

Accession: tr|D7LDD9|D7LDD9_ARALL

Unused ProtScore: 4.37

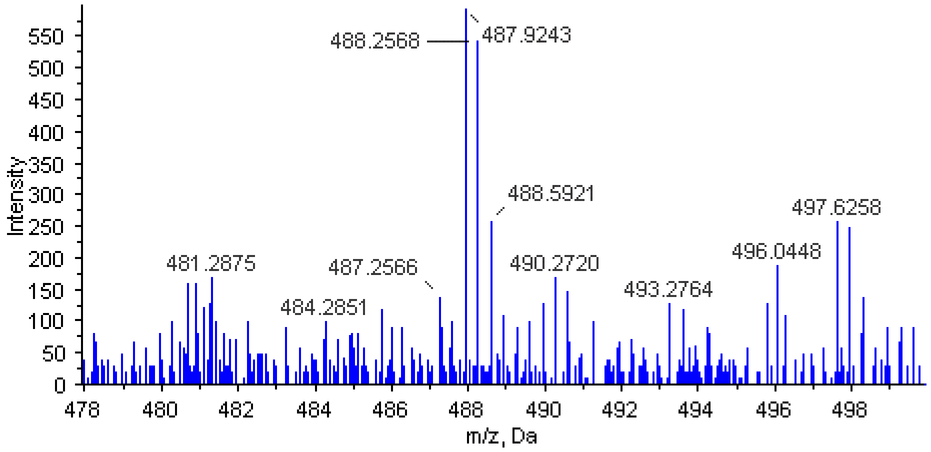
Seq Cov %: 9.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.31

116: 114=E5TL: D5TL=0.21

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MATTSNSVLFLSSDSLSHHHHHHHQQQPLHLPSSRSHSVSLPPNKRSNSLTLRCSTNGDNTSSEKETPI
ELKFPAFPTVMDINQIREILPHRFPFLLVDR**VIEYTPGVSAVAIK**NVTINDNFFPGHFPERPIMPGVLM
IEAMAQVGGIVMLQPEVGGSQ**DNFFFAGIDK**VRFR**KPVIAGDTLVMR**MTLLKFQKRFGLAKMEGKAYVG
GALVCEGEFMMVSAGSS

Protein No.: I-534

Protein name and Species:

Glyceraldehyde 3-phosphate dehydrogenase, putative OS=Ricinus communis GN=RCOM_1574030 PE=3 SV=1

Accession: tr|B9RHV9|B9RHV9_RICCO

Unused ProtScore: 4.35

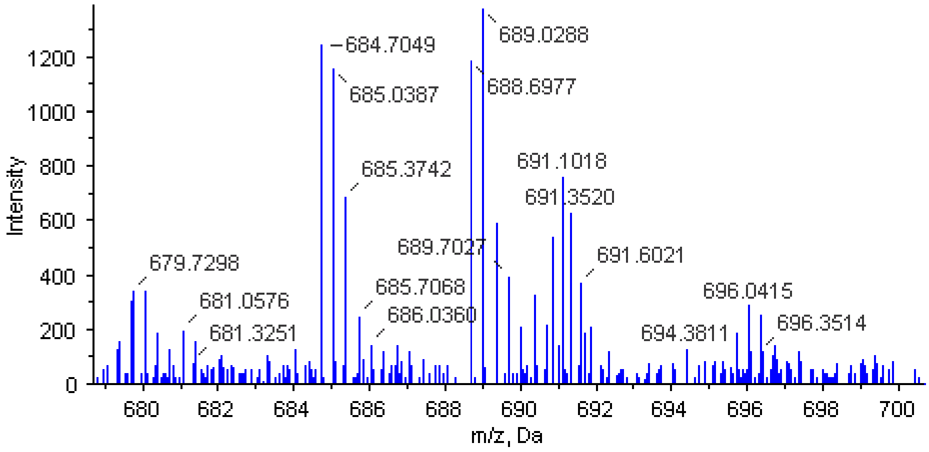
Seq Cov %: 20

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.23

116: 114=E5TL: D5TL=0.36

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAFSCILRSTATSPLIEASRSDLSPSPSDPLQASSVNFNRDLKASKSFFGTSVPTASSSLEACSARSLQ
PIKATVTEMPPTILKSRSDGRTK**IGINGFGR**IGRLVLRIATLR**DDVDVVAVNDPFIDTK**YMAYMLKYDS
THGLFKGHIKVVDESTLEINGKQIKVSSKRDPAEIPWGDHGAEYVVEASGVFTTIDKASAHKKGGAKKV
VISAPSADAPMFVVGVNEQTYKPNMDIVSNASCTTNCLAPLAKVVHEE**FGIVEGLMTTVH**ATTATQKTV
DGPSMKDWRGGR**GAGQNIIPSSTGAAK**AVGKVLPELNGK**LTGMAFR**VPTPNVSVVDLTCRLEKSASYED
VKAAIKYASEGPLK**GILGYTDEDVVSNDFVGDSRSSIFDAK**AGIGLSAAFMKLVSWYDNEWGYSNRVLD
LIEHMALVAAQN

Protein No.: I-536

Protein name and Species:

Glutathione-S-transferase OS=Rheum australe PE=2 SV=1

Accession: tr|B5M1W3|B5M1W3_RHEAU

Unused ProtScore: 4.35

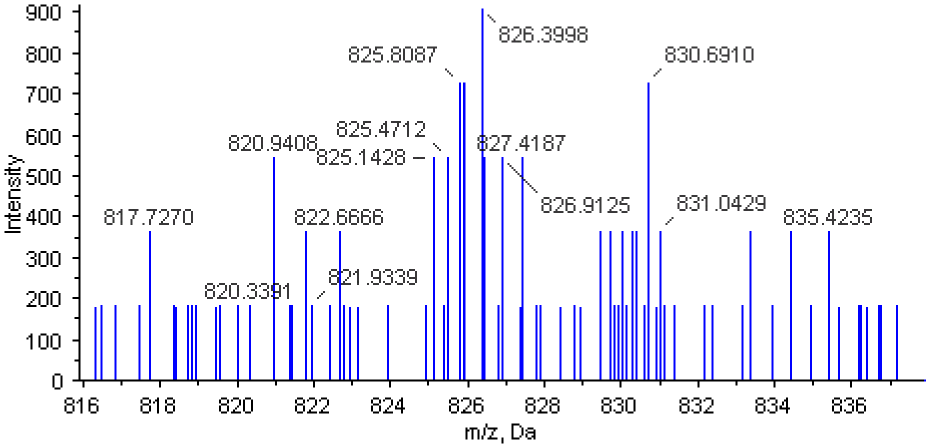
Seq Cov %: 12.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.22

116: 114=E5TL: D5TL=0.56

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAATLPPALDASSPPPPLFDGTTR**LYTSYTCPFAQR**VWITRNYKGLQEKIKLVGINLQNRPDWYKEKVN
PANK**VPALEHDGK**IIVESLDLIKYVDSNFEGPSLYPDEPAKREFGEELLTYVSEFVPKMYGAFKGGDTT
KVADAEFDYLEKALQKFDDGPFFLGQFSLVDIAYAPFIERFQLVIADVWK**YDLTAGRPK**LAEWVEELNK
IEAYKETKTDPDQLLPYLKSRFVAQQ

Protein No.: I-547

Protein name and Species:

Beta-1,3-glucanase OS=Vitis vinifera GN=VIT_05s0077g01150 PE=2 SV=2

Accession: tr|Q9M563|Q9M563_VITVI

Unused ProtScore: 4.31

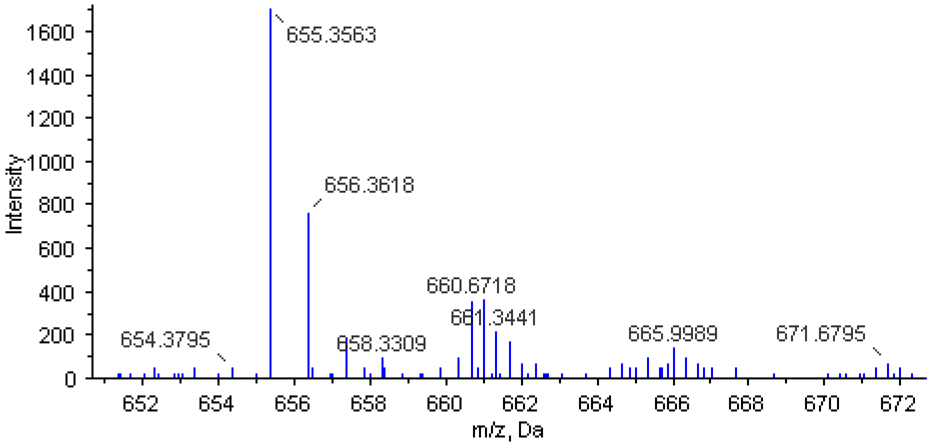
Seq Cov %: 15.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=15.42

116: 114=E5TL: D5TL=3.93

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAAMVLLLGFLLATLQITGVKSVGVCYGMLGNNLPPASQVVALYKSRNIDRMR**IYDPNQAALQALR**GSN
IQLMLGVPNSDLQGLATNPSQAQSWVQRNVRNYWPGVSFR**YIAVGNEV**SPVNGGTSRFAQFVLPAMRNI
RAALA**SAGLQDRVKVSTAIDL**TLLGNSYPPSQGAFRGDVRGYLDPIIRFLVDNK**SPLLANIYPYF**SYSG
NPK**DISLPYALFTANSVVVWDGQR**GYKNLFDAMLDALYSALERAGGASLEVVLSESGWPSAGGFGTTVD
NARTYNSNLIRHVKGGTPKRPGR**AIETYLFAMFDENK**KEPQLEK**HFGLFFPNK**QPKYSINFSGEKPWDV
SSENDTNEESLKSDI

Protein No.: I-549

Protein name and Species:

annexin [Populus tomentosa] OS=Populus trichocarpa GN=POPTRDRAFT_654779 PE=3 SV=1

Accession: tr|B9HFG8|B9HFG8_POPTR

Unused ProtScore: 4.3

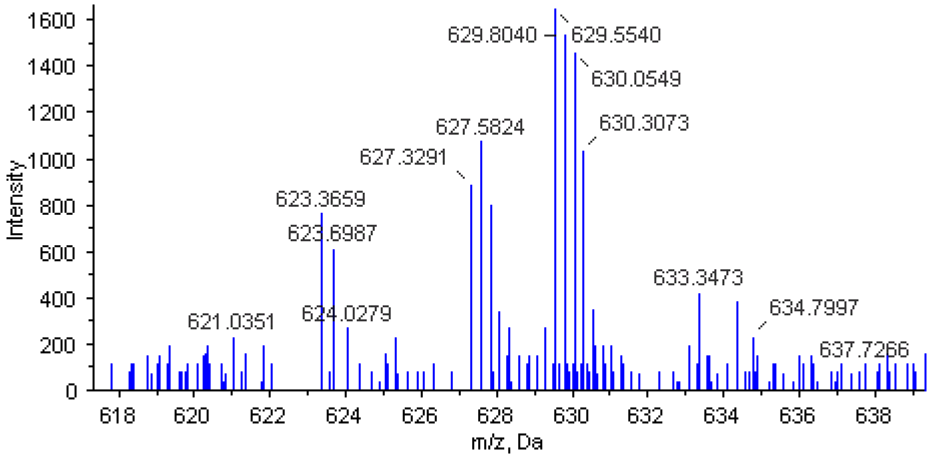
Seq Cov %: 17.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.18

116: 114=E5TL: D5TL=2.47

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MASLKVPASVPPPYEDAEQLHKAFEGWGTNEGLIISILAHRNAAQRNLIRKVYAEAYGQDLLKDLDKEL
SSDFERAVLLWTLDPAERDAYLANEATKRFTSSNWVLMEIACTRSSHDLFKVRQAYHARYKK**SLEEDVA**
YHTTGDFRK**LLVPLVSAFR**YEGEEVNTILAKSEAKILHEKISDKAYSDEEIIRILTTRSK**AQLNATLNH**
YNNAFGNAINKNLKEEADNDFLKLLRATIKCLTYPEKYFEKLLRLSIKKLGTDERALTRVVTTRAEVDM
ERIKEEYHRRNSVTLERDIAGDTSGDYER**MLLALIGHGDA**

Protein No.: I-550

Protein name and Species:

Argininosuccinate synthase, putative OS=Ricinus communis GN=RCOM_0395600 PE=3 SV=1

Accession: tr|B9SS35|B9SS35_RICCO

Unused ProtScore: 4.3

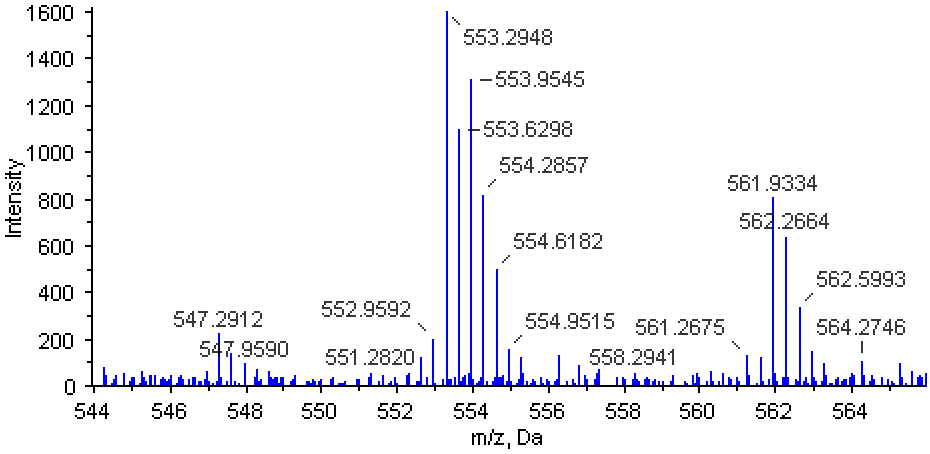
Seq Cov %: 8.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.61

116: 114=E5TL: D5TL=0.40

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAISSSSFNFAVHDSNRDEFLQNHNIPSIKKSPTIFKKLGAKRGELQGIAFAGTKRVILRTHQNKAIQA
VLSSDREVEVSEASKSKGLRGQLNKVVLAYSGGLDTSVIVPWLRENYGCEVVCFTADVGQGLKELEGLE
EKAKASGACQLVVKDLQEEFVRDYIFPCLRAGAIYERKYLLGTSMARPVIAK**AMVDVAKEVGADAVAHG**
CTGKGNDQVRFELTFFALNPELNVVAPWREWDIKGREDAIEYAKKHNVPVPVTKKSIYSRDRNLWHLSH
EGDILEDPANEPNKDMYMMSVDPEDAPNQPEYIEIGIVSGLPVSVNGK**QLSSASLLSQLNEIGGR**HGIG
R**IDMVENR**LVGMKSRGVYETPGGTILFTAARELESLTLDRETMQVKDSLALK**YAELVYAGR**WFDPLRES
MDAFMEKISEKTTGSVTLKLYKGSVLVTSRTSPYSLYR**QDISSFESGK**IYDQADAAGFIRLYGLPMKVR
AMLENGI

Protein No.: I-552

Protein name and Species:

Glycerophosphodiester phosphodiesterase-like protein (Fragment) OS=Manihot esculenta PE=2 SV=1

Accession: tr|Q5PYQ3|Q5PYQ3_MANES

Unused ProtScore: 4.28

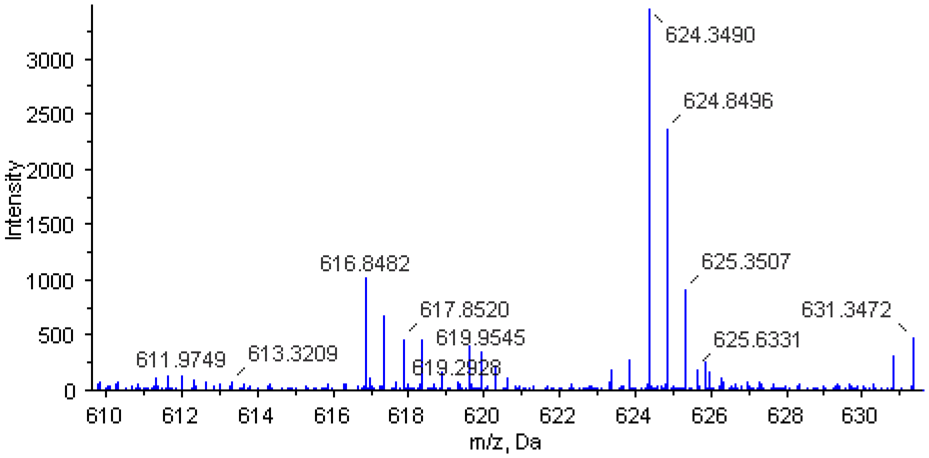
Seq Cov %: 9.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.13

116: 114=E5TL: D5TL=0.25

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MALTCSVLIIFLSLTLVSTATARPIYPLPSKISNGIRKPLQTSRPYNIAHR**GSNGEIPEETAAAYMR**AI
EEGADFIETDILSSKDGVLICFHDVTLDNTTDIAKHNEFTNRKRTYDVQGVNTTGFFTVDFTLEELKTL
RVKQRHPFRDQQYNGKFSIITFEEFIAIALDASR**VVGIYPEMK****NPVFINQHVK**WPGGKRFEDKFVETLK
KYGYKGSYMSKDWLK**QPVFIQSFAPTSLVYISNMTDSPK**IFLIDDIDIPTQDTNQSYWEITSDAYLDYI
KNYVVGH

Protein No.: I-556

Protein name and Species:

DNA-binding protein smubp-2, putative OS=Ricinus communis GN=RCOM_0089600 PE=4 SV=1

Accession: tr|B9SL55|B9SL55_RICCO

Unused ProtScore: 4.24

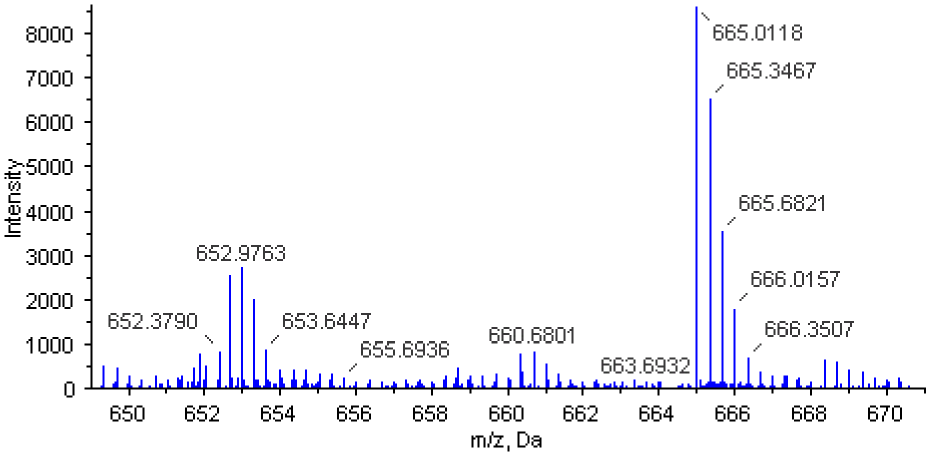
Seq Cov %: 7.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.61

116: 114=E5TL: D5TL=0.68

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MEKDKTKKKLSLQEFVSITSPLLDLEKEAEISASISSGTSRNLDNAQKRGSTILNLKCVDAQTGLMGKT
LLEFQSNKGDVLPSHRFSTHDVVVLKPNKADLGSPALGQGVVYRLKDSSITVAFDDIPEEGLNSPLRLE
KVANEVTYRRMREALIQLSKGVQRGPAADLVPVLFGERQPTMSKKGVTFTPFNSNLDHSQKDAISKALS
SKDVFLLHGPPGTGKTTTVVEIILQEVKRGAK**ILACAASNIAVDNIVER**LVPHRVKLVRLGHPAR**LLPQ**
VLDSALDAQVLKGDNSSLANDIRKEMKALNGKLLKTKDKSTRRDIQKELRTLSKEERKRQQLAVTDVIK
NADVVLTTLTGALSHKLDNTSFDLVIIDEAAQALEIACW**IALLK**GSRCILAGDHLQLPPTIQSVEAEKK
GLGRTLFERLADLYGDEVTSMLTVQYRMHELIMTWSSKELYNSKIKAHPSIAAHMLSDLEGVKRSSATE
PTLLLIDIAGCDMEEKKDEEESTLNEGEADVAVAHAKRLVENGVQASDIGIITPYAAQVVLLKILRSNE
DKLKDVEISTVDGFQGREKEAIIISMVRSNSKKEVGFLSDRRRMNVAVTRARRQCCLVCDTETVTSDGF
LKRLIEYFEEHGEYLSAAEYCNE

Protein No.: I-561

Protein name and Species:

transportin, putative OS=Populus trichocarpa GN=POPTRDRAFT_570025 PE=4 SV=1

Accession: tr|B9I337|B9I337_POPTR

Unused ProtScore: 4.21

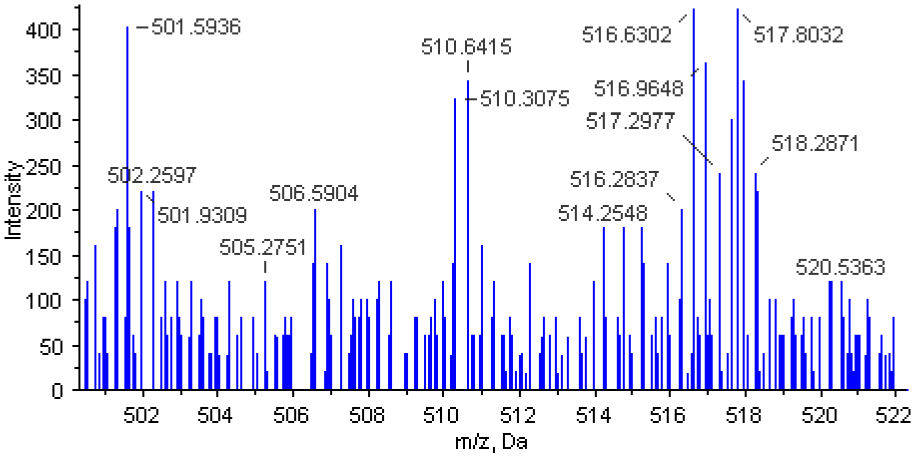
Seq Cov %: 5.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.68

116: 114=E5TL: D5TL=1.63

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MLAVADVLIDAASVLGGDATLRILYVKLAEARTCLGNDHNQWHPAEAALFCIRAISNYVSTVEAEVMPK
IMSLLLELPHEPQLLQTVCLTIGAYSKWLDAALDGFPQLSSVIKILLSGMGKSEDSAAAAAVAFRHICD
DCRRKLCGYFDELFSIYNSAVIGEGSLKVSAGDSLHVVEAFSMVITELPADQAKLALEKLCLPVVTPLQ
EIISQGPDVLEKKLARELTVHIDRLAYIFR**YVNHPEAVADAIQR**LWPILK**AIFDIR**AWDMRTMESLCRA
CKYAVRTSGRLMGITIGAMLEEIQGLYQQHHQPCFLYLSISCHLGMQIFGSDPSCAYYLKNLIEALFKC
TTCLLTNIKDFTARPDIADDCFLLASRCIRYCPQVFIPSAVFPSLVDCSMIGVTVQHREASNSILTFLS
DIFDLAKSSMGEQYLTIRDSVIIPRGSSITR**ILVASLTGALPSSR**LETVTYALLALTRAYGASALEWAR
ESVSLIPSTVVTEVEQTKIFQALTDAASGVDIKTLMGAVEELSDVCRRNRTVQEIVQGALRPLELNLVT
VS

Protein No.: I-562

Protein name and Species:

vacuolar protein sorting-associated protein OS=Populus trichocarpa GN=POPTRDRAFT_833991 PE=4 SV=1

Accession: tr|B9HYZ8|B9HYZ8_POPTR

Unused ProtScore: 4.21

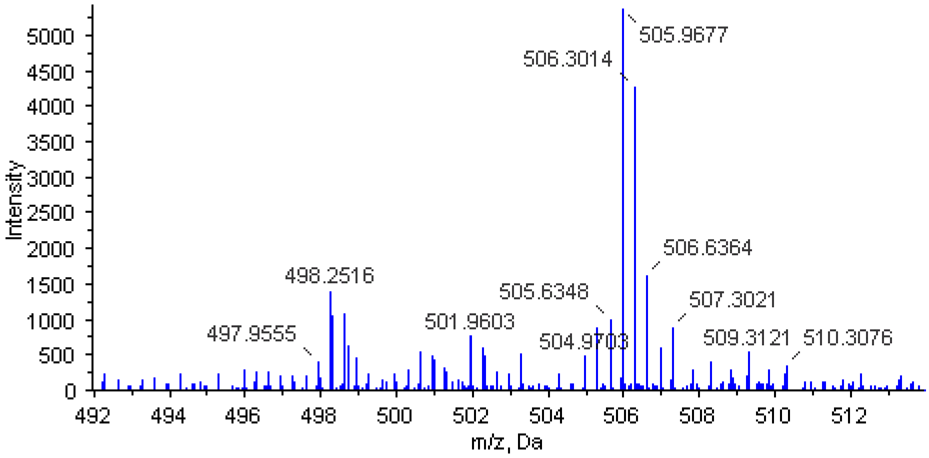
Seq Cov %: 17.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.60

116: 114=E5TL: D5TL=1.66

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MEVKLWNDKREREMYDNFAELYAIIKATEKLEKGYVRDIISSSQYETECQKLIAHFKTLASTFKDTVPS
IERFADTYKMDCPAAINR**LVTSGVPATVEHR**AAAAASSTTSAAVVAECVQNFITAMDSLKLNMVAVDQV
HPLLSDLSASLNK**LSILPPDFEGK**TKMKEWILRLSK**MGAADELTEQQAR**QLHFDLESSYNSFMAALPSA
GT

Protein No.: I-563

Protein name and Species:

Aspartic proteinase, putative OS=Ricinus communis GN=RCOM_1225960 PE=3 SV=1

Accession: tr|B9SFR8|B9SFR8_RICCO

Unused ProtScore: 4.2

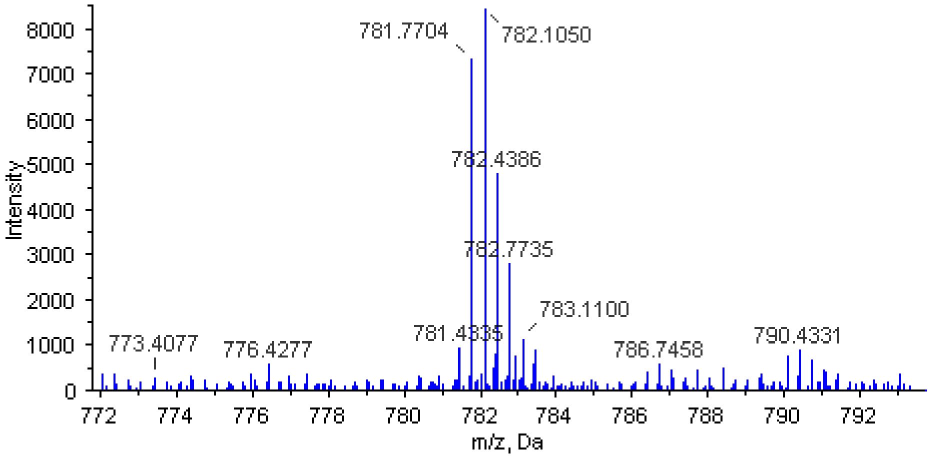
Seq Cov %: 16

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.29

116: 114=E5TL: D5TL=0.42

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGTKSSALWISFVLLLPVVFSLHNDALVRVGLKKKKFDQVNIPAGTVDFKEGEAMRAATKKYNLVENSD
DVDIVELKNYLDAQYYGEIAIGTPPQTFTVIFDTGSSNLWIPSSK**CYFSVACYFHSK**YKASESSTYQKN
GTSAAIRYGTGSISGFFSQDNVKVGDLVIRNQDFIEATK**EPGVTFLAAKFDGILGLGFQEISVGK**AIPV
WYNMVNEGLVKEQVFSFWLNRNVQAEEGGEIVFGGMDPNHYK**GQHTYVPVTQK**GYWQFDMGEVLIGNEI
TGLCADGCK**AIADSGTSLLAGPTTVITQINHAIGASGIVSQECK**TVVEQYGKFILEMLTAQAQPQKICS
QIGFCTFDGTQGVSTNIESVVDKSKETASDGLQQDSACTVCEMIVVWMQNRLRLNETVDQILNYVNKLC
DRLPSPNGESAVDCSSLSSMPIVSFTIGGKAFKLTADQVKGC

Protein No.: I-567

Protein name and Species:

Profilin-1 OS=Hevea brasiliensis PE=1 SV=1

Accession: sp|O65812|PROF1_HEVBR

Unused ProtScore: 4.17

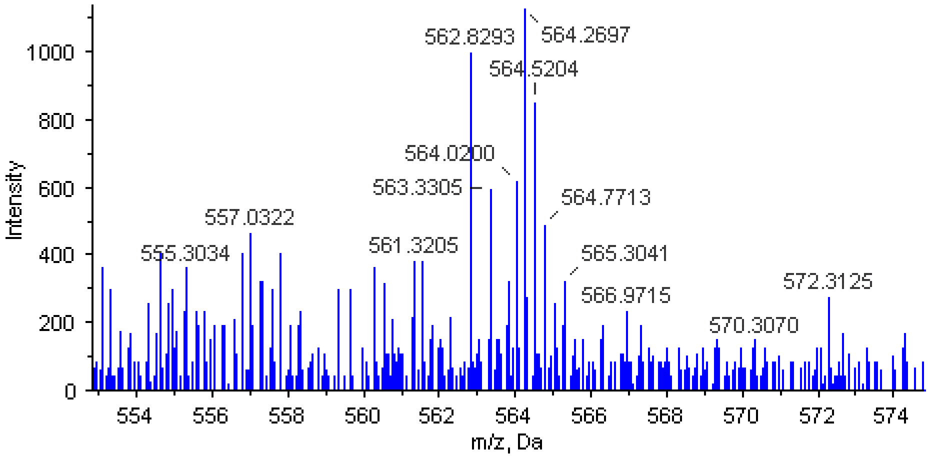
Seq Cov %: 50.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.65

116: 114=E5TL: D5TL=1.98

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSWQTYVDERLMCEIEGNHLTAAAIIGQDGSVWAQSSNFPQFKSEEITAIMSDFDEPGTLAPTGLHLGG
TKYMVIQGEAGAVIRGKKGPGGVTVRKTNQALIIGIYDEPMTPGQCNMIVERLGDYLLEQGM

Protein No.: I-572

Protein name and Species:

ribosomal protein-like,P0 OS=Solanum tuberosum PE=2 SV=1

Accession: tr|Q307Z8|Q307Z8_SOLTU

Unused ProtScore: 4.15

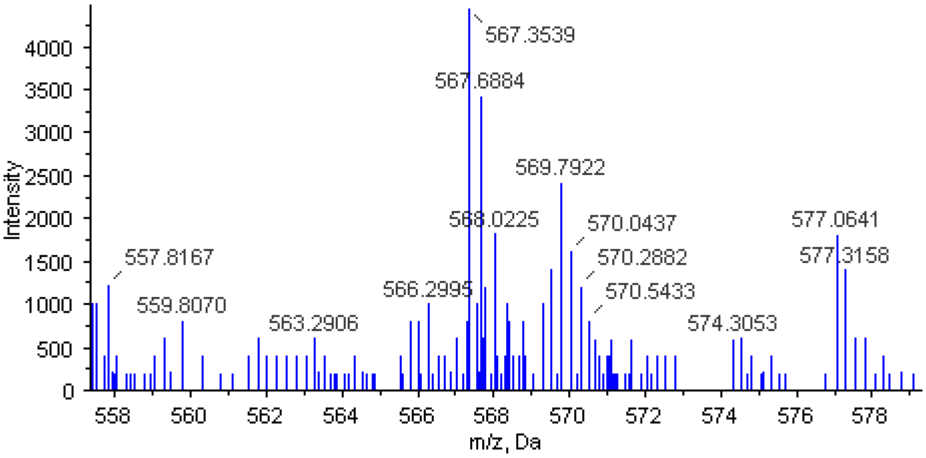
Seq Cov %: 7.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=7.45

116: 114=E5TL: D5TL=2.63

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAPKATKAEKKIAYDTKMCQLLDDFTQVLVAAADNVGSNQLQSIRKGLRGDSVVLMGKNTMMKRTIRVH
AEKTGNETILNLIPLLVGNVGLIFTKGDLKEVSEEVAKYKVGAPARVGLVAPVDVVVPPGNTGLDPSQT
SFFQVLNIPTKINK**GTVEIITPVELIK**KGDK**VGSSEAALLAK**LGIRPFSYGLVVVSVYDNGSVFSPEVL
DLTEDDLIEKFAMGVSMVTSLALAISYPTLAAAPHMFTNAYKNVLAIAVETDYSFPLADKVKEYLADPS
KF**AVAAAPAAAAGSGAAPAAAK**EEEKKEEPAEVSDDDMGFSLFD

Protein No.: I-578

Protein name and Species:

Copper transport protein ATOX1 OS=Hevea brasiliensis GN=CCH PE=4 SV=1

Accession: tr|D4P094|D4P094_HEVBR

Unused ProtScore: 4.13

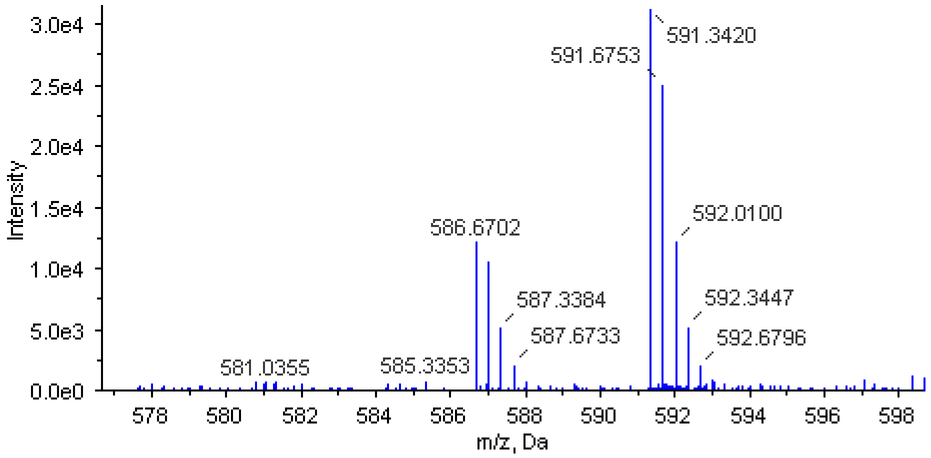
Seq Cov %: 45.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.65

116: 114=E5TL: D5TL=0.52

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSQTVVLK**VGMSCEGCVGAVK**RVLGK**MEGVESYDIDLK**EQKVTVK**GNVQPEAVLQTVSK**TGKKTTFWEAEAPAEPETKPAETVTVA

Protein No.: I-580

Protein name and Species:

auxin-induced protein PCNT115 OS=Glycine max PE=2 SV=1

Accession: tr|C6TIG8|C6TIG8_SOYBN

Unused ProtScore: 4.12

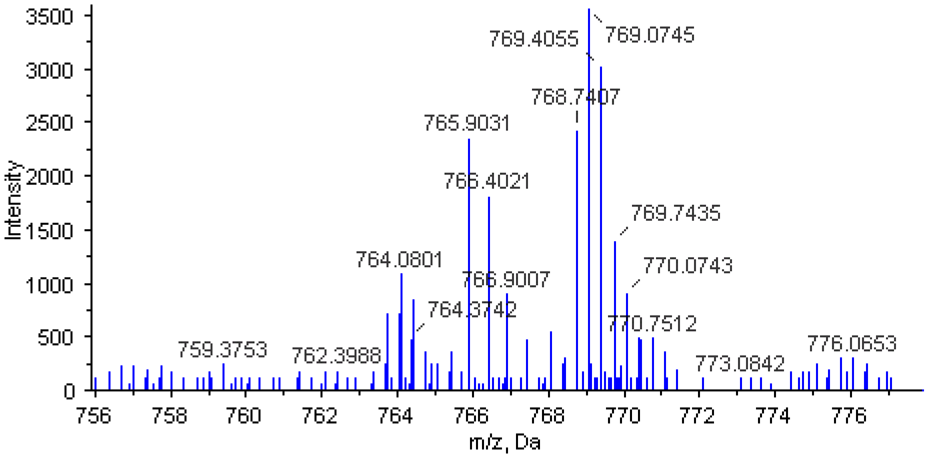
Seq Cov %: 10.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.60

116: 114=E5TL: D5TL=2.02

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MEKLQLHVPRVKLGSQGLEISRLGFGCVGLSGLYNAPLSHEAGCSIIKEAFNMGVTFFDTSDFYGLN**HD**
NEIMIGKALKELPREKVQLATKFGLVRSDGVFAGVKGTPEYVRQCCEASLKRLDVEYIDLYYQHR**VDTS**
VPIEDTMGELKKLVNEGKIKYIGLSQASPDTMKRAHAVHPISALQMEYSLWTR**DIEEEIIPLCR**ELGIG
IVAYSPLGHGFFAGKAAVETLPSQSALAEDARFSGENLEKNKLFYNRIADLASKHSCTPSQLALAWFLH
QGNDIVPIPGTTKIKNLENNVGSVAVKLTNAELSEISDAVPVYEVAGEAPGLGSLSQYTWKFATTPSK

Protein No.: I-584

Protein name and Species:

FH protein interacting protein OS=Populus trichocarpa GN=POPTRDRAFT_809550 PE=4 SV=1

Accession: tr|B9IPT2|B9IPT2_POPTR

Unused ProtScore: 4.09

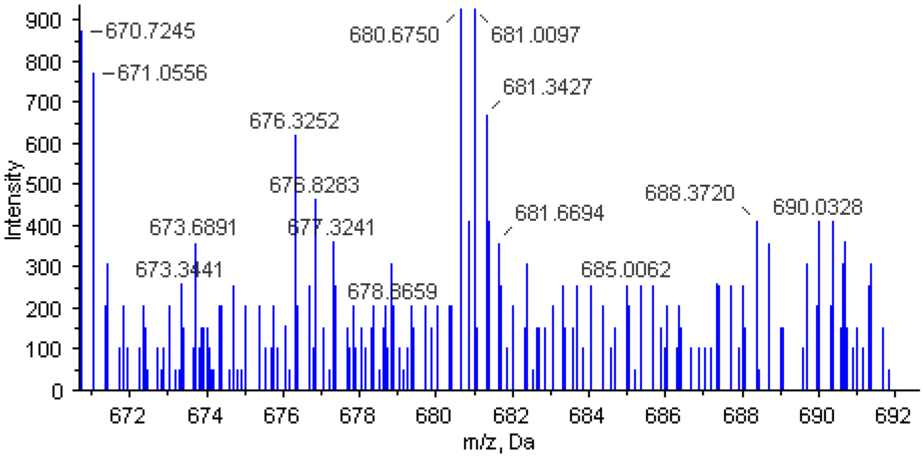
Seq Cov %: 14

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.64

116: 114=E5TL: D5TL=1.17

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MKDHPFSSLIRLNIGGKKFCTTIDTLTQREPDSMLAAMFSGRHTVSEDPDKGYVFIDRDGKHFRHILNW
LR**DGVVPTLTDAEYSELMR**EAVYYQLLGLVEGINSVLTRRREGDELEAELTRADIIKCLQYEKVKFRGV
NFSGLDLSKLDLSYVDFSYASLKNVFFSRANLQCAKFRDVDAEGSIFHNATLRECEFTGANLRGALLAG
ANLKSANLQDACLVDCSFCGADLS**SAHLQTADLTNANLEGANLEGANLK**GAKLNN**ANLKGANLQR**AYLR
HVNLQNTHLEDARLDGANLVGAIR

Protein No.: I-592

Protein name and Species:

Vesicle-associated protein 1 OS=Populus trichocarpa GN=POPTRDRAFT_739862 PE=4 SV=1

Accession: tr|B9MUU5|B9MUU5_POPTR

Unused ProtScore: 4.05

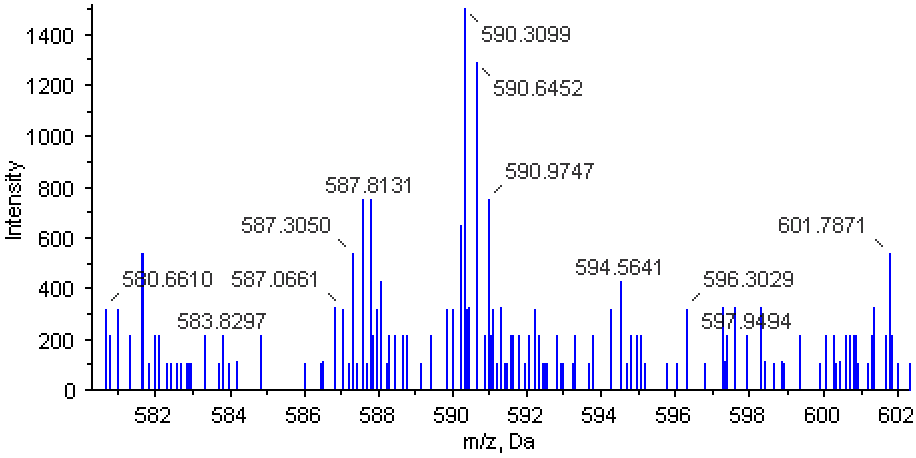
Seq Cov %: 8.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.71

116: 114=E5TL: D5TL=1.69

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSTGELLGIEPLELK**FPFELK**KQISCSLQLSNK**TDNYVAFK**VKTTNPKKYCVRPNAG**IVLPR****STCDVIVTMQAQK**EAPPDMQCKDK**FLLQSVK**ANDGVTVKDINAEMFSKEAGHVVEECKLRVLYVSPPQPPSPVLEGSEEGSPPWGSVSDNGNVNGTDLSTGTRAFVEHLEPQDKPLEAGALISKLTDERNNAIQQNNKLRQE**LELLR**CQGNKNRSGASLMFVIIIGLLGLLLGYLMKKT

Protein No.: I-596

Protein name and Species:

Protease C56, putative OS=Ricinus communis GN=RCOM_0763700 PE=4 SV=1

Accession: tr|B9SJL8|B9SJL8_RICCO

Unused ProtScore: 4.05

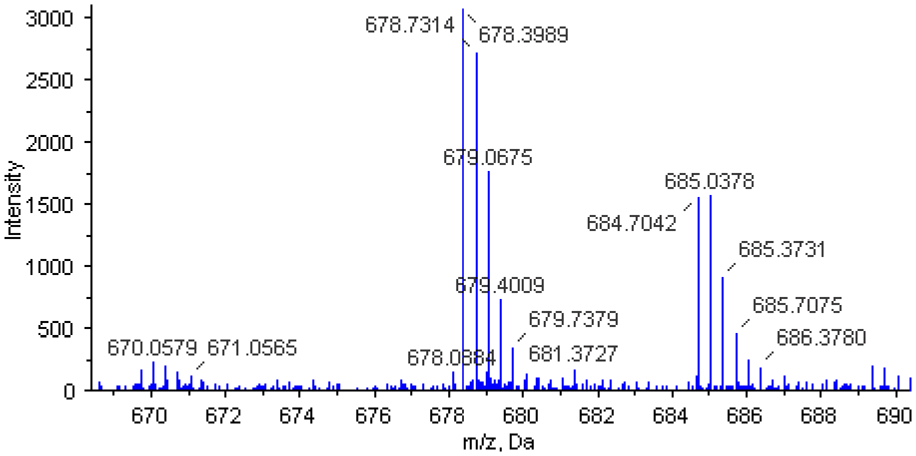
Seq Cov %: 12.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.52

116: 114=E5TL: D5TL=0.31

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSHQKTVFLLCGDYMEDYEAMVPFQALLAYGVAVDAACPGKKAGDYCRTAIHESSGHQTYSESRGHNFT
LNSTFDDIDFGKYDGLVIPGGR**APEYLAMNESVLDCVR**KFADAGKPIASVCHGQLILAAAGLVKGRKCT
AYPPVRPVLIAAGAHWVEPETMASCVADGNLITGATYEGHPEFIQLFVKALGGSITGADKRILFLCGDY
MEDYEVTVPFQSLQALGCHVNAVCPKKKAGDSCPTAVHDFEGDQTYSEKPGHHFTLTASYVGLDVSSYD
ALVLPGGR**APEYLALDETVIALVK**QFMQSKKPVASICHGQQILAAAGVLKGKKCTAYPAVK**LNVVLSGA**
TWLEPDPIDRCYTDENLVTGAAWPGHPEFISQLMALLGIRVSF

Protein No.: I-602

Protein name and Species:

IAA-amino acid hydrolase ILR1-like 4 OS=Arabidopsis thaliana GN=ILL4 PE=1 SV=2

Accession: sp|O04373|ILL4_ARATH

Unused ProtScore: 4.04

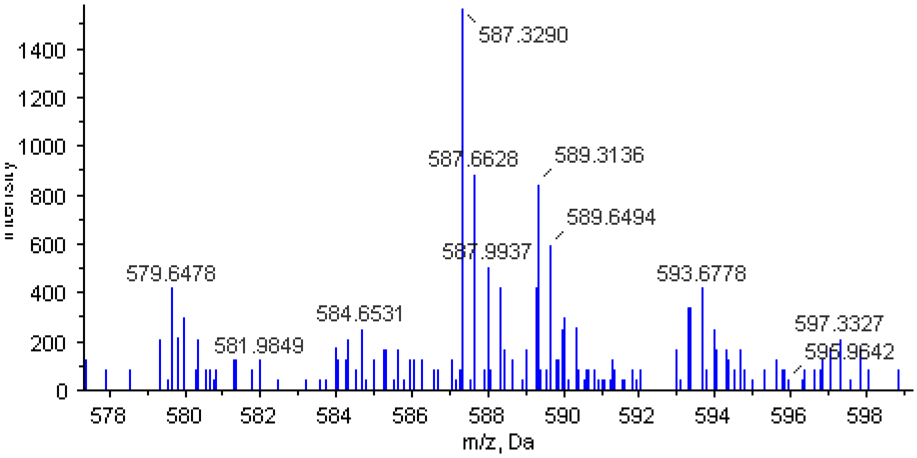
Seq Cov %: 7.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2.31

116: 114=E5TL: D5TL=1.96

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSFFKWVSFVLILHLLNPTLISCSSNGLSQIPSKFLTLAKRNDFFDWMVGIRRRIHENPELGYEEVETS
KLVRAELEKMGVSYKYPVAVTGVVGYVGTGHAPFVALRADMDALAMQEMVEWEHKSKVPGKMHACGHDA
HTTMLLGAAKLLKEHEEELQ**GTVVLVFQPAEEGGGGAK**KIVEAGVLENVSAIFGLHVTNQLALGQVSSR
EGPMLAGSGFFKAKISGKGGHAALPQHTIDPILAASNVIVSLQHLVSR**EADPLDSQVVTVAK**FEGGGAF
NVIPDSVTIGGTFRAFSTKSFMQLKKRIEQVITRQASVNMCNATVDFIEEEKPFFPPTVNDKALHQFFK
NVSGDMLGIENYVEMQPLMGSEDFSFYQQAIPGHFSFVGMQNKARSPMASPHSPYFEVNEELLPYGASL
HASMATRYLLELKASTLNKSNKKDEL

Protein No.: I-605

Protein name and Species:

Putative uncharacterized protein OS=Ricinus communis GN=RCOM_0701460 PE=4 SV=1

Accession: tr|B9SC09|B9SC09_RICCO

Unused ProtScore: 4.03

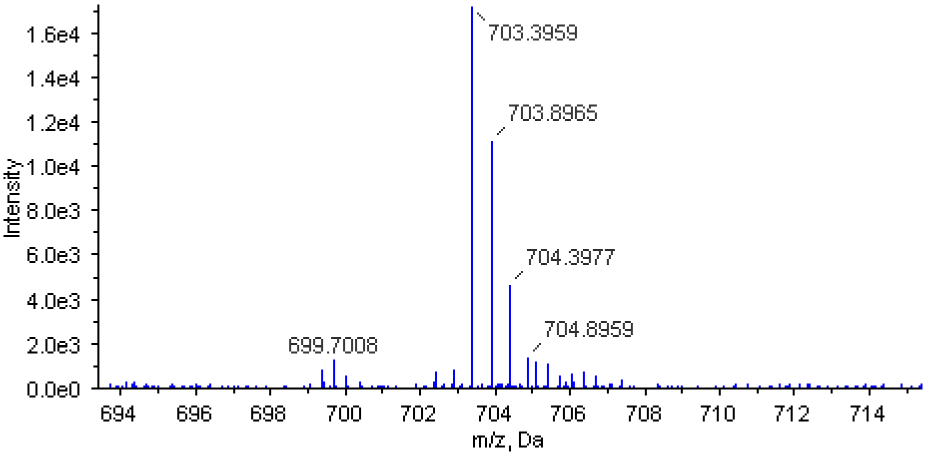
Seq Cov %: 8.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.48

116: 114=E5TL: D5TL=0.56

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAPMLPKSVAIRSEFSRGYAYYMAENEAVRGFIRCEGENILNPYVKIEVETAQIDSKFVHLRFSHTNKY
WGRSGPGFTQDDYWVSATSDQPEEDTSKWSCTLFEPIFDHGFLFLRHVQTGGRVRTDGPIGATGPVSRL
LLYFRNYDNVPYLDFTFFDLGTLCILPKRVAFRGYNDMYLKAEWIERHEYLQFSSDDVNEKAAGYEITM
MPDGHVRLRSNFFNKFWRRSPNWIWADSTDTVGSDRDTLFWPVK**VNDDTIALR**NAGNNR**FCSSLTAERK**
TDCLNAAVATITREAR**LQVEELVFER**SIFNVRFLMEYARIFDERATVAGWGSAENQSEEAATLSITVGY
EDTTSFTFSNSLAITAGVTVGITTGLPRIAEGKIEISTEVTNTLEWNRTTSETRTASATYLANVPARSR
I**RIDYVATRGTCNIPFSYTQR**DRLSHDGSFATTQHVDGVYTGVNYYSFHFEQPQIVPL

Protein No.: I-606

Protein name and Species:

Lipase class 3 family protein [Arabidopsis thaliana] OS=Arabidopsis thaliana PE=4 SV=1

Accession: tr|Q9LUL3|Q9LUL3_ARATH

Unused ProtScore: 4.03

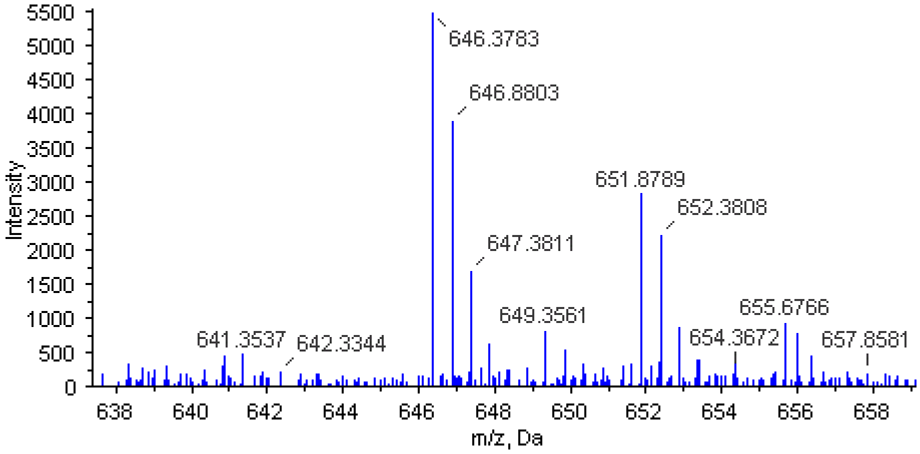
Seq Cov %: 4.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.21

116: 114=E5TL: D5TL=0.40

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MHKDNDSGSGSNPGQVSNYLIVRPHRGGYIDLFRYGVRDDQTSKAKFLEMPDNREWSTITIDEEAEDHR

WVIVVSILVRKIIRLLRTPMEFTGFVVDFFLNLFSANGGFFGLLLRLIQAKVVIPERGSVTFVSTIGQL

DGRISLYKEWNFVEHLEGIDSVDSGRVKIELGSR**GLMDLCVMASKLAYENAK**MNLVEFLDCWNDYQKQM

STQVFVFTDKQK**DANLIVISFR**GTEPFDADDWGTDFDYSWYEVPNVGKLHMGFLEAMGLGNRDDTTTFH

YNLFEQTSSEEENSKKNLLDMVERSAYYAVRVILKRLLSEHENARFVVTGHSLGGALAILFPTLLVLNE

ETEIMKR**LLGVYTFGQPR**IGNREVGLFMKAQLNQPVDRYFRVVYCNDIVPRLPYDDKTFLYKHFGLCLF

YDSFYNETKAEDEPDPNPYGLRYKILGHVIAVWELVRGLTMGYTHGPDYKEGWFRILFRLMGLVIPGLS

DHCMTDYVNSVRLGPDNELQMSSL

Protein No.: I-610

Protein name and Species:

dehydrogenase/reductase SDR family member 12 [Vitis vinifera][Vitis vinifera] OS=Vitis vinifera GN=VIT_18s0157g00200 PE=4 SV=1

Accession: tr|D7SXZ2|D7SXZ2_VITVI

Unused ProtScore: 4.02

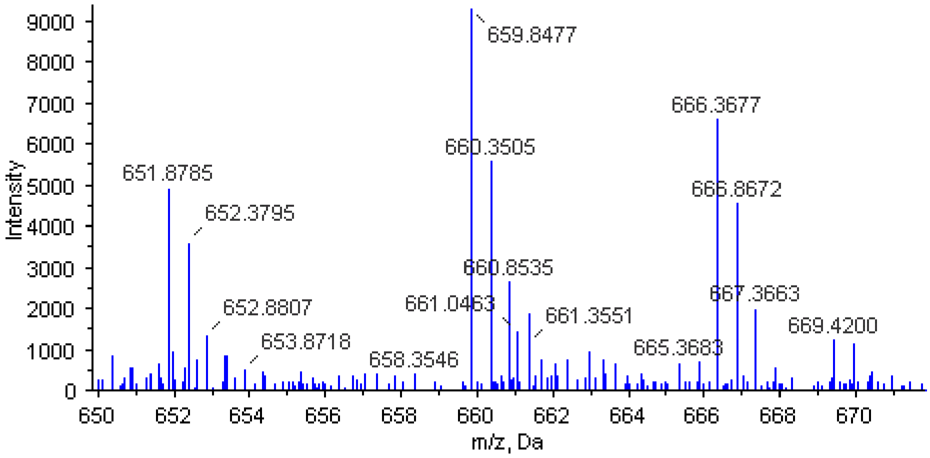
Seq Cov %: 15.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.91

116: 114=E5TL: D5TL=1.58

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MQNPTLHIQIHISIRESIMFILKTWRSIAFGVHGYKNSTKTGFMEHSKNFKSEDMQTQIEGK**NCIVTGA**
NSGIGYATAEGLASRGANVYMVCRNKERGEAALSEIQSK**TGNSNVHLEVCDLSSVSEIK**SFASKFSKKD
VPIHVLVNNAGLLEYNRITTSEGFELNFAVNVLGTFTMTESMLPLLEKAAPDARVITVSSGGMYSVPLT
NDLQFSDDKFDGVTQYARNKR**VQVALTEK**WAEMYKNKGIGFYAMHPGWAETSGLAKSLPGFYKLLSGNL
RTIEEGADTIIWLALQPKEK**LVSGAFYFDR**AEAPKHLMFAATRSSHAMIDSIIGNLRSFSGLSALSS

Protein No.: I-612

Protein name and Species:

UTP-glucose-1-phosphate uridylyltransferase OS=Pyrus pyrifolia PE=2 SV=1

Accession: sp|O64459|UGPA_PYRPY

Unused ProtScore: 4.01

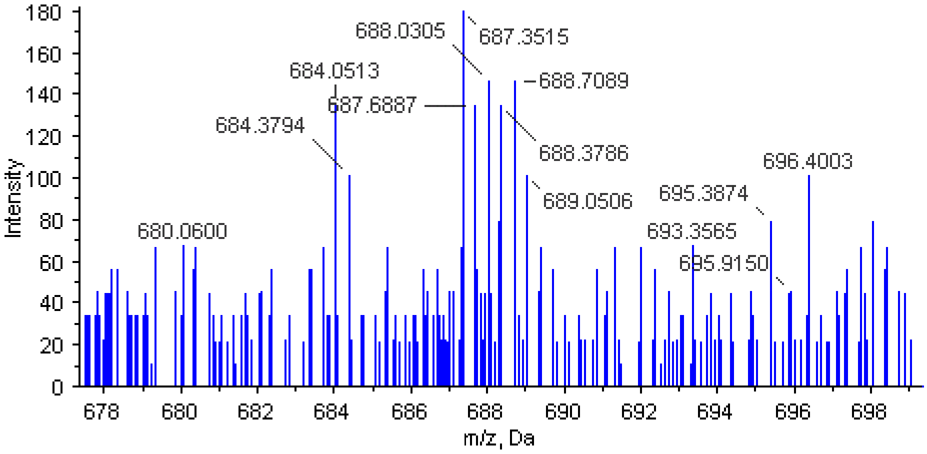
Seq Cov %: 23.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.52

116: 114=E5TL: D5TL=0.27

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAAVATGNVDKLKSDVASLSQISENEKNGFINLVSRYVSGEEAQHVEWSKIQTPTDEVVVPYDGLAPTP
EDPEEIKKLLDKLVVLK**LNGGLGTTMGCTGPKSVIEVR**NGLTFLDLIVIQIENLNNKYGSCVPLLLMNS
FNTHDDTQKIVEKYSK**SNVQIHTFNQSQYPRLVVEDFSPLPSK**GQTGK**DGWYPPGHGDVFPSLK**NSGKL
DLLLSQGKEYVFIANSDNLGAVVDLKILHHLIQKK**NEYCMEVTPK**TLADVKGGTLISYEGR**VQLLEIAQ**
VPDQHVNEFKSIEKFKIFNTNNLWVNLNAIKR**LVEADALKMEIIPNPK**EVDGVK**VLQLETAAGAAIRFF**
NHAIGINVPRSRFLPVK**ATSDLLLVQSDLYTLQDGFVTR**NSARKNPENPTIELGPEFKKVGSYLSRFKS
IPSILELESLKVSGDVWFGAGVVLKGKVTITAKSGVKLEIPDNAVIANKDINGPEDL

Protein No.: I-613

Protein name and Species:

Chitinase OS=Euonymus europaeus PE=2 SV=1

Accession: tr|Q7Y237|Q7Y237_EUOEU

Unused ProtScore: 4.01

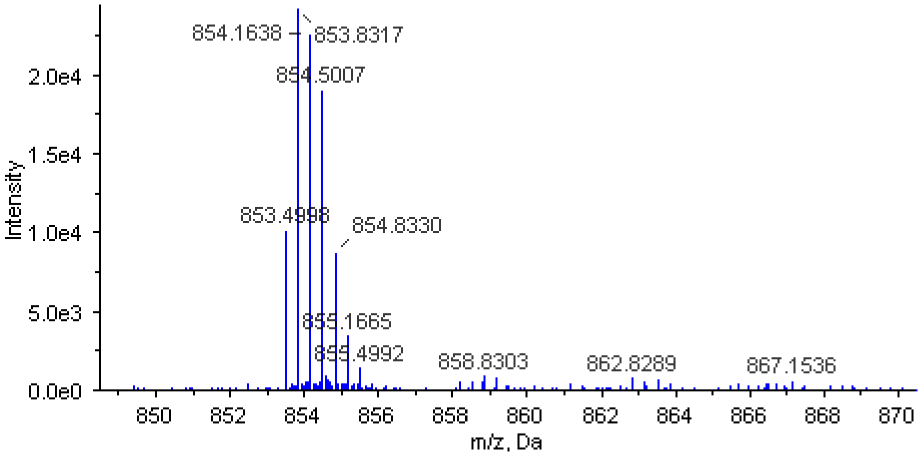
Seq Cov %: 13.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.24

116: 114=E5TL: D5TL=0.21

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MRFWVFTILSLSLSVLGSA**EQCGR**QAGGALCPGGQCCSQYGWCGTTNEYCGQGCQSQCGGSGGGGDIGG
IISRDRFNDILKHRNDNACEGKGFYSHDAFLTAAKAYPAFGTTGDDATRKREIAAFLAQTSHETTGGWP
SAPDGPYSWGYCFVRERNPPSSYCDPNYPCPKQYYGRGPLQLSWNYNYAQAGR**AIGVDLINNPDLVATD**
AVISFKTAIWFWMTAQSPKPSCHDVIIGSWRPSGADTAAGR**VSGYGVITNIINGGIECGK**GQNPQVEDR
IGFFRRYCQILGTGTGNNLDCYNQRPFGARLLLDTI

Protein No.: I-618

Protein name and Species:

HEV1.2 OS=Hevea brasiliensis PE=4 SV=1

Accession: tr|Q6JYQ9|Q6JYQ9_HEVBR

Unused ProtScore: 4

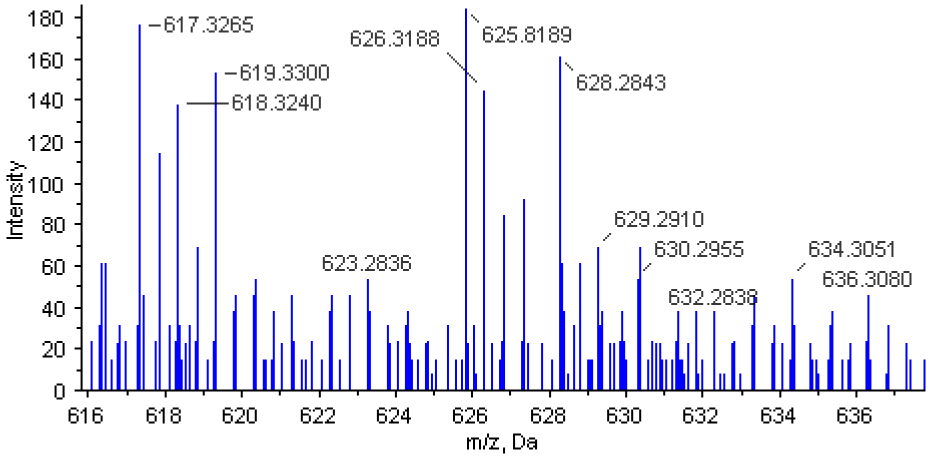
Seq Cov %: 64.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.60

116: 114=E5TL: D5TL=0.33

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MNICMVVLLCLTGVAIAEQCGRQAGGKLCPNNLCCSQYGWCGSSDDYCSPSKNCQSNCKGGGGGGGGSG
GSASNVLATYHLYNPQQHGWDLNAVSAYCSTWDANKPYSWRSKYGWTAFCGPVGAHGQPSCGKCLSVTN
TGTGAKTTVRIVDQCSNGGLDLDVNVFRQLDTDGKGYERGHLTVNYQFVDCGDSFNPLFSIVKSSVIN

Protein No.: I-625

Protein name and Species:

Pyruvate kinase OS=Ricinus communis GN=RCOM_0248610 PE=3 SV=1

Accession: tr|B9ST42|B9ST42_RICCO

Unused ProtScore: 4

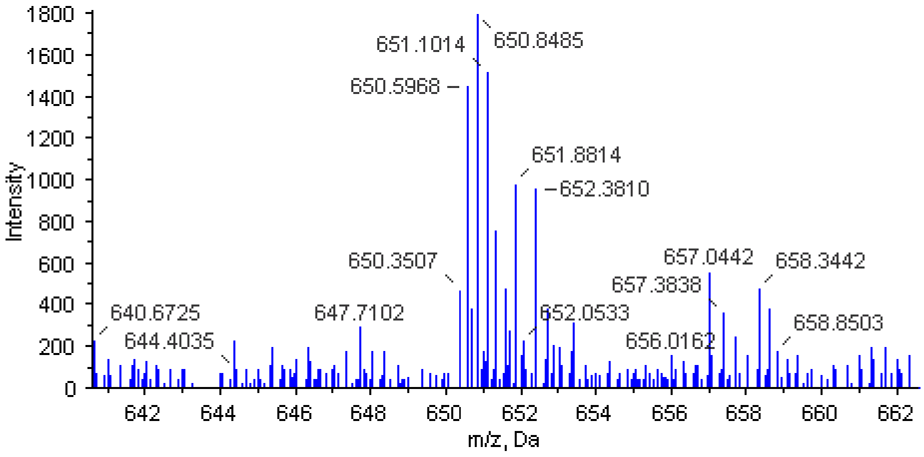
Seq Cov %: 14.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.65

116: 114=E5TL: D5TL=1.05

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MQGGHMVVEEPLRLSSILTPSKPSYLPSLTKIVGTLGPKSRSVETIEACLNAGMSVARFDFSWLDVDYH
QETLNNLRQAMRNAKKLCAVMVDTVGPELPICNQTVKQIELK**ADNRVTITSDVSK**EPSAEILPVNFSGL
SQILKKGDTVFLGQYLFTGSENTSVWLEVLETNGKDVVCLVKNSATLTGFVLMHISQVLSSLPTLTDND
KKVISEWGSCSNVDIISLSYTRNVEDVRELRAFIK**THSLHETQVFAK**IETVEGLKHFDEILQEADGIIL
GR**GNLGIDLPPEK**VFLFQKSAVYK**CNMAGKPVIISR**VVDSMTANLRPTR**AEATDVANAVLDGADGILLG**
AETLRGLYPIDTIRTVGRICAEAEIVCNHSFHFKRISRHVGEPMSHAESVASSAVRAAIKVKAPLIVVF
TSSGAAPRLIAK**YRPPVPVFAVVIPR**LRSNTLKWSFTGSAEARQLLGVRGVYPILASPLVATSGASSEV
STLKVALDHGKSVGLLKPNDQIVVFEKIGDSSVVRIMQLPS

Protein No.: I-628

Protein name and Species:

TBC1 domain family member 13 OS=Populus trichocarpa GN=POPTRDRAFT_174838 PE=4 SV=1

Accession: tr|B9GFV7|B9GFV7_POPTR

Unused ProtScore: 4

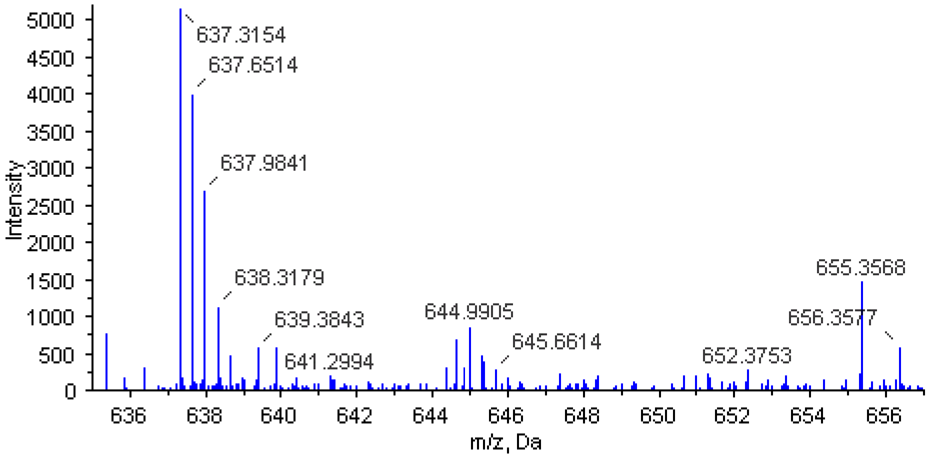
Seq Cov %: 8.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.22

116: 114=E5TL: D5TL=0.22

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

SAAEDISKQALLLTELSKKVINMGELRRIASQGIPDGAGIRSTVWK**LLLGYLAPDR**SLWSSELAKKRSQ
YKHFKEDLLMNPSEIARRLEKTTVLNNDNGKSESRCVLSRSEITHGEHPLSLGKSSVWNQFFQDSEIIE
QIDRDVKRTHPDLHFFSGDSSLAKSNQEALRNILTVFAKLNPGIRYVQGMNEILAPLFYIFKNDPDEEM
AACAEADTFFCFVELLSGFR**DHFCQQLDNSVVGIR**STITRLSQLLKEHDEELWRHLEITTKVNPQFYAF
RWITLLLTQEFNFADSLHIWDTLLSDPEGPQETLLRVCCAM**LILIR**RRLLAGDFTSILKLLQNYPPTNI
SHMLYVANKLR

Protein No.: I-631

Protein name and Species:

Cytochrome b5 OS=Camellia sinensis PE=2 SV=1

Accession: tr|F4YFE3|F4YFE3_CAMSI

Unused ProtScore: 4

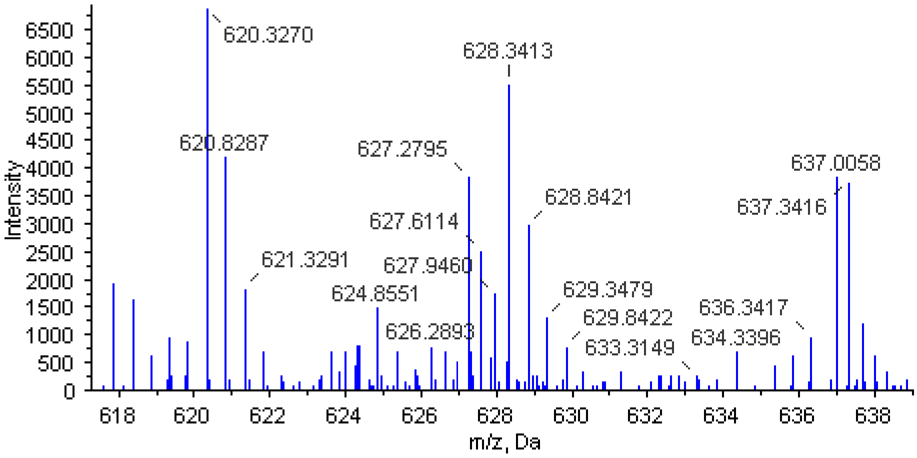
Seq Cov %: 29.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=3.05

116: 114=E5TL: D5TL=2.04

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MASDPKIHTFEEVAKHNKTKDCWLILSGK**VYDVTPFMDDHPGGDEVLLSSTGKDATNDFEDVGHSDSAR**
EMMEKYYIGGIDSSTVPLKRSYIPPQQSHYKPDKTP**EFVIK**IFQFLVPLLILGLAFGVRYYTKEK

Protein No.: I-634

Protein name and Species:

Putative uncharacterized protei OS=Glycine max PE=2 SV=1

Accession: tr|C6TGB0|C6TGB0_SOYBN

Unused ProtScore: 4

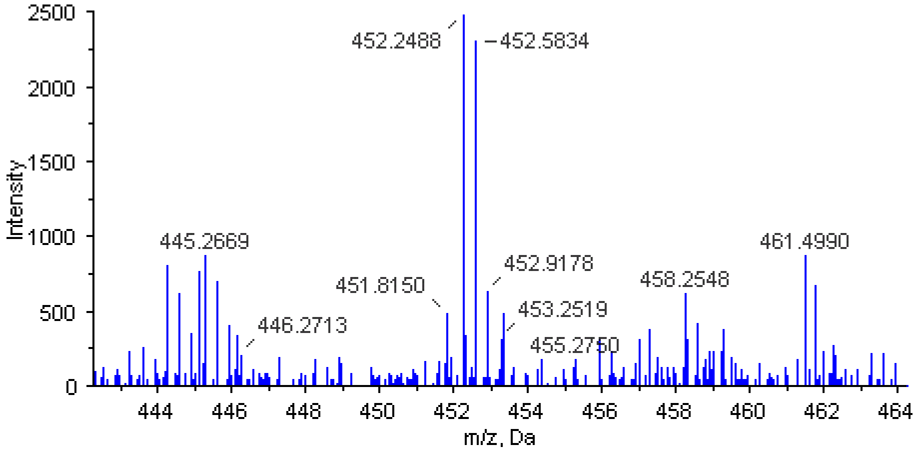
Seq Cov %: 5.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.46

116: 114=E5TL: D5TL=1.44

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MESASELVEFPLLLTPIDSNYRACTIPYRFPSDNPRKPTPTEISWIDLFLNSIPSFKKRAESDTSVPDAAAKAEKFAQRYADILEDLKKDPESHGGPPDCILLCRLRELVLRELGFRDIFKKVKDEENAKAISLSENVVH**LNDAIEDEGK**RLENLVRGIFAGNIFDLGSAQLVEVFSKDGMSFLASCQNLVPRPWVIDDLDTFKLKWSKNPWKKVIIFVDNSGADIILGIMPFARELLRRGSQVVLAANDLPSINDVTCSELVEIISKLKDEDGQLVGVSTSNLLIANSGNDLPVIDLTRVSQELAYLASDADLVTLEGMGRGIETNLYAQFKCDSLKIGMVK**HPEVAQFLGGR**LYDCVFKYNEVSS

Protein No.: I-643

Protein name and Species:

Translation machinery-associated protein 7-like OS=Hevea brasiliensis PE=4 SV=1

Accession: tr|D9IZZ6|D9IZZ6_HEVBR

Unused ProtScore: 4

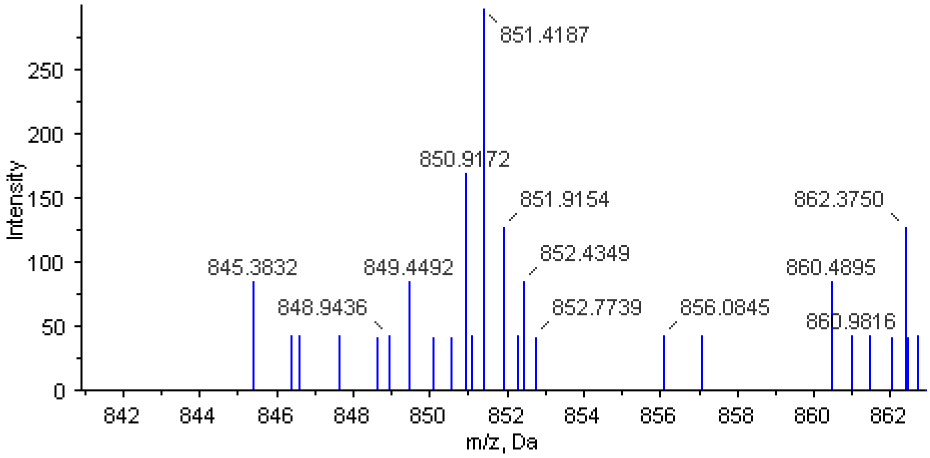
Seq Cov %: 32.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.30

116: 114=E5TL: D5TL=1.26

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSSKQGGKAKPLEQPKAEKK**DYDETDTANIQK**KKEEEKALKELRAKAAQK**GTFGGSGLK**KSGKK

Protein No.: I-648

Protein name and Species:

20 kDa chaperonin, chloroplastic OS=Vitis vinifera GN=VIT_17s0000g03620 PE=3 SV=1

Accession: tr|D7SIZ7|D7SIZ7_VITVI

Unused ProtScore: 3.96

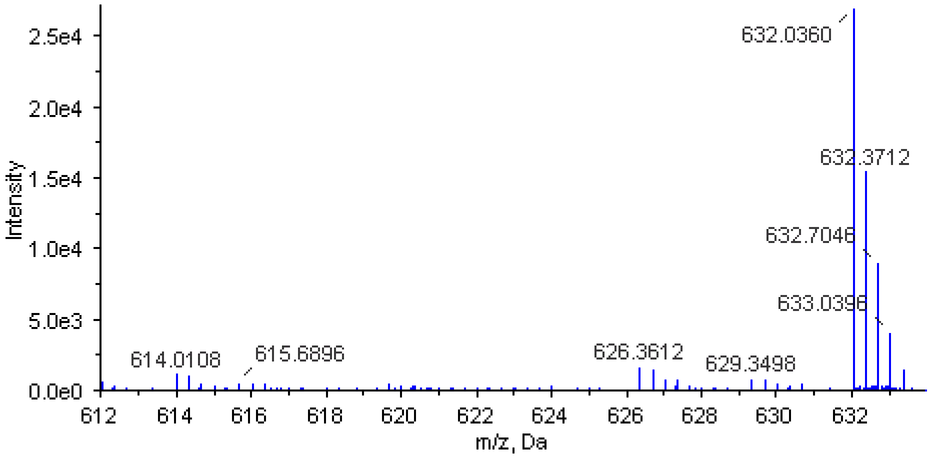
Seq Cov %: 10.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.22

116: 114=E5TL: D5TL=0.59

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MATAPAISTRSLPSFEGLRPSTVRVPLVRLPLRAAGLTQRPVRGLVVRAATSIGPKYTSLKPLADRVLV
KIKTVEEKTGGGILLPTTAQTK**PQGGEVVAVGEGR**TVGKNKVDIGVKTGTSVVYSKYAGTELEFNGSNH
LILK**EDDIVGILETDDIK**DLKPLNDRVLIKVAVAEEKTAGGLLLTEATKEKPSIGTVIAVGPGSLDGEG
NRKPLSLSPGSTIMYSKYAGNEFKGSDGSDYIALRASDVMAVLS

Protein No.: I-650

Protein name and Species:

Ribosomal protein (Fragment) OS=Jatropha curcas PE=2 SV=1

Accession: tr|D1ML39|D1ML39_9ROSI

Unused ProtScore: 3.95

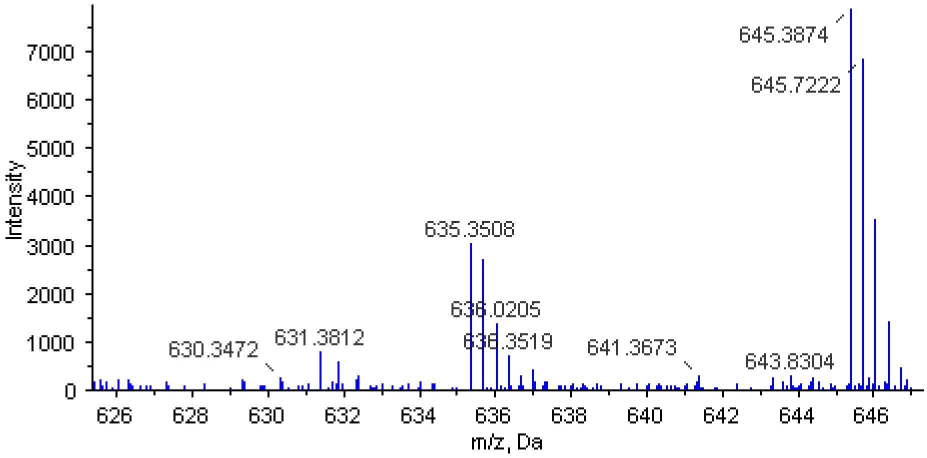
Seq Cov %: 16.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=11.48

116: 114=E5TL: D5TL=2.11

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

QSETLREAISTIMAASVEKKRNFTETIELQ**IGLK**NYDPQKDKCFSGSVKLPHIPRPKMKICMLGDAQHV
EEAEAIGLQWMDVEALKKLNKNKKLVKKLAK**QYHAFLASESVIK**QIPR**LLGPGLNK**AGK**FPTLVTHQES**
LESKVNETKATVKFQLKKVLCMGVAVGNCAMEEKQVFQNVQMSVNFLVSLLKKNWQNVKCLNVKTTMGN
PVRIF

Protein No.: I-651

Protein name and Species:

Calcium lipid binding protein, putative OS=Ricinus communis GN=RCOM_1612600 PE=4 SV=1

Accession: tr|B9RDG1|B9RDG1_RICCO

Unused ProtScore: 3.94

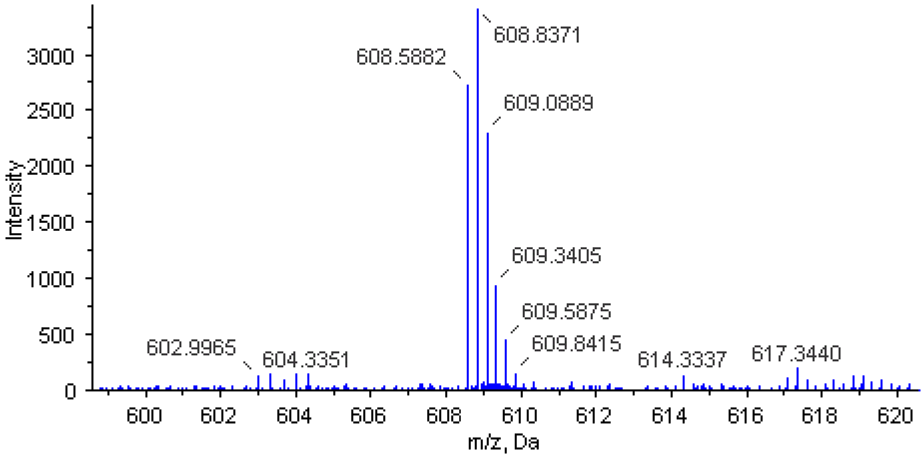
Seq Cov %: 9.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=3.40

116: 114=E5TL: D5TL=2.06

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGLISGIFMGMIFGIAVMAGWKHMMRYRSTKRIAKAVDIK**LLGSLNR**DDLKKICGDNFPDWISFPVFEQ
VKWLNKQLSKLWPFVADAATMVVK**ESVEPLLEDYRPPGITSLK**FNKFSLGTVPPKIEGIRVQSLKKGQI
IMDIDFRWGGDPSIILGVEAALVASIPIQLKDLEVYTVIRVIFQLAEEIPCISAVVIALLSEPKPK**IDY**
VLKAVGGSLTAIPGLSDMIDDTVHSIVTDMLQWPHRVVVPIGGIPVDTSELELKPEGK**LTVTVVK**ANDL
KNMEMIGK**SDPYVVLYIR**PMFKVKSRTIENNLNPVWDQTFEMIAEDKETQSLILEVFDKDIGQDKRLGI
AKLPLIELEAETWKQHELRLLPALDMLKIKDKKDGGTLTIKVLYHAFNKEEQLAALEEEKRIIEERKKL
KEAGVIGSTMDALDGAVGLVGTGIASGVGLVGTGIGAGVGLVGTGVGAGVGIVGSGLGAVGSGLSKAGK
FVGRTFTGQSSKR**SGSSTPVNSVQENGGAKPL**

Protein No.: I-653

Protein name and Species:

Quercetin 3-O-methyltransferase 1 OS=Arabidopsis thaliana GN=OMT1 PE=1 SV=1

Accession: sp|Q9FK25|OMT1_ARATH

Unused ProtScore: 3.92

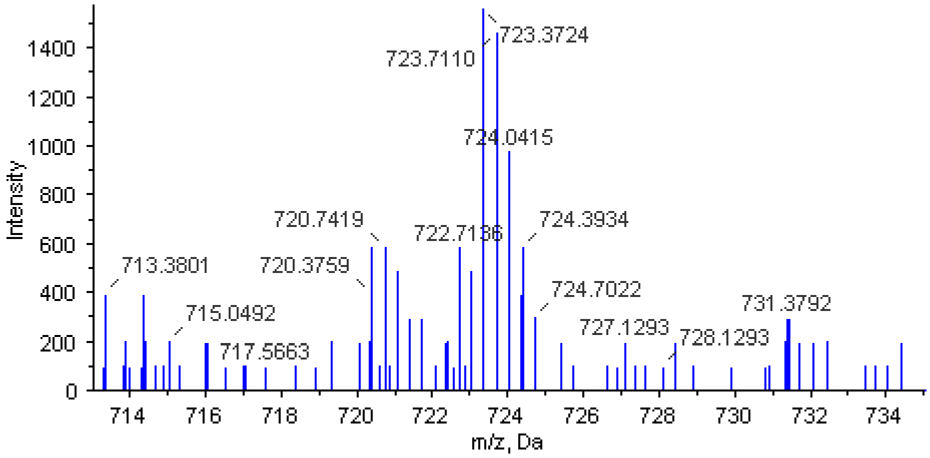
Seq Cov %: 8.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.13

116: 114=E5TL: D5TL=0.70

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGSTAETQLTPVQVTDDEAALFAMQLASASVLPMALK**SALELDLLEIMAK**NGSPMSPTEIASKLPTKNP
EAPVMLDRILRLLTSYSVLTCSNRKLSGDGVERIYGLGPVCKYLTK**NEDGVSIAALCLMNQDK**VLMESW
YHLKDAILDGGIPFNKAYGMSAFEYHGTDPRFNKVFNNGMSNHSTITMKKILETYKGFEGLTSLVDVGG
GIGATLKMIVSKYPNLKGINFDLPHVIEDAPSHPGIEHVGGDMFVSVPK**GDAIFMK**WICHDWSDEHCVK
FLKNCYESLPEDGKVILAECILPETPDSSLSTKQVVHVDCIMLAHNPGGKERTEKEFEALAKASGFKGI
KVVCDAFGVNL**IELLK**KL

Protein No.: I-666

Protein name and Species:

glyceraldehyde-3-phosphate dehydrogenase, NADP-dependent OS=Vitis vinifera GN=VIT_11s0037g00070 PE=3 SV=1

Accession: tr|D7U1A1|D7U1A1_VITVI

Unused ProtScore: 3.83

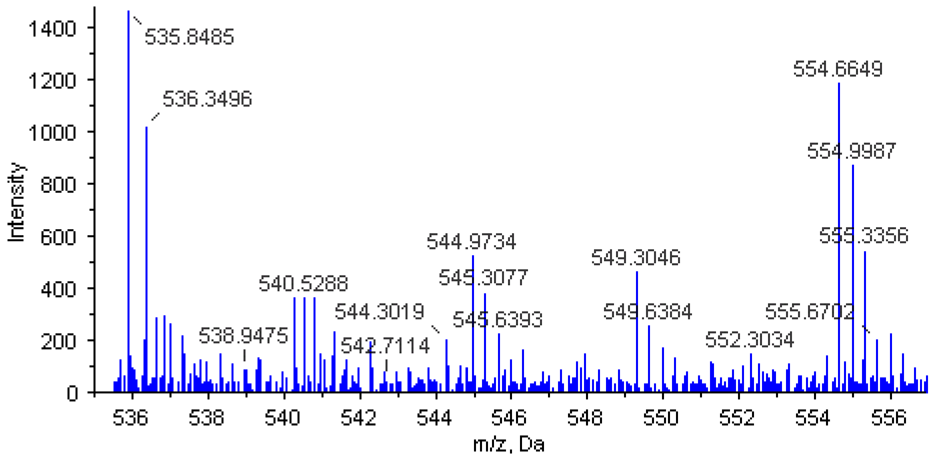
Seq Cov %: 44.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.24

116: 114=E5TL: D5TL=0.99

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAGTGVFAEIIDGDVYKYYSEGEWRKAVSGK**SVAIINPTTR**KTQYR**VQACSQEEVNK**AMEIAKSAQKIW
AKTPLWKR**AELLHK**AAAILKEHK**APIAECLVK**EIAKPAKDAVTEVVR**SGDLVSYTAEEGVR**ILGEGK**FL**
VSDSFPGNERSKYCLTSK**IPLGVILAIPPFNYPVNLAVSK**IAPALIAGNSIVLKPPTQGAVSALHMVHC
FHLAGFPKGVISCVTGK**GSEIGDFLTMHPGVN**CISFTGGDTGVAISKK**AGMIPLQMELGGK**DACIVLED
ADLDLVAANIVK**GGFSYSGQR**CTAVKVVLAMESIADTLVEKVNAKVAKLTVGPPEDDCDITPVVSESSA
NFIEGLVMDAKQK**GATFCQEYRR**EGNLIWPLLLDNVRPDMR**IAWEEPFGPVLPVLRINSVEEGIHHCNA**
SNFGLQGCVFTRDINK**AILISDAMETGTVQINSAPARGPDHFPFQGLKDSGIGSQGITNSINMMTK**IK**S**
TVINLPSPSYTMG

Protein No.: I-668

Protein name and Species:

Neutral leucine aminopeptidase preprotein OS=Solanum lycopersicum GN=LapN PE=2 SV=1

Accession: tr|Q8GZD8|Q8GZD8_SOLLC

Unused ProtScore: 3.82

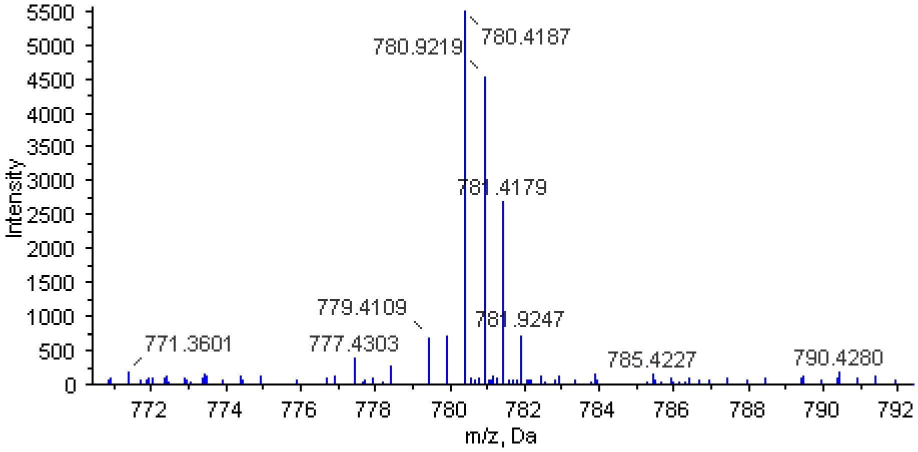
Seq Cov %: 13.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.50

116: 114=E5TL: D5TL=1.13

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAALRVSSALACSSSSSFHSYPSIFTKFQSSPIWSFSISVTPLCSRRAKRMAHSIARDTLGLTHTNQSD
APKISFAAKEIDLVEWKGDILTVGATEKDLARDGNSKFQNPLLQKLDSKLSGLLSEASSEEDFSGKAGQ
STILR**LPGLGSK**RIALVGLGSPTSSTAAYRCLGEAAAAAAKSAQASNIAIALASTDGLSAELKLSSASA
ITTGAVLGTFEDNRFKSESKKPTLK**SLDILGLGTGPEIEK**KIKYAADVCAGVILGRELVNAPANVLTPA
VLAEEAKKIASTYSDVFSANILDVEQCKELKMGSYLAVAAASANPAHFIHLCYKPSSGEIKKK**IALVGK**
GLTFDSGGYNIKTGPGCSIELMKFDMGGAAAVLGAAKALGQIKPAGVEVHFIVAACENMISGTGMRPGD
IITASNGK**TIEVNNTDAEGRLTLADALVYACNQGVEK**IVDLATLTGACVVALGPSIAGIFTPSDDLAKE
VVAASEVSGEKLWRLPMEDSYWDSMK**SGVADMVNTGGR**PGGAITAALFLKQFVNEKVQWMHIDLAGPVW
SDKKKNATGFGVSTLVEWVLKNSTN

Protein No.: I-680

Protein name and Species:

hydrolase domain-containing protein 4-like [Vitis vinifera] OS=Vitis vinifera GN=VIT_18s0001g13610 PE=4 SV=1

Accession: tr|E0CPI5|E0CPI5_VITVI

Unused ProtScore: 3.74

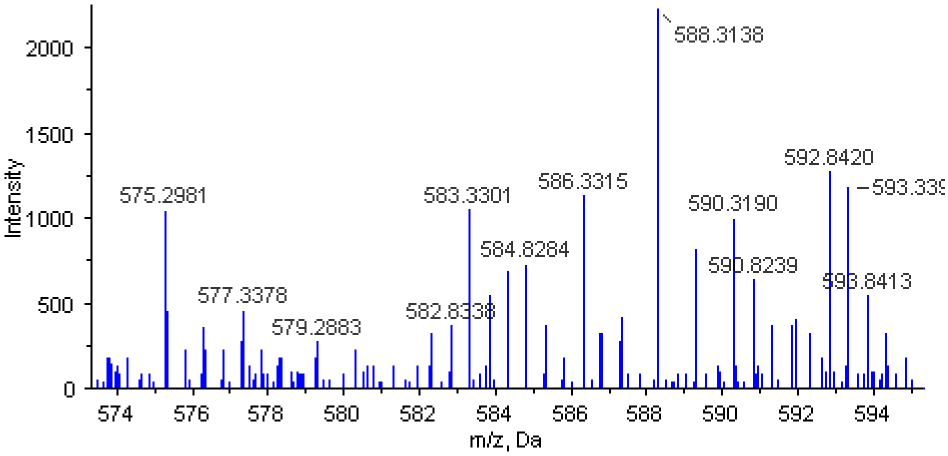
Seq Cov %: 14.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=9.46

116: 114=E5TL: D5TL=2.53

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAEEMTKAELGSSSSTTKSRSLWPSLFRWIPTSTDHIIDAEKR**LLSLVK****TPYVQEQVNIGSGPPGSK**VR
WFRSASNEPR**FINTVTFDSK**DDSPTLVMVHGYGASQGFFFRNFDALARRFR**VIAIDQLGWGGSSRPDFT**
CKSTEETEAWFIDSFEEWRKAKNLSNFILLGHSVGGYVAAKYALKHPEHIQHLILVGPAGFSLESDGKS
EWLTRFRATWKGAVLNHLWESNFTPQKLVRGIGPWGPDLVRKYTSARFSSYSTGDLLTEEESKLLTDYV
YHTVAAK**ASGELCLK**YIFSFGAFARLPLLHSASEWKVPTTFIYGFEDWMNYQGAQEARKQMKVPCEIIR
VPQAGHFVFIDNPSGFHSAVLYACRRFLLPDPDSQSLPEGLTSA

Protein No.: I-683

Protein name and Species:

bifunctional polymyxin resistance protein; UDP-D-apiose/UPD-D-xylose synthetase [Vitis vinifera] OS=Vitis vinifera

Accession: tr|D7SN69|D7SN69_VITVI

Unused ProtScore: 3.7

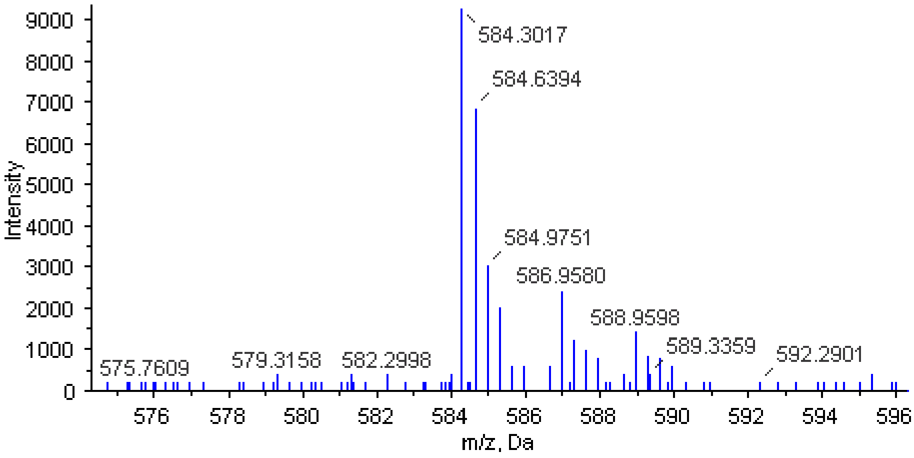
Seq Cov %: 26.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=3.31

116: 114=E5TL: D5TL=2.04

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MASAARLDLDGNAIKPMTIC**MIGAGGFIGSHLCEK**LMAETMHKVLAVDVYSDKIKHLLEPSTHPWSDRI
QFHRINIKHDSR**LEGLIKMADLTINLAAICTPADYNTR**PLDTIYSNFIDALPVVKYCSENNKR**LIHFST**
CEVYGKTIGSFLPKDSPLWQDPTYYVLK**EDASPCIFGPIEK**QRWSYACAKQLIERLIYAEGAENDLEFT
IVRPFNWIGPR**MDFIPGIDGPSEGVPR**VLACFSNNLLRHEPLKLVDGGQSQRTFVYIKDAIEAVLLMID
NPAR**ANGHIFNVGNPNNEVTVR**QLAEMMTEVYAKVSGEPSLEVPTVDVSSK**EFYGEGYDDSDKR**IPDMT
IINKQLGWNPKTSLWDLLESTLTYQHRTYAEAIKQAIAKPVAS

Protein No.: I-687

Protein name and Species:

V-type proton ATPase subunit F OS=Hevea brasiliensis GN=VHA-F PE=2 SV=1

Accession: tr|B8Y6I1|B8Y6I1_HEVBR

Unused ProtScore: 3.68

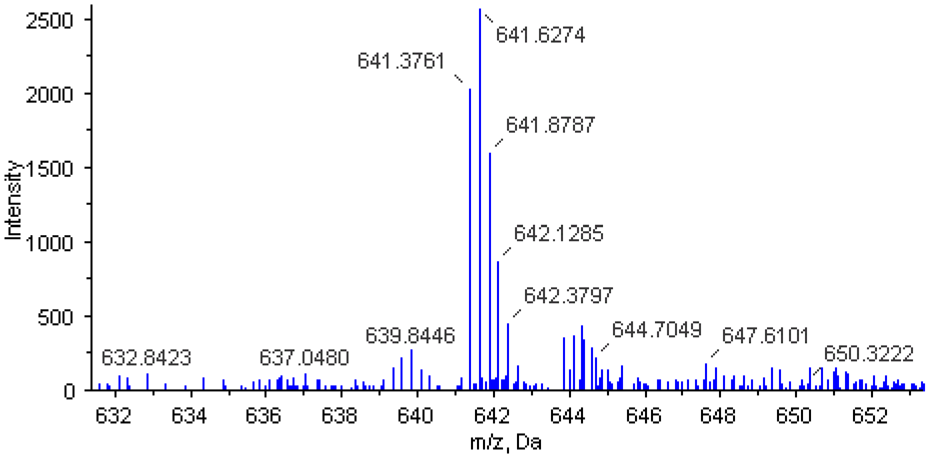
Seq Cov %: 21.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.69

116: 114=E5TL: D5TL=1.54

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MANRVQIPTSNSALIAMIADEDSVVGFLLAGVGNVDLRRK**SNYLLVDSK**TTVKQIEDAFKDFTTREDIA
IVLISQYVANMVR**FLVDSYNKPVPAILEIPSK**DHPYDPAQDSVLSRVKHLFSAESVASERR

Protein No.: I-688

Protein name and Species:

argininosuccinate lyase [Vitis vinifera] OS=Vitis vinifera GN=VIT_18s0001g07590 PE=3 SV=1

Accession: tr|E0CRW7|E0CRW7_VITVI

Unused ProtScore: 3.66

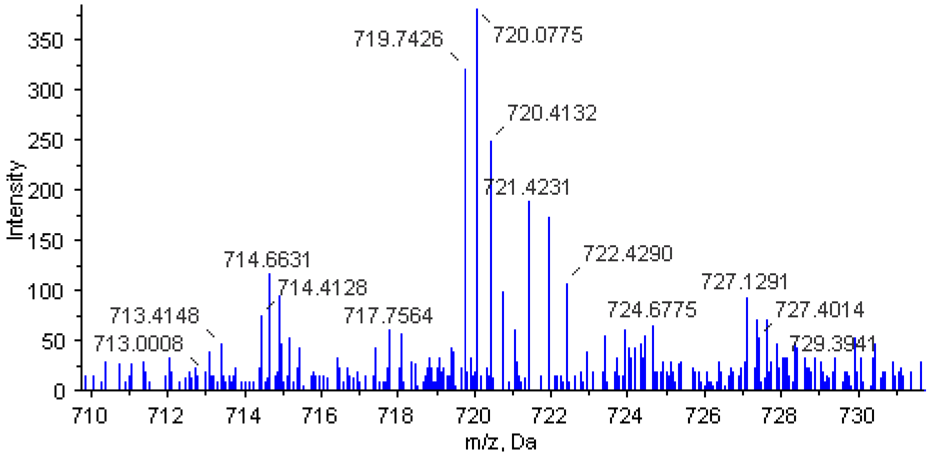
Seq Cov %: 8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.54

116: 114=E5TL: D5TL=0.47

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MKTSATDPSTKKAKEAKLWGGRFEEGVTDAVER**FTESISFDK**ALYKQDIMGSRAHASMLAHQGLISVSD
RDSILQGLDNIERRIEDGEFVWRTDREDVHMNIEAALTDLIGEPAKKLHTARSRNDQVLTDFRLWCRDA
IDNIVARIEHLQVALVTLAMKNENLIVPGYTHLQRAQPILLQHLLLAYVEQLDRDAGRLLDCRQR**LNFC**
PLGACALAGTGLPIDRFMTSHDLGFNAPMRNSIDAVSDRDFVLEFLSANSITAIHLSRLGEEWVLWASE
EFGFLTPSDSVSTGSSIMPQKKNPDPMELVRGKSARVVGDLVTLLVLCKGLPHAYNRDLQEDKEPTFDS
TKTIIGMLEVCAEFAQNITFNREKIKK**ALPAGHLDATTLADYLVK**KGIPFRTSHDIVGKSVALCVSK**NC**
QLQDLSLDELRSVNPVFDEDVYEFLGVENAVKKFCSYGSTGSECVAEQLDFWVTKLQINTAGHK

Protein No.: I-692

Protein name and Species:

Homogentisate 1,2-dioxygenase, putative OS=Ricinus communis GN=RCOM_1743950 PE=4 SV=1

Accession: tr|B9RXB8|B9RXB8_RICCO

Unused ProtScore: 3.63

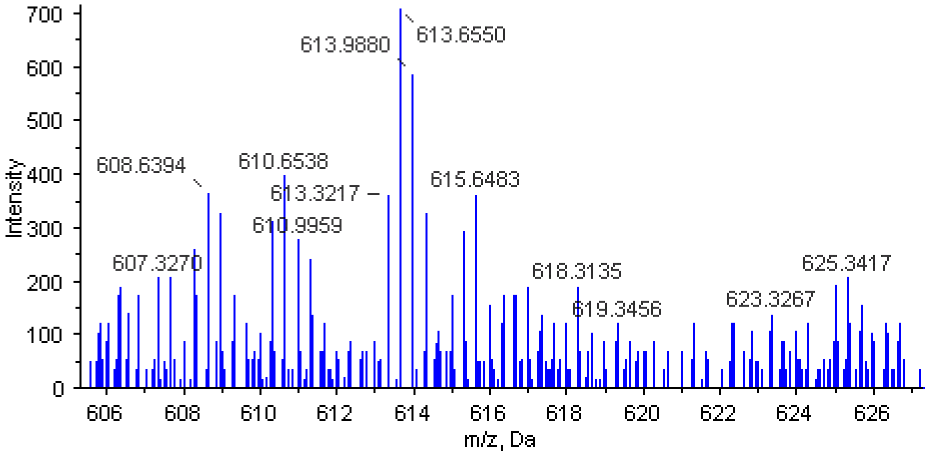
Seq Cov %: 7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.09

116: 114=E5TL: D5TL=0.19

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDNPKSNGRDFPSDDHDYLSGFGNTFESEAIHGALPRGQNSPLICPY**GLYAEQISGSSFTSPR**KLSQRS
WLYRIKPSVTHEPFKPRVPSHGK**IVSEFDK**TDSCTTTPTQLRWKPVDIPDSPTDFIDGLFTICGAGSSF
LRHGFAIHMYTANKSMGNCALCNADGDFLVVPQEGRLWITTECGKLQVSPGEVVVLPQGFRFAVDLPDG
PSRGYVAEIFGTHFQLPDLGPIGANGLAAPRDFLVPKAWYEEGPCPGYTIIQK**FGGELFTAK**QDFSPFN
VVAWHGNFVPYKYDLKKFCPYNTVLIDHSDPSINTVLTASTDKPGVALLDFVIFPPRWLVAEHTFRPPY
YHRNCMSEFMGLIYGGYEAKADGFVPGGASLHSCMTPHGPDTKTYEATIARGNDAGPSRITDTMAFMFE
SCLIPRICLWAVESPFIDHDYYQCWIGLKSHFSHGADSKNGGI

Protein No.: I-694

Protein name and Species:

3-isopropylmalate dehydratase, putative OS=Ricinus communis GN=RCOM_1217310 PE=4 SV=1

Accession: tr|B9SQS5|B9SQS5_RICCO

Unused ProtScore: 3.61

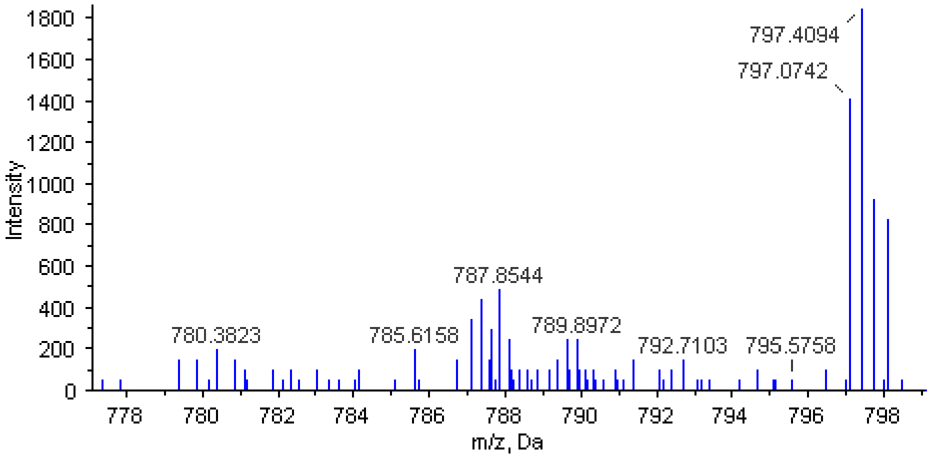
Seq Cov %: 8.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.48

116: 114=E5TL: D5TL=0.67

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MASSAITSPSSS**FITK**KDLGLSAFSSQSSPFYSIPKCKKSISKKVVSVMAPQQSERTPATTGSVKTAMT
MTEKILARASEKSQLSPGENVWVNVDVLMTHDVCGPGSIGIFKREFGQNATVWDREK**IVIIPDHYIFTT**
DERANRNVDILRDFCQEQNVKYFYDIK**DLSNFK**VNPDYKGVCHVALAQEGHCRPGEVLLGTDSHTCTAG
AFGQFATGIGNTDAGFVLGTGKLLLKVPPTLRFVMDGEMPDYLLAKDLILQIIGEISVSGATYKSMEFV
GTTVESLNMEER**MTLCNMVVEAGGK**NGVIPSDSTTFKYLEDKTSVPFEPVYSDEKARFLSEYRFDVSKL
EPLVAKPHSPDNCALARECKDVKIDRVYIGSCTGGKTEDFMAAAKVFLASGKKVKVPTFLVPATQKVWM
DVYSLPVPGSGGK**TCSQIFEEAGCDTPASPSCGACLGGPK**DTYARMNEPMVCVSTTNRNFPGRMGHKEG
QIYLASPYTAAASALTGYVTDPREFLQ

Protein No.: I-700

Protein name and Species:

Protein-L-isoaspartate O-methyltransferase OS=Ricinus communis GN=RCOM_1508020 PE=3 SV=1

Accession: tr|B9RAR0|B9RAR0_RICCO

Unused ProtScore: 3.54

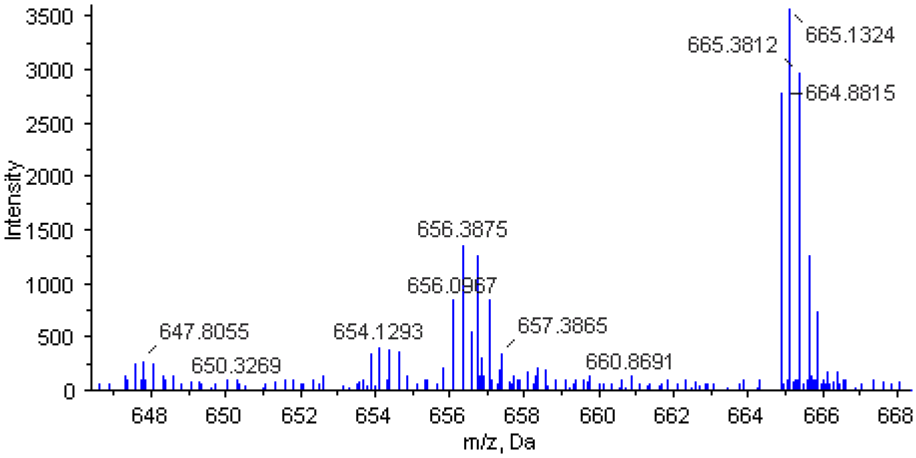
Seq Cov %: 15.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.61

116: 114=E5TL: D5TL=0.87

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MPISPVIAYGCRNYYYVPVPPLKRILTYSFRKNHLHHNNSHRCF**LLLLR**TTTNFHPQFSTFNLIPRKLY
CPFTGNSLFFRMERFFAGSGINKNKAMVEHLQHYGVISSRKVVEVMETIDRALFVPDGTQAYVDSPMPI
GYNATISAPHMHATCLQLLEEHLKPGMHALDVGSGTGYLTACFAIMVGPQGR**AVGVEHIPELVTSSVK**N
ILKSAAAPLLKEGFLSVHIGDGRQGWPEFAPYDAIHVGAAAPEIPQALIDQLKPGGR**MVIPVGNIFQDL**
KVIDKNQDGSISVRSETSVRYVPLTSRDAQLRG

Protein No.: I-703

Protein name and Species:

Heat shock protein 17.5 cytosolic class II OS=Jatropha curcas PE=2 SV=1

Accession: tr|D5JG84|D5JG84_9ROSI

Unused ProtScore: 3.53

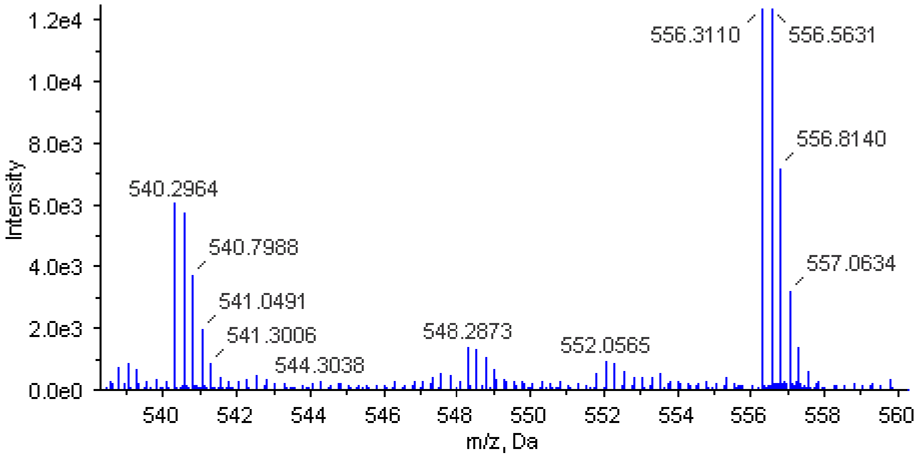
Seq Cov %: 19.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.50

116: 114=E5TL: D5TL=1.34

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDVRFVGLDSPLLHTLQQMMDIGD**DADHKSFNAPTR**TYVRDAK**AMASTPADVKEYPNSYVFIIDMPGLK**
SGDIKVQVEDDNVLLISGERKREEEKEGAKYVRMERRVGKLMRKFALPENANTDAISAVCQDGVLTVTV
QKLPPPEPKKPKTIEVKIA

Protein No.: I-704

Protein name and Species:

Putative uncharacterized protein OS=Vitis vinifera GN=VIT_13s0067g03420 PE=4 SV=1

Accession: tr|D7T494|D7T494_VITVI

Unused ProtScore: 3.52

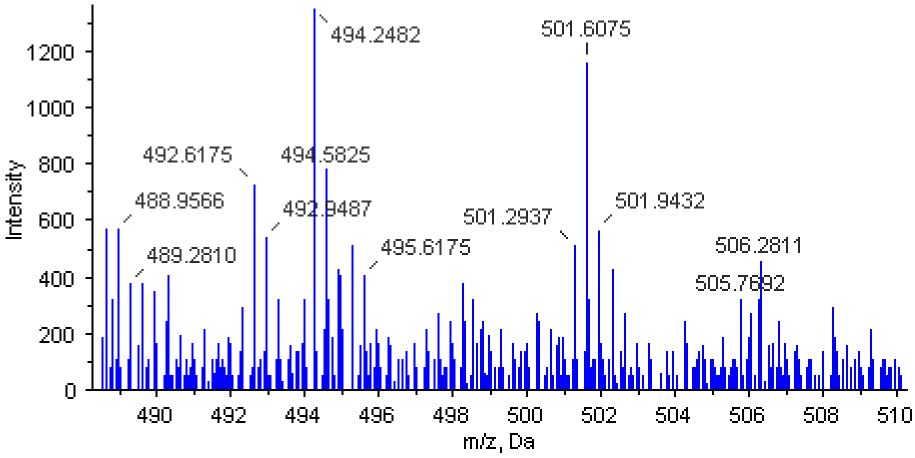
Seq Cov %: 3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.10

116: 114=E5TL: D5TL=0.35

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MKPKAVVNPLVTFEHKRDAYGFAVRPQHLQRYR**EYANIYKEEEEER**SERWNIFLEQQAESAQLPVNGLS
ADEHNKALHGEATEKDVDANPEKVVQKLGSDDSNENVTEKESQGVAETKTHRIQIWTEIRTSLHAIEEM
MSTRVKKRRDSSKNEKETGLGKHHAPVEEARSLKGVSEEDSEDEFYDVERSDPVQDVPSSDSSNASATA
SAGDVVTLETSFPWKEELECLVRGGVPMALRGELWQAFVGVKARRVERYYQELLASEHNVGNKVEQDSS
QTDSLTDGPIKDSLTVTEKWKGQIEKDLPRTFPGHPALDEDGRNALRRLLTAYARHNPSVGYCQAMNFF
AGLLLLLMPEENAFWALMGIIDDYFDGYYSEEMIESQVDQLAFEDLVRERLPKLVNHLDFLGVQVAWVT
GPWFLSIFMNMLPWESVLRVWDVLLFEGNRVMLFKTALALMELYGPALVTTKDAGDAVTLLQSLAGSTF
DSSELVLTACMGYQNVNEARLQELRDKHRAAVIAAVEERSKGLRAWRDSKGLAHKLYGFKHDPGSLAMD
ANQTEQVVDSQANGDMSHMEPGSANVDGFLIGLTENVEIDSVPDLQEQVRWLKVELCKLLEEKRSALLR
AEELETALMEMVKQDNRRQLSAR**VEQLEQEVSELR**QALADKQEQEHAMLQVLVRVEQEQKLTEDARRFA
EQDAAAQRYAAQVLQEKYEEAITSLAQMEKRVVMAETMLEATLQYQSGQVKAQPSPRSHQDSSSARSNQ
ETPQELPTRKIGLLSRPFALGWRDRNKGKPASEEVSDAKPTNEVENPSAQQVESPSTQQKDANGHEVQE
KQ

Protein No.: I-708

Protein name and Species:

Hydrolase, hydrolyzing O-glycosyl compounds, putative OS=Ricinus communis GN=RCOM_0272270 PE=4 SV=1

Accession: tr|B9T139|B9T139_RICCO

Unused ProtScore: 3.46

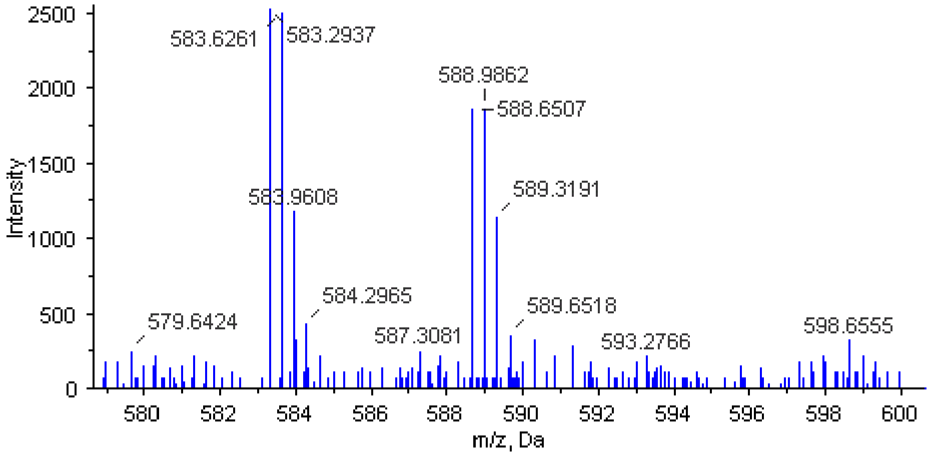
Seq Cov %: 6.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=16.00

116: 114=E5TL: D5TL=3.72

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAWSLQKSEIKPTVRKLEKKGGDRQLDAMTIKPAVRISDRKLIVKDRTILTGLQDNVIATSGSSSSPVE
GVFIGAVFDEENSRHVVPLGTLRDVRFMACFRFKLFWMAQKMGDHGRDIPLETQFLMMETKDGSQLESD
GGNEENQIIYTVFLPLIEGSFRACLQGNDNDELELCLESGDVDTKAASFTHPLFIHAGTDPFGTLTEAV
RAVKLHLKSFRQRHEKKLPAIIDYFGWCTWDAFYQEVTQEGVEAGLKSLSEGGTLPKFVIIDDGWQSVG
GDPQEDDEDKPQPLLRLIGIKENEKFRKKDDPTVGIKNIVNIAKEKYGLKYVYVWHAITGYWGGVRPGV
KEMEEYGSLMKYPKVSEGVLENEPTWRTDVLAVQGLGLMNPKAVYKFYNELHNYLASAGIDGVK**VDVQC**
ILETLGAGLGGRVEITR**QYHQALDASVAR**NFPDNGCIACMSHNTDALYCSKQTAVVR**ASDDFFPR**DPVS
HTIHIAAVAYNSVFLGEFMQPDWDMFHSLHPAAEYHASAR**AISGGPVYVSDEPGK**HDFNVLKK**LVLPDG**
SILRARLPGRPTRDCLFSDPARDGISLLKIWNMNKHTGVLGVYNCQGAAWNCVERKNTFHETKSEALTG
AIKGRDVHLIAEAATDSNWNGDCAVYCHQTAELTTVPYNASLPVSLKVLEHEIFTLTPIKVLAPGFSFA
PLGLIAMYNAGGAIEGLKYEVKGVKLVELDEGYKGENSTVSDERVENISSELVGKICMEVKGCGKFGAY
SSTKPRMCIVDSNIAEFEYDSSSGLVTFNLDNLAEEGRLHLVEVEV

Protein No.: I-710

Protein name and Species:

ATP-citrate synthase, putative OS=Populus trichocarpa GN=POPTRDRAFT_827990 PE=4 SV=1

Accession: tr|B9N432|B9N432_POPTR

Unused ProtScore: 3.44

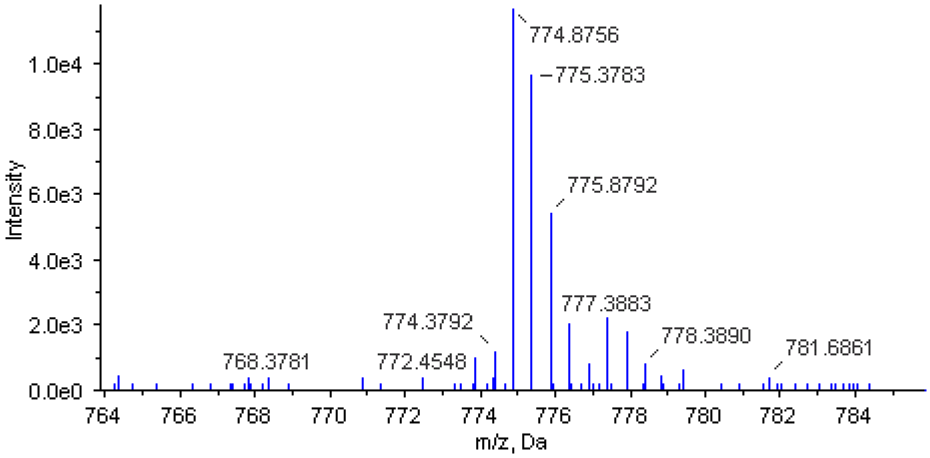
Seq Cov %: 17.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.56

116: 114=E5TL: D5TL=0.61

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MARKKIREYDSKRLLKEHLKRLSGIDLQICSAQVTEGTDFTELTNKEPWLSSTK**LVVKPDMLFGK**RGKS
GLVALNLDLAQVAEFVKARLGAEVEMGGCKAPITTFIVEPFVPHDQEFYISIVSERLGSTISFSECGGI
EIEENWDKVKTIFLPTEKPMTLEACAPLIATLPLEIRGKIGDFIISVFSVFQDLDFSFLEMNPFTLVNG
EPYPLDMR**GELDDTAAFKN**FKKWGNVEFPLPFGRVLSSTESFIHSLDEKTSSSLK**FTVLNPK**GRIWTMV
AGGGASVIYADTVGDLGYASELGNYAEYSGAPNEDEVLQY**ARVVIDCATSDPDGR**KRALLIGGGIAN**FT**
DVAATFNGIIRALREKESKLKAARMHIYVRR**GGPNYQTGLAK**MR**TLGEELGVPLEVYGPEATMTGICK**Q
AIDCIMSTA

Protein No.: I-713

Protein name and Species:

Potassium channel beta, putative OS=Ricinus communis GN=RCOM_1021600 PE=4 SV=1

Accession: tr|B9RWM3|B9RWM3_RICCO

Unused ProtScore: 3.44

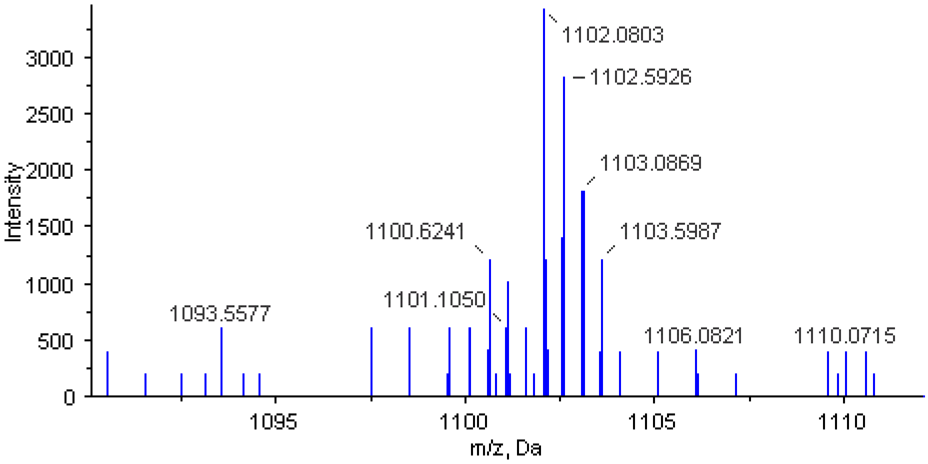
Seq Cov %: 7.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=12.13

116: 114=E5TL: D5TL=2.13

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MQYKNLGRSGLKVSQLSYGAWVSFGNQLDVKEAK**SLLQCCR**DHGVNFFDNAEVYANGRAEEIMGQAIRE
LGWKRSDIVVSTKIFWGGSGPNDKGLSRKHIVEGTKASLKRLDMDYVDVIYCHRPDSSTPIEETIRAMN
HVIDKGWAFYWGTSEWSAQQITEAWGIAER**LDLVGPIVEQPEYNLLSR**HKVESEYLPLYTNYGLGLTTW
SPLASGVLTGKYSRGAIPPDSRFALENYKNLASRSLIDDVLKKVNGLKPIADELGVPLSQLAIAWCAAN
PNVSSVITGATKESQIQENMKAIDVIPLLTPAVMEKIEAVVQSKPKRPDSYR

Protein No.: I-714

Protein name and Species:

Aldehyde dehydrogenase family 7 member A1 OS=Euphorbia characias PE=2 SV=1

Accession: tr|Q5EBY6|Q5EBY6_EUPCH

Unused ProtScore: 3.43

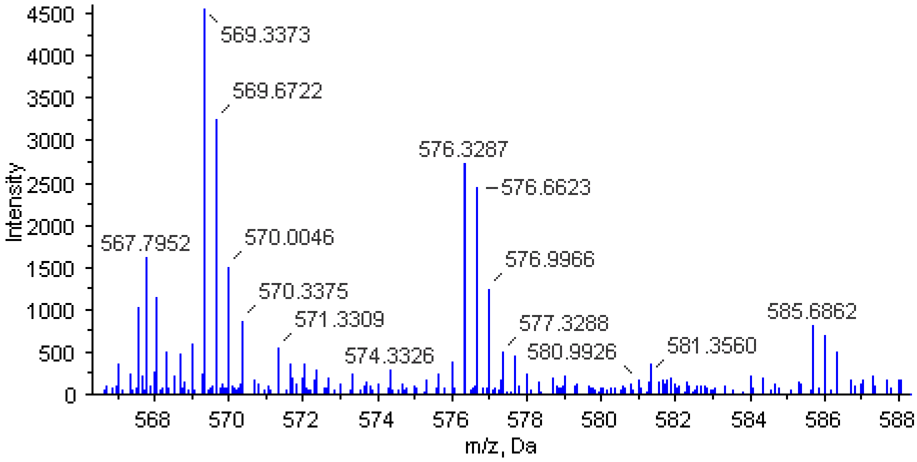
Seq Cov %: 11.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.59

116: 114=E5TL: D5TL=0.68

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGFARKEYEFLSEIGLSERNLGCYVNGTWKANGPVVTTSNPAN**NQAIAEVVEGSIEDYEEGMK**ACSEAA
KIWMQVPAPKRGDIVRQIGDALRGKLEHLGRLVSLEMGKILAEGIGEVQEIIDMCDFCVGLSRQLNGSI
IPSERPNHAMLEMWNPLGIVGVITAFNFPCAVLGWNACIALVCGNCAVWKGAPTTPLMTIATTKLVAEV
LERNNLPLAIFTSFCGGADIGQAIAKDTR**IPLVSFTGSSK**VGLMVQQTVNQRYGKSLLELSGNNAIIVM
DDADIPLAARSILFAAVGTAGQRCTTCRRLILHEKIYDTVLDQLLKSYKQVKIGDPLEKGTLLGPVHTA
ESRKNFEKG**IELIK**SQGGK**ILTGGSVIESEGNYVQPTIVEISSK**AEVVK**EELFAPVLYVMK**FQTLEEAI
EINNSVPQGLSSSIFTRRPDVIFKWLGPHGSDCGIVNVNIPTNGAEIGGAFGGEKATGGGREAGSDSWK
QYMRASTCTINYGSELPLAQGINFG

Protein No.: I-716

Protein name and Species:

Isoflavone reductase, putative OS=Ricinus communis GN=RCOM_1594880 PE=4 SV=1

Accession: tr|B9R7W5|B9R7W5_RICCO

Unused ProtScore: 3.43

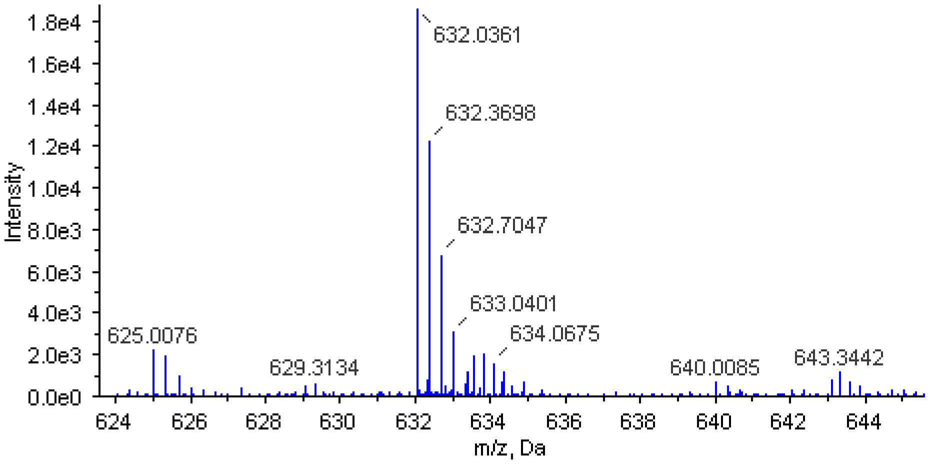
Seq Cov %: 20.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.23

116: 114=E5TL: D5TL=0.48

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MADTSK**ILIIGGTGYIGK**FIVEASAKAGLPTFVLIR**ESTVSDPVK**GKIVENFK**NLGVTLLHGDLYDHES**
LVKAIKQADVVISTLGALQLADQTKVIAAIKEAGNVKR**FFPSEFGTDVDHVHAVEPAK**SAFETKAQIRR
AIEAEGIPYTYAVCNYFASLMIPLLLRPAGDK**VTILGDGNVK**AIFSMEQDIALYTIKAVDDPRTLNKTL
FVNPPMNILTYNELVALEEKKTGKTIEKNYVPEEKVLQDIQTVPMPFNIGLAINHCVFIKGDQTNFEID
PSWGVEASQLYPDVKYTTIAEYFDQTA

Protein No.: I-717

Protein name and Species:

glycine-tRNA ligase 1, mitochondrial OS=Populus trichocarpa GN=POPTRDRAFT_830916 PE=3 SV=1

Accession: tr|B9GZ19|B9GZ19_POPTR

Unused ProtScore: 3.42

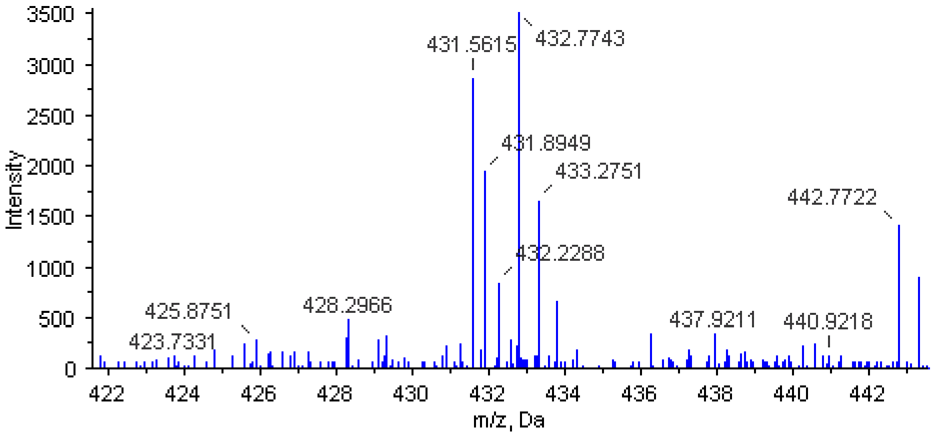
Seq Cov %: 10.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.61

116: 114=E5TL: D5TL=0.79

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAASEDSLRRALAEKQSSIESQGNTVRALKASNAEKATVDEAIEKLNALKLDKSVMEK**QLQAAVNGNGP**
DGSVNKEAFRQAVVNTLERRLFYIPSFKIYRGVAGLYDYGPPGCAVKSNVLSFWRQHFVLEENMLEVDC
PCVTPEVVLKASGHVDK**FTDLMVK**DEKTGTCCRADHLLKDFCNEKIQKDLSISAEKAAELKHVLAILDD
LSAEELGAKIK**EYGITAPDTK**NPLSDPYPFNLMFQTSIGPSGLSPGYMRPETAQGIFVNFKDLYYYNGN
K**LPFAAAQIGQAFR**NEISPRQGLLRVREFTLAEIEHFVDPEYKSHPK**YSEVADLEFLMFPR**ELQISAQS
AKKIQLGEAVSK**GIVNNETLGYFIGR**VYLFLTRLGIDKDRLRFRQHLANEMAHYAADCWDAEIESSYGW
IECVGIADRSAYDLHAHSEK**SGVPLVAHEK**FSEPK**EVEKLVIAPVK**K**ELGLAFK**GNQKKVVEALEAMNE
KEALDMKASLETKGEVEFYVCTLGEKVTIKKNMVSISKEKKKEHQRTFTPSVIEPSFGIGRIIYCLYEH
SFYMRPSK**AGDEQLNVFR**FPPLVAPIKCTVFPLVQNQQYEDVAKIISKTLTAAGISHK**IDITGTSIGK**R
YARTDELGVPFAITVDSISSVTIRERDSKDQIRVDVEEAAPVVKSVTDGHKTWADVWANFPHHSSGSVE
D

Protein No.: I-718

Protein name and Species:

40S ribosomal protein S25-1, putative OS=Ricinus communis GN=RCOM_1447530 PE=4 SV=1

Accession: tr|B9RH67|B9RH67_RICCO

Unused ProtScore: 3.42

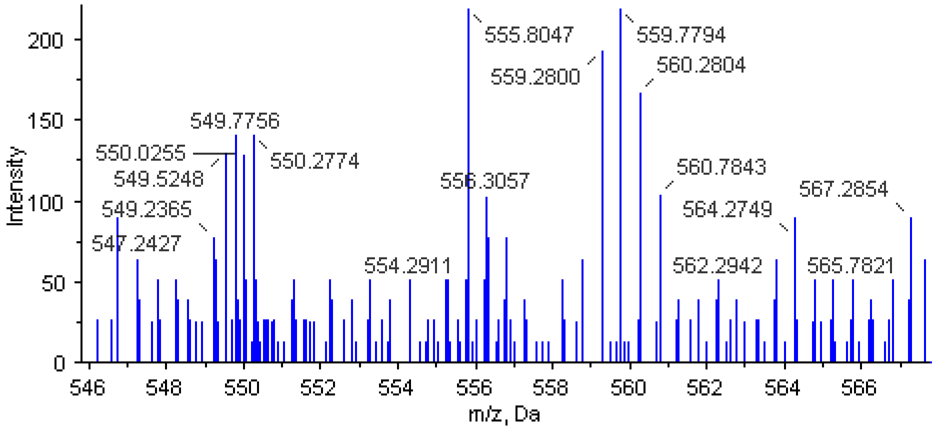
Seq Cov %: 20.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2.07

116: 114=E5TL: D5TL=0.91

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAPKKDKAPPPSSKPAKSGGGKQKKKKWSKGKQKEK**VNNMVLFDQATYDK**LLSEAPKYKLITPSILSDR
LRVNGSLARRAIRELMARGLIRMVSAH**ASQQIYTR**ATNT

Protein No.: I-720

Protein name and Species: **clathrin heavy chain 1 [Vitis vinifera]**

OS=Vitis vinifera GN=VIT_13s0067g01290 PE=4 SV=1

Accession: tr|A5ACP0|A5ACP0_VITVI

Unused ProtScore: 3.4

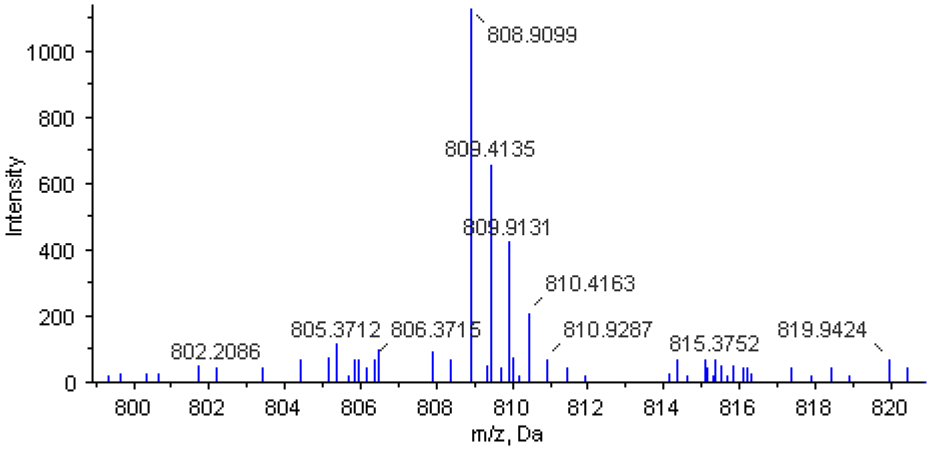
Seq Cov %: 15.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.63;

116: 114=E5TL: D5TL=1.20

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAA**ANAPITMK**EVLTLPSLGISPQFITFTHVTMESDKYLCVR**ETAPQNSVVIIDMNMPMQPLR**RPITAD
SALMNPNTR**ILALKAQLPGTTQDHLQIFNIEMK**AKMKSYQMPEQIVFWKWITPKMLGLVTQTSVYHWSI
EGDSEPVKMFER**TANLVNNQIINYR**CDPSEKWLVLIGIAPGSPERPQLVKGNMQLFSVEQHRSQALEAH
AASFATFKVPGNDQPCTLIGFATK**SFNAGQIVSK**LHVIELGSNPGKPGFTKKQADLFFPPDFADDFPVA
MQISHKYGLIYVITKLGLLFVYDLESASAVYRNRISPDPIFLTAEATSIGGFYAINRRGQVLLATVNEA
AIVPFVSGQLNNLELAVNLAK**RGNLPGAENLVVQR**FQELFAQTK**YKEAAELAAESPQGILR**TPDTVAKF
QSVPMQSGQTPPLLQYFGTLLTRGK**LNAFESLELSR**LVVNQNKK**NLLENWLAEDKLECSEELGDLVK**TV
DTDLALKIYIKARATPKVVAAFAERREFDKILIYSKQVGYTPDYLFLLQTILRSDPQGAVNFALMMSQM
EGGCPIDFNTITDLFLQRNLIREATAF**LLDVLK**PNLPEHGFLQTKVLEINLVTYPNVADAILANGMFSH
YDRPR**IAQLCEK**AGLYVRALQHYTELPDIKRVIVNTHAIEPQALVEFFGTLSREWALECMK**DLLLVNLR**
GNLQIIVQTAKEYSEQLGVDQCVKLFEQFKSYEGLYFFLGSYLSSSEDPDIHFK**YIEAAAK**TGQIKEVE
RVTR**ESNFYDAEK**TKNFLMEAKLPDAR**PLINVCDR**FGFVPDLTHYLYTNNMLRYIEGYVQKVNPSNAPL
VVGQLLDDECPEDFIKGLILSVR**SLLPVEPLVDECEK**RNRLRLLTQFLEHLVSEGSQDVHVHNALGK**II**
IDSNNNPEHFLTTNPYYDSRVVGKYCEK**RDPTLAVVAYR**RGQCDEELINVTNKNSLFKLQARYVVERMD
SDLWEKVLDPDNDYRR**QLIDQVVSTALPESKSPEQVSAAVK**AFMTADLPHELIELLEKIVLQNSAFSGN
FNLQNLLILTAIKADPSR**VMDYINR**LDNFDGPAVGEVAVEAQLFEEAFAIFKKFNLNVQAVNVLLDNIQ
SIER**AVEFAFR**VEEDAVWSQVAKAQLR**EGLVSDAIESFIR**ADDATQF**LDVIRAAEDANVYHDLVR**YLLM
VRQKAKEPKVDSELIYAYAKIDRLGEIEEFILMPN**VANLQNVGDR**LYDEALYEAAKIIFAFISNWAKLA
CTLVKLR**QFQGAVDAAR**KANSSKTWK**EVCFACVDAEEFR**LAQICGLNIIIQVDDLEEVSDYYQNRGCFN
ELISLMESGLGLERAHMGIFTELGVLYARYRPEKLMEHIKLFSTRLNIPKLIRACDEQQHWKELTYLYI
QYDEFDNAATTIMNHSPDAWDHMQFKDVAVK**VANVELYYK**AVHFYLQEHPDLINDLLN**VLALR**VDHTRV
VDIMRKAGHLHLVKPYMVAVQSNNVSAVNEALNGIYVEEEDYDRLR**ESIDMHDNFDQIGLAQK**IEKHEL
LEMRR**VAAYIYK**KAGRWKQSIALSKKDNLYKDAMETASQSGDRELAEELLVYFIEKGKKECFASCLFVC
YDLIRPDIALELAWINNMVDFALPYLLQFIREYAGKVDELVKDK**LEALNEVK**AKEKEEKDVIAQQNMYA
QLLPLALPAPPMPGMGGAGMAGGFVPPPMGSMGMPPMPPFGMPPMGTY

Protein No.: I-723

Protein name and Species:

Unknown protein 1 (Fragment) OS=Vitis rotundifolia PE=1 SV=1

Accession: sp|P86104|UP01_VITRO

Unused ProtScore: 3.4

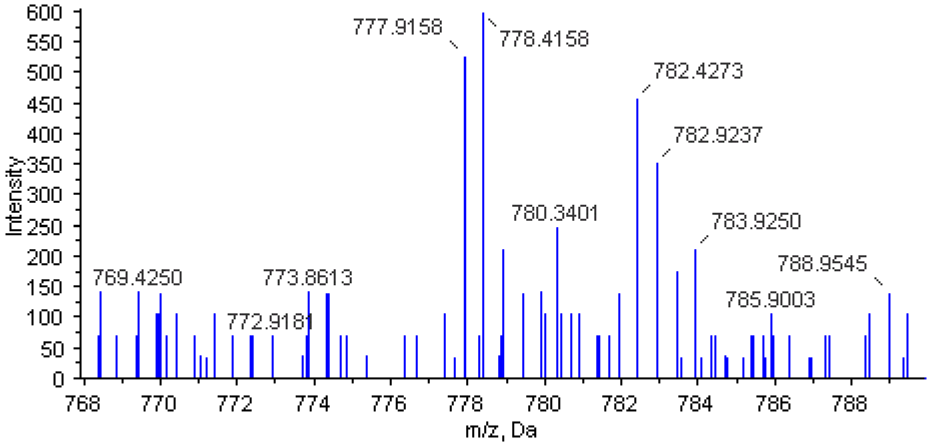
Seq Cov %: 100

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.11

116: 114=E5TL: D5TL=0.58

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

TNAENEFVTIKK

Protein No.: I-729

Protein name and Species:

5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase, putative OS=Ricinus communis GN=RCOM_0952830 PE=3 SV=1

Accession: tr|B9RQ33|B9RQ33_RICCO

Unused ProtScore: 3.37

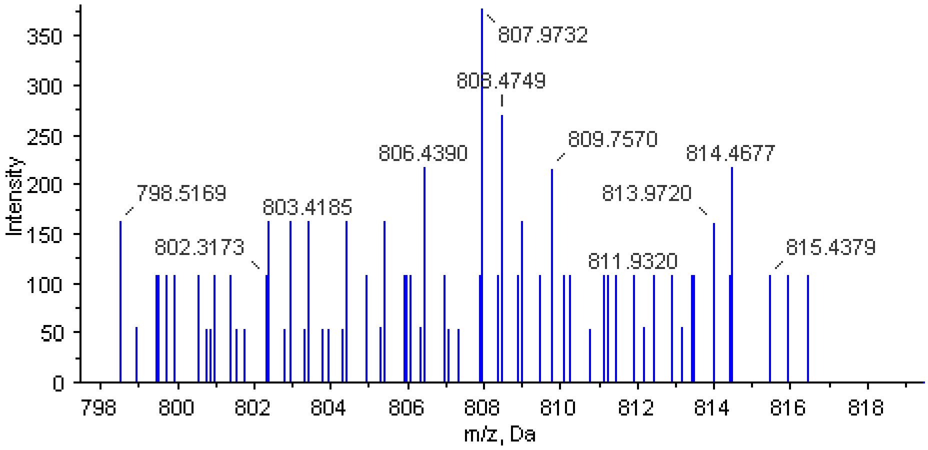
Seq Cov %: 16.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.62

116: 114=E5TL: D5TL=1.09

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MRQVSLNVLAPFTSFRVISLPFSSSTNPSSLSFLPFSFHFPSLSSTSFRAMASHIAGYPRMGPKRELK**F**
ALESFWDGKSSAEDLQKVAAELRASIWKQMADAGTKFIPSNTFSYYDQVLDTTAMLGAVPPRYGWDGGE
IGFDVYFSMAR**GNASVPAMEMTK**WFDTNYHYIVPELGPEVKFSYASHKAVDEYKEAKALGVETVPVLVG
PVSYLLLSKPAKGVEKSFSLLSLIDRILPIYKEVIAELKAAGARWIQFDEPKLVMDLDSHELQAFTNAY
SELEASLSGVHVVVETYFADLPAEAYKTLTSLK**GVTGFGFDLVR**GTKTLDLIKGGFPTGK**FLFAGVVDG**
RNIWANDLASSLDTLHALESAVGKDKVVVSTSCSLLHTAVDLANEPKLDKEIK**SWLAFAAQKVLEVNAL**
AKALAGNRDEAFFSSNALAHASRKSSPR**VTNEAVQQAAAALK**GSDHRRATNVSARLDAQQKKLNLPILP
TTTIGSFPQTLDLRRVRREYKAKKISEDDYVKAIKEEISKVVKIQEELDIDVLVHGEPERNDMVEYFGE
QLSGFAFTANGWVQSYGSR**CVKPPIIYGDVSR**PKAMTVFWSSMAQSMTSRPMK**GMLTGPVTILNWSFVR**
NDQPRHETCYQIALAIKDE**VEDLEKAGITVIQIDEAALR**EGLPLRKSEHAFYLDWAVHSFRITNCGVED
TTQIHTHMCYSNFNDIIHSIINMDADVITIENSRSDEKLLSVFREGVK**YGAGIGPGVYDIHSPRIPSTE**
EIADRINKMLAVLES**NILWVNPDCGLK**TRKYSEVKPALSNMVAATKILRTQLASAK

Protein No.: I-732

Protein name and Species:

Catalytic, putative OS=Ricinus communis GN=RCOM_0300260 PE=4 SV=1

Accession: tr|B9T676|B9T676_RICCO

Unused ProtScore: 3.37

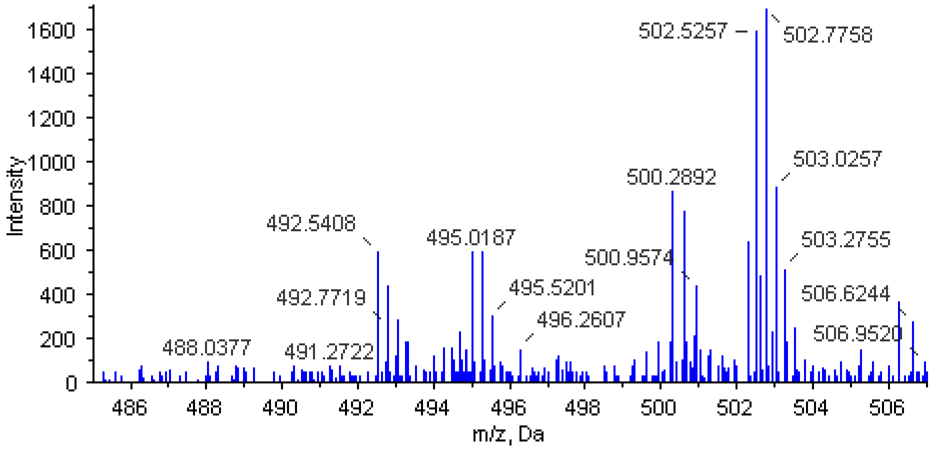
Seq Cov %: 8.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=4.02

116: 114=E5TL: D5TL=11.62

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MEYEGNQQHVLEKYECLLFDVDDTLYPLRSGLSQHVTKNIQEYMVQKLGIEESKVAELCVSLYKLYGTT
LAGLRAIGHNIDYDDFHSFVHGRLPYDIVKPDPVLRNLLHSLPVRKIVFTNADKTHASRVLSRLGLEDC
FEGILSFETLNNTTKGNESVNEDENGVFDINEYTAAPNAGLALPRSPVVCKPFEDAFEQVFKITSINPQ
R**TLFFDDSIR**NLQTGKRLGLTTVWVGSSHR**TEGVDYALESIHNIK**EALPELWDANEKSDGVRYSGRVAI
ETSVKA

Protein No.: I-735

Protein name and Species:

Phagocytic receptor 1b [Vitis vinifera] OS=Vitis vinifera GN=VIT_01s0011g06540 PE=4 SV=1

Accession: tr|D7T8E1|D7T8E1_VITVI

Unused ProtScore: 3.34

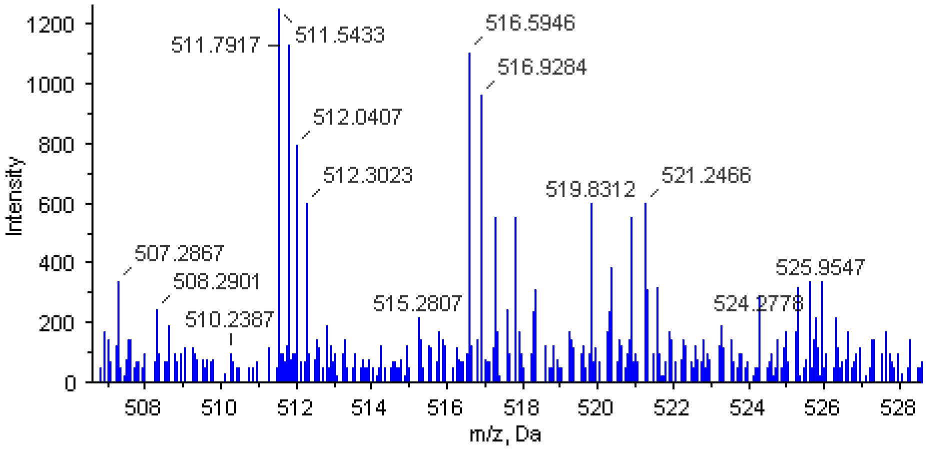
Seq Cov %: 3.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.71

116: 114=E5TL: D5TL=1.29

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MERAMAILVVAVLILLCGSQVRSDASSHRYKAGEAVPLYANK**VGPFHNPSETYR**YFDLPFCVPAHLKEK
KEALGEVLNGDR**LVSAPYK**LDFLREKDSEVVCKKKLKKEEVAQFRAAVAKDYYFQMYYDDLPIWGFIGK
VDKEGKADPSEYKYFLYKHIQFDIRYNKDRVIEINARTDPHSMVDVTDDKDVDVEFMYTVKWTETDAPF
EKRMEKYSQTSSMPHHLEIHWFSIINSCVTVLLLTGFLATILMRVLKNDFIKYAHDEESADDQEETGWK
YIHGDVFRYPKYKSLFAAALGSGTQLFTLTVFIFILALVGVFYPYNRGALFTALVVIYALTSGIAGYTA
TSFYCQLEGTNWVRNLLLTGCLFCAPLFLTFCFLNTVAIIYSATAALPFGTIVVIVLIWTLVTSPLLVL
GGIAGKNSK**AEFQAPCR**TTKYPREIPALPWYRSTIPQMAMAGFLPFSAIYIELYYIFASVWGHRIYTIY
SILFIVFIILLIVTAFITVALTYFQLAAEDHEWWWRSFLCGGSTGLFIYGYCLYYYYARSDMSGFMQTS
FFFGYMACICYGFFLMLGTVGFRASLLFVRHIYRSIKCE

Protein No.: I-738

Protein name and Species:

Dimethylaniline monooxygenase, putative OS=Ricinus communis GN=RCOM_1470740 PE=4 SV=1

Accession: tr|B9RLT7|B9RLT7_RICCO

Unused ProtScore: 3.33

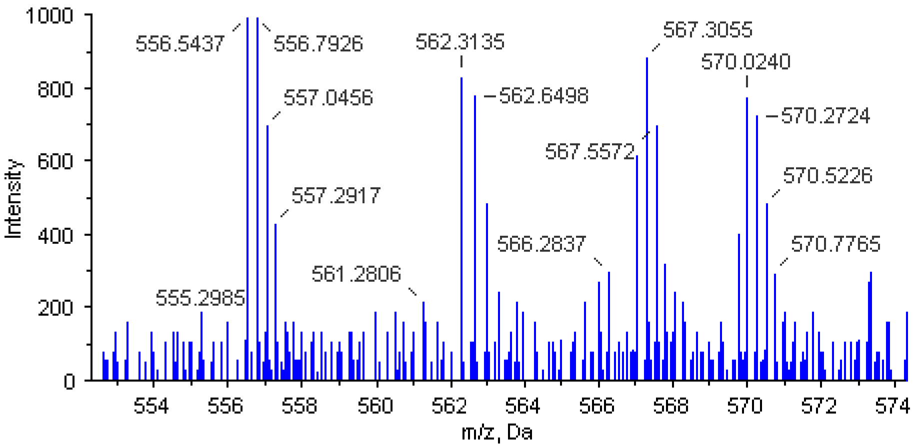
Seq Cov %: 6.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.43

116: 114=E5TL: D5TL=0.25

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MVSDFTRSK**NVCVIGAGPSGLVAAR**ELRKEGHRVVLLEQKDDVGGQWLYEANVESEHPLGKKKFLEVHS
SIYASLRLVSPREIMGYTDFPFLVKKGRDMRRFPGHRELWLYLKDFCDSFGLREMIRFNTRVEYVGMLD
YDELRNDLKWVVKSKEKDSEKAVEEVFDAVVVATGHYSHPKLPFIKGMETWKRKQMHSHIYRVPEPFRN
EVVVVVGNSLSGQDISMELVEVAKEVHLSSKSLDVTLGLSKVISKHENLHLRPQIESLEEDGRVLFADG
SQVIADTILYCTGYTYTFPFLDTKGIVVVEDDRVGPLYEHTFPPSLAPSLSFVGIPRK**IIGFPFFESQA**
KWIAQLLSGKRTLPSWDDMMLSIKQFYQSRDTAGIPKHNTHDIADFEYCDRYADHIGFPHLEEWRKQLC
LSALVNANDNLETYRDSWDDHDLLQEALQSPHFTQLGVQDFIV

Protein No.: I-740

Protein name and Species:

Aminopeptidase M1 [Arabidopsis thaliana] OS=Arabidopsis thaliana GN=APM1 PE=2 SV=1

Accession: tr|Q8VZH2|Q8VZH2_ARATH

Unused ProtScore: 3.31

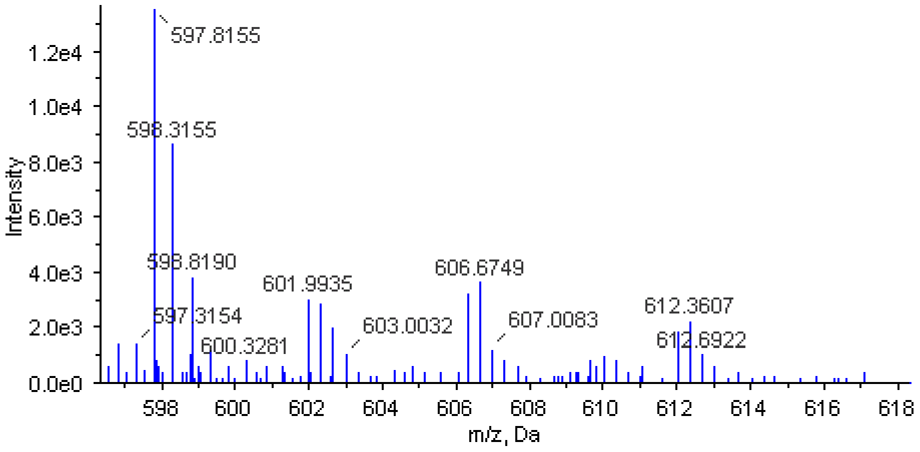
Seq Cov %: 6.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.19

116: 114=E5TL: D5TL=0.38

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDQFKGEPRLPKFAVPKRYDLRLNPDLIACTFTGTVAIDLDIVADTRFIVLNAADLSVNDASVSFTPPS
SSKALAAPKVVLFEEDEILVLEFGEILPHGVGVLKLGFNGVLNDKMKGFYRSTYEHNGEKK**NMAVTQFE**
PADARRCFPCWDEPACKATFKITLEVPTDLVALSNMPIMEEKVNGNLKIVSYQESPIMSTYLVAIVVGL
FDYVEDHTSDGIKVRVYCQVGKADQGKFALHVGAKTLDLFKEYFAVPYPLPKMDMIAIPDFAAGAMENY
GLVTYRETALLYDEQHSAASNKQRVATVVAHELAHQWFGNLVTMEWWTHLWLNEGFATWVSYLATDSLF
PEWK**IWTQFLDESTEGLR**LDGLEESHPIEVEVNHAAEIDEIFDAISYRKGASVIRMLQSYLGAEVFQK**S**
LAAYIKNHAYSNAKTEDLWAALEAGSGEPVNKLMSSWTKQKGYPVVSAKIKDGKLELEQSRFLSSGSPG
EGQWIVPVTLCCGSYEKRKNFLLESKSGAYDLKELLGCSIADGSDKINGTCSWIKINVDQAGFYRVKYD
DSLAAGLRNATESQSLTSIDRYGILDDSFALTMARQQSLASLLTLCSAYKKELDYTVLSNLIAISYKVV
KIGADANQELMSGIKHFFIGVFQFAAGKLGWDPK**QGESHLDAMLR**GEVLTALAVFGHDETLKEAVRRFD
AFLADR**NTPLLPPDIR**RAAYVAVMQRANKSDK**SGYESLLR**VYRETDLSQEKTRILGSLASCPDPTIVQD
VLNFVLSDEVRNQDALYGLSGVSWEGREVAWKWLQEKWEYIGNTWGSGFLITR**FISAVVSPFASFEK**AK
EVEEFFATRSKPSMARTLKQSIERVHINANWVESIKKEDNLTQLVAQLSSN

Protein No.: I-743

Protein name and Species:

Cytochrome P450, putative OS=Ricinus communis GN=RCOM_1517900 PE=3 SV=1

Accession: tr|B9SDH3|B9SDH3_RICCO

Unused ProtScore: 3.29

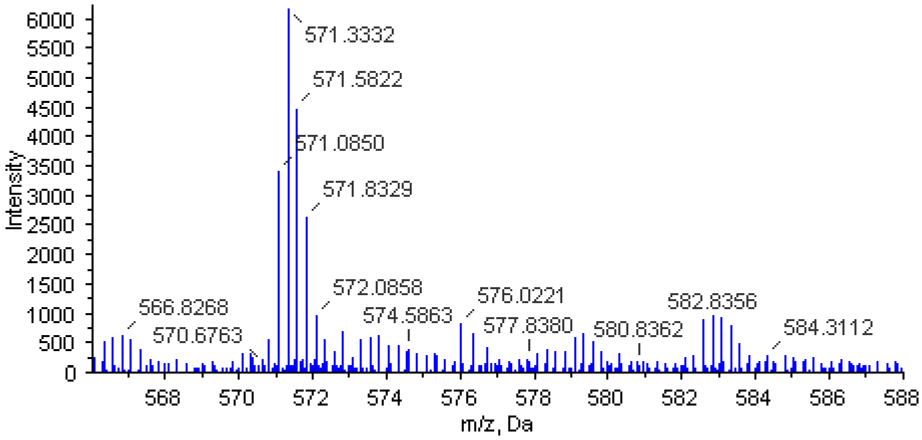
Seq Cov %: 2.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2.11

116: 114=E5TL: D5TL=1.19

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MEIWLFIPISLAVSILLKLVINHLLSTKNSTHKLPPGPSPLPILGSSLWLTTTVFDLESALRSLHSKFG
PLLTLHMGSRPAIFIADRSLAHEALIQNSSIFADRPPALGMEKINTSDQHTISSAFYGPTWRLLRRNLT
AKVLHPSNIKSYSHTRKWVVQILKDRLESEFKERGRIQVMGHFQYAMFCLLAFMCFGDNLEEDQIRKIE
EVQRQLLLNFVEFSVFSFWPSVTKVLFRKRWDEYMQIR**KNQENVLIPLLR**SRKAQRDKETDSVLPYVDT
LMDLGLPDEKRKLEEEEIVSLLSEILNGGTETTATALQWIMANLVKYPHIQEKLYMEIRRIVGEGEDLI
KEDELQKMPFLKAVILEGLRRHPPAHMVVPHAVTEDTVLDKYLIPKNGTVNFMVAEMGWDSKVWKDPMA
FKPERFMGSEYEHEVFDITGSREIKMMPFGLGRRMCPGHGLAMLHLEYLVANMVWSYEWKGMDGNGVDL
SEKLEFSVVMK**NPLQAQISPR**RRHKLIIDKI

Protein No.: I-744

Protein name and Species:

cytochrome b5 reductase 1-like，NADH [Vitis vinifera] OS=Vitis vinifera GN=VIT_13s0047g01190 PE=4 SV=1

Accession: tr|F6HIY1|F6HIY1_VITVI

Unused ProtScore: 3.29

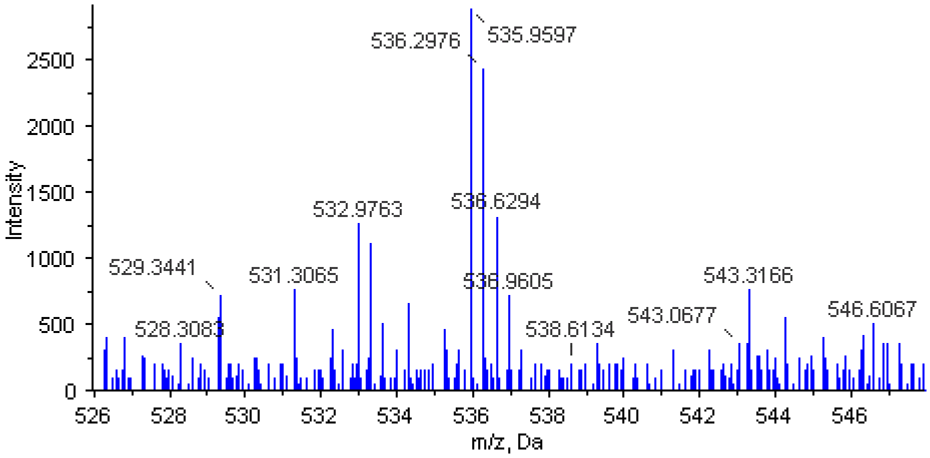
Seq Cov %: 6.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.61

116: 114=E5TL: D5TL=2.01

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MWKMTSTLLPTFRVTWPLKTPGIELSGFAVGLAAVGLAAVYFFYGRRKPKGCLDPERFQDFKLVQKTRI
SHNVGRFRFALPTPTSVFGLPVGQHIICRGKDDQGAEVIRPYTPITLDSDVGFYELVVKMYPKGQMSHH
FRKMREGDTLAVKGPRGRLIYKPGQAKAFGMLAGGTGITPMFQLTR**AILENPK**DKTNVHLIYANISYDD
ILLKDELDGFARKFPNRFKVFYVLSQPPEAWNGGIGHISKEMIEK**HCPAPAPDIQILR**CGPPGMNKAMA
GHLVALGYTPQMQFEF

Protein No.: I-746

Protein name and Species:

40S ribosomal protein S23 OS=Solanum tuberosum PE=2 SV=1

Accession: tr|Q38HT5|Q38HT5_SOLTU

Unused ProtScore: 3.29

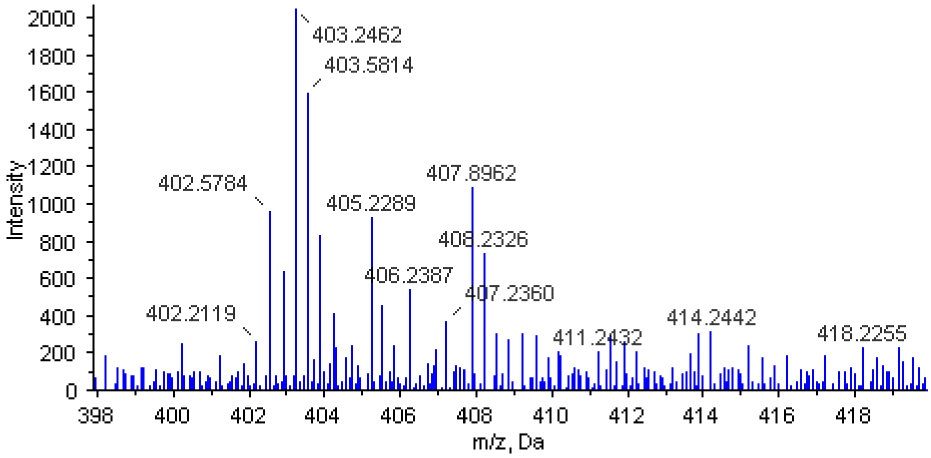
Seq Cov %: 11.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.62

116: 114=E5TL: D5TL=0.41

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGKTRGMGAGRKLKSHRRRQRWADKSYKKSHLGNEWKKPFAGSSHAKGIVLEKIGIEAKQPNSAIRKCA
RVQLIKNGKKIAAFVPNDGCLNYIEENDEVLIAGFGRK**GHAVGDIPGVR**FKVVKVSGVSL**LALFK**EKKE
KPRS

Protein No.: I-757

Protein name and Species:

Very-long-chain enoyl-CoA reductase-like OS=Populus trichocarpa GN=POPTRDRAFT_720621 PE=2 SV=1

Accession: tr|A9PDL9|A9PDL9_POPTR

Unused ProtScore: 3.24

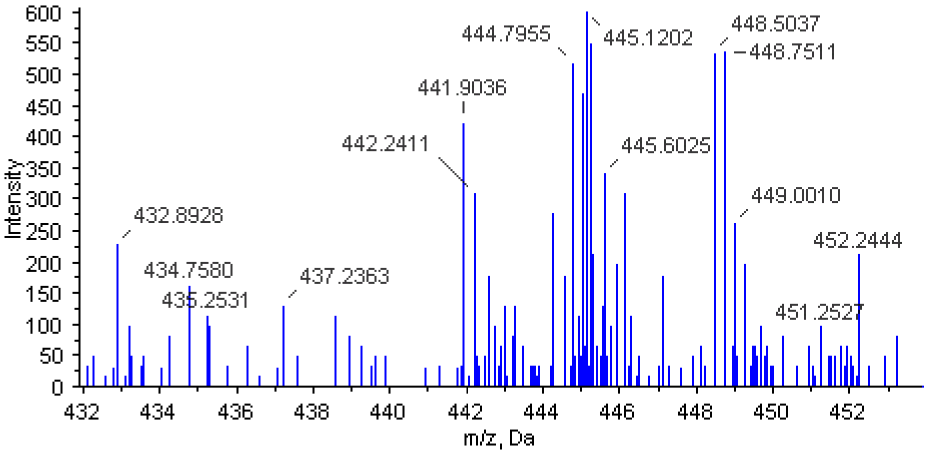
Seq Cov %: 7.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.94

116: 114=E5TL: D5TL=2.66

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MKVTVVSRSGREVIKGGLELSDSATVADLQEAIHKRTKKFYPARQR**LTLPLPPGSK**ERPTVLNYKKNLK
EYQDGNLDSLTILFKDLGPQVSYRTLFFFEYLGPLVLYPFFYYFPVYQFLGYKGEHIMHPVQTYALYYW
CFHYFKR**IMETFFVHRFSHATSPLSNVFR**NCAYYWTFGSYIAYYVNHPLYTPVGDLQMKIGFGFGLVCQ
LANFYCHILLRNLRRPDGNGGYQIPSGFLFNIVTCANYTTEIYQWLGFNIATQTVAGYIFLVVAASIMT
NWALAKHRRLKKLFDGKDGRPKYPRRWVILPPVL

Protein No.: I-758

Protein name and Species:

Suppression of tumorigenicity, putative OS=Ricinus communis GN=RCOM_0712150 PE=4 SV=1

Accession: tr|B9RRB9|B9RRB9_RICCO

Unused ProtScore: 3.22

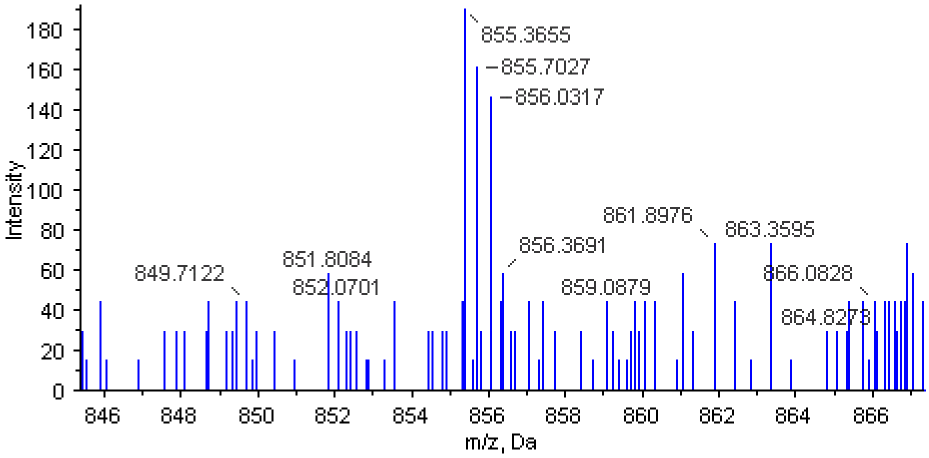
Seq Cov %: 6.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.52

116: 114=E5TL: D5TL=1.68

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAKNEDTGSPGWR**ASLFLQTTEDVARAVAAAAAAATAPR**SPR**PSVVFSSK**DDHGDSQFQKLQRHVTRVL
KGFSSPPPEVKAGTYNPEVLTSQKRQWANFQLQYLDHRSLKEPSRLFESMVVVGLHPNCDLQALQRQYV
ARKSEGSARLQGSPGCQNQSRVEPVLEPQVLFVYPPDKQLPLKYKDLLSFCFPGGMEVHAVEKTPSMSE
LNEILLGQEHLKQSDLSFVFRLQVADDSTLYGCCVLVDEIVQKPSGLLSMISDKRSSCSSLSRYVLTTR
RCYCILSRLPFFELHFGVLNSIFTEERLERLTRHIGAFDLESSEGYDKDENLGYNLDSVSPNYIAAEDR
LDGAAETFQSSLRDSTPGEDNKNHMEHCITEEHIHLLQKGVNDNIVVPVESETEIVSNKGESGGGNLED
SDICVDDLSKKQAEERRLPNAVLPLIR**YYQYESSESSSSFQGSPSEDR**NFRSDIDDTETEEASTSGQED
TNDHMDILEWAKVNNYGSLQIICKYYQLHCPSRGSTLRLHPLEHLHPLEYHRTDETVLHIAGSVIDLRT
CSTSLEFAEAHSALSAEEEATALSTWAVACICGSLRLENVLTLFAGALLEKQIVFVCSNLGILSASVLS
IVPLIRPYQWQSLLMPILPDDMLDFLDAPVPYVVGVKNKTSEVQSKLTNVILVDVNKNQVKSHTIPQLP
KHRELFSSLSPYHAKLVGESYLARKRPVHECTDVQVCYSA

Protein No.: I-759

Protein name and Species:

Peroxidase 12, putative OS=Ricinus communis GN=RCOM_0961200 PE=3 SV=1

Accession: tr|B9SEA1|B9SEA1_RICCO

Unused ProtScore: 3.22

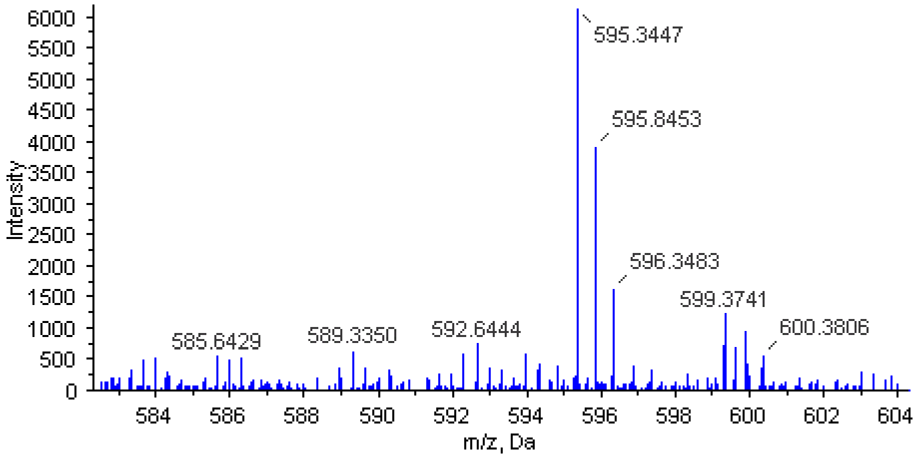
Seq Cov %: 7.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2.49

116: 114=E5TL: D5TL=1.56

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MASANSFTSLLLISCLLLAACFSAIEAQTKPPIKNGLSWTFYKTSCPKAESIIRSELKKIFKK**DVGQAA
GLLR**LHFHDCFVLGCDSSVLLDGSAGGPSEKSELPNLTLRKQAFKIVEDLRARLHKECGR**VVSCSDIVA
IAAR**DSVVLTGGPEYAIPLGRRDGVKFAEINATFEHLVGPTAKVTEILTKLDRKGLDATDAVALSGGHT
IGIGHCTSFTER**LYPSQDPTMDK**TFANNLKLTCPKLDTTNTTFLDIRSPNKFDNK**YYVDLMNR**QGLFTS
DQDLYTDKRTRSIVTSFAINESLFFEKFIIGMIK**MGQLDVLTGNQGEIR**ANCSAINPKKKYIESVAEEE
LGSSSEMR

Protein No.: I-760

Protein name and Species:

elongation factor 2-like OS=Vitis vinifera GN=VIT_19s0027g00760 PE=4 SV=1

Accession: tr|F6H4T7|F6H4T7_VITVI

Unused ProtScore: 3.21

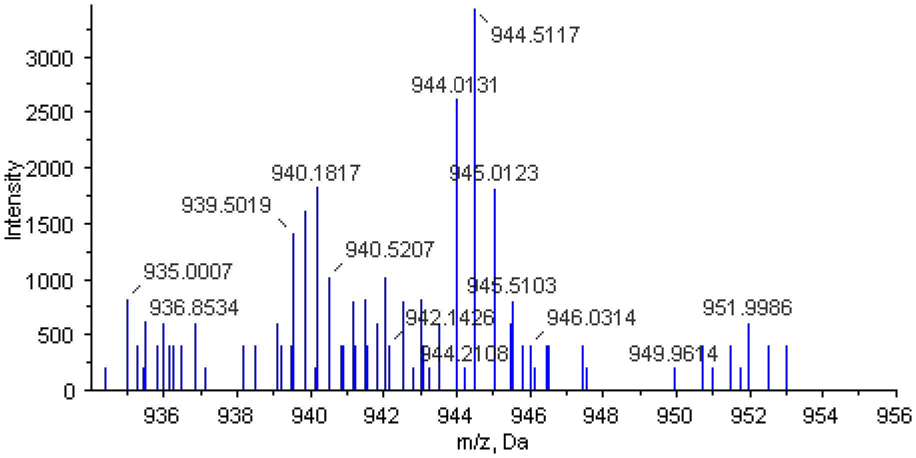
Seq Cov %: 25

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.63

116: 114=E5TL: D5TL=1.51

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDFNRICLPLWVKFTVEELRRIMDYKHNIR**NMSVIAHVDHGKSTLTDSLVAAAGIIAQEVAGDVR**MTDT
RQDEAERGITIK**STGISLYYEMSDESLK**NYRGERQGNEYLINLIDSPGHVDFSSEVTAALRITDGALVV
VDCVEGVCVQTETVLRQALGER**IRPVLTVNK**MDRCFLELQVDGEEAYQTFSRVIENANVIMATYEDPLL
GDVQVYPEKGTVAFSAGLHGWAFTLTNFAKMYASK**FGVDESK**MMERLWGENFFDPSTRKWTTKNTGAPN
CKR**GFVQFCYEPIKQIINTCMNDQK**DK**LWPMLQKLGVTMK**SDEKDLMGKALMKRVMQTWLPASTALLEM
MIFHLPSPSTAQKYR**VENLYEGPLDDIYATAIRNCDPEGPLMLYVSK**MIPASDKGRFFAFGRVFSGKVS
TGLKVR**IMGPNYVPGEKKDLYVK**SVQRTVIWMGKRQETVEDVPCGN**TVAMVGLDQFITK**NATLTNEKES
DAHPIRAMK**FSVSPVVR**VAVQCK**VASDLPK**LVEGLKRLAKSDPMVVCSIEESGEHIIAGAGELHLEICL
KDLQDDFMGGAEIVKSDPVVSFR**ETVLEK**SCRTVMSKSPNKHNR**LYMEAR**PLEEGLAEAIDDGRVGPRD
DPKARSK**ILSEEFGWDK**DLAKK**IWCFGPETTGPNMVVDMCKGVQYLNEIKDSVVAGFQWASKEGALAEE**
NMRGICFEVCDVVLHADAIHRGGGQVIPTAR**RVIYASQLTAKPR**LLEPVYLVEIQAPEQALGGIYSVLN
QKR**GHVFEEMQRPGTPLYNIKAYLPVVESFGFSGTLR**AATSGQAFPQCVFDHWDVMSADPLEAGSTAAQ
LVADIRKRKGLKEQMTPLSEFEDKL

Protein No.: I-763

Protein name and Species:

Cinnamoyl-CoA reductase OS=Hevea brasiliensis GN=CCR PE=2 SV=1

Accession: tr|E9M776|E9M776_HEVBR

Unused ProtScore: 3.19

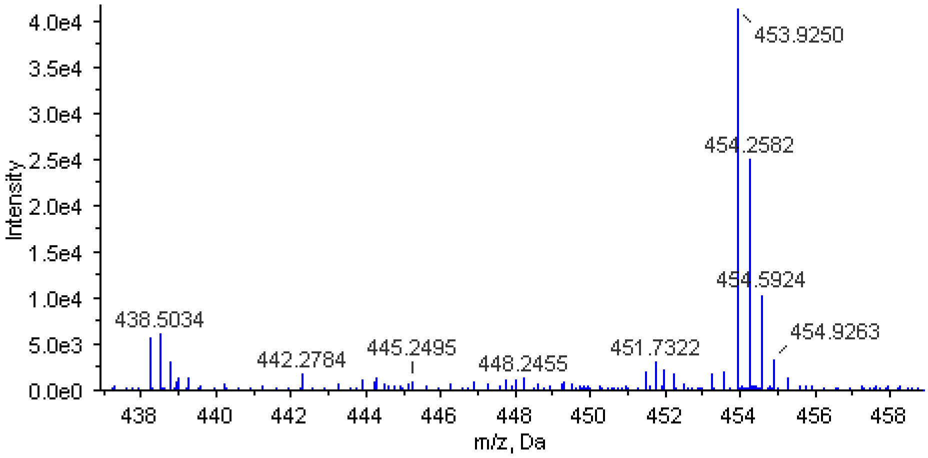
Seq Cov %: 5.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.58

116: 114=E5TL: D5TL=1.02

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MPVDTSSLSGHGQTVCVTGAGGFIASWIVKLLLERGYTVKGTVRNPDDPKNSHLRELEGAKERLTLCK**A**
DLLDYESLRKAIMGCDGVFHAASPVTDDPEQMVEPAVNGTKNVVIAAAEAKVRRVVFTSSIGAVYMDPN
RNPDVVVDESCWSDLDFCKNTKNWYCYGKAVAEQAAWEVAKEKGVDLVAVNPVLVLGPLLQSTVNASII
HILKYLTGSAKTYANSVQAYAHVKDVALAHILVYEIPSASGR**YLCAESVLHR**GEVVEILAKSFPEYPIP
TRCSDEKNPRAKPYKFSNQKLKDLGMEFTPVKQCLYETVKSLQERGHLPIPKQPEDSIRIQS

Protein No.: I-771

Protein name and Species:

Multicopy suppressor of IRA1 OS=Nicotiana tabacum GN=MSI1 PE=2 SV=1

Accession: tr|B0LUS9|B0LUS9_TOBAC

Unused ProtScore: 3.09

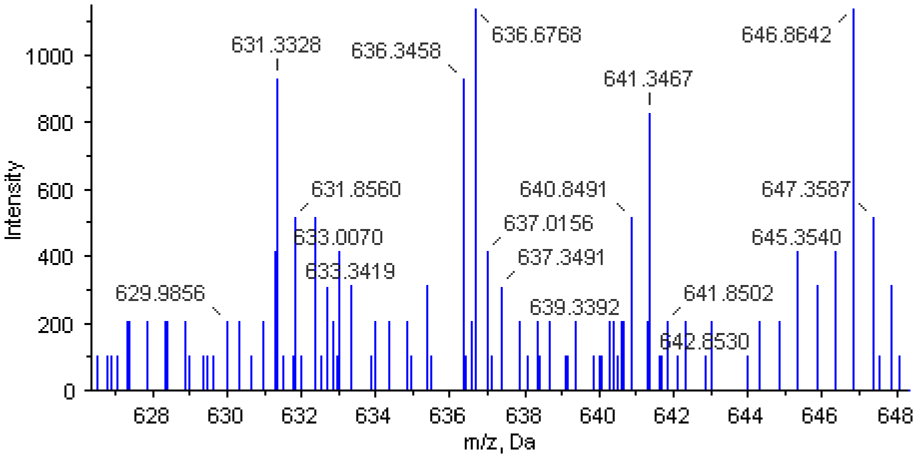
Seq Cov %: 5.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.58

116: 114=E5TL: D5TL=0.52

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGKDEDEMRGEIEERLINEEYKIWKKNTPFLYDLVITHALEWPSLTVEWLPDREEPPGKDYSVQKMILG
THTSENEPNYLMLAQVQLPLEDAENDARHYDDDRSEFGGFGCANGK**VQIIQQINHDGEVNR**ARYMPQNS
FIIATKTISAEVYVFDYSKHPSKPPLDGACNPDLRLRGHSTEGYGLSWSQFKQGHLLSGSDDAQTCLWD
INATPKNK**ALDAMQIFK**IHEGVVEDVAWHLRHEYLFGSVGDDQYLHIWDLRTPSVTKPIQSVVAHQSEV
NCLAFNPFNEWVVATGSTDKTVKLFDLRKISTALHTLDCHKEEVFQVGWNPKNETILASCCLGRRLMVW
DLSRIDEEQTPEDAEDGPPELLFIHGGHTSKISDFSWNPCEDWVVASVAEDNILQIWQMAENIYHDEDD
LPGDDATKAP

Protein No.: I-772

Protein name and Species:

ubiquitin-associated (UBA) zinc-finger and PB1 domain-containing protein OS=Populus trichocarpa GN=POPTRDRAFT_252306 PE=4 SV=1

Accession: tr|B9IEZ0|B9IEZ0_POPTR

Unused ProtScore: 3.06

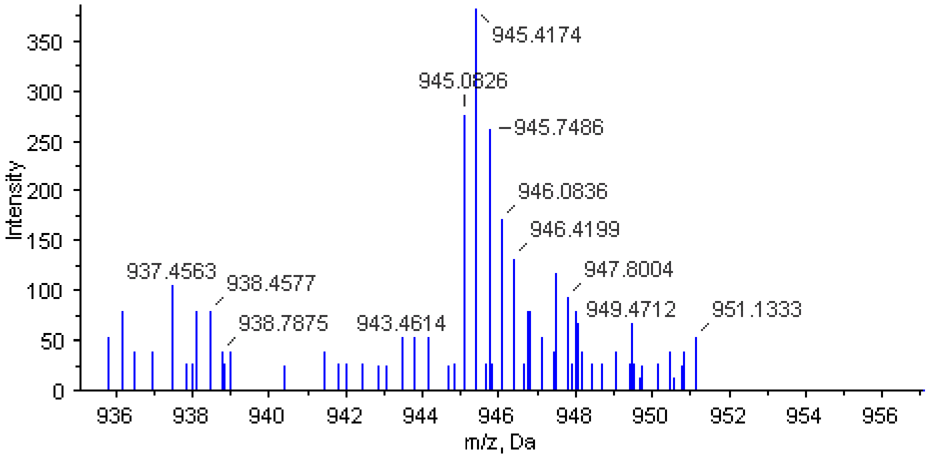
Seq Cov %: 5.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.13

116: 114=E5TL: D5TL=0.57

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

IQVKYSDTLRRFNAHVKENEQLDLDMIALREKIFGLFNFPPDADLTLTYIDEDGDVVTLADDDDLRDVM
RQNLKFLRIDVQLNNDKSGKSNARSSGSSTPMRSPRVQSPLPCLNNGVADVLKSVPEPLREVLSK**ISLD**
LTSKAVASNTVLTELVDCFSKMGQYHLNPTSQSHDGIGAQTGATAPTVLNASKDGGLKEDLLNLNSPLK
TSQEERFENGTKTAMSPHTAVPSPVNLNPNPQISNSHVIKRNNSLNNPMVGMFHR**GVQCDGCGVHPITG**
PRYKSKVK**EDYDLCSICFAEMGNEADYIKMDRPMPYR**NRWSFKGFNDPKSWAIPQPLSKGSYGVKGAQP
KLDSRFVLDVNVSDGTMMPTCTPFTKIWRMRNNGSVAWPQGVRLVWIGGDRFFNTDSVEIEIPVNGVPI
DGELDVAADFVSPALPGRYISYWRMAYPSGGKFGQRVWVLIEVDASLKDPFFKYLNLNESPNYIGSKFP
GVLDMNVQPAVDGCFLEPQNNTLLSEPDVPMVDEQPKSQELKFPIDDALLIGHGVSASAPPQAMPSSVP
VLYPMIDISETVPASTELLPAADASTSPEEVIVENAVEKTLLKELKEMGFKQVDLNKEILRRNEYDLEQ
SVDDLCGVSDWDPILEELQEMGFRDKEMNKLLLKKNNGSIKGVVMDILTGKK

Protein No.: I-774

Protein name and Species:

Vacuolar sorting protein, putative OS=Ricinus communis GN=RCOM_0363260 PE=4 SV=1

Accession: tr|B9SYU2|B9SYU2_RICCO

Unused ProtScore: 3.05

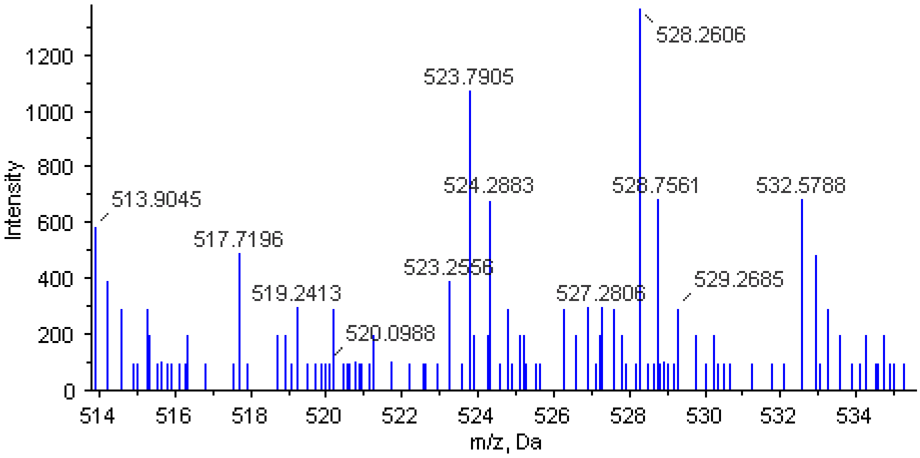
Seq Cov %: 2.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.96

116: 114=E5TL: D5TL=2.06

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MIADGVENEEKWLAAGIAGLQQNAFNMHR**ALDSNNLR**DALKYSAQMLSELRTSKLSPHKYYELYMRAFD
ELRKLEIFFREETRRGCSIIDLYELVQHAGNILPRLYLLCTVGSVYIKSKEAPAKDVLKDLVEMCRGIQ
HPVR**GLFLR**SYLSQVSRDKLPDIGSEYEGDADTVMDAVEFVLQNFTEMNKLWVRMQHQGPAREKEKREK
ERSELRDLVGKNLHVLSQIEGVDLDMYKETVLPRVLEQVVNCKDEIAQFYLMDCIIQVFPDEYHLQTLE
VLLGACPQLQPSVDIKMVLSRLMERLSNYAASSTEVLPEFLQVEAFSKLNHAIGKVIEAQVDMPMFGAV
TLYSSLLTFTLHVHPDRLDYADQVLGACVKKLSNKGKLEDSKATK**QIVALLSAPLEK**YNDVVTALKLSN
YPRVMEYLDNETNKVMATVIIQSIMKNNTRISIADKVEALFELITGLIKDLDGTHEEVDEDDFKEEQNS
VARLIQMLHNDDPEEMYKIICTVRKQIMTGGPKRLPFTVPPLVFSSLKLVRRLQGQEENPFGDESSTTP
KKIFQLLNQMIEALSIVPAPELALRLYLQCAEAANDSDLEPVAYEFFTQAYILYEEDISDSKAQVTALH
LIIGTLQRMHVFGVENRDTLTHKATGYSAKLLKKPDQCRAVYGCAHLFWVDDQDNMKDGERVLICLKRA
LRIANAAQQMANATRGSTGSVTLFVEILNKYLYFFEKGNPQVTVAAIQSLIELITTEMQSDSSTPDPAA
DAFFASTLRYIQFQKQKGGAIGEKYEPLKIVTG

Protein No.: I-778

Protein name and Species:

Phosphoglycerate dehydrogenase OS=Populus trichocarpa GN=POPTRDRAFT_1069632 PE=2 SV=1

Accession: tr|A9PEK1|A9PEK1_POPTR

Unused ProtScore: 3.04

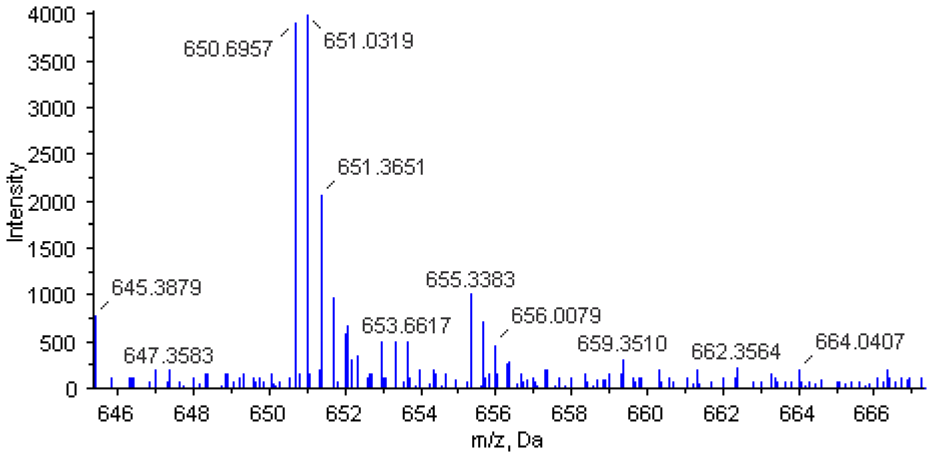
Seq Cov %: 4.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.19

116: 114=E5TL: D5TL=0.54

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAATTSTAASSLLATKKNLSSLSLTSANKLPAFSPLLTSSRRQRFIVLSASLNSKPTVLVAEKLGEA**GI**
NLLKDFANVDCSYNLSPDELCTKISLCDAIIVRSGTKVSREVFESSGGRLKVVGRAGVGIDNVDLAAAT
EHGCLVVNAPTANTVAAAEHGIALMAAMARNVAQADASVKAGKWERNKYVGVSLVGKTLAVMGFGKVGS
EVARRAK**GLGMHVIAHDPYAPADR**ARAIGVELVSFDEAIATADFISLHMPLTPATAKILNDETFAKMKK
GVRIVNVARGGVIDEDALVRALDAGIVAQAALDVFTVEPPPQDSKLVQHERVTVTPHLGASTKEAQEGV
AIEIAEAVVGALKGELASTSVNAPMVPAEVLTELKPYVELAEKLGRLAVQLVSGGSGVKDVKVTYASAR
APDDLDTRVLRAMITKGLIEPISSVFVNLVNADFSAKQRGLRISEERILGDGSPESPLHFIQVQIANVE
SKFASAISENGEIKVEGRVKDGIPHLTKVGSFEVDVSLEGSIILCRQVDQPGMIGKVGSVLGVENVNVS
FMSVGRIAPRKQAVMAIGVDEQPSKETLKKIGDIPAVEEFVFLKL

Protein No.: I-779

Protein name and Species:

Sucrose synthase [Arabidopsis thaliana] OS=Arabidopsis lyrata subsp. lyrata GN=ARALYDRAFT_494980 PE=4 SV=1

Accession: tr|D7MNN8|D7MNN8_ARALL

Unused ProtScore: 3.03

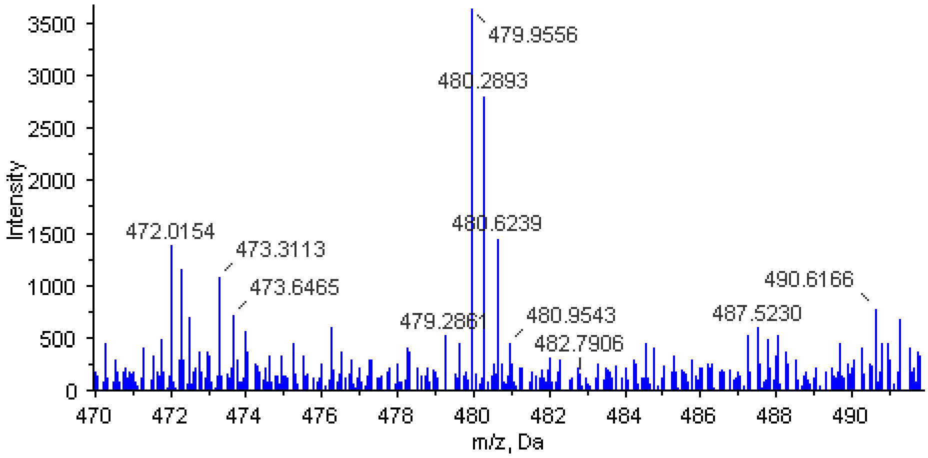
Seq Cov %: 8.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.27

116: 114=E5TL: D5TL=0.33

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MPTGRFETMREWVHDAISAQRNELLSLFSRYVAQGKGILQSHQLIDEFLKTVKVDGTTEDLNKSPFMKV
LQSAEEAIVLPPFVALAIRPRPGVREYVRVNVYELSVDHLTVSEYLRFKEELVNGHANGDYLLELDFEP
FNATLPRPTR**SSSIGNGVQFLNR**HLSSIMFRNKESMEPLLEFLRTHKHDGR**SMMLNDR**IQNIPILQGAL
ARAEEFLSKLPLATPYSEFEFELQGMGFERGWGDTAQKVSEMVHLLLDILQAPDPSVLETFLGRIPMVF
NVVILSPHGYFGQAN**VLGLPDTGGQVVYILDQVRALENEMLLR**IQKQGLEVIPKILIVTRLIPEAKGTT
CNQRLEKVSGTEHAHILRIPFRTEKGILRKWISRFDVWPYLETFAEDASNEISAELQGVPNLIIGNYSD
GNLVASLLASKLGVMQCNIAHALEKTKYPESDIYWRNHEDKYHFSSQFTADLIAMNNADFIITSTYQEI
AGSKNNVGQYESHTAFTMPGLYR**VVHGIDVFDPK**FNIVSPGADMTIYFPYSDKERRLTALHESIEELLF
SAEQNDEHVGLLSDQ**SKPIIFSMAR**LDRVKNLTGLVECYAKNSKLRELANLVIVGGYIDVNQSRDREEM
AEIQKMHSLIEQYDLHGQFRWIAAQMNRARNGELYRYIADTKGVFVQPAFYEAFGLTVVESMTCGLPTF
ATCHGGPAEIIENGVSGFHIDPYHPDQVAATLVSFFETCNTNPNHWVKISEGGLKRIYERYTWKKYSER
LLTLAGVYAFWKHVSKLERRETRRYLEMFYSLKFRDLANSIPLATDEN

Protein No.: I-780

Protein name and Species:

Calcium ATPase OS=Populus trichocarpa GN=POPTRDRAFT_768258 PE=3 SV=1

Accession: tr|B9HPP7|B9HPP7_POPTR

Unused ProtScore: 3.03

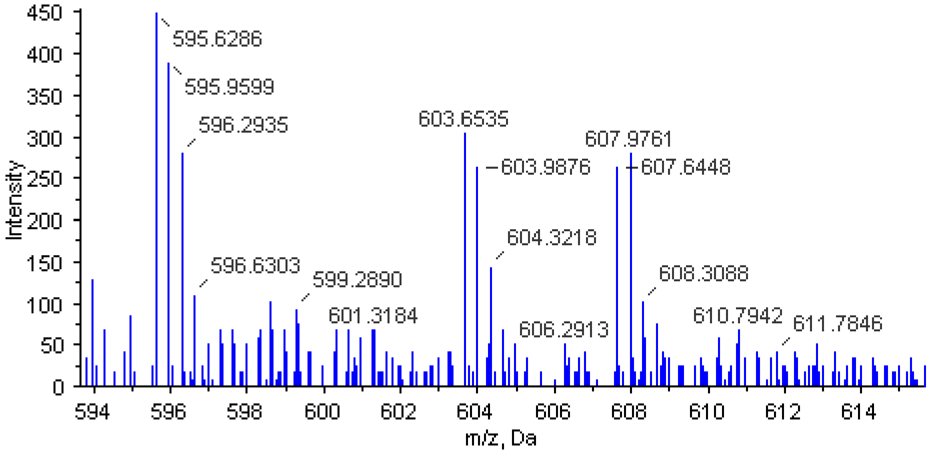
Seq Cov %: 2.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2.01

116: 114=E5TL: D5TL=1.67

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGKGGEDYGERDQNGIESQNQGDIFPAWAKEVKECEEKYAVNREFGLSSADVEKRLKIYGYNELEKHEG
VSIFKLILDQFNDTLVRILLAAAIVSFVLAWYDGEEGGEMGITAFVEPLVIFLILIVNGIVGIWQESNA
EKALEALK**EIQSEHATVIR**DRKKFSSLPAK**ELVPGDIVELR**VGDKVPADMRVLNLISSTLR**VEQGSLTG**
ESEAVSKTAKPVAESTDIQGKKCMVFAGTTVVNGNCICLVTETGMNTEIGKVHSQIHEAAQNEEDTPLK
KKLNEFGEVLTMLIGIICALVWLINLKYFLTWEYVDGWPKNFKFSFEKCTYYFEIAVALAVAAIPEGLP
AVITTCLALGTRKMAQKNALVRKLPSVETLGCTTVICSDKTGTLTTNQMAVSKLVAMGSRVGTLRSFNV
EGTTYSPFDGKIEDWPVGRMDSNLQMIAKIAAVCNDAGVEQSGNHYVAGGMPTEAALKVMVEKMGFPGG
LSKESSLVHEDVLACCRLWNTMEQRIATLEFDRDRKSMGVIVNSSSGKKSLLVKGAVENLLDRSTSIQL
LDGSVVALDRCSKDLILQNLREMSTSALRCLGFAYKEDLSEFRTYSGDEDHPAHQLLLDLHNYSSIESN
LTFVGLAGLRDPPRKEVRQAIEDCKAAGIRVMVITGDNKNTAEAICHEIGVFGPYDDISSKSLTGREFM
GLRDKKTHLRQSGGLLFSRAEPRHKQEIVRLLKEDGEVVAMTGDGVNDAPALKLADIGIAMGIAGTEVA
KEASDMVLADDNFSTIVVAVGEGRSIYNNMKAFIRYMISSNIGEVASIFLTAALGIPEGMIPVQLLWVN
LVTDGPPATALGFNPPDGDVMKKPPRKSDDSLISAWILFRYLVIGFYVGIATVGVFIIWYTRHTFMGID
LSGDGHSLVTYSQLANWGHCESWKNFSASPFTAGSQVFNFDANPCEYLRSGKIKASTLSLTVLVAIEMF
NSLNALSEDCSLVRMPPWVNPWLLLAMSVSFGLHFLILYVPFLAQVFGIVPLSLNEWLLVLAVALPVIL
IDEVLKFVGRLTSGWRHSGSRRPSKSKPE

Protein No.: I-782

Protein name and Species:

Serine/threonine-protein kinase SRK2C OS=Arabidopsis thaliana GN=SRK2C PE=1 SV=1

Accession: sp|Q9M9E9|SRK2C_ARATH

Unused ProtScore: 3.02

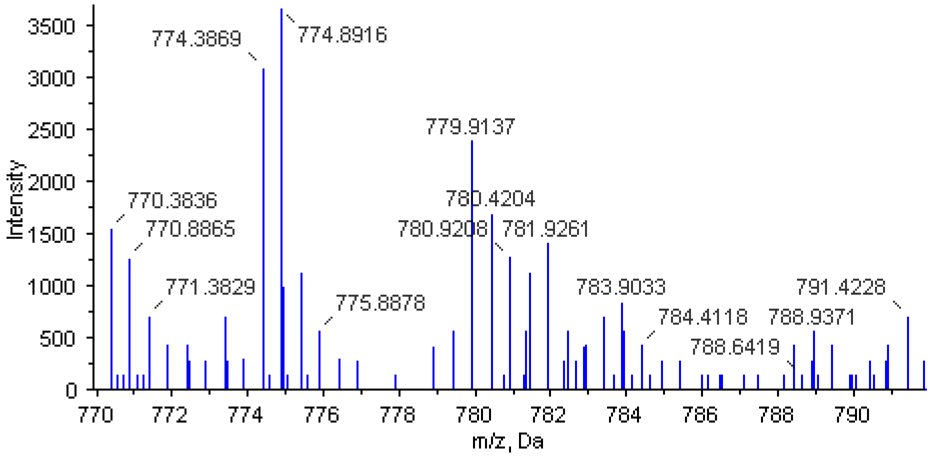
Seq Cov %: 6.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.54

116: 114=E5TL: D5TL=0.27

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MERYEIVKDIGSGNFGVAKLVRDKFSKELFAVKFIERGQKIDEHVQREIMNHR**SLIHPNIIR**FKEVLLT
ATHLALVMEYAAGGELFGRICSAGRFSEDEARFFFQQLISGVNYCHSLQICHRDLK**LENTLLDGSEAPR**
VKICDFGYSKSGVLHSQPKTTVGTPAYIAPEVLSTKEYDGKIADVWSCGVTLYVMLVGAYPFEDPSDPK
DFRKTIGRILKAQYAIPDYVRVSDECRHLLSRIFVANPEKRITIEEIKNHSWFLKNLPVEMYEGSLMMN
GPSTQTVEEIVWIIEEARKPITVATGLAGAGGSGGSSNGAIGSSSMDLDDLDTDFDDIDTADLLSPL

Protein No.: I-783

Protein name and Species:

Nonsense-mediated mRNA decay protein, putative OS=Ricinus communis GN=RCOM_0241560 PE=4 SV=1

Accession: tr|B9T5L2|B9T5L2_RICCO

Unused ProtScore: 3.02

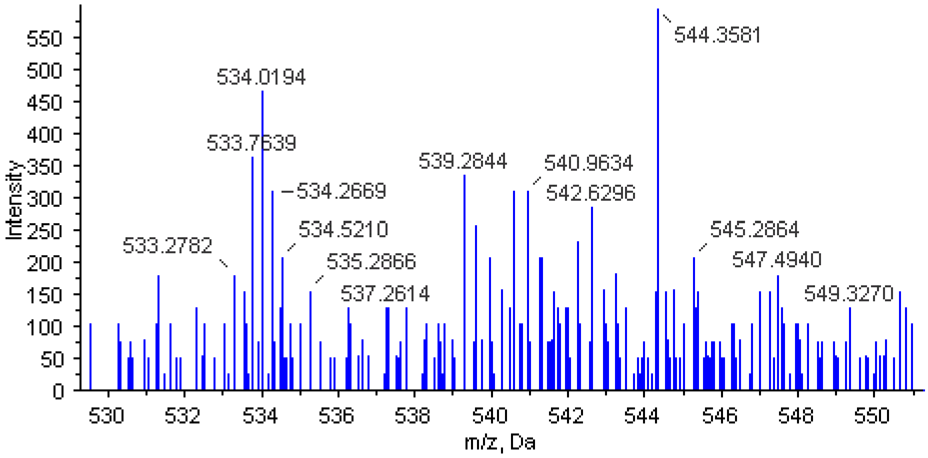
Seq Cov %: 4.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.62

116: 114=E5TL: D5TL=0.38

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAEEAGMFMVRQTIGSVLCCKCGIPMQPNAVNMCVKCLRSEVDITEGLKKRVIIKHCPECDTYLQPPYT
RIKAQLESKELMTFCVRTLDLKHAGVTLVHAEFIWTEPHSKRIKLRCRVQKEVHRGAVLEQSYIVEFVQ
QESMCESCSRVQANPDQWVASVQLRQHVSHRRTFFYLEQLILKHDAAARAIKIKQMDQGIDFFFGNRSH
GVKFVEFLGKVAPVRSRHDKQLVSHDPKSNNYNYK**YTFSVEISPICR**EDLVCLPPKVAVSLGNLGPLVI
CTKVTNSIALLDPLTLRHCYLDGDQYWRSSFKSLLTSRQLVEYIVLDVDIISPEVNIGSSKYAMAEVQV
ARLSDFGKNDTIFFIKTHLGHILKPGDQALGYDLYGANSNDIELDKYK**GLVLPEAILIK**KSYEEKRQRK
RGKPRAWKLKSLEMEVDDSRGRNDQEKMDTEYEQFLRDLEENAELRF**NVSLYR**NKEYQPSEMASVTDGE
DVPSIPLEELLADLDISEMEDAADDMRE

Protein No.: I-784

Protein name and Species:

ADP-ribosylation factor, putative OS=Ricinus communis GN=RCOM_0910690 PE=3 SV=1

Accession: tr|B9RTH6|B9RTH6_RICCO

Unused ProtScore: 3

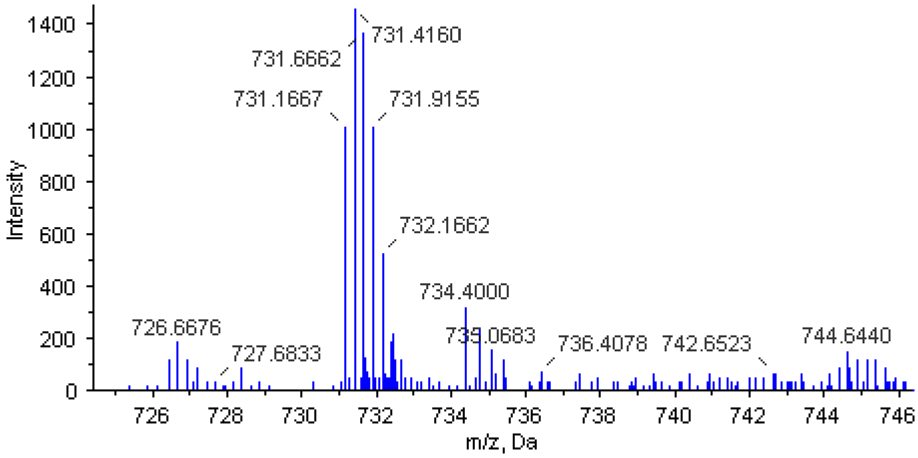
Seq Cov %: 15.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.64

116: 114=E5TL: D5TL=1.77

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGGFISRFWFMLFPAKEYK**IVVVGLDNAGK**TTTLYKLHLGEVVTTHPTVGSNVEELVYKNIR**FEVWDLG**
GQDRLRTSWATYYRGTHAVIAVIDSTDRARISIMKDELFRLLGHEDLQHSVILVLANKQDLK**DAMTPAE**
ITDALSLHSIKNHDWHIQACCALTGEGLYDGLGWIAQRVTGKAPS

Protein No.: I-789

Protein name and Species:

Putative uncharacterized protein OS=Ricinus communis GN=RCOM_1588080 PE=4 SV=1

Accession: tr|B9R730|B9R730_RICCO

Unused ProtScore: 2.98

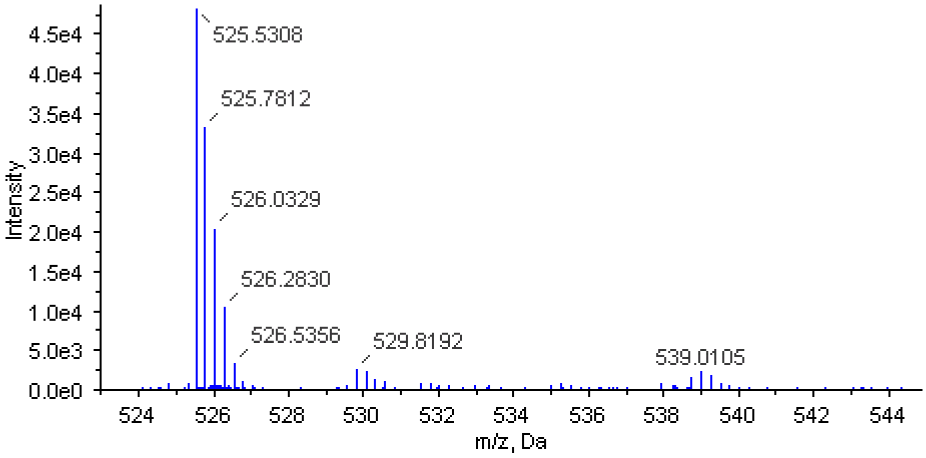
Seq Cov %: 10.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.10

116: 114=E5TL: D5TL=0.14

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSWWWAGAIGAAKKKQEEDDAPRSFQSVALVLGVTGIVGNSLAEILPLSDTPGGPWKVYGVARRPRPTW
NADHPVEYIQCDISDSAETQSKLSQLTDITHIFYVTWTNRQSEDENCEINGLMFR**NVLQAVIPNAPNLR**
HICLQTGAKHYVGPFESLGK**IQTHDPPFTEDLPR**LDAPNFYYTLEDIMFEEVAKKEGLTWSIHRPDQIF
GFSPYSLMNIIGTLCVYATICK**HEGLPLLFPGTK**AAWNCYSVASDADLIAEHQIWASVDPYAKDEAFNC
NNGDVFKWKHFWKVLAEQFGIEEYGFEEGEKRLSLVEMMKGKEAVWEEIVSENQLQPTKLDEVAVWWFV
DLMLGGEAVISSMNKSK**EHGFLGFR**NSKNSFASWIDKMKAYKIVP

Protein No.: I-790

Protein name and Species:

Cycloartenol synthase OS=Ricinus communis PE=1 SV=1

Accession: sp|Q2XPU6|CAS1_RICCO

Unused ProtScore: 2.98

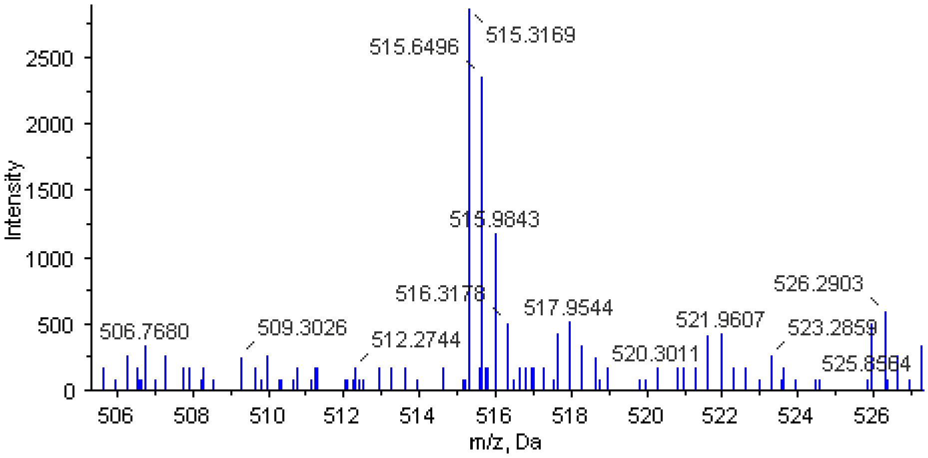
Seq Cov %: 3.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.48

116: 114=E5TL: D5TL=1.16

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MWKLRIAEGSGNPWLRTTNDHIGRQVWEFDSSKIGSPEELSQIENARQNFTKNRFIHKHSSDLLMRIQF
SKENPICEVLPQVKVKESEQVTEEKVKITLRRALNYYSSIQADDGHWPGDYGGPMFLMPGLIIALSITG
ALNAILSEEHKREMCRYLYNHQNRDGGWGLHIEGPSTMFGSVLCYVSLRLLGEGPNEGEGAVERGRNWI
LKHGGATAITSWGKMWLSVLGAYEWSGNNPLPPEMWLLPYILPVHPGRMWCHCR**MVYLPMSYLYGKRFV**
GPITPTVLSLRKELYTVPYHEIDWNQARNQCAKEDLYYPHPMLQDVLWATLHKFVEPILMHWPGKRLRE
KAIQTAIEHIHYEDENTR**YICIGPVNK**VLNMLCCWVEDPNSEAFKLHLPRLYDYLWLAEDGMKMQGYNG
SQLWDTAFAVQAIVSTNLIEEYGPTLKKAHSFIKKMQVLENCPGDLNFWYRHISKGAWPFSTADHGWPI
SDCTAEGIKALMLLSK**IPSEIVGEGLNANR**LYDAVNVVLSLQNGDGGFPTYELSRSYSWLEFINPAETF
GDIVIDYPYVECTSAAIQALTSFRKSYPEHQREEIECCIKKAAKFMEKIQISDGSWYGSWGVCFTYGTW
FGIKGLVAAGKSFGNCSSIRK**ACDFLLSK**QCPSGGWGESYLSCQKKVYSNLEGDRSHVVNTAWAMLSLI
DAGQAERDPTPLHRAARYLINAQMENGDFPQQEIMGVFNRNCMITYAAYRDIFPIWALGEYRCRVLKAS

Protein No.: I-794

Protein name and Species:

Lactoylglutathione lyase [Vitis vinifera] OS=Vitis vinifera GN=VIT_10s0116g01660 PE=4 SV=1

Accession: tr|F6H7L5|F6H7L5_VITVI

Unused ProtScore: 2.95

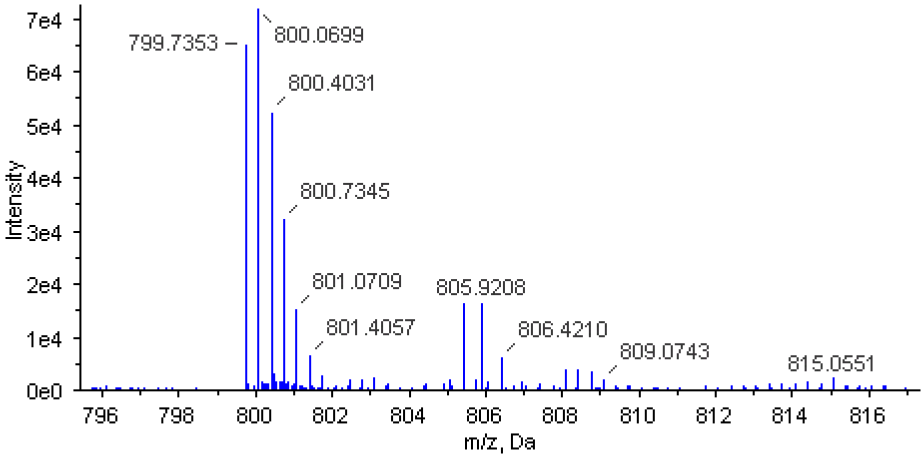
Seq Cov %: 23

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.24

116: 114=E5TL: D5TL=0.19

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAEAAPVVPSDELLEWPKKDKRR**FLHVVYR**VGDLDRTIK**FYTECFGMK**LLRKRDIPEEKYSNAFLGFGP
EETNFVVELTYKEDDETVLEYLLNCFQQQAPRYQLKLLRKVFDPWKLAAPVVPSDELLEWPKKDKRR**FL**
HVVYRVGDLDRTIK**FYTECFGMK**LLRKRDIPEEKYTNAFLGFGPEETNFVVELTYNYGVDKYDIGTGFG
HFAIATQDVYKMVEDIRAKGGIITREPGPVKGGKSVIAFAK**DPDGYIFELIQRGPTPEPLCQVMLR**VGD
LERSIKFYEKALGMKMVKKTDRPEYKYSIAMMGYAEEHETTVLELTYNYGVTEYTK**GNAYAQVAISTDD**
VYKSAEVVNLVTKELGGK**ITRQPGPIPGLNTKITSFLDPDGWKTVLVDNEDFLK**ELHKEE

Protein No.: I-799

Protein name and Species:

protein argonaute 4A-like [Vitis vinifera] OS=Vitis vinifera GN=VITISV_044457 PE=4 SV=1

Accession: tr|A5BG74|A5BG74_VITVI

Unused ProtScore: 2.93

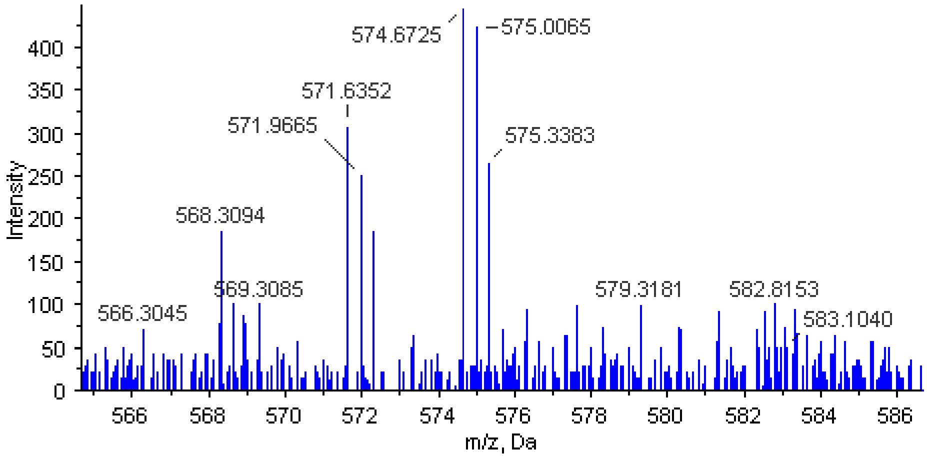
Seq Cov %: 2.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.55

116: 114=E5TL: D5TL=2.21

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MHPRPALMLPCIQPSRPALMLPCIQPLRQSYSSPTSEAHEFHVLQVLYKYLASCNRILKRRLGRFVKNR
TVCPVRWSDRWFERFNAGSTTKRFFETDRTEKLTGRRFDRSDRPNLTMESQXPPNAEPXKRSSSIPNRL
PMARRGLGRTGETIQLVXNHFKVSMHSNANTGAHFYQYNVSLAXEDGHPADAKDIGRKVMDKVHETYHT
EMAXMSFAYDGEKSLFTIGSLPSKKLRFTVVLEDASSNRISTXRNIDXPDDGSDRKRSRRPYHSKTFNV
EISFAAKFPMDSIVRASYGQPSKHLQDAAX**VLDIILR**QHAAKKGCLVVRQSFFDNLPXNFTPLGGGVLG
CRGFNSSFRATQGGLFLNMDVSTTLVIQPDPVRDFLVSNQNVKDMYHIDWSKLCTLVSLQRYTKPLSTQ
QRSSLVEKSRQKPQERMRALKSNKYDANPMLRSSGISISTQFTQVEGRILPTPSSISVVISLQLKSGNG
QDLSPRNGRWNFNNKELAQPTKIDPWLIASFSSRCNMKTLIQDLIKCAKMKGISMGYPAEIFTENPQYM
REPAPVRVDKMISTMMSQFRRLPQFILCILPQKKNCDIYGPWKRQCLSGCGVPTQCIAPSTPV**VNDQYL**
TNLLLKINAKLGGLNSLLTMGYCPSLRLISTIPTLILGMDVSHGSPGRADVPSIAAVVSSRHWPSISQY
RATVRTQSPKLEMIDSLFEPLPNSKDSGIIQACKLLDEQWHPKFMVIIAQKNHHTRFLQNGSPSNVPPG
LSPLYHLQSQVQSGQAGLRITMYCWMSLAFQQMTCSNLCIPCVXLAPVCYAHLAAAQVAQFIKFEDLPE
SSSGHAAAPVPQLPSFHEKVADTMFFC

Protein No.: I-801

Protein name and Species:

S-adenosylmethionine synthase 1 OS=Elaeagnus umbellata GN=SAMS1 PE=2 SV=1

Accession: sp|Q9AT56|METK1_ELAUM

Unused ProtScore: 2.92

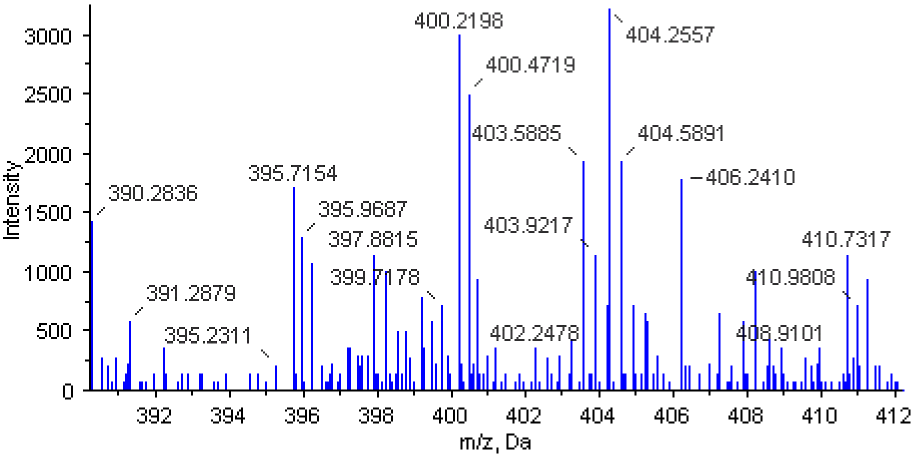
Seq Cov %: 26

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.60

116: 114=E5TL: D5TL=0.96

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

METFLFTSESVNEGHPDK**LCDQISDAVLDACLAQDPDSK**VACETCSKTNMVMVFGEITTK**ANVDYEK**IV
RDTCRAIGFVSDDVGLDADNCK**VLVNIEQQSPDIAQGVHGHFTK****RPEEIGAGDQGH**MFGYATDETPEYM
PLSHVLATKLGARLTEVRKNGTCPWLRPDGK**TQVTVEYYNENGAMVPVR**VHTVLISTQHDETVTNDEIA
ADLKEHVIKPVIPEKYLDEK**TIFHLNPSGRFVIGGPHGDAGLTGR**K**IIIDTYGGWGAHGGGAFSGK**DPT
KVDRSGAYIVRQAAK**SIVANGLAR**RCLVQVSYAIGVPEPLSVFVDSYGTGQIPDKEILNIVK**ENFDFR**P
GMITINLDLKRGGNGRFLKTAGYGHFGRDDPDFTWEIVKPLKWEKPQS

Protein No.: I-807

Protein name and Species:

60S ribosomal protein L14, putative OS=Ricinus communis GN=RCOM_1169110 PE=4 SV=1

Accession: tr|B9SS61|B9SS61_RICCO

Unused ProtScore: 2.9

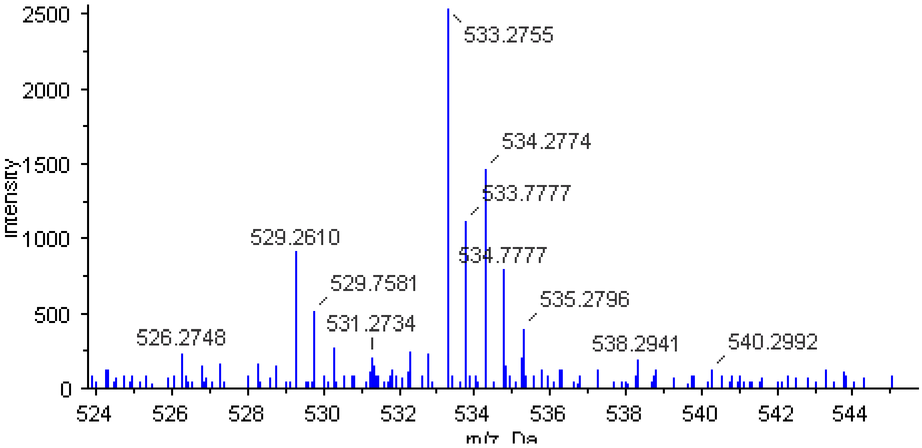
Seq Cov %: 13.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.51

116: 114=E5TL: D5TL=0.33

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MPFKRYVEIGRVALVNYGKDYGKLVVIVDVIDQNR**ALVDAPDMVR**SQMNFKRLQLTDIKIDINRVPKKK
NLIEAMEKADVKNKWESSSWGRKLIVQKRR**AALNDFDR**FKLMLAKIKRGGLIRQELAKLKKETAA

Protein No.: I-808

Protein name and Species:

Thioredoxin (Fragment) OS=Populus trichocarpa GN=PtrTrxh2 PE=3 SV=1

Accession: tr|B9IJS4|B9IJS4_POPTR

Unused ProtScore: 2.9

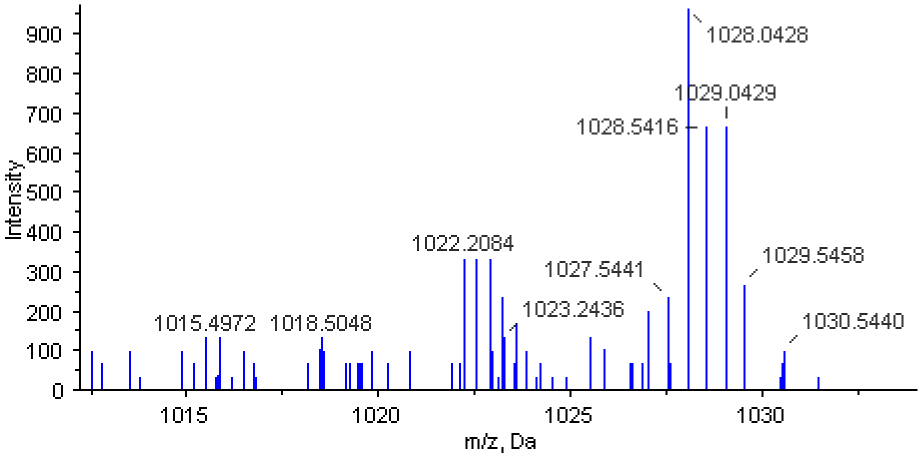
Seq Cov %: 25.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.08

116: 114=E5TL: D5TL=0.30

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

IGSILSYLFGASAAGEDSASDGQSGVTAFHSSARWQLHFNSIKNTNQLMVIDFAASWCGPCKHMEPAVH
AMAAK**FTDVQFAKIDVDELPDVAQEFGVQAMPTFVLVK**KGNEVDRVVGAQKEELQRKIEKHR

Protein No.: I-813

Protein name and Species:

Ras-related protein RABA6b-like OS=Populus trichocarpa GN=POPTRDRAFT_835110 PE=3 SV=1

Accession: tr|B9IEB2|B9IEB2_POPTR

Unused ProtScore: 2.87

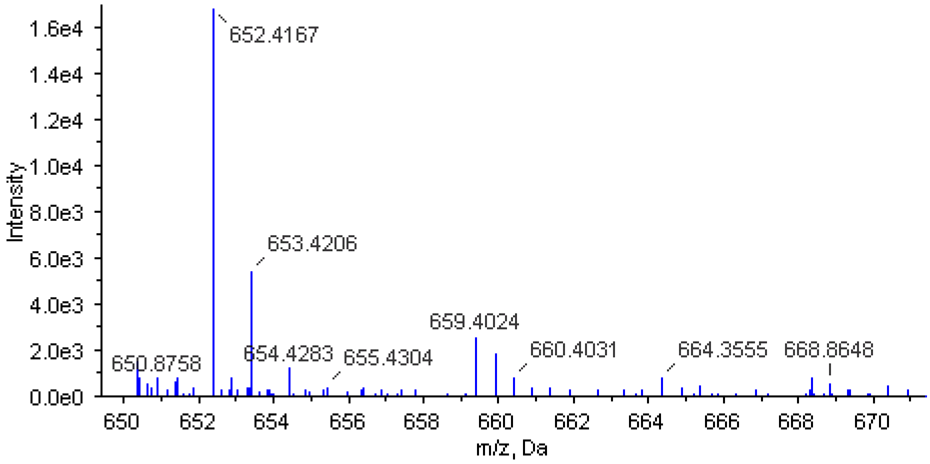
Seq Cov %: 19.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.77

116: 114=E5TL: D5TL=2.51

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MADSYDEECDYLFKAVLIGDSAVGKSNLLSRFSRDEFRLDSKPTIGVEFAYRNIRVG**DKLIKAQIWDTA**
GQERFR**AITSSYYRGALGALLVYDITR**RATFDNVKKWLHELRDFGSSDMVVVLVGNKSDISHLREVDE**D**
DGKNLAETEALYFMETSALENLNVEEAFMQMITRIHEIASQKSLEAKKNETTISTIKALPVGKEVINID
DEVSATKQASYCCSY

Protein No.: I-817

Protein name and Species:

Pro-hevein OS=Hevea brasiliensis GN=HEV1 PE=1 SV=2

Accession: sp|P02877|HEVE_HEVBR

Unused ProtScore: 2.85

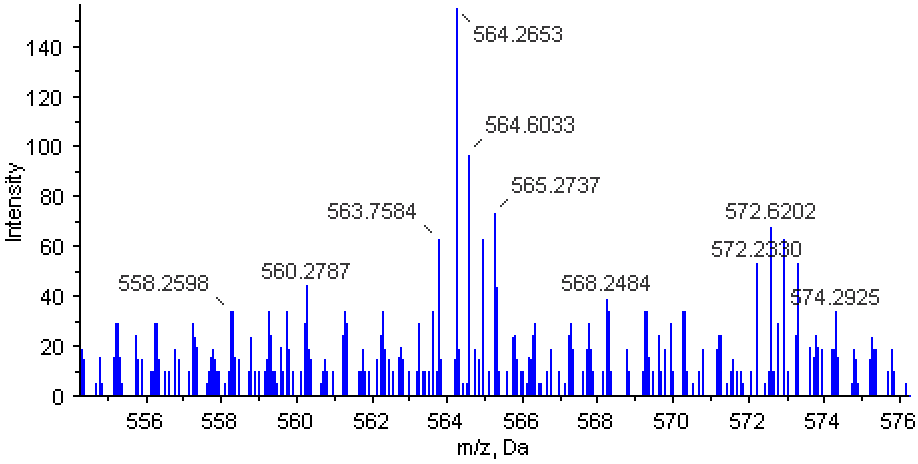
Seq Cov %: 65.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.62

116: 114=E5TL: D5TL=0.34

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MNIFIVVLLCLTGVAIAEQCGRQAGGKLCPNNLCCSQWGWCGSTDEYCSPDHNCQSNCKDSGEGVGGGS
ASNVLATYHLYNSQDHGWDLNAASAYCSTWDANKPYSWRSKYGWTAFCGPVGAHGQSSCGKCLSVTNTG
TGAKTTVRIVDQCSNGGLDLDVNVFRQLDTDGKGYERGHITVNYQFVDCGDSFNPLFSVMKSSVIN

Protein No.: I-819

Protein name and Species:

Monodehydroascorbate reductase I OS=Pisum sativum GN=MDHAR1 PE=4 SV=1

Accession: tr|Q66PF9|Q66PF9_PEA

Unused ProtScore: 2.84

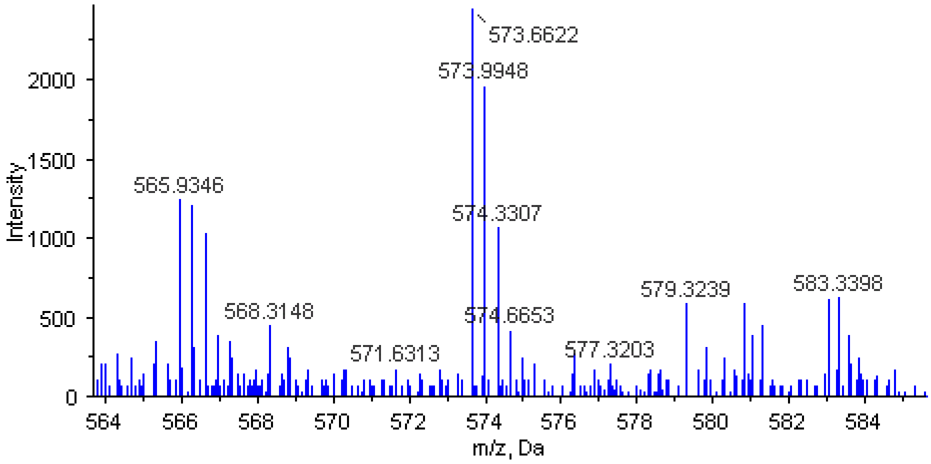
Seq Cov %: 14.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.96

116: 114=E5TL: D5TL=1.18

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MVHSFKYILIGGGVSAGYAAREFVK**QGVHPGELAIISKEAVAPYERPALSK**AYLFPESPAR**LPGFHTCV
GSGGER**LLPEWYSEKGIQLYLSTEIVSADLAAKFLKSANGEHFDYQTLVIATGSAVIRLTDFGVIGANA
KNIFYLREVDDADKLYEAIKRKKNAKAVVVGGGYIGLELSAVLKLNDLDVTMVYPEPWCMPRLFTSEIA
AFYEGYYANK**GINIIKGTVAVGFTANSDGEVK**EVKLKDGRVLEADIVIVGVGGRPQISLFKGQVEEQHG
GIKTDSFFK**TSVPDVYAVGDVATFPLK**LYNDVRRVEHVDHARKSAEQAAKVIFAADVRKSVEEYDYLPY
FYSRSFDLSWQFYGDNVGETVLFGDNDPASSKPKFGTYWIKEGK**VVGAFLEGGTPDENK**AIAKVARAKP
AVEDVNQLAEEGLSFASKI

Protein No.: I-825

Protein name and Species:

eukaryotic initiation factor 4A-3-like [Vitis vinifera] OS=Vitis vinifera GN=VIT_06s0080g00550 PE=4 SV=1

Accession: tr|F6HHF5|F6HHF5_VITVI

Unused ProtScore: 2.81

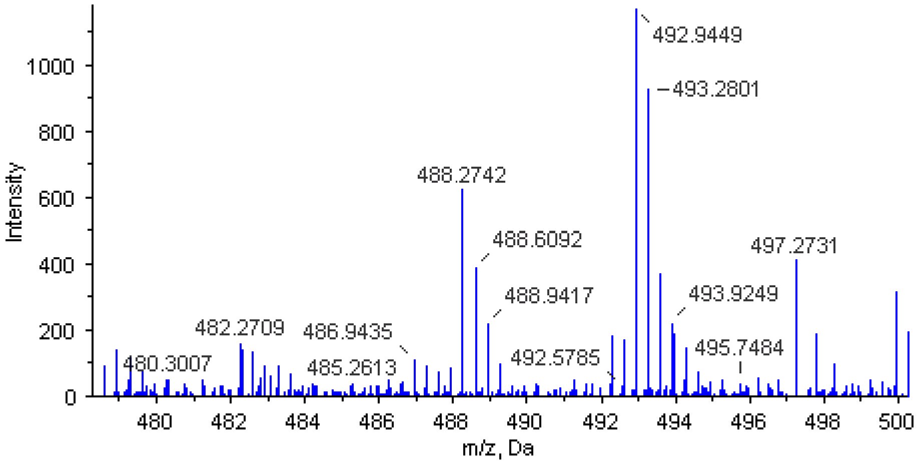
Seq Cov %: 11.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.72

116: 114=E5TL: D5TL=1.18

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAAAATASVVPANRGGRRNGAVDDEKLVFETTEGVEPIMSFDQMGIKDDLLR**GIYAYGFEKPSAIQQR**A
VLPIIQGR**DVIAQAQSGTGK**TSMIALTVCQMVDTSNR**EVQALILSPTR**ELASQTEKVILAIGDFINIQA
HACIGGKSVGEDIRKLEYGVHIVSGTPGRVCDMIKRRTLRTRAIKLLVLDESDEMLSRGFKDQIYDVYR
YLPPELQVVLISATLPNEILEITNKFMTDPVRILVK**RDELTLEGIK**QFFVAVEREEWKFDTLCDLYDTL
TITQAVIFCNTKRKVDWLTEKMRSNNFTVSSMHGDMPQKERDAIMAEFRSGTTRVLITTDVWARGLDVQ
QASHVSLVINYDLPNNRELYIHRIGRSGRFGRKGVAINFVKTDDIKILRDIEQYYSTQIDEMPMNVADL
I

Protein No.: I-827

Protein name and Species:

Ribosomal protein L5A，60S [Hevea brasiliensis] OS=Populus trichocarpa GN=POPTRDRAFT_732569 PE=3 SV=1

Accession: tr|B9IAZ4|B9IAZ4_POPTR

Unused ProtScore: 2.81

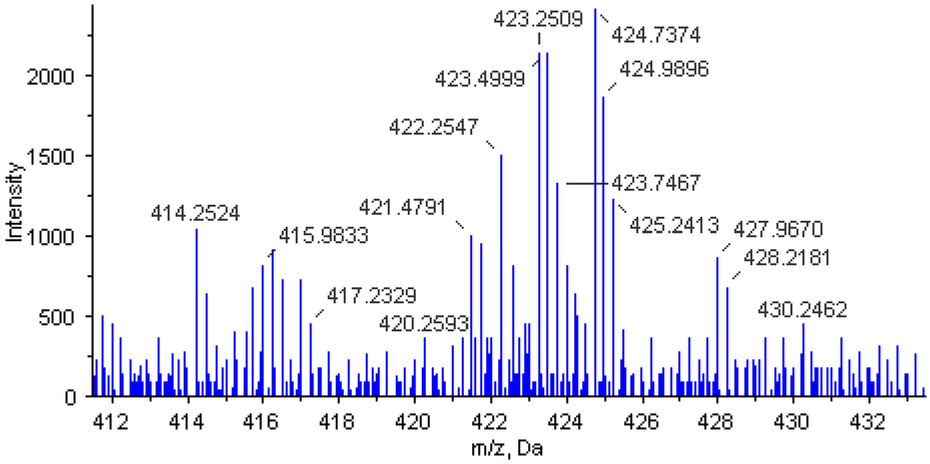
Seq Cov %: 7.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.31

116: 114=E5TL: D5TL=0.35

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAFAKAQKSRAYYKRFQVKFKRRREGKTDYRARIRLINQDKNKYNTPKYRFVMRFTNKDITAQIIHASM
AGDIVVAAAYSHELPRYGLEVGLTNYAAAYCTGLLLARRVLKKLEMDEEYEGNVEATGEDYSVEPADSR
RPFR**ALLDVGLVR**TTTGNRVFGALK**GALDGGLDIPHSDK**RFAGFNKDGK**QLDAEVHR**KYIYGGHVAAYM
RNLMEDEPEKYQSHFSEYIKR**GIEPDNMEELYK**KVHAAIRADPTAKKSEKQLPKEHKRYNLKKLTYEER
KAKLVERLKALNSAADDDEDDE

Protein No.: I-828

Protein name and Species:

60S ribosomal protein L23A-like [Glycine max] OS=Glycine max PE=2 SV=1

Accession: tr|C6SZQ3|C6SZQ3_SOYBN

Unused ProtScore: 2.81

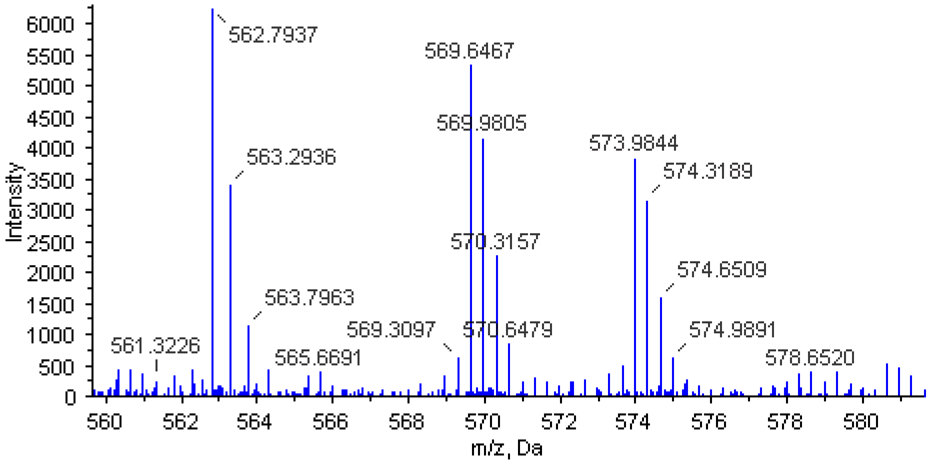
Seq Cov %: 13.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.75

116: 114=E5TL: D5TL=0.48

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAPKVDKKNDPKAQALKTAKAVKSGATFKKKVKKIRTSVTFHRPKTLKKDRNPKYPR**ISAPPR**NK**LDHY**
QILKYPLTTESAMKKIEDNNTLVFIVDLRADKKKIKDAVKK**MYDIQAK**KVNTLIRPDGTKKAYVR**LTPD**
YDALDVANKIGII

Protein No.: I-832

Protein name and Species:

Long chain acyl-CoA synthetase 1-like OS=Populus trichocarpa GN=POPTRDRAFT_850795 PE=4 SV=1

Accession: tr|B9GSW4|B9GSW4_POPTR

Unused ProtScore: 2.78

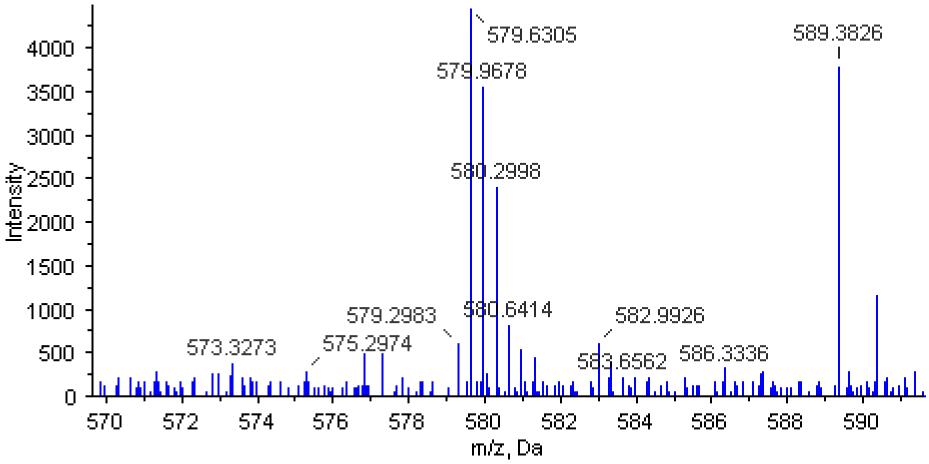
Seq Cov %: 3.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2.21

116: 114=E5TL: D5TL=1.97

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MALKAFAAQVEEGREGKDGK**PSVGPVYR**NLLSKKEYPPLDRDVTTSWDIFSSSAKKYPEYKMLGWRKFV
DGKVGPYVWKTYKEVYDEVLQISSALRASGAEPGYRVGIYGSNCPQWIEAMEACNAQSLVCVPLYDTIG
PRAVNFIIDHAEIDFVFVQDKKVKELLDPDCASAQRLKAIVCFTSLTEEEKDRAAQMGIKSYSWEEYLC
MGKENPSEIFPPQPLSICTIMYTSGTSGDPKGVVILHETVAAFVRGIDLFMEQFEDKMTTDDVYLSFLP
LAHVLDRMIEEYFFRK**GASVGYYHGDLNALR**DDLMELKPTCLAGVPRVFEKIQEGMEIPIKALQELSPL
RRNIFDVLYRYKLGWMNRGYRQK**YASPLADLLAFR**KVKAKLGGRLRLIICGGASLSTEVEEFLRVTSCA
FVIQGYGLTESCGPATMAFPDEMCMLGTVGAVAVYNDLCLEEVPEMGYDPLGNPPCGEICLRGKTLFSG
YYKNPELTRESMKDGWFHTGDIGEILPNGVVKIIDRKKNLIKLSQGEYIAIEYLENVYNNTPIVEDIWI
YGDSCKSMLVAVVVLHEENTKSWAYLNGHMGSFTELCSLHQLQKLVLSELKTTAERNKLKGFEHIKGVI
LESCPFDIEK**DLVTATLK**KKRNKLVSHYRVEIDELYQKLAEGRA

Protein No.: I-835

Protein name and Species:

Ubiquitin carboxyl-terminal hydrolase OS=Ricinus communis GN=RCOM_0004440 PE=3 SV=1

Accession: tr|B9T7A3|B9T7A3_RICCO

Unused ProtScore: 2.77

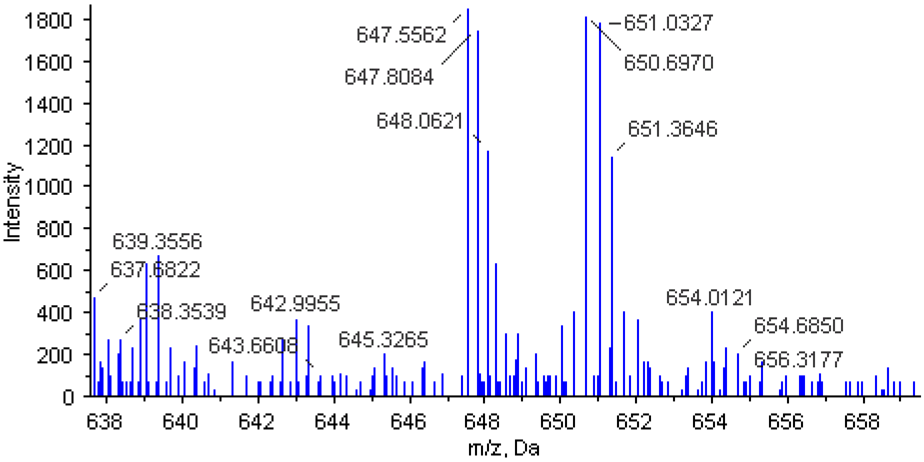
Seq Cov %: 8.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.51

116: 114=E5TL: D5TL=1.02

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MLSVSVKWQKKVFPQVEIDTSQPPYLFKCQLFDLTGVPPERQKIMVKGGLLKDDADWATVGVKEGQK**LM**
MMGTADEIVKAPEK**GPVFMEDLPEEEQVVAVGH**TAGLFNLGNTCYMNSTVQCLHSVPELKSALVKYPSD
RRNDLDQTSHMLTTATR**ELFNELDK**SVKPVAPMQFWMVLRKKYPQFGQLHNGLFMQQDAEECWTQLLYT
LSQSLRPPSPSENPDTVKELFGIDLVSR**IHCQESGEESSETESVYSLK**CHISQDVNHLHEGLKHGLKSE
LEKASPSLGRSAIYLKESCINDLPRYLTVQFVRFFWKRESNQKAKILRKVDYPLELDVYDFCSADLRKQ
LEAPRQILRDEEGRKLGLKVNEKSSGSKDNDVKMTDAEGPSSGSGESSKATSEEGESSHKVSSLTGIYD
LVAVLTHKGRSADSGHYVAWVKQESGKWIEYDDDNPIPQREEDITKLSGGGDWHMAYICMYKARAVPM

Protein No.: I-838

Protein name and Species:

Tubulin beta-7 chain OS=Arabidopsis lyrata subsp. lyrata GN=TUB7 PE=3 SV=1

Accession: tr|D7LLA4|D7LLA4_ARALL

Unused ProtScore: 2.76

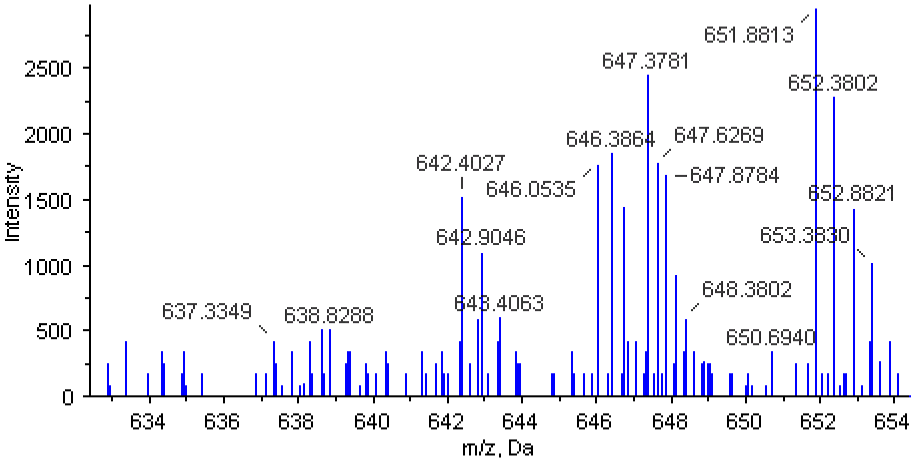
Seq Cov %: 6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.63

116: 114=E5TL: D5TL=1.29

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MR**EILHIQGGQCGNQIGSK**FWEVVNLEHGIDQTGRYHGDSDLQLERVNVYYNEASCGRYVPRAVLMDLE
PGTMDSVRSGPYGQIFRPDNFVFGQSGAGNNWAKGHYTEGAELIDSVLDVVRKEAENCDCLQGFQVCHS
LGGGTGSGMGTLLISKIREEYPDRMMMTFSVFPSPKVSDTVVEPYNATLSVHQLVENADECMVLDNEAL
YDICFRTLKLSTPSFGDLNHLISATMSGVTCCLRFPGQLNSDLRK**LAVNLIPFPR**LHFFMVGFAPLTSR
GSQQYRNLTVPELTQQMWDAKNMMCAADPRHGRYLTASAMFRGKMSTK**EVDEQMLNVQNK**NSSYFVEWI
PNNVKSTVCDIPPTGLKMASTFIGNSTSIQEMFRRVSEQFTAMFRRKAFLHWYTGEGMDEMEFTEAESN
MNDLVSEYQQYQDATADEEGEYEDEEAEYEQEEGY

Protein No.: I-839

Protein name and Species:

Dipeptidyl peptidase IV, putative OS=Ricinus communis GN=RCOM_1243220 PE=4 SV=1

Accession: tr|B9RSG5|B9RSG5_RICCO

Unused ProtScore: 2.75

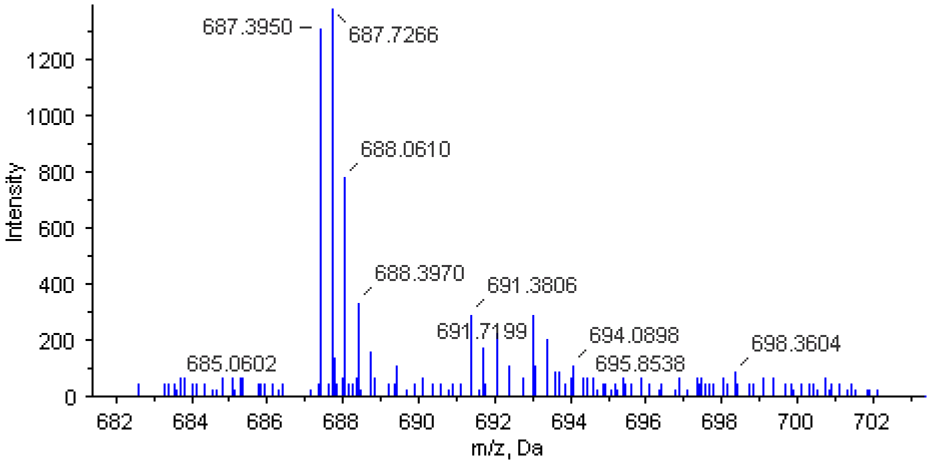
Seq Cov %: 6.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1.77

116: 114=E5TL: D5TL=0.98

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MADNTTPQNLDDCILFPVEDIVQSPLPGYGAPTSISFSPDDALITFLFSRK**VFAFDLK**TFK**QELFFSPP**
DGGLDESNISPEEKLRRERSRERGLGVTQYEWVKTSFKKKAVMVPLPAGIYFQELSSSKPELKLPSSPL
SPIIDPHLSPDGTMLAYVK**DSELHVLNLLYNESK**QLTFGSQGNTVTHGLAEYIAQEEMDRKNGYWWSLD
SKFIAFTQVDSSGIPLFRIMHQGKSSVGLESQEDHAYPFAGASNVKVRLGVVSIAGGSITWMDLVCGGT
EELDNEDEYLTRVNWMRGDILTAQVLNRSHTKLRIIKFDIKTGQGKVILVEEQDKWVNLHDCFTPLDKS
VTKYSGGFIWASEKTGFRHLYLHDANGTCLGPITEGEWMVEQIAGVNEAAGLVYFTATLDGPLEFNLYC
TKLFRDDSQNFLGPVRLTHGKGKHVVVLDHHMR**NFVDIHDSLDFPPR**VLYTSLHDGSVIMPLYEQPFTI
PRFKRLELEPPEIVQVQASDGTILYGALYKPDPTKFGPPPYKTLISVYGGPCVQYVCDSWLNTVDMRAQ
FLRSKGILVWKLDNRGSARRGLKFEGSLKYNAGRIDAEDQLTGTEWLIKQGLAKVGHIGVYGWSYGGYM
SAMILARFPDVFRCAVSGAPVTSWDGYDTFYTEKYMGLPSQNPSGYEYSSVMHHVHKLKGRLLLVHGMI
DENVHFRHTARLVNALVAAGKPYELLIFPDERHTLRWHRSRVYMEERIWEFVERSL

Protein No.: I-840

Protein name and Species:

Glutathione-s-transferase theta, gst, putative OS=Ricinus communis GN=RCOM_1299540 PE=3 SV=1

Accession: tr|B9S069|B9S069_RICCO

Unused ProtScore: 2.75

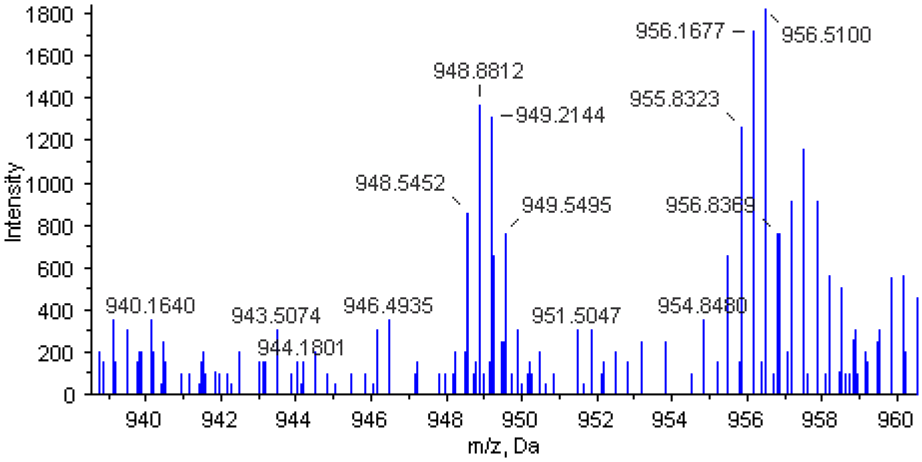
Seq Cov %: 16.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.38

116: 114=E5TL: D5TL=1.15

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSSVEGKLKLYSYWRSSCSCRVR**IALNLKGISYQYIPVNLVK**GEQF**TPEFLK**LNPIGYVPVLVDGDIVI
SDSFAILMYLEDKYPQHPLLPSDLQKK**AISIQAANIVSSSIQPLQNLAVLK**FIEEKVGPDQKVPWVQFH
IEKGFTALEKLLKDHAGKYATGDEVSLADVFLEPQIHAAINRFDVDMNKFPLLLRLHEAYNELPAFQNG
MPDKQLDAPSSSSS

Protein No.: I-844

Protein name and Species:

Pyridoxine kinase, putative OS=Ricinus communis GN=RCOM_1384840 PE=4 SV=1

Accession: tr|B9S7R8|B9S7R8_RICCO

Unused ProtScore: 2.72

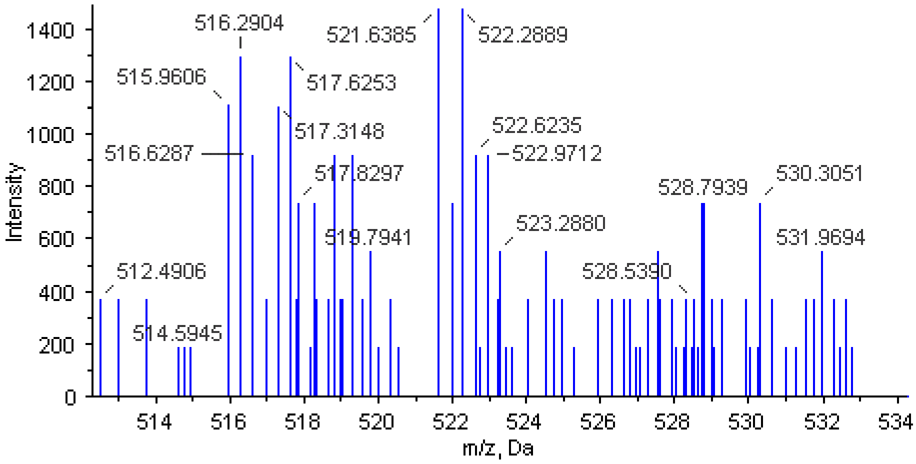
Seq Cov %: 16.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.61

116: 114=E5TL: D5TL=0.51

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAPPILSLALPSGTGRVLSIQSHTVQGYVGNKSAVFPLQILGYDVDPINSVQFSNHTGYPSVKGQVLNG
QQLWDLIEGLEGNDLLYYTHLLTGYIGSVSFLNTILEVVNKLRSINPK**LTYVCDPVMGDEGKLYVPPEL**
VAVYREK**VVPVASMLTPNQFEAEQLTGFR**IVTEKDGREACNTLHAAGPSKVIITSINIDGNLLLVGSHQ
KEKDQPPEQFKIEIPKIPAYFTKYPDNLGTAAELAVSSLQALLQRTVNDYRSVGYDPQSSSLEIRLIQS
QDDIRHPQVKFKAEKYD

Protein No.: I-845

Protein name and Species:

rhamnogalacturonate lyase OS=Populus

Accession: tr|B9H6S4|B9H6S4_POPTR

Unused ProtScore: 2.72

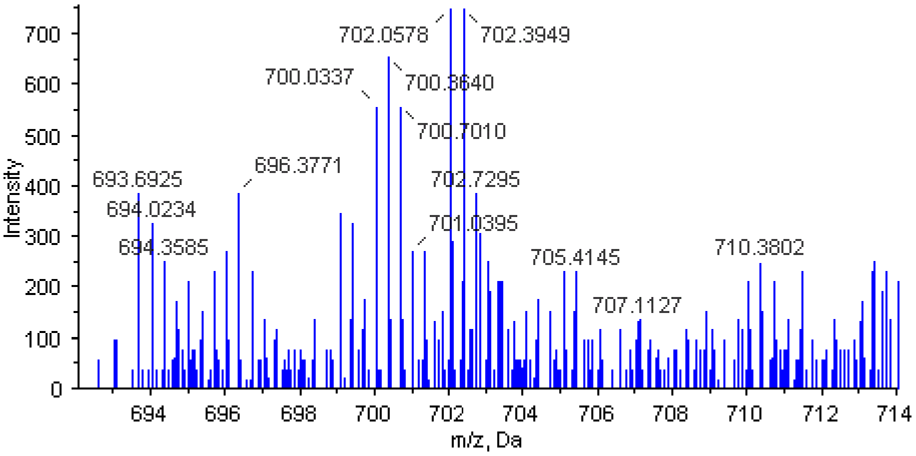
Seq Cov %: 8.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 21

116: 114=E5TL: D5TL=0. 18

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDNGIVQVTLSKPAGIVTGIR**YDGIDNLLEVLNR**ETNRGYWDLHWNPPGGNGIFDVISGTSFRVVVEND
EQVELSFTRMWDSSLEGKYIPLNIDKRFILLRGSSGFYSYAIYEHLQEWPGFDIGETRITFKLRKDKFQ
YMAIADNRQRLMPLPDDRLPGR**CQALAYPEAVILVNPK**LPELTGEVDDKYQYSCENKDNQVHGWICFKP
PVGFWQITPSDEFRTAGPLKQNLTSHVGPTTLAMFHSSHYAGKDLVLSISPGEPWKKVFGPVFIYLNSA
SNGEDPLFLWEDAKMQMMAEVQSWPYSFPASEDFQKSEQRGNVCGRLLVKDRNISDDYILASGAYVGLA
PPGDVGSWQTECKDYQFWTR**ADENGYFSIK**NIRTGDYNLYAWVPGFLGDYRWDAIVNIISGCDMDMGDL
VYEPPR**DGPTLWEIGIPDR**SAAEFYIPGPDPKFMNNLYANHPDRFRQYGLWGRYADLYPDTDLVYTVGL
SDYRKDWFFAQVVRRKDDDTQVGTTWQIKFKLDKVDRNSSYKLRVAIASATLAELQVRVNDAKAQRPLF
TSGLIGRDNAIARHGIHGLYR**LYNVNIPGARLVEGENTIFLTQPR**CTSPFQGLMYDYIRLEGPPFSGSS
NEASSSFK

Protein No.: I-864

Protein name and Species:

Glutaredoxin, grx, putative OS=Ricinus communis GN=RCOM_0936190 PE=4 SV=1

Accession: tr|B9RZ84|B9RZ84_RICCO

Unused ProtScore: 2.65

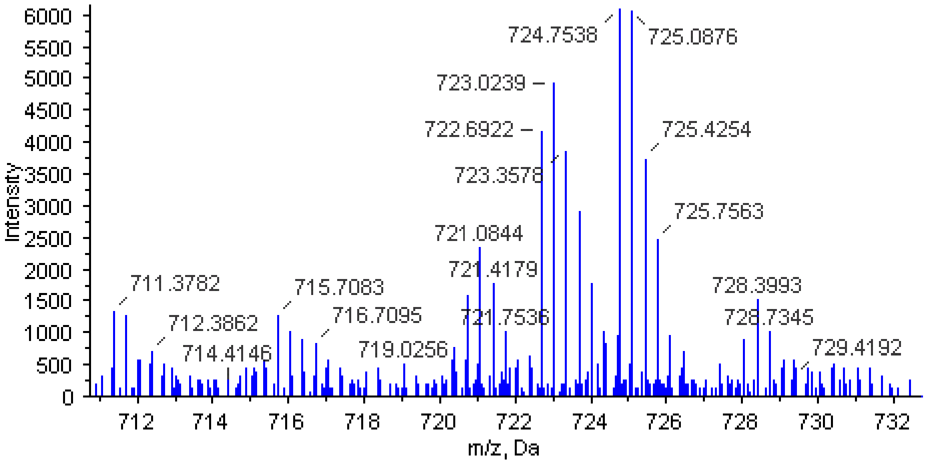
Seq Cov %: 9.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.62

116: 114=E5TL: D5TL=1.00

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGGSVKEVHSKTELDDVRSSGVPVIVHFWASWCDASKHMDQVFSHLSTDFPNAHFLRVEAEEQPEISEE
FSVSAVPFFVFFKDGKKVDSLEGADPSSLANKVAKAAGSVKSGEPAAPASLGMAAGPSILETVKELAKD
NGPSQVSNKVQPGLNDALEKRLQQLINSHPVMLFMKGSPEAPRCGFSQKIVDILKDEAVK**FGSFDILSD**
NEIREGLKKFSNWPTFPQLYCKGELLGGCDIAIAMHESGELKDVFRDHGVDTNSSEEVKVSEGGNGKGG
ISESTGLSSTLTSRLESLINSSPVMLFMKGKPDEPKCGFSRKVVDILREEK**VNFDSFDILSDDEVR**QGL
KVYSNWSSYPQLYIKGELIGGSDIVLEMQKSGELKRVLVEKGISPKGTLEDRLRSLVASSHVMLFMKGS
PDAPRCGFSSKVVNALR**EEGVSFGSFDILSDEEVR**QGLKVFSNWPTFPQLYYKGELIGGCDIIMELKNN
GELKSTLSE

Protein No.: I-868

Protein name and Species:

programmed cell death protein 5-like [Vitis vinifera] OS=Vitis vinifera GN=VIT_10s0003g02790 PE=4 SV=1

Accession: **tr|D7TK03|D7TK03_VITVI**

Unused ProtScore: **2.65**

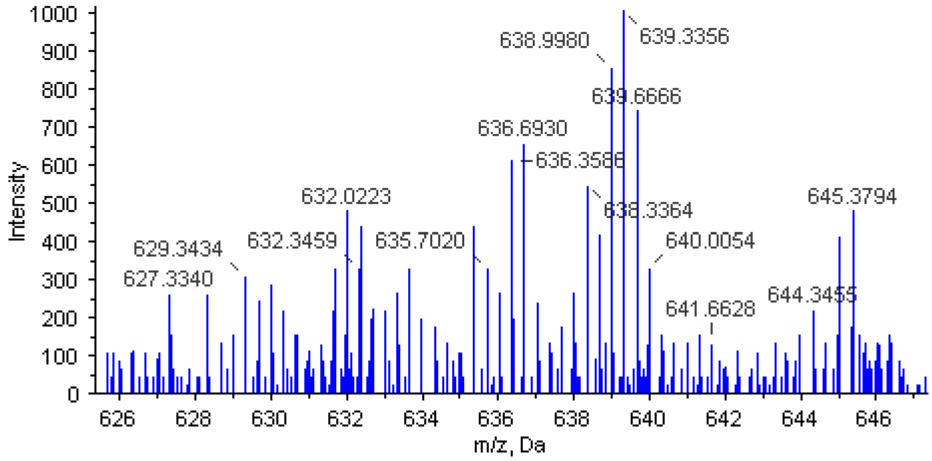
Seq Cov %: **23.5**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 54

116: 114=E5TL: D5TL=0. 47

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MQELMAQHGVGNHQNSEQQKAQEDAKREADERR**QMMLSQILSSEAR**ERLARIALVKPEKAR**GVEDVLLR**
AAQMGQIVEKVSEER**LISLLEQINNQTTK**QTKVTIQRRRSVLEDDD

Protein No.: I-869

Protein name and Species:

14 kDa zinc-binding protein-like [Vitis vinifera] OS=Vitis vinifera GN=VITISV_029944 PE=4 SV=1

Accession: tr|A5BDT4|A5BDT4_VITVI

Unused ProtScore: 2.64

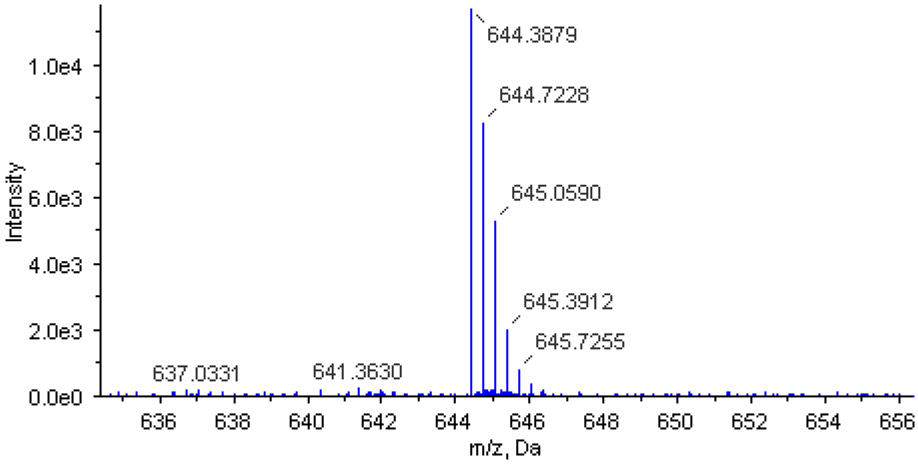
Seq Cov %: 5.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 30

116: 114=E5TL: D5TL=0. 34

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MNPSNKSRNQSRVGDINSRLGVIASHLSSAYMASEKGAAVAATPSDSPTIFDKIINKEIPATIVYEDDK
VLAFR**DIAPQAPTHILLIPK**VKDGLTGLSKYIFSSVLYTGQLKTPRHKCYCALHFERTAIHETEYCFLL
RFNLGESLSLNHMGLTLGCICSVDLVMESVGRLLANWRRHYMSIGSRVTFNRVLLIKCSYALHILLIPG
SIRNTWEIGDGFSLVRVRPRRELFDWLELGV**VLAIR**DLERMTEALLGKWLWKFVVEXDSSXRVVFESQC
CYSRELRDFDVCGDHGTQSLPMVQPMRGGRITPTRLACARRMGRAWIIYQFPRNSEAYVGKLTWTIWQV
VLMVFRGFMXFIFQAEERHSVILGHLLYTAKLVAK**QEGLEDGFR**IVINDGPSACQSVYHIHVHLLGGRQ
MNWPPG

Protein No.: I-870

Protein name and Species:

Adenylosuccinate synthetase 2, chloroplastic OS=Ricinus communis GN=PURA2 PE=3 SV=1

Accession: sp|B9SL58|PURA2_RICCO

Unused ProtScore: 2.64

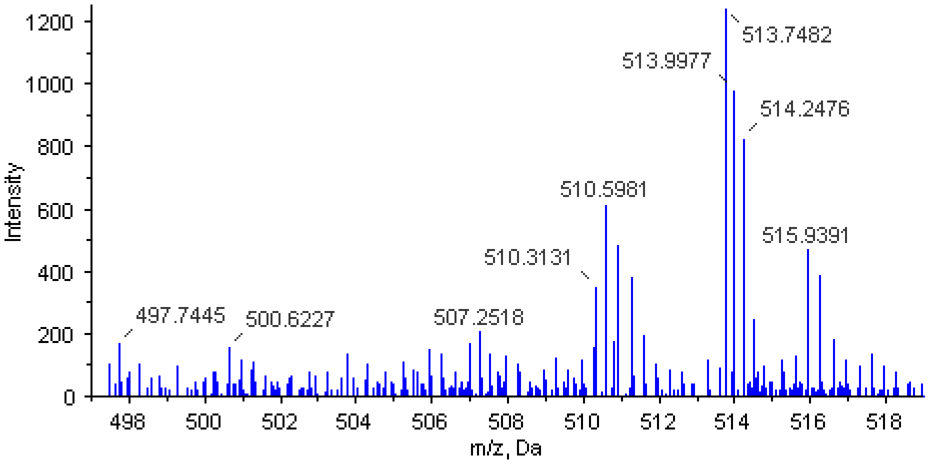
Seq Cov %: 7.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.53

116: 114=E5TL: D5TL=2.38

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSFTSSLRLDTNPITSPKWVHRQVPLRPHRNFVVCSIKSPSTPSLNLATDSASTDSLSRINSLSQVSGV
LGCQWGDEGKGKLVDILAQHFDIVAR**CQGGANAGHTIYNSEGK**KFALHLVPSGILNEDTLCVIGNGVVV
HLPGLFKEIDGLESSGVSCTGRILVSDRAHLLFDFHQEVDGLREAELAKSFIGTTRRGIGPCYASKAIR
NGIRVSDLRHMDTFPQKLDILLSDAASRFQGFKYGPEMLREEVEKYKRYAERLEPFIADTVHVMNESIE
QKKKILVEGGQATMLDIDFGTYPFVTSSSPSAGGICTGLGIAPRAVGDLIGVVKAYTTRVGSGPFPTEI
LGQGGDLLRFAGQEFGTTTGRPRRCGWLDIVALKYCCQINGFSSLNLTKLDVLSDLPEIQLGVAYKHAD
GTPFKSFPADLR**LLEQLK**VEYEVLPGWKSDISSIRNYADFPKAAQQYVER**IEELVGVPVHYIGVGPGR**D
ALIYK

Protein No.: I-871

Protein name and Species:

60S ribosomal protein L4, putative OS=Ricinus communis GN=RCOM_0819810 PE=4 SV=1

Accession: tr|B9SGS2|B9SGS2_RICCO

Unused ProtScore: 2.63

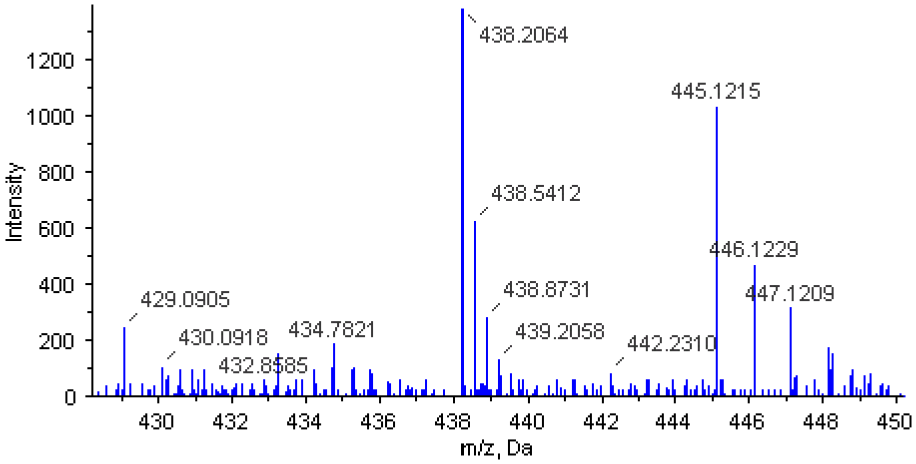
Seq Cov %: 11

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2. 68

116: 114=E5TL: D5TL=0. 54

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAAAAAAARPLVTVQSLPSQNDMATDAVTTVPLPDSMKASLRPDIVSFVHAQMSKNSRQPYAVSKRAGH
QTSAESWGTGRAVSRIPRVPGGGTHR**AGQGAFGNMCR**GGRMFAPTKIWRRWHRKINVNQKRYALVSAIA
ASAIPSLVMARGHK**VESVPEMPLVISDSAESIEK**TSTALKVLKEIGAYPDVEKAKDSHAIRPGKGKMRN
RRYISRKGPLIVYGSEGAKLVKAFRNIPGVEVANVERLNLLKLAPGGHLGRFVIWTKSAFEK**LDSIYGS**
FQKSSEKKKGYVLPRSKMVNADISRIINSDEVQSVVNPIKKEVNRAPLKKNPLK**NLNVMLK**LNPYAKAA
RRMSLLAEAQRVKAKKEKLDKKRKTVTKEEAAAIRAAGKAWYQTM**ISDSDYTEFENFSK**WLNVSQ

Protein No.: I-879

Protein name and Species:

Phosphofructokinase;pyrophosphate-fructose 6-phosphate 1-phosphotransferase OS=Populus trichocarpa GN=POPTRDRAFT_761666 PE=4 SV=1

Accession: tr|B9H5X2|B9H5X2_POPTR

Unused ProtScore: 2.61

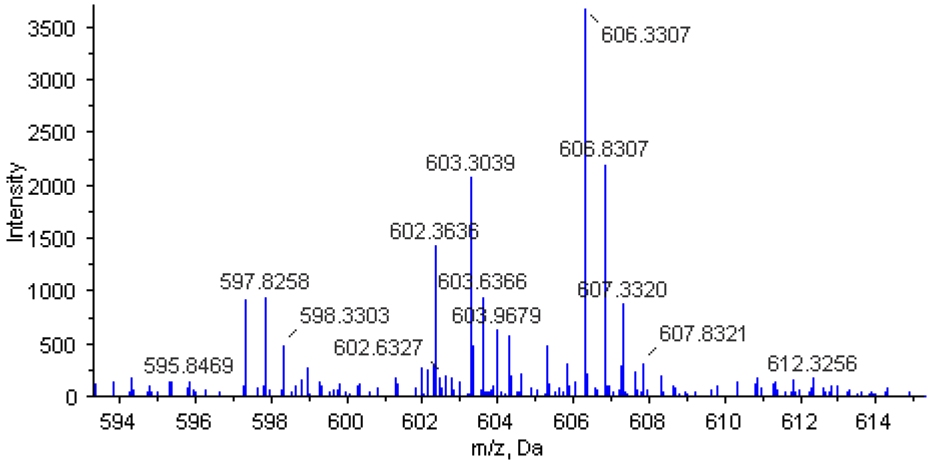
Seq Cov %: 30.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 30

116: 114=E5TL: D5TL=1.01

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDSDFGIPRELSDLQKLR**SLYQPELPPCLQGTAVR**VELGDATTAADPADVHSISRSFPL**TYGQPLAHFL**
RASAKVSDAQIITDHPAFR**VGIVFCGR**QSPGGHNVIWGLHNALKIHNPN**STLLGFLGGSEGLFAQKTLE**
ITDDILSTYKNQGGYDLLGRTKDQIR**TTEQVNAALTACK**DLK**LDGLVIIGGVTSNTDAAQLAETFAEAK**
CPTK**VVGVPVTLNGDLKNQFVETNVGFDTICKVNSQLISNVCTDALSAEK**YYYFIRLMGRK**ASHVALEC**
TLQSHPNMVILGEEVAASKLTLFDLTTQICDAVQARAVQDKNHGVILLPEGLIESIPEVYALLK**EIHGL**
LRHGVAPDNISSQLSPWTSALFEFLPPYIKKQLLLHPESDDSAQLSQIETEKLLAHLVETEMNKRLKEG
TYTGKK**FNAICHFFGYQAR**GSLPSKFDCDYAYVLGHISYHILAAGLNGYMATVTNLKNPVNKWR**CGAAP**
ITAMMTVKRWAQSPGASSIGK**PAIHPATVDLK**GKAYELLRQNAGRFWMDDLYRNPGPLQFDGPGADSKA
VTLCVEDQDYMGGIKKLQEYLDKVRNIVKPGCSQEVLKAALSVMSSVTDVLSVMSSTSSNGQTPL

Protein No.: I-885

Protein name and Species:

Thioredoxin OS=Jatropha curcas PE=3 SV=1

Accession: tr|E9JFW4|E9JFW4_9ROSI

Unused ProtScore: 2.61

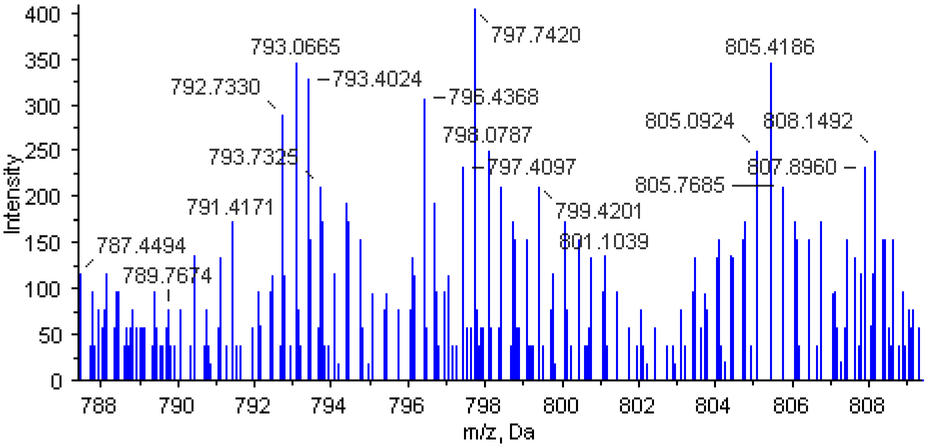
Seq Cov %: 15.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1. 77

116: 114=E5TL: D5TL=0. 79

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAEEGQVIACHTVEAWNEQLEKGKESKTLIVVDFTATWCGPCRFITPILQDLAKK**MPHVTFLK**VDVDEL
R**TVAEDWAVEAMPTFMFLK**EGKIVDKVVGAKKEELQMTIVKHATEVAAA

Protein No.: I-886

Protein name and Species:

Nucleoside diphosphate kinase OS=Vitis vinifera GN=VIT_02s0025g01500 PE=3 SV=1

Accession: tr|A5BVN4|A5BVN4_VITVI

Unused ProtScore: 2.6

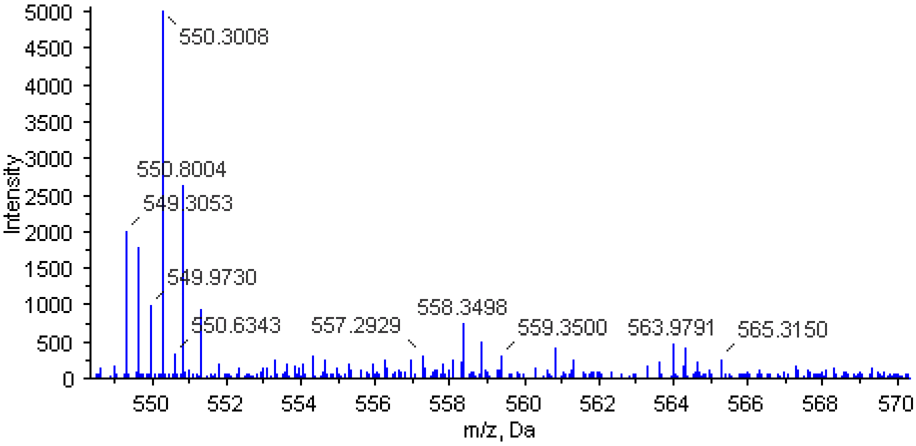
Seq Cov %: 8.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 64

116: 114=E5TL: D5TL=0. 97

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSSQICRSASRAARSLLSASKSSNLLAEGRAVAAVAALSSRGKPFLSSFGNAGSGNAYRGWLSSVLALP
AAAYMMQEQELHATEMER**TFIAIKPDGVQRGLIAEILSR**FERKGFKLVAIKIVVPSKDFAQKHYHDLKE
RPFFNGLCDFLSSGPVVAMVWEGEGVIKYGRKLIGATDPQKSEPGTIRGDLAVVVGRNIIHGSDGPETA
KDEINLWFKPEELVNYSSNAEKWIYGVN

Protein No.: I-888

Protein name and Species:

Coated vesicle membrane protein, putative OS=Ricinus communis GN=RCOM_0911000 PE=3 SV=1

Accession: **tr|B9RTJ5|B9RTJ5_RICCO**

Unused ProtScore: **2.59**

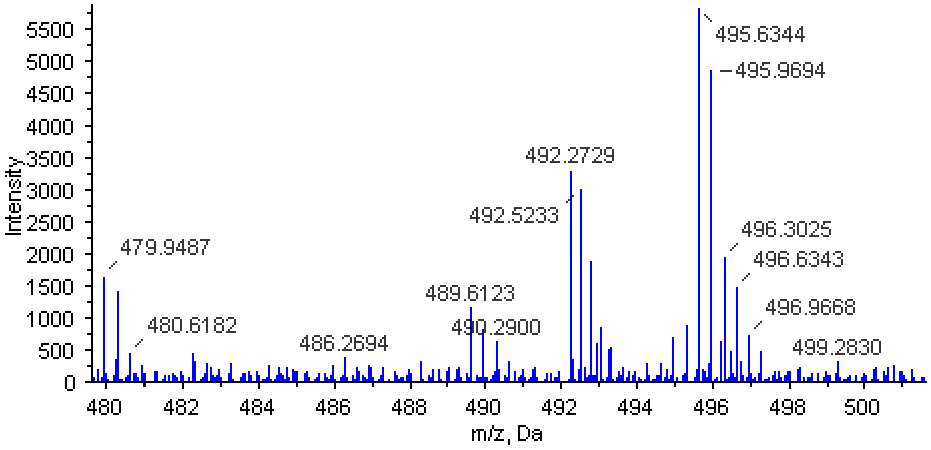
Seq Cov %: **10**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=7. 31

116: 114=E5TL: D5TL=2. 19

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MTRRQIYVVGILLLMNLIGRISSLSVTVNDVECVYEYVLYEGDTVSGNFVVVDHDIFWSSDHPGIDLTV
TSPADNVVHTVKGTSGDKFEFKAPRSGMYKFCFHNPYSTPETVSFYIHVGHIPNAHDLAK**DEHLNPINV**
KIAELR**EALESVTAEQK**YLKARDARHRRTNESTRKRVIGYTVGEYILLGLVSTLQVVYIRRLFSKSVAY
NRV

Protein No.: I-900

Protein name and Species:

Glutathione transferase GSTL3 [Populus trichocarpa] OS=Populus trichocarpa GN=POPTRDRAFT_281791 PE=3 SV=1

Accession: tr|B9MT66|B9MT66_POPTR

Unused ProtScore: 2.53

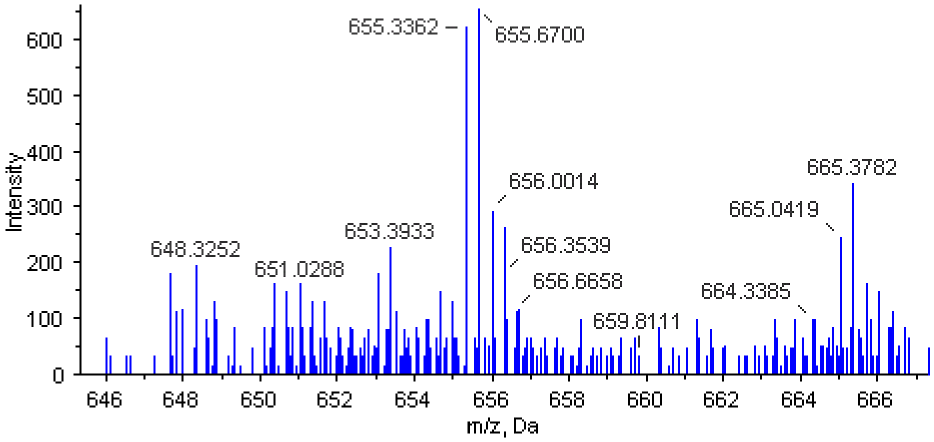
Seq Cov %: 15

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 47

116: 114=E5TL: D5TL=0. 24

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

PLDATAEQPPLFDGTTK**LYTCYTCPFAQR**VWITRNFKG**LQDEIK**LVPLILQNRPAWYPEKVYPPNK**VPS
LEHNGK**ITGESLDLIKYLESNFEGPSLLPKDPAKKEFAEELFSYTDKFNGTVYTAFKGDLAK**EAGPAFD
YLENALHK**FDDGPFFLGKEF**SLVDIAYIPFVER**LNIFLLEVFKYDIAAGRQKLAAWIEEVNK**IEAYK**QT
KTDPK**ELVEFYK**K

Protein No.: I-903

Protein name and Species:

177 protein OS=Arabidopsis thaliana GN=LSH10 PE=2 SV=1

Accession: **tr|Q9S7R3|Q9S7R3_ARATH**

Unused ProtScore: **2.53**

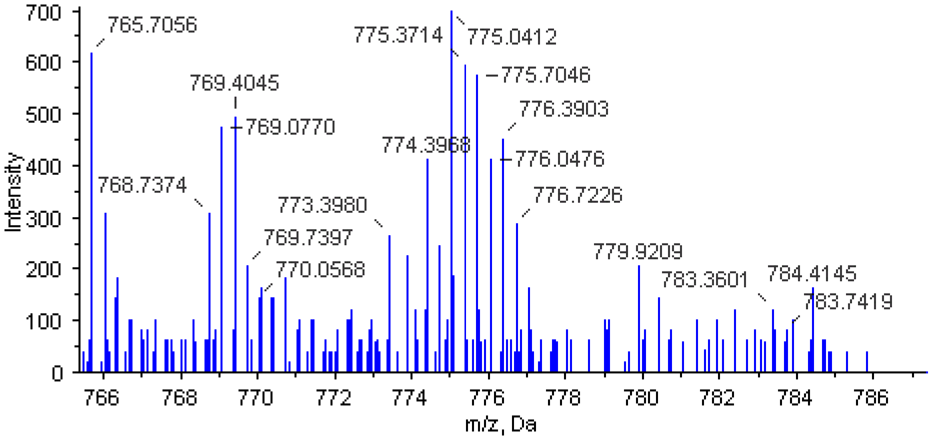
Seq Cov %: **11.9**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 46

116: 114=E5TL: D5TL=0. 22

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSSPRERGKSLMESSGSEPPVTPSRYESQKRRDWNTFGQYLKNQRPPVPMSHCSCNHVLDFLR**YLDQFG**
KTKVHVPGCMFYGQPEPPAPCTCPLRQAWGSLDALIGRLR**AAYEENGGPPETNPFASGAIR**VYLREVRE
CQAKARGIPYKKKKKKKPTPEMGGGREDSSSSSSSFSFS

Protein No.: I-904

Protein name and Species:

Protein disulfide isomerase OS=Gossypium hirsutum GN=GHPDI12 PE=2 SV=1

Accession: tr|G1ED19|G1ED19_GOSHI

Unused ProtScore: 2.53

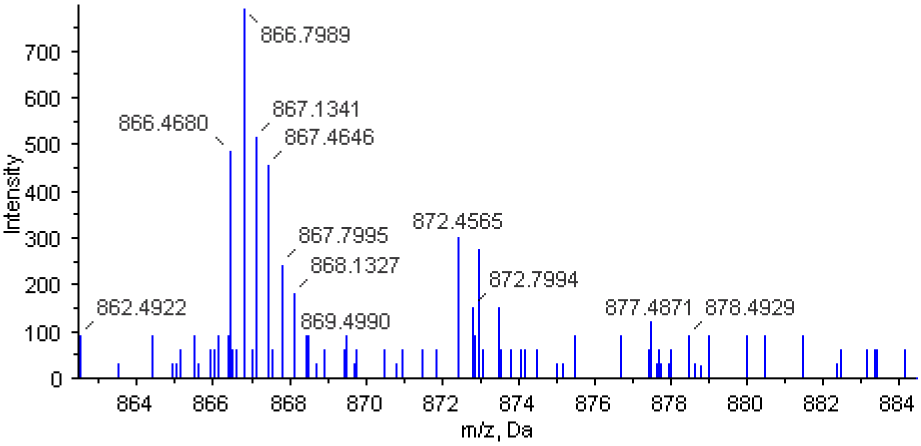
Seq Cov %: 7.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2. 36

116: 114=E5TL: D5TL=1. 50

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MKSQICLAFGTLALLLASALADDVVVLTEANFDKEVGQDRGVLIEFYAPWCGHCKKLAPEYEKLGATFK
KAKSVLIGKVDCDEHKSLCSKYGVQGYPTVQWFPKGSLEPKKYEGTSTAEAPVEFVNTEGGTNVKIATL
PSNVAVLNADNFDEIVLDETKDVLVEFYAPWCGHCKNLAPTYEKVATAFK**SEEDVVIANLDADK**YRDLA
EKYGISGFPTLKFFPKGNKAGEDYDGGR**DLDDFVSFINEK**CGTSRDAKGQLTSTAGILSSLDALVKEFV
AASADEKKVVFSK**IEEEVEK**LKGSTARHGKIYLKAAKSCLEKGADYPKKEIERLQRMLDKSISPAKADE
FTLKKNILSTFASS

Protein No.: I-905

Protein name and Species:

Glutathione S-transferase,2,4-D inducible OS=Glycine max GN=GSTa PE=1 SV=1

Accession: tr|O49235|O49235_SOYBN

Unused ProtScore: 2.52

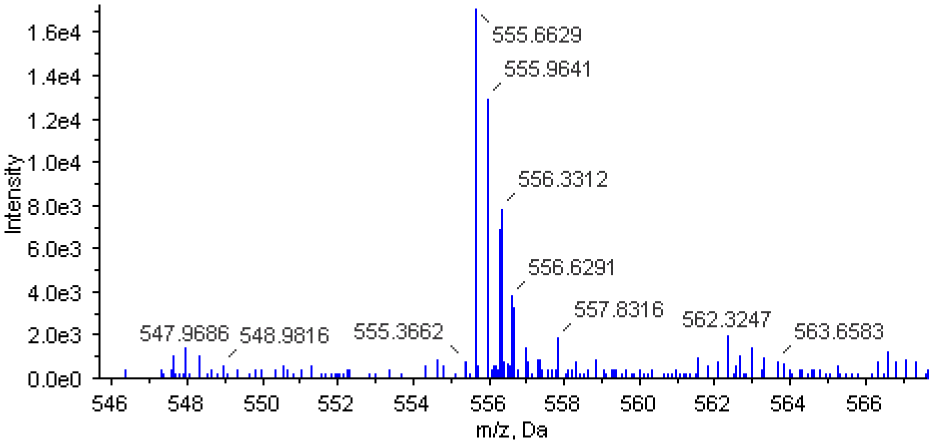
Seq Cov %: 9.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 35

116: 114=E5TL: D5TL=0. 16

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSDEVVLLDFWPSPFGMRVR**IALAEK**GIKYEYKEEDLRNK**SPLLLQMNPVHK**KIPVLIHNGKPICESLI
AVQYIEEVWNDRNPLLPSDPYQRAQTRFWADYVDKKIYDLGRKIWTSKGEEKEAAK**KEFIEALK**LLEEQ
LGDKTYFGGDNLGFVDIALVPFYTWFKAYETFGTLNIESECPKFIAWAKRCLQKESVAKSLPDQQKVYE
FIMDLRKKLGIE

Protein No.: I-907

Protein name and Species:

Cysteine synthase OS=Medicago truncatula PE=2 SV=1

Accession: tr|B7FKU7|B7FKU7_MEDTR

Unused ProtScore: 2.5

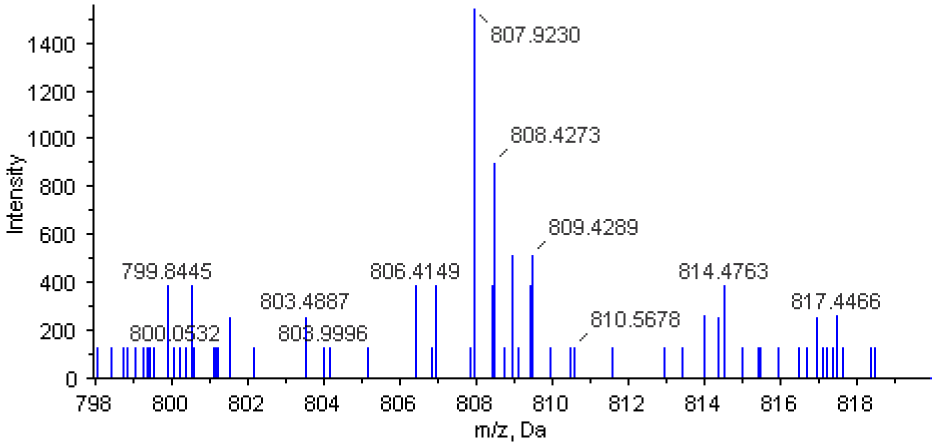
Seq Cov %: 19.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 59

116: 114=E5TL: D5TL=1. 07

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAVERSGIAK**DVTELIGK**TPLVYLNRLADGCVARVAAK**LELMEPCSSVK**DR**IGYSMIADAEEK**GLITPG
QSVLIEPTSGNTGIGLAFMAAAKGYK**LIITMPASMSLER**RIILLAFGAELVLTDPAKGMKGAVQK**AEEL
LAK****TPNAYILQQFENPANPK**VHYETTGPEIWKGTDGKIDAFVSGIGTGGTITGAGKYLKEQNSNIKLIG
VEPVESPVLSGGKPGPHKIQGIGAGFVPGVLEVNLIDEVVQISSDEAIETAK**LLALK**EGLFVGISSGAA
AAAAIKIAK**RPENAGK****LIVVVFPSFGER**YLSSVLFESVRREAETMTFEP

Protein No.: I-914

Protein name and Species:

trehalose-phosphate synthase [UDP-forming] 9 [Arabidopsis thaliana] OS=Arabidopsis lyrata subsp. lyrata GN=ARALYDRAFT_889930 PE=4 SV=1

Accession: tr|D7KNJ9|D7KNJ9_ARALL

Unused ProtScore: 2.48

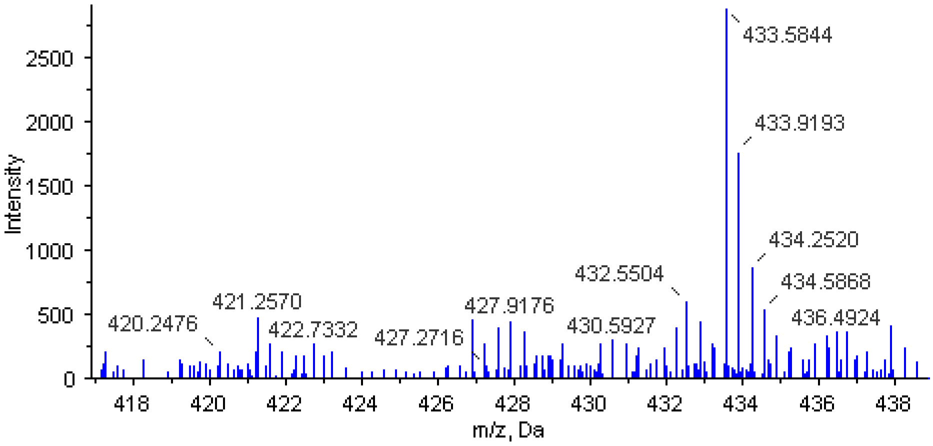
Seq Cov %: 3.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1. 89

116: 114=E5TL: D5TL=1. 96

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MVSRSCANFIDLASWDLLDFPQTQRALPRVMTVPGIISELDGGYSDGSSDVNSSSSSRERKIIVANMLP
LQAKRDTESGQWCFSWDEDSLLLQLRDGFSSDTEFVYIGSLNADIGTSEQEEVSHKLLLDFNCVPTFLP
KEMQEKFYLGFCKHHLWPLFHYMLPMFPDHGDRFDRRLWQAYVSANKIFSDRVMEVINPEEDYVWIHDY
HLMVLPTFLRKRFNRIKLGFFLHSPFPSSEIYRTLPVRDDLLRGLLNCDLIGFHTFDYARHFLSCCSRM
LGLDYESKR**GHIGLDYFGR**TVFIKILPVGIHMGRLESVLNLPSTAAKMKEIQEQFKGKKLILGVDDMDI
FKGISLKLIAMERLFETYWHMRGKLVLIQIVNPARATGKDVEEAKRETYSTVKRINERYGSAGYQPVIL
IDRLVPRYEKTAYYAMADCCLVNAVRDGMNLVPYKYIICRQGTPGMDKAMGISHDSPRT**SMLVVSEFIG**
CSPSLSGAIRVNPWDVDAVSEAVNLALTMGETEKRLRHEKHYHYVSTHDVGYWAKSFMQDLERACREHY
NKRCWGIGFGLSFRVLSLSPSFRKLSIDHIVSTYRTTQRRAIFLDYDGTLVPESSIIKTPNAEVLSVLK
SLCGDPKNTVFVVSGRGWESLSDWLSPCENLGIAAEHGYFIRWSSKREWETCYSSAEAEWKTMVEPVMR
SYMDATDGSTIEFKESALVWHHQEADPDFGACQAKELLDHLESVLANEPVVVKRGQHIVEVKPQGVSKG
LAVEKVIHRMVEDGNPPDMVMCIGDDRSDEDMFESILSTVTNPDLPMPPEIFACTVGRKPSKAKYFLDD
VSDVLKLLGGLAAASSSRKPEDQQQSSSLHTQVAFESII

Protein No.: I-921

Protein name and Species:

Adaptin ear-binding coat-associated protein, putative OS=Ricinus communis GN=RCOM_0553580 PE=4 SV=1

Accession: tr|B9SGK0|B9SGK0_RICCO

Unused ProtScore: 2.45

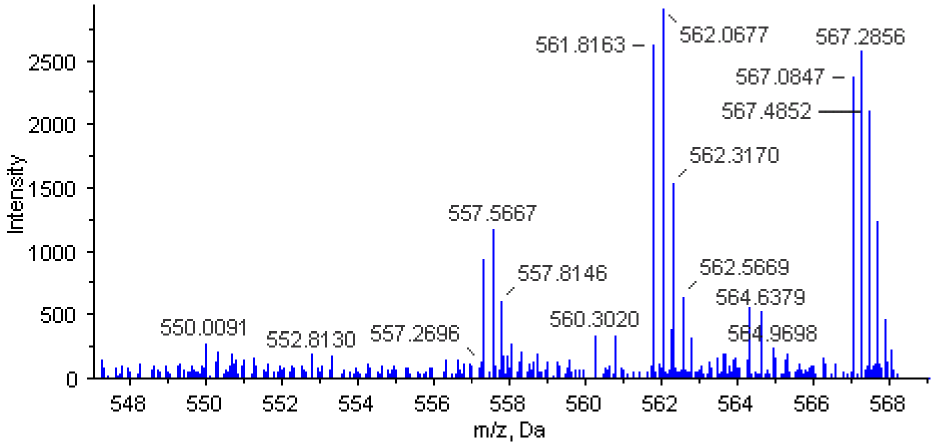
Seq Cov %: 6.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 27

116: 114=E5TL: D5TL=0. 99

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MLRKHLGPVHSPISSQPPPVSDDSIILPQPEAVLDRRVIQKGKYRPKSDVLIKWKGAPREDATWENEWR
FTKSYLDYLNPFHAYDEGNLSWMAAAEAEPATMSMVRRAIPNASSLEEGNRVLRGNWLKTIEQHHQQYS
GKSIISDILDVGCSVGVSTRFLADKFPLAKVTGLDLSPHFLSVAQFKEKKGAPRKNPINWIHANGEDTG
LPSKSYDLVTIAFVVHECPERAINGLLREAYRLLRPGGTIALTDSSPKSKILQIMEIEVKDLNDQEKET
EETEAIELVLFHVSECYVYLIPPRKSAASCRADEWNVNKWAWEGMLKVISKGEECIIKLEDKTTGELYA
RAFLR**DGEPHPVEPVIDSSR**YFVLR**IEENIGGR**LRHAFIGIGFRERTEAYDFQAALHDHMKYLNKKK**TA**
EEMEQHFQKTSTVDYSLKEGETLVLQIKNKSGSGMKSKILDQGLNNLSLEEKGEQKELILGIKLPPPPP
APVSPVTSPRFPSDLPPKISLDGTSIDNSPRLRKEEAKEQHSPDNESTQDIPDDDFGDFQAAG

Protein No.: I-929

Protein name and Species:

Putative uncharacterized protein OS=Ricinus communis GN=RCOM_0186330 PE=4 SV=1

Accession: tr|B9T8C2|B9T8C2_RICCO

Unused ProtScore: 2.41

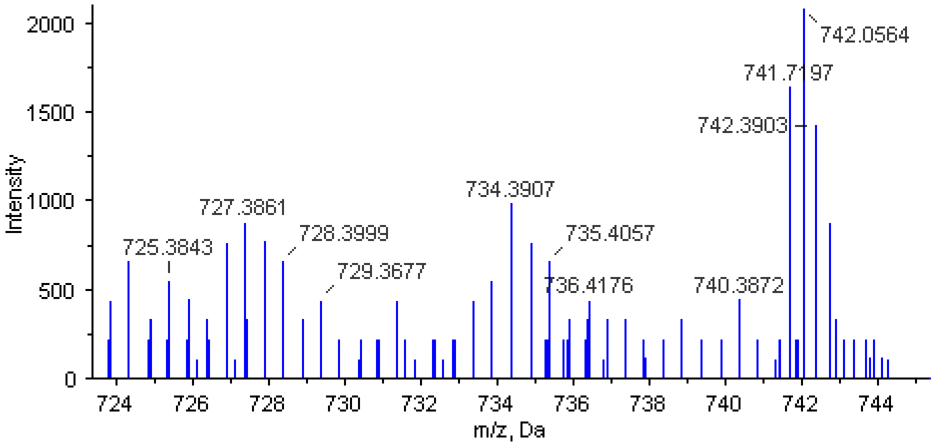
Seq Cov %: 6.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 61

116: 114=E5TL: D5TL=0. 29

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSMLDSFFNKGFKATKCKTLLKLTIPRIKLLRNRREIQIKQMRRDIAKLLETGQEATARIRVEHIIREE
NMMAAQEILELFCELISVRLPIIEAQRECPLDLK**EAISSICFAAPR**CADLQELLQVQMLFVSKYGREFV
AAATELMPECGVNRQLIELLSVRAPSPDVKLKLLKEIAEEHELDWDPAASETELLKKHEDLLNGPTQFV
SGSKLPLPEEKHEEALNSVPDQAHNEQPDSDSDFETLDFPEVPKVALRPSANTASAPEMLPIPPAAQRG
IEHEPSNLSANYENLAQECHLENEDLTEEEPVATKDGTANIVDAKEEKQFLPFISPPVSSTSFSTRPST
SPPISRTK**SEFNVDLQDVIAAAQAAAETAER**AAAAARLAATLAQARISVLTKKNSEKFPECSDENPFHV
DTPDQSPTTEKPHFGHQHSFDGPSGVSSYLHLHQQHEDHQPSELHDLPSFEKLKMEYDSPPSDLVHEQQ
SVRHQPQRLPSMDDDAYFSYPNLFTSQNPNLGSSAQSGTGNSHSAHDV

Protein No.: I-938

Protein name and Species:

Glutathione-s-transferase theta (Fragment) OS=Jatropha curcas PE=2 SV=1

Accession: tr|D6BRD9|D6BRD9_9ROSI

Unused ProtScore: 2.37

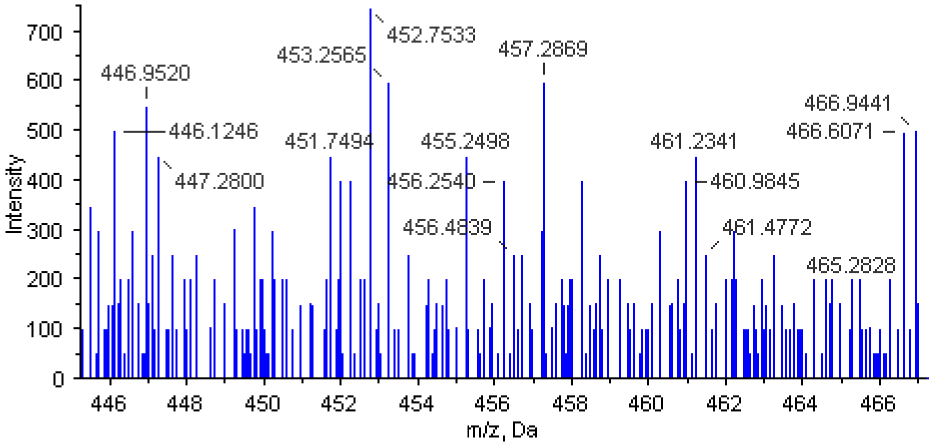
Seq Cov %: 15.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2. 27

116: 114=E5TL: D5TL=2. 11

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAVIKVHGNPISTATQRVLATLYEKDLEFEFVHIDLATGEHKR**EPFISLNPFGQVPALEHGDLK**LFESR
AITQYITHENPDKGTQLLCPGKVKMPILTVWMEVEAQKFEPAASKLNWEVFLKPIFGLTTDSAAVEANE
AELSKVLDVYEARLAQSKYLACDCFTLVDLHHLPNLQLLLLTQSKKLIESRPHVSAWAADITARPAWAK
VLAMQRV

Protein No.: I-944

Protein name and Species:

Fructose-bisphosphate aldolase OS=Arabidopsis lyrata subsp. lyrata GN=ARALYDRAFT_482625 PE=3 SV=1

Accession: tr|D7LJ40|D7LJ40_ARALL

Unused ProtScore: 2.35

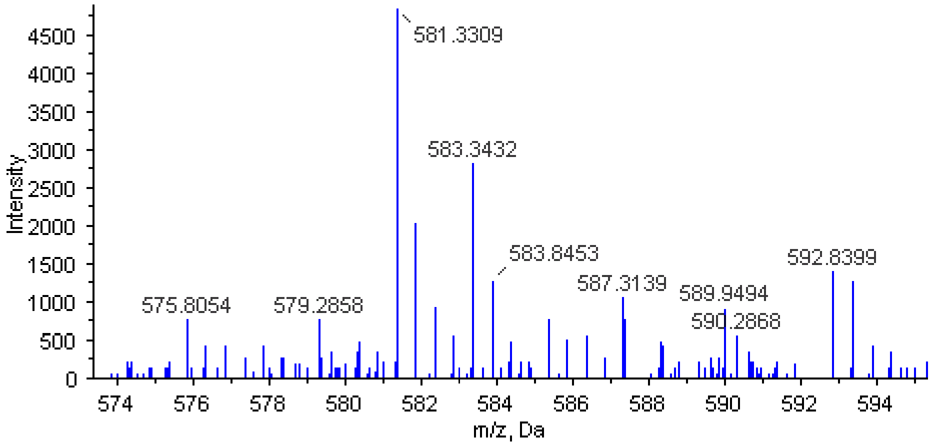
Seq Cov %: 28.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 52

116: 114=E5TL: D5TL=0. 22

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSCFTTK**FADELIANAAYIGTPGKGILAADESTGTIGKRLASINVENVESNRR**ALRELLFTTPGALPCL
SGVILFEETLYQKSSNGTPFVDMLKSAGVLPGIKVDKGTVELAGTNAE**TTTQGLDGLGDR**CKK**YYEAGA**
RFAKWRAVLKIGQNEPSELAIHENAYGLARYAVICQENGLVPIVEPEILVDGSHDIHKCAAVTER**VLAA**
CYKALSDHHVLLEGTLLKPNMVTPGSESA**KVAPEVIAEHTVR**ALQR**TVPAAVPAIVFLSGGQSEEEATR**
NLNAMNKLKTKKPW**SLSFSFGRALQQSTLK**TWGGKEENVK**KAQEAFLVR**CK**ANSEATLGTYK**GDAKLGE
GAAESLHVKDYKY

Protein No.: I-945

Protein name and Species:

coatomer subunit delta OS=Populus trichocarpa GN=POPTRDRAFT_824854 PE=4 SV=1

Accession: tr|B9ICR4|B9ICR4_POPTR

Unused ProtScore: 2.35

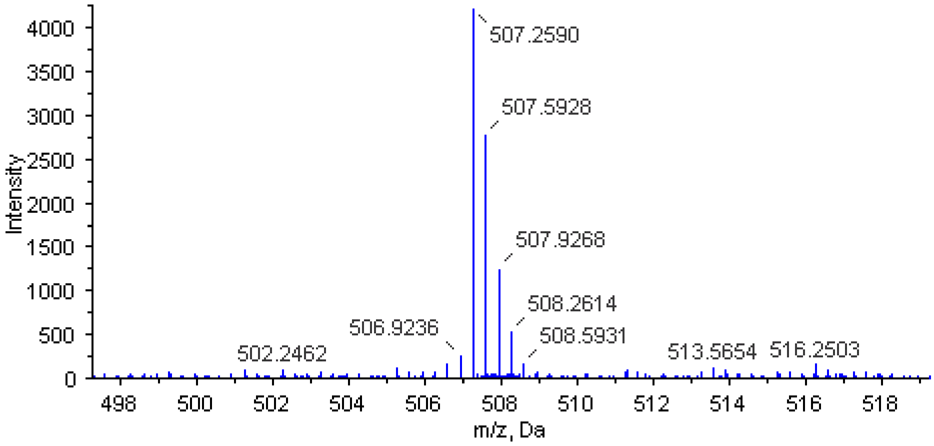
Seq Cov %: 5.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 20

116: 114=E5TL: D5TL=0. 47

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MVVLAASIVSKNGKVLVSRQFVDMSRIR**IEGLLAAFPK**LIGSGK**QHTYVETENVR**YVYQPIEAMYLLLV
TNKQSNILEDLDTLRLLSKLVPEYTMSLDEEGICQTAFELIFAFDEVISLGHK**ENVTVAQVKQYCEMES**
HEEKLHKLVLQNKIDETKRRMKEEASKIDQMKIEKNRGNKGGFMSSMGSGRIESSFNDMSISSGGGGGF
GSGSGFGLTSDVDSFSSKPKGRQPSSATAPPKGLGMKLGKTQR**TNQFLESLK**AEGEMIVEDVQPSKSTQ
YTSAAQKLTDPVTLTAEEKLNVTLKRDGGMSHFDVQGHLSLQILNQEDGLIQVQIETGGNPGVIFKTHP
NVNKELFANENILGLRDPSRPFPACQTGDAGVGLLKWRMQSVDESMVPLTINCWPSESGNETYVSIEYE
ASSMFDLRNVVIAVPLPALREAPNVRQIDGEWRYDARNSILEWSILLIDNSNRSGSMEFVVPSGDSSAF
FPITVQ**FSATSTYSELK**VANILPLKGGAPPKFSQRTQLITENYQVV

Protein No.: I-948

Protein name and Species:

Adenylyl cyclase-associated protein OS=Populus trichocarpa GN=POPTRDRAFT_556459 PE=3 SV=1

Accession: tr|B9H0Q2|B9H0Q2_POPTR

Unused ProtScore: 2.34

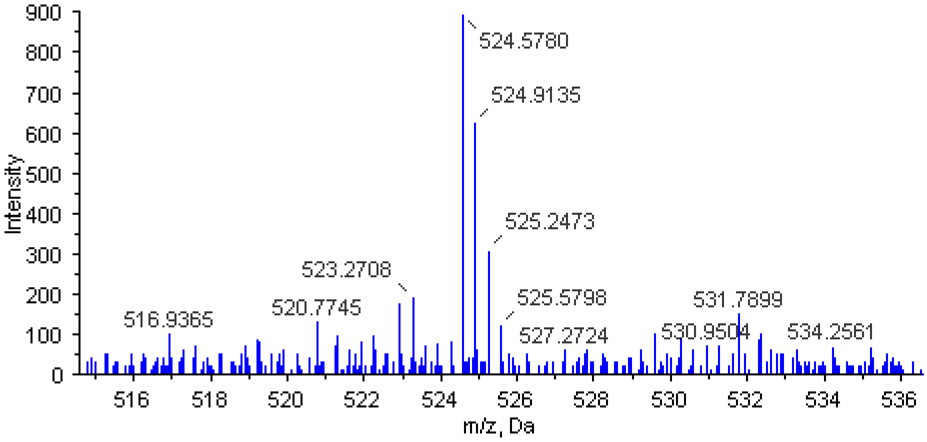
Seq Cov %: 8.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 40

116: 114=E5TL: D5TL=0. 54

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MEERLMARLESAVARLEALSLRGGSVAGSGGDDASATDPSIVAFEDFMGAYLGRVSSAGEKIGGQVLAV
TKILEQALNMQKELLIKIKQTQKPDLAGLAEFLKPLNEVIMKANSMTEGRRSDFFNHLKAAADSSTALA
WIAYTGKDCGMSMPIAHVEESWQMAEFYNNK**ILVEYK**SKDPNHVEWAKALK**ELYLPGLR**DYVKSHYPLG
PVWSATAKAKAAAPSAPAPPPPPPASLFTSESSSPSSSKPKVGMAAVFQEISSGKPVTSGLRKVTDNMK
TKNRADRTGVVGASEKESRTSSPSFSKAGPPK**LELQMGR**KWVVENQIGRKNLVIDDCDAK**QSVYIFGCK**
DSVLQVQGKVNNITIDKCTKMGVVFTDVVAACEIVNCSGVEVQCQGSAPTISVDNTGGCQLYLSKGSLG
ASITTAKSSEINILVPGAEPDGDLVEHALPQQFIHTFK**DGQFETTPVSHSGG**

Protein No.: I-949

Protein name and Species:

Annexin-like protein RJ4 OS=Fragaria ananassa PE=2 SV=2

Accession: sp|P51074|ANX4_FRAAN

Unused ProtScore: 2.34

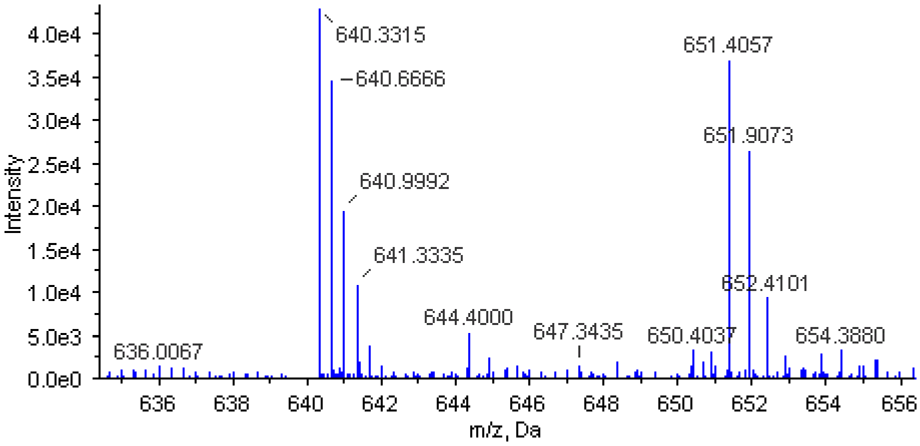
Seq Cov %: 6.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 09

116: 114=E5TL: D5TL=0. 37

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MATLVSPPNFCAKEDAEALRKSVKGWGTNEKAIISILGHRNAGQRKEIRAAYEQLYQEDLLKPLESELS
GDFEKAVYRWTLDPADR**DAVLANVAIK**KSTDVYNVIIEISCIHSPEELLAVRRAYQLRYKHSVEEDLAA
HTTGDIR**KLLVALVTAYR**YDGHEINAKLAN**SEADILHDAIK**DKAFNHEEIIRILSTRSKTQLMATFNKY
RDDQGISISKNLLEEGANDFQKALHTAIRCLNDPKKYFEKVLRNAIKR**VGTDEDALTRVIVTR**AERDLR
DIKEVYYKKNSVPLEQAVAKDTSGDYKAFLLTLLGKED

Protein No.: I-952

Protein name and Species:

Fructose-bisphosphate aldolase OS=Codonopsis lanceolata PE=2 SV=1

Accession: tr|Q2WFK8|Q2WFK8_9ASTR

Unused ProtScore: 2.33

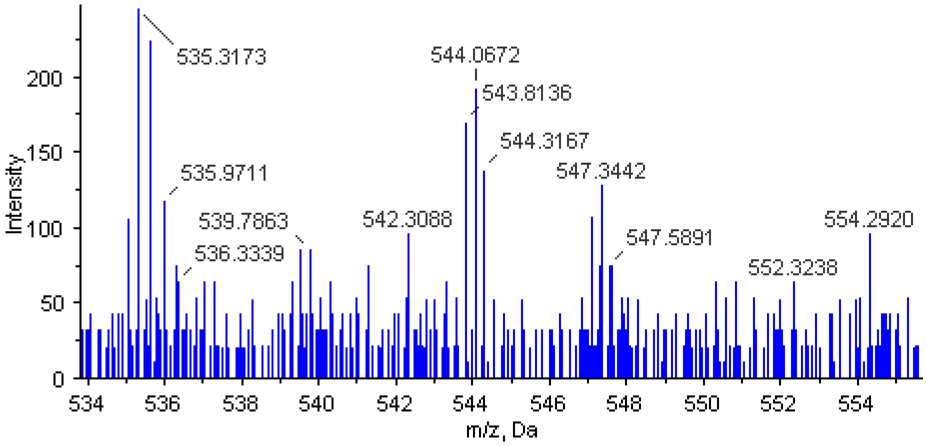
Seq Cov %: 23.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 47

116: 114=E5TL: D5TL=0. 33

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSCYKGK**YADELIANATYIGTPGKGILAADESTGTIGKR**LSSINVENIESNRWALRELLFCTPGALQYL
SGVILFEETLYQKTAAGKPFVDVLKENGVLPGIKVDKGTVVLAGTNGETTTQGLDGLGARCAQYYAAGA
RFAKWRAVLN**IGPNEPSQLAINENANGLAR**YAIICQENGLVPIVEPEILVDGAHDIAKCADVTER**VLAA**
CYKALNDHHVLLEGTLLKPNMVTPGSDSAKVAPEVVAEYTIRALQRTMPAAVPAVVFLSGGQSEEQATV
NLNAINKYKGKKPWSLTFSFGR**ALQQSTLK**AWAGKEENVAKAQAAFLARCKANSEATLGTYEGGASLSE
GAAESLHVKDYKY

Protein No.: I-975

Protein name and Species:

dolichol-phosphate mannosyltransferase OS=Populus trichocarpa GN=POPTRDRAFT_801608 PE=4 SV=1

Accession: tr|B9H5H4|B9H5H4_POPTR

Unused ProtScore: 2.28

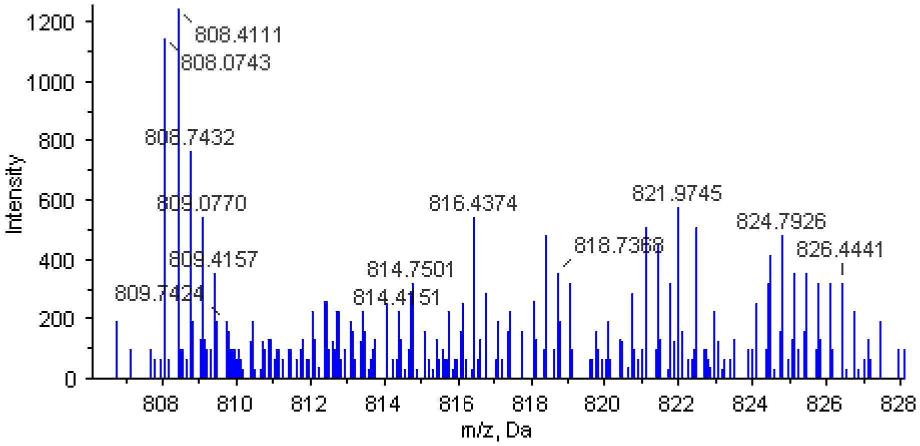
Seq Cov %: 14.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1. 77

116: 114=E5TL: D5TL=2. 07

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MEKNNRYSIIVPTYNERLNIALIVYLIFKHLQDVEFEIIVVDDGSPDGTQEVVKQLQKVYGEDRILLRP
RAKKLGLGTAYIHGLKHASGNFVVIMDADLSHHPKYLPSFIKK**QLETGASIVTGTR**YVKGGGVHGWNLM
RKLTSR**GANVLAQTLLWPGVSDLTGSFR**LYKK**SVLEDIISSVVSK**GYVFQMEMIVRASRKGYQIEEVPI
TFVDRVFGSSK**LGGSEIVEYLK**GLAYLLVTT

Protein No.: I-981

Protein name and Species:

Predicted protein OS=Populus trichocarpa GN=POPTRDRAFT_818483 PE=4 SV=1

Accession: tr|B9H739|B9H739_POPTR

Unused ProtScore: 2.26

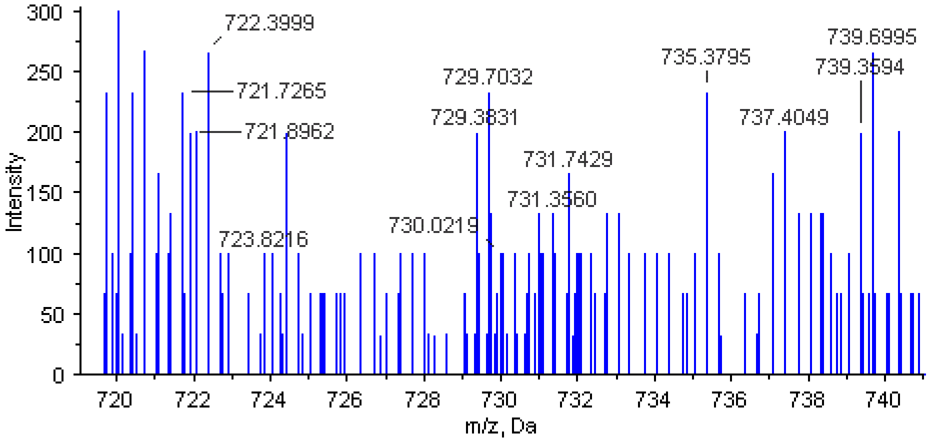
Seq Cov %: 9.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 61

116: 114=E5TL: D5TL=1. 05

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MERSTPVRKPHTSTADLLTWSETPPPDSPSVGSAPRPTRSHQPSDGISK**VVFGGQVTEEEFESLNK**RKP
CSGYKMKEMTGSGIFAANGEDDTAESGSANPIPNSKTGLRMYQQAIAGISHISFAEDDSVSPKKPTTLP
EVAKQRELSGTLESESDAKLKKQISGAKSKELSGHDIFAPPPEILPRPTTVRALALQESIQLGEPSPHD
PVGGQQPSEESVVKTAKKINNQK**FNELSGNDIFK**GDAPPSSAEKPLSVAKLREMSGNDIFADGKVESRD
FLGGVRKPPGGESSIALV

Protein No.: I-982

Protein name and Species:

Phospholipase D OS=Fragaria ananassa PE=2 SV=1

Accession: **tr|Q533V0|Q533V0_FRAAN**

Unused ProtScore: **2.25**

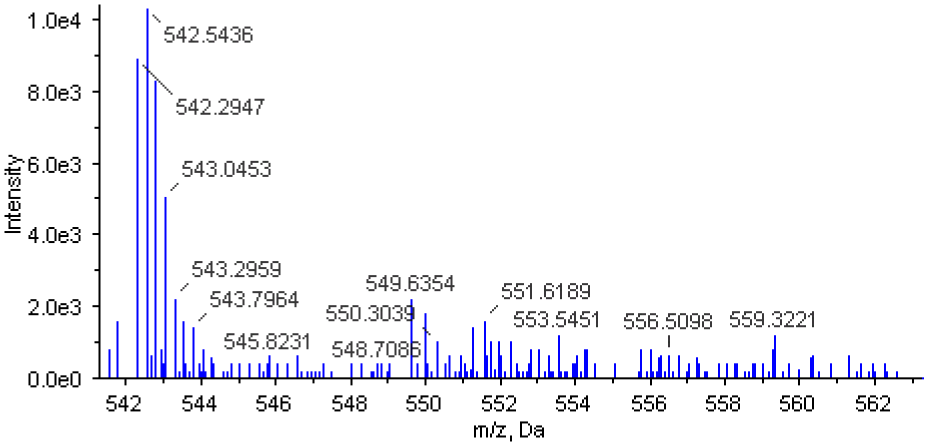
Seq Cov %: **11.6**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 29

116: 114=E5TL: D5TL=0. 24

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGDSAEHWLHGTLHATIYEVDKLHGSSGNFLRKITGKLEETVGLGKGVSKLYATVDLERARVGRTRVIE
KEPSNPNWSESFHIYCAHVAANVIFTVKESNPIGASLIGRAYVPVEQLIEGEEVDTWAKILDDKKNPVH
GEPKIHVKLQFFHVSKDRSWGQGIKSPKFPGVPFTFFSQRQGCRVSLFQDAHVPDKFIPK**IPLAGGK**YY
EPHRCWEDIFDAITNAKHLIYITGWSVYTEISLIRDSRRPK**SGGDITIGELLK**KKASEGVR**VLMLVWDD**
RTSVGLLKKDGLMATHDEETAQFFQNTDVNCVLCPRNPDGGGSIVQGAQISTMFTHHQKIVVVDSEMPN
GGSQSRR**IVSFVGGLDLCDGRYDTPFHSLFR**TLDTAHHDDFHQPNFTGASITKGGPREPWHDIHSRLEG
PIAWDVLFNFEQRWRKQGGKDVLVQLRELDNVIIPPSPVMFPDDHETWNVQLFR**SIDGGAAFGFPDSPE**
DAARAGLVSGKDNIIDR**SIQDAYIHAIR**RAKNFIYIENQYFLGSSFAWAADGIKPEDIGASHVIPRELS
LKIADKIANGERFTVYVVVPMWPEGIPESASVQAILDWQRRTMEMMYKDIKQALDKHGVEEDPR**NYLTF**
FCLGNREVKKDGEYEPSEAPEADSDYIRAQEARRFMIYVHTK**MMIVDDEYIIIGSANINQR**SMDGARDS
EIAMGAYQPHHLSVREPARGQIHGFRMALWYEPLGMLDETFLQPESVECIK**KVNQIADK**YWDLYSSETL
EHDLPGHLLRYPVGVTSEGEVTELPGFEFFPDTKARVLGAKSDYLPPILTT

Protein No.: I-990

Protein name and Species:

Malic enzyme OS=Populus trichocarpa GN=POPTRDRAFT_737670 PE=3 SV=1

Accession: tr|B9ILT5|B9ILT5_POPTR

Unused ProtScore: 2.23

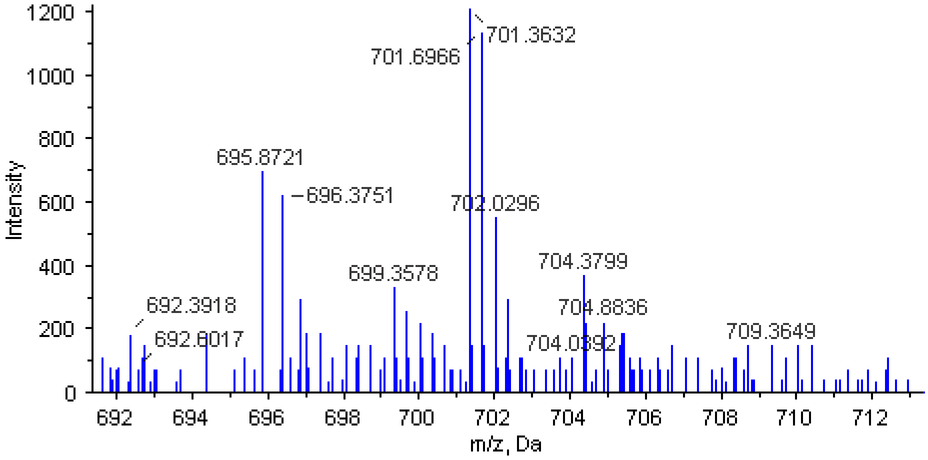
Seq Cov %: 7.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.59

116: 114=E5TL: D5TL=1.25

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MESTLKEMRDGASVLDMDPKSTVGGGVEDVYGEDRATEDQLVTPWTISVASGFTLLRDPQHNKGLAFTE
KERDAHYLRGLLPPATISQQLQEKKLMNTIRQYQLPLQKYTAMMELEERNERLFYKLLIDNVEELLPVV
YTPTVGEACQK**YGSIFK**RPQGLYISLKEKGKVLDVLKNWPQKSIQVIVVTDGER**ILGLGDLGCQGMGIP**
VGKLSLYTALGGVRPSACLPVTIDVGTNNEQLLKDEF**YIGLR**QKRATGQEYSELLHEFMTAVKQNYGEK
VLIQFEDFANHNAFDLLAKYGTTHLVFNDDIQGTAAVVLAGLISALKLLGGSLADHTFLFLGAGEAGTG
IAELIALEMSRRSKTPLEETRKKIWLTDSKGLIVSSRKESLQHFKKPWAHEHEPVKG**LLEVVK**AIKPTV
LIGTSGVGKTFTKEVIEAMASFNEKPLILALSNPTSQSECTAEEAYTWTKGK**AIFASGSPFDPVEYEGK**
VFVPGQSNNAYIFPGLGLGLVISGAIRVHDDMLLAAAEALAGQIKEEYLAKGLIYPPLSNIRKISVQ**IA**
ANVAAKAYELGLATRLPRPENLVKHAESCMYSPAYRYYR

Protein No.: I-993

Protein name and Species:

Signal recognition particle 68 kDa protein, putative OS=Ricinus communis GN=RCOM_1503780 PE=4 SV=1

Accession: tr|B9RA70|B9RA70_RICCO

Unused ProtScore: 2.23

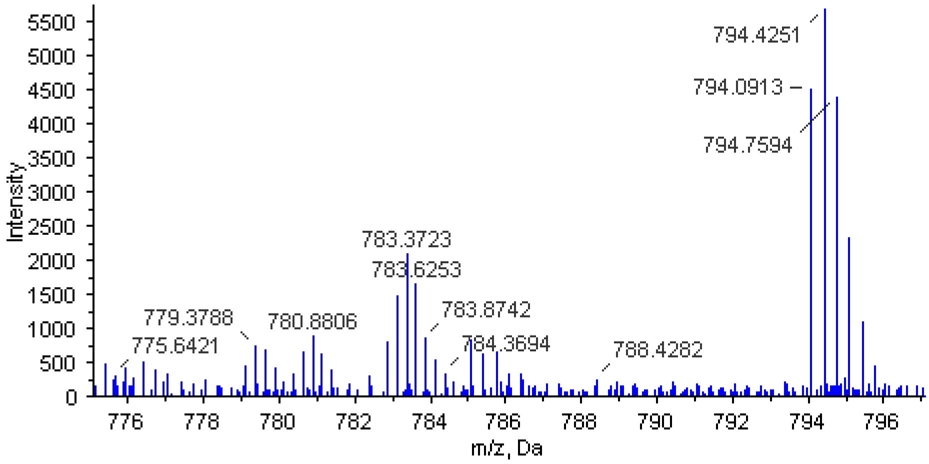
Seq Cov %: 6.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2. 91

116: 114=E5TL: D5TL=0.86

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAMDIDGPKSNNSEQISPRYSINVLQLLKSAQMQHGLRHGDYTRYRRYCTARLRRLYKSLKFTHGRGKY
TRRAITESTVTEVRFLHLVLYSAERAWSHAMEKRQLPDGPNARQRIYLIGRLRKAVQWANLFSQLCAAK
GDSRTSLEAEAYAAYMNGNLLFEQDRNWDTALKNFISARAVYEELGKYGDLENQVLCRERVEELEPSIR
YCRHKIGQSNLQTSDLLQIGEMEGPALDLFKTKLEAVMAEARSQQAASLTEFHWLGHKFPISNAKTRVA
ILKAQELEKDLHGSAADSLPAEKKLVVFDKIFAAYHEARSCIR**SDLVSAGNADSVKDDLSGLDK**AVSAV
LGQRTIERNQLLVSIAKSKFIKRRDDKNEKLTRPEELVR**LYDLLLQNTSDLSDLVSSGR**DTKPEEVAFS
EDCALRSLAFRAQRCFYLAKSYSLAGKRTEAYSLYCRARSLSENALQKFQSLNNTDEIMVKELKTLYNE
CRSNSCIEHASGIMEDEKAPENLSKKVSAISLSGGDKKVEKFLLEKLDVYESAVGDPHVKAPPRIEVFP
PAFQTIPRNPIILDLAYNYIDFPSLENRMKKDKKGFISRLWR

Protein No.: I-1002

Protein name and Species:

Hydrolase； Leukotriene A-4 hydrolase, putative OS=Ricinus communis GN=RCOM_1071200 PE=4 SV=1

Accession: tr|B9SD61|B9SD61_RICCO

Unused ProtScore: 2.2

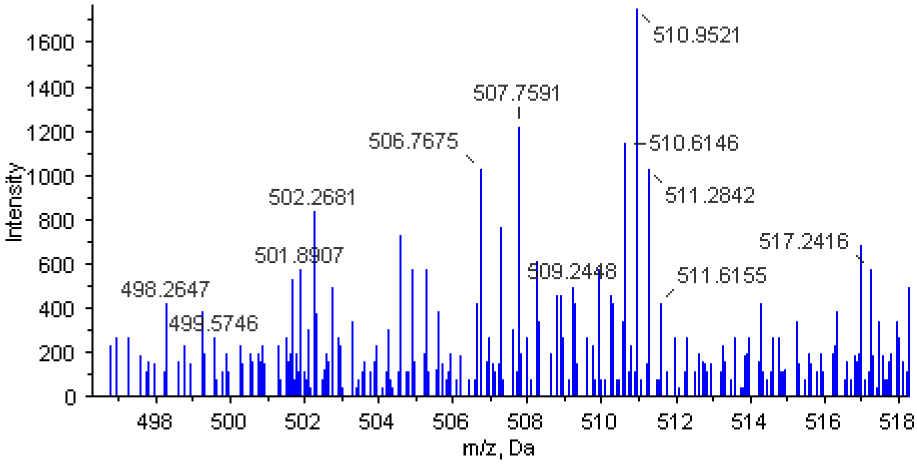
Seq Cov %: 5.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=6. 19

116: 114=E5TL: D5TL=3. 09

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAPVDPHSYTDSTHPLTTHISLSLYFDFSASTIHGTALFSLSTPHTGHISLDTRSLTVHKIADPVTRAL
IPFSLSPEIDPIKGCHLTLSLQNQSSFLILYSTSPSSSALQWLSPPQTFGKAQPFVYTQCQSIHARSVF
PCQDTPAARICYSARLNIPRQLAAVMSARHCHRRAPVSGDVENSIDEGTDFDLKSIWCGEGRVIEEFVM
EQPIPPYLFAF**AVGELGFR**EVGPRTRIYSENVGDVLDAAAREFSGTEEMIRQGEKLFGEYEWERFDLLV
LPPSFPYGGMENPRMVFLTPTVIKGDSSGAQVVAHELAHSWTGNLITNTNNNHFWLNEGFTTYAERRIV
EVVQGEDKAVLNIGIGWRGLNEEVERFKDNMEFTKLK**TNQENADPDDMYSQVPYEK**GFQFLWRIERQIG
RPAFDEFLKKYIATFKFKSIDTDMFLDFLKANVPGIEKDIDLQLWTEGTGIPPDAYEPVSNVYTKIISL
AHEFKLGTMPGEVEVADWQGQEWELYLENLPK**SVEASQIIALDAR**YRLSESKDYEVKVAFLELAILSGC
KDYFSAVEKTLKEVGRMKYLRPLYTALVQGTGKEEEKILAKRVFAEARDCYHPIAQGVVEAIFAKHL

Protein No.: I-1008

Protein name and Species:

Alanine aminotransferase [Medicago truncatula] OS=Medicago truncatula PE=2 SV=1

Accession: tr|B7FM77|B7FM77_MEDTR

Unused ProtScore: 2.19

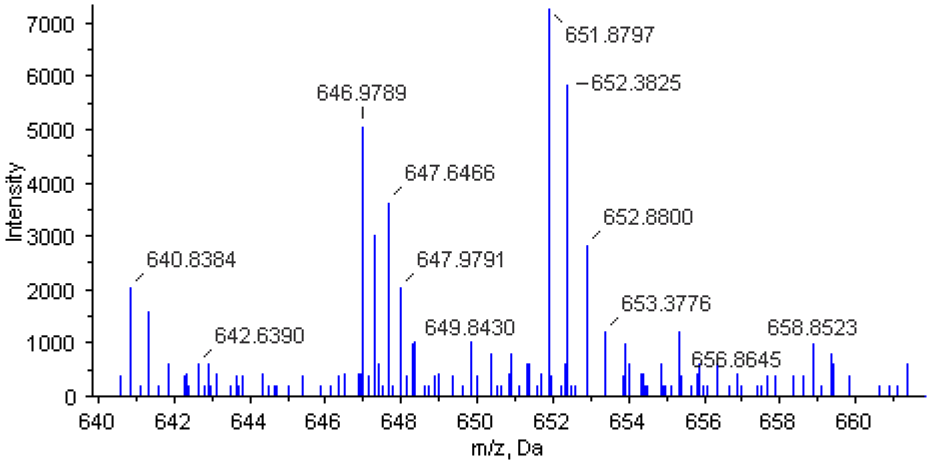
Seq Cov %: 5.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=5. 06

116: 114=E5TL: D5TL=1. 54

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MRKSAADRFRHLFNRSLVFVRNQNQQYHHPSPLRSLSSMASDSPFPVTAQNINPQVLKCQYAVRGEIVT
LAQNLQKALQANPDAHSFDEIIYCNIGNPQSLGQQPITFFREVLALCDYPALLDKSETQGLFSADSIER
AWQLVDQIPGRATGAYSHSQGIQGLRDTIAAGIEERDGFPCNANDIFLTDGASPAVHMMMQLLIRSEKD
GILCPIPQYPLYSASITLHGGHLVPYYLDEATGWGLEISELKKQLEEAKSKGISVRALAAINPGNPTGQ
VLAEDNQR**AIVEFCKQEGLVLLADEVYQENVYVPEK**KFHSFKKVSRSMGYGDNDICLVSFQSVSKGYHG
ECGKR**GGYMEVTGFSPDVR**EQIYKVASANLCSNITGQILASLIMSPPKVGDESYESFMAERGAILSSLT
TRAKALEEALNKLEGVTCNK**AEGAMYLFPR**IRLPEKAIKAAEAEKSAPDAFYCKRLLNATGIVVVPGSG
FGQVPGTWHFRCTILPQEDRIPAIVTRLTEFHQKFMDEFRD

Protein No.: I-1016

Protein name and Species:

Ras-related protein Rab11B OS=Nicotiana tabacum GN=RAB11B PE=2 SV=1

Accession: sp|Q40521|RB11B_TOBAC

Unused ProtScore: 2.18

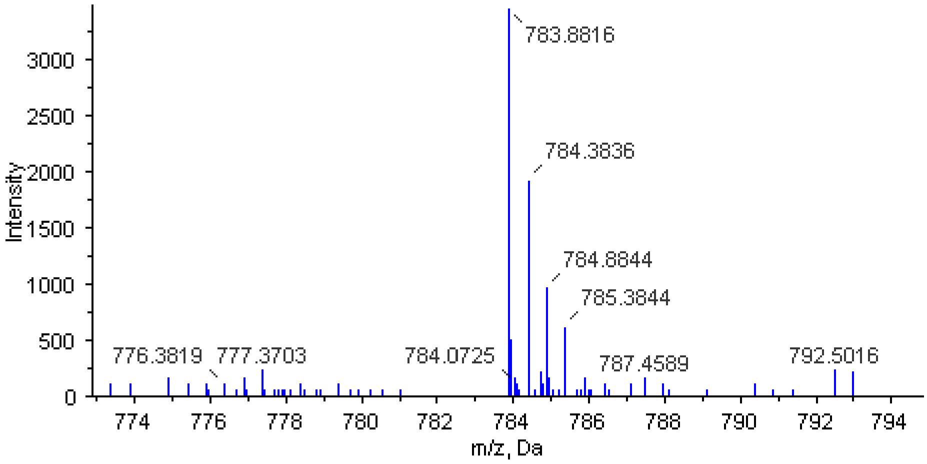
Seq Cov %: 33.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 35

116: 114=E5TL: D5TL=1. 21

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAGGYR**AEDDYDYLFKLVLIGDSGVGK**SNLLSRFSRNEFNLESK**STIGVEFATR**SIRVDDKIVK**AQIWD TAGQER**YR**AITSAYYR**GAVGALVVYDITR**HVTFENVER**WLKELRDHTDQNIVIMLVGNKADLRHLRAVS TEDAKAFAERENTFFMETSALESLNVENAFTEVLTEIYKVVCR**KALEVGDDPAALPK**GQTINVGKDDVS AVKKVGCCSS

Protein No.: I-1019

Protein name and Species:

guanine nucleotide-binding protein subunit beta OS=Vitis vinifera GN=VIT_17s0000g02750 PE=4 SV=1

Accession: tr|A5BV59|A5BV59_VITVI

Unused ProtScore: 2.17

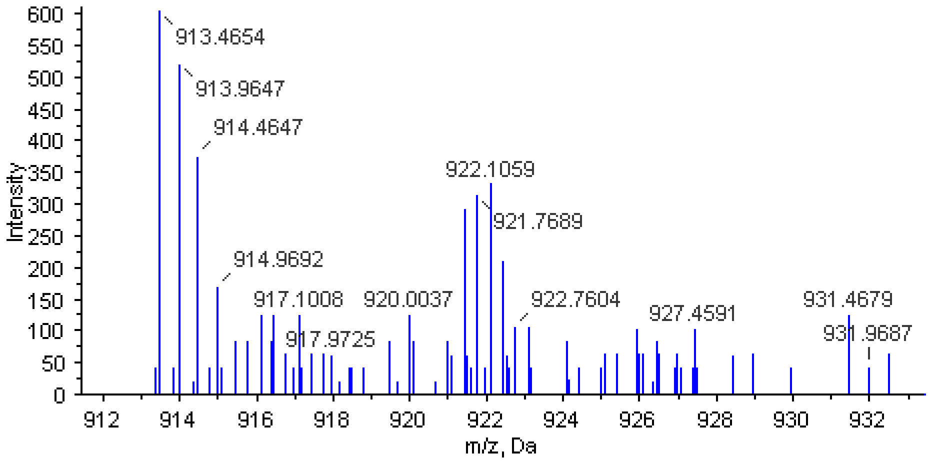
Seq Cov %: 12.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1. 67

116: 114=E5TL: D5TL=0. 30

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAETLVLRGTMRAHTDMVTAIATPIDNSDMIVTSSRDKSIILWHLTKDDK**TYGVPR**RRLTGHSHFVQDV
VLSSDGQFALSGSWDGELRLWDLAAGTSARRFVGHTKDVLSVAFSVDNRQIVSASRDRTIKLWNTLGEC
KYTIQDADAHSDWVSCVRFSPNNLQPTIVSASWDRTVKVWNLTNCKLR**ATLAGHGGYVNTVAVSPDGSL**
CASGGKDGVILLWDLAEGKRLYSLDAGAIIHALCFSPNRYWLCAATEQSIKIWDLESK**SIVEDLK**VDLK
TEAEKSEDTTTTAKKKGKIIYCTSLSWSADGSTLFSGYTDGVVRVWGIGRY

Protein No.: I-1026

Protein name and Species:

Indole-3-acetic acid-amido synthetase GH3.5, putative OS=Ricinus communis GN=RCOM_0236810 PE=4 SV=1

Accession: tr|B9T6N8|B9T6N8_RICCO

Unused ProtScore: 2.15

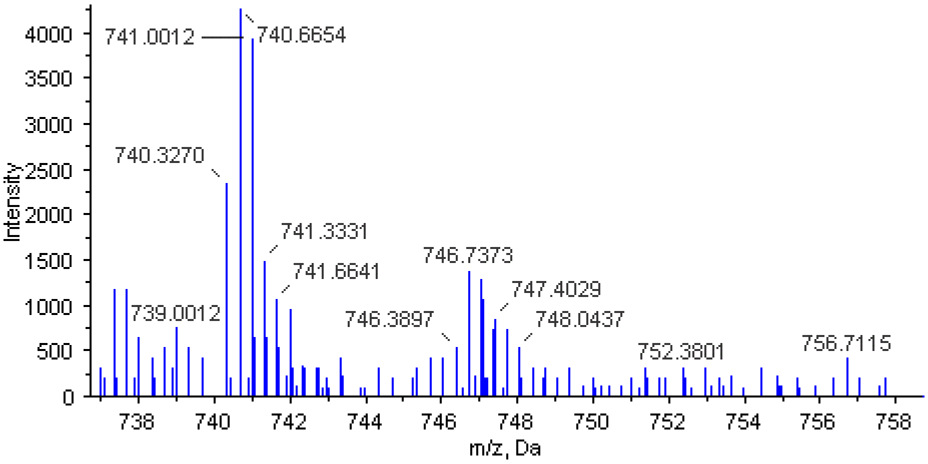
Seq Cov %: 3.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2. 38

116: 114=E5TL: D5TL=1. 60

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MTKNAERVQKETLKK**ILEENGSAEYLQNLGLDGR**TDPESFKICVPICTHGDLEPYIQRIADGDSSPVLT
GKPITTISLSSGTTQGKPKYVPFTDQLLDNTLQIFRTSFAYRNREFPLENGKALEFVFSSKQGKTK**GGL**
AAGTATTNLFRNPNYKTALEELQFKSCSPREVIFGSDFHQSLYCHLLCGLIFREDIQFVFSTFAHSIVL
AFRTFEQVWEELCDDIRNGELSSRITAPSIRTAMSHLLKPNAELADLIHTKCSGLSNWYGLIPELFPNA
KYIYGIMTGSMEPYLKKLRHYAGELPLLSADYGASEGWIAANVNPLLPPELATFAVLPDIGYFEFIPLR
RNGDHIYSEPKPIGLSDVKIGEEYEILVTNFAGFYRYRLGDVVKVMGFHNSTPELKFVCRRSLLLSINI
DKNTEK**DLQLVVEEAAK**LLADEKLEVVDFSSLADRSTDPGHYVIFWEISGEPTAEVLQECCNCLDR**SFL**
DAGYVTSRKVKAIGPLELRVVHRGTFQKILDHYLGLGAAVSQFKTPRCVGPANNVVSQILSNNVAKSYV
STAF

Protein No.: I-1029

Protein name and Species:

Vesicle transport protein-lik OS=Populus trichocarpa GN=POPTRDRAFT_584135 PE=4 SV=1

Accession: **tr|B9N7F9|B9N7F9_POPTR**

Unused ProtScore: **2.15**

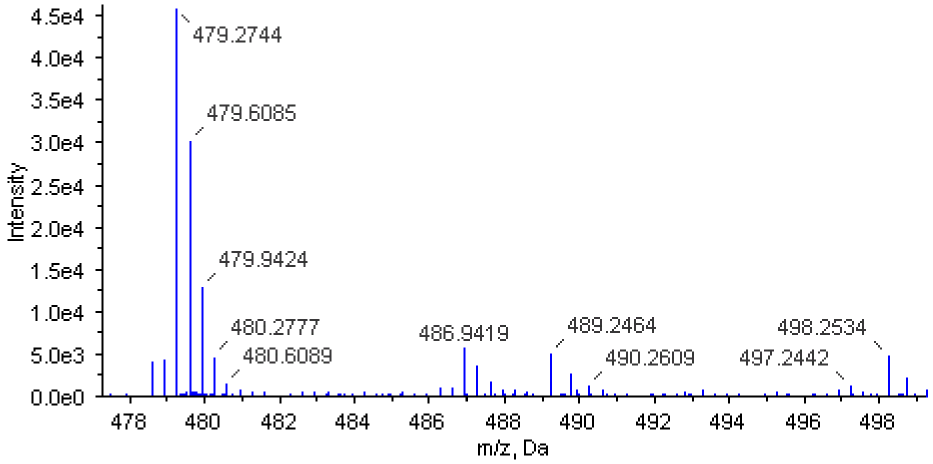
Seq Cov %: **11.9**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1. 66

116: 114=E5TL: D5TL=1. 74

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MVKLTMIARVTDGLPLAEGLDDGRDVKDAEMYKQQVKALFKNLASGHNDASRMSVETGPYVFHYIIEGR
VCYLTMCDRSYPKKLAFQYLEDLKYEFERVNGAQIETAARPYAFIKFDTFIQKTKKLYQDTRTQRNVAK
LNDELYEVHQIMTRNVQEVLGVGEKLDQVSQMSSRLTSESRIYAEKARDLNRQALIRKWAPVAIVLGVV
FLLFWVKTKLW

Protein No.: I-1030

Protein name and Species:

Proteasome subunit alpha type OS=Populus trichocarpa GN=POPTRDRAFT_818935 PE=2 SV=1

Accession: tr|A9PCM5|A9PCM5_POPTR

Unused ProtScore: 2.14

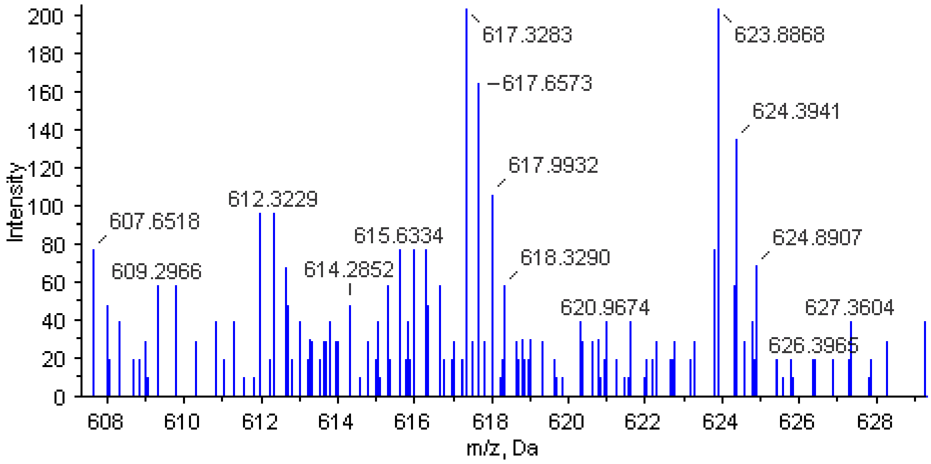
Seq Cov %: 10

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 27

116: 114=E5TL: D5TL=0. 38

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSRRYDSRTTIFSPEGRLYQVEYAMEAIGNAGSAIGILSKDGVVLVGEKKVTSKLLQTSTSTEKMYKID
DHVACAVAGIMSDANILINTARIQAQRYTFAYQEPMPVEQLVQSLCDTKQGYTQFGGLRPFGVSFLFAG
WDKNYGFQLYMSDPSGNYSGWK**AGAIGANNQAAQSMLK**QDYKDEITR**EEAVQLALK**VLSKTMDSTSLTS
EKLELAEVFLSPSGNVKYQVCSPDVLSKLLVKFGVTQPAAETS

Protein No.: I-1037

Protein name and Species:

Aminoacyl-tRNA synthetase-like OS=Populus trichocarpa GN=POPTRDRAFT_552617 PE=3 SV=1

Accession: tr|B9GTA1|B9GTA1_POPTR

Unused ProtScore: 2.13

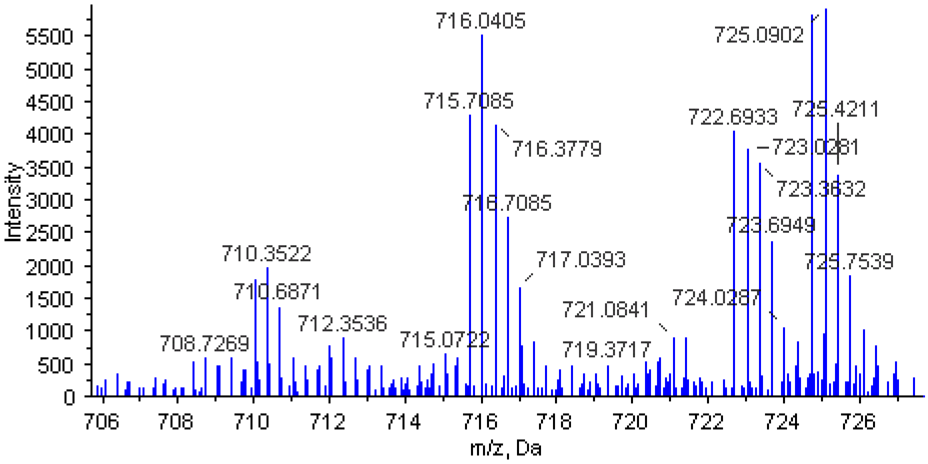
Seq Cov %: 18.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 28

116: 114=E5TL: D5TL=0. 22

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MADGKKKEVKKETGLGLTFKKEENFGEWYSEVVVNGEMIEYYDISGCYILRPWSMSIWETMQAFFDVEI
KKMKIK**NCYFPLFVSSSVLQK**EKDHIEGFAPEVAWVTKAGKSDLEVPVAIR**PTSETVMYPYFSK**WIRGH
RDLPLK**LNQWCNVVR**WEFSNPTPFIRSREFLWQEGHTAFASKQEADEEVLQILELYRR**IYEEFLAIPVI**
KGKKSEMEK**FAGGLYTTSVEAFIPNTGRGIQGATSHCLGQNFAKMFEINFENEK**GEKGMAWQNSWAYST
RTIGVMVMVHGDDKGLVLPPK**VASVQVIVVPVPYK**DADTQGIFDACAATVDTLCEAGIRAEADFRENYS
PGWKYSHWEMKGVPLRIEIGPKDLANNQVRAVRRDNAAKVDISRDSLMEKVKDMLDDIQQRLFDAAKQK
RDACIQVVKTWGEFKEALSQRKMILAPWCDEEEVERDVKERTRGEMGAAKSLCSPFDQPELPEGTACFA
SGKPAKKWTYWGRSY

Protein No.: I-1044

Protein name and Species:

Chorismate synthase OS=Vitis vinifera GN=VIT_13s0019g04190 PE=3 SV=1

Accession: tr|D7TMA3|D7TMA3_VITVI

Unused ProtScore: 2.12

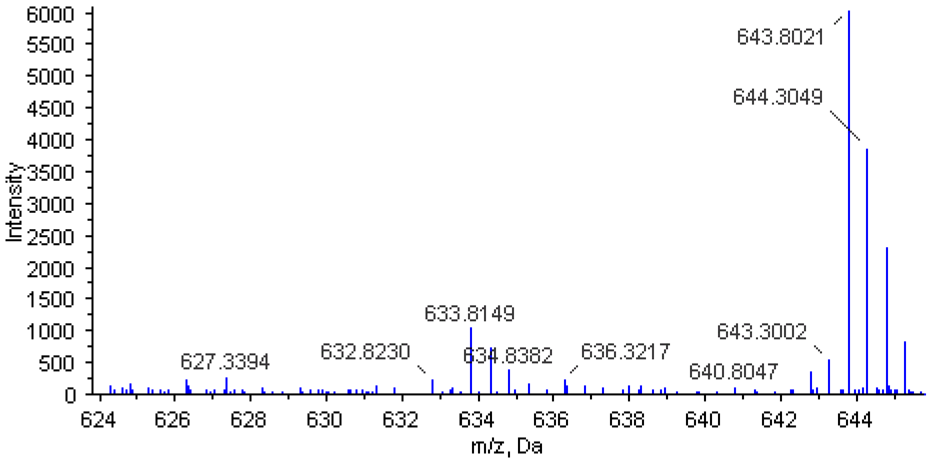
Seq Cov %: 6.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 60

116: 114=E5TL: D5TL=1. 09

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MASSLSSKPFLTSPSTDGASGFGSLRKLSFPSVRYAIRPTHRRTLEIQA**AGSTYGTYFR**VTTYGESHGG
GVGCIIDGCPPRLPLTEADMQIDLDRRRPGQSRITTPRKETDTCRIYSGVAEGMTTGSPIMVNVPNTDQ
RGNDYTEMSKAYRPSHADATYDFKYGVRSVQGGGRSSARETIGRVAAGAVAKKILKNFSGTEVLAYVSQ
VHKVVLPEDLVDHETLALDQIESNIVRCPDPEYAEKMIAAIDAVRVR**GDSVGGVVTCIVR**NIPRGLGSP
VFDK**LEAELAK**AALSLPATKGFEFGSGFAGTFMTGSEHNDEFFTDAHGRIRTRTNRSGGIQGGISNGEI
INIRIGFKPTSTIGKKQHTVTRDKQETELIARGRHDPCVVPRAVPMVEAAVALVLVDQLMAQYAQCELF
PINPALQEPLEFRDPELAGTHI

Protein No.: I-1049

Protein name and Species:

pantothenate kinase OS=Vitis vinifera GN=VIT_08s0007g07660 PE=4 SV=1

Accession: tr|F6HLA1|F6HLA1_VITVI

Unused ProtScore: 2.12

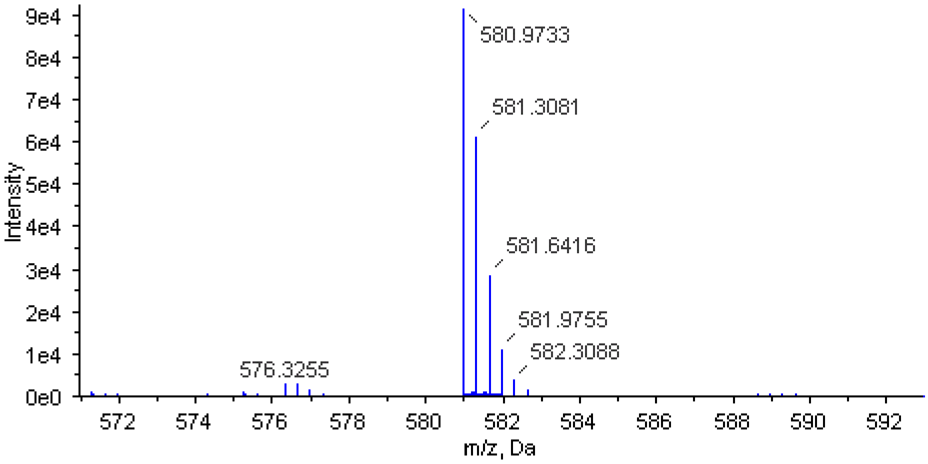
Seq Cov %: 3.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 47

116: 114=E5TL: D5TL=1. 01

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MEFPFGHHHHTHHHRPEYGAGEEEEYLQPPPPPPLIHPPPPPPAYFHGEDEPPPPAYFYGEDEPPPPRA
QVHHISHADPPRPPPSSHVHHISHVEDQGFGRENYTHEGPPYARPPPVSYSASAPVRHVSHHLNPQQPQ
GTEQVETHHLHHLPGFLHHHNEAHGVGSNLSNKPTVRVFCKAKPNHSLTILDGKVYLAPSNKTDMLQHW
IKDEK**YSTSVKDEEGFPSFALVNK**ATGQAMKHSIGASHPVQLIPYNPDVLDESVLWTESKDLGDNFRSI
RMINNIHLNVDALHGDRSHGSVHDCTTIVLNKWKKGDNQLWKISLYFENPFPSQLTQSIPLSLNLSLCE
C

Protein No.: I-1051

Protein name and Species:

Carotenoid cleavage dioxygenase 1 OS=Rosa damascena GN=CCD1 PE=2 SV=1

Accession: tr|A9Z0V7|A9Z0V7_ROSDA

Unused ProtScore: 2.11

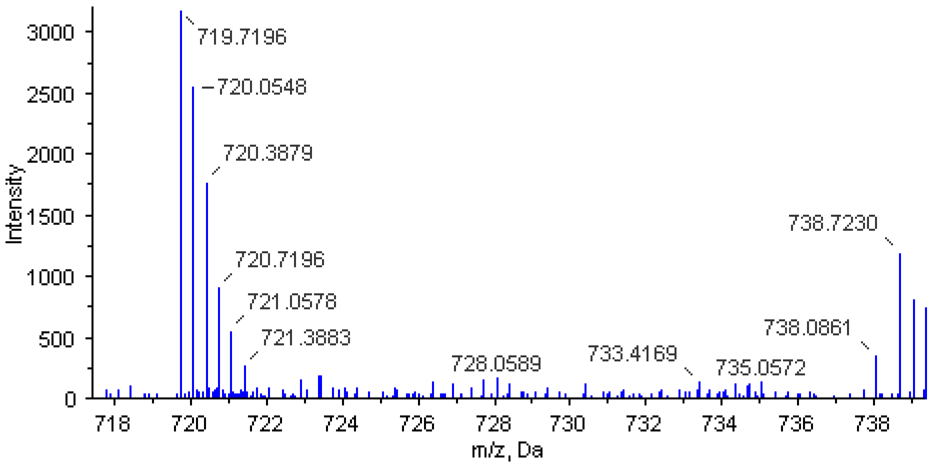
Seq Cov %: 4.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 60

116: 114=E5TL: D5TL=0. 93

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAEVVEKRHDDDVKEKLKSNGIVVPNPKPSKGVTSTLVDTVEKLIVKLMYDSSQPHHYLAGNFAPVIEE

TPPTKDLHVIGHLPDCLNGEFVRVGPNPKFAPVAGYHWFDGDGMIHGMRIKDGKATYVSRYVKTSRLKQ

EEYFGGAKFMKVGDLKGLFGLLMVYMQQLRAKLKVLDLSYGHGTGNTAFVYHHGKLLALSEGDKPYVLK

VLEDGDLQTVGLLDYDKRLKHSFTAHPKVDPFTGEMFTFGYSHDPPYVTYRVISKDGFMHDPIPITVPA

PVMMHDFAITENYAIFMDLPLYFRPKEMVKEGKLIFSFDETKKARFGVLPRYAKDDLLIRWFELPNCFI

FHNANAWEEEDEVVLMTCRLENPDLDMVNGPIKKKLDNFKNELYEMRFNLKTGLATQKKLSESAVDFPR

VNESYTGRKQRYVYGTTLDSIAKVTGIVKFDLHAAPEIGKTKIEVGGNVQGLYDLGPGRFGSEAIFVPR

VPGITSEEDDGYLIFFVHDENTGKSAIHVLDAKTMSGDPVAIVELPHRVPYGFHAFFVTEEQLQEQAKF

Protein No.: I-1059

Protein name and Species:

Nucleoredoxin, putative OS=Ricinus communis GN=RCOM_1599380 PE=4 SV=1

Accession: tr|B9R8F0|B9R8F0_RICCO

Unused ProtScore: 2.1

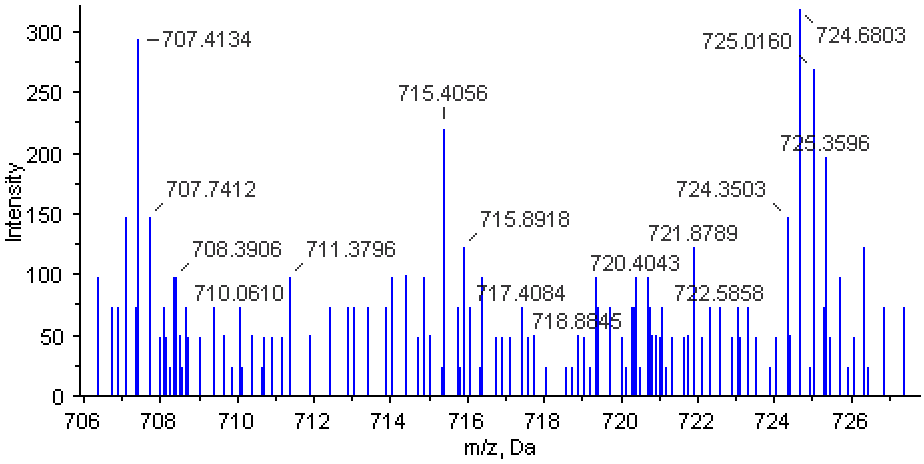
Seq Cov %: 11.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.56

116: 114=E5TL: D5TL=0.75

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MCHYLRLPLALHLRYKVKVSELEGKVIGLYFSANWYPPCRNFNQVLAGVYEQLKENGSNFEVVFVSSDE
NLDAFNNYRALMPWLSIPFSDLETKKALDRKFNIEGVPCLVILQPKDDKEEATLHDGVDLLYR**FGVQAF**
PFTKERLEELKMQEKEKHESQTLTNLLTNHDRDYLFAHPAPKQVPVASLIGKTIGLFFSAQWCRPGMKF
TPKLISIYHKIKQMLRERESEDFEIVFVSTDRDQEGFDSYFNTMPWLALPFGDPTIKTLTK**YFDVQGIP**
CLIIIGPNGKTITKNGR**NLINLYQENAYPFTEAK**VELLEKQMEEEFKSLPRSEYHVGHKHELNLVTEGT
GGGPYICCDCDEQGSGWAYQCLECGYEVHPKCVRVVEPGSTRAR

Protein No.: I-1062

Protein name and Species:

Structural molecule, putative OS=Ricinus communis GN=RCOM_1168960 PE=4 SV=1

Accession: tr|B9SS56|B9SS56_RICCO

Unused ProtScore: 2.09

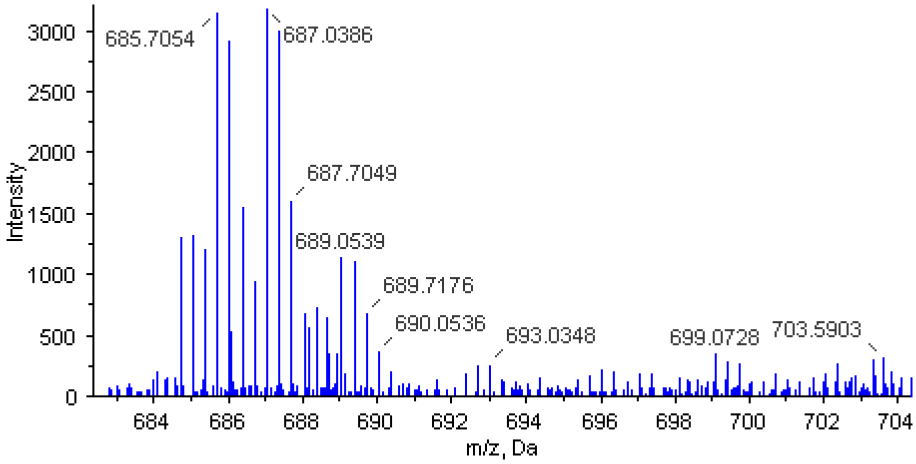
Seq Cov %: 11.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 65

116: 114=E5TL: D5TL=1. 15

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDTLTSLLHPPSFSSSFINHSSSSSSSFTIKAFPKRRLFYINNNTGKSLPVVKSALDEVPVLDPPPPPP
PPPPPFGNERENNKLVASLKLKLLSIVSGLNRGLAASEDDLQKADAAAK**ELEAVGGLVDLSNDIDK**LQG
RWKLIYSSAFSSRTLGGSRPGPPTGRLLPITLGQVFQRIDVLNKDFDNIVELQLGAPWPLPPVEVTATL
AHKFELIGSAKVKITFEKTTVK**TTGNLSQLPPLEIPR**IPDALRPPSNTGSGDFEVTYVDADTRITRGDR
GELRVFVIA

Protein No.: I-1065

Protein name and Species:

Ribosomal protein L3A OS=Nicotiana tabacum GN=RPL3A PE=2 SV=1

Accession: tr|Q6TKR0|Q6TKR0_TOBAC

Unused ProtScore: 2.08

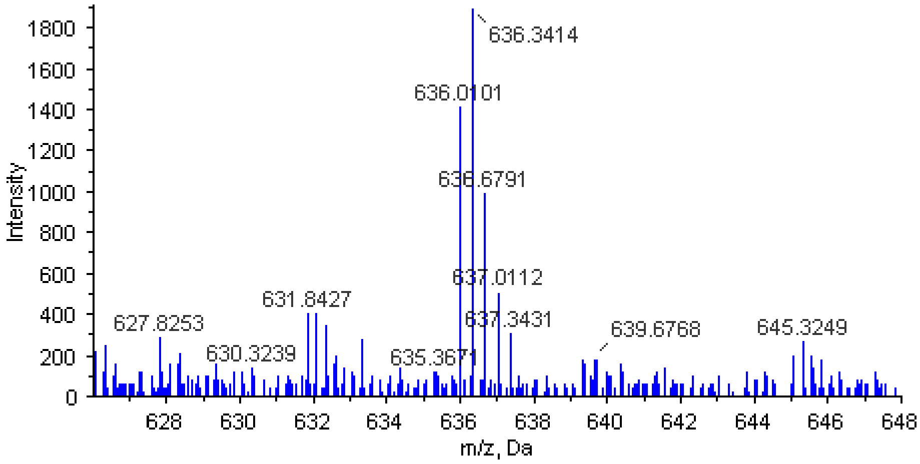
Seq Cov %: 8.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1. 66

116: 114=E5TL: D5TL=2. 75

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSHRKFEHPR**HGSLGFLPR**KRAARHRGKVKAFPKDDPNKPCK**LTAFLGYK**AGMTHIVRDVEKPGSKLHK
KETCEAVTIIETPPMVIVGVVGYVKTPRGLRCLNTVWAQHLSEELKRRFYKNWCKSKKKAFLKYSKKYE
SDEGKKDIQTQLEKLKKYACVIR**VLAHTQIR**KMKGLKQKKAHLMEIQVNGGTIAQK**VDFAYGFFEKQVP**
VDAVFQKDEMIDIIGVTKGKGYEGVVTRWGVTRLPRKTHRGLRKVACIGAWHPARVSYTVARAGQNGYH
HRTEMNKKVYKLGKAGQESHAAVTDFDRTEK**DITPMGGFPHYGVVK**DDYLLIKGCCVGPKKRVVTLRQS
LLNQTSR**VALEEIK**LKFIDTSSKFGHGRFQTTQEKQKFYGRLKG

Protein No.: I-1066

Protein name and Species:

Glutamate decarboxylase isozyme 3 OS=Nicotiana tabacum PE=2 SV=1

Accession: tr|Q94KK8|Q94KK8_TOBAC

Unused ProtScore: 2.08

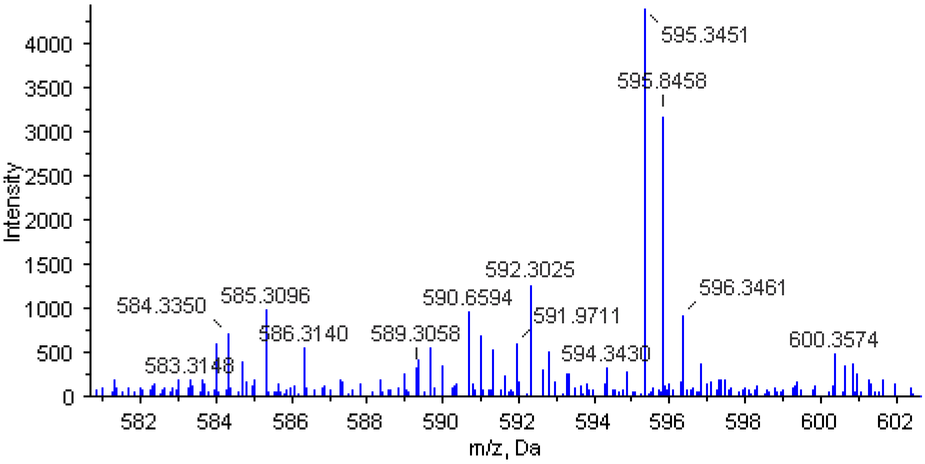
Seq Cov %: 8.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2. 21

116: 114=E5TL: D5TL=0. 92

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MVLSKTSSESDVSVHSTFASRYVRTSLPRFEMAENSIPKEAAFQIINDELMLDGNPRLNLASFVTTWME
PECDKLMMDSINK**NYVDMDEYPVTTELQNR**CVNMIARLFNAPLEEKETAVGVGTVGSSEAIMLAGLAFK
RNWQNKRKAEGKPYNKPNIVTGANVQVCWEKFANYFEVELKEVKLREGYYVMDPVQAVEMVDENTICVA
AILGSTLNGEFEDVK**LLNDLLIEK**NKQTGWNTPIHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSGH
KYGLVYAGIGWVIWRTKQDLPEELIFHINYLGADQPTFTLNFSK**GSSQVIAQYYQLIRLGYEGYR**NVME
NCRENAIVLREGLEKTGRFNIVSKDEGVPLVAFSLKDNSRHNEFEVSETLRRFGWIVPAYTMPADAQHV
TVLRVVIREDFSRTLAERLVLDIVKVLHELDTLPARLSAKLEEVKLVKNGKKFELEVQREVTNYWKKFV
LARKAPVC

Protein No.: I-1067

Protein name and Species:

Aminopeptidase OS=Citrus unshiu GN=ORF12 PE=4 SV=1

Accession: tr|F8WL79|F8WL79_CITUN

Unused ProtScore: 2.08

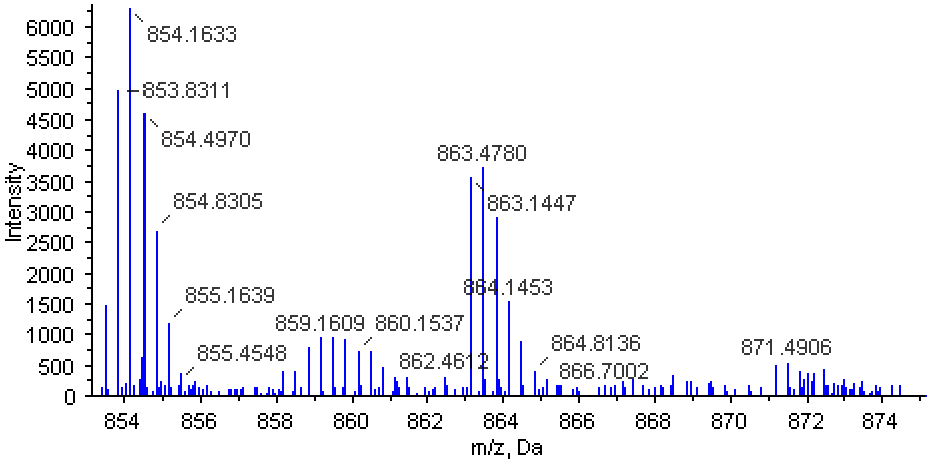
Seq Cov %: 4.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 59

116: 114=E5TL: D5TL=0. 41

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MEEFKGQPRLPKFAVPKRYDIRLTPDLTSCKFGGSVAIDVDVVGDTKFIVLNAADLTINNRSVSFTNKA
SSKALEPTKVELVEADEILVLEFAETLPTGMGVLAIGFEGVLNDKMKGFYRSSYELNGEKK**NMAVTQFE**
PADARRCFPCWDEPACKATFK**ITLDVPSELVALSNMPVIDEK**VDGNMKTVSYQESPIMSTYLVAVVIGL
FDYVEDHTSDGTVTISIDSHGIKVRVYCQVGKANQGKFALNVAVKTLELYKEYFAVPYSLPKLDMIAIP
DFAAGAMENYGLVTYRETALLYDDQHSAAANKQRVATVVAHELAHQWFGNLVTMEWWTHLWLNEGFATW
VSYLAADSLFPEWK**IWTQFLDECTEGLR**LDGLAESHPIEVEVNHTGEIDEIFDAISYRKGASVIRMLQN
YLGAECFQRSLASYIKKYACSNAKTEDLWAALEEGSGEPVNKLMNSWTKQKGYPVISVKVREEKLELEQ
ELLGCSISKEGDNGGWIKLNVNQTGFYRVKYDKDLAARLGYAIEKKQLSETDRFGILDDHFALCMARQQ
TLTSLLTLMASYSEETEYTVLSNLITISYKIGRIAADARPELLDYLKQFFISLFQNSAELFICRKLGWD
SKPGESHLDALLRGEIFTALALLGHKETLNEASKRFHAFLADRTTPLLPPDIRKAAYVAVMQKVSASDR
SGYESLLRVYRETDLSQEKTRILSSLASCPDVNIVLEVLNFLLSSEVRSQDAVYGLAVSIEGRETAWKW
LKASGVLSKEVNFDPIPSSINGRISSITGTTSQRPGVLVFLSHALSAQLSHRFVVYTSQIMCSVFQLLH
MCTSNVFPLIPFLFLSAVWHAQFASYEKVREVEEFFSSRCKPYIARTLRQSIERVQINAKWVESIRNEG
HLAEAVKELAYRKY

Protein No.: I-1071

Protein name and Species:

serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform [Vitis vinifera] OS=Vitis vinifera GN=VIT_17s0000g03870 PE=4 SV=1

Accession: tr|D7SIX7|D7SIX7_VITVI

Unused ProtScore: 2.07

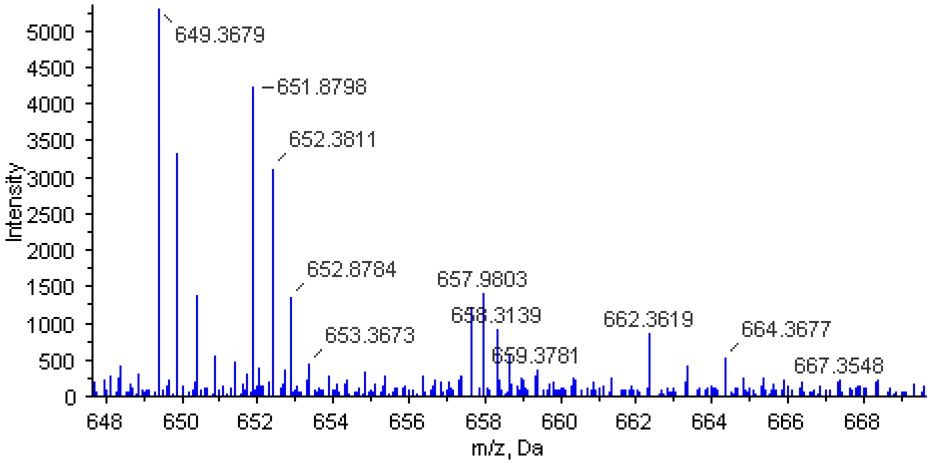
Seq Cov %: 14.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 16

116: 114=E5TL: D5TL=0. 28

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MKDTDFFFSALLKLVEGSSLSSPKFQDGLRLPHLRSQILLFPNCPFLFSHFHCSEMAMIDEPLYPIAVL
IDELKNEDIQLRLNSIRRLSTIARALGEERTRKELIPFLSENNDDDDEVLLAMAEELGVFIPYVGGVEH
ANVLLPPLETLCTVEETCVRDK**AVESLCR**IGAQMREPDLVESFIPLVKRLAAGEWFTARVSSCGLFHIA
YPSAPETLKTELR**AIYSQLCQDDMPMVR**RSAASNLGKFAATVEAAHLK**ADIMSIFEDLTQDDQDSVRLL**
AVEGCAALGKLLEPQDCVAH**ILPVIVNFSQDK**SWRVR**YMVANQLYELCEAVGPEPTR**SDLVPAYVRLLR
DNEAEVRIAAAGKVTKFCR**ILNPELAIQHILPC**VKELSSDSSQHVR**SALASVIMGMAPVLGK**DATIDQL
LPIFLSLLKDEFPDVRLNIISKLDQVNQVIGIDLLSQSLLPAIVELAEDRHWRVRLAIIEYIPLLASQL
GVGFFDDKLGALCMQWLKDKVYSIRDAAANNVKRLAEEFGPDWAMQHIIPQVLDMINNPHYLYRMTILH
AISLLAPVMGPEITCSKLLPVVINAAKDRVPNIKFNVAK**VLQSLTPIVDQSVVDKTIRPCLVELSEDPD**
VDVRFFASQALQASDQIMMSS

Protein No.: I-1072

Protein name and Species:

Long-chain acyl-CoA synthetase 4 OS=Ricinus communis GN=LACS4 PE=2 SV=1

Accession: tr|B3TZ27|B3TZ27_RICCO

Unused ProtScore: 2.07

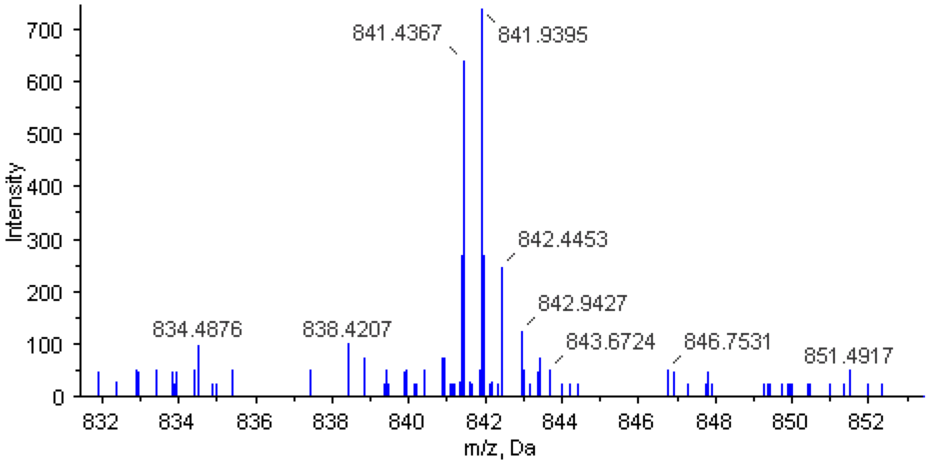
Seq Cov %: 6.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 42

116: 114=E5TL: D5TL=1. 36

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAQQRQRKYLIEVEKAKEAKDGK**PSVGPVYR**SLFAKDGFPPPIPGLDSCWDVFRMSVEKYPNNPMLGHR
EFVNGKAGKYVWQTYKQVYDLVIKVGNAIRSCGVEPGEKCGIYGANSAEWIMSMEACNAHGLYCVPLYD
TLGAGAVEYIICHAEVSIAFVEEKKIPELLKTFPSAAQYIKTIVSFGNIAREQREEMEKFGLVAYSWED
FLKLGENKQYDLPEKKKSDICTIMYTSGTTGDPKGVMISNDSIVTIIAGVRRLLESVNEQLTSEDVYLS
YLPLAHIFDRVIEELFISHGASIGFWRGDVK**LLIEDIGELKPTIF**CAVPRVLDRIHSGLTQKISSGGFL
KNKLFNLAYSYKLSCMKKGLAHDEASPLSDKLVFDKVKQGLGGKVRLILSGAAPLAIHVEAFLRVVSCA
HVLQGYGLTETCAGTFVSLPNEMAMLGTVGPPVPNVDVCLESVPEMNYDALSSTPRGEICVRGSTVFAG
YYKREDLTKEVLIDGWFHTGDIGEWQADGSLKIIDRKKNIFKLSQGEYVAVENLENIYGLASDVDSIWV
YGNSFESFLVAVVNPNKQALEHWAQENSVDGDFKSLCENPRAK**QYIIGELTK**IGKEKKLKGFESIK**AVH**
LDPEPFDIERDLLTPTYKKKRPQLLKYYQKVIDDMYKNASKPSA

Protein No.: I-1081

Protein name and Species:

Malate dehydrogenase OS=Vitis vinifera GN=VIT_07s0005g03350 PE=3 SV=1

Accession: tr|F6HZK0|F6HZK0_VITVI

Unused ProtScore: 2.06

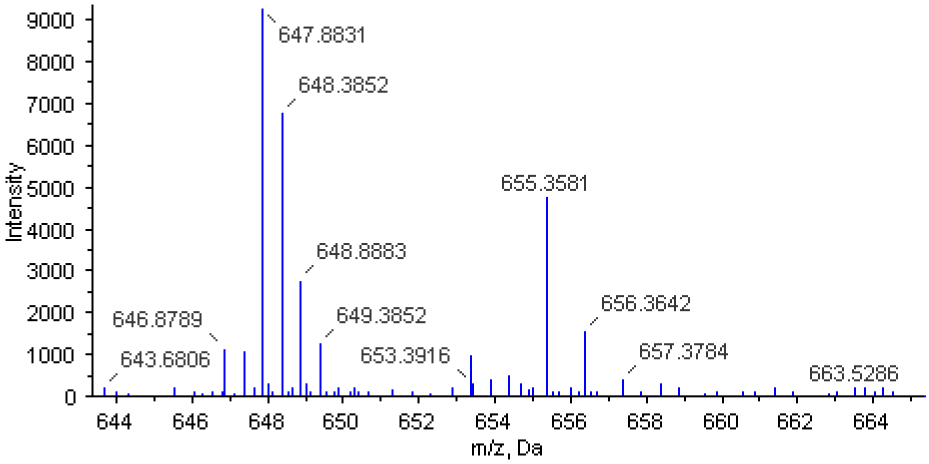
Seq Cov %: 27.4

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 28

116: 114=E5TL: D5TL=0. 62

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAEDVPRGQTSGLTKSSGTQRRFPLPCSPAIPTMAKEPVR**VLVTGAAGQIGYALVPMIAR**GVMLGADQP
VILH**MLDIPPAAEALNGVKMELVDAAFPLLK**GVVATTDVVEACTGVNIAVM**VGGFPR**KEGMERKDVMSK
NVSIYKSQASALEN**HAAANCKVLVVANPANTNALILKEFAPSIPEK**NISCLTRLDHNRALGQVSER**LNV**
QVSDVKNVIIWGNHSSTQYPDVNHATVKTPAGEKPVRGLVGDDAWLNGEFITTVQQRGAAIIKARKLSS
ALSAASAACDHIRDWVLGTPEGTWVSMGVYSDGSYNVPAGLIYSFPVTCCAGEWK**IVQGLHIDEFSR**KK
LDLTAQELSEEKELAYSCLS

Protein No.: I-1082

Protein name and Species:

Aspartyl aminopeptidase-like protein OS=Populus trichocarpa GN=POPTRDRAFT_835204 PE=3 SV=1

Accession: tr|B9IF79|B9IF79_POPTR

Unused ProtScore: 2.06

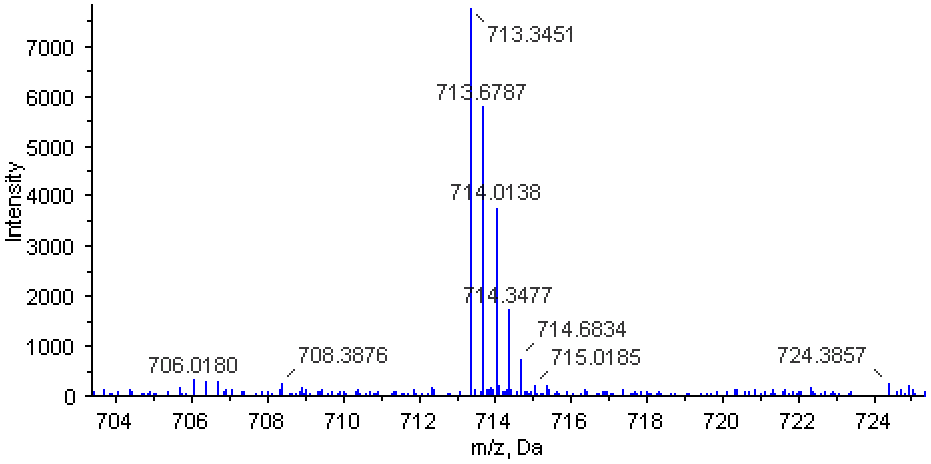
Seq Cov %: 8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2. 05

116: 114=E5TL: D5TL=1. 06

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MANNNKEQEYCVASDLIDFLNASPTAFHAVEEAKRRLKNAGYEQVSERHDWKLEAGKRYFFTRNHSTIL
AFAIGKK**YVAGNGFYIVGAHTDSPCLK**LKPVSKVTKGGFLEVGVQTYGGGLWHTWFDRDLTVAGRVIVK
EEKDGLVSYSHRLVRIEEPIMRVPTIAIHLERTVNTDGFKVNTQSQLLPVLATSIKAELNKAAAENGPV
KSEEVQADGKKSDKGTISSKHHSLVLEMIANQIGCKVDDICDFELQACDTQPSLIAGAAKEFIFSGRLD
NLCSSFCSLK**ALIDATSSESDLEDESGVR**MVALFDHEEIGSDSAQGAGSPVMLDALSRITSSFNSDSKL
LPKAIQKSFLVSADMAHALHPNYMDKHEENHQPKLHGGLVIKHNANQR**YATNAITSFLFR**EIATKHDLP
TQDFVVRNDMGCGSTIGPILASGVGIR**TVDVGAPQLSMHSIR**EMCSVDDVKYSYEHFKAFFQDISHLDA
KITVDM

Protein No.: I-1085

Protein name and Species:

L-allo-threonine aldolase, putative OS=Arabidopsis thaliana GN=T27C4.17 PE=4 SV=1

Accession: tr|Q9M835|Q9M835_ARATH

Unused ProtScore: 2.06

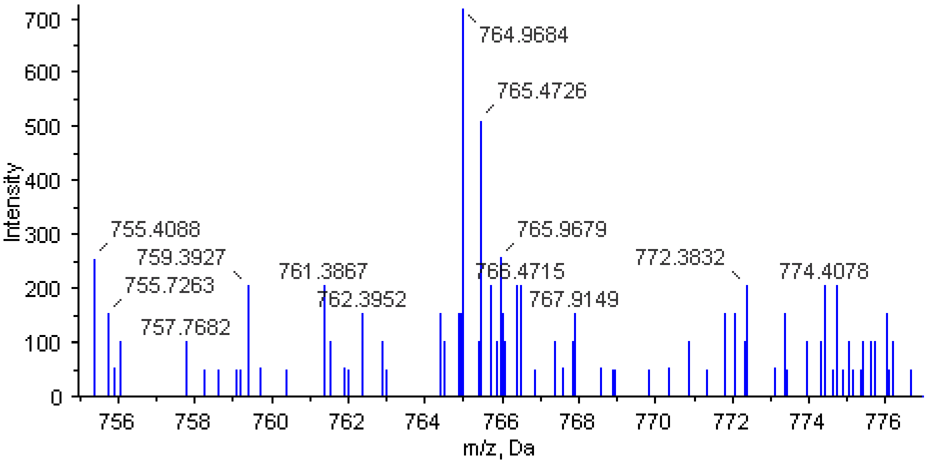
Seq Cov %: 7.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1. 58

116: 114=E5TL: D5TL=1. 04

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MVTPTTIRTVDLRSDTVTKPTESMRSAMANAEVDDDVLGNDPTALRLEKEVAEIAGKEAAMFVPSGTMG
NLISVLVHCDERGSEVILGDDSHIHIYENGGVSSLGGVHPRTVKNEEDGTMEIGAIEAAVRSPKGDLHH
PVTK**LICLENTQANCGGR**CLPIEYIDKVGELAKKHGLKLHIDGARIFNASVALGVPVKRIVQAADSVSI
CLSK**GIGAPVGSVIVGSK**KFITKARWLRKTLGGGMRQIGVLCAAALVALHENVAKLEDDHKKARVLAEG
LNRIERLRVNVAAVETNIVNPKFGAEEACKSLEDVGVLVIPQATFRIRIVLHHQISDVDVEYVLSCFEV
CSLLSSTDMCFDIFNFFATLYSFID

Protein No.: I-1120

Protein name and Species:

Exportin-1 OS=Solanum lycopersicum GN=Xpo1 PE=2 SV=1

Accession: tr|D1MAF2|D1MAF2_SOLLC

Unused ProtScore: 2.03

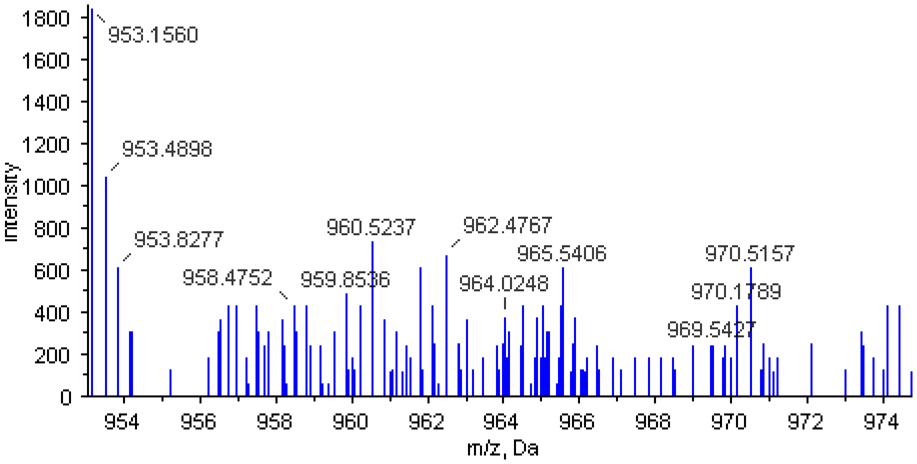
Seq Cov %: 10.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 60

116: 114=E5TL: D5TL=4. 17

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAAEKLR**DLSQPIDVSLLDATVAAFYGTGSK**EERAAADHILRDLQNNPDMWLQVVHILSSTQSLNTKFFALQVLEGVIKYRWNALPVEQRDGMKNYISEVIVKLSSDEASLRRERLYISKLNIILVQILKHEWPARWR**SFIPDLVAAAK**TSETICENCMAILK**LLSEEVFDFSR**GEMTQQKIKELKQSLNSEFQLIHELCLYVLSVSHRTELIRATLATLHAFLSWIPLGYIFESTLLEILLKFFPLPSYRNLTLQCLTEVAALNFGDFYNEQYIKMYTIFMGQLQSVLPPNTSIPEAYANGSNEEQAFIQNLALFFTSFFKSHIRVLESSQENIGALLVGLEYLINISYVDDTEVFKVCLDYWNSLVLELFEAAHHNLDNPAMTTNMMGLQMPLLSGMNDGLGAQLMQRRQLYSGPMSKLRLLMISR**MAKPEEVLIVEDENGNIVR**ETMK**DNDVLVQYK**IMRETLIYLSHLDHDDTEKQMLKKLSNQLNGEDWSWNNLNTLCWAIGSISGSMVEEQENRFLVMVIR**DLLNLCEITK**GKDNK**AVIASNIMYVVGQYPR**FLRAHWKFLKTVVNKLFEFMHETHPGVQDMACDTFLKIVQKCKRKFVVVQVGENEPFVSELLTTLPTTIADLEPHQIHTFYESVGQMIQAEPDPQKRDEYLQRLMELPNQRWNEIIGQARQSVDYLKDQDVIRAVLNILQTNTSAASSLGTYFLPQISLIFLDMLNVYR**MYSELISTSIAQGGPYASR**TSIVKLLRSVKRETLK**LIETFLDK**AEDQSHIGK**QFVPPMMDPVLGDYAR**NVPDARESEVLSLFATIINKYKGAMIEDVPRIFEAAFQCTLEMITKNFEDYPEHRLKFFSLLRAIATHCFAALIRLSSEQLKLVMDSIIWAFRHTERNIAETGLNLLLAMLKNFQNSEFANQFYRTYYLTIEQEIFAVLTDTFHKPGFKLHVLVLQHLFCMVVMLSEPLWDASTVPCSYPNNVEFVREYTIKLLSTSFPNMTAAEVTQFVSGLFDSTNDLPTFKNHIRDFLVQSK**EFSAQDNKDLYAEEAAAQR**ERERQRMRSIPGLIAPNEIQDEMVDS

Protein No.: I-1121

Protein name and Species:

Glucose 4-6-dehydratase, putative OS=Ricinus communis GN=RCOM_0464520 PE=4 SV=1

Accession: tr|B9SR17|B9SR17_RICCO

Unused ProtScore: 2.03

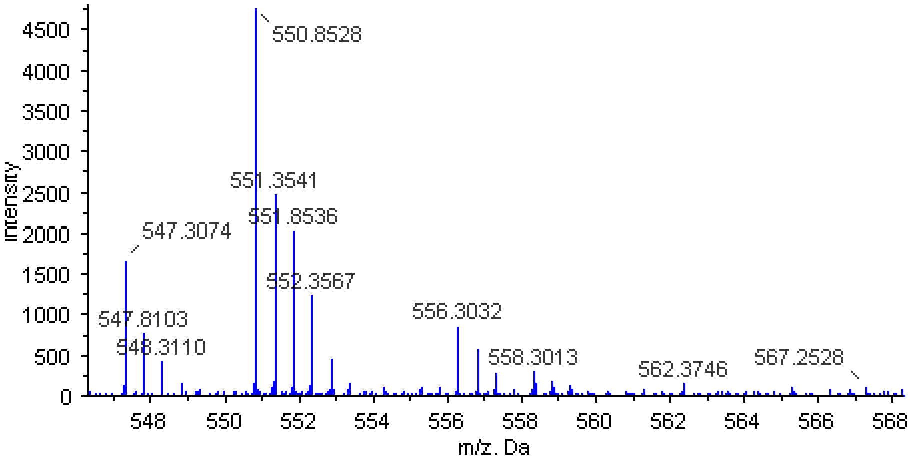
Seq Cov %: 25.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2. 13

116: 114=E5TL: D5TL=0. 82

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAKEVSNGDHSSASKPPPTPSPLRFSKFFQSNMR**ILVTGGAGFIGSHLVDK**LMENEK**NEVIVVDNYFTG**
SKDNLKKWIGHPRFELIRHDVTEPLLIEVDQIYHLACPASPIFYKYNPVKTIK**TNVIGTLNMLGLAK**RV
GARILLTSTSEVYGDPLVHPQEESYWGNVNPIGVRSCYDEGKR**VAETLMFDYHR**QHGIEIRIAR**IFNTY**
GPRMNIDDGR**VVSNFIAQAVR****NEPLTVQAPGTQTRSFCYVSDMVDGLIR**LMEGENTGPINIGNPGEFTM
LELAETVKELINPDVEIAKVENTPDDPRQRKPDITKAKELLGWEPKIKLR**DGLPLMEDDFR**LRLGVPRK
K

Protein No.: I-1130

Protein name and Species:

copper transport protein [Arabidopsis thaliana] OS=Arabidopsis thaliana PE=4 SV=1

Accession: tr|Q8LCK3|Q8LCK3_ARATH

Unused ProtScore: 2.03

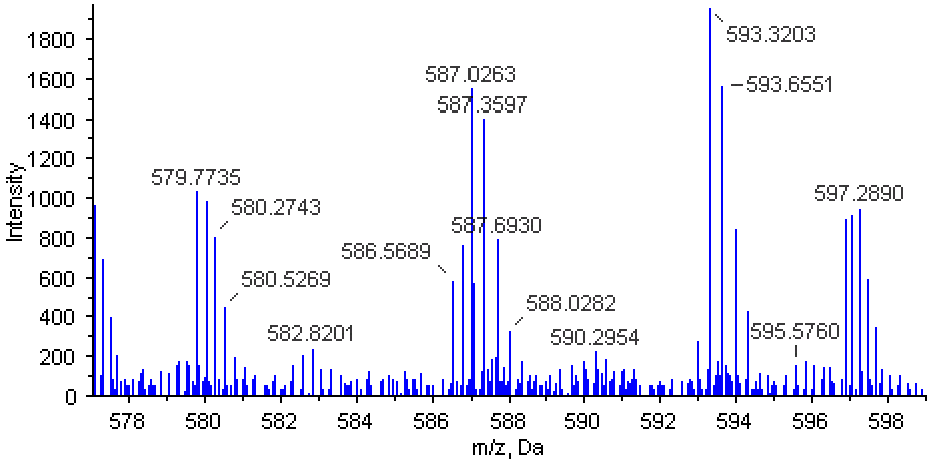
Seq Cov %: 23.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 42

116: 114=E5TL: D5TL=0. 88

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAQKVVLK**VLTMTDDK**TKQK**AIEAAADIFGVDSIAADMK**DQK**LTVIGLMDAVAVVK**KLKKVGK**VDLISV**
GPAKEEKKEEKKEEKKKEKKEEKKEEKKEEEPKK

Protein No.: I-1136

Protein name and Species:

V-type H+-transporting ATPase subunit I; At2g21410/F3K23.17 OS=Arabidopsis thaliana GN=VHA-A2 PE=2 SV=1

Accession: tr|Q9SJT7|Q9SJT7_ARATH

Unused ProtScore: 2.02

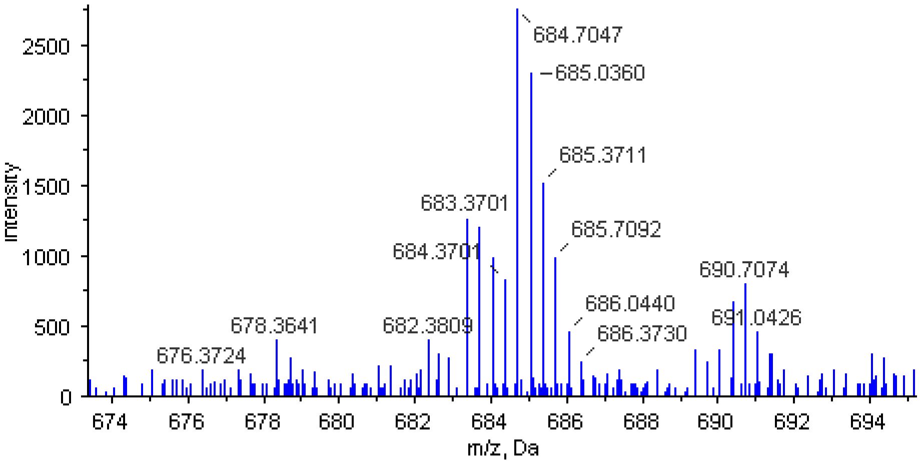
Seq Cov %: 3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 51

116: 114=E5TL: D5TL=1. 13

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAESHGGGGGCCPPMDLMRSEPMQLVQVIVPMESAHLTVSYLGDLGLVQFKDLNSEKSPFQRTYAAQIK
RCGEMARKIRFFKEQMSKAGVTPKETLDRENDIDLDDVEVKLEELEAELVEINANNDKLQRSYNELVEY
KLVLEKAGEFFASAHRSATAQQSEIETEQVGEDLLEAPLLQEEKSVDPTKQVKLGFLTGLVPREKSMVF
ERILFRATRGNIFIRQSVIEESVVDPNSGEKAEKNVFVVFYSGERAKSKILK**ICEAFGANR**YPFSEDLG
KQAQMMTEVSGRLSELKTTIGAGLDQRNILLETIGDKFEQWNLKIRKEKAIYHTLNMLSLDVTKKCLVG
EGWSPVFAATEIQDALHRAAVDSNSQVGSIFQVLRTKEMPPTFFRTNK**FTTAFQEIVDAYGVAK**YQEAN
PSVFTIVTFPFLFAVMFGDWGHGICLLLATMYLILREKKLSSQKLGDIMEMAFGGRYVIFMMSLFSIYT
GLIYNEFFSIPYPLFASSAYDCRDVSCSEATTIGLIKTRDTYPFGVDPVWHGTRSELPFLNSLKMKMSI
LIGVAQMNLGIIMSFFNAKFFKSAVNIWFQFVPQMIFLNCLFGYLSVLIIIKWCTGSQADLYHVMIYMF
LSPMDDLGENQLFPNQKIVQLTFLFLALVSVPWMLLPKPFILKKQHEARHQGLSYAQLDETDESLQVET
NGGGHGHEEFEFSEIFVHQLIHTIEFVLGAVSNTASYLRLWALSLAHSELSSVFYEKVLLMAWGFNNVF
IWIVGILVFIFATVGVLLVMETLSAFLHALRLHWVEYQNK**FYEGDGYK**FAPFTFTLVGNEDE

Protein No.: I-1137

Protein name and Species:

Translation elongation factor OS=Populus trichocarpa GN=POPTRDRAFT_814408 PE=3 SV=1

Accession: tr|B9IF97|B9IF97_POPTR

Unused ProtScore: 2.02

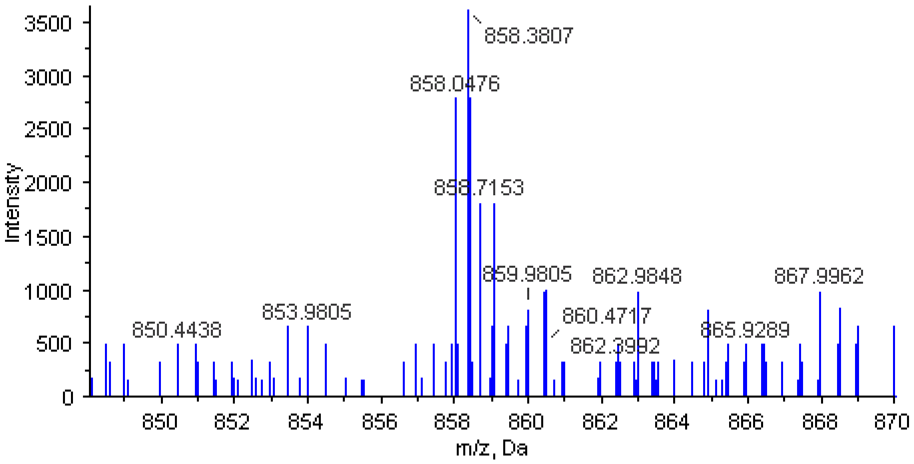
Seq Cov %: 26.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 61

116: 114=E5TL: D5TL=0. 53

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

M**AVTFYDLTSAAGLK**KLDDFLLSRSYISGYQASKDDLTVYSALSSAPSAEHVNVYRWYTHIDALLRISG
VEAEGCGVVVKGSAPITEEAIATPPSAETK**AAEDDDDDVDLFGEETEEEK**KAAEERAATVKAASKKKE
SGK**SSVLLDVKPWDDETDMK****KLEEAVR**SVEMEGLLWGASK**LVPVGYGIK**KLTIMLTIVDDLVSVDTLIE
ERLTTEPINEYVQSCDIVAFNKKGSR

Protein No.: I-1155

Protein name and Species:

Galactinol-sucrose galactosyltransferase OS=Populus trichocarpa GN=POPTRDRAFT_762165 PE=4 SV=1

Accession: tr|B9HA87|B9HA87_POPTR

Unused ProtScore: 2.01

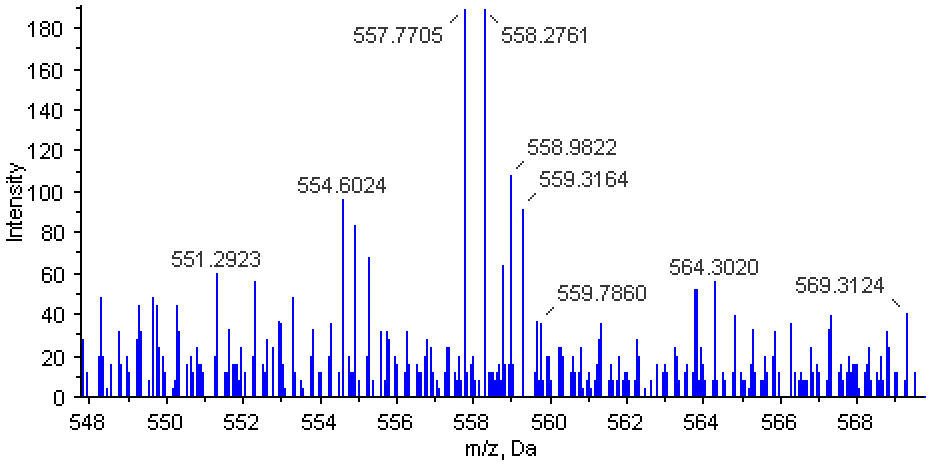
Seq Cov %: 8.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=11. 07

116: 114=E5TL: D5TL=3. 94

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MTIKPAVRISDGKLIVKDRTILTGVPDNVIATSGSTSGPVEGVFLGAVFDQENSRHVTSLGALRDVRFM
ACFRFKLWWMAQKMGDQGR**DIPLETQFLLVETK**DGSHLESDGGDEDNQVVYTVFLPLIEGSFRACLQGN
VSDELELCLESGDAETKTSSFTHTLFIHAGTDPFRTITEAVRAVKLHLKTFRQRHEKRLPGIIDHFGWC
TWDAFYQEVTQEGVEAGLQSLASGGTPPKFVIIDDGWQSVGGDPEEETNGQDVKKQDQQPLLRLTGIKE
NAKFQKKDDPAAGIKSIVNIAKEKYGLKYVYVWHAITGYWGGVRPGVKEMEEYGSMMKYPMVSKGVVEN
EPIWKNDALTLQGLGLVNPKNVYRFYNELHSYLAAAGIDGVK**VDVQCILETLGAGLGGR**VELTR**QYHQA**
LDASVARNFLDNGCIACMSHNTDALYCSKQTAVVR**ASDDFYPR**DPVSHTIHIAAVAYNSVFLGEFMQPD
WDMFHSLHAAAEYHASARAISGGPIYVSDAPGKHNFELLKKVVLPDGSILRARLPGRPTSDCLFSDPAR
DGVSLLKIWNMNKFTGVLGVYNCQGAAWSSTERKNAFHQTTTEALTGTIRGRDVHLVAEAATDPNWDGN
CAFYCHRTGELITLPYNAALPVSLK**VLEHDIFTVTPIK**VLAPGFSFAPLGLINMFNAGGAIEGLKYEVK
GKVCVEVKGCGKFGAYSSAKPRKCIVDSNVVDFVYDSNSGLVGFNLDSLLEEGKLRIVEIEL

Protein No.: I-1157

Protein name and Species:

Pyrophosphate-energized membrane proton pump 3 [Vitis vinifera] OS=Vitis vinifera GN=VIT_09s0054g00700 PE=3 SV=1

Accession: **tr|D7SS21|D7SS21_VITVI**

Unused ProtScore: **2.01**

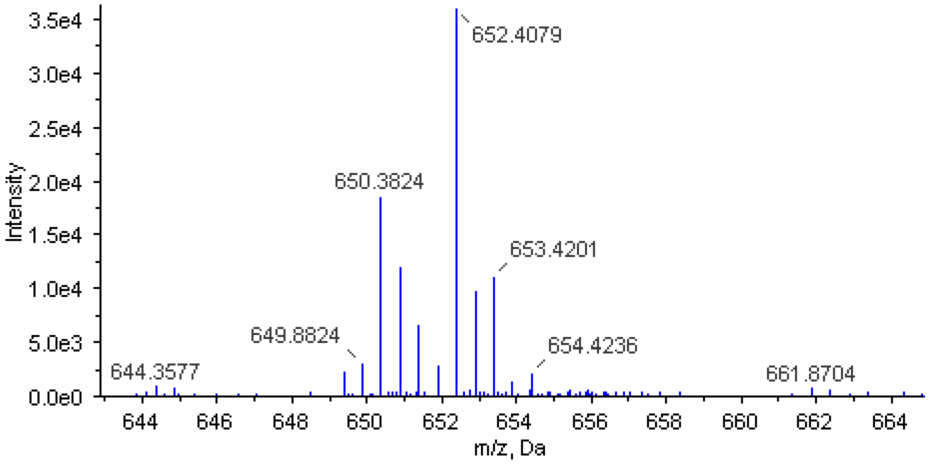
Seq Cov %: **3.8**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1. 60

116: 114=E5TL: D5TL=1. 63

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDDDVESGALGPYQDKPRIFPNMRSKSYTPLIFRIFMGINVRVLFVLLLLGLGAVFYVGARTSPILVFV
FSVCIISFLLSVYLTKWVLAKDEGPPEMAQISDAIRDGAEGFFRTQYGTISKMAMLLALVILSIYLFRS
TTPQQESSGIGRSTTAYITVAAFLLGALCSGIAGYVGMWVSVRANVRVSSAARRSAREALQIAVRAGGF
SALVVVGMAVIGVAILYATFYVWLGVDSTGSMKVTDLPLLLVGYGFGASFVALFAQLGGGIYTK**AADVG**
ADLVGKVEQGIPEDDPR**NPAVIADLVGDNVGDCAAR**GADLFESIAAEIISAMILGGTMAQRCKIEDPSG
FILFPLVIHSFDLVISSVGIFSIRGTRDSGVKSPVEDPMAILQKGYSITIILAVLTFGLSTRWLLYTEQ
APSAWMNFALCGLVGIMTAYVFVWITKYYTDYKHEPVRTLALSSSTGHGTNIIAGVSLGLESTALPVIV
ISISIVSAFWLGQTSGLVDETGNPTGGLFGTAVATMGMLSTAAYVLTMDMFGPIADNAGGIVEMSQQPE
SVREITDLLDAVGNTTKATTKGFAIGSAALASFLLFSAYMDEVSAFAHEPFKQVDIAIPEVFVGGLLGS
MLIFLFSAWACSAVGRTAQEVVNEVRRQFIERPGIMDYKEKPDYGRCVAIVASASLREMIKPGALAIVS
PIVVGFLFRILGYYTGHPLLGAKVVASMLMFATVAGILMALFLNTAGGAWDNAKKYIETGALGGKGSDA
HKAAVTGDTVGDPFKDTAGPSLHVLIKMLATITLVMAPVFL

Protein No.: I-1171

Protein name and Species:

Glyceraldehyde-3-phosphate dehydrogenase OS=Dimocarpus longan PE=2 SV=1

Accession: tr|C0LDX2|C0LDX2_9ROSI

Unused ProtScore: 2

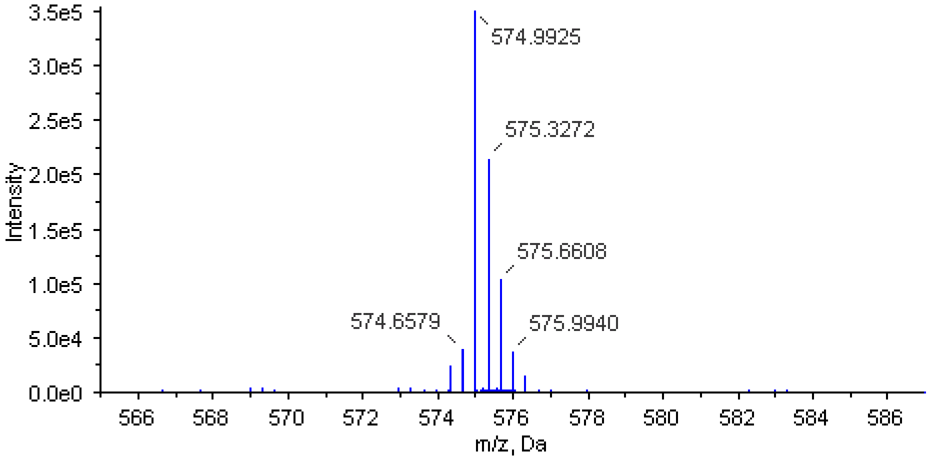
Seq Cov %: 33.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 61

116: 114=E5TL: D5TL=0. 22

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGKIK**IGINGFGR**IGRLVARVILQSDDVELVAVNDPFIDTTYMTYMFKYDSVHGPWKHHELKVKDSKTL
LFGEKAVTVFGIR**NPEEIPWQETGAEYVVESTGVFTDK**EK**AAAHLK**GGAK**KVVISAPSK**DAPMFVVGVN
EH**EYKPEIDIVSNASCTTNCLAPLAK**VINDK**FGIVEGLMTTVHSITATQK**TVDGPSMKDWRGGR**AASFN**
IIPSSTGAAKAVGK**VLPSLNGKLTGMAFR**VPTVDVLVVDLTVRLEKKASYDEIKAAIKEAADGKLK**GIL**
GYTEDDVVSTDFVGDNRSSIFDAKAGIALNDFFVKLVSWYDNEWGYSSRVVDLIRHMAKC

Protein No.: I-1172

Protein name and Species:

Ras-related protein Rab7 OS=Populus trichocarpa GN=POPTRDRAFT_712938 PE=2 SV=1

Accession: tr|A9P8Q6|A9P8Q6_POPTR

Unused ProtScore: 2

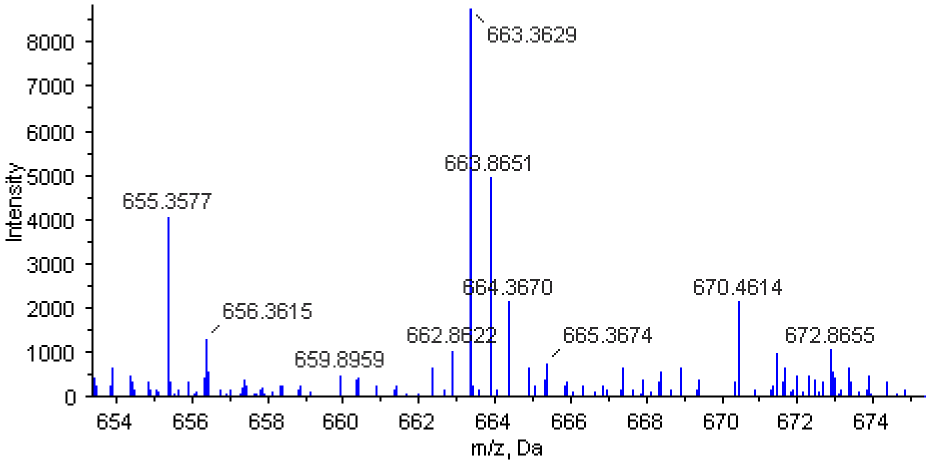
Seq Cov %: 73.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 62

116: 114=E5TL: D5TL=1. 21

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MPSRRRTLLK**VIILGDSGVGKTSLMNQYVNK**KFSNQYK**ATIGADFLTKEVQFEDRLFTLQIWDTAGQER**
FQSLGVAFYRGADCCVLVYDVNSMKSFDHLNNWR**EEFLIQASPSDPENFPFVVLGNK**VDVDGGNSRVVS
EKKARAWCASK**GNIPYFETSAKEGVNVEEAFQCIAKNALKSGEEEEIYLPDTIDVGSSSQPR**STGCEC

Protein No.: I-1173

Protein name and Species:

Heat shock protein 80 (Fragment) OS=Euphorbia esula PE=2 SV=1

Accession: tr|Q9M5X2|Q9M5X2_EUPES

Unused ProtScore: 2

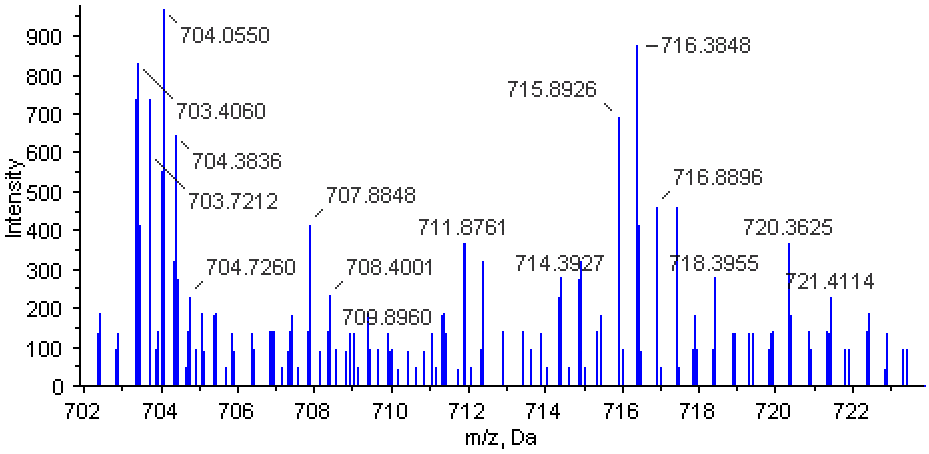
Seq Cov %: 40.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=3.22

116: 114=E5TL: D5TL=1.02

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

VKVIRKNLVKKCIELFQEIAENKEDYNKFYESFSKNLK**LGIHEDSQNK**TK**LAELLR**YHSTK**SGDEMTSL**
KDYVTRMKEGQS**DIYYITGESKKAVENSPFLEK**LKKKGYEVLF**MVDAIDEYAVGQLK**EFEGKK**LVSATK**
EGLKIDESEDEKKKKDELKEQ**FEGLCK**VIKDVLGDRVEK**VVVSDRVVDSPCCLVTGEYGWTANMER**IMK
AQALRDSSMAGYMSSKK**TMEINPENPIMDELRK**RADADKNDKSVKDLVLLLFETALLTSGFSLDDPNTF
GNRIHRMLK**LGLSIDEDAGEGDADMPALEEADADAEGSK**MEEVD

Protein No.: I-1179

Protein name and Species:

Coatomer subunit gamma OS=Populus trichocarpa GN=POPTRDRAFT_821185 PE=3 SV=1

Accession: **tr|B9HRP1|B9HRP1_POPTR**

Unused ProtScore: **2**

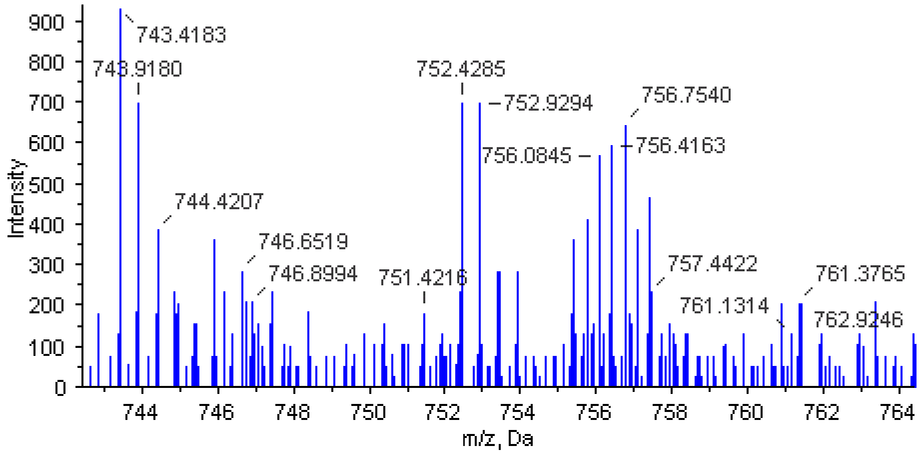
Seq Cov %: **11.3**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1. 58

116: 114=E5TL: D5TL=0. 71

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAQPLVKKDDDHDDEAEYSPFLGIEKGAVLQEARVFNDPQLDPRRCSQVITKLLYLLNQGDYFTKTEAT
EVFFSVTKLFQSKDFGLRRMVYLIIKELSPSADEVIIVTSSLMKDMNSKTDMYRANAIRVLCR**ITDGTL**
LTQIERYLKQAIVDKNPVVASAALVSGIHLLQTNPEIVKRWSNEVQEAVQSRAALVQFHALALLQQIRQ
NDRLAVSKLVTSLTRGTVRSPMAQCLLIRYASQVIRESANTQTGDRPFYDFLESCLRHK**AEMVIFEAAR**
AITELSGVTNRELTPAITVLQLFLSSSKPVLRFAAVRTLNKVAMTHPMAVTNCNIDMESLISDQNR**SIA**
TLAITTLLKTGNESSVDRLMKQITNFMSDIADEFKIVVVEAIRSLCLKFPLKYRSLMNFLSNILREEGG
FEYKKAIVDSIVILIRDIPEAKESGLLHLCEFIEDCEFTYLSTQILHFLGIEGPKTTDPSKYIRYIYNR
VHLENATVRAAAVSTLAKFGAMVDALKPR**IFVLLR**R**CIFDSDDEVRDR**TTLYLSTLGGDGEVVETDRDT
KTFLFGDLDIPLVNLETSLK**NYEPSEEPFDIDSVPK**EVKSQPLAEKKAPGK**KPTGLGAPPAGPPSTVDA**
YERLLSSIPEFSDFGKPFK**SSAPVELTEAETEYAVNVVK**HIFDRHVVFQYNCTNTIPEQLLENVSVIVD
SSEADNFAEVASKPLRSLPYDTPGQTFVAFEKPKGITAVGKFSNTLRFIVKEVDPTTGEAEEDGVEDEY
QLEDLEVVAADYMMK**VGVSNFR**NAWESMGDEFEH**VDEYGLGPR**ENLAEAVIAVINLLGMQPCEGTEVVA
TNSRSHTCLLSGVFLGNVRVLARLQFGIHGSRDVAMKLAVRSEDEAVSDTIHEIVSSG

Protein No.: I-1180

Protein name and Species:

Actin-like protein (Fragment) OS=Eperua grandiflora GN=Act PE=3 SV=1

Accession: **tr|D5K0Z8|D5K0Z8_9FABA**

Unused ProtScore: **2**

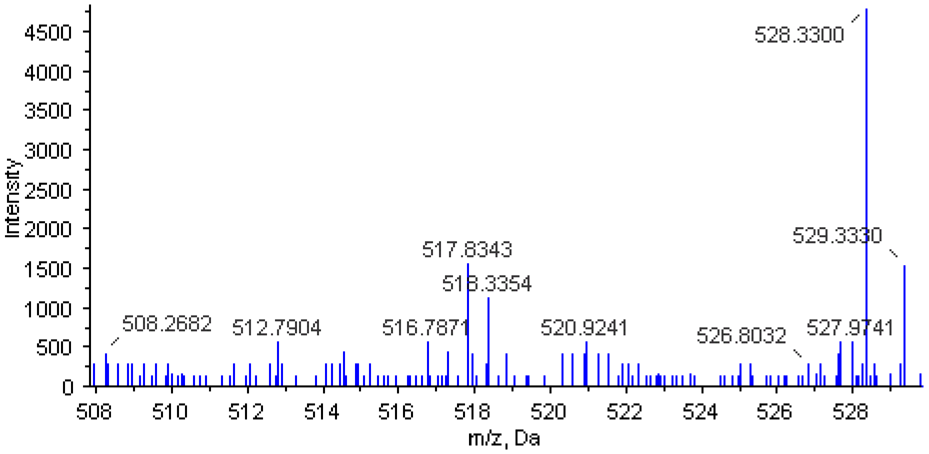
Seq Cov %: **37**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 60

116: 114=E5TL: D5TL=0. 29

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

FNAPAMYVAIQAVLSLYASGR**TTGIVLDSGDGVSHTVPIYEGYALPHAILR**LDLAGR**DLTDALMK**ILTE
RGYSFTTTAEREIVRDMKEKLAYIALDYEQELETSKTSSAVEK**SYELPDGQVITIGNER**FRCPEVLFQP
SMIGMEAA

Protein No.: I-1186

Protein name and Species:

Luminal-binding protein 5 OS=Populus trichocarpa GN=POPTRDRAFT_570800 PE=3 SV=1

Accession: **tr|B9I7J3|B9I7J3_POPTR**

Unused ProtScore: **2**

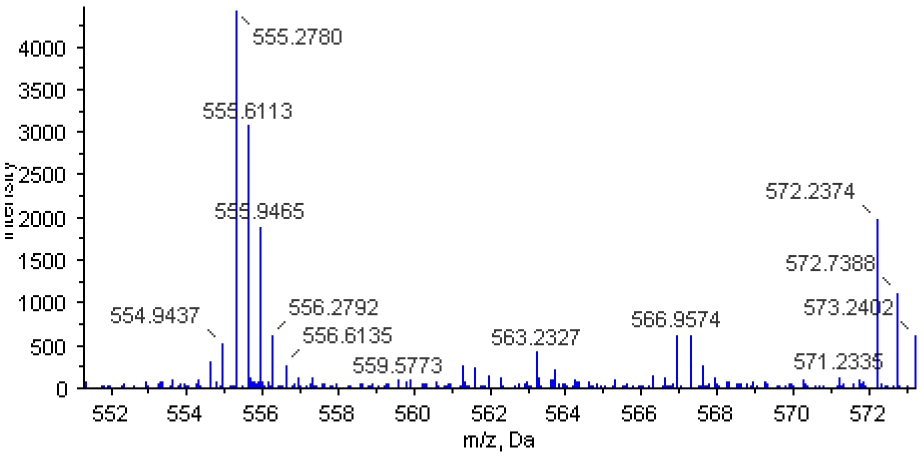
Seq Cov %: **8.5**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 60

116: 114=E5TL: D5TL=0. 25

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MRVKHKAAFAFLFLFVSEYYFLGLVVAADDGPKLGTVIGIDLGTTYSCVAVSR**DGHVEIIANDQGNR**VT
PSWVAFTDTERLIGEAAKNQAPMNPERTIFGVKRLIGRKFDDPEVQRDIKFLPYKVVNKDGKSYIQVKV
KGETKVFSPEEISAMILGKMKETAESYLGKK**IKNAVVTVPAYFNDAQR**QATKDAGIIAGLNVPR**IINEP**
TAAAIAYGLDKKGGDMNILVYDLGGGTFDVSILTIDNGVFEVLSTSGDTHLGGEDFDQRLMDYFINLVK
KKYNKDMSKDKKALGKLRRECERAKRALSSQHQVRVEIESLIDGIDFSEPITRARFEELNMDLFKKTLG
IVKKAMDDAGLKKADIKEIVLVGGSTRIPKVQEMLKEYFDGKEPNKGVNPDEAVAYGAAVQGGILSGEG
GEETKGLLLLDVTPLSLGIETVGGVMTKLIPRNTVIPTKKSQIFTTYQDQQTTVSIKVYEGERSLTKDC
RELGRFDLSGIPPAPRGVPQIEVTFEVDANGILHVKAEDKAAKKSQS**ITITNDK**GR**LSQEEIDR**MVK**EA**
EEMAEEDKKVREKIDARNKLETYIYNMRSTINDKDKLADKIDSDDKERIETALKEALEWLDDNQNAEKD
DYEEKLKEVEEVCDPVIKQVYEKSGSSADSEYEEPNDEL

Protein No.: I-1188

Protein name and Species:

Glyceraldehyde 3-phosphate dehydrogenase (Fragment) OS=Mallotus pierrei GN=G3pdh PE=3 SV=1

Accession: tr|B2X0F6|B2X0F6_9ROSI

Unused ProtScore: 2

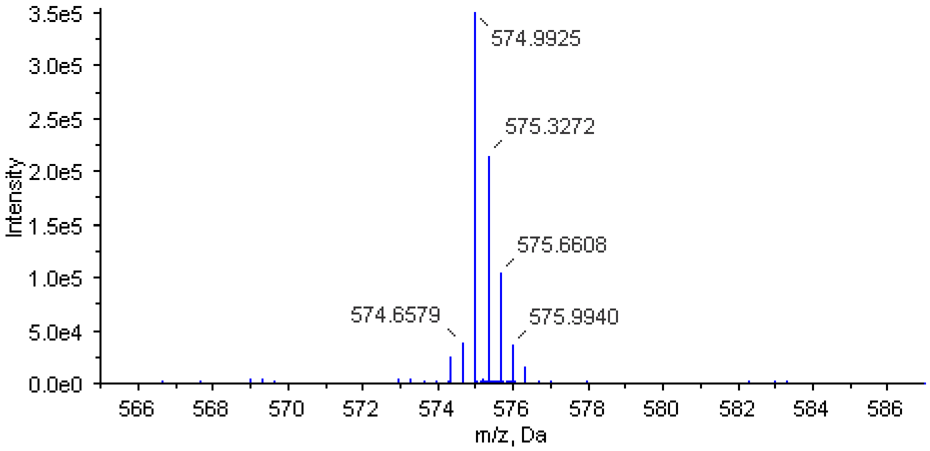
Seq Cov %: 45.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.65

116: 114=E5TL: D5TL=0.53

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

VXSITATQKTVDGPSMKDWRGGR**AASFNIIPSSTGAAK**AVGKVLPSLNGK**LTGMSFRVPTVDVSVVDLT**
VRLEKEASYDDIK**TAIKEESEGK**LKGILGYTED

Protein No.: I-1191

Protein name and Species:

Myosin-Vb-like [Vitis vinifera] OS=Vitis vinifera GN=VIT_13s0320g00070 PE=4 SV=1

Accession: **tr|F6GZ28|F6GZ28_VITVI**

Unused ProtScore: **2**

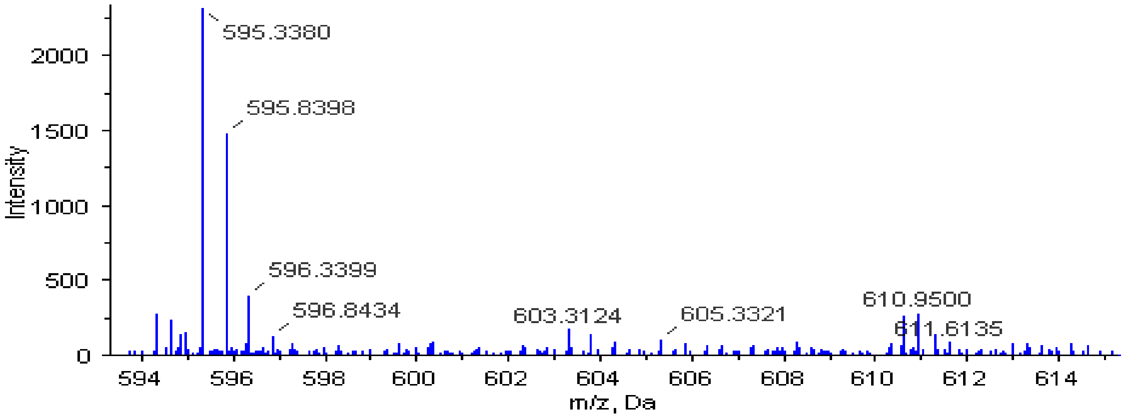
Seq Cov %: **2.9**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2. 58

116: 114=E5TL: D5TL=1. 98

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MIKGTPVNIIVGSHAWAEDPDAAWIDGEVIGIEGRNATIVTTDGKTIVADISNIYPKDTEAPPAGVDDM
TKLAYLHEPGVLHNLASRFALNEIYTYTGNILIAVNPFQRLPHLYDIHMMGQYKGAAFGELSPHLFAVA
DTCYRAMINEQK**SQSILVSGESGAGK**TETTKMLMRYLAFMGGRSGTEGR**TVEQQVLESNPVLEAFGNAK**
TVKNNNSSRFGKFVEIQFDKHGKISGAAVRTYLLERSR**VCQVSDPER**NYHCFYMLCAAPPEDVKKFKLG
DPRSFHYLNQTNCYEVANVNDAREYLETRNAMDVVGISQDEQDAIFRVVAAILHLGNIGFIKGKEADSS
KLKDEKALYHLRTAAELLMCDEKALEDSLCQRVIVTPDGNITKPLDPDLAVFSRDALAKTVYSRLFDWI
VDKINSSIGQDPNATSIIGVLDIYGFESFKINSFEQLCINLTNEKLQQHFNQHVFKMEQEEYKREEINW
SYVEFIDNQDVLDLIEKKPGGIIALLDEACMFPKSTHETFAQKMYQTYKGHKRFSKPKLARTDFTINHY
AGDVIYQADQFLDKNK**DYVVAEHQALLNASK**CPFVANLFPLLSEEASKQSKFSSIGTRFKQQLQALMET
LSTTEPHYIRCVKPNAVLKPAIFENFNVLNQLRCGGVLEAIRISCAGYPTKRTFDEFFDRFGMLAPDVL
DGADEKSACIAICDRMGLKGYQIGKTKVFLR**AGQMAELDAR**RTEVLANAARRIQRQIQTHLTRKEFIRQ
RRATIHMQKLWRAQLARKLYESMRREAASVCVQKNVRAHTARRNYTNLQASAMAIQTGLRAMAARNEFR
YRRRTKAATLIQTQWRGFQAFSAYNQQKKATLTLQCLWRGRAARKELRKLRMAARETGALKEAKDKLEK
RVEELTWRLEFEKHLRIDVEEAKGQEISKLQNALLEMQVQLEEAHAAIIREKEAAKIAIEQAPPVLKEV
PVVDNTKMDLLKNQNEELEGEVSELKKMVAEFEQKYCEAQKENTARLKEAEESFTRTSQLQETIERLEL
NLSNLEAENQVLRQQALVASTNEDLFEEMKILKDKIANLESENEVLRNQPTSIEQVAALERVPPQVKSF
DNGHKMEEELQTTKELVPFAPILTKQRSLTDRQQENHDVLIKCLMEDKRFDKNRPVAACIVYKALLQWR
SFEAEKTNIFDRIIHTIRSSIESQESISNLAYWLSTTSTLLFLVQSTLKASNTPNVTSFRSRNSPTTLF
GRMAQGLRSSSFPMGVSSGYSGMVGKPNTHSKVEPKYPALLFKQHLTAYLEKIYGMIRDSLKKEISPFL
NLCIQAPRSTRARSIRGSSKNIHSNIVAKQQASNIHWQNIVNSLDHTLGIMSENHVPSMITRKIFSQVF
SFINVQLFNSLLLRRECCSFSNGEYVKAGLQELEQWCFKAKDEFAGSSWDELQHIRQAVGFLVLHQKPQ
KFLDDITNELCPMLSIPQIYRIGTMFWDDKYGTHGLSPDVIGKMRVLMTEDSINMPNNSFLLDVDSRIP
FSMEEMSRSLIDINLSYVDPPPLLRQRSDFHFLLQPTD

Protein No.: I-1195

Protein name and Species:

Fructokinase-5-like [Vitis vinifera] OS=Vitis vinifera GN=VIT_15s0048g01260 PE=3 SV=1

Accession: **tr|D7U7P5|D7U7P5_VITVI**

Unused ProtScore: **2**

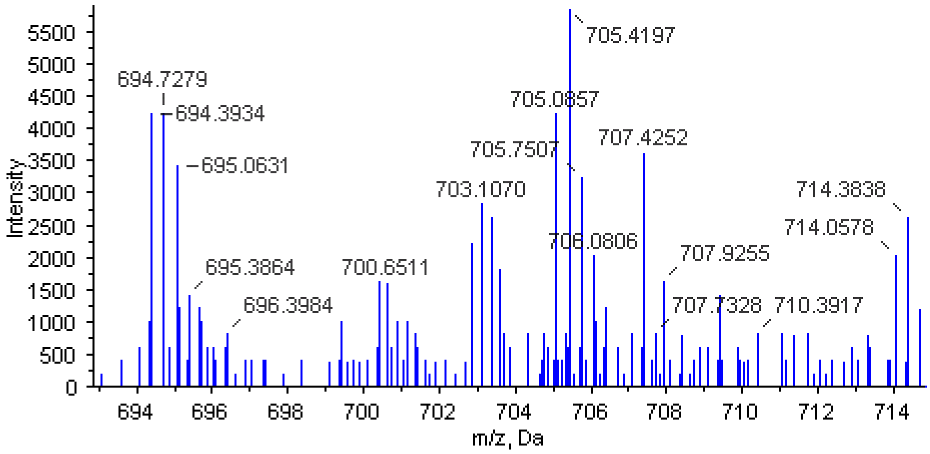
Seq Cov %: **11.3**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2. 05

116: 114=E5TL: D5TL=1. 05

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSKSNRSKDDEARMSGCCFPVNLDRSMKSGLSFKKSSSGSFKGESQEKRPLVVCFGEMLIDFVPTVGGVSLSESPAFKKAPGGAPANVAVGISR**LGGSSAFIGK**VGEDEFGFMLADILKQNNVDSSGMRFDRNAR**TALAFVTLR**DDGEREFMFFRNPSADMLLRESELDANLIKKASIFHYGSISLIEEPCKSAHLAAMNIARKSGSILSYDPNLRLPLWPSPETARKTIMSIWNQADLIK**ISEEEITFLTGGDDPNDDNVVLK**KLYHSNLKLLVVTEGSNGCRYYTKEFKGRVTGVKVKAVDTTGAGDAFVGGILNSLAADLNLYKNEEKLREALLFANACGAITVTERGAIPALPTKEAVLQILPKANA

Protein No.: I-1196

Protein name and Species:

Ripening-reduced alpha-L-arabinofuranosidase OS=Carica papaya PE=2 SV=1

Accession: tr|C9EA44|C9EA44_CARPA

Unused ProtScore: 2

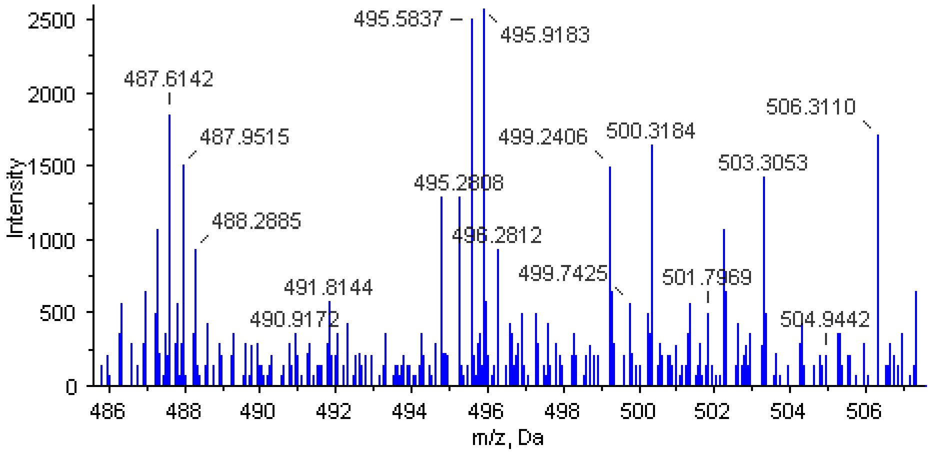
Seq Cov %: 5.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.65

116: 114=E5TL: D5TL=0.53

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MLWADYAKFLCGEVTMSSCKAASSFSSFLCFFLGACCVYQCFALEVGANVTARLIVDASQGASRPMPET
LFGIFFEQEINHAGAGGLWDELVSNRGGFEAGGPNTPSNIDPWSIIGDESSVTVSTERSSCFERNKVAL
R**MEVLCDSR**GANICPSGGVGVYNPGFWGIFLCQNIEQGKKYKVVLYVRSPGAIDLSVSLTSSNGSRTLA
SSNVIASSSDVSNWTKKELLLEAKGTDPHSRLQLTTARKGVIWLDQVSAMPLDTYKVQGHGFRSDLVEM
LLDIKPRFIRFPGGGCFVEGEWLRNAFRWKESIGPWEERPGHFGDVWNYWTDDGLGYFEFLQVGLAEDL
GALPIWVFNNGIGISHNDQVDTSTVLPFVQLQEALDSIEFARGDPDSRWGSVR**AAMGHPEPFDLR**FVAL
GNEDCWKKNYWPGNYLRFYYAIKRAFPDIK**IISNCDGSSR**QLDHPTDYYDFHVVYTSSSNLFSMSHKFD
HASRNGPKVW**AFVSEYAVTGK**DAGTGSLLAALAEAGF**LIGLEK**NSDLVEMTSYAPLFVNVNDRRWNPDA
IVFDSYRQYGTPSYWVQQFFAESSGATLLNSTLQIDSTSLIASAISWQDEKADKKYIRINVNFGSNAVT
LRIYVDGMDPNVARLSGLTETVLRSDNVMDENSFENPEKVRLLFLFLLENAGEDIEVELSPHSFTSFDL
LKEYANIRIAGFDSFSKSST

Protein No.: I-1203

Protein name and Species:

Ras-related protein RHN1-like [Glycine max] OS=Glycine max PE=2 SV=1

Accession: tr|C6TED4|C6TED4_SOYBN

Unused ProtScore: 2

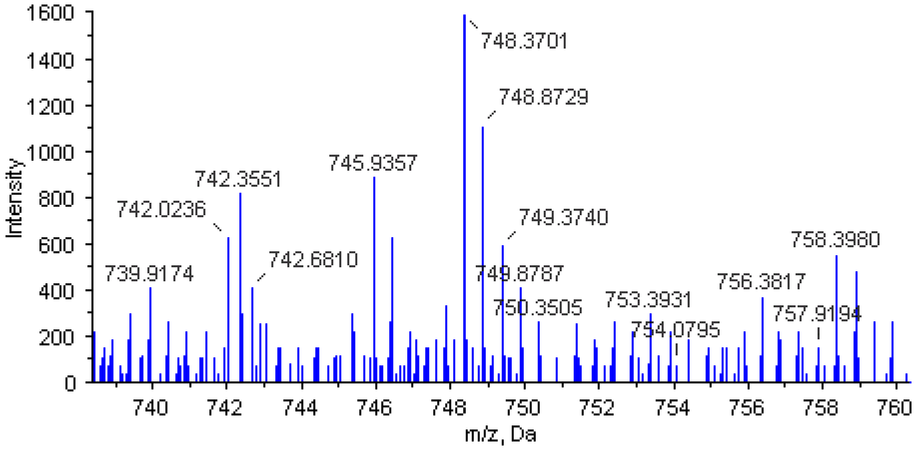
Seq Cov %: 16.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1. 85

116: 114=E5TL: D5TL=1. 08

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MATIGHNNLNAKLVGPSSLFSISFCFFFLSQSFSIPMMFSPCSFHQVLLGDMGAGKSSLVLRFVKGQFL
EFQESTIGAAF**FSQTLAVNDATVKFEIWDTAGQER**YHSLAPMYYRGAAAAIIVYGITSSDSFTRAKKWV
QELQKQGNPNMVMALAGNKADLEDKRKVTAEEARVYAEENGLFFMETSAK**TASNVNDIFYEIAK**RLPRA
QPAQNPAGMVLVDRPAEGTRAASCCS

Protein No.: I-1206

Protein name and Species:

Enolase OS=Helianthus annuus GN=ENO1 PE=2 SV=1

Accession: tr|A9P745|A9P745_HELAN

Unused ProtScore: 2

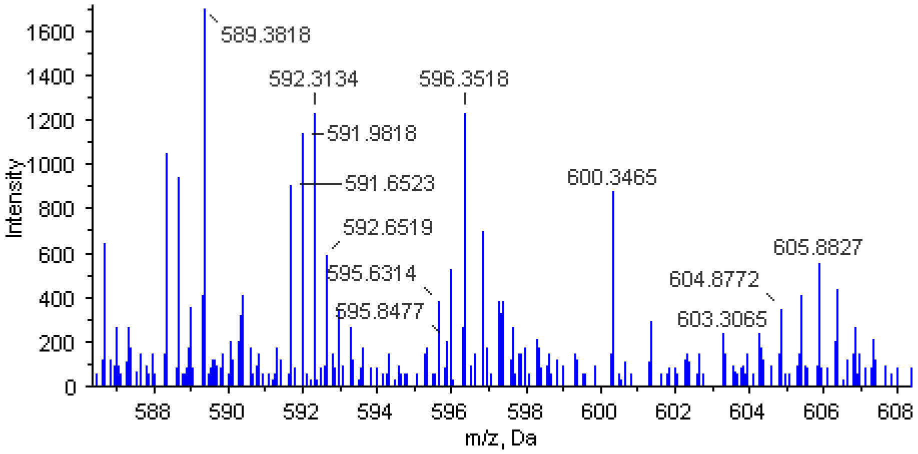
Seq Cov %: 6.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 19

116: 114=E5TL: D5TL=0. 23

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MALAPPTTTTSLSNPLLSSKPSLSSPFVNLPTVSRRSPTKFTVRNSVSVAQSPSVSAAKSSTVKSVKAR
QIIDSRGNPTVEVDLVTDGLYRSAVPSGASTGIYEALELRDGDKSVYGGKGVLNAVKNINEVLGPKLIG
VDVRNQAEFDGIMLEIDGTPNKSKLGANAILGVSLSACRAGAGAKSIPLYKHIQEISGTKELVMPVPAF
NVINGGSHAGNNLAMQEFMILPVGATSFAEALRMGSEVYHTLKGIIKAK**YGQDACNVGDEGGFAPNVQD**
NREGLVLLIDAIEKAGYTGKIKIGMDVAASE**FLTK**DGKYDLNFKKQPNDGAHVLSAPSLGDLYREFVRD
FPIVSIEDPFDQDDWTSWTSLQSSVDIQLV**GDDLLVTNPK**RIAEGIQKK**ACNALLLK**VNQIGTVTESIQ
AALDSKAAGWGVMVSHRSGETEDNFIADLSVGLASGQIKTGAPCRSERLAKYNQLLRIEEELGNVRYAG
EAFRSP

Protein No.: I-1207

Protein name and Species:

Rubber elongation factor protein, putative OS=Ricinus communis GN=RCOM_1433280 PE=4 SV=1

Accession: tr|B9RFA8|B9RFA8_RICCO

Unused ProtScore: 2

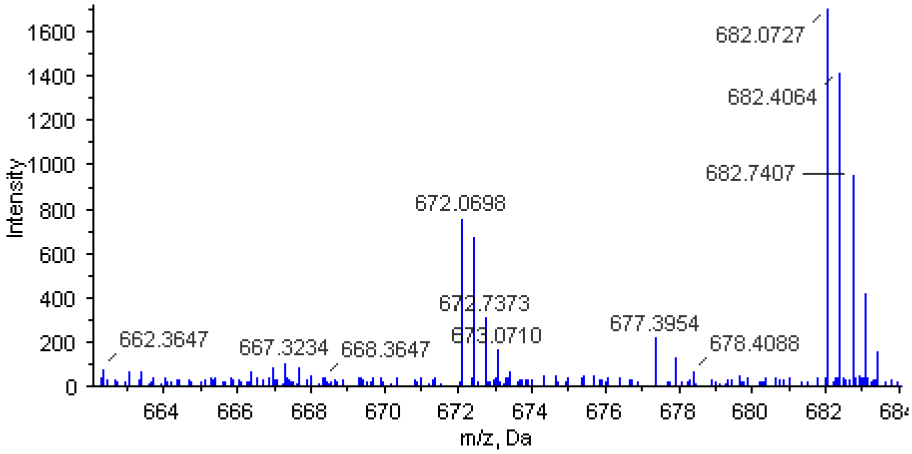
Seq Cov %: 11.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1. 51

116: 114=E5TL: D5TL=0. 72

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAEQNVNLQQQMAKENEERLKYLEFVQVAALHAVMTFANLYVYAKDK**AGPLKPGVETVEGTVK**SVVGPV
YDKFHDVPIEVLKFVDRKVDESVTKLDRRVPPVVK**QVSAQAYSVAR**EAPVAARAVASEVQRTGVKETAS
GLAKTLYAMYEPKAKELYSKYEPKAEQCAVSAWRK**LNQLPLFPQVAQVFVPTAAYCSEK**YNQTVVSTAE
KGYR**VSSYLPLVPTQK**IAQVFRNEVPESAPIASS

Protein No.: I-1210

Protein name and Species:

RNA recognition motif-containing protein [Arabidopsis thaliana]

OS=Arabidopsis thaliana GN=At4g17720 PE=2 SV=1

Accession: tr|Q8LA96|Q8LA96_ARATH

Unused ProtScore: 2

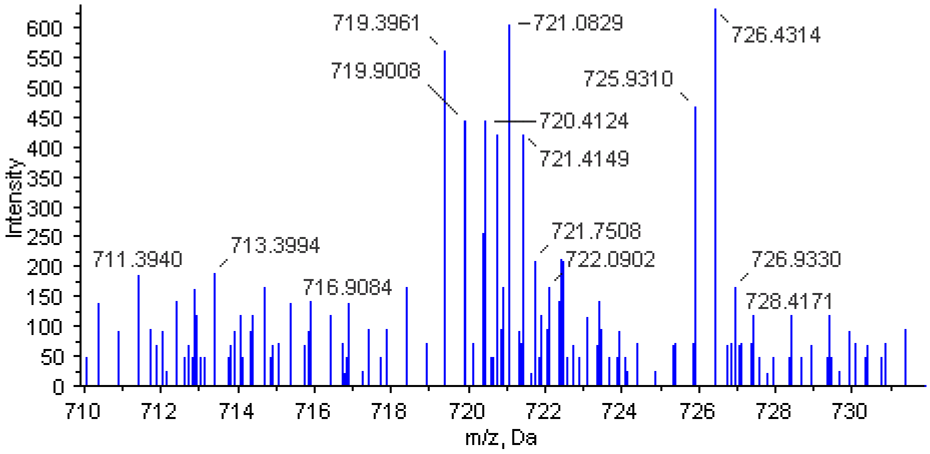
Seq Cov %: 6.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=5. 40

116: 114=E5TL: D5TL=1. 25

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MTMTTVKVSNVSLGATDRDLKEFFSFSGDILYLETQSETERTKLAYVTFKDLQGAETAVLLSGATIVDS
SVIVSMAPDYQLSPEALASLEPKDSNKSPKAGDSVLRK**AEDVVSSMLAK**GFILGKDAIAKAKSVDEKHQ
LTSTASAKVASFDKKIGFTDKINTGTVVVGEKVREVDQKYQVSEKTKSAIAAAEQT**VSNAGSAIMK**NRY
VLTGATWVTGAFNKVAKAAEEVGQKAKEKVGMAEEEDKRKVVDEFARVHLSESPKAASSTQEAERESKL
SESPEAKKDSEHLEPQSKPLQQQSPPPMASAPAPAQP

Protein No.: I-1211

Protein name and Species:

GTP-binding protein OS=Nicotiana tabacum GN=SUP1 PE=2 SV=1

Accession: tr|Q40581|Q40581_TOBAC

Unused ProtScore: 2

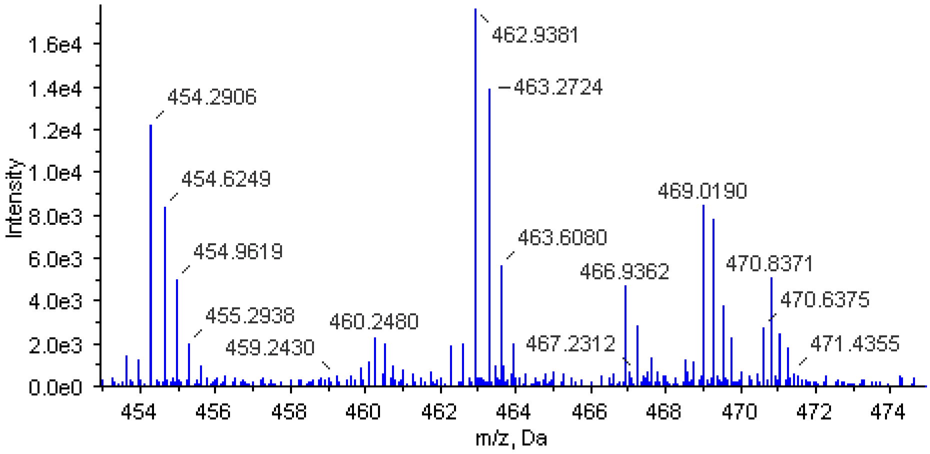
Seq Cov %: 5.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 20

116: 114=E5TL: D5TL=0. 51

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MVNVEDGKPEEAIKPEKTNGEDSAMAEEGEAGDDEKPDIPEDELKDEAHPDLEPKNVEPKGIAGKEASP
PEDIQDEVEVNKKRHLNVVFIGHVDAGK**STIGGQILLLSGQVDDR**TIQKYEREAKDKNRESWYMAYIMD
TNEEERVKGITVEVGRAHFETDTTR**FTILDAPGHK**SYVPNMISGRSQADIGLLVISARKGEFETGYERG
GQTREHVQLAKTLGVTKFLVVVNKMDDPTVNWSKERYDEIESKMVPFLRSSGYNVKKDVQFLPISGLLG
SNLKTRMEKSVCPWWNGPCLFETLDAVEVPPRDPNGPLRMPIIDKFKDMGTVVMGKIESGSIHEGDNLL
IIPNKAAVKVLAIFCDEDKVRHVGPGENVRVRLSGVEEDDILSGFVLCSVAKPIHAVTEFVAQLQILEL
LDNAIFTAGYKAVLHIHSVVEECEIVELMQQIDLKTKKPMKKKPLFVKNGAIVLCRVQVNNLICVEKFS
DFAQLGRFTLRTEGKTVAVGKITALPTVADNA

Protein No.: I-1214

Protein name and Species: **FAS-associated factor 2 OS=Populus trichocarpa GN=POPTRDRAFT_548279 PE=4 SV=1**

Accession: **tr|B9GK93|B9GK93_POPTR**

Unused ProtScore: **2**

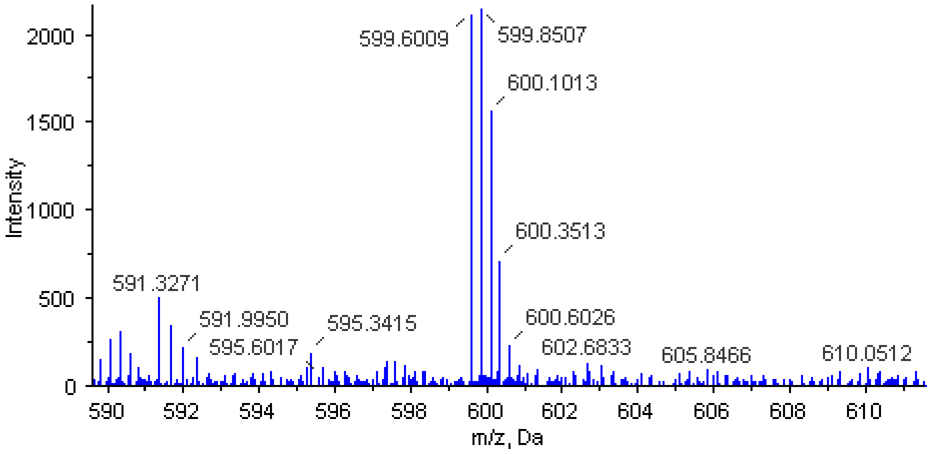
Seq Cov %: **6.3**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 48

116: 114=E5TL: D5TL=1. 01

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MVDVADKLACFRAITGLEDSDLCTEILQAHNWDLELAISSFTSNHSDNHPFSSSYTATDTTATAVDPSN
ATIHRSDSTSIVPAGAPPPGLAWKIVTLPISVISGSLGLISGAVGFGLWAAGGVLSYSLGFIGLGSNSG
RGGDSSAQLVTVSAASREAMEFVAQFERDYGSGSSTRPNFVSEGFMDALTRSRNTFKLLFVYLHSPDHL
DTPAFCEGTLCSEVLSAFVNENFVAWGGSIRGSEGFKMSNSLKASRFPFCAVVMSSTNQRIVLLQHVEG
PK**SPEEMLVILQR**VLEQSAPVLVTARLEAEERTTNMR**LREEQDAAYR**AALEADQARERQQREEQERLER
EAAEAERKRREEEEARDRAASEAAENEAALARMRQEK**ALSLGAEPEKGPDVTQVLVR**FPTGERKERRFH
CAATIQSLYDYVDSLGSLNVENYSLVSNFPRVVYGTDKVSLSLKEAGLHPQASLFVELN

Protein No.: I-1225

Protein name and Species:

carboxymethylenebutenolidase, putative OS=Vitis vinifera GN=VITISV_041925 PE=4 SV=1

Accession: tr|A5AEX6|A5AEX6_VITVI

Unused ProtScore: 2

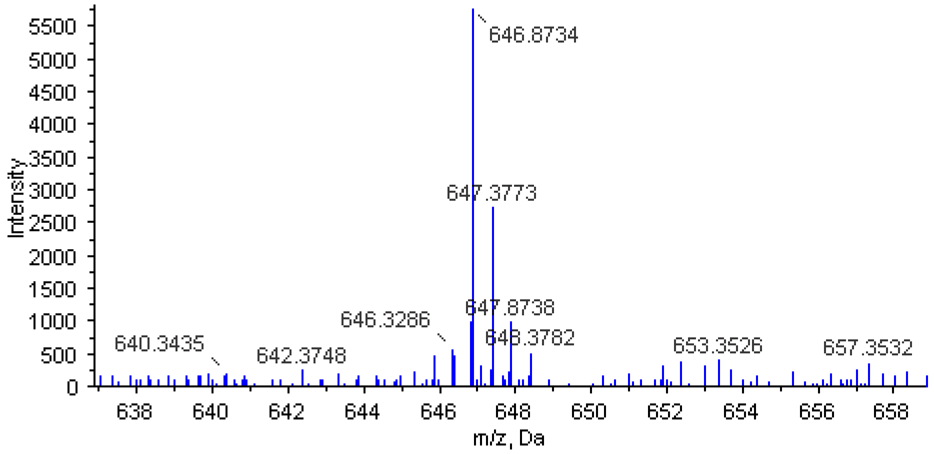
Seq Cov %: 3.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 66

116: 114=E5TL: D5TL=0. 63

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAESASSPFKKIQIQR**DDTTFDAYVVGK**EDAPGIVVVQEWWGVDYEVKNHALK**ISQLDPGFKALIPDLY**
RGKVGLDVAEAQHLMDGLDWQGAVKDICASVNWLKANGSQKVGVTGYCMGGALSIASSVLLPEVDAVVA
FYGVPSSELADPAKAKAPVQAHFGELDSFVGFSDVTAAKALEEKLKASGVPYEVHIYPGNGHAFMNRSP
EGIQRRKGMGMPDEDEDAVGLAWSRFRAWMSCYLSP

Protein No.: I-1228

Protein name and Species:

Prefoldin subuni OS=Populus trichocarpa GN=POPTRDRAFT_714512 PE=4 SV=1

Accession: **tr|B9H401|B9H401_POPTR**

Unused ProtScore: **2**

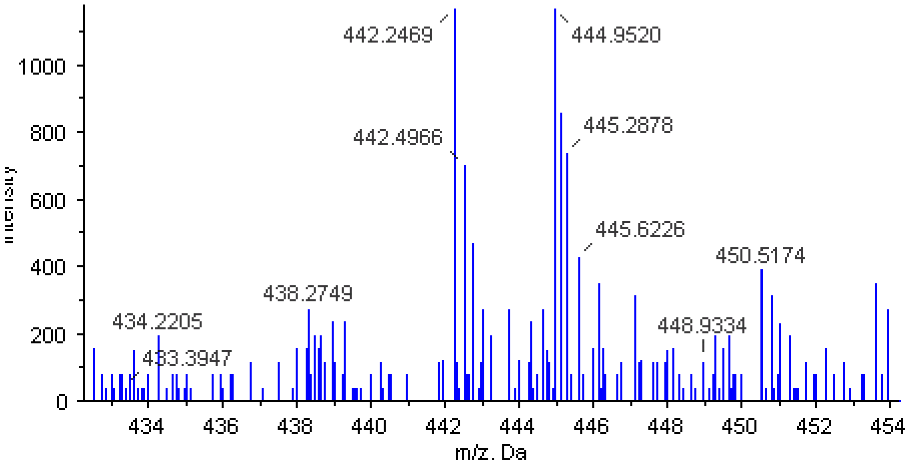
Seq Cov %: **16.8**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 61

116: 114=E5TL: D5TL=0. 52

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

AIRELQRDLENKANDLSKLQKDIAKNHQVRKKYTIQLGENELVLK**ELDLLNEGANVYKLIGPVLVK**QDL
AEANANVSKRIEYISAELKRLDGTLQDLEEKQNSKKDAIFKLQQRIQSFQAGKAKA

Protein No.: I-1231

Protein name and Species:

60S ribosomal protein L14-2-like [Vitis vinifera] OS=Vitis vinifera GN=VIT_05s0049g01310 PE=4 SV=1

Accession: tr|D7SZI9|D7SZI9_VITVI

Unused ProtScore: 2

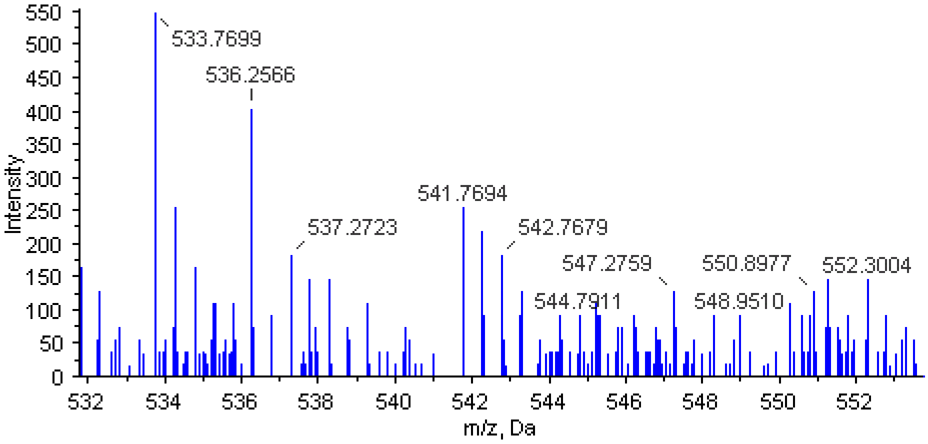
Seq Cov %: 8.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2. 29

116: 114=E5TL: D5TL=3. 08

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MEFFNLYNLHGHKVLNQIRLISGFNSPKKAQRASKPNTIVTQRSRTQIGPKRTIKKPRKTLSPVSPSTP
LASSIFPLPAVSRALANMPFKRYVEVGRVALVNYGKDYGRLVVIVDVIDQNR**ALVDAPDMVR**CQMNFKR
LSLTDIKIDIKRVPKKKTLIEAMTAADVKNKWENSSWGRKLIVQKRR**ASLNDFDR**FKIMLAKIKRGGVI
RQELAKLKKQTAS

Protein No.: I-1236

Protein name and Species:

chitinase 1 OS=Populus trichocarpa GN=POPTRDRAFT_557015 PE=4 SV=1

Accession: tr|B9HQZ2|B9HQZ2_POPTR

Unused ProtScore: 2

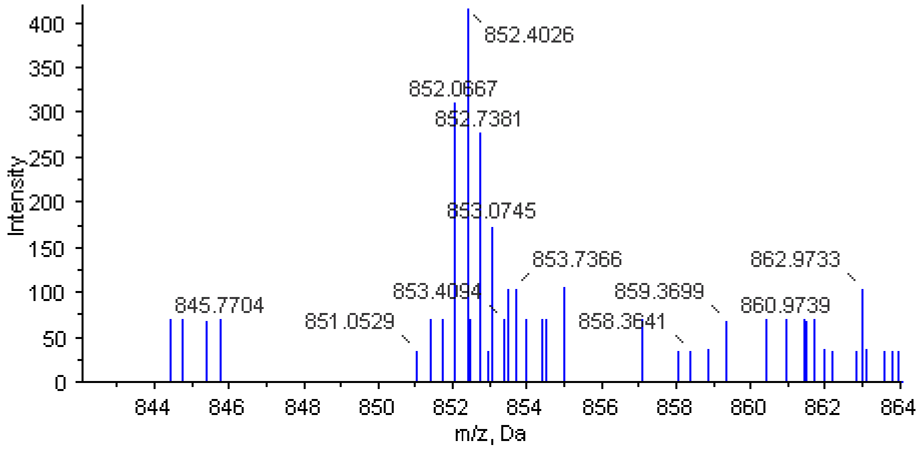
Seq Cov %: 6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 52

116: 114=E5TL: D5TL=0. 37

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MKMWVFTVFSLLLSLLLGGSAEQCGSQAGGALCPGGLCCSQFGWCGSTNDYCGNGCQSQCGGASGGDLG
SIISSEKFDEMLKHRNDGGCPGKGFYTYSAFISAANAFPGFGTTGDADTRKREIAAFLGQTSHETTGGW
QTAPDGPYAWGYCFVK**EQNPGSYCSPSSTYPCADGK**QYYGRGPVQLSWNYNYGQCGKAIGVDLLNNPDL
VATDPVISFKTAIWFWMTAQSPKPSCHSVITGNWSPSGADSAAGRVPGYGVLTNIINGGLECGMGWKQQ
VEDR**IGFYK**R**YCDLLGVGYGNNLDCYNQK**SFANGLLDMVDSM

Protein No.: I-1247

Protein name and Species:

ADP-ribosylation factor, putative OS=Ricinus communis GN=RCOM_0060350 PE=3 SV=1

Accession: tr|B9SYE9|B9SYE9_RICCO

Unused ProtScore: 2

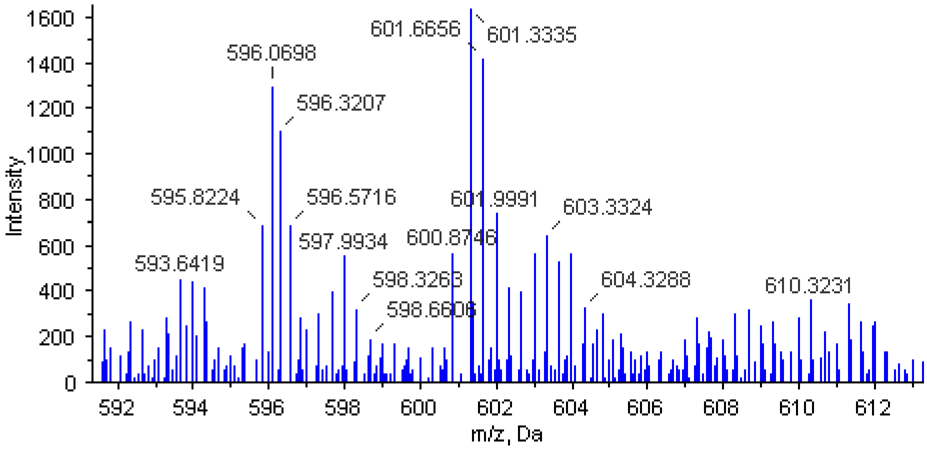
Seq Cov %: 8.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 34

116: 114=E5TL: D5TL=0. 82

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGLLDSLLNWLRSLFFKQEMELSLVGLQNAGKTSLVNAVATGGYSEDMIPTVGFNMRKVTKGNVTIKLW
DLGGQRRFRTMWERYCRGVSAILYVVDAADRDSVPIARSELHDLVVKPSLSGIPLLVLGNKIDKSEALS
K**QALVDQLGLESITDR**EVCCYMISCKDSVNIDVVIDWLIKHSKTAK

Protein No.: I-1275

Protein name and Species:

V-type proton ATPase subunit F OS=Ricinus communis GN=RCOM_1381970 PE=3 SV=1

Accession: **tr|B9S7V3|B9S7V3_RICCO**

Unused ProtScore: **2**

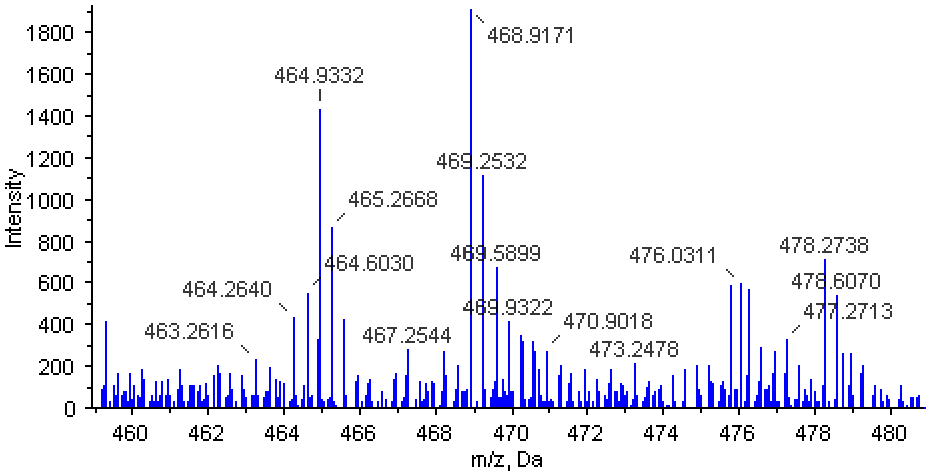
Seq Cov %: **9.2**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 61

116: 114=E5TL: D5TL=1. 16

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MANRNQIRTNNSALIAMIADEDTVVGFLLAGVGNVDLRRKTNYLLVDSKTTVKQIEDAFKDFTTREDIA
IVMISQYVANMIRFVVDSYNKPVPAILEIPSKDHPYDPSQDSVLSRVK**HLFSAESVASGR**R

Protein No.: I-1278

Protein name and Species:

nuclear transport factor 2 isoform 1 OS=Populus trichocarpa GN=POPTRDRAFT_548036 PE=2 SV=1

Accession: tr|A9PBT2|A9PBT2_POPTR

Unused ProtScore: 2

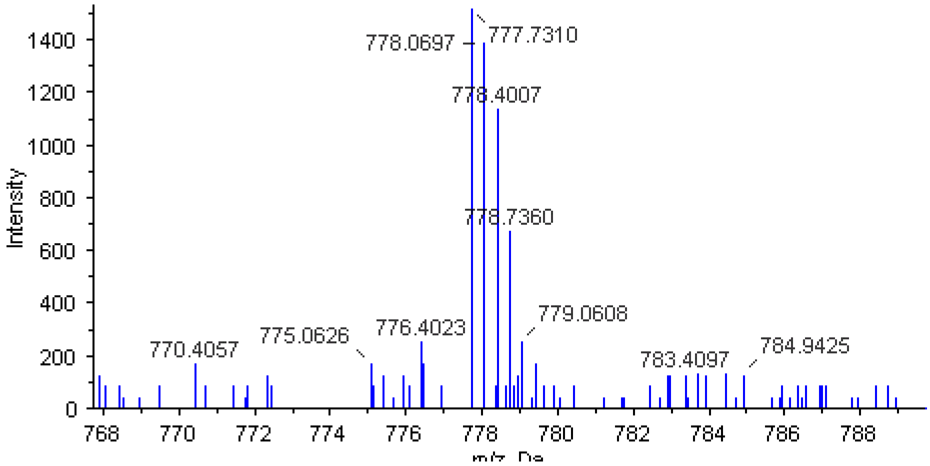
Seq Cov %: 27.6

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.39

116: 114=E5TL: D5TL=0.95

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDPDQVAKAFVEHYYSTFDANR**AGLANLYQDGSMLTFEGQK**TQGSQNIVAKLIALPFQQCKHLITTVDC
QPSGPAGGMLVF**VSGNLQLAGEQHALK**FSQMFHLMPTPQGSFYVFNDIFRLNYA

Protein No.: I-1281

Protein name and Species:

nuclear transport factor, putative OS=Populus trichocarpa PE=4 SV=1

Accession: tr|A9PE14|A9PE14_POPTR

Unused ProtScore: 2

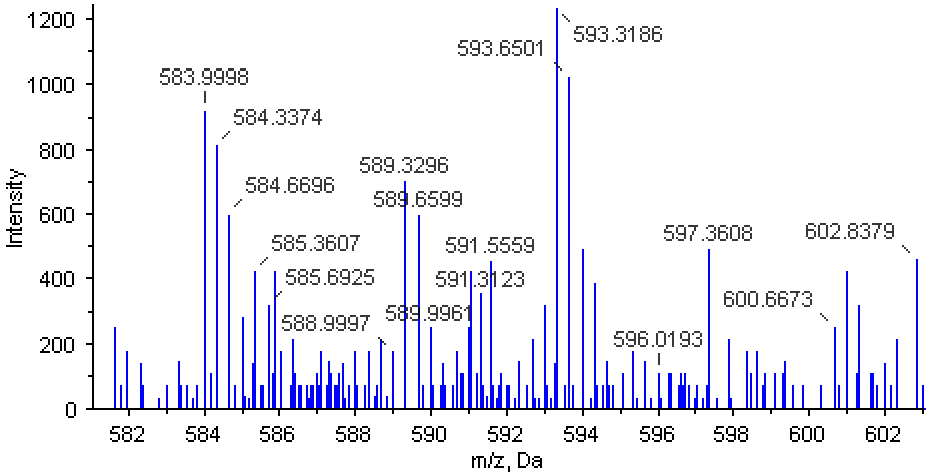
Seq Cov %: 29.8

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 51

116: 114=E5TL: D5TL=1. 43

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDPDTVAKAFVEHYYNMFDSNR**AGLANLYQDASMLTFEGQK**TQGSQNIVAKLTALPFHQCKHHITTVDC
QPSGPAGGMLVF**VSGNLQLAGEQHALK**FSQGSYYVYNDIFRLNYA

Protein No.: I-1318

Protein name and Species:

Putative uncharacterized protein OS=Vitis vinifera GN=VIT_01s0011g00830 PE=4 SV=1

Accession: **tr|F6HF70|F6HF70_VITVI**

Unused ProtScore: **2**

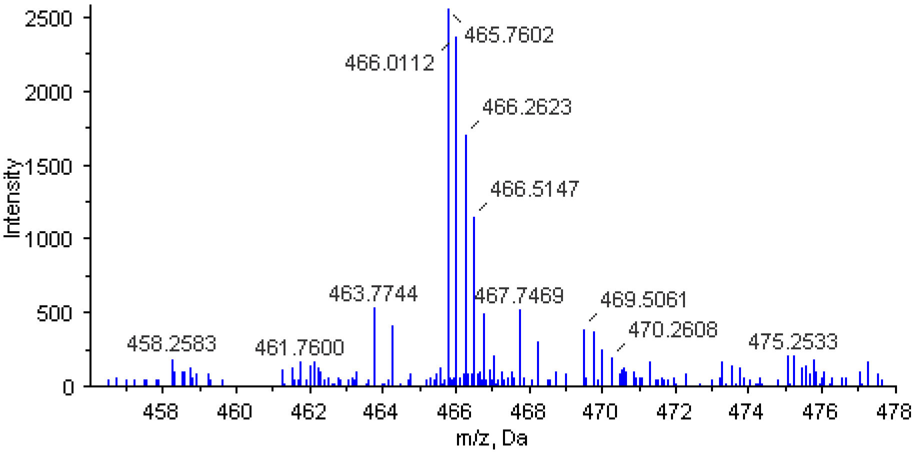
Seq Cov %: **8.9**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 52

116: 114=E5TL: D5TL=0. 12

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MMMVKQHGHDTVKEASPPHISTGEGGVKASSPLFDPSLCKTSSEFLSFQTSMDPTSHHRPGSHPQKHHQ
PSSSELLSSAKVVAEAAQASFHHESEKVDKSR**VAGAAADILGAASHYGK**LEEKSFGKYVEKAETYLHQY
QSSHSTTTTINSGHSTTNTTETHSSSHSGGGDSHSGGGYGDYLKMAEGFLKKY

Protein No.: I-1320

Protein name and Species:

heat shock factor-binding protein-like OS=Ricinus communis GN=RCOM_1439840 PE=4 SV=1

Accession: **tr|B9T0W0|B9T0W0_RICCO**

Unused ProtScore: **2**

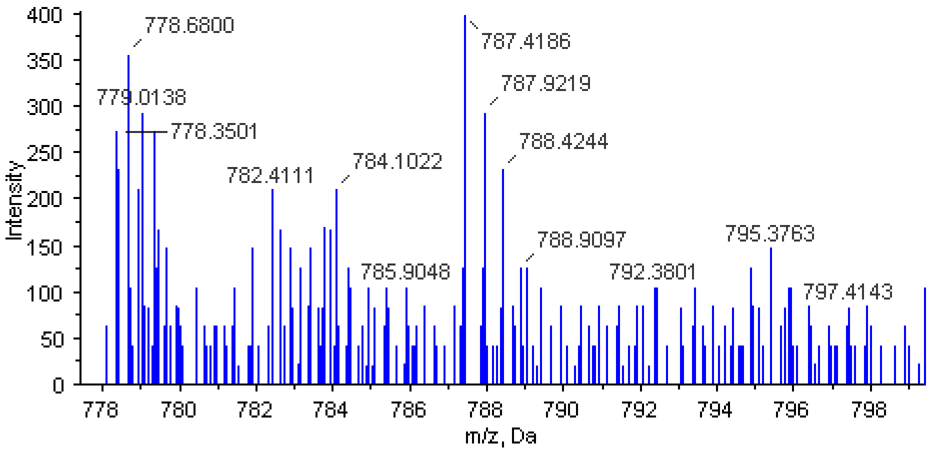
Seq Cov %: **16.7**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2. 07

116: 114=E5TL: D5TL=1. 03

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDGHD**SEDPK**QSTADMTVFVQNLLQQMMGTR**INDLEQSINDLR**SEMGVEGSPSPLCQSKQKSGEENQDD
ALA

Protein No.: I-1336

Protein name and Species:

Calcium lipid binding protein, putative OS=Ricinus communis GN=RCOM_0491050 PE=4 SV=1

Accession: tr|B9SXV3|B9SXV3_RICCO

Unused ProtScore: 1.95

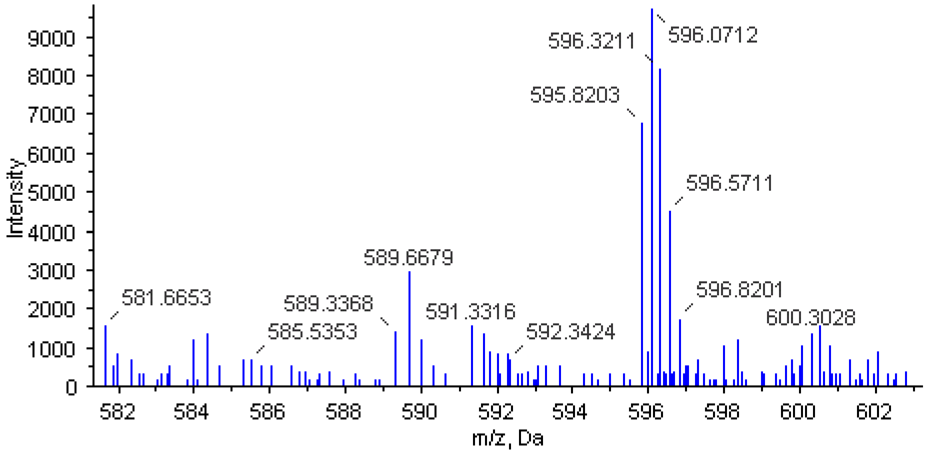
Seq Cov %: 11.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1. 67

116: 114=E5TL: D5TL=4. 33

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGFFSTIFGFCGFGVGISMGLVIGYYLFIFFQPTDVKEPEIRPLVEEDSETLQRMLPEIPLWVKNPDYD
RIDWLNKFLEYMWPYLDKAICKTAKNIATPIIAEQIPKYKIDSVEFETLTLGTLPPTFSGMKVYVTDEK
ELILEPCLK**WAGNPNVTVAVK**AFGLK**ATAQVVDLQVFALPR**ITLKPLVPSFPCFATIYVSLMEKPHVDF
GLK**LSGADIMSIPGLYR**L**VQEIIK**DQVANMYLWPKTLEVQVMDPAKALKRPVGILNVKVVRAMKLKKK**D**
LLGASDPYVKIK**LTEDKLPSK**KTTVKHKNLNPEWNEEFNLVVKDPETQAVEFHVYDWEQVGKHDK**MGMN**
VVPLKELSPEEPKLTTLDLLKNMDLNDSQNEKSRGQWRLH**VEVVSTSSR**MGLLHPK**ESLGYVDISLADV**
VSNKRINEKFHLIDSKNGRIQIELQWRTSS

Protein No.: I-1337

Protein name and Species:

heat shock 70 kDa protein, mitochondrial-like [Vitis vinifera] OS=Vitis vinifera GN=VIT_00s0415g00030 PE=3 SV=1

Accession: tr|F6HCT7|F6HCT7_VITVI

Unused ProtScore: 1.94

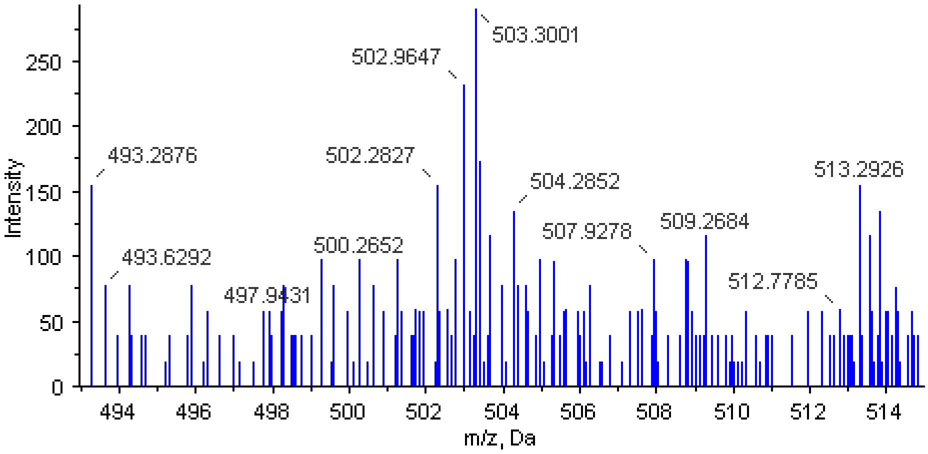
Seq Cov %: 4.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1. 96

116: 114=E5TL: D5TL=1. 54

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MATSVLLRCLKRRDLQSSSLAAYRSLTGNAKTSVSTSPAVQKWASYIRPFSSKPAGNDVIGIDLGTTNS
CVSVMEGKNAKVIENSEGARTTPSVVAINQKGELIVGTPAKRQAVTNPTNTVFGTKRLIGRRFDDPQTQ
KEMKMVPFKIVRAPNGDAWVEANGQQYSPSQIGAFVLTKMKETAEAYLGKTVSKAVITVPAYFNDAQRQ
ATKDAGRIAGLDVQRIINEPTAAALSYGLNNKEGLIAVFDLGGGTFDVSILEISNGVFEVKATNGDTFL
GGEDFDNALLEFLVSEFKRTEGIDLTKDRLALQRLREAAEKAKIELSSTSQTDINLPFITADASGAKHL
NITLTRSKFEALVDKLIERTRNPCKSCLKDAGISVKEVDEVLLVGGMTRVPK**VQEVVAEIFGK**SPSK**GV**
NPDEAVAMGAAIQGGILRGDVKELLLLDVTPLSLGIETLGGIFTRLINR**NTTIPTK**KSQVFSTAADNQT
QVGVKVLQGEREMATDNKLLGEFELVGIPPAPRGMPQIEVTFDIDANGIVTVSAKDKSTGKEQQITIRS
SGGLSDDEIEKMVKEAELHAQRDQERK**ALIDIR**NSADTTIYSIEKSLDEYRDKIPAEVAKEIEAAVADL
RDAMQKENIDEIKAKLDAANKAVSKIGQHMSGGSGGAASGGSEGSTSSDQTPEAEYEQAKK

Protein No.: I-1341

Protein name and Species:

Predicted protein OS=Populus trichocarpa GN=POPTRDRAFT_1115857 PE=4 SV=1

Accession: tr|B9N560|B9N560_POPTR

Unused ProtScore: 1.92

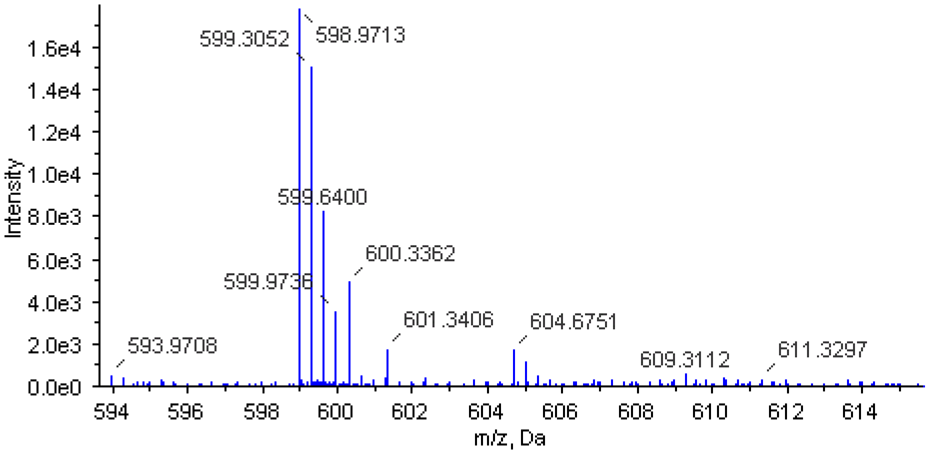
Seq Cov %: 11.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 62

116: 114=E5TL: D5TL=0. 58

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MNPQQQQQQQQQQQQNPVDPDQPLLPTIKIHHHPSPPRHPHPPSATPTLTPTTRRK**IGVAVDLSDESAY**
AVRWSVHHYIRPGDSVILLHVSPTSVLLGADWGPLPLSTPTQSQLDLLNNNSKFNSEIDSKTKNENSEK
PQPRQEDDFDAFTASKAADIARPLKEAQIPYKIHIVKDHDMKERLCLEIER**LGLSAVIMGSR**GFGAAIR
GSDERLGSVSDYCVHHCFCPVVVVRYPEDKDCGRD

Protein No.: I-1346

Protein name and Species:

Serine/threonine-protein kinase, putative OS=Ricinus communis GN=RCOM_1590280 PE=4 SV=1

Accession: tr|B9R7B8|B9R7B8_RICCO

Unused ProtScore: 1.91

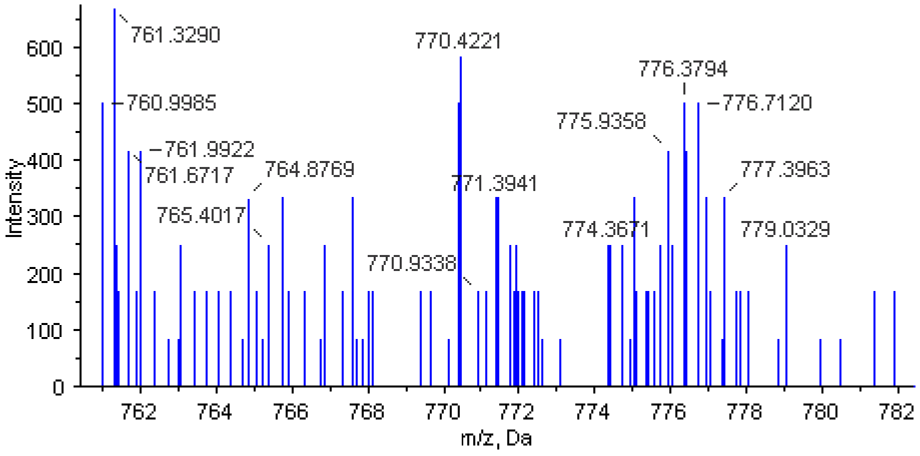
Seq Cov %: 5.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=1. 71

116: 114=E5TL: D5TL=3. 28

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDGGDGTVRLGALNLRPDR**SGFDSGPDVSVSSPVTR**QKAAAAKQFIENHYKNYLQGLQDRKDRRQALQR
RAQEARISNEEQEEMMRNLERRETEYMRLQRRKIGIDDFEQLTVIGKGAFGEVRLCRAKSTGEIFAMKK
LKKSEMLSRGQVEHVRSERNLLAEVDSRCIVKLFYSFQDSDFLYLIMEYLPGGDIMTLLMREDILSEDV
ARFYIAESILAIQSIHQHSYVHRDIKPDNLILDKNGHLK**LSDFGLCK**PLDDKYSSILLENEDISQEGTN
EAGGHSGSEAPWSMPKEVLQQWKRNRRALAYSTVGTLDYMAPEVLLKKGYGMECDWWSLGAILYEMLLG
YPPFCSDDPRITCRKIINWKTCLKFPDEPKISNEAKDLICHLLCDVETRLGTRGVDELKAHPWFRCTQW
DMLYEMEAAYKPVVNGDLDTQNFEK**FPDLEGPPSAIPR**VGPWRKMLTSKDTNFIGFTFKKSDVINSMES
SGTYAKSNASSKAPSLISLLGRIDLQETAELEGEHTLQS

Protein No.: I-1348

Protein name and Species:

Putative uncharacterized protein OS=Ricinus communis GN=RCOM_0632890 PE=4 SV=1

Accession: tr|B9S119|B9S119_RICCO

Unused ProtScore: 1.89

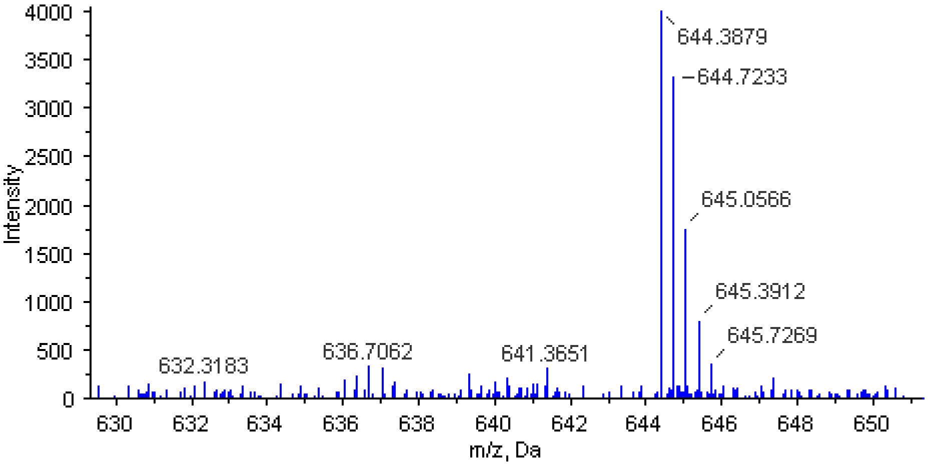
Seq Cov %: 10.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 33

116: 114=E5TL: D5TL=1. 16

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MASQRIANHRDEAEIYLGESLCKQKSIELLEEIRLPKGLLPLDDIVEVGYNRTTGFVWLKQKNSKNHRF
REIGR**NVNYDTEVTAFVEDR**RMKRLTGVKSKELLIWVTISDIYVDHNDNSK**ITFGNPSGISR**TFPVSAF
QLQEEKK

Protein No.: I-1353

Protein name and Species:

chitinase，class I (Fragment) OS=Hevea brasiliensis GN=rq30 PE=2 SV=1

Accession: **tr|Q949H3|Q949H3_HEVBR**

Unused ProtScore: **1.87**

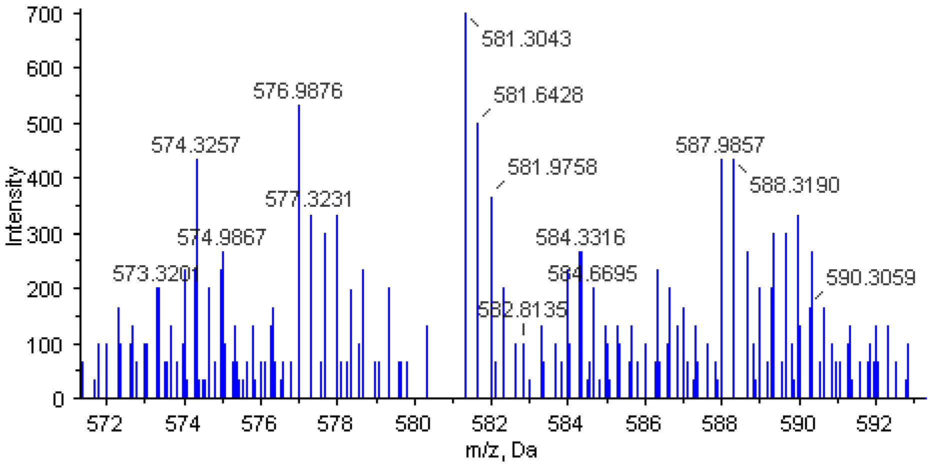
Seq Cov %: **7.1**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 45

116: 114=E5TL: D5TL=0. 51

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

EQCGRQAGGALCPGGLCCSQYGWCANTPEYCGSGCQSQCDGGGGGEDGGIDLGSIISR**STFEEMLK**HRN
DAACPAK**GFYTYDAFISAAK**AFPAFGTTGDVDTCKREIAAFFGQTSHATTGGWPTAPDGPYAWGYCYKE
ELNQASSYCSPSPAYPCAPGKKYYGRGPIQLSWNYNYGQCGQALGLDLLNNPDLVATDRVISFKAAIWF
WMTPQFPKPSCHDVITGQWSPTGHDISAGRAPGYGVITNIINGGLECGRGWDARVEDR**IGFYK**RYCDMF
AVGYGSNLDCYNQTPFGLG

Protein No.: I-1355

Protein name and Species:

GTP-binding protein OS=Populus trichocarpa GN=POPTRDRAFT_1073333 PE=3 SV=1

Accession: tr|B9H023|B9H023_POPTR

Unused ProtScore: 1.86

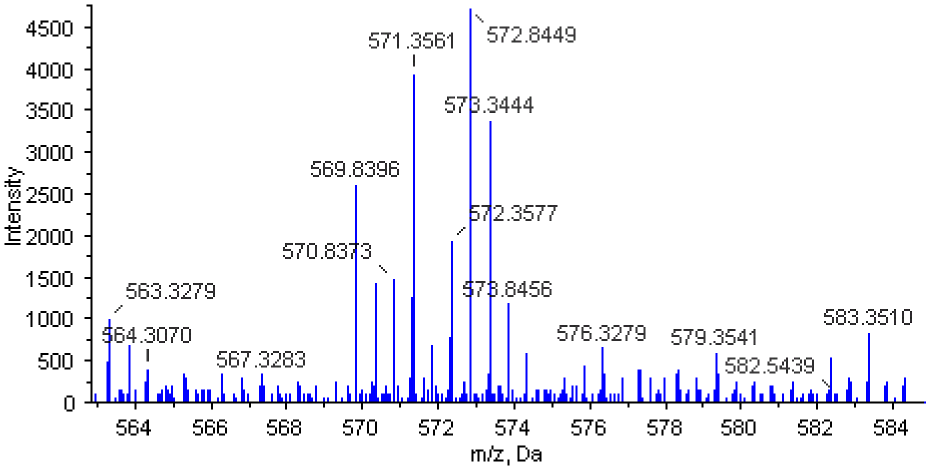
Seq Cov %: 22

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2. 75

116: 114=E5TL: D5TL=0. 78

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MSNSSENEVESLPQSIEEKHQELVVSHVPIVSSFNERIR**PLLDAVDK**LRHLQ**VMKEGIQLPTIVVVGDQ**
SSGKSSVLESLAGISLPRGQGICTRVPLIMRLQHHTAPEPEFSLEFNGKTVPTSEAK**IANAISLATDEI**
AGNAKGISNTPLTLVVKKNGVPDLTMVDLPGITRVPVHGQPENIYEQIADIIMEYIRPDESIILNVLSA
TVDFTTCESIRMSQKVDKNGERTLAVVTKADR**APEGLLEKVTADDVNIGLGYVCVR**NRIGDESYEEARK
EEADLFENHPLLSKIDK**SMVGIPVLAQKLVQIQATIIAR**CLPEIVRKINEK**LNASISELNR**MPKTLSSV
GEALTTFMSIVGSAKESLNKIIVR**GEYDEYLEDKNMHCTAR**LVEMLNQYSGELHNCSENDLTGNFLMDE
IQVLEEAKGIELPNFLPRTTFLSILQKKVEKVSHIPVAFVEKVWTYIEGVVISVLMHHSENYHQLQLST
RRAGHSLIARMKEHSRNWVTEIVQMEKLTDYTSNPEYMNDWNKLMAQQHDFTRNVLENGYVATFKIEGL
GVVPIAGLRGYEQHVLLQAFDLKMRMTAYWKIVLRRLVDFMALHLQF**CARNLVNK**EMEEEIVQELVGRH
DGAIERMLEESPAVAAKREKLNVSIKLLRESNN**VLGNIMDK**IASNI

Protein No.: I-1387

Protein name and Species:

ubiquitin 11 OS=Medicago truncatula PE=2 SV=1

Accession: tr|B7FLK9|B7FLK9_MEDTR

Unused ProtScore: 1.77

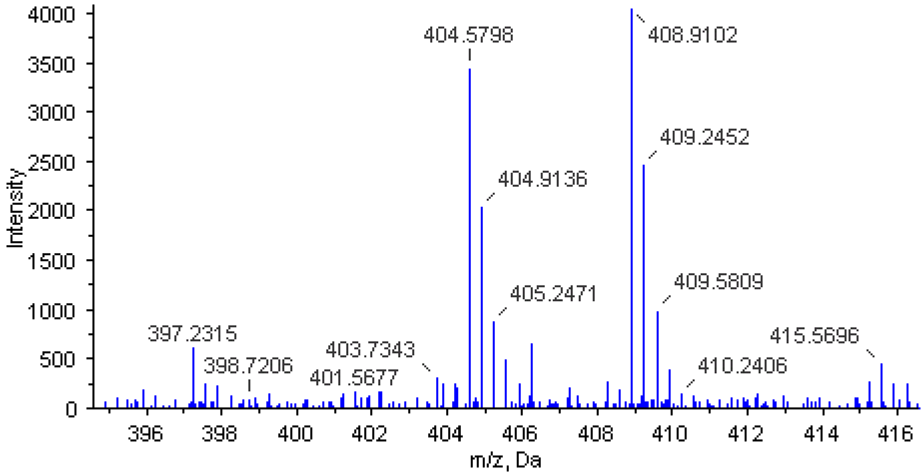
Seq Cov %: 77.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.24

116: 114=E5TL: D5TL=0.82

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MQIFVKTLTGKTITLEVESSDTIDNVKAKIQNKEGIPPDQQRLIFAGKQLEDGRTLADYNIQKESTLHL
VLRLRGGMQIFVKTLTGKTITLEVESSDTIDNVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLADYNIQ
KESTLHLVLRLRGGMQIFVKTLTGKTITLEVESSDTIDNVKAKIQDKEGIPPDQQRLIFAGKQLEDGRT
LADYNIQKESTLHLVLRLRGGF

Protein No.: I-1404

Protein name and Species:

Conserved hypothetical protein [Ricinus communis] OS=Ricinus communis GN=RCOM_1445010 PE=4 SV=1

Accession: tr|B9RGW6|B9RGW6_RICCO

Unused ProtScore: 1.7

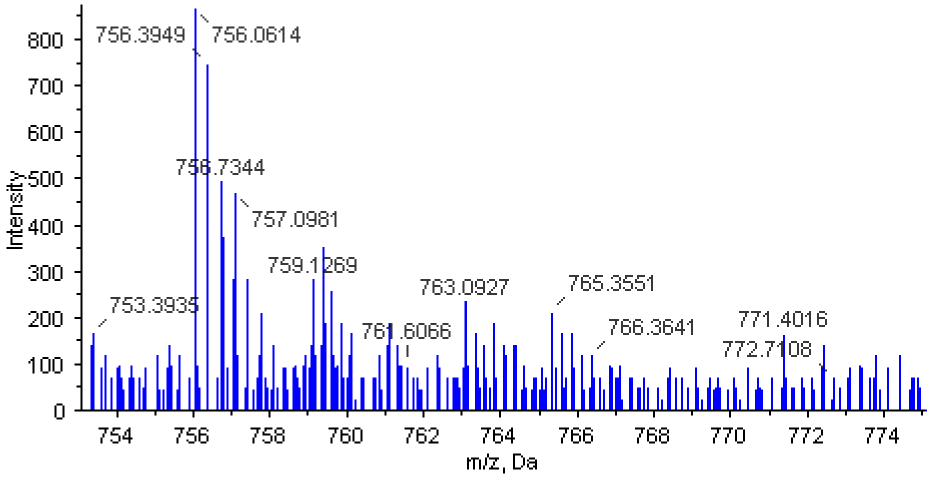
Seq Cov %: 7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2. 94

116: 114=E5TL: D5TL=3. 98

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDKNTTKKKEVIRLERESVIPILKPKLVMTLANLIEHTSDRAEFLKLCKRIEYTIRAWYLLQFEDLMQL
YSLFDPVSGAQKLQQQNLSPEEIDVLEQNFLTYLFQVMDKSNFKIATEEEIEVAHSGQYLLNLPISVDE
SKLDKEVLKKYFAAHPREDLPD**FVDK**YVIFRRGIGIDRTTDYFIMEKVDMLIARFWAYILRLTRVEKLL
RRRSSMRCKKDPKKNDEINSEADQNDLCVERIRLENMELSVRNLLSSTTIQEPTFDRIIVVYRRASSKL
KKERGIYVKHFKNIPMADMEIVLPEKKNPGLTPMDWVKFLGSAIVGLVALVSSLEMPKADLWVIFAVLS
AVIGYFAKTYFTFQANLAAYQNLITQSMYDKQLDSGK**GTLLHLCDDVIQQEVK**EVIISFFILMEQGKAT
MQDLDLR**CEELIQEEFGESCNFDVDDAVLK**LEK**LGIVAR**DTIGRYYCVGLKRANEIIGTTTEELVLKAK
QGARRRTKSEVKPAERSKTQEQKILMHHIRRLQGQRRKAMGSLCSIISYLCDFFGLNSNQIPGSAGVWS
CYG

Protein No.: I-1407

Protein name and Species:

Predicted protein OS=Populus trichocarpa GN=POPTRDRAFT_806336 PE=3 SV=1

Accession: **tr|B9I2G0|B9I2G0_POPTR**

Unused ProtScore: **1.69**

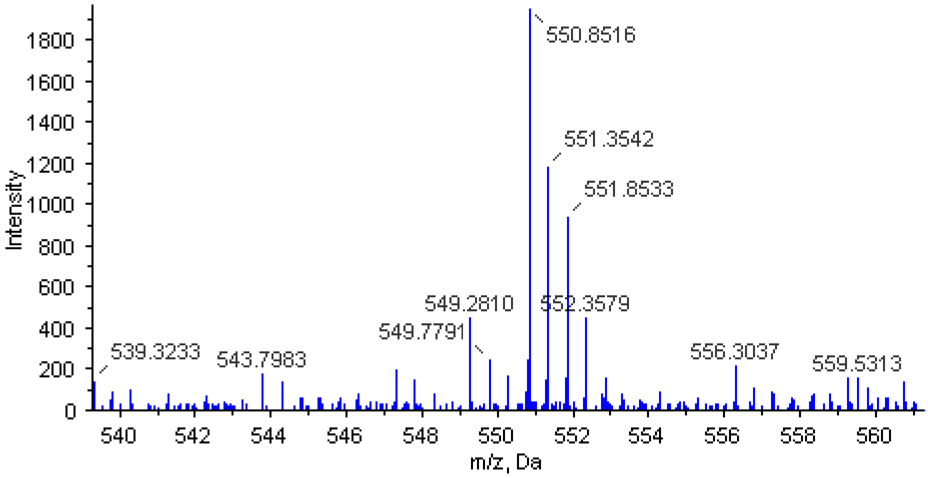
Seq Cov %: **1.5**

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 59

116: 114=E5TL: D5TL=0. 56

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MKNFLKKLHIMPNQSQDAEGSNSSRGHKSSNESSSDNKFLHSRLQENKPFSGLSNWLSSVANRKKGARR
DSVSSTSRDPDVEEEFQIQLALELSAR**EDPEAVQIEAVK**QISLGSCAPEHTLAELIAYRYWNYNALSYD
DKVLDGFYDLYGIMTESTSDKMPSLVDLQATPVSGGVTWEAVLVNRAADANLLKLEKKALEIAVKSRSE
SQVFIGSALVRRLAVLVSDYMGGAVGDPSNLSRAWRSLSYSLKANLGSMVLPLGSLTIGLPRHRALMFK
VLADSVGIPCRLVKGHLYTGSDDVAMNFVKIDDGREYIVDLTADPGTLIPSDAAGSHIEYDDSFFSSSP
FSRDIDSYRIASSSSGHTSDSHEGASLTKLSKGEEESTISLNDFGKISIAEKVPVRELPGRPIYPSAHA
RSPSWTEGVSSPSVRRMKVKDVSQYMIDAAKENPQLAQKLHDVLLESGVVAPPNLFTEIYAEQLNASTA
EATSPTEGKDGHKQRTEIRYVKDQDDLVPARFFPLLPPNELPYKSSSPGNQPEQSKPSEFTPVKYVKNV
PVAAAAAAAAAVVASSMVVAAAKSSTDSNLELPVAAAATATAAAVMATTAAVNKQYVQGARSDGDADSA
GYEPHGSGDKGSGGRGKGERISDRLAVNVRSKSDAGLDDVAECEIPWEEITLGERIGLGSYGEVYRGDW
HGTEVAVKRFLDQDITGEALAEFRSEVRIMKRVRHPNVVLFMGAVTRAPNLSIVTEFIPRGSLYRLLHR
PNNQLDDRRRLRMALDAARGMNYLHSCTPMIVHRDLKSPNLLVDKNWVVK**VCDFGLSR**IKNSTFLSSRS
TAGTAEWMAPEVLRNEPSDEKCDVYSFGVILWELSTLQQPWGGMNPMQVVGAVGFQHRSLDIPNDMDPA
IADIIRKCWQTDPRLRPTFAEIMAALKLLQKPITGPQVPRPNAPLRSGH

Protein No.: I-1418

Protein name and Species:

aspartate-tRNA ligase, cytoplasmic-like OS=Populus trichocarpa GN=POPTRDRAFT_652970 PE=3 SV=1

Accession: tr|B9HBL6|B9HBL6_POPTR

Unused ProtScore: 1.65

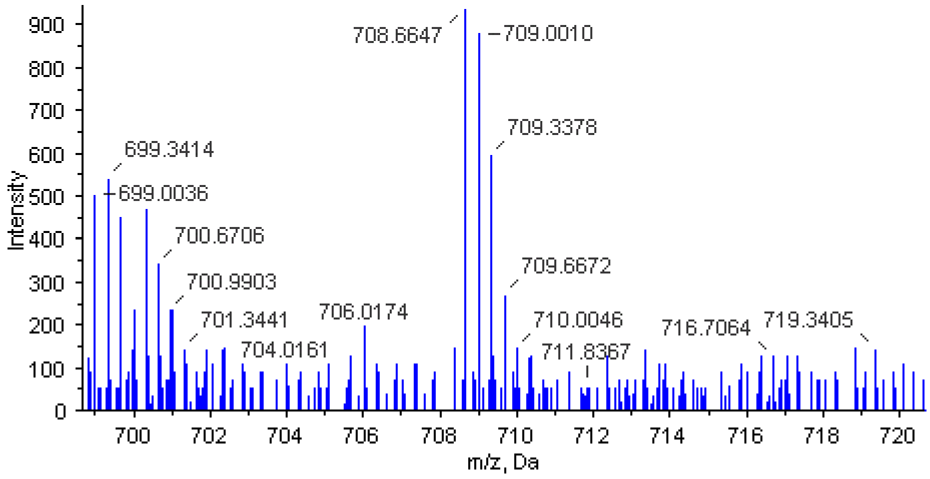
Seq Cov %: 7.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 10

116: 114=E5TL: D5TL=0. 21

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MNPQNQRAKKLQRRKQQSKRSYVAVRKPLWPAAAASSLSIEEDPLAANYGNIPLQDLQSKVEADLKAWT
QVGDLTHELKEKEVLIRGRAQTTRAVGKNMAFVVVREKGFTVQCVVTARPDVVSKQMVKFAAGLSRESI
VDIHGVVSVPSIAIKGTTQQVEIQVSKLYCVDK**AMPTLPINIEDASR**SEK**EIEEALEAGEQLVR**VNQDT
RLNYRVLDFRTSANQGIFRIQCQVCNIFRQFLLSEDFVEIHTPKLIAGSSEGGSAVFKLDYKGQAACLA
QSPQLHKQMAICGDFGRVFEIGPVFRAEDSYTHRHLCEFTGLDVEMEIKQHYTEVMDIVDHLFVTMFDH
LNKKCSKYLEAVGRQYPFEPLKYLPKTLRLRFEEGVQMLK**EAGVEIDPYGDLNTESER**K**LGQLVLEK**YG
TEFYILHRYPLAVRPFYTMPCYDDPKYSNSFDVFIRGEEIISGAQRVHVPEFLVERAQACGIDVSTIST
YIDSFRYGAPPHGGFGAGLERVVMLFCGLNNIRKTSLFPRDPLRIAP

Protein No.: I-1426

Protein name and Species:

random slug protein 5 isoform 2 [Vitis vinifera] OS=Vitis vinifera GN=VIT_18s0001g12420 PE=4 SV=1

Accession: tr|F6H1I3|F6H1I3_VITVI

Unused ProtScore: 1.61

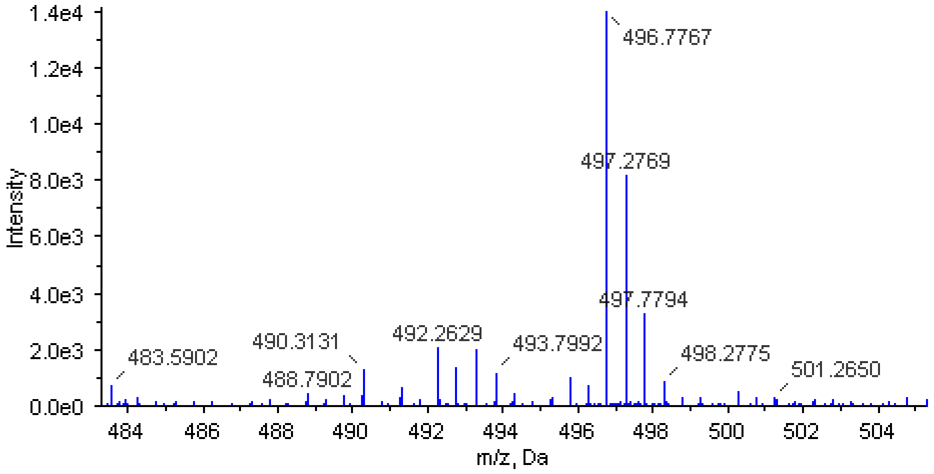
Seq Cov %: 8.3

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 17

116: 114=E5TL: D5TL=0. 93

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MISEEVSVFLDAHLSQQKYPTMLRLWGKSHHDQEKDLQKSDSKVHELK**AALGPLSGR**SLQYCNDACLKR
YLEARNWNVDKSKKMLEETLTWRSTYKPEEIRWSDVATEGETGKVFRANFHDRHGRTVLILRPGKQNTT
ALDNQVRHLVYLLENAILNLPEDQEQMVWLIDFTGMTFSNSVPIKTARDTIN**ILQNHYPER**LFLAFLYS
PPRIFEAFWKAVKYLLDAKTFQKVKFVYPKDKNSVELMSSYFDVENLPTDFGGKATMN**YDHEEFSR**LMT
QDDVKSANLWGFGDKLQHVSNGHSVAEVSPEPACLAPAS

Protein No.: I-1434

Protein name and Species:

HMG-CoA synthase 2 OS=Hevea brasiliensis GN=HMGS2 PE=2 SV=1

Accession: tr|Q6QLW8|Q6QLW8_HEVBR

Unused ProtScore: 1.58

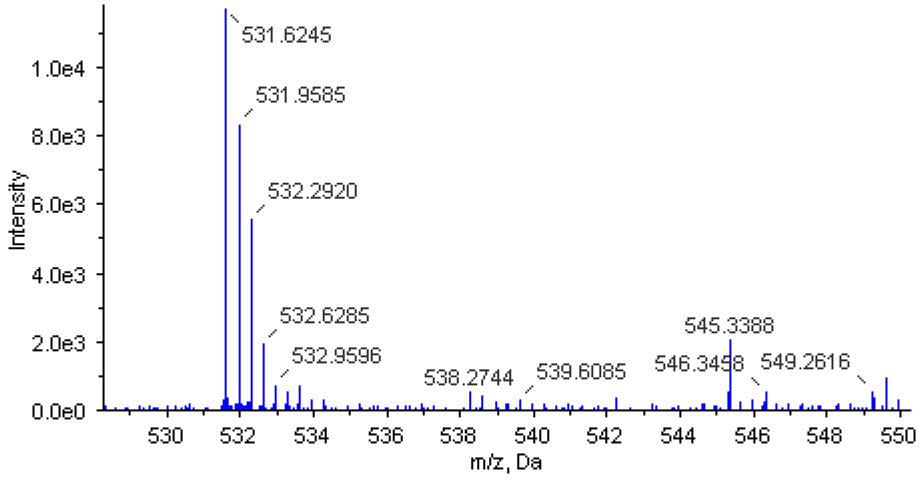
Seq Cov %: 32.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 58

116: 114=E5TL: D5TL=0. 73

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MAKNVGILAMDIYFPPTYVQQEALEAHDGASKGKYTIGLGQDCMAFCTEVEDVISMSLTAVTSLLEK**YNIDPNQIGRLEVGSETVIDK**SKSIK**TFLMQIFEK**FGNTDIEGVDSANACYGGTAALFNCVNWVESNSWDGR**YGLVVCTDSAVYAEGPAR**PTGGAAAIAMLIGPEAPIAFESKFRGSHMSHAYDFYK**PNLASEYPVVDGKLSQTCYLMALDSCYK**HFCAKYEKLEGKQFSISDAEYFVFHSPYNKLVQKSFAR**LVFNDFVRNASSIDDAAK**EK**LAPFSTLSGDESYQNR**DLEK**VSQQVAKPLYDAKVQPTTLIPK**QVGNMYTASLYAAFASLLHNKHTELAGKRVILFSYGSGLTATMFSLR**LHEGQHPFSLSNIATVMNVAGK**LKTRHEFPPEK**FAVIMK**LMEHRYGAKDFVTSKDCSILAPGTYYLTEVDTMYRRFYAQK**AVGDTVENGLLANGH**

Protein No.: I-1437

Protein name and Species:

methyl transferase [Populus tomentosa] OS=Populus trichocarpa GN=POPTRDRAFT_1101018 PE=4 SV=1

Accession: tr|B9IEB9|B9IEB9_POPTR

Unused ProtScore: 1.57

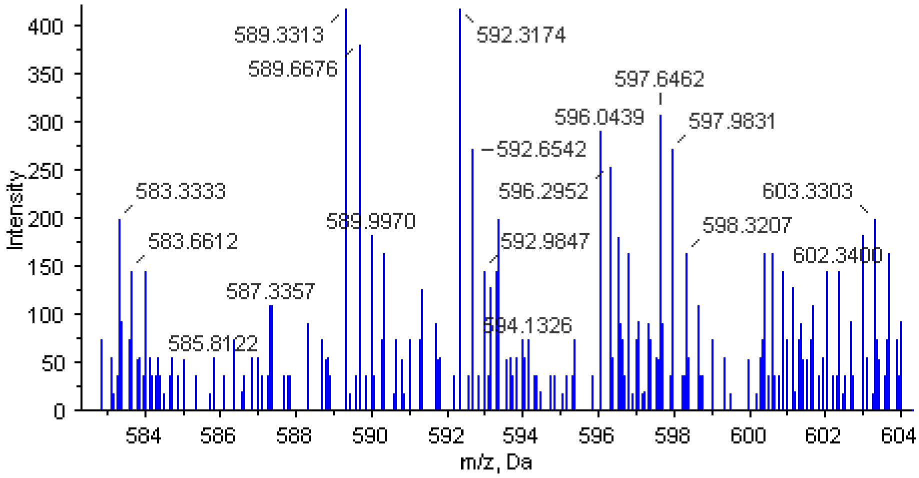
Seq Cov %: 5.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=3. 73

116: 114=E5TL: D5TL=7. 78

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDNISDLSVNAMMLDSKASELDKEERPEILSLLPPYEGKTVLELGAGIGRFTGELAQKAGQVVALDFIE
SAIKKNENINGHYKNVKFMCADVTSPDLNISEGSVDLIFSNWLLMYLSDKEVENLVERMVKWVKVDGFI
FFRESCFHQSGDSKRKYNPTHYREPRFYTKVFKECHTRDGSGDSFELSLVGCKCISAYVKNKKNQNQAM
KLDHLILWICWIWQKVSSYEDK**GFQRFLDNVQYK**SNGILRYERVFGQGYVSTGGIETTKEFVGKLDLKP
GQKVLDVGCGIGGGDFYMAENFDVEVVGIDLSINMISFALERAIGLKCSVEFEVADCTTK**TYPDNTFDV**
IYSRDTILHIQDKPALFRSFFKWLKPGGKVLISDYCKCDGTPSPEFAEYIKQRGYDLHDVKAYGQMLRD
AGFDEVVAEDRTDQFNKVLQRELNAIEKDKDEFIHDFSEGDYNDIVGGWKAKLIRSSSGEQRWGLFIAK
KK

Protein No.: I-1453

Protein name and Species:

chitinase Class Ib, OS=Limonium bicolor PE=2 SV=1

Accession: tr|Q1W6C5|Q1W6C5_9CARY

Unused ProtScore: 1.53

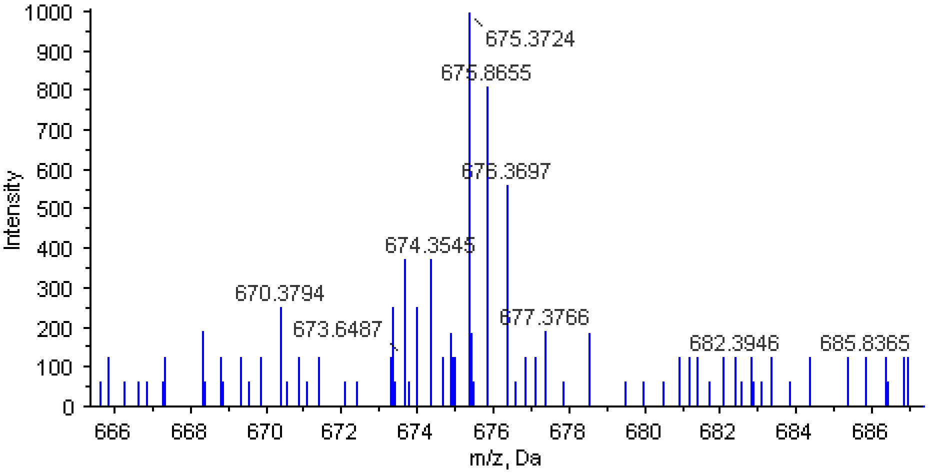
Seq Cov %: 5.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 64

116: 114=E5TL: D5TL=0. 51

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MKTTLILTAAALPFLLLISFSSAEQCGSQAGGAVCPNGLCCSKYGWCGSTDTYCKDGCQSQCGGTTPTP
TTPTPTPTQGGDVSSIISQSNFDEMLKHRNDNACSGHGFYTYAAFISAAQSFPGFGTTGDTDTRKRELA
AFLGQTSHETTGGWAAAPDGPYAWGYCF**VQEQGASGAFCTSPEYPCAPGK**QYYGRGPIQLTHNYNYAQA
GTAINQDLINNPDLVATDPTISFKTAIWFWMTPQSNKPSSHDVITGKWTPSSADSAAGR**VPGYGVITNI**
INGGLECGKGSIAKQEDR**IGFYK**RYCDVLGVGYGNNLDCNSQRPFA

Protein No.: I-1459

Protein name and Species:

Dynamin, putative OS=Ricinus communis GN=RCOM_0718390 PE=3 SV=1

Accession: tr|B9SBH8|B9SBH8_RICCO

Unused ProtScore: 1.51

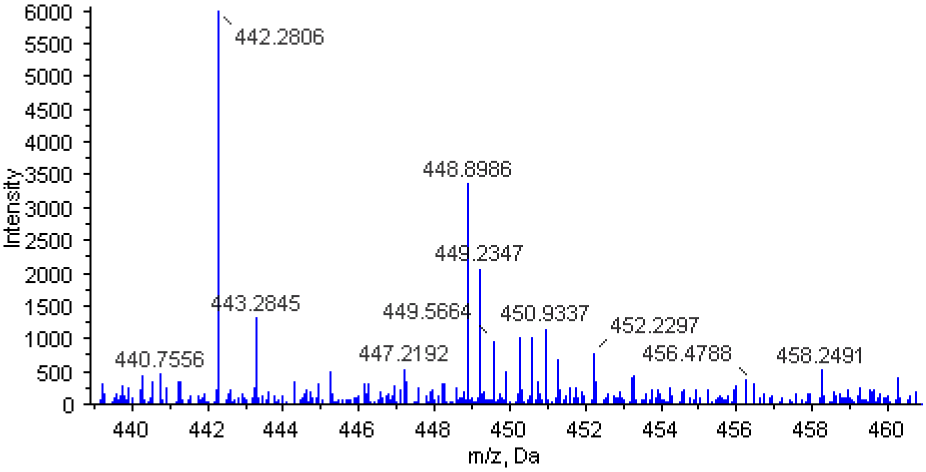
Seq Cov %: 8.9

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.60

116: 114=E5TL: D5TL=0. 56

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MENLISLVNKIQRACTALGDHGEESALPTLWDSLPSIAVVGGQSSGKSSVLESIVGKDFLPRGAGIVTR
RPLVLQLHRVDEGKEYAEFMHLPRKKFSDFAAVRKEISDETDRETGRSKQISTVPIHLSIYSPNVVNLT
LIDLPGLTKVAVDGQPESIVLDIENMIRSYIEKPNCIILAISPANQDLATSDAIKISREVDPKGERTFG
VLTKVDLMDK**GTDAVDILEGK**SYKLQFPWIGVVNRSQADINKSVDMIAARRKEREYFQNSTEYRHLAHR
MGSEHLGKMLSKHLEQVIKSR**IPGLQSLINK**TIAELEGELSRLGKPVATDAGGKLYMIMEICRSFDQIF
KEHLDGIRPGGDKIYLVFDNQLPAALKRLQFDKHLSIDNVRK**LITEADGYQPHLIAPEQGYR**RLIESTL
VTIRGPAEAAVDAVHVLLKELVQKSINETLELKQYPTLR**VEVSNAAIESLDR**MREESKKATLQLVDMEC
CYLTVEFFRKLPQDIEK**GGNPTHSIFDR**YNDSYLRRVGSNVLSYVNMVCGSLRNSIPKSVVYCQVRDAK
RSLLDYFFAELGKKETKQLSSLLDEDPAVMQRRISLAKRLELYRSAQAEIDAVAWAK

Protein No.: I-1464

Protein name and Species:

Alanine aminotransferase 1 OS=Glycine max GN=AlaAT1 PE=2 SV=1

Accession: tr|A8IKE1|A8IKE1_SOYBN

Unused ProtScore: 1.5

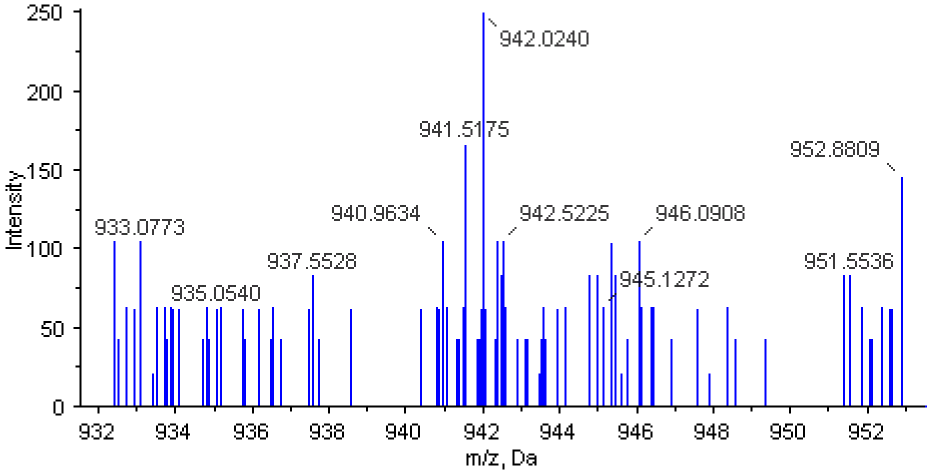
Seq Cov %: 7.2

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 60

116: 114=E5TL: D5TL=0. 94

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MASDSPFPVTAQNINPKVLKCEYAVRGEVVTLAQNLQKDLQANPGSHPFDEILYCNIGNPQSLGQQPIT
FFR**EVLALCDHPAILDKSETQGLFSTDAIQR**AWQIVDQIPGRATGAYSHSQGVKGLRDTIAAGIEERDG
FPANPDDIFMTDGASPAVHNMMQLLIRSENDGILCPIPQYPLYSASIALHGGCLVPYYLDEATGWGLEI
PELKKQLEAAKSKGINVRALVVINPGNPTGQVLGEANQRDIVEFCK**QEGLVLLADEVYQENVYVPEK**KF
HSFKKVSRSMGYGENDITLVSFQSVSKGYHGECGKR**GGYMEVTGFSAEVR**EQIYKVASVNLCSNISGQI
LASLVMSPPKVGDESYDSFMAEKENILASLARRAK**TLEDAFNKLEGVTCNK**AEGAMYLFPQIRLSEKAI
KAAEAANATPDNFYCKRLLNATGVVVVPGSGFGQVPGTWHFRCTILPPEEKIPAIVTRLTEFHEKFMDE
FRD

Protein No.: I-1467

Protein name and Species:

L-lactate dehydrogenase OS=Arabidopsis thaliana PE=2 SV=1

Accession: tr|Q8LBD5|Q8LBD5_ARATH

Unused ProtScore: 1.49

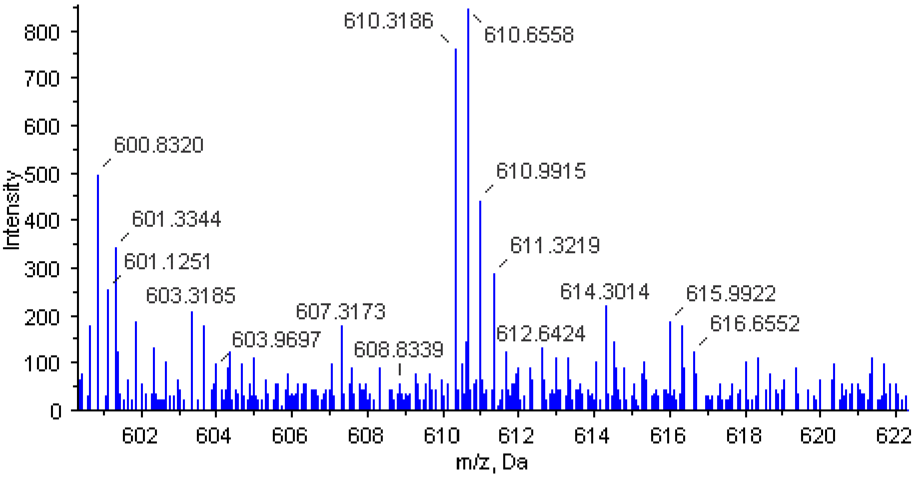
Seq Cov %: 20.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 52

116: 114=E5TL: D5TL=0. 24

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MEKNASTSSLKDLGPSGLDLTSAFFKPIHNSDPSLPSNRRTKVSVVGVGNVGMAIAQ**TILTQDLADEIA**
LVDAKPDKLR**GEMLDLQHAAAFLPR**TK**ITASVDYEVTAGSDLCIVTAGAR**QNPGESR**LNLLQR**NVALFR
HIIPPLAKASPDSILIIVSNPVDVLTYVAWKLSGFPVNR**VLGSGTNLDSSR**FRFLIADHLDVNAQDVQA
FIVGEHGDSSVALWSSISVGGIPVLSFLEKNQIAYEKQTLEDIHQAVVGSAYEVIGLKGYTSWAIGYSV
ANLARTILRDQRKIHPVTVLARGFYGVDGGDVFLSLPALLGRNGVVAVTNVHMTDEEAEKLQKSAKTIL
EMXSQLGL

Protein No.: I-1479

Protein name and Species:

S-formylglutathione hydrolase-like [Glycine max] OS=Glycine max PE=2 SV=1

Accession: tr|C6TB50|C6TB50_SOYBN

Unused ProtScore: 1.43

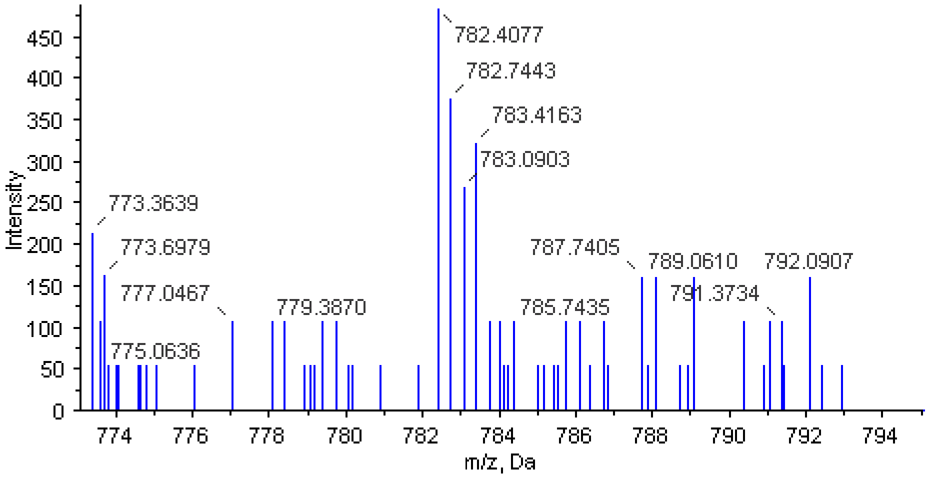
Seq Cov %: 14.7

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0.64

116: 114=E5TL: D5TL=0. 79

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MDTRPTEISSGK**MFGGYNK**RFKHFSLTLGCSMNFHIYFPPSPSPSHKFPVLYFLSGLTCTDENFIFKSG
AQR**AASAEGVALVAPDTSPR**GLNVEGEADSWDLGVGAGFYLNATQEKWKNWRMYDYVVKELPKLLSDNF
PQLEISK**ASIFGH**SMGGHGA**LTIFLK**NQDKYK**SVSAFAPIANPINCPWGQK**AFSNYLGDNKFEWEDYDA
TRLVTKFPNVSSTILIDQGEDDKFLPDQLLPHKFEEACKKANVPLLLRFQPGYDHLYYFIATFIDDHIR
HHAQAFRLN

Protein No.: I-1487

Protein name and Species:

Aminotransferase YbdL-like OS=Vitis vinifera GN=VIT_18s0001g03300 PE=4 SV=1

Accession: tr|E0CR92|E0CR92_VITVI

Unused ProtScore: 1.4

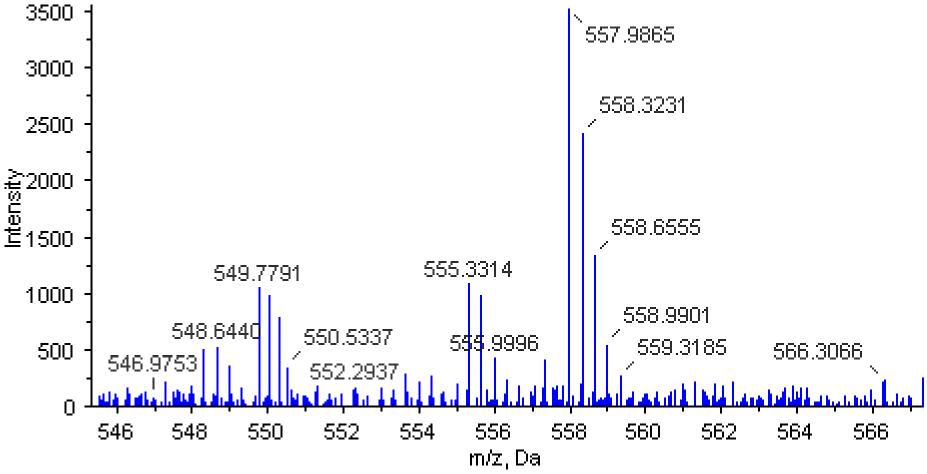
Seq Cov %: 5.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2. 25

116: 114=E5TL: D5TL=1. 82

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MASASTVSAPNTEAEQTHNPPQPLQVAKRLEKFKTTIFTQMSMLAIKHGAINLGQGFPNFDGPEFVKEA
AIQAIKDGKNQYARGYGVPDLNSAVADRFKKDTGLVVDPEKEVTVTSGCTEAIAATMLGLINPGDEVIL
FAPFYDSYEATLSMAGAQIKSITLRPPDFAVPMDELKSAISKNTR**AILINTPHNPTGK**MFTREELNVIA
SLCIENDVLVFTDEVYDKLAFEMDHISMASLPGMYERTVTMNSLGKTFSLTGWKIGWTVAPPHLTWGVR
QAHSFLTFATCTPMQWAAATALR**APDSYYEELK**RDYSAKK**AILVEGLK**AVGFRVYPSSGTYFVVVDHTP
FGLKDDIAFC**EYLIK**EVGVVAIPTSVFYLHPEDGKNLVRFTFCKDEGTLRAAVERMKEKLKPKQ

Protein No.: I-1494

Protein name and Species:

Putative uncharacterized protein OS=Vitis vinifera GN=VIT_19s0014g01520 PE=4 SV=1

Accession: tr|F6H2P8|F6H2P8_VITVI

Unused ProtScore: 1.39

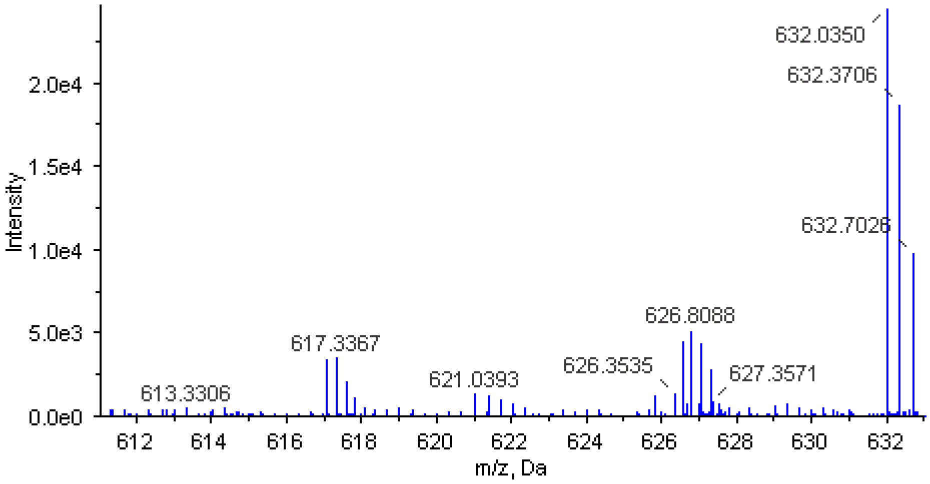
Seq Cov %: 6.5

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=0. 13

116: 114=E5TL: D5TL=0. 29

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MALRHLTPLSPLSPFTRIPPRRCFTQKPFSLSVSASMGSSSRKVLVPIAHGSEPMEAVII**IDVLR**R**AGA**
DVTVASVEKRLQVDACHGVKIVADALISDCADTGFDLISLPGGMPGAATLRDCGMLESMVKKHAADGQL
YAGICAAPAVALGSWGLMKGLKATCYPSFMEQLSSTATTVESRVQQDGKVVTSRGPGTTMEFSVSLVEQ
LYGKEKANEVSGPLVMCSNLGDKFIMAELNPIDWKCDNPQILVPIANGTEEMEAVIIIDFLRRAK**ANVV**
VASVEDKLEIVASRKVKLVADVLLDEAVK**LSYDLIVLPGGLGGAQ**AFASSEKLVNLLKNQRESNKPYGA
ICASPALVLEPHGLLKGKKATAFPALCSKLSDQSEIENRVLVDGNLITSRGPGTSMEFALAIIEKFFGH
GK**ALELAK**VMLFSSQ

Protein No.: I-1523

Protein name and Species:

succinyl-CoA ligase [ADP-forming] subunit alpha-1, mitochondrial-like [Glycine max] OS=Glycine max PE=2 SV=1

Accession: tr|C6TNV4|C6TNV4_SOYBN

Unused ProtScore: 1.31

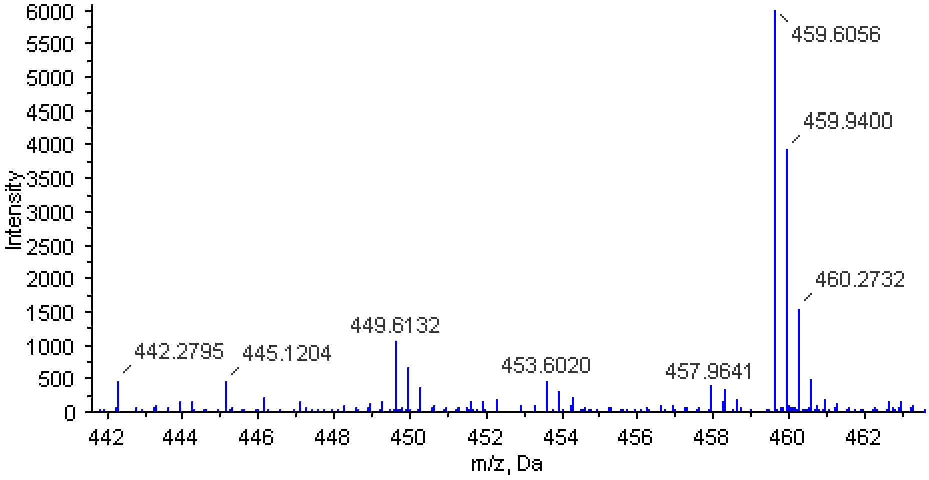
Seq Cov %: 3.1

ITRAQ Changed Ratio:

117: 115=E3TL: D3TL=2.11

116: 114=E5TL: D5TL=1.52

Annotated typical Precursor MS Region:



Sequence Coverage and Matched peptides: in different color

MGRQAVTKLLSSIASRRHGLRLFSAASPAV**FVDK**STRVICQGITGKNGTFHTEQAIEYGTNMVGGVTPK
KGGTEHLGLPVFNTVAEAKAETKANASVIYVPPPFAAAAIMEAMEAELDLVVCITEGIPQHDMVRVKAA
LNRQSKTRLIGPNCPGIIKPGECKIGIMPGYIHKPGRIGIVSRSGTLTYEAVFQTTAVGLGQSTCVGIG
GDPFNGTNFVDCLQKFLTDPQTEGIILIGEIGGTAEEDAAALIKDSGTEKPVVAFIAGLTAPPGRRMGH
AGAIVSGGKGTAQDKIKTLREAGVMVVESPAK**IGAAMLDVFK**QRGLVQ

Supplementary Figure S5:
Supplemental spectra and MALDI TOF/TOF MS /MS identification information

Annotated spectra for the 59 phosphorlated latex proteins on identified by TOF, TOF/TOF and LC-MALDI MS/MS.

CID: collision induced desorption;

MALDI TOF:

matrix assisted laser desorption/ionization time of flight;

MS: mass spectrometry;

PMF: peptide mass fingerprinting;

PFF: peptide fragment fingerprinting.

Spot No.: **P1**

NCBI accession No.: **gi|123650**

Species: *Petunia x hybrida*

Protein name: **Heat shock cognate 70 kDa protein**

Mascot score: **97**

Sequence coverage %: **40**

Matched peptides No.: **24**

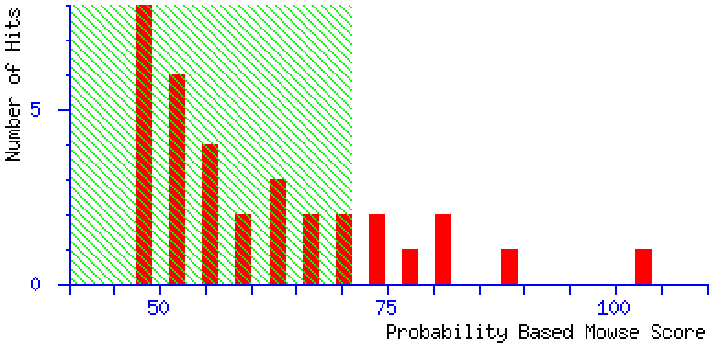
Total peptides No.: **41**

Calculated Mr: **71581**

Calculated *p*I: **5.11**

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red:

1 EGPAIGIDLG TTYSCVGVWQ HDRVEIIAND QGNRTTPSYV GFTDTERLIG
51 DAAKNQVAMN PINTVFDAKR LIGRRFSDPS VQSDIKLWPF KVIPGPGDKP
101 MIVVTYKGEE KQFAAEEISS MVLTK**MKEIA** **EAYLGTTIKN** **AVVTVPAYFN**
151 **DSQR**QATK**DA** **GVIAGLNVMR** **IINEPTAAAI** **AYGLDKK**ASS AGEKNVLIFD
201 LGGGTFDVSL LTIEEGIFEV K**ATAGDTHLG** **GEDFDNRMVN** **HFVQEFK**RKN
251 KK**DISGNPRA** LRRLRTACER AKR**TLSSTAQ** **TTIEIDSLYE** **GIDFYSTITR**
301 **ARFEELNMDL** **FRKCMEPVEK** CLRDAKMDK**S** **SVHDVVLVGG** **STR**IPKVQQL
351 LQDFFNGKEL CKSINPDEAV AYGAAVQAAI LSGEGNEKVQ DLLLLDVTPL
401 SLGLETAGGG MTVLIPRNTT IPTKK**EQVFS** **TYSDNQPGVL** **IQVYEGER**AR
451 TKDNNLLGKF ELSGIPPAPR **GVPQITVCFD** **IDANGILNVS** **AEDK**TTGQKN
501 KITITNDKGR LSK**EEIERMV** **QEAEK**YKSED EELKKKVEAK **NALENYAYNM**
551 **RNTIKDDKIN** **SQLSAADKKR** **IEDAIDEAIK** WLDNNQLAEA DEFEDK**MKEL**
601 **ESICNPIIAK** MYQGGAGGAT MDEDGPSVGG SAGSQTGAGP KIEEVD

Spot No.: **P2**

NCBI accession No.: **gi| 249262** Species: *Manihot esculenta*

PFF score: [54]

Protein name: linamarase

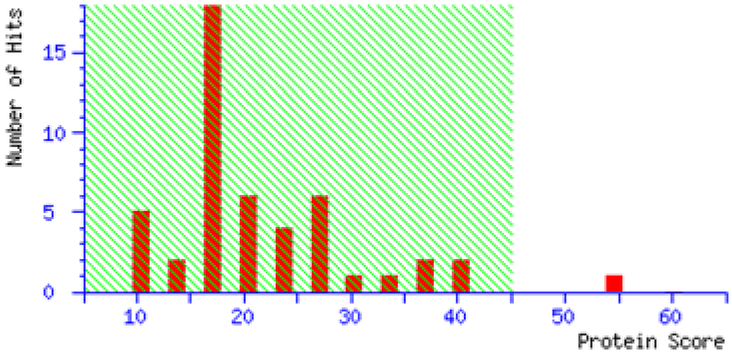
Matched peptides No.: [1] Sequence coverage %: [3]

Matched sequences: R.ILDGSNGDVAVDFYNR.Y

Calculated Mr: **61448** Calculated *p*I: **5.52**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

```
  1 MLVLFISLLA LTRPAMGTDD DDDNIPDDFS RKYFPDDFIF GTATSAYQIE
 51 GEATAKGRAP SVWDIFSKET PDRILDGSNG DVAVDFYNRY IQDIKNVKKM
101 GFNAFRMSIS WSRVIPSGRR REGVNEEGIQ FYNDVINEII SNGLEPFVTI
151 FHWDTPQALQ DKYGGFLSRD IVYDYLQYAD LLFERFGDRV KPWMTFNEPS
201 AYVGFAHDDG VFAPGRCSSW VNRQCLAGDS ATEPYIVAHN LLLSHAAAVH
251 QYRKYYQGTQ KGKIGITLFT FWYEPLSDSK VDVQAAKTAL DFMFGLWMDP
301 MTYGRYPRTM VDLAGDKLIG FTDEESQLLR GSYDFVGLQY YTAYYAEPIP
351 PVDPKFRRYK TDSGVNATPY DLNGNLIGPQ AYSSWFYIFP KGIRHFLNYT
401 KDTYNDPVIY VTENGVDNYN NESQPIEEAL QDDFRISYYK KHMWNALGSL
451 KNYGVKLKGY FAWSYLDNFE WNIGYTSRFG LYYVDYKNNL TRYPKKSAHW
501 FTKFLNISVN ANNIYELTSK DSRKVGKFYV M
```

Spot No.: **P3**

NCBI accession No.: **gi| 224100473** Species: *Populus trichocarpa*

PFF score: [112]

Protein name: predicted protein

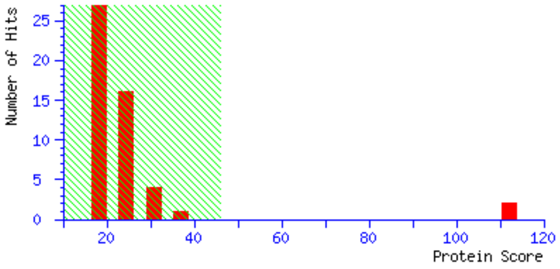
Matched peptides No.: [1] Sequence coverage %: [3]

Matched sequences: R.SPPIEEVIQAGVVPR.F

Calculated Mr: **46093** Calculated *p*I: **4.54**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 GVWSEDGNLQ LESTTQFRKL LSIER**SPPIE** **EVIQAGVVPR** FVEFLVREDF
51 PQLQFEAAWA LTNIASGTSE NTKVVIDHGA VPIFVKLLGS PSDDVREQAV
101 WALGNVAGDS PKCRDLVLSH GALIPLLAQL NEHAKLSMLR NATWTLSNFC
151 RGKPQPPFEQ VRPALPALER LVHSTDEEVL TDSCWALSYL SDGTDDKIQA
201 VIEAGVCPRL VELLLHPSPS VLVPALRTVG NIVTGDDMQT QVKALLAFCL
251 FVPSFAVIEN GLIGPLVNLL QNAEFDIKKE AAWAVSNATS GGTHEQIKFL
301 VSQGCIKPLC DLLVSPDPRI VTVSLEGLEN ILKVGEAEKN LGNSGDANFY
351 AQMIDDAEGL EKIENLQSHD NNEIYEKAVK ILETYWLEED DETLPSGDGA
401 QQGFQFGGNG VQVPSGGFNF

Spot No.: **P4**

NCBI accession No.: **gi| 249262** Species: *Manihot esculenta*

PFF score: [56]

Protein name: linamarase

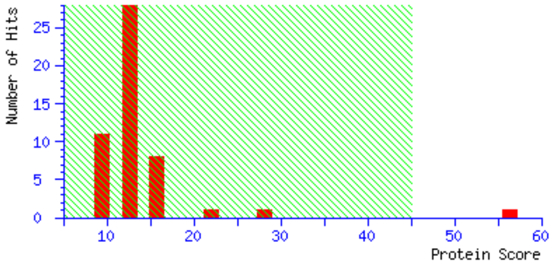
Matched peptides No.: [1] Sequence coverage %: [3]

Matched sequences: R.ILDGSNGDVAVDFYNR.Y;

Calculated Mr: **61448** Calculated *p*I: **5.52**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

```
  1 MLVLFISLLA LTRPAMGTDD DDDNIPDDFS RKYFPDDFIF GTATSAYQIE
 51 GEATAKGRAP SVWDIFSKET PDRILDGSNG DVAVDFYNRY IQDIKNVKKM
101 GFNAFRMSIS WSRVIPSGRR REGVNEEGIQ FYNDVINEII SNGLEPFVTI
151 FHWDTPQALQ DKYGGFLSRD IVYDYLQYAD LLFERFGDRV KPWMTFNEPS
201 AYVGFAHDDG VFAPGRCSSW VNRQCLAGDS ATEPYIVAHN LLLSHAAAVH
251 QYRKYYQGTQ KGKIGITLFT FWYEPLSDSK VDVQAAKTAL DFMFGLWMDP
301 MTYGRYPRTM VDLAGDKLIG FTDEESQLLR GSYDFVGLQY YTAYYAEPIP
351 PVDPKFRRYK TDSGVNATPY DLNGNLIGPQ AYSSWFYIFP KGIRHFLNYT
401 KDTYNDPVIY VTENGVDNYN NESQPIEEAL QDDFRISYYK KHMWNALGSL
451 KNYGVKLKGY FAWSYLDNFE WNIGYTSRFG LYYVDYKNNL TRYPKKSAHW
501 FTKFLNISVN ANNIYELTSK DSRKVGKFYV M
```

Spot No.: **P5**

NCBI accession No.: **gi| 29170601** Species: *Hevea brasiliensis*

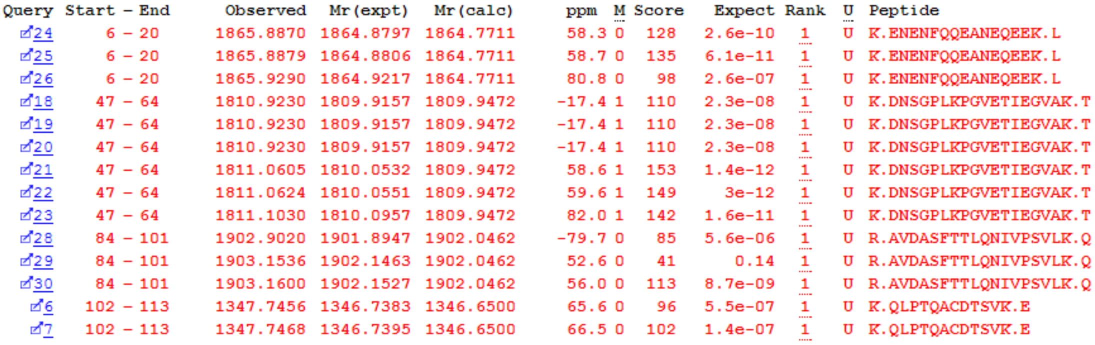
PFF score: [502]

Protein name: Small rubber particle protein

Matched peptides No.: [12] Sequence coverage %: [53]

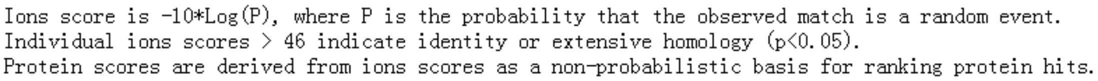
Calculated Mr: **12769** Calculated *p*I: **4.61**

Matched sequences:

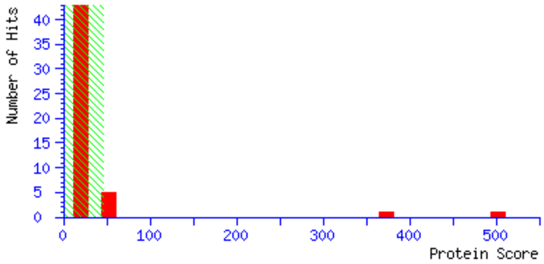


Query	Start – End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Expect	Rank	U	Peptide
24	6 – 20	1865.8870	1864.8797	1864.7711	58.3	0	128	2.6e-10	1	U	K.ENENFQQEANEQEEK.L
25	6 – 20	1865.8879	1864.8806	1864.7711	58.7	0	135	6.1e-11	1	U	K.ENENFQQEANEQEEK.L
26	6 – 20	1865.9290	1864.9217	1864.7711	80.8	0	98	2.6e-07	1	U	K.ENENFQQEANEQEEK.L
18	47 – 64	1810.9230	1809.9157	1809.9472	-17.4	1	110	2.3e-08	1	U	K.DNSGPLKPGVETIEGVAK.T
19	47 – 64	1810.9230	1809.9157	1809.9472	-17.4	1	110	2.3e-08	1	U	K.DNSGPLKPGVETIEGVAK.T
20	47 – 64	1810.9230	1809.9157	1809.9472	-17.4	1	110	2.3e-08	1	U	K.DNSGPLKPGVETIEGVAK.T
21	47 – 64	1811.0605	1810.0532	1809.9472	58.6	1	153	1.4e-12	1	U	K.DNSGPLKPGVETIEGVAK.T
22	47 – 64	1811.0624	1810.0551	1809.9472	59.6	1	149	3e-12	1	U	K.DNSGPLKPGVETIEGVAK.T
23	47 – 64	1811.1030	1810.0957	1809.9472	82.0	1	142	1.6e-11	1	U	K.DNSGPLKPGVETIEGVAK.T
28	84 – 101	1902.9020	1901.8947	1902.0462	-79.7	0	85	5.6e-06	1	U	R.AVDASFTTLQNIVPSVLK.Q
29	84 – 101	1903.1536	1902.1463	1902.0462	52.6	0	41	0.14	1	U	R.AVDASFTTLQNIVPSVLK.Q
30	84 – 101	1903.1600	1902.1527	1902.0462	56.0	0	113	8.7e-09	1	U	R.AVDASFTTLQNIVPSVLK.Q
6	102 – 113	1347.7456	1346.7383	1346.6500	65.6	0	96	5.5e-07	1	U	K.QLPTQACDTSVK.E
7	102 – 113	1347.7468	1346.7395	1346.6500	66.5	0	102	1.4e-07	1	U	K.QLPTQACDTSVK.E

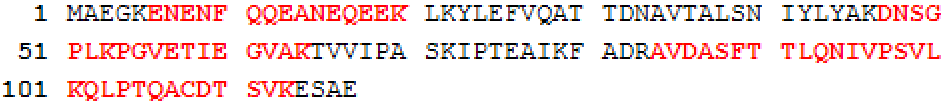
Probability Based Mowse Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:



1 MAEGK**ENENF** **QQEANEQEEK** LKYLEFVQAT TDNAVTALSN IYLYAK**DNSG**
51 **PLKPGVETIE** **GVAK**TVVIPA SKIPTEAIKF ADR**AVDASFT** **TLQNIVPSVL**
101 **KQLPTQACDT** **SVK**ESAE

Spot No.: **P6**

NCBI accession No.: **gi| 29170601** Species: *Hevea brasiliensis*

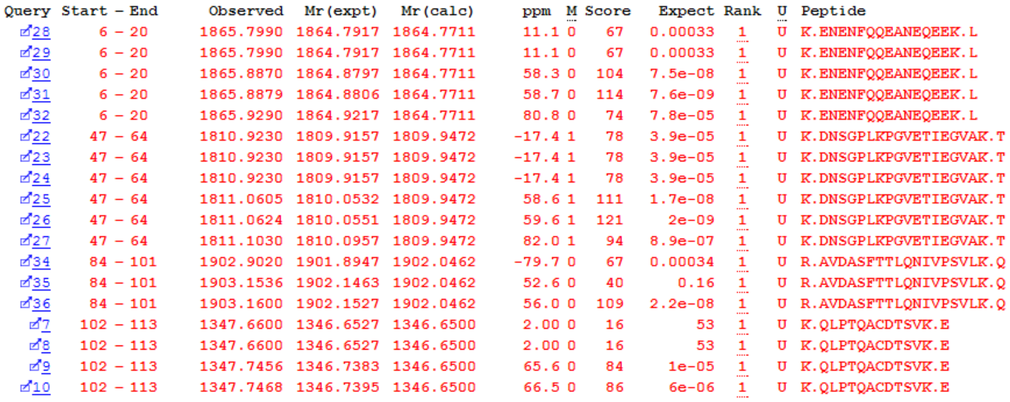
PFF score: [429]

Protein name: Small rubber particle protein

Matched peptides No.: [18] Sequence coverage %: [53]

Calculated Mr: **12769** Calculated *p*I: **4.61**

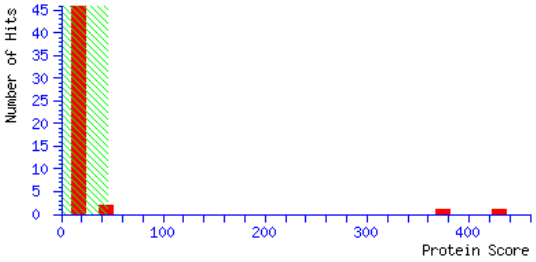
Matched sequences:



Query	Start – End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Expect	Rank	U	Peptide
28	6 – 20	1865.7990	1864.7917	1864.7711	11.1	0	67	0.00033	1	U	K.ENENFQQEANEQEEK.L
29	6 – 20	1865.7990	1864.7917	1864.7711	11.1	0	67	0.00033	1	U	K.ENENFQQEANEQEEK.L
30	6 – 20	1865.8870	1864.8797	1864.7711	58.3	0	104	7.5e-08	1	U	K.ENENFQQEANEQEEK.L
31	6 – 20	1865.8879	1864.8806	1864.7711	58.7	0	114	7.6e-09	1	U	K.ENENFQQEANEQEEK.L
32	6 – 20	1865.9290	1864.9217	1864.7711	80.8	0	74	7.8e-05	1	U	K.ENENFQQEANEQEEK.L
22	47 – 64	1810.9230	1809.9157	1809.9472	-17.4	1	78	3.9e-05	1	U	K.DNSGPLKPGVETIEGVAK.T
23	47 – 64	1810.9230	1809.9157	1809.9472	-17.4	1	78	3.9e-05	1	U	K.DNSGPLKPGVETIEGVAK.T
24	47 – 64	1810.9230	1809.9157	1809.9472	-17.4	1	78	3.9e-05	1	U	K.DNSGPLKPGVETIEGVAK.T
25	47 – 64	1811.0605	1810.0532	1809.9472	58.6	1	111	1.7e-08	1	U	K.DNSGPLKPGVETIEGVAK.T
26	47 – 64	1811.0624	1810.0551	1809.9472	59.6	1	121	2e-09	1	U	K.DNSGPLKPGVETIEGVAK.T
27	47 – 64	1811.1030	1810.0957	1809.9472	82.0	1	94	8.9e-07	1	U	K.DNSGPLKPGVETIEGVAK.T
34	84 – 101	1902.9020	1901.8947	1902.0462	-79.7	0	67	0.00034	1	U	R.AVDASFTTLQNIVPSVLK.Q
35	84 – 101	1903.1536	1902.1463	1902.0462	52.6	0	40	0.16	1	U	R.AVDASFTTLQNIVPSVLK.Q
36	84 – 101	1903.1600	1902.1527	1902.0462	56.0	0	109	2.2e-08	1	U	R.AVDASFTTLQNIVPSVLK.Q
7	102 – 113	1347.6600	1346.6527	1346.6500	2.00	0	16	53	1	U	K.QLPTQACDTSVK.E
8	102 – 113	1347.6600	1346.6527	1346.6500	2.00	0	16	53	1	U	K.QLPTQACDTSVK.E
9	102 – 113	1347.7456	1346.7383	1346.6500	65.6	0	84	1e-05	1	U	K.QLPTQACDTSVK.E
10	102 – 113	1347.7468	1346.7395	1346.6500	66.5	0	86	6e-06	1	U	K.QLPTQACDTSVK.E

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

```
  1 MAEGKENENF QQEANEQEEK LKYLEFVQAT TDNAVTALSN IYLYAKDNSG
 51 PLKPGVETIE GVAKTVVIPA SKIPTEAIKF ADRAVDASFT TLQNIVPSVL
101 KQLPTQACDT SVKESAE
```

Spot No.: **P7**

NCBI accession No.: **gi| 224071449** Species: *Populus trichocarpa*

PFF score: [75]

Protein name: predicted protein

Matched peptides No.: [1] Sequence coverage %: [2]

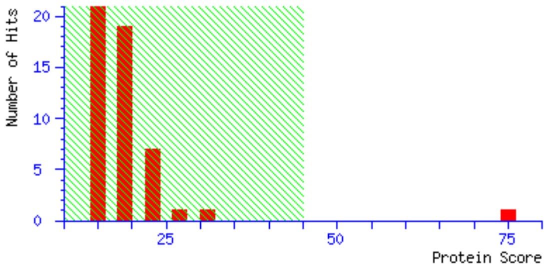
Matched sequences: K.NKIDVIPHYPGR.L;

K.IDVIPHYPGR.L

Calculated Mr: **47121** Calculated *p*I: **5.28**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MDGTSEATWP EILGSRNWDN LLDPLDLSLR KLILRCGDFC QATYDAFNND
51 QNSRYCGTSR YGKRNFFHKV MLDNPENYQV SSFLYATARV SLPEAFLLHS
101 LSRDSWDRET NWIGYIAVTS DEQTKTLGRR EIYIAFRGTT RNYEWVDILG
151 AKLKSAKPLL RGATSTTHDQ ESSSSSDDDD DKVPKVMLGW LTMYISDDPN
201 SPFTKLSARA QLLAHIKELR ERYKDDDLSI IFTGHSLGAS LSILSAFDLV
251 ENGITDIPVS AFVFGSPQVG NKEFNERFNK YPNLKVLHIK **NKIDVIPHYP**
301 **GR**LMGYVYTG IEFEIDTRKS PSLKDSKNPS DWHNLQAMLH IVAGWNGEEQ
351 EFELKVKRSL ALVNKSSEFL KDECLVPGIW WVEKNKGMVR NEDGEWVLAP
401 PDEEDLPVPE C

Spot No.: **P8**

NCBI accession No.: **gi| 32186890** Species: *Gossypium hirsutum*

PFF score: [519]

Protein name: actin

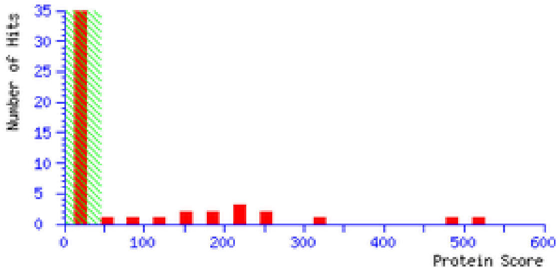
Matched peptides No.: [8] Sequence coverage %: [37]

Matched sequences: K.YPIEHGIVSNWDDMEK.I;
K.IWHHTFYNELR.V;
R.VAPEEHPVLLTEAPLNPK.A;
R.TTGIVLDSGDGVSHTVPIYEGYALPHAILR.L;
K.LAYVALDYEQELETAK.S;
K.NYELPDGQVITIGAER.F;
R.KDLYGNIVLSGGSTMFPGIADR.M + Oxidation (M);
K.GEYDESGPSIVHR.K

Calculated Mr: **41917** Calculated *p*I: **5.31**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

```
  1 MADGEDIQPL VCDNGTGMVK AGFAGDDAPR AVFPSIVGRP RHTGVMVGMG
 51 QKDAYVGDEA QSKRGILTLK YPIEHGIVSN WDDMEKIWHH TFYNELRVAP
101 EEHPVLLTEA PLNPKANREK MTQIMFETFN VPAMYVAIQA VLSLYASGRT
151 TGIVLDSGDG VSHTVPIYEG YALPHAILRL DLAGRDLTDA LMKILTERGY
201 MFTTTAEREI VRDMKEKLAY VALDYEQELE TAKSSSSVEK NYELPDGQVI
251 TIGAERFRCP EVLFQPSFIG MEAAGIHETT YNSIMKCDVD IRKDLYGNIV
301 LSGGSTMFPG IADRMSKEIT ALAPSSMKIK VVAPPERKYS VWIGGSILAS
351 LSTFQQMWIS KGEYDESGPS IVHRKCF
```

Spot No.: **P9**

NCBI accession No.: **gi| 14423933**   Species: *Hevea brasiliensis*

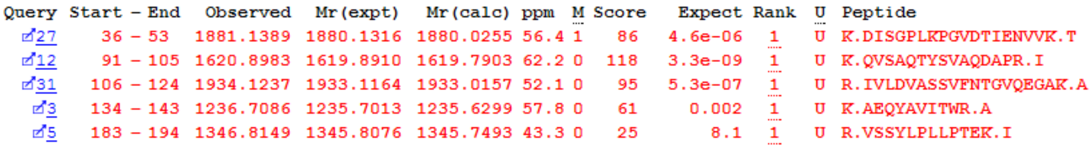
PFF score: [384]

Protein name: Small rubber particle protein

Matched peptides No.: [5]   Sequence coverage %: [36]

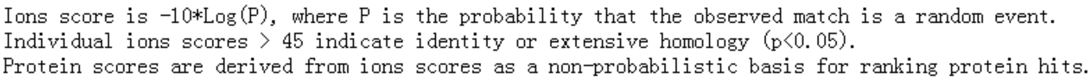
Calculated Mr: **22331**   Calculated *p*I: **4.80**

Matched sequences:

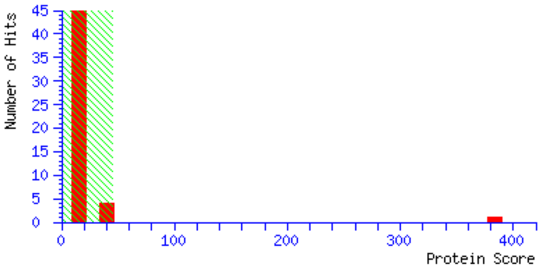


```
Query Start - End  Observed  Mr(expt)  Mr(calc) ppm  M Score  Expect Rank  U Peptide
  27    36 - 53  1881.1389 1880.1316 1880.0255 56.4 1   86  4.6e-06   1   U K.DISGPLKPGVDTIENVVK.T
  12    91 - 105 1620.8983 1619.8910 1619.7903 62.2 0  118  3.3e-09   1   U K.QVSAQTYSVAQDAPR.I
  31   106 - 124 1934.1237 1933.1164 1933.0157 52.1 0   95  5.3e-07   1   U R.IVLDVASSVFNTGVQEGAK.A
   3   134 - 143 1236.7086 1235.7013 1235.6299 57.8 0   61    0.002   1   U K.AEQYAVITWR.A
   5   183 - 194 1346.8149 1345.8076 1345.7493 43.3 0   25      8.1   1   U R.VSSYLPLLPTEK.I
```

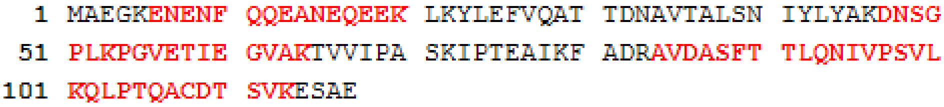
Probability Based Mowse Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:



1 MAEGK**ENENF QQEANEQEEK** LKYLEFVQAT TDNAVTALSN IYLYAK**DNSG**
51 **PLKPGVETIE GVAK**TVVIPA SKIPTEAIKF ADR**AVDASFT TLQNIVPSVL**
101 **KQLPTQACDT SVK**ESAE

Spot No.: **P10**

NCBI accession No.: **gi| 224071449** Species: *Populus trichocarpa*

PFF score: [71]

Protein name: predicted protein

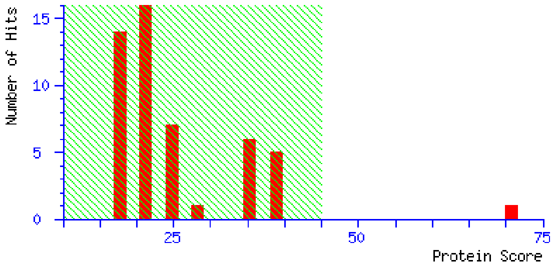
Matched peptides No.: [1] Sequence coverage %: [2]

Matched sequences: K.IDVIPHYPGR.L;

Calculated Mr: **47121** Calculated *p*I: **5.28**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MDGTSEATWP EILGSRNWDN LLDPLDLSLR KLILRCGDFC QATYDAFNND
51 QNSRYCGTSR YGKRNFFHKV MLDNPENYQV SSFLYATARV SLPEAFLLHS
101 LSRDSWDRET NWIGYIAVTS DEQTKTLGRR EIYIAFRGTT RNYEWVDILG
151 AKLKSAKPLL RGATSTTHDQ ESSSSSDDDD DKVPKVMLGW LTMYISDDPN
201 SPFTKLSARA QLLAHIKELR ERYKDDDLSI IFTGHSLGAS LSILSAFDLV
251 ENGITDIPVS AFVFGSPQVG NKEFNERFNK YPNLKVLHIK NK**IDVIPHYP**
301 **GR**LMGYVYTG IEFEIDTRKS PSLKDSKNPS DWHNLQAMLH IVAGWNGEEQ
351 EFELKVKRSL ALVNKSSEFL KDECLVPGIW WVEKNKGMVR NEDGEWVLAP
401 PDEEDLPVPE C

Spot No.: **P11**

NCBI accession No.: **gi| 224071449** Species: *Populus trichocarpa*

PFF score: [52]

Protein name: predicted protein

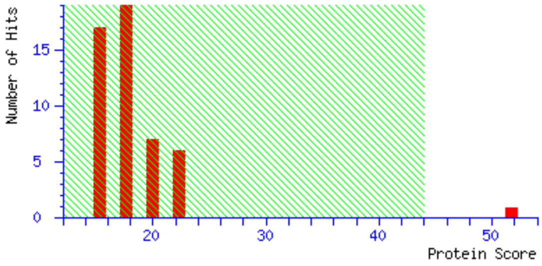
Matched peptides No.: [1] Sequence coverage %: [2]

Matched sequences: K.IDVIPHYPGR.L;

Calculated Mr: **47121** Calculated *p*I: **5.28**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

```
  1 MDGTSEATWP EILGSRNWDN LLDPLDLSLR KLILRCGDFC QATYDAFNND
 51 QNSRYCGTSR YGKRNFFHKV MLDNPENYQV SSFLYATARV SLPEAFLLHS
101 LSRDSWDRET NWIGYIAVTS DEQTKTLGRR EIYIAFRGTT RNYEWVDILG
151 AKLKSAKPLL RGATSTTHDQ ESSSSSDDDD DKVPKVMLGW LTMYISDDPN
201 SPFTKLSARA QLLAHIKELR ERYKDDDLSI IFTGHSLGAS LSILSAFDLV
251 ENGITDIPVS AFVFGSPQVG NKEFNERFNK YPNLKVLHIK NKIDVIPHYP
301 GRLMGYVYTG IEFEIDTRKS PSLKDSKNPS DWHNLQAMLH IVAGWNGEEQ
351 EFELKVKRSL ALVNKSSEFL KDECLVPGIW WVEKNKGMVR NEDGEWVLAP
401 PDEEDLPVPE C
```

Spot No.: **P12**

NCBI accession No.: **gi| 224071449** Species: *Populus trichocarpa*

PFF score: [106]

Protein name: predicted protein

Matched peptides No.: [2] Sequence coverage %: [2]

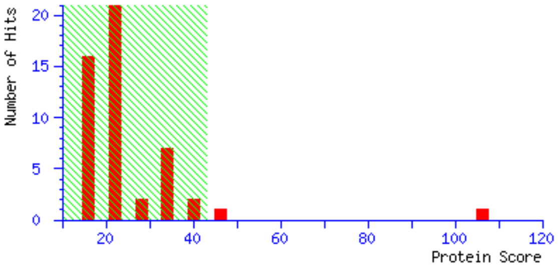
Matched sequences: K.NKIDVIPHYPGR.L;

K.IDVIPHYPGR.L;

Calculated Mr: **47121** Calculated *p*I: **5.28**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 43 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

```
  1 MDGTSEATWP EILGSRNWDN LLDPLDLSLR KLILRCGDFC QATYDAFNND
 51 QNSRYCGTSR YGKRNFFHKV MLDNPENYQV SSFLYATARV SLPEAFLLHS
101 LSRDSWDRET NWIGYIAVTS DEQTKTLGRR EIYIAFRGTT RNYEWVDILG
151 AKLKSAKPLL RGATSTTHDQ ESSSSSDDDD DKVPKVMLGW LTMYISDDPN
201 SPFTKLSARA QLLAHIKELR ERYKDDDLSI IFTGHSLGAS LSILSAFDLV
251 ENGITDIPVS AFVFGSPQVG NKEFNERFNK YPNLKVLHIK NKIDVIPHYP
301 GRLMGYVYTG IEFEIDTRKS PSLKDSKNPS DWHNLQAMLH IVAGWNGEEQ
351 EFELKVKRSL ALVNKSSEFL KDECLVPGIW WVEKNKGMVR NEDGEWVLAP
401 PDEEDLPVPE C
```

Spot No.: **P13**

NCBI accession No.: **gi| 1550740** Species: *Arabidopsis thaliana*

PFF score: [51]

Protein name: GDP-associated inhibitor

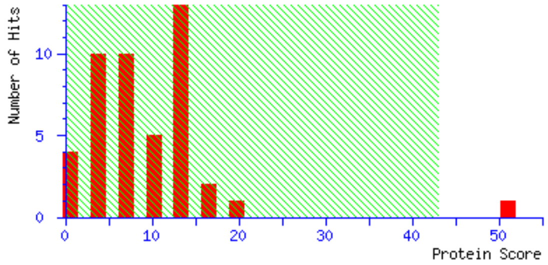
Matched peptides No.: [1] Sequence coverage %: [5]

Matched sequences: R.FQGGSPYIYPLYGLGELPQAFAR.L;

Calculated Mr: **50269** Calculated *p*I: **5.49**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 43 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

```
  1 MDEEYEVIVL GTGLKECILS GLLSVDGLKV LHMDRNDYYG GESTSLNLNQ
 51 LWKKFRGEEK APAHLGSSRD YNVDMMPKFM MANGKLVRVL IHTDVTKYLS
101 FKAVDGSYVF VQGKVQKVPA TPMEALKSPL MGIFEKRRAG KFFSYVQEYD
151 EKDPKTHDGM DLRRVTTKDL IAKFGLKEDT IDFIGHAVAL HCNDNHLHQP
201 AYDTVMRMKL YAESLARFQG GSPYIYPLYG LGELPQAFAR LSAVYGGTYM
251 LNKPECKVEF DEEGKVSGVT SEGETAKCKK VVCDPSYLTN KVRKIGRVAR
301 AIAIMSHPIP NTNDSQSVQV ILPQKQLGRK SDMYVFCCSY SHNVAPKGKF
351 IAFVSTDAET DNPQTELQPG IDLLGPVDEL FFDIYDRYEP VNEPTLDNCF
401 ISTSYDATTH FDTTVVDVLN MYKLITGKEL DLSVDLNPAS AAEEE
```

Spot No.: **P14**

NCBI accession No.: **gi| 255552291** Species: *Ricinus communis*

PFF score: [144]

Protein name: short chain dehydrogenase, putative

Matched peptides No.: [3] Sequence coverage %: [11]

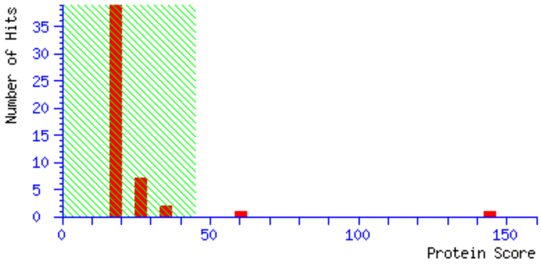
Matched sequences: K.VALVTGGDSGIGR.A;

K.AEGAKDPIAIPTDVGFEENCR.K;
K.DPIAIPTDVGFEENCR.K

Calculated Mr: **32148** Calculated *p*I: **6.50**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MATRRGYRFP PQSQDKQPGK EYLMHPLPEF INPHYKPSNK LQDK**VALVTG**
51 **GDSGIGR**AVS YYFTLEGATV AFTYVKGRED KDKDHILKIL HEVK**AEGAKD**
101 **PIAIPTDVGF** **EENCR**KVIDQ IMSEYGKIDI LVNNAGEAHY STTIEDITDP
151 MLERVFRTNI FGHFFMSRHA LKHMKEGGCI INTASVAAYA GFSFMVDYSS
201 TKGAVVAFTR SLALQLIDRG IRVNAVAPGS VWTPFQPSTL SAEQVAQVGS
251 GVPMDRAAQP YEIAPSFVFL ASNDCSSYFT GQVLHPNGMF

Spot No.: **P15**

NCBI accession No.: **gi| 218157**Species: ***Oryza sativa***

PFF score: [174]

Protein name: cytoplasmic aldolase

Matched peptides No.: [2]   Sequence coverage %: [3]

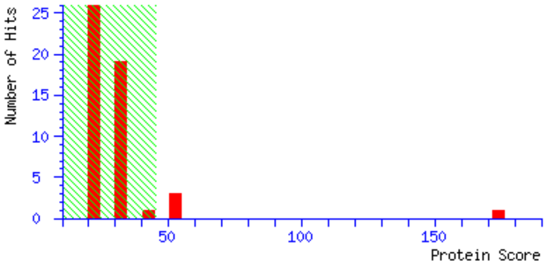
Matched sequences: K.KVAPEVIAEYTVR.T;

K.VAPEVIAEYTVR.T;

Calculated Mr: **39151**   Calculated *p*I: **6.56**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MSAYCGKYKD ELIKNAAYIG TPGKGILAAD ESTGTIGKRF ASINVENVED
51 NRRAFRELLF CTPGALQYIS GVILFDETLY QKTKDGKPFV DILKEAGALP
101 GIKVDKGTIE VAGTDKETTT QGHDDLGKQC AKYYEAGARF AKWRAVLKIG
151 PNQPSQLAID LNAQGLACYA IICQENGLVP IVEPEILVDG PHDIDRCAYV
201 SEVVLAACYK ALNEHHVLLE GTLLKPNMVT PGSDAK**KVAP** **EVIAEYTVR**T
251 LQRTVPPAVP AIVFLSGGQS EEEATLNLNA MNKLSAKKPW SLSFSFGRAL
301 QQSTLKAWAG KTENVEKARA AFLVRCKANS EATLGTYKGD AVLGEGAAES
351 LHVKDYKY

Spot No.: **P16**

NCBI accession No.: **gi| 218157** Species: *Oryza sativa Japonica Group*

PFF score: [125]

Protein name: cytoplasmic aldolase

Matched peptides No.: [2]　　　　　Sequence coverage %: [3]

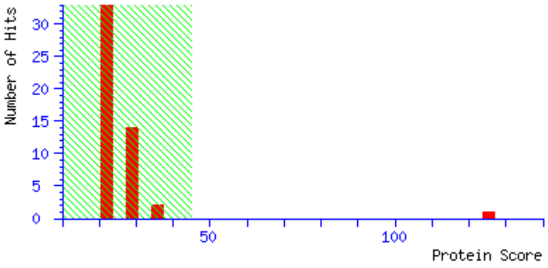
Matched sequences: K.KVAPEVIAEYTVR.T;

K.VAPEVIAEYTVR.T;

Calculated Mr: **39151**　　　　　Calculated *p*I: **6.56**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MSAYCGKYKD ELIKNAAYIG TPGKGILAAD ESTGTIGKRF ASINVENVED
51 NRRAFRELLF CTPGALQYIS GVILFDETLY QKTKDGKPFV DILKEAGALP
101 GIKVDKGTIE VAGTDKETTT QGHDDLGKQC AKYYEAGARF AKWRAVLKIG
151 PNQPSQLAID LNAQGLACYA IICQENGLVP IVEPEILVDG PHDIDRCAYV
201 SEVVLAACYK ALNEHHVLLE GTLLKPNMVT PGSDAK**KVAP** **EVIAEYTVR**T
251 LQRTVPPAVP AIVFLSGGQS EEEATLNLNA MNKLSAKKPW SLSFSFGRAL
301 QQSTLKAWAG KTENVEKARA AFLVRCKANS EATLGTYKGD AVLGEGAAES
351 LHVKDYKY

Spot No.: **P17**

NCBI accession No.: **gi| 14423933** Species: *Hevea brasiliensis*

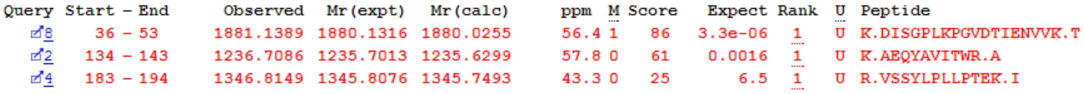
PFF score: [171]

Protein name: Small rubber particle protein

Matched peptides No.: [3] Sequence coverage %: [19]

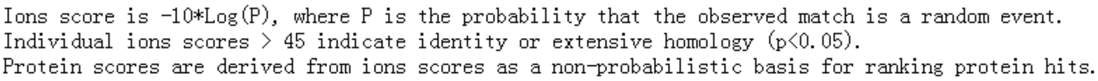
Calculated Mr: **22331** Calculated *p*I: **4.80**

Matched sequences:

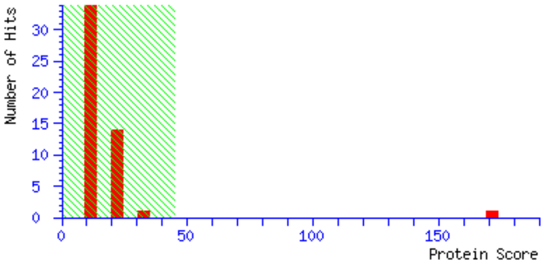


```
Query Start - End     Observed  Mr(expt)  Mr(calc)    ppm  M Score   Expect Rank  U  Peptide
   8    36 - 53     1881.1389 1880.1316 1880.0255    56.4 1    86   3.3e-06   1   U  K.DISGPLKPGVDTIENVVK.T
   2   134 - 143    1236.7086 1235.7013 1235.6299    57.8 0    61    0.0016   1   U  K.AEQYAVITWR.A
   4   183 - 194    1346.8149 1345.8076 1345.7493    43.3 0    25       6.5   1   U  R.VSSYLPLLPTEK.I
```

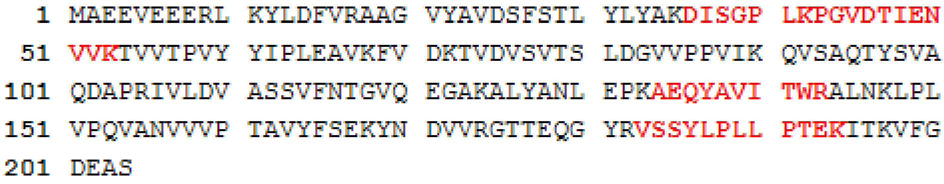
Probability Based Mowse Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:



1 MAEEVEEERL KYLDFVRAAG VYAVDSFSTL YLYAK**DISGP** **LKPGVDTIEN**

51 **VVK**TVVTPVY YIPLEAVKFV DKTVDVSVTS LDGVVPPVIK QVSAQTYSVA

101 QDAPRIVLDV ASSVFNTGVQ EGAKALYANL EPK**AEQYAVI** **TWR**ALNKLPL

151 VPQVANVVVP TAVYFSEKYN DVVRGTTEQG YR**VSSYLPLL** **PTEK**ITKVFG

201 DEAS

Spot No.: **P18**

NCBI accession No.: **gi| 118489480**

Species: *Populus trichocarpa x Populus deltoids*

PFF score: [74]

Protein name: unknown

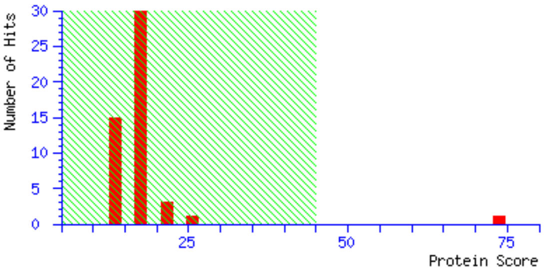
Matched peptides No.: [2]   Sequence coverage %: [3]

Matched sequences: R.KLLVALVSAYR.Y;
K.LLVALVSAYR.Y

Calculated Mr: **35859**   Calculated *p*I: **8.42**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



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

1 MAHLEALAKA FTGLGVDEKS LIENLGKSHP EQRTLFRKKT PQLFIEDERS
51 FERWNDHCVR LLKHEFVRFK NALVLWAMHP WERDARLVKE ALKKGPQSYG
101 VIVEIACTRS SEELLGARKA YHSLFDQSIE EDVATHIHGS ER**KLLVALVS**
151 **AYR**YEGPKVK EDAAKSEAKI LANAIKNGNK KNPIEDEEVI RILSTRSKAH
201 LKVACKHYKE VSGNNIHEDL DPSDLILKET VECLCTPHAY FSKVLDEAMS
251 SNAHKNTKKG LTRVIVTRAD VDMKEIKEEY MNLFGVSLSK KIEEKANGNY
301 RDFLVTLITR DN

Spot No.: **P19**

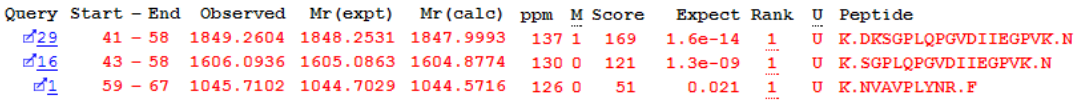
NCBI accession No.: **gi|132270**   Species: *Hevea brasiliensis*

PFF score: [341]

Protein name: Rubber elongation factor protein

Matched peptides No.: [3]   Sequence coverage %: [19]

Matched sequences:

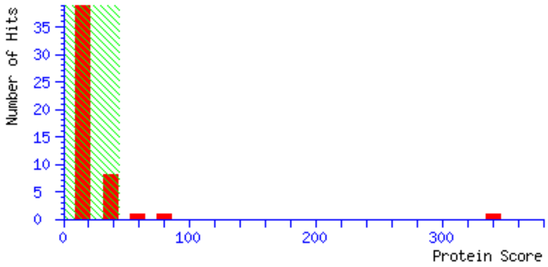


Query	Start – End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Expect	Rank	U	Peptide
29	41 – 58	1849.2604	1848.2531	1847.9993	137	1	169	1.6e-14	1	U	K.DKSGPLQPGVDIIEGPVK.N
16	43 – 58	1606.0936	1605.0863	1604.8774	130	0	121	1.3e-09	1	U	K.SGPLQPGVDIIEGPVK.N
1	59 – 67	1045.7102	1044.7029	1044.5716	126	0	51	0.021	1	U	K.NVAVPLYNR.F

Calculated Mr: **14713**   Calculated *p*I: **5.04**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

```
  1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK DKSGPLQPGV
 51 DIIEGPVKNV AVPLYNRFSY IPNGALKFVD STVVASVTII DRSLPPIVKD
101 ASIQVVSAIR AAPEAARSLA SSLPGQTKIL AKVFYGEN
```

Spot No.: **P20**

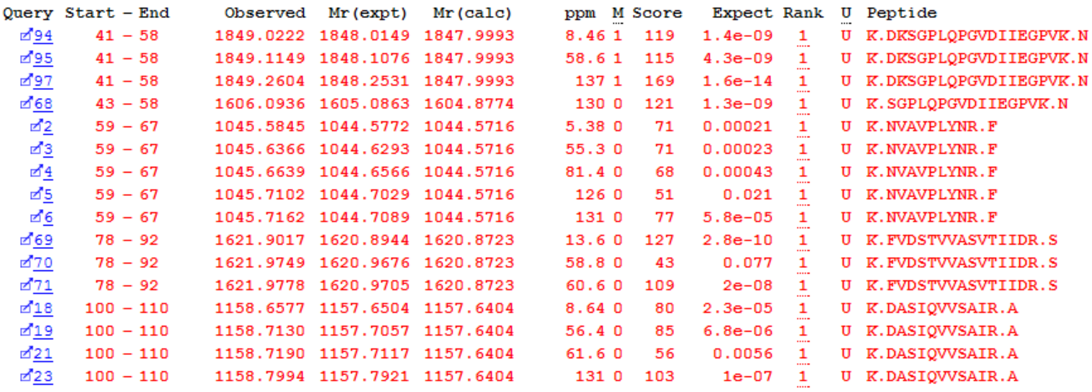
NCBI accession No.: **gi|132270** Species: *Hevea brasiliensis*

PFF score: [597]

Protein name: Rubber elongation factor protein

Matched peptides No.: [16] Sequence coverage %: [38]

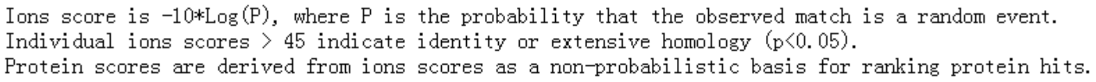
Matched sequences:



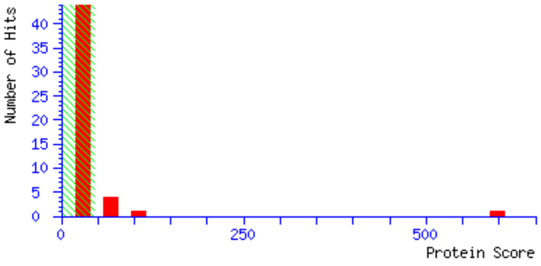
Query	Start – End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Expect	Rank	U	Peptide
94	41 – 58	1849.0222	1848.0149	1847.9993	8.46	1	119	1.4e-09	1	U	K.DKSGPLQPGVDIIEGPVK.N
95	41 – 58	1849.1149	1848.1076	1847.9993	58.6	1	115	4.3e-09	1	U	K.DKSGPLQPGVDIIEGPVK.N
97	41 – 58	1849.2604	1848.2531	1847.9993	137	1	169	1.6e-14	1	U	K.DKSGPLQPGVDIIEGPVK.N
68	43 – 58	1606.0936	1605.0863	1604.8774	130	0	121	1.3e-09	1	U	K.SGPLQPGVDIIEGPVK.N
2	59 – 67	1045.5845	1044.5772	1044.5716	5.38	0	71	0.00021	1	U	K.NVAVPLYNR.F
3	59 – 67	1045.6366	1044.6293	1044.5716	55.3	0	71	0.00023	1	U	K.NVAVPLYNR.F
4	59 – 67	1045.6639	1044.6566	1044.5716	81.4	0	68	0.00043	1	U	K.NVAVPLYNR.F
5	59 – 67	1045.7102	1044.7029	1044.5716	126	0	51	0.021	1	U	K.NVAVPLYNR.F
6	59 – 67	1045.7162	1044.7089	1044.5716	131	0	77	5.8e-05	1	U	K.NVAVPLYNR.F
69	78 – 92	1621.9017	1620.8944	1620.8723	13.6	0	127	2.8e-10	1	U	K.FVDSTVVASVTIIDR.S
70	78 – 92	1621.9749	1620.9676	1620.8723	58.8	0	43	0.077	1	U	K.FVDSTVVASVTIIDR.S
71	78 – 92	1621.9778	1620.9705	1620.8723	60.6	0	109	2e-08	1	U	K.FVDSTVVASVTIIDR.S
18	100 – 110	1158.6577	1157.6504	1157.6404	8.64	0	80	2.3e-05	1	U	K.DASIQVVSAIR.A
19	100 – 110	1158.7130	1157.7057	1157.6404	56.4	0	85	6.8e-06	1	U	K.DASIQVVSAIR.A
21	100 – 110	1158.7190	1157.7117	1157.6404	61.6	0	56	0.0056	1	U	K.DASIQVVSAIR.A
23	100 – 110	1158.7994	1157.7921	1157.6404	131	0	103	1e-07	1	U	K.DASIQVVSAIR.A

Calculated Mr: **14713** Calculated *p*I: **5.04**

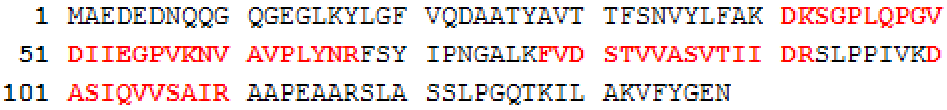
Probability Based Mowse Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:



```
  1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK DKSGPLQPGV
 51 DIIEGPVKNV AVPLYNRFSY IPNGALKFVD STVVASVTII DRSLPPIVKD
101 ASIQVVSAIR AAPEAARSLA SSLPGQTKIL AKVFYGEN
```

Spot No.: **P21**

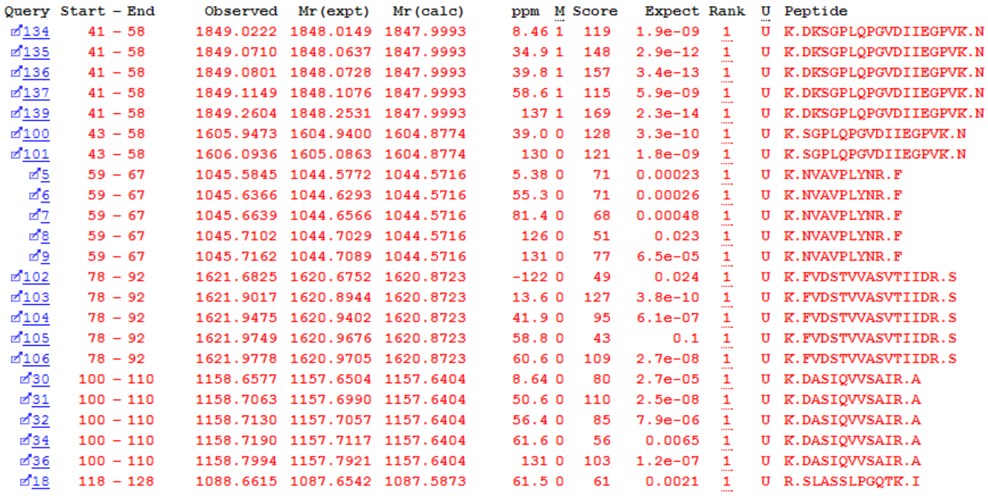
NCBI accession No.: **gi|132270** Species: *Hevea brasiliensis*

PFF score: [672]

Protein name: Rubber elongation factor protein

Matched peptides No.: [23] Sequence coverage %: [46]

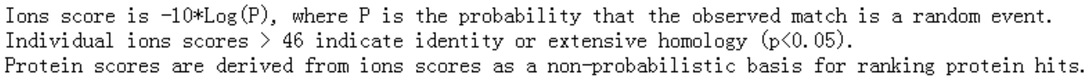
Matched sequences:



Query	Start – End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Expect	Rank	U	Peptide
134	41 – 58	1849.0222	1848.0149	1847.9993	8.46	1	119	1.9e-09	1	U	K.DKSGPLQPGVDIIEGPVK.N
135	41 – 58	1849.0710	1848.0637	1847.9993	34.9	1	148	2.9e-12	1	U	K.DKSGPLQPGVDIIEGPVK.N
136	41 – 58	1849.0801	1848.0728	1847.9993	39.8	1	157	3.4e-13	1	U	K.DKSGPLQPGVDIIEGPVK.N
137	41 – 58	1849.1149	1848.1076	1847.9993	58.6	1	115	5.9e-09	1	U	K.DKSGPLQPGVDIIEGPVK.N
139	41 – 58	1849.2604	1848.2531	1847.9993	137	1	169	2.3e-14	1	U	K.DKSGPLQPGVDIIEGPVK.N
100	43 – 58	1605.9473	1604.9400	1604.8774	39.0	0	128	3.3e-10	1	U	K.SGPLQPGVDIIEGPVK.N
101	43 – 58	1606.0936	1605.0863	1604.8774	130	0	121	1.8e-09	1	U	K.SGPLQPGVDIIEGPVK.N
5	59 – 67	1045.5845	1044.5772	1044.5716	5.38	0	71	0.00023	1	U	K.NVAVPLYNR.F
6	59 – 67	1045.6366	1044.6293	1044.5716	55.3	0	71	0.00026	1	U	K.NVAVPLYNR.F
7	59 – 67	1045.6639	1044.6566	1044.5716	81.4	0	68	0.00048	1	U	K.NVAVPLYNR.F
8	59 – 67	1045.7102	1044.7029	1044.5716	126	0	51	0.023	1	U	K.NVAVPLYNR.F
9	59 – 67	1045.7162	1044.7089	1044.5716	131	0	77	6.5e-05	1	U	K.NVAVPLYNR.F
102	78 – 92	1621.6825	1620.6752	1620.8723	-122	0	49	0.024	1	U	K.FVDSTVVASVTIIDR.S
103	78 – 92	1621.9017	1620.8944	1620.8723	13.6	0	127	3.8e-10	1	U	K.FVDSTVVASVTIIDR.S
104	78 – 92	1621.9475	1620.9402	1620.8723	41.9	0	95	6.1e-07	1	U	K.FVDSTVVASVTIIDR.S
105	78 – 92	1621.9749	1620.9676	1620.8723	58.8	0	43	0.1	1	U	K.FVDSTVVASVTIIDR.S
106	78 – 92	1621.9778	1620.9705	1620.8723	60.6	0	109	2.7e-08	1	U	K.FVDSTVVASVTIIDR.S
30	100 – 110	1158.6577	1157.6504	1157.6404	8.64	0	80	2.7e-05	1	U	K.DASIQVVSAIR.A
31	100 – 110	1158.7063	1157.6990	1157.6404	50.6	0	110	2.5e-08	1	U	K.DASIQVVSAIR.A
32	100 – 110	1158.7130	1157.7057	1157.6404	56.4	0	85	7.9e-06	1	U	K.DASIQVVSAIR.A
34	100 – 110	1158.7190	1157.7117	1157.6404	61.6	0	56	0.0065	1	U	K.DASIQVVSAIR.A
36	100 – 110	1158.7994	1157.7921	1157.6404	131	0	103	1.2e-07	1	U	K.DASIQVVSAIR.A
18	118 – 128	1088.6615	1087.6542	1087.5873	61.5	0	61	0.0021	1	U	R.SLASSLPGQTK.I

Calculated Mr: **14713** Calculated *p*I: **5.04**

Probability Based Mowse Score:



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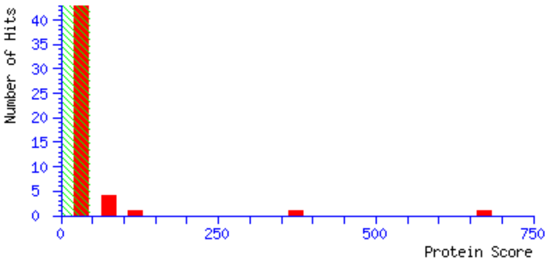
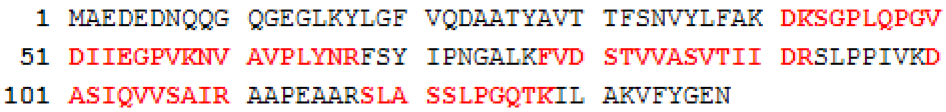
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:



1 MAEDEDNQQG QGEGLKYLGF VQDAATYAVT TFSNVYLFAK **DKSGPLQPGV**
51 **DIIEGPVKNV** **AVPLYNR**FSY IPNGALK**FVD** **STVVASVTII** **DR**SLPPIVK**D**
101 **ASIQVVSAIR** AAPEAAR**SLA** **SSLPGQTK**IL AKVFYGEN

Spot No.: **P22**

NCBI accession No.: **gi| 38154482** Species: *Nicotiana benthamiana*

PFF score: [197]

Protein name: molecular chaperone Hsp90-1

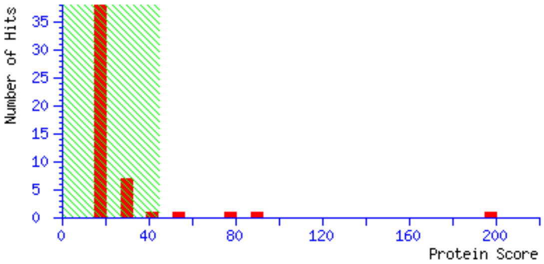
Matched peptides No.: [5] Sequence coverage %: [8]

Matched sequences: K.ADLVNNLGTIAR.S;
K.HNDDEQYVWESQAGGSFTVTR.D;
K.RAPFDLFDTR.K;
R.APFDLFDTR.K;
K.GIVDSEDLPLNISR.E

Calculated Mr: **80340** Calculated *p*I: **4.94**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEAETFAFQ AEINQLLSLI INTFYSNKEI FLRELISNSS DALDKIRFES
51 LTDKSKLDAQ PELFIHIIPD KTNNSLTIID SGIGMTK**ADL** **VNNLGTIAR**S
101 GTKEFMEALA AGADVSMIGQ FGVGFYSAYL VAEKVIVTTK **HNDDEQYVWE**
151 **SQAGGSFTVT** **R**DTSGDNLGR GTKITLFLKE DQLEYLEERR LKDLIKKHSE
201 FISYPISLWV EKTIEKEISD DEEEEEKKDE EGKVEEVDEE KEKEEKKKKK
251 VKEASNEWSL VNKQKPIWMR KPDEITKEEY AAFYKSLTND WEEHLAVKHF
301 SVEGQLEFKA ILFVPK**RAPF** **DLFDTR**KKPN NIKLYVRRVF IMDNCEELIP
351 EYLSFVK**GIV** **DSEDLPLNIS** **R**EMLQQNKIL KVIRKNLVKK CVELFFEIAE
401 NKEDYDKFYE AFSKNLKLGI HEDSQNRSKF AELLRYHSTK SGDEMTSLKD
451 YVTRMKEGQN DIYYITGESK KAVENSPFLE KLKKKGYEVL YMVDAIDEYS
501 IGQLKEFEGK KLVSATKEGL KLDESEDEKK KQEELKEKFE GLCKVIKDVL
551 GDKVEKVVVS DRVVDSPCCL VTGEYGWTAN MERIMKAQAL RDSSMAGYMS
601 SKKTMEINPE NAIMEELRKR ADADKNDKSV KDLVLLLFET ALLTSGFSLE
651 EPNTFGNRIH RMLKLGLSID DDSGDADVDM PALEDAEADA EGSKMEEVD

Spot No.: **P23**

NCBI accession No.: **gi| 1708314** Species: *Ipomoea nil*

PFF score: [126]

Protein name: RecName: Full=Heat shock protein 83

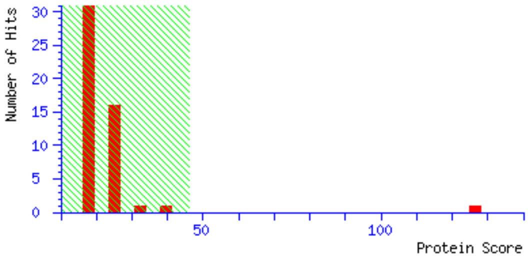
Matched peptides No.: [5] Sequence coverage %: [8]

Matched sequences: K.LDAQPELFIR.L;
K.ADLVNNLGTIAR.S;
K.ITLFLKEDQLEYLEER.R;
K.RAPFDLFDTR.K;
K.LGIHEDSQNR.A

Calculated Mr: **81055** Calculated *p*I: **4.95**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

```
  1 MADVQMAEAE TFAFQAEINQ LLSLIINTFY SNKEIFLREL ISNASDALDK
 51 IRFESLTDKS KLDAQPELFI RLVPDKTNKT LSIIDSGVGM AKADLVNNLG
101 TIARSGTKEF MEALQAGADV SMIGQFGVGF YSAYLVAEKV IVTTKHNDDE
151 QYIWESQAGG SFTVTRDVDG EQLGRGTKIT LFLKEDQLEY LEERRIKDLV
201 KKHSEFISYP IYLWTEKTTE KEISDDEDDE PKKEEEGDIE EVDEDKEKEG
251 KKKKKIKEVS HEWQLINKQK PIWLRKPEEI TKEEYASFYK SLTNDWEDHL
301 AVKHFSVEGQ LEFKAILFVP KRAPFDLFDT RKKMNNIKLY VRRVFIMDNC
351 EELIPEYLGF VKGVVDSDDL PLNISREMLQ QNKILKVIRK NLVKKCIEMF
401 NEIAENKDDY NKFYEAFSKN LKLGIHEDSQ NRAKLADLLR YYSTKSGDEL
451 TSLKDYVTRM KEGQKDIYYI TGESKKAVEN SPFLERLKKK GYEVLFMVDA
501 IDEYAVGQLK EYDGKKLVSA TKEGLKLEDD DEEEKKKREE KKKSFENLCK
551 IIKDILGDKV EKVVVSDRIV DSPCCLVTGE YGWTANMERI MKAQALRDSS
601 MSSYMSSKKT MEINPDNGIM EELRKRAEAD KNDKSVKDLV LLLFETALLT
651 SGFSLDDPNT FGARIHRMLK LGLSIDEEEA GDDADMPALE EEAGEESKME
701 EVD
```

Spot No.: **P24**

NCBI accession No.: **gi| 20559**   Species: *Petunia x hybrida*

PFF score: [136]

Protein name: hsp70 (AA 6 - 651)

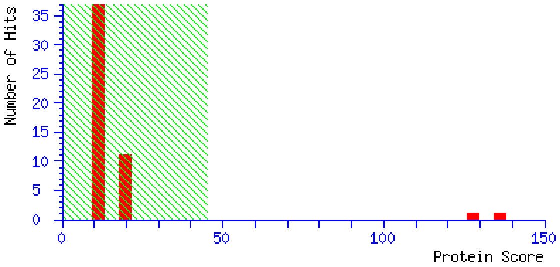
Matched peptides No.: [4]   Sequence coverage %: [11]

Matched sequences: K.NAVVTVPAYFNDSQR.Q;
R.TLSSTAQTTIEIDSLYEGIDFYSTITR.A;
R.ARFEELNMDLFR.K;
K.EQVFSTYSDNQPGVLIQVYEGER.A

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

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 EGPAIGIDLG TTYSCVGVWQ HDRVEIIAND QGNRTTPSYV GFTDTERLIG
51 DAAKNQVAMN PINTVFDAKR LIGRRFSDPS VQSDIKLWPF KVIPGPGDKP
101 MIVVTYKGEE KQFAAEEISS MVLTKMKEIA EAYLGTTIK**N** **AVVTVPAYFN**
151 **DSQR**QATKDA GVIAGLNVMR IINEPTAAAI AYGLDKKASS AGEKNVLIFD
201 LGGGTFDVSL LTIEEGIFEV KATAGDTHLG GEDFDNRMVN HFVQEFKRKN
251 KKDISGNPRA LRRLRTACER AKR**TLSSTAQ** **TTIEIDSLYE** **GIDFYSTITR**
301 **ARFEELNMDL** **FR**KCMEPVEK CLRDAKMDKS SVHDVVLVGG STRIPKVQQL
351 LQDFFNGKEL CKSINPDEAV AYGAAVQAAI LSGEGNEKVQ DLLLLDVTPL
401 SLGLETAGGG MTVLIPRNTT IPTKK**EQVFS** **TYSDNQPGVL** **IQVYEGER**AR
451 TKDNNLLGKF ELSGIPPAPR GVPQITVCFD IDANGILNVS AEDKTTGQKN
501 KITITNDKGR LSKEEIERMV QEAEKYKSED EELKKKVEAK NALENYAYNM
551 RNTIKDDKIN SQLSAADKKR IEDAIDEAIK WLDNNQLAEA DEFEDKMKEL
601 ESICNPIIAK MYQGGAGGAT MDEDGPSVGG SAGSQTGAGP KIEEVD

Spot No.: **P25**

NCBI accession No.: **gi| 255566038** Species: *Ricinus communis*

PFF score: [118]

Protein name: Phospholipase C 3 precursor, putative

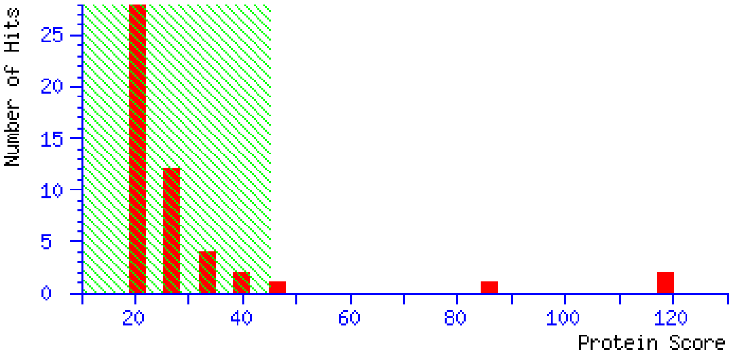
Matched peptides No.: [2] Sequence coverage %: [4]

Matched sequences: K.TVVVLVQENR.S;
K.HCEKGELPNYVVIEPR.Y

Calculated Mr: **59111** Calculated *p*I: **5.08**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MAAESSTSAN EYPIK**TVVVL** **VQENR**SFDHM LGWLKTLNPE IDGVTGQESN
51 PISTSDLNSS LVFFRDQAAY VDPDPGHSIQ AIYEQVFGVE WTEAALSSEN
101 AVSPKMNGFA QNAERTQQGM AETVMNGFRP EAVPVYKELA MNFAVCDRWF
151 ASIPTSTQPN RLYLHSATSH GATSNDTKML AEGFPQKTIF ESMHEAGFSF
201 GIYFQQVPTT LFYRNLRKIK YLKNFHQFDL QFKK**HCEKGE** **LPNYVVIEPR**
251 YYDLLSIPAN DDHPSHDVSE GQKFVKEVYE ALRASPQWNE MLFIIIYDEH
301 GGFYDHVPTP ATGIPTPDDI VGPAPYLFKF DRLGVRVPAV LISPWIEPGT
351 VLHGPSGPQE TSEFEHSSIA ATVKKLFNLK EFLTKRDEWA GTFESVLTRT
401 SPRTDCPVTL TEPVKLRSRG ANEEANISEF QQELVQLAAV LNGDHGTDIY
451 PHKLVESMKV SEAANYVENA FKRFYEEYEK ARDGGVDESE VIALVKTEAL
501 AIITNTSASS KSFIQKLFSC IVCDN

Spot No.: **P26**

NCBI accession No.: **gi| 4235430** Species: *Hevea brasiliensis*

PFF score: [80]

Protein name: latex-abundant protein

Matched peptides No.: [3] Sequence coverage %: [9]

Matched sequences: R.SAEPGDLLFVHYSGHGTR.L;

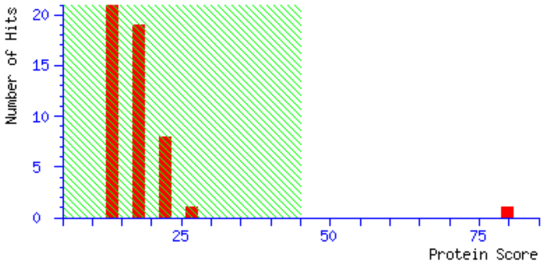
R.EFVDQVPHGCR.I;

K.QTIQDAFESR.G

Calculated Mr: **46443** Calculated *p*I: **5.01**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MAKKAVLIGI NYPGTKAELK GCINDVKRMY RCLVDRYGFS EEDITVLIDI

51 DESYIQPTGK NIRRVLTDLV R**SAEPGDLLF** **VHYSGHGTR**L PAETGEDDDT

101 GFDECIVPCD MNLITDDDFR **EFVDQVPHGC** **R**ITVVSDSCH SGGLIDEAKE

151 QIGESTKRKE EESESGFGFK SFLK**QTIQDA** **FESR**GVHLPS DLHHHHGHRD

201 EEDFDNRVVE EDYGDSGYVK SKSLPLSTLI EILKQKTGKD DIDVGKLRPT

251 LFDMFGDDAS PKVKKFMKVI LNKLRHGDGE SGGGGFLGMV GSLAQEFLKH

301 KLDENDESYV KPALETEVDS KQEVYAGKTK RSLPDGGILI SGCQTDQTSA

351 DASPSGKSSE AYGALSNAIQ TIIAETDGAV TNQELVLKAR KMLKKQGFTQ

401 KPGLYCSDDH VEASFVC

Spot No.: **P27**

NCBI accession No.: **gi| 297833008** Species: *Arabidopsis lyrata subsp. Lyrata*

PFF score: [53]

Protein name: phosphoesterase family protein

Matched peptides No.: [2]   Sequence coverage %: [3]

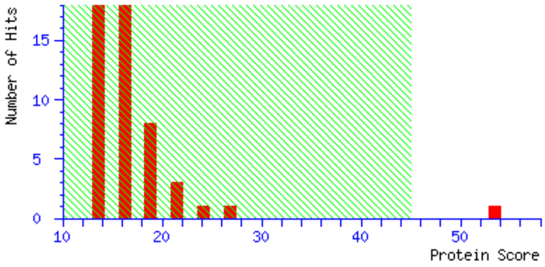
Matched sequences: K.TVVVLVQENR.S;

K.LPNYVVIEPR.Y

Calculated Mr: **59395**   Calculated *p*I: **5.21**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MGEETSSGGG SSSSPIK**TVV** **VLVQENR**SFD HMLGWFKELN PEIDGVSESE
51 PRSNPISTSD PNSAQVFFGK ESQNIDPDPG HSFQAIYEQV FGKPFSDESP
101 YPYPKMNGFV QNAEAITKGM SEKVVMQGFP PEKLPVFKEL VQEFAVCDRW
151 FSSLPSSTQP NRLYVHAATS NGAFSNDTNT LVRGFPQRTV FESLEESGFT
201 FGIYYQSFPN CLFYRNMRKL KYVDNFHQYH LSFKRHCKEG K**LPNYVVIEP**
251 **R**YFNILSAPA NDDHPKNDVA EGQNLVKEIY EALRASPQWN QILFVVVYDE
301 HGGYYDHVPT PVTGVPNPDG LVGPEPYNFK FDRLGVRVPA LLISPWIEPK
351 TVLHEPNGPE PTSQFEHSSI PATLKKIFNL KSFLTKRDEW AGTFDAVINR
401 TSPRTDCPVT LPELPRARDI DIETQEEDED LTDFQIELIQ AAAVLNGDHI
451 KDIYPFKLAD NMKVLDAARY VEEAFTRFHG ESKKAKEGGL DEHEIVDLSK
501 GSTRHSSPKS FVQKFFSCLI CDN

Spot No.: **P28**

NCBI accession No.: **gi| 226530579** Species: *Zea mays*

PFF score: [108]

Protein name: uncharacterized protein LOC100272911

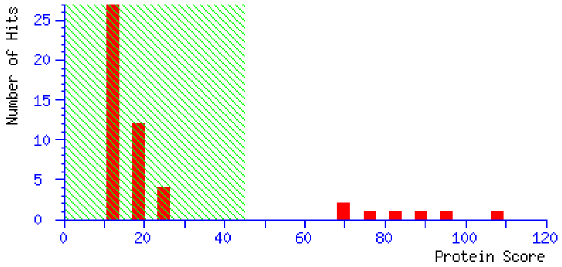
Matched peptides No.: [4] Sequence coverage %: [11]

Matched sequences: K.NAVITVPAYFNDSQR.Q;
R.IINEPTAAAIAYGLDKK.A;
K.ATAGDTHLGGEDFDNR.L;
K.SQIHDVVLVGGSTR.I

Calculated Mr: **62054** Calculated *p*I: **5.23**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MKMWPFKVVP GPADKPMIVV TYKGEEKKFS AEEISSMVLT KMKEIAEAYL
51 STTIK**NAVIT** **VPAYFNDSQR** QATKDAGVIA GLNVTR**IINE** **PTAAAIAYGL**
101 **DKK**ATSTGEK NVLIFDLGGG TFDVSILTIE EGIFEVK**ATA** **GDTHLGGEDF**
151 **DNR**LVNHFVM EFKRKHKKDI SGNPRALRRL RTACERAKRT LSSTAQTTIE
201 IDSLYEGIDF YATITRARFE ELNMDLFRKC MEPVEKCLRD AKMDK**SQIHD**
251 **VVLVGGSTRI** PKVQQLLQDF FNGKELCKSI NPDEAVAYGA AVQAAILSGE
301 GNQKVQDLLL LDVTPLSLGL ETAGGVMTVL IPRNTTIPTK KEQVFSTYSD
351 NQPGVLIQVY EGERTRTKDN NLLGKFELTG IPPAPRGVPQ INVTFDIDAN
401 GILNVSAEDK TTGKKNKITI TNDKGRLSKE EIERMVQEAE KYKTEDEEVK
451 RKVEARNALE NYAYNMRNTV RDEKIASKLP ADDKKKIEDT IEDAIKWLDG
501 NQLAEAEEFE DKMKELESIC NPIISQMYQG GAGAAGMDED VPGGGAGNGG
551 GSGAGPKIEE VD

Spot No.: **P29**

NCBI accession No.: **gi|149938954**   Species: *Actinidia chinensis*

PFF score: [133]

Protein name: G6PD1

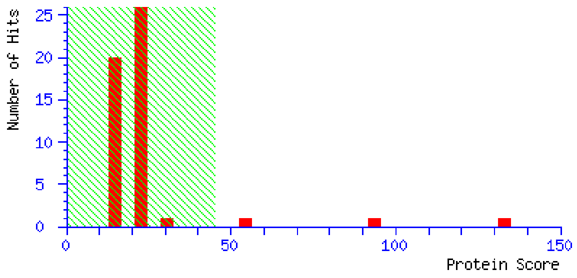
Matched peptides No.: [3]   Sequence coverage %: [7]

Matched sequences: R.QGFLQSNEVHIFGYAR.T;
R.GGYFDEYGIIR.D;
R.YQGVTIPEAYER.L

Calculated Mr: **59276**   Calculated *p*I: **6.75**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MGSGAWTIEK RSTFRNESFS KEYVTVSETG CLSIIVLGAS GDLAKKKTFP
51 ALFNLYR**QGF** **LQSNEVHIFG** **YAR**TKISDDE LRNRIRGYLI QGSGSSDKQL
101 EEVSKFLQLI KYISGSYDSG EGFQLLDKEI SGYEFSKNTV EGSSRRLFYL
151 ALPPSVYPSV CKMIKNNCMN KSDLGGWTRI VVEKPFGKDL GSAEQLSAQI
201 GELFDEPQIY RIDHYLGKEL VQNLLVLRFA NRFFLPLWNR DNIANVQIVF
251 REDFGTEGR**G** **GYFDEYGIIR** DIIQNHLLQV FCLVAMEKPV SLKPEHIRDE
301 KVKVLQSVVP IKDEEVVLGQ YKGYRDDPTV PDNSNTPTFA TVVLRVHNER
351 WEGVPFILKA GKALNSRKAE IRIQFKDVPG DIFKCQKQGR NEFVIRLQPL
401 EAMYMKLTVK QPGLEMSTVQ SELDLSYGQR **YQGVTIPEAY** **ER**LILDTIRG
451 DQQHFVRRDE LKAAWEIFTP LLHRIDDGEV KPLTYQLGSR GPAEADQLLE
501 RAGYVQTHGY IWIPPTL

Spot No.: **P30**

NCBI accession No.: **gi|226493285** Species: *Zea mays*

PFF score: [53]

Protein name: flavonol 4-sulfotransferase

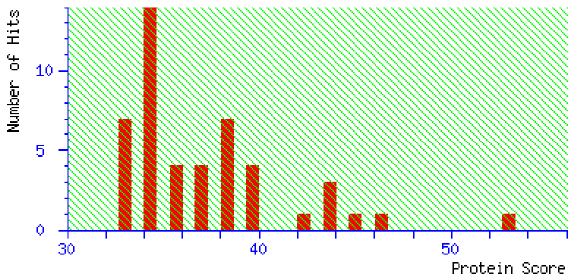
Matched peptides No.: [12] Sequence coverage %: [38]

Matched sequences: -.MAAAACNPVAPSGPVPFK.D;-.MAAAACNPVAPSGPVPFKDVDDGSVPEHTPK.E;M.AAAACNPVAPSGPVPF;K.DR.LYQGFWLPEHWVPGTIVFQR.R;R.LYQGFWLPEHWVPGTIVFQRR.F;K.ALAFATAAR.T;R.LAEFMGR.P + Oxidation (M);R.PFSAAEEAAGDVAAVVELCSFDEM;K.G + Oxidation (M);R.YRPMPR.D;K.GVAGDWANHMTPEMAAR.L + 2 Oxidation (M);K.GVAGDWANHMTPEMAARLDGIFR.E;K.LQGTGLIFS.-

Calculated Mr: **38183** Calculated *p*I: **6.26**

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 73 are significant (p<0.05).



Matched peptide sequences: shown in Bold Red:

1 **MAAAACNPVA** **PSGPVPFKDV** **DDGSVPEHTP** **K**EEFGDLVAA LPSRQQSILE
51 LR**LYQGFWLP** **EHWVPGTIVF** **QRR**FTPRPDD VILASYPKCG TTWLK**ALAFA**
101 **TAAR**TAYPPG GARHPLRRLN PHDCVPFIDE IFASGEEAKL EALPSPRLMN
151 THLPYALLPA PVTATATGCR VAYVCRDPKD MVVSLWHFLR RAKPDLLFAD
201 TFESVCDGTV VVGPVWDHVL SYWRASVAAP DRALFLRYED MLRDPGGNVR
251 R**LAEFMGRPF** **SAAEEAAGDV** **AAVVELCSFD** **EMK**GLEVNRP GSGTAGR**YRP**
301 **MPR**DAFFRK**G** **VAGDWANHMT** **PEMAARLDGI** **FREKLQGTGL** **IFS**

Spot No.: **P31**

NCBI accession No.: **gi|224071449** Species: *Populus trichocarpa*

PFF score: [104]

Protein name: predicted protein

Matched peptides No.: [2] Sequence coverage %: [2]

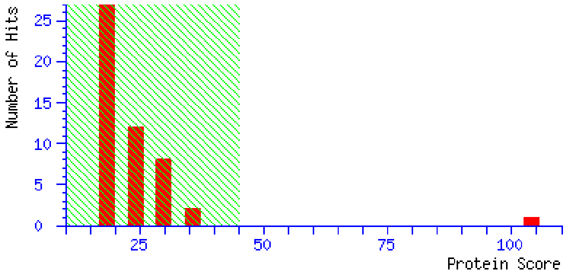
Matched sequences: K.NKIDVIPHYPGR.L;

K.IDVIPHYPGR.L

Calculated Mr: **47121** Calculated *p*I: **5.28**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

1 MDGTSEATWP EILGSRNWDN LLDPLDLSLR KLILRCGDFC QATYDAFNND
51 QNSRYCGTSR YGKRNFFHKV MLDNPENYQV SSFLYATARV SLPEAFLLHS
101 LSRDSWDRET NWIGYIAVTS DEQTKTLGRR EIYIAFRGTT RNYEWVDILG
151 AKLKSAKPLL RGATSTTHDQ ESSSSSDDDD DKVPKVMLGW LTMYISDDPN
201 SPFTKLSARA QLLAHIKELR ERYKDDDLSI IFTGHSLGAS LSILSAFDLV
251 ENGITDIPVS AFVFGSPQVG NKEFNERFNK YPNLKVLHIK **NKIDVIPHYP**
301 **GR**LMGYVYTG IEFEIDTRKS PSLKDSKNPS DWHNLQAMLH IVAGWNGEEQ
351 EFELKVKRSL ALVNKSSEFL KDECLVPGIW WVEKNKGMVR NEDGEWVLAP
401 PDEEDLPVPE C

Spot No.: **P32**

NCBI accession No.: gi|1916805 Species: *Hevea brasiliensis*

PFF score: [219]

Protein name: latex patatin homolog

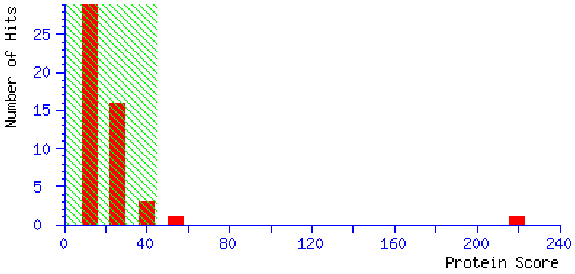
Matched peptides No.: [5] Sequence coverage %: [21]

Matched sequences: K.LQDLDGPDAR.I;
R.DNYDPIHSIGPIYDGEYLR.E;
K.SLDCEDYYLR.I;
R.IQDDTLTGEESSGHIATEENLQR.L;
R.INLDTGRLESIPGAPTNEAAIAK.F

Calculated Mr: **43035** Calculated *p*I: **5.00**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

1 MATGSTTLTQ GKKITVLSID GGGIRGIIPG IILASLESK**L** **QDLDGPDAR**I
51 ADYFDIIAGT STGGLITTML TAPNEDKKPM YQAKDIKDFY LENCPKIFPK
101 ESR**DNYDPIH** **SIGPIYDGEY** **LR**ELCNNLLK DLTVKDTSTD VIIPTFDIKL
151 LLPVIFPSDD AKCNALKNAR LADVCISTSA APVLLPAHSF TTEDDKNIHT
201 FELIDGGVAA TNPTLLALTH IRNEIIRQNP RFIGANLTES KSRLVLSLGT
251 GKSEYKEKYN ADMTSKWRLY NWALYNGNSP AVDIFSNASS DMVDSHLSAL
301 FK**SLDCEDYY** **LRIQDDTLTG** **EESSGHIATE** **ENLQR**LVEIG TELLEKQESR
351 **INLDTGRLES** **IPGAPTNEAA** **IAK**FAKLLSE ERKLRQLK

Spot No.: **P33**

NCBI accession No.: **gi|6707018** Species: *Hevea brasiliensis*

PFF score: [196]

Protein name: latex protein allergen Hev b 7

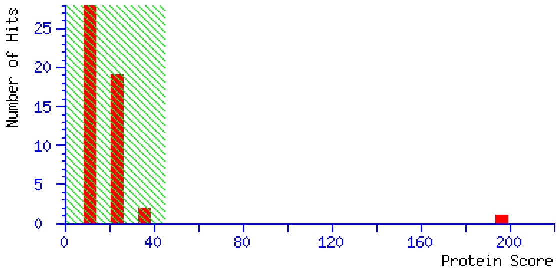
Matched peptides No.: [5] Sequence coverage %: [22]

Matched sequences: K.LQDLDGPDAR.I;
R.DNYDPIHSIGPIYDGEYLR.E;
K.LLLPVIFSSDDAK.C;
R.IQDDTLTGEESSGHIATEENLQR.L;
R.INLDTGRLESIPGAPTNEAAIAK.F

Calculated Mr: **43107** Calculated *p*I: **5.00**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

```
  1 MATGSTPLTQ GKKITVLSID GGGIRGIIPG IILASLESKL QDLDGPDARI
 51 ADYFDIIAGT STGGLITTML TAPNEDKKPM YQAKDIKDFY LENCPKIFPK
101 ESRDNYDPIH SIGPIYDGEY LRELCNNLLK DLTVKDTLTD VIIPTFDIKL
151 LLPVIFSSDD AKCNALKNAR LADVCISTSA APVLLPAHSF TTEDDKNIHT
201 FELIDGGVAA TNPTLLALTH IRNEIIRQNP RFIGANLTES KSRLVLSLGT
251 GKSEYKEKYN ADMTSKWRLY NWALYNGNSP AVDIFSNASS DMVDFHLSAL
301 FKSLDCEDYY LRIQDDTLTG EESSGHIATE ENLQRLVEIG TELLEKQESR
351 INLDTGRLES IPGAPTNEAA IAKFAKLLSE ERKLRQLK
```

Spot No.: **P34**

NCBI accession No.: **gi|32186890** Species: *Gossypium hirsutum*

PFF score: [392]

Protein name: actin

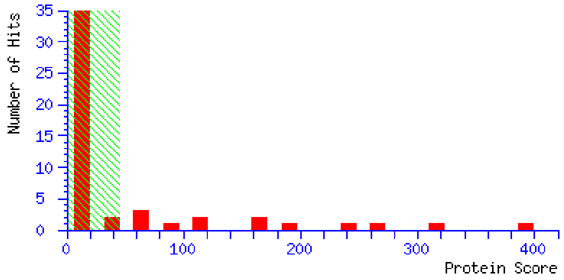
Matched peptides No.: [7] Sequence coverage %: [29]

Matched sequences: K.IWHHTFYNELR.V;
R.VAPEEHPVLLTEAPLNPK.A;
R.TTGIVLDSGDGVSHTVPIYEGYALPHAILR.L;
K.NYELPDGQVITIGAER.F;
R.KDLYGNIVLSGGSTMFPGIADR.M + Oxidation (M);
K.DLYGNIVLSGGSTMFPGIAD;
R.M + Oxidation (M);
K.GEYDESGPSIVHR.K

Calculated Mr: **41917** Calculated *p*I: **5.31**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MADGEDIQPL VCDNGTGMVK AGFAGDDAPR AVFPSIVGRP RHTGVMVGMG
51 QKDAYVGDEA QSKRGILTLK YPIEHGIVSN WDDMEK**IWHH** **TFYNELRVAP**
101 **EEHPVLLTEA** **PLNPK**ANREK MTQIMFETFN VPAMYVAIQA VLSLYASGR**T**
151 **TGIVLDSGDG** **VSHTVPIYEG** **YALPHAILR**L DLAGRDLTDA LMKILTERGY
201 MFTTTAEREI VRDMKEKLAY VALDYEQELE TAKSSSSVEK **NYELPDGQVI**
251 **TIGAER**FRCP EVLFQPSFIG MEAAGIHETT YNSIMKCDVD IR**KDLYGNIV**
301 **LSGGSTMFPG** **IADR**MSKEIT ALAPSSMKIK VVAPPERKYS VWIGGSILAS
351 LSTFQQMWIS **KGEYDESGPS** **IVHR**KCF

Spot No.: **P35**

NCBI accession No.: gi|255552291 Species: *Ricinus communis*

PFF score: [141]

Protein name: short chain dehydrogenase, putative

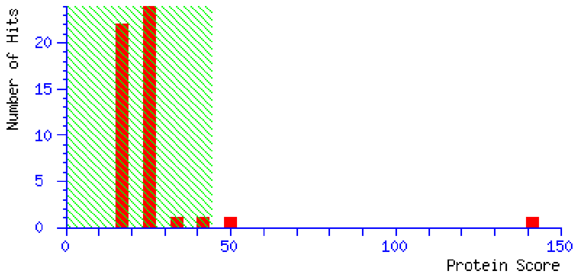
Matched peptides No.: [2] Sequence coverage %: [10]

Matched sequences: K.VALVTGGDSGIGR.A;
K.DPIAIPTDVGFEENCR.K

Calculated Mr: **32148** Calculated *p*I: **6.50**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



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

1 MATRRGYRFP PQSQDKQPGK EYLMHPLPEF INPHYKPSNK LQDK**VALVTG**
51 **GDSGIGR**AVS YYFTLEGATV AFTYVKGRED KDKDHILKIL HEVKAEGAK**D**
101 **PIAIPTDVGF** **EENCR**KVIDQ IMSEYGKIDI LVNNAGEAHY STTIEDITDP
151 MLERVFRTNI FGHFFMSRHA LKHMKEGGCI INTASVAAYA GFSFMVDYSS
201 TKGAVVAFTR SLALQLIDRG IRVNAVAPGS VWTPFQPSTL SAEQVAQVGS
251 GVPMDRAAQP YEIAPSFVFL ASNDCSSYFT GQVLHPNGMF

Spot No.: **P36**

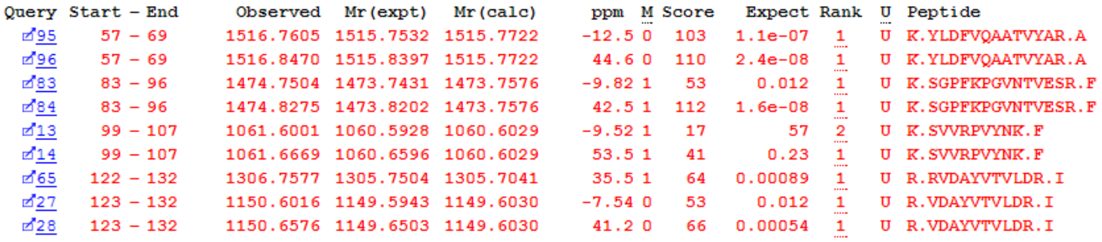
NCBI accession No.: **gi|38122474**   Species: *Hevea brasiliensis*

PFF score: [393]

Protein name: Rubber elongation factor protein

Matched peptides No.: [9]   Sequence coverage %: [26]

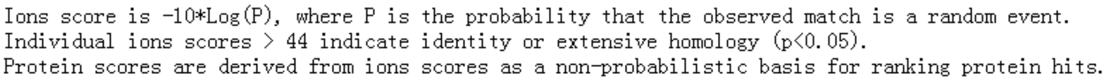
Matched sequences:



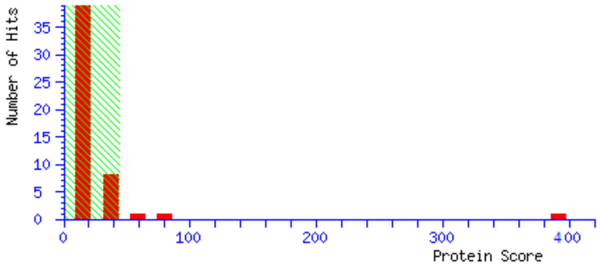
Query	Start – End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Expect	Rank	U	Peptide
95	57 – 69	1516.7605	1515.7532	1515.7722	-12.5	0	103	1.1e-07	1	U	K.YLDFVQAATVYAR.A
96	57 – 69	1516.8470	1515.8397	1515.7722	44.6	0	110	2.4e-08	1	U	K.YLDFVQAATVYAR.A
83	83 – 96	1474.7504	1473.7431	1473.7576	-9.82	1	53	0.012	1	U	K.SGPFKPGVNTVESR.F
84	83 – 96	1474.8275	1473.8202	1473.7576	42.5	1	112	1.6e-08	1	U	K.SGPFKPGVNTVESR.F
13	99 – 107	1061.6001	1060.5928	1060.6029	-9.52	1	17	57	2	U	K.SVVRPVYNK.F
14	99 – 107	1061.6669	1060.6596	1060.6029	53.5	1	41	0.23	1	U	K.SVVRPVYNK.F
65	122 – 132	1306.7577	1305.7504	1305.7041	35.5	1	64	0.00089	1	U	R.RVDAYVTVLDR.I
27	123 – 132	1150.6016	1149.5943	1149.6030	-7.54	0	53	0.012	1	U	R.VDAYVTVLDR.I
28	123 – 132	1150.6576	1149.6503	1149.6030	41.2	0	66	0.00054	1	U	R.VDAYVTVLDR.I

Calculated Mr: **19570**   Calculated *p*I: **5.06**

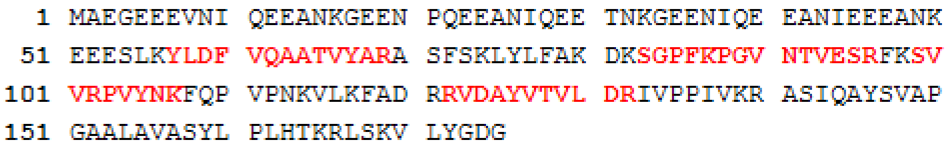
Probability Based Mowse Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:



1 MAEGEEEVNI QEEANKGEEN PQEEANIQEE TNKGEENIQE EANIEEEANK
51 EEESLK**YLDF** **VQAATVYAR**A SFSKLYLFAK DK**SGPFKPGV** **NTVESR**FK**SV**
101 **VRPVYNK**FQP VPNKVLKFAD R**RVDAYVTVL** **DR**IVPPIVKR ASIQAYSVAP
151 GAALAVASYL PLHTKRLSKV LYGDG

Spot No.: P37

NCBI accession No.: **gi|334854634** Species: *Hevea brasiliensis*

PFF score: [288] Protein name： elicitor-responsive protein

Matched peptides No.: [3] Sequence coverage %: [26]

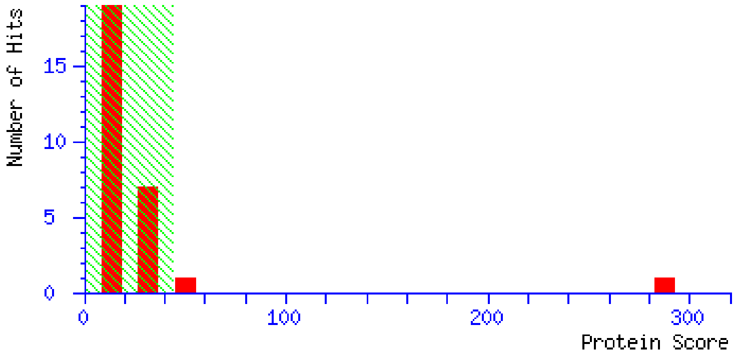
Matched sequences:

```
Start - End    Observed     Mr(expt)    Mr(calc)  ppm     Miss Sequence
    2 - 14    1295.8593   1294.8520   1294.7860    51     0   M.PLGTVEVLLVGAK.G   (Ions score 90)
   47 - 55    1075.5344   1074.5271   1074.4618    61     0   K.GSEPEWNEK.F   (Ions score 53)
   56 - 70    1687.8898   1686.8825   1686.7989    50     0   K.FSFEVSDGDTELTLK.I   (Ions score 145)
```

Calculated Mr: **15249** Calculated *p*I: **4.06**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red

```
  1 MPLGTVEVLL VGAKGLENTD FLNGVDPYVV LACRTQEQKS SVASGKGSEP
 51 EWNEKFSFEV SDGDTELTLK IMDSDVGAAD DFVGEATIPL EPLFLEGNLP
101 STAYKVVKEQ EYKGEITVGL TFTPEVEMDN VGVDGYDFRL
```

Spot No.: **P38**

NCBI accession No.: **gi| 14423933**   Species: *Hevea brasiliensis*

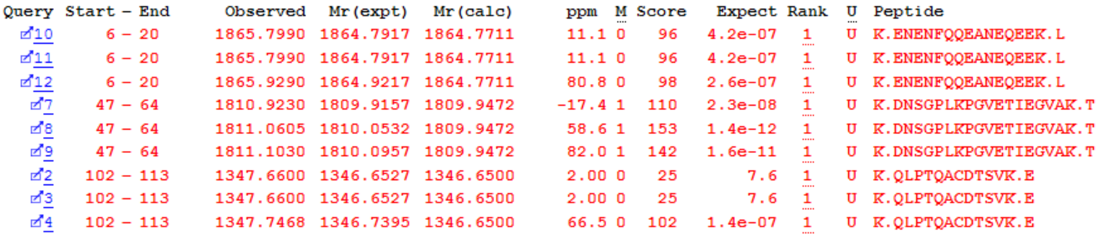
PFF score: [353]

Protein name: Small rubber particle protein

Matched peptides No.: [9]   Sequence coverage %: [38]

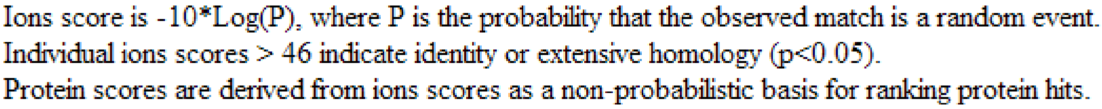
Calculated Mr: **22331**   Calculated *p*I: **4.80**

Matched sequences:

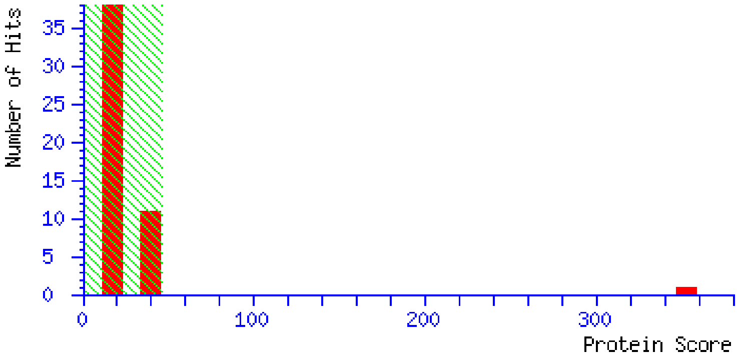


Query	Start – End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Expect	Rank	U	Peptide
10	6 – 20	1865.7990	1864.7917	1864.7711	11.1	0	96	4.2e-07	1	U	K.ENENFQQEANEQEEK.L
11	6 – 20	1865.7990	1864.7917	1864.7711	11.1	0	96	4.2e-07	1	U	K.ENENFQQEANEQEEK.L
12	6 – 20	1865.9290	1864.9217	1864.7711	80.8	0	98	2.6e-07	1	U	K.ENENFQQEANEQEEK.L
7	47 – 64	1810.9230	1809.9157	1809.9472	-17.4	1	110	2.3e-08	1	U	K.DNSGPLKPGVETIEGVAK.T
8	47 – 64	1811.0605	1810.0532	1809.9472	58.6	1	153	1.4e-12	1	U	K.DNSGPLKPGVETIEGVAK.T
9	47 – 64	1811.1030	1810.0957	1809.9472	82.0	1	142	1.6e-11	1	U	K.DNSGPLKPGVETIEGVAK.T
2	102 – 113	1347.6600	1346.6527	1346.6500	2.00	0	25	7.6	1	U	K.QLPTQACDTSVK.E
3	102 – 113	1347.6600	1346.6527	1346.6500	2.00	0	25	7.6	1	U	K.QLPTQACDTSVK.E
4	102 – 113	1347.7468	1346.7395	1346.6500	66.5	0	102	1.4e-07	1	U	K.QLPTQACDTSVK.E

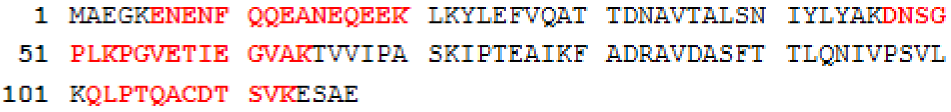
Probability Based Mowse Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:



1 MAEGK**ENENF** **QQEANEQEEK** LKYLEFVQAT TDNAVTALSN IYLYAK**DNSG**
51 **PLKPGVETIE** **GVAK**TVVIPA SKIPTEAIKF ADRAVDASFT TLQNIVPSVL
101 K**QLPTQACDT** **SVK**ESAE

Spot No.: **P39**

NCBI accession No.: **gi| 14423933** Species: *Hevea brasiliensis*

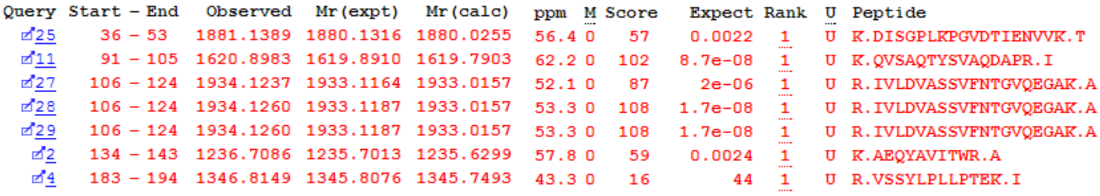
PFF score: [342]

Protein name: Small rubber particle protein

Matched peptides No.: [7] Sequence coverage %: [36]

Calculated Mr: **22331** Calculated *p*I: **4.80**

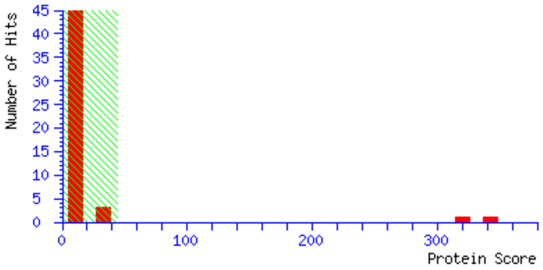
Matched sequences:



Query	Start – End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Expect	Rank	U	Peptide
25	36 – 53	1881.1389	1880.1316	1880.0255	56.4	0	57	0.0022	1	U	K.DISGPLKPGVDTIENVVK.T
11	91 – 105	1620.8983	1619.8910	1619.7903	62.2	0	102	8.7e-08	1	U	K.QVSAQTYSVAQDAPR.I
27	106 – 124	1934.1237	1933.1164	1933.0157	52.1	0	87	2e-06	1	U	R.IVLDVASSVFNTGVQEGAK.A
28	106 – 124	1934.1260	1933.1187	1933.0157	53.3	0	108	1.7e-08	1	U	R.IVLDVASSVFNTGVQEGAK.A
29	106 – 124	1934.1260	1933.1187	1933.0157	53.3	0	108	1.7e-08	1	U	R.IVLDVASSVFNTGVQEGAK.A
2	134 – 143	1236.7086	1235.7013	1235.6299	57.8	0	59	0.0024	1	U	K.AEQYAVITWR.A
4	183 – 194	1346.8149	1345.8076	1345.7493	43.3	0	16	44	1	U	R.VSSYLPLLPTEK.I

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAEEVEEERL KYLDFVRAAG VYAVDSFSTL YLYAK**DISGP** **LKPGVDTIEN**
51 **VVK**TVVTPVY YIPLEAVKFV DKTVDVSVTS LDGVVPPVIK **QVSAQTYSVA**
101 **QDAPRIVLDV** **ASSVFNTGVQ** **EGAK**ALYANL EPK**AEQYAVI** **TWR**ALNKLPL
151 VPQVANVVVP TAVYFSEKYN DVVRGTTEQG YR**VSSYLPLL** **PTEK**ITKVFG
201 DEAS

Spot No.: **P40**

NCBI accession No.: **gi| 29170601**   Species: *Hevea brasiliensis*

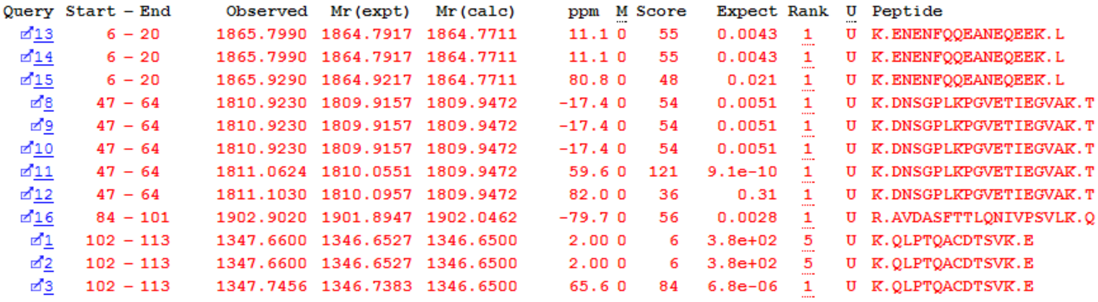
PFF score: [316]

Protein name: Small rubber particle protein

Matched peptides No.: [12]   Sequence coverage %: [53]

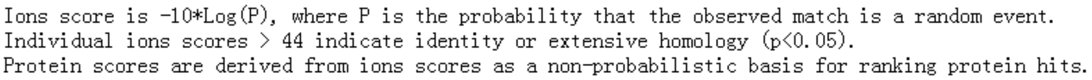
Calculated Mr: **12769**   Calculated *p*I: **4.61**

Matched sequences:

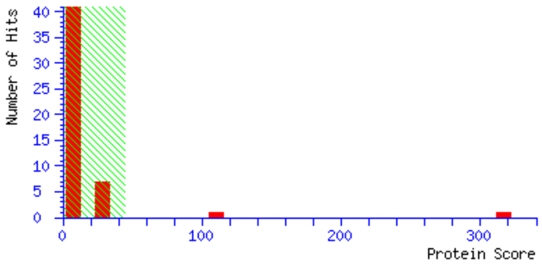


Query	Start – End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Expect	Rank	U	Peptide
13	6 – 20	1865.7990	1864.7917	1864.7711	11.1	0	55	0.0043	1	U	K.ENENFQQEANEQEEK.L
14	6 – 20	1865.7990	1864.7917	1864.7711	11.1	0	55	0.0043	1	U	K.ENENFQQEANEQEEK.L
15	6 – 20	1865.9290	1864.9217	1864.7711	80.8	0	48	0.021	1	U	K.ENENFQQEANEQEEK.L
8	47 – 64	1810.9230	1809.9157	1809.9472	-17.4	0	54	0.0051	1	U	K.DNSGPLKPGVETIEGVAK.T
9	47 – 64	1810.9230	1809.9157	1809.9472	-17.4	0	54	0.0051	1	U	K.DNSGPLKPGVETIEGVAK.T
10	47 – 64	1810.9230	1809.9157	1809.9472	-17.4	0	54	0.0051	1	U	K.DNSGPLKPGVETIEGVAK.T
11	47 – 64	1811.0624	1810.0551	1809.9472	59.6	0	121	9.1e-10	1	U	K.DNSGPLKPGVETIEGVAK.T
12	47 – 64	1811.1030	1810.0957	1809.9472	82.0	0	36	0.31	1	U	K.DNSGPLKPGVETIEGVAK.T
16	84 – 101	1902.9020	1901.8947	1902.0462	-79.7	0	56	0.0028	1	U	R.AVDASFTTLQNIVPSVLK.Q
1	102 – 113	1347.6600	1346.6527	1346.6500	2.00	0	6	3.8e+02	5	U	K.QLPTQACDTSVK.E
2	102 – 113	1347.6600	1346.6527	1346.6500	2.00	0	6	3.8e+02	5	U	K.QLPTQACDTSVK.E
3	102 – 113	1347.7456	1346.7383	1346.6500	65.6	0	84	6.8e-06	1	U	K.QLPTQACDTSVK.E

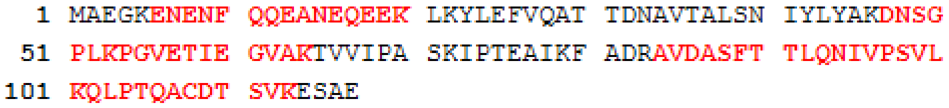
Probability Based Mowse Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:



1 MAEGK**ENENF QQEANEQEEK** LKYLEFVQAT TDNAVTALSN IYLYAK**DNSG**
51 **PLKPGVETIE GVAK**TVVIPA SKIPTEAIKF ADR**AVDASFT TLQNIVPSVL**
101 **KQLPTQACDT SVK**ESAE

Spot No.: **P41**

NCBI accession No.: **gi|2832430** Species: *Hevea brasiliensis*

PFF score: [261]

Protein name: prohevein

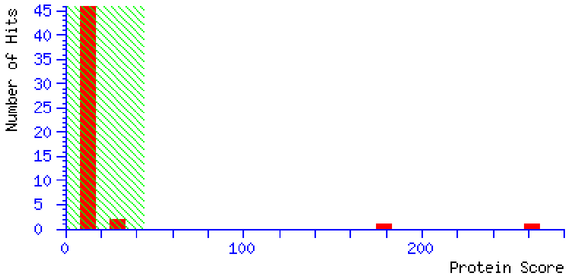
Matched peptides No.: [3] Sequence coverage %: [26]

Matched sequences: K.YGWTAFCGPVGAHGQPSCGK.C;
R.IVDQCSNGGLDLDVNVFR.Q;
R.QLDTDGKGYER.G

Calculated Mr: **20852** Calculated *p*I: **5.64**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

1 EQCGRQAGGK LCPNNLCCSQ WGWCGSTDEY CSPDHNCQSN CKDSGEGVGG
51 GSASNVLATY HLYNSQDHGW DLNAASAYCS TWDANKPYSW RSK**YGWTAFC**
101 **GPVGAHGQPS** **CGK**CLSVTNT GTGAKATVR**I** **VDQCSNGGLD** **LDVNVFRQLD**
151 **TDGKGYER**GH LTVNYQFVDC GDSFNPLFSV MKSSVIN

Spot No.: **P42 (S9)**

NCBI accession No.: **gi|388503664** Species: *Lotus japonicus*

Protein name： **unknown**

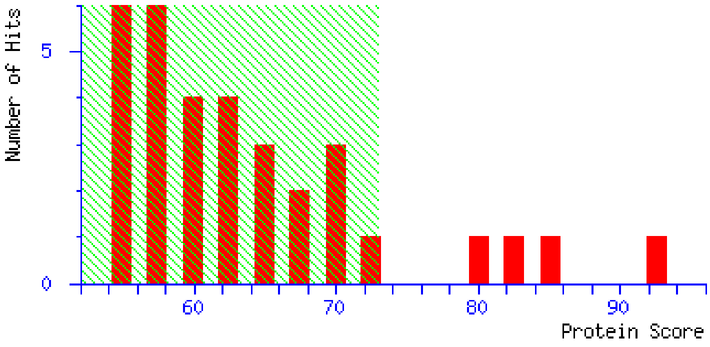
Mascot score: **93** Sequence coverage %: **45**

Matched peptides No.: **13** Total peptides No.: **48**

Calculated Mr: **29537** Calculated *p*I: **4.79**

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 73 are significant ($p<0.05$).



Matched peptide sequences: shown in Bold Red:

1 MASSK**DRGTF** **VYVAKLAEQA** **ER**YEEMVDSM KKVANLDVEL TVEER**NLLSV**
51 **GYKNVIGAR**R ASWR**ILSSIE** **QK**EETKGNDV NAKR**IKEYR**Q KVESELADIC
101 NDVMRVIDEH LIPSATAGES TVFYYKMK**GD** **YYRYLAEFK**S GNEK**KEAADQ**
151 **SMKAYESATT** **AAEAELPPTH** **PIRLGLALNF** **SVFYYEILNS** **PERACHLAK**Q
201 AFDEAISELD TLNEESYK**DS** **TLIMQLLR**DN LTLWTSDIPE EGEDSLKAND
251 TAKVGGGEDA E

Spot No.: **P43**

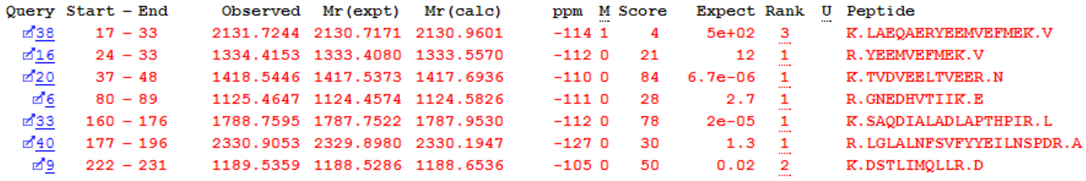
NCBI accession No.: **gi|326694865** Species: *Hevea brasiliensis*

PFF score: [294]

Protein name: 14-3-3 protein 2

Matched peptides No.: [7] Sequence coverage %: [32]

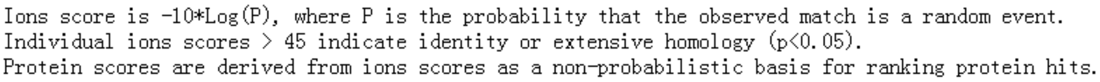
Matched sequences:



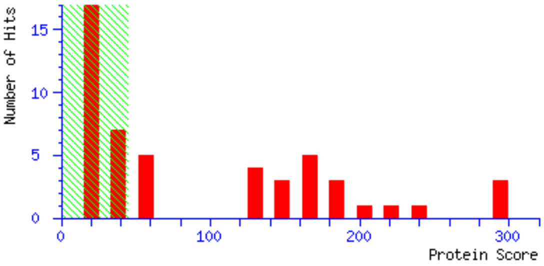
Query	Start – End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Expect	Rank	U	Peptide
38	17 – 33	2131.7244	2130.7171	2130.9601	-114	1	4	5e+02	3		K.LAEQAERYEEMVEFMEK.V
16	24 – 33	1334.4153	1333.4080	1333.5570	-112	0	21	12	1		R.YEEMVEFMEK.V
20	37 – 48	1418.5446	1417.5373	1417.6936	-110	0	84	6.7e-06	1		K.TVDVEELTVEER.N
6	80 – 89	1125.4647	1124.4574	1124.5826	-111	0	28	2.7	1		R.GNEDHVTIIK.E
33	160 – 176	1788.7595	1787.7522	1787.9530	-112	0	78	2e-05	1		K.SAQDIALADLAPTHPIR.L
40	177 – 196	2330.9053	2329.8980	2330.1947	-127	0	30	1.3	1		R.LGLALNFSVFYYEILNSPDR.A
9	222 – 231	1189.5359	1188.5286	1188.6536	-105	0	50	0.02	2		K.DSTLIMQLLR.D

Calculated Mr: **29931** Calculated *p*I: **4.76**

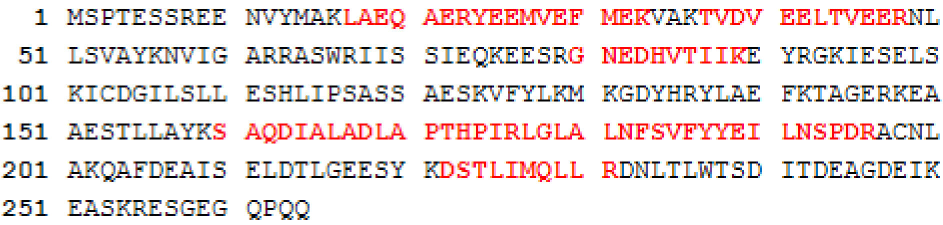
Probability Based Mowse Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:



1 MSPTESSREE NVYMAK**LAEQ** **AERYEEMVEF** **MEK**VAK**TVDV** **EELTVEERN**L
51 LSVAYKNVIG ARRASWRIIS SIEQKEESR**G** **NEDHVTIIK**E YRGKIESELS
101 KICDGILSLL ESHLIPSASS AESKVFYLKM KGDYHRYLAE FKTAGERKEA
151 AESTLLAYK**S** **AQDIALADLA** **PTHPIRLGLA** **LNFSVFYYEI** **LNSPDR**ACNL
201 AKQAFDEAIS ELDTLGEESY **KDSTLIMQLL** **R**DNLTLWTSD ITDEAGDEIK
251 EASKRESGEG QPQQ

Spot No.: P44 (S85)

NCBI accession No.: **gi|224099853** Species: ***Populus trichocarpa***

PFF score: [69] Protein name: **putative protein**

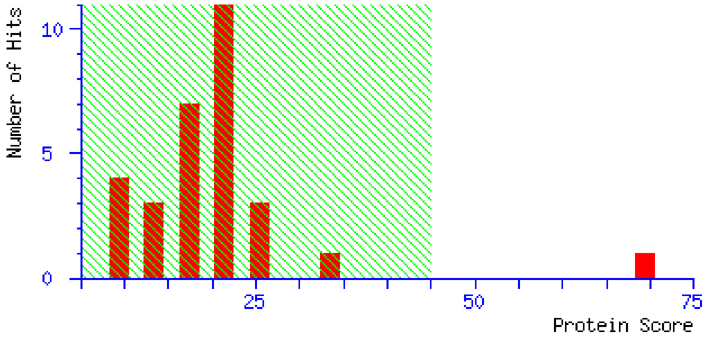
Matched peptides No.: [2] Sequence coverage %: [5]

Matched sequences: S FEHPLNELKP VPR

Calculated Mr: **27448** Calculated *p*I: **5.84**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red

1 MLAVFDNTVA KCPDALQSPH SAPASSALKD GFLANHFASQ HPGSVTVNLG
51 TSGLISHSVE KQNPFLPRLF AVVDDIFCLF QGHIDNVAVL KQQYGLNKTA
101 NEVIVVIEAY RTLRDRGPYP ADQVVKDIQG KFAFILYDST SKATFFAADA
151 DGSVPFFWGA DSEGNLVLSD DVQIVQKGCG KSFAPFPKGC FFTTSGGLR**S**
201 **FEHPLNELKP** **VPR**VDSSGQV CGATFKVDAE TKKESVGMPR VDSSYNWSSN
251 Y

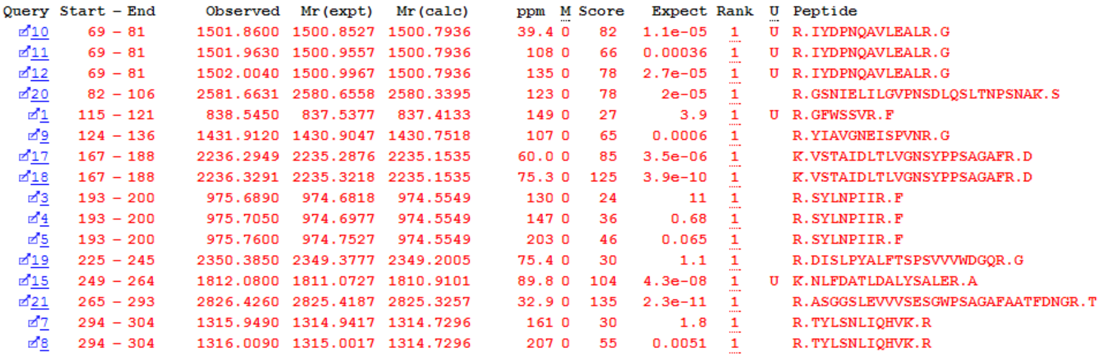
Spot No.: P45

NCBI accession No.: **gi|124365253**   Species: ***Hevea brasiliensis***

PFF score: [745]   **Protein name: beta-1,3-glucanase**

Matched peptides No.: [16]   Sequence coverage %: [44]

Matched sequences:

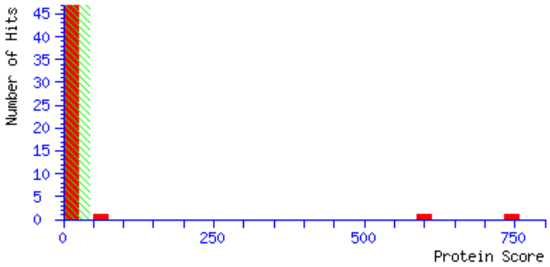


Query	Start – End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Expect	Rank	U	Peptide
10	69 – 81	1501.8600	1500.8527	1500.7936	39.4	0	82	1.1e-05	1	U	R.IYDPNQAVLEALR.G
11	69 – 81	1501.9630	1500.9557	1500.7936	108	0	66	0.00036	1	U	R.IYDPNQAVLEALR.G
12	69 – 81	1502.0040	1500.9967	1500.7936	135	0	78	2.7e-05	1	U	R.IYDPNQAVLEALR.G
20	82 – 106	2581.6631	2580.6558	2580.3395	123	0	78	2e-05	1		R.GSNIELILGVPNSDLQSLTNPSNAK.S
1	115 – 121	838.5450	837.5377	837.4133	149	0	27	3.9	1	U	R.GFWSSVR.F
9	124 – 136	1431.9120	1430.9047	1430.7518	107	0	65	0.0006	1		R.YIAVGNEISPVNR.G
17	167 – 188	2236.2949	2235.2876	2235.1535	60.0	0	85	3.5e-06	1		K.VSTAIDLTLVGNSYPPSAGAFR.D
18	167 – 188	2236.3291	2235.3218	2235.1535	75.3	0	125	3.9e-10	1		K.VSTAIDLTLVGNSYPPSAGAFR.D
3	193 – 200	975.6890	974.6818	974.5549	130	0	24	11	1		R.SYLNPIIR.F
4	193 – 200	975.7050	974.6977	974.5549	147	0	36	0.68	1		R.SYLNPIIR.F
5	193 – 200	975.7600	974.7527	974.5549	203	0	46	0.065	1		R.SYLNPIIR.F
19	225 – 245	2350.3850	2349.3777	2349.2005	75.4	0	30	1.1	1		R.DISLPYALFTSPSVVVWDGQR.G
15	249 – 264	1812.0800	1811.0727	1810.9101	89.8	0	104	4.3e-08	1	U	K.NLFDATLDALYSALER.A
21	265 – 293	2826.4260	2825.4187	2825.3257	32.9	0	135	2.3e-11	1		R.ASGGSLEVVVSESGWPSAGAFAATFDNGR.T
7	294 – 304	1315.9490	1314.9417	1314.7296	161	0	30	1.8	1		R.TYLSNLIQHVK.R
8	294 – 304	1316.0090	1315.0017	1314.7296	207	0	55	0.0051	1		R.TYLSNLIQHVK.R

Calculated Mr: **41543**   Calculated *p*I: **9.40**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red

1 MAISSSTSGT SSSLPSRTTV MLLLFFFTAS VGITDAQVGV CYGMQGNNLP
51 PVSEVIALYK KSNITRMR**IY** **DPNQAVLEAL** **RGSNIELILG** **VPNSDLQSLT**
101 **NPSNAK**SWVQ KNVR**GFWSSV** **RFRYIAVGNE** **ISPVNR**GTAW LAQFVLPAMR
151 NIHDAIRSAG LQDQIK**VSTA** **IDLTLVGNSY** **PPSAGAFR**DD VR**SYLNPIIR**
201 FLSSIRSPLL ANIYPYFTYA GNPR**DISLPY** **ALFTSPSVVV** **WDGQR**GYK**NL**
251 **FDATLDALYS** **ALERASGGSL** **EVVVSESGWP** **SAGAFAATFD** **NGRTYLSNLI**
301 **QHVK**RGTPKR PKRAIETYLF AMFDENKKQP EVEKHFGLFF PNKWQKYNLN
351 FSAEKNWDIS TEHNATILFL KSDM

Spot No.: **P46**

NCBI accession No.: **gi| 224102193**

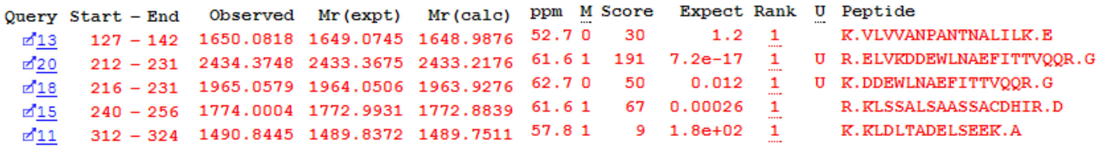
Species: ***Populus trichocarpa***

PFF score: [347]

Protein name： NAD-dependent malate dehydrogenase

Matched peptides No.: [5]　　　　Sequence coverage %: [19]

Matched sequences:

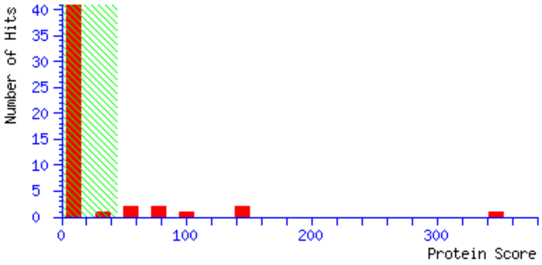


Query	Start – End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Expect	Rank	U	Peptide
13	127 – 142	1650.0818	1649.0745	1648.9876	52.7	0	30	1.2	1		K.VLVVANPANTNALILK.E
20	212 – 231	2434.3748	2433.3675	2433.2176	61.6	1	191	7.2e-17	1	U	R.ELVKDDEWLNAEFITTVQQR.G
18	216 – 231	1965.0579	1964.0506	1963.9276	62.7	0	50	0.012	1	U	K.DDEWLNAEFITTVQQR.G
15	240 – 256	1774.0004	1772.9931	1772.8839	61.6	1	67	0.00026	1		R.KLSSALSAASSACDHIR.D
11	312 – 324	1490.8445	1489.8372	1489.7511	57.8	1	9	1.8e+02	1		K.KLDLTADELSEEK.A

Calculated Mr: **36093**　　　　Calculated *p*I: **6.11**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MAKEPVRVLV TGAAGQIGYA LVPMIARGVM LGPDQPVILH MLDIPPAAEA
51 LNGVKMELVD AAFPLLKGVV ATTDVVEACT GVNIAVMVGG FPRKEGMERK
101 DVMSKNVSIY KSQASALEKH AAANCK**VLVV** **ANPANTNALI** **LK**EFAPSISE
151 KNITCLTRLD HNRALGQISE RLSVQVCDVK NVIIWGNHSS SQYPDVNHAT
201 VKTPAGEKPV R**ELVKDDEWL** **NAEFITTVQQ** **R**GAAIIKAR**K** **LSSALSAASS**
251 **ACDHIR**DWVL GTPEGTWVSM GVYSDGSYNV PAGLIYSFPV TCQNGEWKIV
301 QGLSIDEFSR K**KLDLTADEL** **SEEK**ALAYSC LS

Spot No.: **P47**

NCBI accession No.: **gi| 255578278**

Species: ***Ricinus communis***

PFF score: [75]

Protein name：**hypothetical protein RCOM_053778**

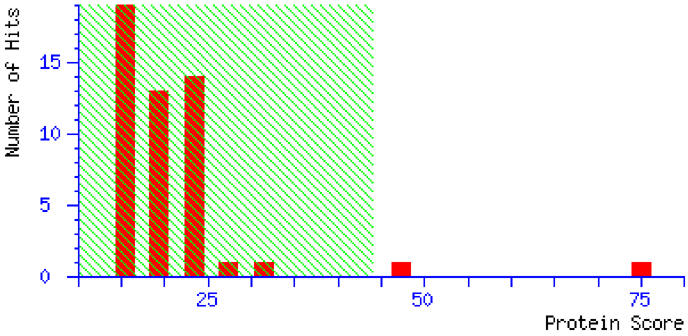
Matched peptides No.: [2] Sequence coverage %: [6]

Matched sequences: **K.QESEYGSGGYGR.R; R.KPSYGEEGGYGER.T**

Calculated Mr: **41389** Calculated *p*I: **4.65**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MPYYTRSEDD VNDFDEFDPT PYGGGYDLAL TYGRPLPPSD ETCYQNSAIA
51 DDDVDYDRPN FTSYAEPSAY NDDILQEEYN SYSRPKPRPG FIPGGGIGGD
101 PYSRPHAAPG FQPGSGGYGG VSEYEKPSGY GRRPDSEYGS GGYGGGTEYE
151 RPSGEDYGSG HGRKQDSEYG SGGYGRRPES EYGSGGGYER PSSEEYGSGY
201 GRK**QESEYGS** **GGYGR**RPEAE YGSGYGGRPE TEYGGGGGSE YGGGYGR**KPS**
251 **YGEEGGYGER** TEYERPSYGD DPPRRPGYGR QDDEYERPSY ERKSDDDNDG
301 SRRKYGGDDD EKGYQKKYGG YGDDDDEEGS RRKYGYGGEE ESYGRKKYGD
351 DGSDDDEKKH HRHKHHQHKH SDDE

Spot No.: **P48**

NCBI accession No.: **gi|255552291** Species: *Ricinus communis*

PFF score: [201]

Protein name: short chain dehydrogenase, putative

Matched peptides No.: [2] Sequence coverage %: [7]

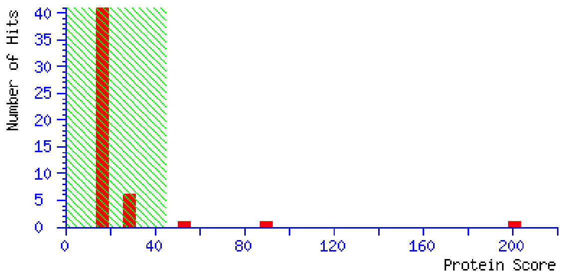
Matched sequences: K.AEGAKDPIAIPTDVGFEENCR.K;

K.DPIAIPTDVGFEENCR.K

Calculated Mr: **32148** Calculated *p*I: **6.50**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

```
  1 MATRRGYRFP PQSQDKQPGK EYLMHPLPEF INPHYKPSNK LQDKVALVTG
 51 GDSGIGRAVS YYFTLEGATV AFTYVKGRED KDKDHILKIL HEVKAEGAKD
101 PIAIPTDVGF EENCRKVIDQ IMSEYGKIDI LVNNAGEAHY STTIEDITDP
151 MLERVFRTNI FGHFFMSRHA LKHMKEGGCI INTASVAAYA GFSFMVDYSS
201 TKGAVVAFTR SLALQLIDRG IRVNAVAPGS VWTPFQPSTL SAEQVAQVGS
251 GVPMDRAAQP YEIAPSFVFL ASNDCSSYFT GQVLHPNGMF
```

Spot No.: **P49**

NCBI accession No.: **gi|255581753**   Species: *Ricinus communis*

PFF score: [175]

Protein name: adenosine kinase, putative

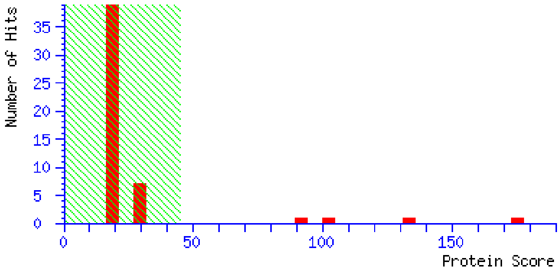
Matched peptides No.: [3]   Sequence coverage %: [11]

Matched sequences: K.RPENWALVEK.A;
K.VLPYMDYVFGNETEAR.T + Oxidation (M);
R.AGCYAANVIIQR.S

Calculated Mr: **38058**   Calculated *p*I: **5.17**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



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

1 MASYEGILLG MGNPLLDISA VVDEDFLNKY EIKLNNAILA EDKHLPMYEE
51 MANNSNVEYI AGGATQNSIK VAQWMLQIPG ATSYMGCIGK DKFGEEMTKN
101 SKKAGVNVHY YEDETAPTGT CGVCVVGGER SLVANLSAAN CYKSEHLK**RP**
151 **ENWALVEK**AK YFYIAGFFLT VSPESIQLVA EHAAANNKIF TMNLSAPFIC
201 EFFKDAQEK**V** **LPYMDYVFGN** **ETEAR**TFAKV HGWETDNVEE IAKKISQWPK
251 ASGTHKRITV ITQGADPVVV AEDGKVKLFP VILLPKEKLV DTNGAGDAFV
301 GGFLSQLVQE KPIEECVR**AG** **CYAANVIIQR** SGCTYPEKPD FS

Spot No.: **P50**

NCBI accession No.: **gi|4588474**   Species: *Brassica napus*

PFF score: [96]

Protein name: phosphoinositide-specific phospholipase C

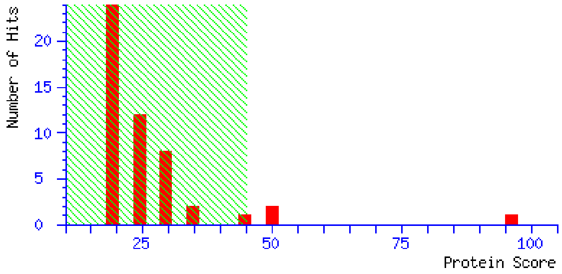
Matched peptides No.: [2]   Sequence coverage %: [3]

Matched sequences: R.VIELDIWPNSNKNDIDVLHGR.T;
K.NDIDVLHGR.T

Calculated Mr: **66632**   Calculated *p*I: **5.79**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MSKQTYKVCF CFNRRFRYTA SEAPRDVKTL FDKYSENGVM TVDHLQRFLI
51 DVQKQDKATK EDAQSIINAA SSLLHSNGLH LDAFFKYLFG DSNPPLALHE
101 VHQDMDAPIS HYFIFTGHNS YLTGNQLSSD CSEVPIIDAL KKGVR**VIELD**
151 **IWPNSNKNDI** **DVLHGR**TLTS PVELIKCLRA IKTHAFEVSD YPVVVTLEDH
201 LTPELQSKVA EMVTEIFGEI LFTPPVGESL KEFPSPNSLK RRIIISTKPP
251 KEYKEGKDED VVQKGKALGD EEVWGREVPS FIERNKSGDK DDLDDEEDND
301 EDDDVEKFKK NAPPQYKHLI AIHAGKPKGS ITACLKVDPD KVRRLSLSEE
351 QLEKAAEKYA KQIVRFTQQN LLRIYPKGTR VTSSNYNPLV GWSHGAQMVA
401 FNMQGYGRSL WLMQGMFRAN GGCGYIKKPD ILLKGGSDSD IFDPKTTLPV
451 KTTLRVTIYM GEGWYFDFRH THFDQYSPPD FYTRVGIAGV PADTVMKKTK
501 TLEDNWVPSW DEVFEFPLTV PELALLRLEV HEYDMSEKDD FGGQTCLPVW
551 ELQEGIRSFP LHNRKEEKYK SVKLLVKVEF V

Spot No.: **P51**

NCBI accession No.: **gi|255578278** Species: *Ricinus communis*

PFF score: [95]

Protein name: hypothetical protein RCOM_0537780

Matched peptides No.: [2] Sequence coverage %: [6]

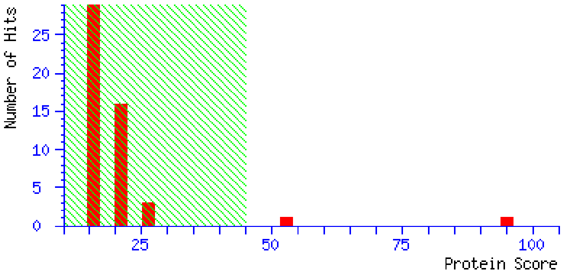
Matched sequences: K.QESEYGSGGYGR.R;

R.KPSYGEEGGYGER.T

Calculated Mr: **41389** Calculated *p*I: **4.65**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MPYYTRSEDD VNDFDEFDPT PYGGGYDLAL TYGRPLPPSD ETCYQNSAIA
51 DDDVDYDRPN FTSYAEPSAY NDDILQEEYN SYSRPKPRPG FIPGGGIGGD
101 PYSRPHAAPG FQPGSGGYGG VSEYEKPSGY GRRPDSEYGS GGYGGGTEYE
151 RPSGEDYGSG HGRKQDSEYG SGGYGRRPES EYGSGGGYER PSSEEYGSGY
201 GRK**QESEYGS** **GGYGR**RPEAE YGSGYGGRPE TEYGGGGGSE YGGGYGR**KPS**
251 **YGEEGGYGER** TEYERPSYGD DPPRRPGYGR QDDEYERPSY ERKSDDDNDG
301 SRRKYGGDDD EKGYQKKYGG YGDDDDEEGS RRKYGYGGEE ESYGRKKYGD
351 DGSDDDEKKH HRHKHHQHKH SDDE

Spot No.: **P52**

NCBI accession No.: **gi|255552291** Species: *Ricinus communis*

PFF score: [67]

Protein name: short chain dehydrogenase, putative

Matched peptides No.: [3] Sequence coverage %: [11]

Matched sequences: K.VALVTGGDSGIGR.A;

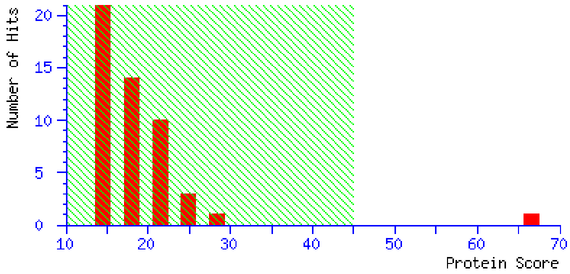
K.AEGAKDPIAIPTDVGFEENCR.K;

K.DPIAIPTDVGFEENCR.K

Calculated Mr: **32148** Calculated *p*I: **6.50**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MATRRGYRFP PQSQDKQPGK EYLMHPLPEF INPHYKPSNK LQDK**VALVTG**
51 **GDSGIGR**AVS YYFTLEGATV AFTYVKGRED KDKDHILKIL HEVK**AEGAKD**
101 **PIAIPTDVGF** **EENCR**KVIDQ IMSEYGKIDI LVNNAGEAHY STTIEDITDP
151 MLERVFRTNI FGHFFMSRHA LKHMKEGGCI INTASVAAYA GFSFMVDYSS
201 TKGAVVAFTR SLALQLIDRG IRVNAVAPGS VWTPFQPSTL SAEQVAQVGS
251 GVPMDRAAQP YEIAPSFVFL ASNDCSSYFT GQVLHPNGMF

Spot No.: **P53**

NCBI accession No.: **gi|224057068** Species: *Populus trichocarpa*

PFF score: [279]

Protein name: predicted protein

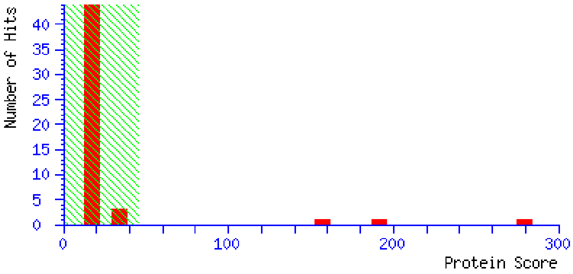
Matched peptides No.: [7] Sequence coverage %: [35]

Matched sequences: K.CPDTNYLFMGDYVDR.G + Oxidation (M);
R.QITQVYGFYDECLR.K;
R.VQEVPHEGPMCDLLWSDPDDR.C + Oxidation (M);
R.GAGYTFGQDISEQFNHTNNLK.L;
R.AHQLVMEGYNWGHEQK.V + Oxidation (M);
K.VVTIFSAPNYCYR.C;
K.GHTFIQFEPAPR.R

Calculated Mr: **36330** Calculated *p*I: **5.08**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MSLDSVATNA HGNLDEEISQ LMQCKPLSEQ EVRALCEKAK EILMDESNVQ
51 PVKSPVTICG DIHGQFHDLA ELFRIGGK**CP** **DTNYLFMGDY** **VDR**GYYSVET
101 VTLLVALKVR YPQRITILRG NHESR**QITQV** **YGFYDECLR**K YGNANVWKIF
151 TDLFDYFPLT ALVESEIFCL HGGLSPSIET LDNIRNFDR**V** **QEVPHEGPMC**
201 **DLLWSDPDDR** CGWGISPR**GA** **GYTFGQDISE** **QFNHTNNLK**L IAR**AHQLVME**
251 **GYNWGHEQKV** **VTIFSAPNYC** **YR**CGNMASIL EVDDCK**GHTF** **IQFEPAPR**RG
301 EPDVTRRTPD YFL

Spot No.: **P54**

NCBI accession No.: **gi|2832430** Species: *Hevea brasiliensis*

PFF score: [181]

Protein name: prohevein

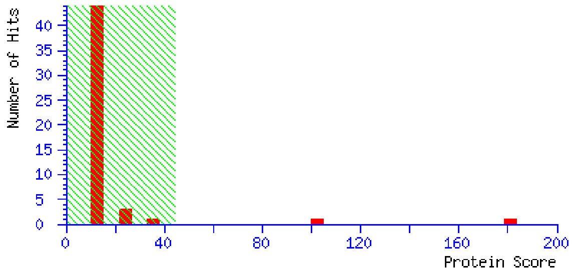
Matched peptides No.: [3] Sequence coverage %: [26]

Matched sequences: K.YGWTAFCGPVGAHGQPSCGK.C;
R.IVDQCSNGGLDLDVNVFR.Q;
R.QLDTDGKGYER.G

Calculated Mr: **20852** Calculated *p*I: **5.64**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 EQCGRQAGGK LCPNNLCCSQ WGWCGSTDEY CSPDHNCQSN CKDSGEGVGG
51 GSASNVLATY HLYNSQDHGW DLNAASAYCS TWDANKPYSW RSK**YGWTAFC**
101 **GPVGAHGQPS** **CGK**CLSVTNT GTGAKATVR**I** **VDQCSNGGLD** **LDVNVFRQLD**
151 **TDGKGYER**GH LTVNYQFVDC GDSFNPLFSV MKSSVIN

Spot No.: **P55**

NCBI accession No.: **gi|224071449** Species: *Populus trichocarpa*

PFF score: [55]

Protein name: predicted protein

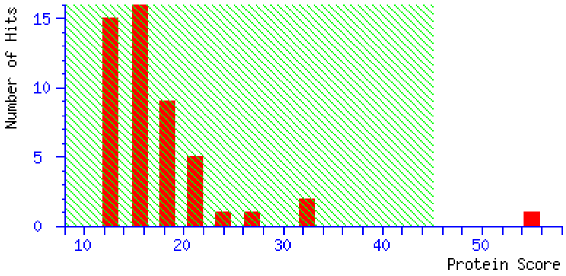
Matched peptides No.: [2] Sequence coverage %: [2]

Matched sequences: K.NKIDVIPHYPGR.L;
K.IDVIPHYPGR.L

Calculated Mr: **47121** Calculated *p*I: **5.28**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

1 MDGTSEATWP EILGSRNWDN LLDPLDLSLR KLILRCGDFC QATYDAFNND
51 QNSRYCGTSR YGKRNFFHKV MLDNPENYQV SSFLYATARV SLPEAFLLHS
101 LSRDSWDRET NWIGYIAVTS DEQTKTLGRR EIYIAFRGTT RNYEWVDILG
151 AKLKSAKPLL RGATSTTHDQ ESSSSSDDDD DKVPKVMLGW LTMYISDDPN
201 SPFTKLSARA QLLAHIKELR ERYKDDDLSI IFTGHSLGAS LSILSAFDLV
251 ENGITDIPVS AFVFGSPQVG NKEFNERFNK YPNLKVLHIK **NKIDVIPHYP**
301 **GR**LMGYVYTG IEFEIDTRKS PSLKDSKNPS DWHNLQAMLH IVAGWNGEEQ
351 EFELKVKRSL ALVNKSSEFL KDECLVPGIW WVEKNKGMVR NEDGEWVLAP
401 PDEEDLPVPE C

Spot No.: **P56**

NCBI accession No.: **gi|218157** Species: *Oryza sativa Japonica Group*

PFF score: [58]

Protein name: cytoplasmic aldolase

Matched peptides No.: [2] Sequence coverage %: [3]

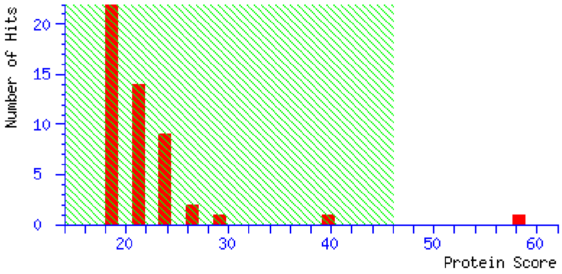
Matched sequences: K.KVAPEVIAEYTVR.T;

K.VAPEVIAEYTVR.T

Calculated Mr: **39151** Calculated *p*I: **6.56**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 46 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MSAYCGKYKD ELIKNAAYIG TPGKGILAAD ESTGTIGKRF ASINVENVED
51 NRRAFRELLF CTPGALQYIS GVILFDETLY QKTKDGKPFV DILKEAGALP
101 GIKVDKGTIE VAGTDKETTT QGHDDLGKQC AKYYEAGARF AKWRAVLKIG
151 PNQPSQLAID LNAQGLACYA IICQENGLVP IVEPEILVDG PHDIDRCAYV
201 SEVVLAACYK ALNEHHVLLE GTLLKPNMVT PGSDAK**KVAP** **EVIAEYTVR**T
251 LQRTVPPAVP AIVFLSGGQS EEEATLNLNA MNKLSAKKPW SLSFSFGRAL
301 QQSTLKAWAG KTENVEKARA AFLVRCKANS EATLGTYKGD AVLGEGAAES
351 LHVKDYKY

Spot No.: **P57**

NCBI accession No.: **gi|15219412**   Species: *Arabidopsis thaliana*

PFF score: [120]

Protein name: phosphoglycerate kinase

Matched peptides No.: [3]   Sequence coverage %: [6]

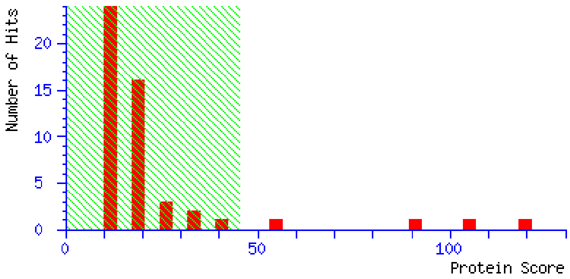
Matched sequences: K.YSLKPLVPR.L;

K.KLAALADVYVNDAFGTAHR.A;
K.LAALADVYVNDAFGTAHR.A

Calculated Mr: **42162**   Calculated *p*I: **5.49**

Probability Based Mowse Score:

```
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.
```



Matched peptide sequences: shown in Bold Red:

```
  1 MATKRSVGTL KEADLKGKSV FVRVDLNVPL DDNSNITDDT RIRAAVPTIK
 51 YLMGNGSRVV LCSHLGRPKG VTPKYSLKPL VPRLSELLGV EVVMANDSIG
101 EEVQKLVAGL PEGGVLLLEN VRFYAEEEKN DPEFAKKLAA LADVYVNDAF
151 GTAHRAHAST EGVAKFLKPS VAGFLMQKEL DYLVGAVANP KKPFAAIVGG
201 SKVSTKIGVI ESLLNTVDIL LLGGGMIFTF YKAQGLSVGS SLVEEDKLDL
251 AKSLMEKAKA KGVSLLLPTD VVIADKFAPD ANSKIVPATA IPDGWMGLDI
301 GPDSIKTFSE ALDTTKTIIW NGPMGVFEFD KFAAGTEAVA KQLAELSGKG
351 VTTIIGGGDS VAAVEKVGLA DKMSHISTGG GASLELLEGK PLPGVLALDE
401 A
```

Spot No.: **P58**

NCBI accession No.: **gi|356513072** Species: *Glycine max*

PFF score: [121]

Protein name: phosphoglucomutase,cytoplasmic-like

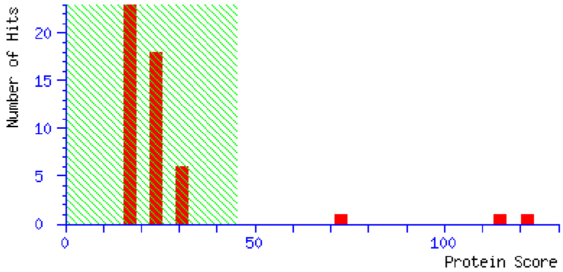
Matched peptides No.: [4] Sequence coverage %: [6]

Matched sequences: R.VETTPFDGQKPGTSGLR.K;
K.SIFDFESIR.K;
K.SIFDFESIRK.L;
K.LVTVEDIVR.Q

Calculated Mr: **63702** Calculated *p*I: **5.33**

Probability Based Mowse Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences: shown in Bold Red:

1 MVLFNVSR**VE** **TTPFDGQKPG** **TSGLR**KKVKV FVQPHYLHNF VQSTFNALTV
51 EKVRGATLVV SGDGRYFSKE AIQIITKMSA ANGVRRVWIG QNGLLSTPAV
101 SAVIRERVGA DGSRATGAFI LTASHNPGGP HEDFGIKYNM ENGGPAPEGI
151 TDKIYENTTT INEYLIASDL PDVDITTTGV TSFTGPEGPF DVEVFDSASD
201 YIKLMK**SIFD** **FESIRK**LLSS PKFTFCYDAL HGVGGAYAKS IFVDELGAQE
251 SSLLNCTPKE DFGGGHPDPN LTYAKELVAR MGLGKSEPQD DPPEFGAASD
301 GDADRNMILG KRFFVTPSDS VAIIAANAVE AIPYFSAGLK GVARSMPTSA
351 ALDVVAKHLN LKFFEVPTGW KFFGNLMDAG LCSVCGEESF GTGSDHIREK
401 DGIWAVLAWL SILAYKNKDK LEDK**LVTVED** **IVR**QHWATYG RHYYTRYDYE
451 NVDAGAAKEL MAYLVKLQSS LSEVNQIIKG IRSDVSNVVH GDEFEYNDPV
501 DGSISSHQGI RYLFEDGSRL IFRLSGTGSE GATIRLYIEQ YEKDPSKIGR
551 LSNEALAPLV EVALKLSKME EFTGRSAPTV IT

Spot No.: **P59**

NCBI accession No.: **gi|255568794** Species: *Ricinus communis*

PFF score: [95]

Protein name: nucleoredoxin, putative

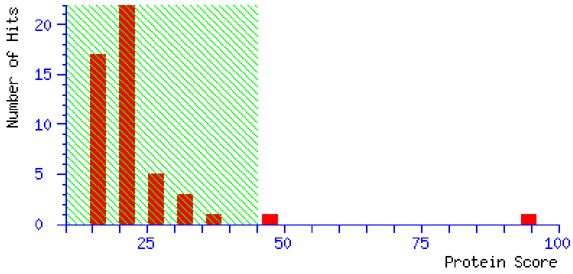
Matched peptides No.: [3] Sequence coverage %: [5]

Matched sequences: R.VEYFRQEEENAK.K;
K.LIEAYHEIK.A;
K.KCDFDLHPK.C

Calculated Mr: **63728** Calculated *p*I: **5.46**

Probability Based Mowse Score:

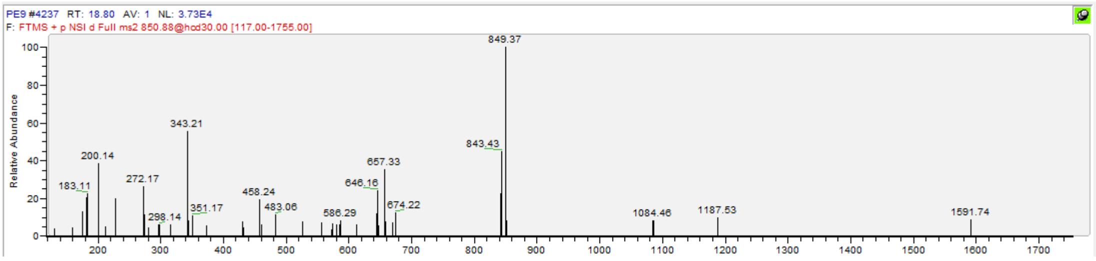
Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

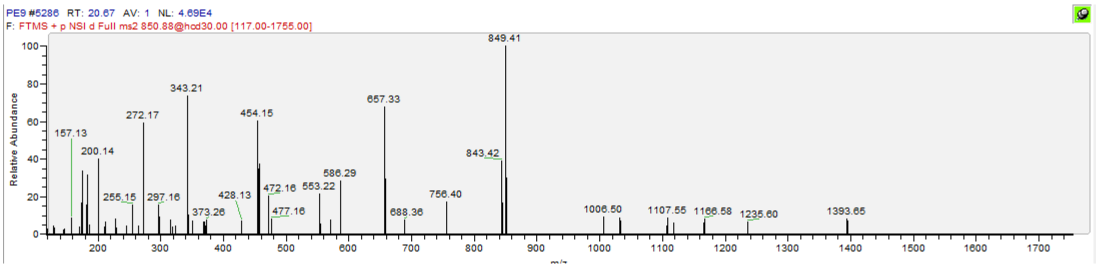


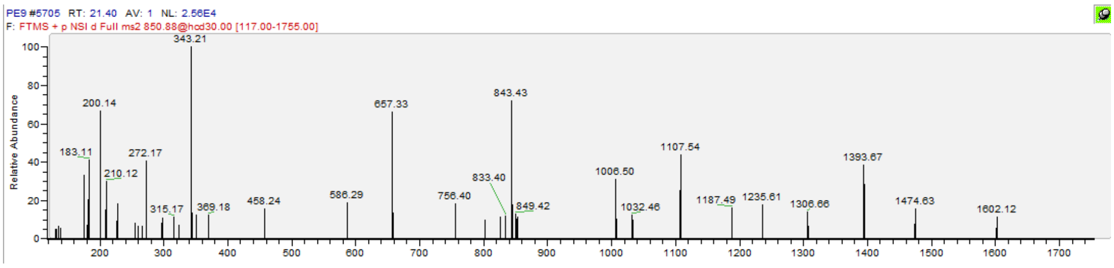
Matched peptide sequences: shown in **Bold Red:**

1 MADDPVIDVS HDLLSLLSSD DRDFLIRSNG DQVKISNLVG KIVGLYFSGS
51 WCGPCRHFTP NLVQVYEELS LKGDFEVVFI SSDRDAESFD AYFSKMPWLA
101 IPFSDQETCK HLKDLFKVRG IPNLVFLDAD GKVSCDQGVR FIREYGAEGY
151 PFTPER**VEYF** **RQEEENAK**KN QTLSSILVSS SRDFLISKDG TKIPVSELEG
201 KMVGLYFSVH SHRLCLDFTP RLEEVYKKLK EKGEKFEVVL ISMDYDENNF
251 KQGLETMPWL ALPFEDKSRE RLARYFELSA LPTLVIIGED GKTLNKNVAE
301 LIEGHGIQAY PFTPEKLVEL AEIEKARLEA QTLESVLVHG DKDFVIEESG
351 SKVPVSELVG KNILLYFSAK WCPPCRAFLP K**LIEAYHEIK** AKDNAFEIIF
401 ISSDRDQSSF DEFYTEMPWL ALPFGDDRKT ILQRKFKIKG IPAAIAISPT
451 GKTLTKEARE HITAYGADAY PFNEDHLKQL NDKQEEIAKG WPEKVRHELH
501 PEHELVRMKR NGYGCDGCKE AGSGWSFYCK **KCDFDLHPK**C ALKKEENGEK
551 VKK

Determination of the phosphorylated amino sites of small rubber particle protein (SRPP) in protein spot P6.

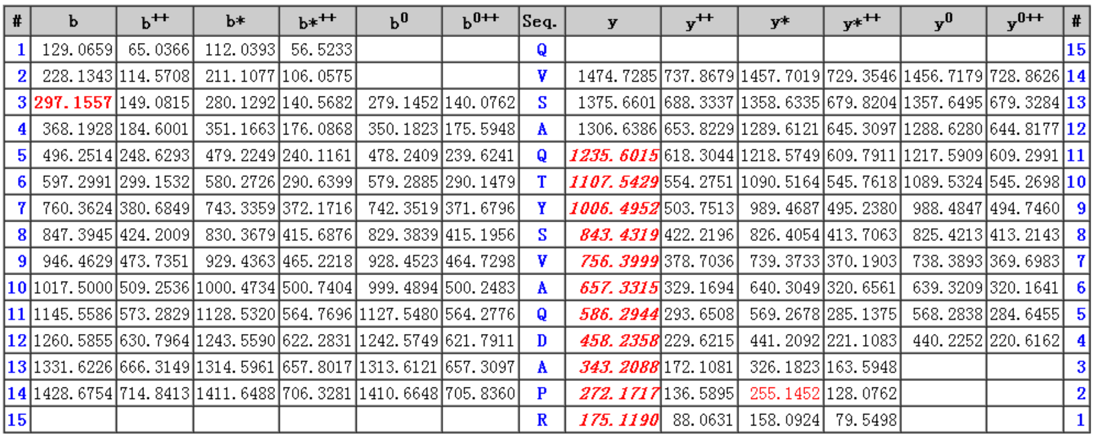




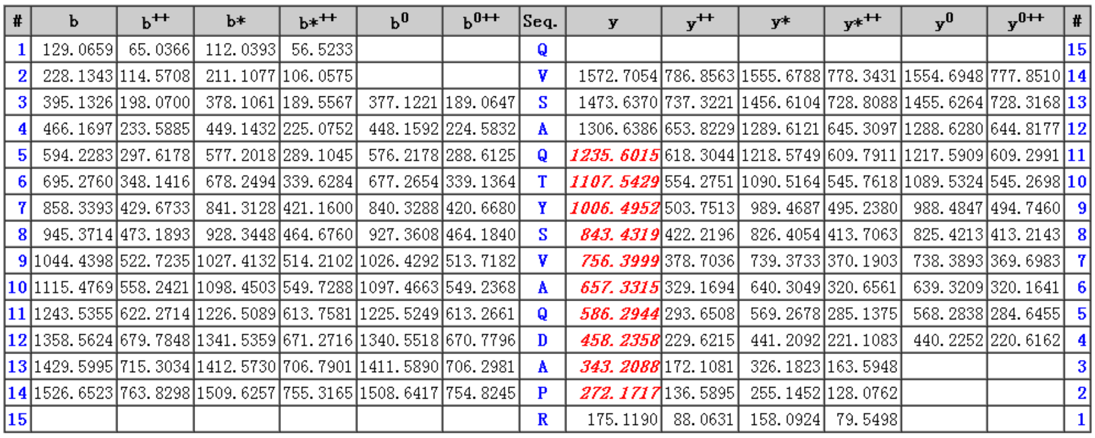


MS/MS Fragmentation of **QVSpAQTYpSVAQDAPR**

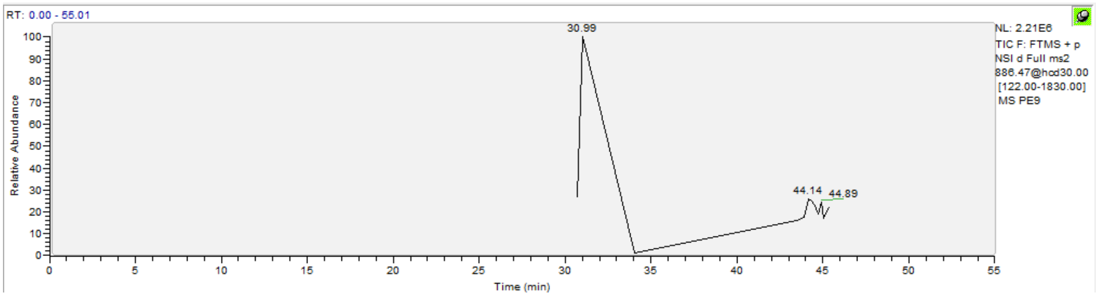
#	b	b^{++}	b*	$b*^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							15
2	228.1343	114.5708	211.1077	106.0575			V	1572.7054	786.8563	1555.6788	778.3431	1554.6948	777.8510	14
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	S	1473.6370	737.3221	1456.6104	728.8088	1455.6264	728.3168	13
4	386.2034	193.6053	369.1769	185.0921	368.1928	184.6001	A	1386.6049	693.8061	1369.5784	685.2928	1368.5944	684.8008	12
5	514.2620	257.6346	497.2354	249.1214	496.2514	248.6293	Q	1315.5678	658.2876	1298.5413	649.7743	1297.5573	649.2823	11
6	615.3097	308.1585	598.2831	299.6452	597.2991	299.1532	T	*1187.5092*	594.2583	1170.4827	585.7450	1169.4987	585.2530	10
7	858.3393	429.6733	841.3128	421.1600	840.3288	420.6680	Y	1086.4616	543.7344	1069.4350	535.2211	1068.4510	534.7291	9
8	945.3714	473.1893	928.3448	464.6760	927.3608	464.1840	S	*843.4319*	422.2196	826.4054	413.7063	825.4213	413.2143	8
9	1044.4398	522.7235	1027.4132	514.2102	1026.4292	513.7182	V	756.3999	378.7036	739.3733	370.1903	738.3893	369.6983	7
10	1115.4769	558.2421	1098.4503	549.7288	1097.4663	549.2368	A	*657.3315*	329.1694	640.3049	320.6561	639.3209	320.1641	6
11	1243.5355	622.2714	1226.5089	613.7581	1225.5249	613.2661	Q	*586.2944*	293.6508	569.2678	285.1375	568.2838	284.6455	5
12	1358.5624	679.7848	1341.5359	671.2716	1340.5518	670.7796	D	*458.2358*	229.6215	441.2092	221.1083	440.2252	220.6162	4
13	1429.5995	715.3034	1412.5730	706.7901	1411.5890	706.2981	A	*343.2088*	172.1081	326.1823	163.5948			3
14	1526.6523	763.8298	1509.6257	755.3165	1508.6417	754.8245	P	*272.1717*	136.5895	255.1452	128.0762			2
15							R	175.1190	88.0631	158.0924	79.5498			1

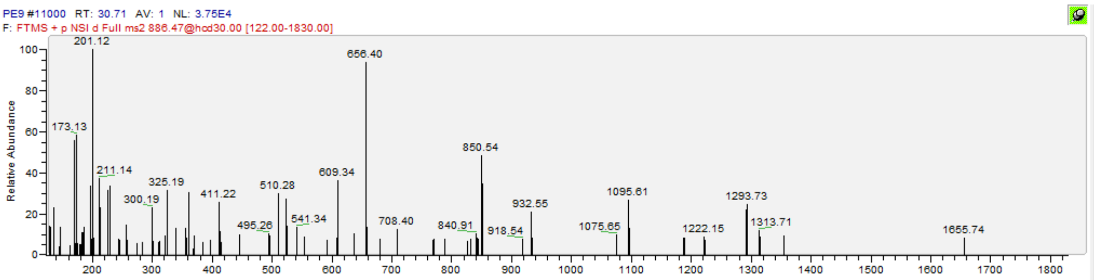


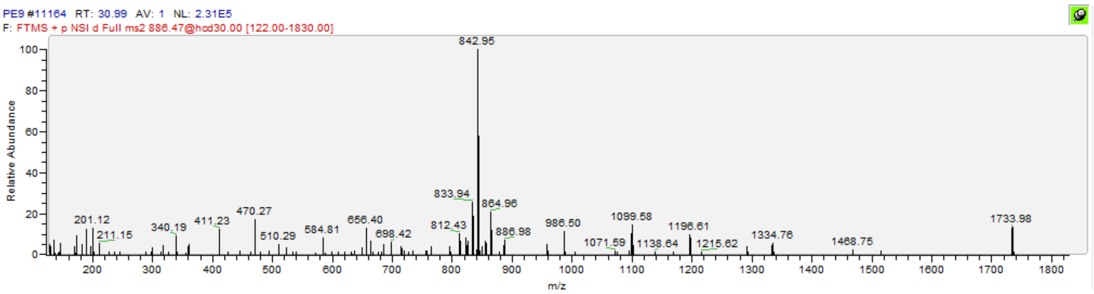
#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	129.0659	65.0366	112.0393	56.5233			Q							15
2	228.1343	114.5708	211.1077	106.0575			V	1474.7285	737.8679	1457.7019	729.3546	1456.7179	728.8626	14
3	297.1557	149.0815	280.1292	140.5682	279.1452	140.0762	S	1375.6601	688.3337	1358.6335	679.8204	1357.6495	679.3284	13
4	368.1928	184.6001	351.1663	176.0868	350.1823	175.5948	A	1306.6386	653.8229	1289.6121	645.3097	1288.6280	644.8177	12
5	496.2514	248.6293	479.2249	240.1161	478.2409	239.6241	Q	1235.6015	618.3044	1218.5749	609.7911	1217.5909	609.2991	11
6	597.2991	299.1532	580.2726	290.6399	579.2885	290.1479	T	1107.5429	554.2751	1090.5164	545.7618	1089.5324	545.2698	10
7	760.3624	380.6849	743.3359	372.1716	742.3519	371.6796	Y	1006.4952	503.7513	989.4687	495.2380	988.4847	494.7460	9
8	847.3945	424.2009	830.3679	415.6876	829.3839	415.1956	S	843.4319	422.2196	826.4054	413.7063	825.4213	413.2143	8
9	946.4629	473.7351	929.4363	465.2218	928.4523	464.7298	V	756.3999	378.7036	739.3733	370.1903	738.3893	369.6983	7
10	1017.5000	509.2536	1000.4734	500.7404	999.4894	500.2483	A	657.3315	329.1694	640.3049	320.6561	639.3209	320.1641	6
11	1145.5586	573.2829	1128.5320	564.7696	1127.5480	564.2776	Q	586.2944	293.6508	569.2678	285.1375	568.2838	284.6455	5
12	1260.5855	630.7964	1243.5590	622.2831	1242.5749	621.7911	D	458.2358	229.6215	441.2092	221.1083	440.2252	220.6162	4
13	1331.6226	666.3149	1314.5961	657.8017	1313.6121	657.3097	A	343.2088	172.1081	326.1823	163.5948			3
14	1428.6754	714.8413	1411.6488	706.3281	1410.6648	705.8360	P	272.1717	136.5895	255.1452	128.0762			2
15							R	175.1190	88.0631	158.0924	79.5498			1

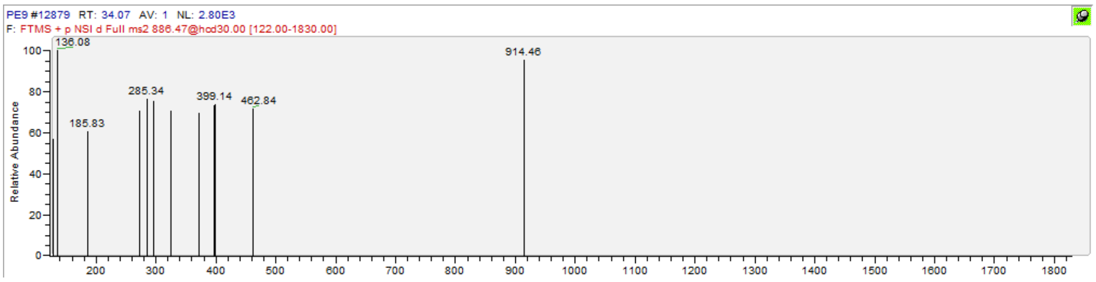


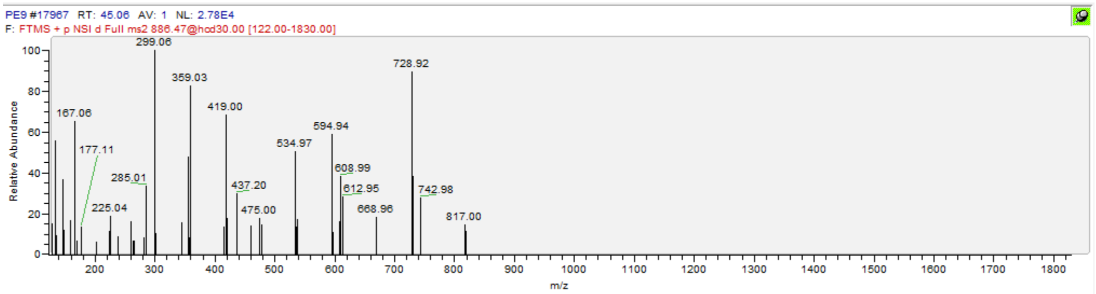
#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	129.0659	65.0366	112.0393	56.5233			Q							15
2	228.1343	114.5708	211.1077	106.0575			V	1572.7054	786.8563	1555.6788	778.3431	1554.6948	777.8510	14
3	395.1326	198.0700	378.1061	189.5567	377.1221	189.0647	S	1473.6370	737.3221	1456.6104	728.8088	1455.6264	728.3168	13
4	466.1697	233.5885	449.1432	225.0752	448.1592	224.5832	A	1306.6386	653.8229	1289.6121	645.3097	1288.6280	644.8177	12
5	594.2283	297.6178	577.2018	289.1045	576.2178	288.6125	Q	1235.6015	618.3044	1218.5749	609.7911	1217.5909	609.2991	11
6	695.2760	348.1416	678.2494	339.6284	677.2654	339.1364	T	1107.5429	554.2751	1090.5164	545.7618	1089.5324	545.2698	10
7	858.3393	429.6733	841.3128	421.1600	840.3288	420.6680	Y	1006.4952	503.7513	989.4687	495.2380	988.4847	494.7460	9
8	945.3714	473.1893	928.3448	464.6760	927.3608	464.1840	S	843.4319	422.2196	826.4054	413.7063	825.4213	413.2143	8
9	1044.4398	522.7235	1027.4132	514.2102	1026.4292	513.7182	V	756.3999	378.7036	739.3733	370.1903	738.3893	369.6983	7
10	1115.4769	558.2421	1098.4503	549.7288	1097.4663	549.2368	A	657.3315	329.1694	640.3049	320.6561	639.3209	320.1641	6
11	1243.5355	622.2714	1226.5089	613.7581	1225.5249	613.2661	Q	586.2944	293.6508	569.2678	285.1375	568.2838	284.6455	5
12	1358.5624	679.7848	1341.5359	671.2716	1340.5518	670.7796	D	458.2358	229.6215	441.2092	221.1083	440.2252	220.6162	4
13	1429.5995	715.3034	1412.5730	706.7901	1411.5890	706.2981	A	343.2088	172.1081	326.1823	163.5948			3
14	1526.6523	763.8298	1509.6257	755.3165	1508.6417	754.8245	P	272.1717	136.5895	255.1452	128.0762			2
15							R	175.1190	88.0631	158.0924	79.5498			1











MS/MS Fragmentation of **TVVTpPVYYIPLEAVK**

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	102.0550	51.5311	84.0444	42.5258	T							15
2	201.1234	101.0653	183.1128	92.0600	V	1670.8805	835.9439	1653.8539	827.4306	1652.8699	826.9386	14
3	300.1918	150.5995	282.1812	141.5942	V	1571.8121	786.4097	1554.7855	777.8964	1553.8015	777.4044	13
4	481.2058	241.1065	463.1952	232.1013	T	1472.7437	736.8755	1455.7171	728.3622	1454.7331	727.8702	12
5	578.2586	289.6329	560.2480	280.6276	P	*1291.7297*	646.3685	1274.7031	637.8552	1273.7191	637.3632	11
6	677.3270	339.1671	659.3164	330.1618	V	1194.6769	597.8421	1177.6503	589.3288	1176.6663	588.8368	10
7	840.3903	420.6988	822.3797	411.6935	Y	*1095.6085*	548.3079	1078.5819	539.7946	1077.5979	539.3026	9
8	1003.4536	502.2305	985.4431	493.2252	Y	*932.5451*	466.7762	915.5186	458.2629	914.5346	457.7709	8
9	1116.5377	558.7725	1098.5271	549.7672	I	769.4818	385.2445	752.4553	376.7313	751.4713	376.2393	7
10	1213.5905	607.2989	1195.5799	598.2936	P	*656.3978*	328.7025	639.3712	320.1892	638.3872	319.6972	6
11	1326.6745	663.8409	1308.6640	654.8356	L	559.3450	280.1761	542.3184	271.6629	541.3344	271.1708	5
12	1455.7171	728.3622	1437.7065	719.3569	E	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
13	1526.7542	763.8808	1508.7437	754.8755	A	317.2183	159.1128	300.1918	150.5995			3
14	1625.8226	813.4150	1607.8121	804.4097	V	246.1812	123.5942	229.1547	115.0810			2
15					K	147.1128	74.0600	130.0863	65.5468			1

Mascot Search Results

Peptide View

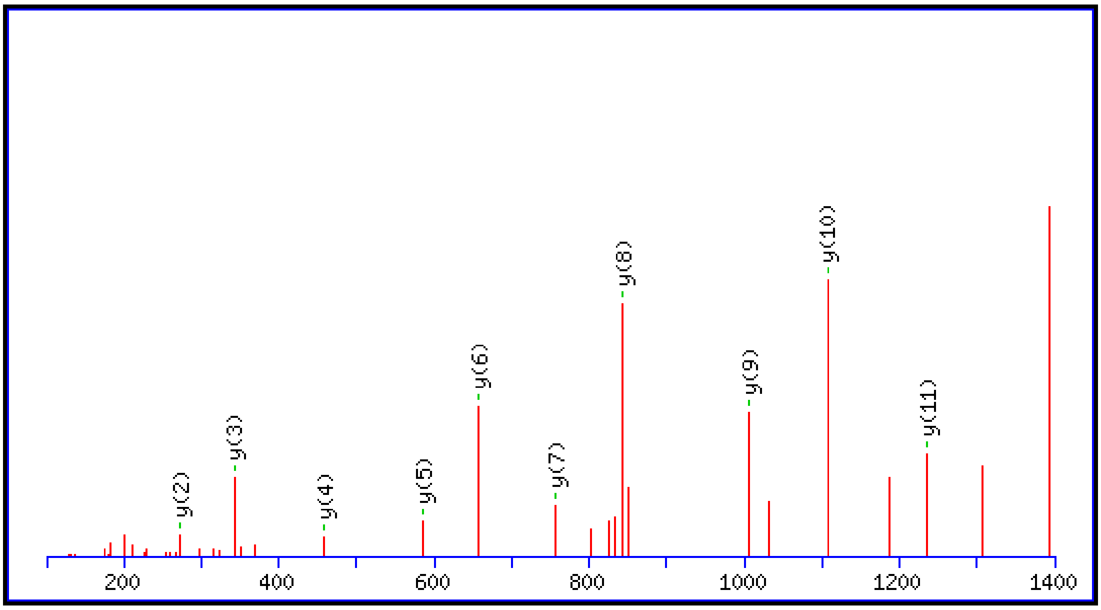
MS/MS Fragmentation of **QVSAQTYSVAQDAPR**

Found in **SRPP_HEVBR** in **SwissProt**, Small rubber particle protein OS=Hevea brasiliensis GN=SRPP PE=1 SV=1

Match to Query 9859: 1699.749968 from(850.882260,2+) intensity(277497.1200) scans(5705) rawscans(sn5705) rtinseconds(1283.9872) index(3303)

Title: 3304: Scan 5705 (rt=1283.99)

Data file tempfile



Monoisotopic mass of neutral peptide Mr(calc): 1699.7567

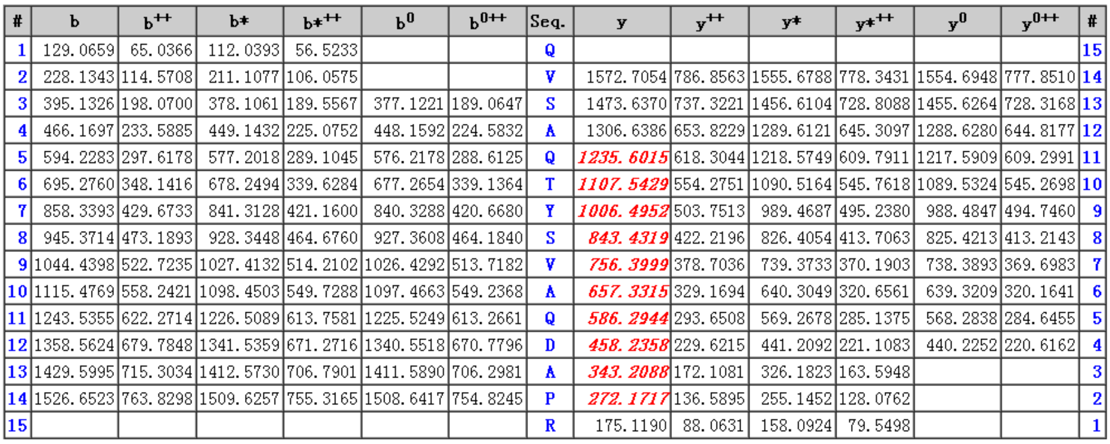
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

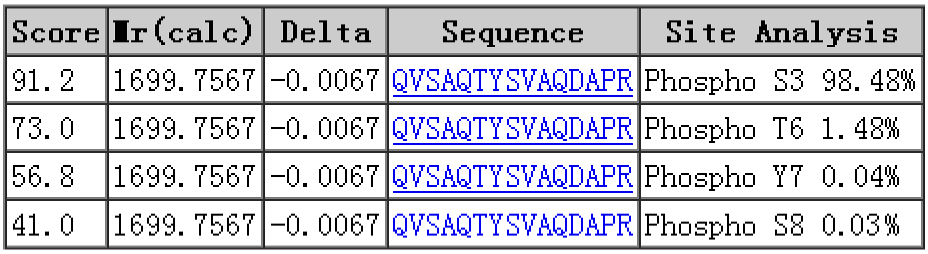
Ions Score: 91 Expect: 2.8e-009

Matches : 10/242 fragment ions using 13 most intense peaks



#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							15
2	228.1343	114.5708	211.1077	106.0575			V	1572.7054	786.8563	1555.6788	778.3431	1554.6948	777.8510	14
3	395.1326	198.0700	378.1061	189.5567	377.1221	189.0647	S	1473.6370	737.3221	1456.6104	728.8088	1455.6264	728.3168	13
4	466.1697	233.5885	449.1432	225.0752	448.1592	224.5832	A	1306.6386	653.8229	1289.6121	645.3097	1288.6280	644.8177	12
5	594.2283	297.6178	577.2018	289.1045	576.2178	288.6125	Q	***1235.6015***	618.3044	1218.5749	609.7911	1217.5909	609.2991	11
6	695.2760	348.1416	678.2494	339.6284	677.2654	339.1364	T	***1107.5429***	554.2751	1090.5164	545.7618	1089.5324	545.2698	10
7	858.3393	429.6733	841.3128	421.1600	840.3288	420.6680	Y	***1006.4952***	503.7513	989.4687	495.2380	988.4847	494.7460	9
8	945.3714	473.1893	928.3448	464.6760	927.3608	464.1840	S	***843.4319***	422.2196	826.4054	413.7063	825.4213	413.2143	8
9	1044.4398	522.7235	1027.4132	514.2102	1026.4292	513.7182	V	***756.3999***	378.7036	739.3733	370.1903	738.3893	369.6983	7
10	1115.4769	558.2421	1098.4503	549.7288	1097.4663	549.2368	A	***657.3315***	329.1694	640.3049	320.6561	639.3209	320.1641	6
11	1243.5355	622.2714	1226.5089	613.7581	1225.5249	613.2661	Q	***586.2944***	293.6508	569.2678	285.1375	568.2838	284.6455	5
12	1358.5624	679.7848	1341.5359	671.2716	1340.5518	670.7796	D	***458.2358***	229.6215	441.2092	221.1083	440.2252	220.6162	4
13	1429.5995	715.3034	1412.5730	706.7901	1411.5890	706.2981	A	***343.2088***	172.1081	326.1823	163.5948			3
14	1526.6523	763.8298	1509.6257	755.3165	1508.6417	754.8245	P	***272.1717***	136.5895	255.1452	128.0762			2
15							R	175.1190	88.0631	158.0924	79.5498			1

All matches to this query



Score	Mr(calc)	Delta	Sequence	Site Analysis
91.2	1699.7567	-0.0067	QVSAQTYSVAQDAPR	Phospho S3 98.48%
73.0	1699.7567	-0.0067	QVSAQTYSVAQDAPR	Phospho T6 1.48%
56.8	1699.7567	-0.0067	QVSAQTYSVAQDAPR	Phospho Y7 0.04%
41.0	1699.7567	-0.0067	QVSAQTYSVAQDAPR	Phospho S8 0.03%

Supplementary Figure S6: Antibody information

Antibody name: WR-1

Protein name: sucrose transporter 3

Plant species: *Hevea brasiliensis*

NCBI Accession No.: gi |227809927

Antibody tag sequence: ISGMLVQPIVGYHSC

Protein sequence：

1 metdptkesk lpsseplppp pplvppppas sklrkivmva siaagiqfgw alqlslltpy
61 vqllgiphtw aafiwlcgpi sgmlvqpivg yhsdrctsrf grrrpfiagg alavavavfl
121 igyaadlgql sgdpvakspk praiavfvvg fwildvannm lqgpcralla dlsganqkkt
181 rianalysff mavgnvlgfa agsythlyki fpftktkacd vycanlkscf fisivllltl
241 tvlaliyvre kpwspergnt aagdeeeede gasesspmpf fseifaslkn lqkpmwilll
301 vtclnwvawf pfllfdtdwm grevyggdsn gnpvqvrlyd rgvragalgl mlnsvvlgft
361 slgvevlara vggvkrlwgi vnfilsfclf mtilitkmae shrrfatvgg gatvplpppg
421 dvkagalalf avmgvpqait ysipfalasi fcntagagqg lslgvlnlsi vipqmvvsvv
481 sgpwdalfgg gnlpafvvgg vaaaasgifa ftllpspqpd apsaktsrav taafh

Gene sequence：

1 atggagactg atcctacgaa agaatccaaa ctcccctctt ctgaacctct tccacctcct
61 ccgcccctag ttcctccacc acccgcttca agcaagctta gaaagattgt aatggtggcc
121 tccatagctg ctggtatcca gtttggctgg gctttgcagc tctctctttt gacaccttac
181 gttcagcttc ttggtatacc tcacacatgg gctgctttca tctggctatg tggacccatt
241 tcaggaatgc ttgtccagcc aattgtcggc tatcatagtg atcgttgcac ctcccgtttt
301 ggccgtcgcc gcccttttat tgcaggcggt gctttggccg ttgctgtagc tgttttcctt
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421 ccacgagcta tagccgtgtt tgtcgttggg ttctggattc ttgacgtcgc taataacatg
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541 cgtatagcta atgcactgta ctccttcttc atggccgtcg ggaacgttct tggctttgcc
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661 gtttactgtg caaatctgaa atcttgtttc tttatctcca ttgtcttgct tttaactctc
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781 gctgccggtg acgaggagga ggaggacgag ggggcgtcgg agtcttctcc gatgccgttc
841 ttcagtgaga tatttgcatc tttgaagaat ctgcaaaaac ccatgtggat ccttcttctg
901 gtgacgtgcc tgaactgggt tgcatggttt ccattcttgt tgttcgatac tgattggatg
961 ggtagagagg tatacggcgg agattcaaac ggaaatcccg ttcaagtgag gttgtatgat
1021 cgtggggtgc gcgctggtgc actgggtctg atgcttaact cggtggtttt ggggttcacc

1081 tcccttggtg tggaggtgct ggcgcgtgct gtcggaggag tgaaaagatt gtggggtata
1141 gtgaatttca ttctttcatt ttgtttgttc atgacgatct tgatcaccaa aatggctgaa
1201 tcccacagaa ggttcgccac cgtgggaggc ggcgccacgg ttcccttgcc accacctgga
1261 gacgtcaagg ctggtgcatt ggcccttttt gcggtgatgg gtgtacctca agctataact
1321 tacagtattc cttttgcttt ggcatcaata ttttgtaaca ctgctggtgc tggtcaagga
1381 ctttctttgg gagttctgaa tctttcaatt gttataccac agatggtggt gtcagtagta
1441 agcggaccat gggatgcatt atttggaggg ggtaatctac cagcttttgt ggtgggaggg
1501 gttgctgccg cggccagtgg aatatttgca ttcaccttac tcccatctcc gcagcctgat
1561 gccccctccg ccaagacttc aagggctgtc acagctgcct tccattga

Antibody name: WR-3

Protein name: **hydroxymethylglutaryl coenzyme A reductase**

Plant species: *Hevea brasiliensis*

NCBI Accession No.: gi |16417954

Antibody tag sequence: CEDRSPTTPKASDA

Protein sequence:

1 mdttgrlhhr khatpvedrs pttpkasdal plplyltnav fftlffsvay yllhrwrdki
61 rnstplhivt lseivaivsl iasfiyllgf fgidfvqsfi arashdvwdl edtdpnylid
121 edhrlvtcpp anistkttii aaptklptse pliaplvsee demivnsvvd gkipsysles
181 klgdckraaa irrealqrmt rrsleglpve gfdyesilgq ccempvgyvq ipvgiagpll
241 lngreysvpm attegclvas tnrgckaiyl sggatsvllk dgmtrapvvr fasatraael
301 kffledpdnf dtlavvfnks srfarlqgik csiagknlyi rfscstgdam gmnmvskgvq
361 nvleflqsdf sdmdvigisg nfcsdkkpaa vnwiegrgks vvceaiikee vvkkvlktnv
421 aslvelnmlk nlagsavaga lggfnahagn ivsaifiatg qdpaqnvess hcitmmeavn
481 dgkdlhisvt mpsievgtvg ggtqlasqsa clnllgvkga nkespgsnsr llaaivagsv
541 lagelslmsa iaagqlvksh mkynrsskdm skaas

Gene sequence:

1 atggacacca ccggccggct ccaccaccga aagcatgcta cacccgttga ggaccgttct
61 ccgaccactc cgaaagcgtc ggacgcgctt ccgcttcccc tctacctgac caacgcggtt
121 ttcttcacgc tgttcttctc ggtggcgtat tacctccttc accggtggcg cgacaagatc
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1141 aatttttgtt cggataagaa gcctgctgct gtaaattgga ttgaaggacg tggcaaatca

1201 gttgtttgtg aggcaattat caaggaagag gtggtgaaga aggtgttgaa aaccaatgtg
1261 gcctccctag tggagcttaa catgctcaag aatcttgctg gttctgctgt tgctggtgct
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1381 caggatccag cacagaatgt tgagagttct cattgcatta ccatgatgga agctgtcaat
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1501 ggtggaactc aacttgcatc tcagtctgct tgtctcaatt tgcttggggt gaagggtgca
1561 aacaaagagt cgccaggatc aaactcaagg ctccttgctg ccatcgtagc tggttcagtt
1621 ttggctggtg agctctcctt gatgtctgcc attgcagctg ggcagcttgt caagagtcac
1681 atgaagtaca acagatccag caaagatatg tctaaagctg catcttag

Antibody name: WR-4

Protein name: **hydroxymethylglutaryl coenzyme A synthase**

Plant species: *Hevea brasiliensis*

NCBI Accession No.: gi |16417956

Antibody tag sequence: YKHFCAKYEKFEGK

Protein sequence：

1 maknvgilav diyfpptfvq qealeahdga skgkytiglg qdcmafctev edvismslta
61 vtslldkyni dpkqigrlev gsetvidksk siktflmqif ekfgntdieg vdstnacygg
121 taalfncvnw vessswdgry glvvctdsav yaegparptg gaaaiailvg pdapiafesk
181 frgshmshay dfykpnlase ypvvdgklsq tcylmaldsc ykhfcakyek fegkqfsisd
241 aeyfvfhspy nklvqksfar lvfndfvrna ssidetakek lapfsnlsgd esyqnrdlek
301 vsqqvakply dakvkpttli pkqvgnmyta slyaafasll hskhtelagk rvtlfsygsg
361 ltatmfslrl hegqhpfsls niasvmnvag klkarhelpp ekfvdimklm ehrygakdfv
421 tskdcsllas gtyyltevds lyrrfyaqka vgntvengll angh

Gene sequence：

1 atggcaaaga atgtgggaat tctcgctgtg gacatctact ttcctcctac ctttgttcag
61 caggaagcac tggaggctca tgatggtgca agcaaaggga aatacaccat tggacttgga
121 caggattgca tggcattttg tactgaggtg gaagatgtca tctcaatgag tttgactgca
181 gttacttcac tcctcgacaa gtataatatt gatcctaaac aaatcggtcg tctggaagtt
241 ggcagtgaga ctgtgatcga caagagcaaa tctattaaaa ccttcttgat gcaaattttc
301 gagaaattcg gaaacactga cattgaaggc gttgactcaa caaatgcatg ttatgggggg
361 actgcagctt tattcaactg tgtcaattgg gttgagagca gttcatggga tggacgctat
421 ggacttgtag tgtgtactga cagtgcggtc tatgcagagg gtccagcccg accaactgga
481 ggagctgcag ccattgcgat tttagtaggt ccagatgcac ctattgcttt tgaaagcaaa
541 tttagggga gccatatgtc tcatgcttat gatttttaca agcccaacct ggctagtgaa
601 tatccagttg tggatggcaa gctttcccaa acatgctacc tcatggctct tgattcttgc
661 tacaaacatt tctgtgccaa gtatgagaaa tttgaaggca agcaattctc tatttctgat
721 gctgaatatt ttgtatttca ttctccttac aacaagcttg tacagaaaag ctttgctcgt
781 ttggtgttca atgactttgt gaggaatgcc aggtctattg atgagactgc taaagaaaag
841 ctggcaccgt tttcaaattt atctggtgat gaaagctacc aaaaccggga tcttgaaaag
901 gtatcccaac aagttgccaa gcccctttat gatgcgaaag tgaaaccaac cactttgata
961 ccaaagcaag ttggcaatat gtacactgca tctttgtatg cagcatttgc atccctcctt
1021 cacagtaaac atactgaatt ggcaggcaag cgggtgacac tgttctctta tgggagtggg
1081 ttgacagcca caatgttctc attgcgacta catgaaggcc aacatccctt tagcttgtca
1141 aacattgcat ctgtgatgaa tgttgcagga aagttgaagg caagacatga gcttcccca
1201 gagaagtttg taaacatcat gaagctaatg gagcaccggt acggagctaa agactttgtg
1261 agaagcaagg attgcagcct cttggcttct ggaacatact atctcacaga agttgacagc

1321 ttgtatcgaa gattctatgc ccagaaggct gttggcaaca cagttgagaa tggtttgctg
1381 gctaatggtc attga

Antibody name: WR-5

Protein name: phosphomevalonate kinase

Plant species: *Hevea brasiliensis*

NCBI Accession No.: gi |16417948

Antibody tag sequence: DEIKPDSWAWAWTDC

Protein sequence：

1 mavvasapgk vlmtggylil erpnagivls tnarfyaivk piydeikpds wawawtdvkl
61 tspqlaresl yklslknlal qcvsssasrn pfveqavqfa vaaahatldk dkknvlnkll
121 lqglditilg tndfysyrne ieacglpltp eslaalpsfs sitfnveean gqnckpevak
181 tglgssaamt tavvaallhh lglvdlsssc kekkfsdldl vhiiaqtahc iaqgkvgsgf
241 dvssavygsh ryvrfspevl ssaqdagkgi plqevisnil kgkwdhertm fslpplmsll
301 lgepgtggss tpsmvgalkk wqksdtqksq etwrklsean saletqfnil sklaeehwda
361 ykcvidscst knsekwieqa tepsreavvk allgsrnaml qirnymrqmg eaagvpiepe
421 sqtrlldttm nmdgvllagv pgaggfdavf avtlgdsgtn vakawsslnv lallvredpn
481 gvllesgdpr tkeittavfa vhi

Gene sequence：

1 atggctgtag ttgcttctgc tccgggtaag gtgttgatga ctgggggtta cctcatattg
61 gaaagaccca atgcagggat tgtactcagc acaaatgctc gattctatgc cattgtgaag
121 cctatttacg atgaaatcaa acctgatagt tgggcatggg catggactga tgtgaaatta
181 acatctcccc aactagcaag ggaaagcttg tacaaattgt cactgaaaaa tttagctctt
241 cagtgtgtct cttcaagtgc atcaaggaac ccatttgtgg aacaagcagt gcaatttgct
301 gtagcagctg cacatgcaac acttgacaaa gataagaaga atgtcttaaa caagctactc
361 ttgcaaggtc ttgatattac aatattaggt accaatgact tctattcata ccgaaatgag
421 attgaagcat gtggactccc tttgacacca gaatcattgg ctgcacttcc ttctttttcc
481 tcaatcacct tcaatgtaga ggaagcaaat ggacaaaact gcaagcctga ggtagctaaa
541 actggattgg gttcatcagc agcaatgacc actgctgtag ttgctgcttt acttcatcac
601 cttggattgg ttgatctttc atcctcttgt aaagagaaga aattttctga tcttgatttg
661 gtacatataa tagcccaaac tgcccattgt attgcacaag ggaaagtcgg cagtggattt
721 gatgttagtt ctgcagttta tggcagtcat cgatacgtgc gcttctctcc agaagtgctt
781 tcctctgctc aggatgctgg gaaaggaatt ccattacagg aagtcatttc taacatccta
841 aaaggaaaat gggaccatga gaggactatg ttttccttgc caccattgat gagcctgcta
901 ctaggtgagc caggaactgg aggatcttcc acgccatcaa tggtaggtgc tctaaagaaa
961 tggcagaagt ctgatactca gaaatcccaa gaaacatgga gaaagttgtc agaggcaaat
1021 tcagcacttg aaacgcaatt caatatttta agcaagctcg cagaagaaca ttgggacgcg
1081 tataaatgtg tgatagacag ttgcagcaca aaaaactcag agaagtggat tgagcaggca
1141 actgaaccca gccgagaagc agttgttaaa gcattattag gatcaagaaa tgccatgctt
1201 cagatcagaa attacatgcg ccagatgggt gaggctgcag gtgttccgat agagcctgaa

1261 tcacagactc gacttttgga tactactatg aatatggatg gagtcttgtt ggctggagtt
1321 cctggagcag gtgggtttga tgcagtcttc gctgttacct taggggactc tggtaccaat
1381 gtggcaaaag cttggagttc actcaatgtt ctggccctgt tggttagaga agaccctaat
1441 ggtgttttgt tagaaagcgg cgatccaaga accaaggaaa tcacaacagc tgtttttgca
1501 gttcatattt ga

Antibody name: WR-6

Protein name: mevalonate kinase, MEVK

Plant species: *Hevea brasiliensis*

NCBI Accession No.: gi |16417946

Antibody tag sequence: DVSITEKEEKLEEC

Protein sequence:

1 mevkarapgk iilsgehavv hgstavaasi nlytyvtlsf ataenddslk lqlkdlalef
61 swpigrirea lsnlgapsss trtscsmesi ktisalveee nipeakialt sgvsaflwly
121 tsiqgfkpat vvvtsdlplg sglgssaafc valsaallaf sdsvnvdtkh lgwsifgesd
181 lellnkwale gekiihgkps gidntvsayg nmikfksgnl triksnmplk mlvtntrvgr
241 ntkalvagvs ertlrhpnam sfvfnavdsi snelaniiqs papddvsite keekleelme
301 mnqgllqcmg vshasietvl rttlkyklas kltgaggggc vltllptlls gtvvdkaiae
361 lescgfqcli agiggngvef cfggss

Gene sequence:

1 atggaagtta aagcaagagc tccagggaaa atcattctct ccggtgaaca cgcagtggtg
61 cacggatcca ctgcagtcgc tgcatccatt aatctctaca cctatgtcac cctttctttt
121 gctactgctg agaatgatga ttcactgaaa cttcagctca aggatctggc actagaattt
181 tcatggccaa ttggtagaat cagagaggca ttatctaact taggtgctcc ttcctcttca
241 acacgcacct cttgctcgat ggaatcaatt aagacaattt cagctttggt tgaagaagaa
301 aatatcccag aggcaaaaat tgcactcact tctggagtgt cagccttttt atggttatat
361 acttctattc aaggatttaa gcctgccacc gtagttgtca cttctgatct tccactgggt
421 tcaggcctag gatcatctgc tgcattttgt gttgccctct cagctgctct gcttgctttc
481 tcagactctg taaatgtgga cacaaagcac ctagggtggt caatatttgg agagtctgac
541 cttgaattat taaacaaatg ggctctcgaa ggtgaaaaga taattcatgg aaagccatct
601 ggaatagaca acactgtcag cgcatatggc aacatgatca agttcaagtc tggtaatctg
661 actcgcatca agtccaacat gccgctcaaa atgctcgtca ctaacacaag agttgggagg
721 aacacaaaag cactggttgc tggtgtttca gagagaacct tacggcaccc taatgccatg
781 agttttgttt ttaatgccgt tgattctatc agtaatgagc tggctaacat catccagtca
841 cctgctccag atgatgtgtc cataactgag aaggaagaga agctagaaga gttaatggaa
901 atgaatcaag gcttgcttca atgcatgggg gtcagccatg cttctataga aactgttctt
961 cggacaactt tgaaatacaa gttagcttcc aagctgactg gagcaggggg tggggggtgc
1021 gtgctgacac tgttaccaac cctgctatca ggaacagttg ttgacaaagc aattgctgaa
1081 ttggagtcat gcggatttca atgtttgatt gctggaatcg gtgggaatgg tgttgagttt
1141 tgctttggtg gttcatcctg a

Antibody name: WR-7

Protein name: **farnesyl diphosphate synthase, FADS**

Plant species: *Hevea brasiliensis*

NCBI Accession No.: gi |22676905

Antibody tag sequence: IPRILKKHFRGKAYC

Protein sequence：

1 madlkstflk vysvlkqell edpafewtpd srqwvermld ynvpggklnr glsvidsykl
61 lkegqeltee eiflasalgw ciewlqayfl vlddimdssh trrgqpcwfr vpkvgliaan
121 dgillrnhip rilkkhfrgk ayyvdlldlf nevefqtasg qmidlittle gekdlskytl
181 slhrrivqyk tayysfylpv acalliagen ldnhivvkdi lvqmgiyfqv qddyldcfgd
241 petigkigtd iedfkcswlv vkalelcnee qkkvlyehyg kadpasvakv kvlynelklq
301 gvfteyenes ykklvtsiea hpskpvqavl ksflakiykr qk

Gene sequence：

1 atggcggatc tgaagtcaac tttcttgaag gtctactctg tcctcaagca ggagctcctt
61 gaggatccgg ctttcgaatg gacaccagat tcccgtcaat gggttgagcg gatgttggac
121 tacaatgtgc ctggagggaa gctgaatagg gggctttctg taattgacag ctacaaattg
181 ttgaaagaag gacaggaatt aacagaagaa gagatctttc ttgcaagtgc tcttggttgg
241 tgtattgaat ggcttcaagc ctattttctt gtacttgatg acattatgga tagctctcat
301 acacgacgtg gtcagccttg ctggtttagg gtgcccaagg ttggtctgat tgcagcaaat
361 gatgggattt tgcttcgcaa tcacattccc aggattctta aaaagcactt ccgagggaag
421 gcatactatg tagatcttct agatttgttt aatgaggtgg agtttcaaac agcctcagga
481 cagatgatag atctaattac aacacttgaa ggagaaaagg atttatccaa atacactttg
541 tcactccacc ggagaattgt tcagtacaaa actgcctact actcatttta ccttcctgtt
601 gcttgtgcat tgctcatagc gggtgagaat ctggacaatc atattgttgt aaaagacatt
661 cttgttcaga tgggaatcta cttccaagta caggatgatt atttggattg ctttggtgat
721 cccgagacaa ttggtaagat aggaacagat atagaagatt ttaagtgttc atggttggtc
781 gtgaaggctt tagaactttg caatgaagaa caaaagaaag tgttatatga gcactatggg
841 aaagctgacc cagccagtgt agcaaaggtg aaggtccttt ataatgagct gaagcttcag
901 ggggtattta cggagtatga gaatgaaagc tataagaaac tagtaacctc tattgaagct
961 catcctagca agccggtgca agcagtgttg aagtcctttt tggccaaaat ttacaagaga
1021 cagaaataa

Antibody name: WR-8

Protein name: **cis-prenyltransferase, CIST**

Plant species: *Hevea brasiliensis*

NCBI Accession No.: gi |40716449

Antibody tag sequence: CDNFRRKPHEVQYV

Protein sequence:

1 mklytgerps vfrllgkymr kglygiltqg pipthlafil dgnrrfakkh klpeggghka
61 gflallnvlt ycyelgvkya tiyafsidnf rrkphevqyv mnlmlekieg mimeesiina
121 ydicvrfvgn lkllsepvkt aadkimrata nnskcvllla vcytstdeiv haveesseln
181 snevcnnqel eeanatgsgt viqtenmesy sgiklvdlek ntyinpypdv lirtsgetrl
241 snyllwqttn cilyspyalw peiglrhvvw svinfqrhys ylekhkeylk

Gene sequence:

1 atgaaattat acaccggtga gaggccaagt gtgttcagac ttttagggaa gtatatgaga
61 aaagggttat atggcatcct aacccagggt cccatcccta ctcatcttgc cttcatattg
121 gatggaaaca ggaggtttgc taagaagcat aaactgccag aaggaggtgg tcataaggct
181 ggatttttag ctcttctgaa cgtgctaact tattgctatg agttaggagt gaaatatgcg
241 actatctatg cctttagcat cgataatttt cgaaggaaac ctcatgaggt tcagtacgta
301 atgaatctaa tgctggagaa gattgaaggg atgatcatgg aagaaagtat catcaatgca
361 tatgatattt gcgtacgttt tgtgggtaac ctgaagcttt taagtgagcc agtcaagacc
421 gcagcagata agattatgag ggctactgcc aacaattcca aatgtgtgct tctccttgct
481 gtatgctata cttcaactga tgagatcgtg catgctgttg aagaatcctc tgaattgaac
541 tccaatgaag tttgtaacaa tcaagaattg gaggaggcaa atgcaactgg aagcggtact
601 gtgattcaaa ctgagaacat ggagtcgtat tctggaataa aacttgtaga ccttgagaaa
661 aacacctaca taaatcctta tcctgatgtt ctgattcgaa cttctgggga gacccgtctg
721 agcaactact tactttggca gactactaat tgcatactgt attctcctta tgcactgtgg
781 ccagagattg gtcttcgaca cgtggtgtgg tcagtaatta acttccaacg tcattattct
841 tacttggaga aacataagga atacttaaaa taa

Antibody name: WR-9

Protein name: Rubber elongation factor

Plant species: *Hevea brasiliensis*

NCBI Accession No.: gi |132270

Antibody tag sequence: drslppivkd asiqvvsa

Protein sequence:

1 maedednqqg qgeglkylgf vqdaatyavt tfsnvylfak dksgplqpgv diiegpvknv
61 avplynrfsy ipngalkfvd stvvasvtii drslppivkd asiqvvsair aapeaarsla
101 sslpgqtkil akvfygen

Gene sequence:

1 ttttgatctt ccatttttgc aaaaggaaat cttcgattat ggctgaagac gaagacaacc
61 aacaagggca gggggagggg ttaaaatatt tgggttttgt gcaagacgcg gcaacttatg
121 ctgtgactac cttctcaaac gtctatcttt ttgccaaaga caaatctggt ccactgcagc
181 ctggtgtcga tatcattgag ggtccggtga agaacgtggc tgtacctctc tataataggt
241 tcagttatat tcccaatgga gctctcaagt ttgtagacag cacggttgtt gcatctgtca
301 ctattataga tcgctctctt cccccaattg tcaaggacgc atctatccaa gttgtttcag
361 caattcgagc tgccccagaa gctgctcgtt ctctggcttc ttctttgcct gggcagacca
421 agatacttgc taaggtgttt tatggagaga attgagcccc aatttgcacc aattgcttcc
481 aactaagcaa gttaatgata tgctcaagaa tatatatcta ttgtgagctt tttttatgtt
541 ctcatcctga gtgttgagac tatgttttcg tttgaatatt atactgtgtt ttattatgtg
601 ttttgaatat tcataatgag aataaagggc caattgaatt attggccaat atgtaatgat
661 acataaattt cgtgattgag t

Antibody name: WR-10

Protein name: Small rubber particle protein

Plant species: *Hevea brasiliensis*

NCBI Accession No.: gi |14423933

Antibody tag sequence: gvvppvik qvsaqtysv

Protein sequence：

1 maeeveeerl kyldfvraag vyavdsfstl ylyakdisgp lkpgvdtien vvktvvtpvy

61 yipleavkfv dktvdvsvts ldgvvppvik qvsaqtysva qdaprivldv assvfntgvq

121 egakalyanl epkaeqyavi twralnklpl vpqvanvvvp tavyfsekyn dvvrgtteqg
181 yrvssylpll ptekitkvfg deas

Gene sequence：

1 ataatcagtt gatagcttcc acagtgtttt ccgaaaggca aatctttttt caaacttcag

61 cgactgcgtt ttgaatttgt gatttttaaa ggaaattttc aattatggct gaagaggtgg

121 aggaagagag gctaaagtat ttggattttg tgcgagcggc tggagtttat gctgtagatt

181 ctttctcaac tctctacctt tatgccaagg acatatctgg tccattaaaa cctggtgtcg

241 atactattga gaatgtggtg aagaccgtgg ttactcctgt ttattatatt ccccttgagg

301 ctgtcaagtt tgtagacaaa acggtggatg tatcggtcac tagcctagat ggcgttgttc

361 ccccagttat caagcaggtg tctgcccaaa cttactcggt agctcaagat gctccaagaa

421 ttgttcttga tgtggcttct tcagttttca acactggtgt gcaggaaggc gcaaaagctc

481 tgtacgctaa tcttgaacca aaagctgagc aatatgcggt cattacctgg cgtgccctca

541 ataagctgcc actagttcct caagtggcaa atgtagttgt gccaaccgct gtttatttct

601 ctgaaaagta caacgatgtt gttcgtggca ctactgagca gggatataga gtgtcctctt

661 atttgccttt gttgcccact gagaaaatta ctaaggtgtt tggagatgag gcatcataat

721 ctgcactgga tttggttatt tatctattgt gagctttttt atatgtactt attcagtgtt

781 tagaataagt ctttggtggt gtgttttgga tgtggaataa agggccaatt gcattgttgg

841 tcaatatata attatgtata acatttcgtg atttgagttg gaatctaaag gttttacaaa

901 aaaaaaaaaa aaaaaaaaaa aa

Antibody name: WR-11

Protein name: **hydroxynitrile lyase**

Plant species: *Hevea brasiliensis*

NCBI Accession No.: gi |**1223884**

Antibody tag sequence: CIENYKPDKVYKVE

Protein sequence:

1 mafahfvlih tichgawiwh klkpllealg hkvtaldlaa sgvdprqiee igsfdeysep
61 lltflealpp gekvilvges cgglniaiaa dkycekiaaa vfhnsvlpdt ehcpsyvvdk
121 lmevfpdwkd ttyftytkdg keitglklgf tllrenlytl cgpeeyelak mltrkgslfq
181 nilakrpfft kegygsikki yvwtdqdeif lpefqlwqie nykpdkvykv eggdhklqlt
241 ktkeiaeilq evadtyn

Gene sequence:

1 atggcattcg ctcattttgt tcttattcat accatatgcc acggtgcatg gatttggcac
61 aagctcaaac ccctccttga ggcacttggc cacaaggtta ctgcactgga ccttgcagca
121 agcggcgttg acccaaggca aattgaggag attggctcat ttgatgagta ttctgaaccc
181 ttgttgacgt tcttggaggc actccctcca ggggaaaagg tgattctggt tggcgagagc
241 tgtggaggac tcaatatagc aattgctgct gataaatact gtgaaaagat tgcagctgct
301 gttttccaca attcagtatt gccagacacc gagcactgcc catcttacgt cgtggataag
361 ctcatggagg tgtttcccga ctggaaagac accacgtatt ttacgtacac taaagatggc
421 aaggagataa ctggattgaa actgggcttc acgcttctga gggaaaattt atataccctt
481 tgcggtcctg aggaatatga actggcgaag atgttgacaa ggaagggatc attatttcaa
541 aatattttag ctaagcgacc attcttcact aaggaaggtt acggatcgat taagaaaatt
601 tatgtgtgga ccgaccaaga cgaaatattt ttacctgaat ttcaactctg gcaaatagaa
661 aactataaac cagacaaggt ttataaggtc gaaggtggag atcataaatt gcagcttaca
721 aagactaagg agatcgctga aattctccaa gaggtggctg atacctataa ttga

Antibody name: WR-12

Protein name: superoxide dismutase (manganese)

Plant species: *Hevea brasiliensis*

NCBI Accession No.: gi |**348137**

Antibody tag sequence: CQLHHQKHHQTYIT

Protein sequence：

1 malrslvtrk nlpsafkaat glgqlrglqt fslpdlpydy galepaisge imqlhhqkhh
61 qtyitnynka leqlndaiek gdsaavvklq saikfngggh vnhsifwknl apvregggel
121 phgslgwaid adfgslekli qlmnaegaal qgsgwvwlal dkelkklvve ttanqdplvt
181 kgptlvpllg idvwehayyl qyknvrpdyl kniwkvmnwk yasevyakec pss

Gene sequence：

1 atggctctgc gatctctagt gacccgaaag aacctaccct cagccttcaa ggccgccaca
61 gggctagggc aactgcgggg attgcagacc ttctctctcc ccgatctccc ttacgactat
121 ggtgccctgg agcccgcgat tagcggcgag ataatgcagc tgcatcacca gaaacatcac
181 cagacttata ttactaacta caacaaggct ctcgagcaac tcaacgacgc tatagagaag
241 ggcgattctg ctgccgtcgt caagttgcag agcgccatca agttcaacgg tggaggtcat
301 gtcaaccact ccattttctg gaagaatctt gcccccgtcc gtgaaggagg tggtgaactc
361 ccgcatggtt cccttggttg ggctattgac gcagattttg gctcattgga aaagttgata
421 caattaatga atgcagaagg tgctgcgctg caaggatctg gatgggtgtg gcttgccttg
481 gacaaagaat tgaagaagct tgtggttgag accactgcaa accaggatcc attggtaact
541 aaaggaccaa ctttagttcc tttgcttggt attgatgttt gggagcatgc atactactta
601 cagtacaaaa atgtcagacc agactatcta aagaacatat ggaaagtaat gaattggaag
661 tatgcaagtg aagtgtatgc caaagaatgc ccttcttctt ag

Antibody name: WR-13

Protein name: **rubber peroxidase 1**

Plant species: *Hevea brasiliensis*

NCBI Accession No.: gi |109809965

Antibody tag sequence: NFNNTNSPDPTLNC

Protein sequence：

1 mhisplmlva ialyailvgs srplayaqls ptfydqscpn vsniirgviq eslqsdsrig
61 aslirlhfhd cfvngcdasi lldntdties ekqaaannns argfdvvdtm karlesacpg
121 ivscadiltv saqqsvdlag gptwtnllgr rdsltasrsq anlsipgpfe tldqlkskft
181 avglnnntdl valsgahtfg raqcrtfspr lynfnntnsp dptlnttylq tlqqicpqgg
241 ngsvitnldl ttsdtfdney fsnllvgegl lqsdqelfnt tgadtvaivq nfsanqtaff
301 esfvesmlrm gnlsvltgti geirlncskv ngnssagaet llvssm

Gene sequence：

1 atgcatatct ctccattgat gttggtggcg atagctttat atgcaatttt agttggatca
61 tcaagacccc tggcctacgc tcagctatct ccaacatttt atgatcaaag ctgcccaaac
121 gtctccaaca ttattcgtgg agtcatccaa gaatccttgc aatctgattc caggattggt
181 gccagcctca tcaggcttca tttccatgac tgctttgtca atggttgcga tgcatcaatt
241 ttgttggaca atactgatac tatagagagt gagaaacaag ctgctgcaaa taacaactca
301 gctagaggtt ttgatgttgt tgatacaatg aaggctagat tggagagtgc ttgtcctggc
361 attgtttctt gtgctgatat tctaactgtt tcagctcaac aatctgttga tttggcagga
421 gggccaacat ggacaaatct acttggaaga agagatagct taacagcaag cagaagtcaa
481 gctaatctta gcattccagg tcctttcgag acccttgacc agctcaagtc caagttcacc
541 gccgtaggcc tcaacaacaa taccgatcta gttgccctat ctggtgctca cacgtttgga
601 agagctcaat gcagaacatt tagcccccgt ttgtacaact tcaataacac taattctcca
661 gacccaacat tgaacacaac atatctgcaa acgcttcaac aaatatgtcc acaaggagga
721 aatgggagtg taataactaa tcttgatctc acaacttctg atacctttga taatgaatat
781 ttctccaatc ttctagttgg agaaggcctt ctccagagtg atcaagaact atttaacact
841 actggggctg atactgttgc tattgttcaa aattttagtg ctaatcagac tgcttttttt
901 gaaagctttg tggagtccat gctcagaatg ggaaatctca gcgttttaac aggaactatt
961 ggagagatta gattgaattg cagcaaagtt aatggaaatt catcagctgg agcagaaact
1021 cttcttgtta gctccatgta g

Antibody name: WR-14

Protein name: **calcium-dependent protein kinase 1, CDPK**

Plant species: *Hevea brasiliensis*

NCBI Accession No.: gi |289413843

Antibody tag sequence: CRQNQQQQSYYQQPE

Protein sequence:

1 mgccsskekp skseankgyr sggtgnlrqn qqqqsyyqqp eyqqqqavqh pkmtvpqtqt
61 qtpqtrpqqp qastpppvra aptnltarsv qtpqtilgkp ledikqyysl gkelgrgqfg
121 vtylctenst ghiyacksil krklinkgdr edikrevqim qhlsgqpniv efrgsyedrq
181 svhvvmelca ggelfdriia kghyserdaa rickdivnvv hachfmgvmh rdlkpenfll
241 askdegamlk ttdfglsvfi eegktyrniv gsayyvapev lrrsygkeid iwsagvilyi
301 llsgvppfwa etekgifdai legyidfess pwpsisdsak dlvrrmltqd pkrritsaqv
361 ldhpwikdgg aasdkpidsa vlsrmkqfra mnklkklalk viaenlseee ikglkamftn
421 mdtdksgtit yeelktglar lgsrlsetev kqlmeaadvd gngaidyief isatmhryrl
481 erdehlykaf qyfdkdssgy itrdelesam meygmgdeas ikeiisevdt dndgkinyee
541 fctmmrrgvq qpgklf

Gene sequence:

1 atgggttgtt gtagcagcaa ggagaagcct tcaaaatcag aggctaataa agggtacagg
61 tcaggaggca ctggtaattt aaggcagaac caacaacaac aatcttatta tcaacaacca
121 gaataccagc aacaacaggc cgtgcagcac ccaaaaatga ccgtccctca aactcaaaca
181 caaaccccgc aaacaaggcc ccaacaacct caggcatcaa cccccccctcc agtaagagca
241 gcacctacga accttacagc aagatcagtt caaacgccac agaccattct gggcaaaccc
301 ttggaagaca ttaagcagta ctacagtcta gggaaagaac tgggtagagg ccaatttggt
361 gttacttatt tgtgcacaga gaattccact ggccacattt atgcctgcaa atccatactg
421 aagagaaaac taatcaataa gggtgacaga gaagatatca agagagaggt tcagattatg
481 cagcacttgt ctgggcagcc aaatattgta gagtttaggg gttcctatga ggataggcaa
541 tctgttcatg ttgtgatgga gctttgtgct ggaggggaac tttttgatcg tattattgct
601 aaagggcatt attcggagag agatgccgct aggatttgca aggatattgt gaatgtggtg
661 cacgcttgcc attttatggg agtgatgcac cgtgatctca agccggagaa tttcttgctg
721 gctagcaagg atgagggagc aatgttgaag accactgatt ttggactgtc tgtgttcatt
781 gaggaaggga aaacataccg taatatagtt ggtagtgctt attatgttgc tcctgaagta
841 ttgaggcgta gttatggaaa ggaaatagat atttggagtg caggagttat tttgtatatt
901 ctactcagtg gtgtacctcc attttgggct gaaactgaaa aaggaatatt tgatgctatt
961 ctagaaggat acattgattt tgaaagttca ccatggccat caatatctga cagtgccaaa
1021 gatctggtca ggagaatgct gactcaggac ccaaaaaggc gaattacttc agcacaagtt
1081 cttgaccatc catggattaa agatggaggt gcagcatcag acaagccaat agatagtgca
1141 gttctctcta gaatgaagca attcagggca atgaataagc tcaagaagct agcattaaag

1201 gttattgctg aaaatctctc tgaagaagaa attaaaggtc ttaaagcaat gttcacaaac
1261 atggacactg acaagagtgg cacaatcacc tatgaagagc tgaagacagg tttagctcga
1321 cttgggtcaa ggctctctga aactgaagtt aaacaattaa tggaagctgc cgatgtggat
1381 ggaaatggag caatcgacta cattgagttt atctctgcta caatgcatag atatcgactg
1441 gaaagagatg agcatctata caaagcattt cagtactttg ataaggatag cagtgggtat
1501 ataacaagag atgaattaga gtctgccatg atggagtatg gtatgggaga tgaggccagt
1561 attaaggaaa taatttctga ggtggataca gataatgatg ggaaaatcaa ctatgaagaa
1621 ttctgcacta tgatgagacg tggagtacaa caaccaggaa agcttttcta g

Antibody name: WR-15

Protein name: **ethylene-inducible protein, ETHI**

Plant species: *Hevea brasiliensis*

NCBI Accession No.: gi |1209317

Antibody tag sequence: GLGEAMVGINLNDKC

Protein sequence:

1 magtgvvavy gngaitetkk spfsvkvgla qmlrggvimd vvnpeqaria eeagacavma
61 lervpadira qggvarmsdp qlikeikqsv tipvmakari ghfveaqile aigidyvdes
121 evltpadeen hinkhnfrip fvcgcrnlge alrriregaa mirtkgeagt gnvieavrhv
181 rsvmgdirll rnmdddevft fakkiaapyd lvmqtkqlgr lpvvqfaagg vatpadaalm
241 mqlgcdgvfv gsgvfksgdp arraraivqa vthysdpdml aevscglgea mvginlndkk
301 verfanrse

Gene sequence:

1 atggctggaa ctggggtggt ggcagtttac ggcaacggag caatcaccga aaccaaaaag
61 tcccctttt ccgtgaaggt gggtctagcc cagatgctaa gaggcggtgt tatcatggac
121 gtcgtaaatc ccgagcaggc ccgcatagcc gaggaggctg gcgcttgtgc tgtcatggct
181 ttggagcgtg tgccagccga tatccgcgct caaggtggcg tcgcgcgcat gagcgaccct
241 cagcttatca aagaaattaa acagtccgtt accatccccg tcatggccaa ggcccgcatc
301 ggccacttcg tggaggccca aattcttgaa gccataggca tcgattacgt cgacgagagc
361 gaagtgctta cccctgccga cgaagagaac cacatcaaca aacataattt ccgtatcccc
421 ttcgtttgcg gttgtaggaa cttaggcgag gcgcttcgaa ggatacgcga aggagccgcc
481 atgattagga ccaaaggtga agcaggaaca gggaatgtta tcgaagcggt taggcacgtg
541 aggtctgtga tgggtgatat taggcttttg aggaatatgg acgacgatga ggtgttcact
601 ttcgccaaga agattgctgc gccgtacgat ttggttatgc agacgaagca gctagggagg
661 ctacctgtgg tgcagttcgc ggcgggaggg gtcgcgacgc cggcggatgc ggctttgatg
721 atgcagttgg gttgcgatgg ggtgtttgtg gggtctgggg tgttcaagag cggggacccc
781 gcaaggaggg ccagagcaat tgtgcaggcg gtgacgcatt atagcgatcc cgacatgctc
841 gcggaggtga gttgcggtct cggtgaggct atggtgggta tcaatttaaa cgacaagaag
901 gtggaaaggt tcgcaaacag gtcggaatag

Antibody name: WR-16

Protein name: **ethylene receptor, ETHR**

Plant species: *Hevea brasiliensis*

NCBI Accession No.: gi |56900932

Antibody tag sequence: QQNPVGYTVPIQLPC

Protein sequence:

1 meacnciepq wpadellmky qyisdffial ayfsipleli yfvkksavfp yrwvlvqfga
61 fivlcgathl inlwtftmhs rtvaivmtta kvltaavsca talmlvhiip dllsvktrel
121 ilknkaaeld remglirtqe etgrhvrmlt heirstldrh tilkttlvel grtlaleeca
181 lwmptrsgle lqlsytlrqq npvgytvpiq lpvinkvfsc nravkispnc pvarirpfag
241 kympgevvav rvpllhlsnf qindwpelst kryalmvlml psdsarqwha yelelvevva
301 dqvavalsha aileesmrar dllmeqnval dlarreaeta irarndflav mnhemrtpmh
361 aiialssllq etgltpeqrl mvetilkssn llatlindvl dlsrledgsl qldlgtfnlr
421 avfrevlnli kpiasvkklp vtlnlapdlp eyaigdekrl mqtilnvvgn avkfskegni
481 sitafvarpe slrdlrfpdf fpvpsddhfy lrvqvkdegl ginlqdipkl ftkfaqnqsl
541 atrnsggsgl glaickrfvn lmeghiwies eglgkgctai fvvklailec sneskhpfmq
601 ngpkpnqgak qtsfmgpess llmddtggyq dgnkrtfwgt lxcdxttvss sdeclrvvxl
661 dhkvvfmdvc mpdglellsa ymkdftkrhe rplivalywn ankvtkencm kvgmdgvilk
721 pvsvdkmrgv lsdllehrvl feam

Gene sequence:

1 atggaggcat gcaattgtat tgagccacaa tggccagcgg atgaattgtt gatgaagtac
61 caatatattt cagatttctt cattgctctt gcttatttct ccattcctct agagctcatt
121 tattttgtta agaaatcagc agtttttcct tatagatggg tgctggtgca gtttggtgct
181 tttatagttt tatgtggggc aacacatctt attaacttat ggacttttac catgcattca
241 cgaactgtgg ctattgtaat gaccacagca aaagttttga ctgctgcagt ttcatgcgca
301 accgccctta tgcttgtaca cataattcct gatcttttga gtgttaaaac tagagaacta
361 attttgaaaa acaaggctgc agagcttgat agagagatgg gcctgatccg tacacaggaa
421 gaaacaggcc ggcatgttag gatgctgact catgagatca ggagcacact tgatagacat
481 accatactaa agaccacact tgttgaactg ggaaggacat tggcattgga agagtgtgcc
541 ttatggatgc ccaccaggtc tggattagag cttcaacttt cctacactct tcgtcagcag
601 aatcctgttg gatatactgt gcctatccag cttcctgtga ttaataaagt attcagttgt
661 aaccgtgctg taaaaatatc acctaactgt ccagtggcaa gaatacgtcc ttttgcagga
721 aaatatatgc ctggagaggt ggttgctgtt cgagtcccac ttcttcatct ctctaatttc
781 caaattaatg attggcctga gctttctacc aaacgctatg ctttgatggt tttgatgctt
841 ccctcagata gtgcaaggca gtggcatgct tatgagttgg agcttgttga agtagttgct
901 gaccaggtgg ctgttgctct atcacatgct gctatcttag aagagtcaat gagggcaagg
961 gatcttctta tggagcagaa tgttgcactt gatcttgcaa ggagagaagc agaaacagct

1021 atccgtgctc gcaatgattt cttagctgtc atgaaccatg agatgagaac tcccatgcat
1081 gcaattattg cactttcttc cttactgcaa gaaactggac tgacgcctga gcagcgcctg
1141 atggttgaga caattcttaa gagtagtaac ctgttggcta ctttaataaa tgatgtatta
1201 gacctttcaa ggcttgaaga tggcagtctt cagcttgacc tgggaacttt taatctacgt
1261 gctgtattca gggaggtcct taacttgatc aagcctattg catctgttaa aaagttgcct
1321 gttactttaa atttagctcc agatttgcca gaatatgcca ttggtgatga gaaacgtctt
1381 atgcaaacca ttttaaatgt tgttggtaat gctgtgaagt tctctaaaga aggcaacatc
1441 tcaataactg cttttgttgc tagaccagaa tcattaagag atcttcggtt tcctgatttt
1501 ttcccagtgc caagtgatga tcacttttat ttgcgtgtac aggtaaaaga tgagggacta
1561 ggtataaacc tccaagatat tcctaagttg tttactaaat ttgcacaaaa tcaatcattg
1621 gcaaccagaa attctggtgg cagtggactt ggccttgcaa tttgtaagag gtttgtaaat
1681 cttatggaag gacacatctg gatagagagt gaaggacttg gcaagggatg cactgctatc
1741 tttgttgtaa aacttgctat tcttgagtgc tcaaatgaat cgaagcatcc tttcatgcag
1801 aatgggccca agccaaatca aggggccaaa caaacttctt ttatggggcc tgaaagttct
1861 ttgttaatgg atgatacggg gggttaccag gacggtaaca aaaggacttt ttggggcact
1921 ttggnttgtg atgngaccac tgtgagctcc agcgatgagt gtttacgagt agtttntctg
1981 gaccacaagg tggtatttat ggatgtgtgc atgcctgatg gtttggagtt gctatccgca
2041 tacatgaaag atttcacaaa acgtcatgaa aggccattaa tagtggcgct ttactggaac
2101 gcaaacaagg tgacaaagga aaactgcatg aaggtcggca tggatggtgt aatactgaaa
2161 cctgtctctg ttgacaagat gaggggtgtt ttatcagatc ttctggagca tcgggttcta
2221 ttcgaggcca tgtaa

Antibody name: WR-17

Protein name: **glutathione reductase, GLUR**

Plant species: *Hevea brasiliensis*

NCBI Accession No.: gi |186920319

Antibody tag sequence: CMKNTISGRQEKTVM

Protein sequence:

1 avfcipplsv vglseeqaie qakndilvft stfnpmknti sgrqektvmk lvvdaetdkv
61 lgasmcgpda peiiqgiava lkcgatkaql dstvgihpst aeefctm

Gene sequence:

1 gcagtgtttt gcataccacc tttgtctgta gtaggcctca gtgaagagca ggcaatagag
61 caagcaaaaa atgatatatt ggttttcact tcaaccttca atcctatgaa gaatactatc
121 tctggacggc aagagaagac agtgatgaag cttgttgttg atgctgagac agataaagtt
181 cttggagctt caatgtgtgg gcctgatgct cctgaaatta tacagggaat tgctgttgca
241 ttgaagtgcg gagcaacaaa ggcccaattg gacagcacgg tgggaataca cccttctact
301 gctgaggaat tctgtaccat g

Antibody name: WR-23

Protein name: **latex cyanogenic beta glucosidase, LACG**

Plant species: *Hevea brasiliensis*

NCBI Accession No.: gi |31580730

Antibody tag sequence: LDDKLRVRYFKGYLC

Protein sequence：

1 mmkekflkeh pyllekevsr sdfppnflfg vatsayqieg gcreggrgps iwdafshtkg
61 tildgsngdv avdhyhryke dieliaklgf dayrfslsws rifpdglgtk vneegiafyn
121 niinallekg iepyitlyhw dlplhlqesm ggwlnkeivk yfaiyadtcf asfgdrvkkw
181 itlneplqta vngfdtgila pgkhehsyte pflashhqil ahatavsiyr smykdnqgge
241 vglvvdcewa esnsdkiedk aaaakrlefq lgwylhplyy gdypevmrki lggglpkfse
301 edkellrnsl dfiglnhyss rfikhvtdsp aecyyykaqe ierlakwedg epigeraase
361 wlyvrpwglr kvlnyivqry nnpiiyvten gmddedssap lhemlddklr vryfkgylaa
421 vaqaikdgad vrgyfawsll dnfewaqgyt krfgliyvdy knglarhpks saywfmrflk
481 gdegkngke

Gene sequence：

1 atgatgaagg agaaattctt gaaggaacat ccatatttgc tggaaaagga ggtctctcgc
61 tctgattttc ctcctaattt tctctttggt gttgccactt ctgcctatca gattgaaggt
121 ggctgcaggg aaggtggtag aggtcctagt atatgggatg ctttttcaca caccaaagga
181 actattcttg atggaagcaa tggtgatgtg gcagtggatc attatcatcg atacaaggaa
241 gacattgaac tcatcgctaa gttggggttt gatgcttatc gattttcctt atcatggtct
301 cgcattttcc ctgatggttt gggaaccaaa gtcaatgaag aagggatagc attctataac
361 aatatcatta atgctcttct tgaaaagggt atagagccat atataactct gtaccattgg
421 gatctcccct tgcatcttca agagtcaatg ggagggtggt tgaataagga aattgtaaaa
481 tactttgcaa tctatgcaga cacttgcttt gcaagttttg gtgatagagt taagaaatgg
541 attactctaa atgagcctct ccaaacagca gtaaatggat ttgatactgg aatacttgct
601 cctggaaaac atgaacattc atatacagaa ccatttttgg cttcacacca ccagatcttg
661 gcccatgcaa cagctgtttc catataccgc agtatgtaca aagacaatca aggaggagaa
721 gtaggcttgg tggtggactg tgaatgggct gaatctaatt cagataaaat tgaagataaa
781 gctgctgctg caaaacggct tgagtttcag cttggatggt atttgcatcc tttatattat
841 ggagactatc ctgaagttat gcgtaaaata ctgggaggtg ggctcccaaa attctcagag
901 gaagataagg aattacttag gaactcactt gacttcattg gtctaaatca ctattcttca
961 agattcatca agcatgttac agatagccct gcagaatgct attactataa agcccaagaa
1021 attgagagac ttgctaaatg ggaagatggt gagccaatcg gcgagagggc agcatcagaa
1081 tggctctatg ttcgtccttg gggacttcgg aaggttctca attacatagt ccagagatac
1141 aataatccca taatttacgt tactgagaat ggtatggatg atgaagactc cagtgcccct
1201 ctccatgaaa tgctagatga caaactgaga gttcgctatt ttaaaggata ccttgctgca

1261 gttgctcagg caatcaaaga cggagcagat gtgaggggat attttgcatg gtcattgttg
1321 gacaattttg aatgggctca aggttatacc aagcgttttg gtttgatcta tgtggattac
1381 aagaatggac ttgctcgcca cccaaagtct tctgcttatt ggttcatgag gttcttgaaa
1441 ggtgatgaag ggaaaaatgg caaagagtga

Antibody name: WR-25

Protein name: **beta-cyanoalanine synthase, CYAS**

Plant species: *Hevea brasiliensis*

NCBI Accession No.: gi |326909405

Antibody tag sequence: CQRIRDLPKNLPGTK

Protein sequence:

1 matlrnllkk ksltsnelai rrfvsseaaa espsfaqrir dlpknlpgtk iktevsqlig
61 rtplvylnkm segcgayiav kqemmqptas ikdrpafsmi ndaekknlit pgktvliept
121 sgnmgismaf maamkgykmv ltmpsytsle rrvtmkafga elivtdptkg mggtvkkayd
181 llestpnafm lqqfsnpans kihfettgpe iwedtlghvd ifvmgigsgg tvsgvgqylk
241sqnpnvkiyg vepaesnvln ggkpgphqim gngvgfkpdi ldmdvmekvl evssedavkm
301 arrlaleegl mvgissgant vaalrlarmp enkgklivtv hpsfgeryls svlfeelrye
361 aanmqpvpvd

Gene sequence:

1 atggctactc ttaggaactt gttgaagaaa aaatctttaa cgtccaacga gcttgctata
61 aggaggttcg tctcttccga ggctgctgct gaatctcctt cttttgctca aagaatcagg
121 gatctgccca agaatctccc tggaactaaa atcaagactg aagtttctca acttattggg
181 agaactcccc ttgtttatct taacaaaatg agtgaaggat gtggagctta catagccgtc
241 aagcaagaga tgatgcaacc aactgccagc atcaaagaca ggccggcgtt ttcaatgatc
301 aatgatgcag aaaagaagaa tttaatcact cccgggaaga cggtcttgat agagccaaca
361 tctggtaata tggggattag tatggctttt atggcagcca tgaaaggata caagatggtt
421 ctaaccatgc cctcttacac aagcttggag agaagggtga ctatgaaggc atttggagct
481 gagctaattg tcactgatcc caccaagggg atgggtggaa cagttaagaa ggcctatgat
541 cttttggaat ccacaccaaa tgctttcatg ctacaacaat tttcaaatcc tgcaaattct
601 aagatccatt ttgaaacgac aggtcctgaa atttgggagg atacacttgg tcatgttgac
661 atctttgtaa tgggaatagg cagtggagga acagtctctg gcgttgggca gtaccttaaa
721 tctcaaaatc ctaatgttaa gatatatggg gtggagcctg ctgaaagtaa tgtgctcaac
781 ggtggtaaac caggtcctca tcaaattatg ggtaacggag ttggatttaa accagacata
841 ttggacatgg atgtaatgga aaaggttctt gaggttagca gtgaagatgc agtaaaaatg
901 gctaggagat tggcattgga ggaggggctt atggtgggaa tatcatctgg agccaacaca
961 gttgctgcac ttagacttgc tagaatgcca gagaacaaag gaaaactcat cgtgactgtt
1021 catccaagtt tcggggagcg atacttgtca tctgtcctgt ttgaagaact gagatatgag
1081 gctgcaaaca tgcaaccagt tccagttgac taa

Antibody name: WR-28

Protein name: ascorbate peroxidase, ACPX

Plant species: *Hevea brasiliensis*

NCBI Accession No.: gi |27449248

Antibody tag sequence: HPGREDKPEPPPEC

Protein sequence：

1 mtknypkvse eyqkaidkak rklrgfiaek gcaplmlria whsagtydan tktggpfgtm
61 rhaaeqahaa nngldiavrl lepikqqfpi lsyadfyqla gvvaveitgg peipfhpgre
121 dkpepppegr lpnatkgadh lrevfgktmg lsdkdivvls gghtlgrchk ersgfdgpwt
181 anplifdnsf ftellagqke gllqlptdtv lvtdpvfrpy vekyaadeda ffadyaeahv
241 klselgfaea

Gene sequence：

1 atgacgaaga actacccaaa agttagtgaa gagtaccaga aggccattga taaggccaag
61 aggaagctca ggggtttcat cgctgagaag ggctgtgctc ctctcatgct ccgtatcgca
121 tggcactcag ctggaactta cgacgcgaac accaagactg gaggtccatt tggaaccatg
181 aggcacgcag cggagcaggc ccatgctgct aacaatgggc tggatattgc tgtcagactc
241 cttgagccca tcaagcagca gttccctatc ctctcctatg ctgacttcta tcagcttgct
301 ggtgttgttg ccgttgagat cactggtggg cctgagatcc cattccaccc tggcagagag
361 gacaagcctg aaccacctcc agaaggtcgt ctgcctaatg ctactaaagg tgctgatcac
421 ttgagggagg tctttggcaa aaccatgggt ctcagtgaca aggatatcgt tgttctctct
481 ggtggccaca ccctgggaag gtgccacaag gagcgctctg gttttgacgg gccctggact
541 gctaacccac tcatctttga caattctttc ttcacggagc tcttggctgg acagaaggaa
601 ggccttctac aattgccaac tgacaccgtt cttgttaccg atcctgtctt ccgcccatat
661 gttgaaaaat atgctgctga tgaagatgca ttctttgctg attatgctga ggcccatgtg
721 aagctctccg agctggggtt tgctgaggct taa

Antibody name: WR-29

Protein name: **heat-shock protein 70, HSP70**

Plant species: *Hevea brasiliensis*

NCBI Accession No.: gi |186898205

Antibody tag sequence: EKYKAEDEEVKKKC

Protein sequence:

1 mapktegkai gidlgttysc vgvwqndrve iiandqgnrt tpsyvaftdt erligdaakn
61 qvamnpqntv fdakrligrr fsdpsvqsdm khwpfkvisg pgdkpmivvq ykgeekqfap
121 eeissmvltk mkeiaeaylg qtvknavitv payfndsqrq atkdagaiag vnvmriinep
181 taaaiaygld kkgsstgekn vlifdlgggt fdvslltiee gifevkatag dthlggedfd
241 nrlvnhfvae fkgkhkkdis tnaralrrlr tarerakrtl sstsqttiei dslyegidfy
301 atitrarfee lnmdlfrkcm epvekclrds kidksqvhdv vlvggstrip kvqqllqdif
361 ngkelcksin pdeavaygaa vqaailsgeg dekvqdllll dvtplslgie taggvmtvli
421 prnttiptkk eqifstysdn qpgvliqvye gerartkdnn llgkfeltgi ppaprgvpqi
481 nvcfdidang ivnvsaedkt agvknkitit ndkgrlskee iermvqeaek ykaedeevkk
541 kveaknslen yaynmrntvk ddkfagklap adkgkiekai detiewldrn qlaeveefed
601 klkeleglcn piiakmyqgg aggdvpvgga empnsnygkt ssggsgagpk ieevd

Gene sequence:

1 atggcgccaa aaactgaagg caaggccatt ggtatcgatc ttggcaccac ctacagctgc
61 gtgggtgtgt ggcagaacga ccgggttgag atcatagcca atgatcaggg caacagaact
121 actccttctt atgttgcctt cactgacacc gagcgtctca ttggggatgc agctaagaac
181 caagttgcta tgaaccctca aaacactgtc tttgatgcca aacgtctcat tggtaggcgg
241 ttttctgatc cttctgtgca gagcgacatg aagcactggc ctttcaaggt tatttctggt
301 cctggtgata agcctatgat tgtggtgcaa tacaaaggtg aagaaaagca atttgcgcct
361 gaggagattt cttctatggt gctaaccaag atgaaggaga ttgcagaggc ttatctgggt
421 cagacagtga agaatgccgt gatcacagtg cctgcttatt tcaatgactc gcaaaggcag
481 gccaccaagg atgctggtgc tattgcaggg gtgaacgtca tgagaattat caatgagcct
541 acagctgcag ccattgctta cggtttggac aagaaaggtt cgagtactgg agaaaagaac
601 gtgttgattt tcgatcttgg tggagggaca tttgatgttt ctcttctgac gatcgaggag
661 ggtatatttg aagtgaaggc aacagctgga gacacccacc ttggaggaga ggacttcgat
721 aataggcttg tcaaccattt cgttgcagag ttcaagggga agcacaagaa ggatattagt
781 actaatgcga gagccttgag aaggttgaga accgcccgcg agagggcaaa gaggactctg
841 tcttcaacct cgcaaacaac cattgagatt gattctctct acgaagggat tgatttctat
901 gcgaccatca ctagagcaag atttgaagag ctgaacatgg atttgtttag aaagtgcatg
961 gaacccgtgg agaaatgtct tcgtgactcc aagatcgata agagtcaagt tcatgacgtt
1021 gtgctcgttg gtgggtcaac aagaattcct aaagttcagc aacttttgca agatatcttc
1081 aacggaaagg agctctgcaa gagcataaac cccgacgagg ctgtcgctta tggagcagct

1141 gtccaagctg caattcttag tggtgaaggg gatgagaaag ttcaagattt acttctcttg
1201 gatgttactc ctctcagcct cggaattgag actgctggtg gtgtaatgac agtcttgatt
1261 ccaaggaaca ccactattcc taccaaaaaa gagcaaatct tctctacata ctctgataat
1321 caaccaggag tgcttattca ggtgtatgaa ggtgaaagag ctagaaccaa ggataataat
1381 cttcttggaa aattcgagct caccggaatc cctcctgcac ccagaggcgt tcctcagatt
1441 aatgtgtgtt tcgacattga cgccaatggt attgtgaatg tctctgctga ggataagact
1501 gctggagtga agaacaagat aacaatcact aacgataaag gaagattgag caaggaagag
1561 attgaaagaa tggtgcaaga agcagagaag tacaaagcag aggatgagga ggtgaagaag
1621 aaggtggagg ccaagaactc tttggagaac tacgcataca acatgagaaa tacagtgaag
1681 gatgacaagt tcgccggaaa attggctcca gccgacaagg ggaagattga aaaggcaatt
1741 gatgagacta ttgagtggtt ggacagaaac caattagcag aggtggagga gtttgaggac
1801 aagttgaagg agcttgaggg cttgtgcaat ccaattattg caaagatgta tcagggcggt
1861 gctgggggtg acgtaccagt gggtggcgcc gaaatgccga acagcaacta tggcaagact
1921 agctccggcg gttctggtgc cgggcccaag atcgaagaag ttgattaa

Antibody name: WR-30

Protein name: **aquaporin**

Plant species: *Hevea brasiliensis*

NCBI Accession No.: gi |307826678

Antibody tag sequence: CQSQDDKDYTEPPA

Protein sequence：

1 megkeedvrl gankyretqp igtsaqsqdd kdyteppaap lfepteltsw sfyragiaef
61 iatflflyis vltvmgvvka ptkcstvgiq giawsfggmi falvyctagi sgghinpavt
121 fglflarkls ltralyymvm qclgaicgag vvkgfegrhq ytllgggans vnpgytkgdg
181 lgaeivgtfv lvytvfsatd akrnardshv pilaplpigf avflvhlati pitgtginpa
241 rslgaaiifn kdkgwddhwi fwvgpfigaa laalyhqvvi raipfkk

Gene sequence：

1 atggagggca aggaagaaga tgttagattg ggagctaaca aatataggga gacgcagccc
61 attggtacgt cagctcagag ccaagatgac aaggactaca ctgaaccacc agcagcgccg
121 ctgttcgagc caacggagct cacttcttgg tccttttaca gggctggtat tgcagagttc
181 atagccactt tcttgttctt atacatctct gttttgactg tcatgggtgt agttaaggca
241 cccaccaagt gttcgactgt tgggattcag gggatagctt ggtcctttgg tggcatgatc
301 ttcgctcttg tctattgtac tgctggcatt tcaggaggtc acataaaccc ggcggtgacg
361 tttgggctgt ttttggcaag gaaactgtcc ttgacaaggg ctttgtacta catggtgatg
421 cagtgccttg gagccatatg tggtgctggt gtagtgaaag gatttgaagg gcgtcaccag
481 tatactttgt tgggtggtgg tgccaatagt gtgaacccag gttacaccaa aggtgatggg
541 cttggtgctg aaattgttgg cacctttgtt cttgtctaca ctgtcttctc tgctactgat
601 gccaaacgta atgccagaga ctcccatgtt cctattttgg cacctttgcc aattgggttc
661 gctgtgttct tggtgcactt ggctaccatc ccaattacag gaactggtat caacccagct
721 cgtagtcttg gtgcagcaat catcttcaac aaggacaagg gctgggatga tcactggatt
781 ttctgggtgg gtccattcat tggagcagca cttgcagctc tataccacca agttgtgatc
841 agagccatcc ctttcaagaa gtga

Antibody name: WR-31

Protein name: Geranylgeranyl diphosphate synthase, GGDS

Plant species: *Hevea brasiliensis*

NCBI Accession No.: gi |14325238

Antibody tag sequence: QEQLAGFDPEKAAPC

Protein sequence：

1 mssvnlgswv htsyvlnqat rsrsksksfs lpfnplksla isfayrkser pissvsaiit
61 keeetlqeeq nnpppsfdfk symlqkgnsi nqaleaaipl qepakihesm rysllaggkr
121 vrpalclaac elvggndsma mpaacavemi htmslihddl pcmdnddlrr gkptnhivfg
181 edvavlagda llafafehia vstlnvssar ivravgelak aigaeglvag qvvdinsegs
241 sevdleklef ihihktakll egavvlgail gggtdeevek lrkyardigl lfqvvddild
301 vtkssqelgk tagkdlvadk vtypkllgie ksrefaekln keaqeqlagf dpekaaplia
361 lanyiahrqn

Gene sequence：

1 atgagttcag tgaatttggg ctcatgggtt cacacctcct acgtcttaaa ccaagctacc
61 agatccagat ccaaatccaa atccttctct ctacctttca atcctctaaa aagtttagca
121 atttcctttg cttatagaaa atcagagcga cccatttcat ctgtctctgc gattattacc
181 aaggaagaag aaactcttca agaagagcag aataatccac caccctcttt tgatttcaaa
241 tcctacatgc tccaaaaagg caattccatt aaccaagctt tagaagctgc cattccactc
301 caagaacccg ctaaaattca cgagtctatg cgttattccc tcttggccgg cggcaagagg
361 gtacgaccgg ccctctgcct cgctgcgtgt gagcttgttg gtgggaatga ctccatggcg
421 atgcctgctg catgcgctgt ggaaatgatt catactatgt ctcttatcca tgatgacctc
481 ccttgcatgg ataacgacga tctccgccgt ggcaagccca ccaatcacat cgtgtttgga
541 gaggacgtgg cggttctcgc cggtgacgca ctcctagcat ttgcttttga acacatcgct
601 gtttctactt taaatgtttc ttctgctaga attgtccggg cagttgggga attagcgaag
661 gcgatcgggg cagaagggtt agttgctggc caagtagttg atataaattc tgagggctca
721 tctgaggtgg atttagagaa gcttgaattt attcacatcc acaagaccgc taagttgttg
781 gagggggctg tggtgctagg ggctatattg ggcggaggaa ccgatgagga agtggagaaa
841 ttgaggaaat atgctaggga tattgggttg ttgttccaag ttgttgacga tattcttgat
901 gtgactaaat catcccaaga attggggaaa actgcaggca aggacttggt ggcggacaag
961 gttacatatc ccaagctttt ggggattgag aagtcgaggg aatttgcaga gaagctgaat
1021 aaggaagctc aggagcagct ggctggattt gatcctgaaa aggcagctcc attgattgct
1081 ttggctaatt acatcgctca caggcaaaac taa

Supplementary Figure S7: **Primers used for RT-PCR**

Protein name: 14-3-3 protein

Spot No.: I-27

Accession No.: tr|F2YZ43|F2YZ43_HEVBR

Primer sequences:

Primer-up: CGTGGATGTTGAGGAGCTAACTG

Primer-down: CAGAAGTCCAGAGTGTCAGATTGTC

Protein name: (ACAT) Acetyl-CoA C-acetyltransferase

Spot No.: I-13

Accession No.: tr|A9ZMZ4|A9ZMZ4_HEVBR

Primer sequences:

Primer-up: GGTTGGATGCTTCTCAAGTTGATTAC

Primer-down: CAAGAGTTCGCCCCATCGTG

Protein name: (ACPX) Ascorbate peroxidase

Spot No.: I-228

Accession No.: tr|Q8GZP1|Q8GZP1_HEVBR

Primer sequences:

Primer-up: GGCTGGATATTGCTGTCAGACTC

Primer-down: CGGAAGACAGGATCGGTAACAAG

Protein name: (ADPF) actin-depolymerizing factor

Spot No.: S-170

Accession No.: gi|298362843

Primer sequences:

Primer-up: TGCGGCTACTGTATCCAAACC

Primer-down: CTGCTTCACCATCCCACAAAC

Protein name: (ABAS) Abscisic acid stress ripening-related protein 1

Spot No.: I-160

Accession No.: tr|Q6XNP8|Q6XNP8_HEVBR

Primer sequences:

Primer-up: GGCACAAGATAAAAGAGGAGGTAGC

Primer-down: GCGTATGGAGTTAAAAGGGATGG

Protein name: (ATPS) ATP synthase subunit beta

Spot No.: I-188

Accession No.: sp|P29685|ATPBM_HEVBR

Primer sequences:

Primer-up: GTTGGTCTAACTGGGCTAACTGTGG

Primer-down: TCTTGGTGGTTGTAATACGCTCTTG

Protein name: (CIAD)Cinnamyl alcohol dehydrogenase

Spot No.: I-254

Accession No.: tr|E9M774|E9M774_HEVBR

Primer sequences:

Primer-up: TGGTCCTATAATGATGTCTACACCGAT

Primer-down: CTTGTTCAACCCAAAGTGGCTAAG

Protein name: (CIBP)Citrate-binding protein

Spot No.: S-145

Accession No.: sp|Q39962|CBPR_HEVBR

Primer sequences:

Primer-up: GATCCAACTGATGGGTTCACTGAG

Primer-down: GCTTGATGTTTTTCCACCTTGATTC

Protein name: Copper transport protein ATOX1

Spot No.: I-578

Accession No.: tr|D4P094|D4P094_HEVBR

Primer sequences:

Primer-up: GAAAGGAAACGTGCAGCCAGAG

Primer-down: ACCGAGTGTCGTATAAGGGTGCT

Protein name: chitinase

Spot No.: D-72

Accession No.: gi|3451147

Primer sequences:

Primer-up: GCAACGAAGGAACTCTAACACAAAC

Primer-down: GAATCCGAGAAATCAGCACATCC

Protein name: caffeic acid 3-O-methyltransferase

Spot No.: D-125

Accession No.: gi|380468126

Primer sequences:

Primer-up: AGTTGATGTGGGCGGTAATAGTG

Primer-down: TGTCGGGTCCTCTCTTTTCCTC

Protein name: Cysteine protease

Spot No.: I-252

Accession No.: tr|Q155L4|Q155L4_HEVBR

Primer sequences:

Primer-up: CTTGTTCTTCGCTTCCACCTTGT

Primer-down: GGTCCGATTCTCCGAGTTATGCT

Protein name: Cis-prenyl transferase

Spot No.: I-351

Accession No.: tr|A9ZN23|A9ZN23_HEVBR

Primer sequences:

Primer-up: GGTCCCATCCCTACTCATCTTGC

Primer-down: CTCATACTCTGATCTGCTGCGGTC

Protein name: Cis-prenyl transferase OS=Hevea brasiliensis

Spot No.: I-1585

Accession No.: tr|Q8W3U4|Q8W3U4_HEVBR

Primer sequences:

Primer-up: GGAGGTGGTCATAAGGCTGGAT

Primer-down: TCTGCTGCGGTCTTGAGTGG

Protein name: Cu/Zn superoxide dismutase

Spot No.: D-17

Accession No.: gi|27449246

Primer sequences:

Primer-up: GTTATTACCAGCAGTGAGGGCATTAG

Primer-down: GACCTTCGTGAAAAACAACTGACC

Protein name: eukaryotic translation initiation factor 5A

Spot No.: S-91

Accession No.: gi|33325129

Primer sequences:

Primer-up: CGCAAGAATGGTTACATCGTC

Primer-down: TCCCTTCCACTCAATAGCAATC

Protein name: Eukaryotic translation initiation factor

Spot No.: I-98

Accession No.: tr|B9SJV6|B9SJV6_RICCO

Primer sequences:

Primer-up: CGCAAGAATGGTTACATCGTC

Primer-down: TCCCTTCCACTCAATAGCAATC

Protein name: Eukaryotic translation initiation factor 1Aa

Spot No.: I-673

Accession No.: tr|F8RW94|F8RW94_HEVBR

Primer sequences:

Primer-up: AAGGGAAAGGGAGGTAAGAATAGGA

Primer-down: GATAGTCACGCAGCCCAACAAGT

Protein name: eukaryotic translation elongation factor

Spot No.: D-8

Accession No.: gi|255565836

Primer sequences:

Primer-up: TGCCACGGCTCAGAAGTATCG

Primer-down: GCAACCTTACATTGAACAGCCAC

Protein name: Enolase 1

Spot No.: D-6

Accession No.: gi|14423688

Primer sequences:

Primer-up: CGTTGCTAACCTCGCTGGTAAC

Primer-down: GCATAGTGCTCCCAGTCATCTTG

Protein name: Esterase

Spot No.: D-95

Accession No.: gi|51315784

Primer sequences:

Primer-up: GATTTTATCGCCGAGAGTTTCAATC

Primer-down: ACCGTCGTCTGCTGTAACTGTATCT

Protein name: Elicitor-responsive protein

Spot No.: I-30

Accession No.: tr|F8SKC5|F8SKC5_HEVBR

Primer sequences:

Primer-up: AATGCCTCTAGGAACTGTTGAAGTC

Primer-down: ACCGAAAATCGTATCCATCCAC

Protein name: Farnesyl diphosphate synthase

Spot No.: I-133

Accession No.: tr|Q8L7F4|Q8L7F4_HEVBR

Primer sequences:

Primer-up: ATGGGTTGAGCGGATGTTGG

Primer-down: CTGGGAATGTGATTGCGAAGC

Protein name: Gamma-glutamylcysteine synthetase

Spot No.: I-1621

Accession No.: tr|D5LYI6|D5LYI6_HEVBR

Primer sequences:

Primer-up: TGCCAGCATTTTGGGTAGGAT

Primer-down: GTTCTAACCACCTCAGCCACTTCA

Protein name: Beta-1,3-glucanase

Spot No.: I-2

Accession No.: tr|D1M8S7|D1M8S7_HEVBR

Primer sequences:

Primer-up: ATCTCCAAAGCCTTACCAATCC

Primer-down: TGGTGAAGTGAACAAAGCATAGG

Protein name: Glutaredoxin

Spot No.: I-264

Accession No.: tr|B3FNP8|B3FNP8_HEVBR

Primer sequences:

Primer-up: TGGATACTGAGGGCGATGGAA

Primer-down: CTTTTAAGCAGAAGCCTTAGCAAGAG

Protein name: Glyoxylase I

Spot No.: I-812

Accession No.: tr|E9KK00|E9KK00_HEVBR

Primer sequences:

Primer-up: CTCCAAGTGACCCAGTTGAAAGA

Primer-down: GAAATACCAATATGTCCAAAGCCAC

Protein name: (GLUS) glutamine synthetase

Spot No.: S-56

Accession No.: gi|2213877

Primer sequences:

Primer-up: TGGTACGGCATTGAGCAAGAATAC

Primer-down: AGCAACGCCCCATAAGAAAGTG

Protein name: (GSTF) glutathione-S-transferase tau 1

Spot No.: D-53

Accession No.: gi|333690873

Primer sequences:

Primer-up: ATGGACTACAAAGGGAGATGAGCA

Primer-down: GCACCTCTTAGCCCAAGCAATC

Protein name: Pro-hevein

Spot No.: I-817

Accession No.: sp|P02877|HEVE_HEVBR

Primer sequences:

Primer-up: CTATGTTGTAGCCAGTATGGGTGG

Primer-down: GTAGTTCACTGTAAGATGACCTCGTTC

Protein name: Hevein

Spot No.: I-1357

Accession No.: tr|Q7M1L9|Q7M1L9_HEVBR

Primer sequences:

Primer-up: CTATGTTGTAGCCAGTATGGGTGG

Primer-down: GTAGTTCACTGTAAGATGACCTCGTTC

Protein name: Hevamine

Spot No.: D-93

Accession No.: gi|157831407

Primer sequences:

Primer-up: CATAGAGCATGGTTCAACCCTGTAC

Primer-down: GACCAAAGCATAACACCTCCGTAC

Protein name: (Hev b5) Major latex allergen Hev b 5

Spot No.: I-5

Accession No.: sp|Q39967|ALL5_HEVBR

Primer sequences:

Primer-up: CAAGAAACCGCCGATGCTACA

Primer-down: CGGAACTTCTGTGGTGGCTGTC

Protein name: (HMGR) Hydroxymethylglutaryl coenzyme A reductase

Spot No.: I-119

Accession No.: tr|Q547W6|Q547W6_HEVBR

Primer sequences:

Primer-up: TCCGTCGTGGATGGGAAGAT

Primer-down: TGGTCGCCATTGGAACAGAGT

Protein name: (HMGS) Hydroxymethylglutaryl coenzyme A synthase

Spot No.: I-22

Accession No.: tr|Q944F8|Q944F8_HEVBR

Primer sequences:

Primer-up: CAGTGCGGTCTATGCAGAGGGT

Primer-down: GCAAGAATCAAGAGCCATGAGGT

Protein name: (HMGS-2) HMG-CoA synthase 2

Spot No.: I-1434

Accession No.: tr|Q6QLW8|Q6QLW8_HEVBR

Primer sequences:

Primer-up: TGATCCTAACCAAATCGGTCGTC

Primer-down: GCGTCCATCCCATGAATTACTCT

Protein name: Heat shock protein

Spot No.: I-11

Accession No.: tr|Q71EE1|Q71EE1_HEVBR

Primer sequences:

Primer-up: GGAGAATATGGCTGGACTGCTAAC

Primer-down: CGTCAATGCTCAGACCCAGTTTC

Protein name: latex protein allergen Hev b 7

Spot No.: D-76

Accession No.: gi|6707018

Primer sequences:

Primer-up: TTCTTCTCCCAGTCATCTTCTCATC

Primer-down: CTTTCAAGCCTGCCAGTATCC

Protein name: (LAP1) latex abundant protein 1

Spot No.: D-111

Accession No.: gi|37901124

Primer sequences:

Primer-up: ACTATGATTATCCCGACTTCACCTG

Primer-down: TCACATAGATTGCACAACGGAAC

Protein name: (LAC) latex cystatin

Spot No.: D-102

Accession No.: gi|268321205

Primer sequences:

Primer-up: GGCAAAACTAGGAGGTGTTAAGGAAG

Primer-down: GCTGTAGAGTCTGAAGGGGCATC

Protein name: (MEVD) Mevalonate disphosphate decarboxylase

Spot No.: I-18

Accession No.: tr|Q944G0|Q944G0_HEVBR

Primer sequences:

Primer-up: CACCACAGGAATGCGTGAGACT

Primer-down: CGTTCATGTAGAAAATTGGAGGACA

Protein name: (MEVK) Mevalonate kinase

Spot No.: I-1957

Accession No.: tr|Q944G2|Q944G2_HEVBR

Primer sequences:

Primer-up: TCTGATCTTCCACTGGGTTCAGG

Primer-down: CTTGATGCGAGTCAGATTACCAGAC

Protein name: MYC2

Spot No.: I-159

Accession No.: tr|D2CRK4|D2CRK4_HEVBR

Primer sequences:

Primer-up: AAGAGGAAGAACCCAACTGAACG

Primer-down: ATCGGTGCTCTGATTGTCGGT

Protein name: (NUDK) nucleoside diphosphate kinase 1

Spot No.: S-93

Accession No.: gi|312985291

Primer sequences:

Primer-up: CTAATCACTGTGGAGCGCTTG

Primer-down: CGGGTGAAGGCTGCTTGA

Protein name: Invertase 2

Spot No.: I-50

Accession No.: tr|E9KF95|E9KF95_HEVBR

Primer sequences:

Primer-up: CACCAGAGGCGGTCTTGATTACT

Primer-down: TCAGAAAAGCCAGGGCACTAGG

Protein name: (PDBP) Pyridoxal biosynthesis protein PDX1

Spot No.: I-150

Accession No.: sp|Q39963|PDX1_HEVBR

Primer sequences:

Primer-up: AGTCCGTTACCATCCCCGTCA

Primer-down: CATTCCCTGTTCCTGCTTCACC

Protein name: (PHOT)Phosphoglyceride transfer family protein

Spot No.: I-175

Accession No.: tr|Q6J6I5|Q6J6I5_HEVBR

Primer sequences:

Primer-up: GATTTGATGAGAAGCCAACCCAC

Primer-down: CATATTAGCCTGGTTGCTTTAATCG

Protein name: (PROI) Protease inhibitor protein

Spot No.: I-366

Accession No.: tr|B3FNP9|B3FNP9_HEVBR

Primer sequences:

Primer-up: TCGGGACAAACGGGGACAT

Primer-down: GGTAATAAATTCGTTGTTTAGCCAATG

Protein name: (PPCI) Peptidyl-prolyl cis-trans isomerase

Spot No.: I-33

Accession No.: tr|B3FNQ1|B3FNQ1_HEVBR

Primer sequences:

Primer-up: GCGGATACAACGCCACGAAC

Primer-down: CCCTCCACAACTCTACCAAACACC

Protein name: Profilin-1

Spot No.: I-567

Accession No.: sp|O65812|PROF1_HEVBR

Primer sequences:

Primer-up: CTGCCATTATGAGTGACTTTGACG

Primer-down: TGTCTTCCTAACAGTAACACCACCAG

Protein name: prohevein

Spot No.: D-10

Accession No.: gi|2832430

Primer sequences:

Primer-up: GAAGGTGTTGGTGGTGGAAGTG

Primer-down: TGATGATTTCATAACGGAGAATAGAGG

Protein name: Pseudo-hevein

Spot No.: D-140

Accession No.: tr|Q6KF83|Q6KF83_HEVBR

Primer sequences:

Primer-up: GATGGGATTTGAACGCTGTAAGTG

Primer-down: TGGAGAATAGAGGGTTGAAGGAATC

Protein name: Rab4

Spot No.: I-227

Accession No.: tr|F2VXU6|F2VXU6_HEVBR

Primer sequences:

Primer-up: CTTCCTCTTGCCTGTTGCCTCT

Primer-down: GCAGCTTAATTGTCTTGCCATCC

Protein name: (REF-1) rubber elongation factor

Spot No.: D-85

Accession No.: gi|38122474

Primer sequences:

Primer-up: CAAGGACAAGTCTGGTCCATTC

Primer-down: TATGAACATCCAAAACACACGAC

Protein name: Rubber elongation factor

Spot No.: D-139

Accession No.: gi|132270

Primer sequences:

Primer-up: CAAAGACAAATCTGGTCCACTG

Primer-down: AAACATAGTCTCAACACTCAGGATG

Protein name: (SRPP-1) small rubber particle protein

Spot No.: D-99

Accession No.: gi|29170601

Primer sequences:

Primer-up: CCGTTGAAGCCTGGGGTC

Primer-down: CCACATCCAAAACACACCACC

Protein name: Small rubber particle protein

Spot No.: I-66

Accession No.: tr|Q84T87|Q84T87_HEVBR

Primer sequences:

Primer-up: CGTGTTCCGCCAGTTGTCAAG

Primer-down: GTAGGCACCAAAGGCAAATAAGAG

Protein name: (SRPP-3) Small rubber particle protein

Spot No.: D-52

Accession No.: gi|14423933

Primer sequences:

Primer-up: TGAAGAGGTGGAGGAAGAGAGG

Primer-down: CCACATCCAAAACACACCACC

Protein name: (TMAP) Translation machinery-associated protein

Spot No.: I-643

Accession No.: tr|D9IZZ6|D9IZZ6_HEVBR

Primer sequences:

Primer-up: AGCAAGGTGGAAAAGCAAAGC

Primer-down: CTTGAGCCCAGAACCTCCGA

Protein name: Ubiquitin-protein ligase 2a

Spot No.: I-943

Accession No.: tr|F8RWT0|F8RWT0_HEVBR

Primer sequences:

Primer-up: AGACTGATGAGGGATTTTAGGAGGT

Primer-down: TGACTGGATTGATGTGAGTATGGC

Protein name: (VHA-F) V-type proton ATPase subunit F

Spot No.: I-687

Accession No.: tr|B8Y6I1|B8Y6I1_HEVBR

Primer sequences:

Primer-up: TGCTGATGAGGACTCAGTAGTTGGA

Primer-down: CCTGTGCAGGATCATAAGGATGG

Protein name: (50KP) 50 kDa protein; major latex allergen Hev b 4

Spot No.: D-2

Accession No.: gi|37719658

Primer sequences:

Primer-up: GGAAGATTTTCTGATGGTCGCAC

Primer-down: CACGATATGTCGAATTGCCACAG

Protein name: (VHAE) V-type proton ATPase subunit E

Spot No.: D-58

Accession No.: gi|356528948

Primer sequences:

Primer-up: ATGGTCAGATTCATCCGTCAGG

Primer-down: TGTGGTTAATGCCATGAAAGAGG

Protein name: calmodulin

Spot No.: D-105

Accession No.: gi|354318

Primer sequences:

Primer-up: TCACTGGGACAGAATCCTACCG

Primer-down: CTTCTCGCCAAGGTTTGTCATC

Protein name: (CDCP) cell division cycle protein

Spot No.: D-130

Accession No.: gi|351727028

Primer sequences:

Primer-up: GGTGGTGTTAGAAAACAGATGGC

Primer-down: CCAATGACAATAACATGAGCACG

The abbreviations for the proteins were:

ATPS, ATP synthase subunit beta; ACAT, Acetyl-CoA C-acetyltransferase; REF, rubber elongation factor; SRPP, small rubber particle protein; VHAF, V-type proton ATPase subunit; ACPX, Ascorbate peroxidase; GGCS, Gamma-glutamylcysteine synthetase; VHAE, V-type proton ATPase subunit E; GLUS, glutamine synthetase; GSTF, glutathione-S-transferase;HSP70, heat shock protein 70; PDBP, Pyridoxal biosynthesis protein; CAMT, caffeic acid 3-O-methyltransferase;CYSP,Cysteine protease; CIPT, Cis-prenyl transferase; ETIF, eukaryotic translation initiation factor; ETEF, eukaryotic translation elongation factor; ELRP, Elicitor-responsive protein; LAC, latex cystatin; TMAP, Translation machinery-associated protein; COPT, Copper transport protein; 50KP, 50 kDa protein; Gluc, beta-1,3-glucanase; CDCP, cell division cycle protein; ABAS, Abscisic acid stress ripening-related protein; ADPF, actin-depolymerizing factor; PROI, Protease inhibitor protein; HMGR, Hydroxymethylglutaryl coenzyme A reductase; HMGS, Hydroxymethylglutaryl coenzyme A synthase; PPCI, Peptidyl-prolyl cis-trans isomerase; MEVD, Mevalonate disphosphate decarboxylase; MEVK, Mevalonate kinase; ProH, prohevein; PseuH, Pseudo-hevein; FADS, Farnesyl diphosphate synthase; GLUD, Glutaredoxin; LAP, latex abundant protein; CIAD, Cinnamyl alcohol dehydrogenase; CIBP, Citrate-binding protein; SOD, Superoxide dismutase; NUDK, nucleoside diphosphate kinase; PHOT, Phosphoglyceride transfer family protei; SUCT, sucrose transporter; PHOK, phosphomevalonate kinase; HYDL, hydroxynitrile lyase; CDPK, calcium-dependent protein kinase; ETHI, ethylene-inducible protein; GLUR, glutathione reductase; LACG, latex cyanogenic beta glucosidase; CYAS, beta-cyanoalanine synthase; GGDS, geranylgeranyl diphosphate synthase.

Supplementary Table S1 MS identification of high abundant rubber latex proteins 2-DE gels

Spot No.[a]	Vol%[b]	Exper.[c] *p*I/M*r*	Thero.[d] *p*I/M*r*	M.S.[e] Score	NCBI No.[f]	Plant species	Protein name
1	4.47	4.96/14	5.04/14.7	122	132270	*H. brasiliensis*	Rubber elongation factor protein
2	4.18	4.92/13	5.04/14.7	142	132270	*H. brasiliensis*	Rubber elongation factor protein
3	3.09	4.88/13	5.04/14.7	95	132270	*H. brasiliensis*	Rubber elongation factor protein
4	2.69	4.8/22	4.8/22.3	119	14423933	*H. brasiliensis*	Small rubber particle protein
5	1.12	4.9/23	4.8/22.3	122	14423933	*H. brasiliensis*	Small rubber particle protein
6	1.24	4.82/23	4.8/22.3	135	14423933	*H. brasiliensis*	Small rubber particle protein
7	0.0296	4.72/14	4.61/12.8	[121]	29170601	*H. brasiliensis*	small rubber particle protein
8	0.034	4.74/14	4.61/12.8	[110]	29170601	*H. brasiliensis*	small rubber particle protein
9	0.0969	4.88/26	4.79/29.5	93	388503664	*L. japonicus*	unknown
10	0.434	4.98/40	5.0/43.0	209	3288200	*H. brasiliensis*	latex allergen
11	0.834	5.01/40	5.0.43.1	172	6707018	*H. brasiliensis*	latex protein allergen Hev b 7
12	0.214	5.07/49	5.01/46.4	82	4235430	*H. brasiliensis*	latex-abundant protein
13	0.135	5.05/49	5.01/46.6	96	4235430	*H. brasiliensis*	latex-abundant protein
14	0.335	5.09/54	5.07/71.1	103	20559	*P. hybrida*	hsp70 (AA 6 - 651)
15	0.513	5.16/40	5.31/42.0	142	58013197	*I. tinctoria*	actin
16	0.0655	5.21/52	5.2/69.1	174	225429795	*V. vinifera*	V-type proton ATPase, subunit A
17	0.137	5.29/47	7.56/59.9	92	357480067	*M. truncatula*	Leucine aminopeptidase
18	0.139	5.31/44	5.91/30.8	81	219885949	*Z. mays*	unknown
19	0.309	5.28/33	5.93/34.3	[101]	242059605	*S. bicolor*	hypothetical protein
20	0.145	5.18/15	8.01/11.2	[86]	30575570	*C. paradisi*	HSP19 class II, partial
21	0.458	5.33/16	5.73/15.7	83	27449246	*H. brasiliensis*	Cu/Zn superoxide dismutase
22	0.656	5.61/15	8.29/35.1	[60]	37806305	*O. sativa*	hypothetical protein
23	0.0912	5.55/33	9.46/35.3	85	10946499	*H. brasiliensis*	beta-1,3-glucanase
24	0.363	5.62/36	6.01/36.0	82	78216493	*M. domestica*	cytosolic malate dehydrogenase
25	0.567	5.77/32	6.41/36.0	[81]	257219562	*J. curcas*	annexin-like protein
26	0.852	5.69/27	8.72/34.1	[56]	3451147	*H. brasiliensis*	chitinase
27	0.442	5.75/30	9.45/38.9	97	4469175	*H. brasiliensis*	beta-1,3-glucanase
28	0.652	6.89/33	9.4/41.5	99	124365253	*H. brasiliensis*	beta-1,3-glucanase
29	0.803	6.85/34	9.4/41.5	109	124365253	*H. brasiliensis*	beta-1,3-glucanase
30	0.728	6.75/33	7.1/36.9	86	255540341	*R. communis*	glyceraldehyde 3-phosphate dehydrogenase
31	0.447	6.87/35	7.7/36.8	121	4539543	*N. tabacum*	glyceraldehyde-3-phosphate dehydrogenase
32	0.139	5.6/45	5.68/51.9	99	32527831	*P. tremuloides*	UDP-glucose pyrophosphorylase
33	0.104	5.55/39	5.0/43.1	171	6707018	*H. brasiliensis*	latex protein allergen Hev b 7
34	0.111	5.49/48	5.49/48.0	123	158144895	*G. hirsutum*	enolase
35	0.131	4.95/40	5.0/43.0	[81]	3288200	*H. brasiliensis*	latex allergen
36	0.0215	4.91/39	5.0/43.0	[138]	1916805	*H. brasiliensis*	latex patatin homolog
37	0.122	5.03/40	5.12/43.0	152	41581137	*H. brasiliensis*	latex allergen hev b 7.02
38	0.0897	5.06/40	5.12/43.0	142	41581137	*H. brasiliensis*	latex allergen hev b 7.02
39	0.0134	5.11/72	5.13/90.4	136	255556934	*R. communis*	Transitional endoplasmic reticulum ATPase
40	0.183	5.16/42	5.31/41.9	125	149938964	*A. deliciosa*	ACT1
41	0.0147	5.39/46	9.34/41.4	83	159489771	*C. reinhardtii*	predicted protein

42	0.0412	5.46/44	5.57/48.0	97	14423688	*H. brasiliensis*	Enolase 1
43	0.0132	5.54/62	5.62/111	90	23503558	*L. japonicus*	phosphoenolpyruvate carboxylase
44	0.0841	5.51/38	9.61/62.6	82	382929047	*H. hirsuta*	maturase K (chloroplast)
45	0.142	5.52/34	9.45/38.9	156	4469175	*H. brasiliensis*	beta-1,3-glucanase
46	0.045	5.65/33	9.45/38.9	126	4469175	*H. brasiliensis*	beta-1,3-glucanase
47	0.0134	5.65/27	6.18/35.9	[65]	225438145	*V. vinifera*	malate dehydrogenase, cytoplasmic
48	0.177	5.63/28	6.18/35.9	[85]	225438145	*V. vinifera*	malate dehydrogenase, cytoplasmic
49	0.0563	5.2/33	6.5/32.1	[75]	255552291	*R. communis*	short chain dehydrogenase, putative
50	0.057	4.75/15	4.61/12.8	[240]	29170601	*H. brasiliensis*	small rubber particle protein
51	0.638	5.05/13	5.04/14.7	103	132270	*H. brasiliensis*	Rubber elongation factor protein
52	0.339	5.15/13	5.04/14.7	115	132270	*H. brasiliensis*	Rubber elongation factor protein
53	0.0984	5.28/17	5.57/17.5	[61]	115187464	*A. hypogaea*	thioredoxin fold
54	0.0297	5.64/16	6.22/34.3	84	34538473	*H. vulgare*	caleosin 1
55	0.201	5.72/15	9.57/19.2	88	225440278	*V. vinifera*	hypothetical protein
56	0.0897	5.07/54	5.81/39.5	83	2213877	*H. brasiliensis*	glutamine synthetase
57	0.0301	5.1/54	5.21/71.5	102	172050753	*C. spinosa*	70 kDa heat shock protein
58	0.0356	5.12/54	5.18/71.9	[151]	762844	*S. lycopersicum*	Hsc70
59	0.0783	5.0/57	4.98/80.4	107	356552478	*G. max*	heat shock cognate protein 80-like
60	0.0132	5.01/56	5.07/52.1	[51]	356510919	*G. max*	UDP-glycosyltransferase 75D1-like
61	0.0163	5.03/49	5.49/47.1	144	255560725	*R. communis*	dead box ATP-dependent RNA helicase
62	0.0271	5.06/46	5.01/46.4	[142]	4235430	*H. brasiliensis*	latex-abundant protein
63	0.0401	4.91/46	4.65/41.4	[76]	255578278	*R. communis*	hypothetical protein
64	0.0176	5.14/46	5.15/47.1	[98]	5302811	*A. thaliana*	serine protease-like protein
65	0.0171	5.13/51	5.85/63.3	102	2506277	*P. sativum*	60 kDa chaperonin subunit beta
66	0.0193	5.16/54	5.27/72.0	88	255543357	*R. communis*	heat shock protein, putative
67	0.025	5.18/48	4.54/46.1	[91]	224100473	*P. trichocarpa*	predicted protein
68	0.0265	5.21/48	5.72/56.3	84	31580730	*H. brasiliensis*	latex cyanogenic beta glucosidase
69	0.0379	5.27/44	5.44/50.1	83	2501850	*N. tabacum*	GDP dissociation inhibitor
70	0.0152	5.3/44	5.44/50.1	[202]	2501850	*N. tabacum*	GDP dissociation inhibitor
71	0.549	5.21/43	5.42/47.2	147	359478860	*V. vinifera*	26S protease regulatory subunit 6B
72	0.126	5.13/42	5.28/47.1	[128]	224071449	*P. trichocarpa*	phospholipase A
73	0.0841	5.12/40	5.37/41.9	178	32186912	*G. hirsutum*	actin
74	0.0304	4.98/34	4.79/48.0	[70]	297816956	*A. lyrata*	hypothetical protein
75	0.0404	4.9/32	4.72/28.9	[74]	3264769	*P. armeniaca*	late embryogenesis-like protein
76	0.0574	4.93/32	5.24/42.0	81	168066110	*P. patens*	predicted protein
77	0.0683	4.89/30	4.79/29.5	109	388503664	*L. japonicus*	unknown
78	0.0174	5.0/35	4.84/24.3	[71]	115468882	*O. sativa*	Os06g0608500
79	0.0627	5.06/33	5.51/61.1	[104]	356532109	*G. max*	phosphoglycerate mutase
80	0.0124	5.05/31	5.11/59.2	90	224056489	*P. trichocarpa*	predicted protein
81	0.185	5.14/34	6.5/32.1	[174]	255552291	*R. communis*	short chain dehydrogenase, putative
82	0.133	5.29/38	5.49/39.3	91	2073448	*L. japonicus*	glutamine synthetase
83	0.0563	5.1/31	6.07/27.5	[204]	192912956	*E. guineensis*	aluminum-induced protein
84	0.0517	5.06/28	5.12/32.9	[254]	255559601	*R. communis*	alpha-soluble nsf attachment protein
85	0.0808	4.98/27	5.84/27.4	[69]	224099853	*P. trichocarpa*	predicted protein

86	0.438	5.17/21	5.06/19.6	[410]	38122474	*H. brasiliensis*	rubber elongation factor
87	0.0478	5.21/22	5.06/19.6	[226]	38122474	*H. brasiliensis*	rubber elongation factor
88	0.0734	5.13/21	5.06/19.6	116	38122474	*H. brasiliensis*	rubber elongation factor
89	0.0575	5.14/23	5.06/19.6	99	38122474	*H. brasiliensis*	rubber elongation factor
90	1.88	4.62/19	4.06/15.2	[496]	334854634	*H. brasiliensis*	elicitor-responsive protein
91	0.156	5.35/17	5.6/17.7	[95]	33325129	*H. brasiliensis*	eukaryotic translation initiation factor 5A
92	0.0403	5.37/16	5.39/18.0	[180]	224144943	*P. trichocarpa*	predicted protein
93	0.299	6.68/13	6.85/16.3	84	312985291	*H. brasiliensis*	nucleoside diphosphate kinase 1
94	0.376	6.74/16	5.63/22.7	96	123062	*H. brasiliensis*	Pro-hevein
95	0.274	6.61/15	7.77/20.7	[70]	313586569	*H. brasiliensis*	hypothetical protein 19
96	0.0897	6.65/14	7.77/20.7	94	313586569	*H. brasiliensis*	hypothetical protein 19
97	0.414	6.78/16	8.94/40.7	84	4835766	*A. thaliana*	transfactor (WERBP-1)
98	0.0367	5.42/22	5.06/19.6	99	38122474	*H. brasiliensis*	rubber elongation factor
99	0.107	5.34/24	5.71/26.1	[73]	3377751	*M. crystallinum*	glutathione S-transferase
100	0.0804	5.35/26	6.17/27.5	[49]	1709761	*S. oleracea*	Proteasome subunit alpha type-4
101	0.0483	5.47/26	5.78/27.5	[434]	27449248	*H. brasiliensis*	ascorbate peroxidase
102	0.142	5.48/26	6.0/27.5	[193]	211906460	*G. hirsutum*	triosephosphate isomerase
103	0.0357	5.22/21	5.06/19.6	125	38122474	*H. brasiliensis*	rubber elongation factor
104	0.345	5.75/19	8.72/34.1	153	3451147	*H. brasiliensis*	chitinase
105	0.15	5.75/23	8.44/29.9	93	157831407	*H. brasiliensis*	Chain A, Crystal Structures Of Hevamine
106	0.231	5.74/24	8.44/29.9	99	157831407	*H. brasiliensis*	Chain A, Crystal Structures Of Hevamine
107	0.148	5.77/20	8.72/34.1	83	3451147	*H. brasiliensis*	chitinase
108	0.0327	5.52/33	5.89/27.9	[89]	3127890	*C. arietinum*	cysteine synthase, O-acetyl-lyase
109	0.0761	5.39/37	5.44/40.0	[163]	114199044	*M. domestica*	caffeic acid O-methyltransferase
110	0.0405	5.38/44	5.57/48.0	158	14423688	*H. brasiliensis*	Enolase 1
111	0.0239	5.39/44	5.57/48.0	175	14423688	*H. brasiliensis*	Enolase 1
112	0.0339	5.38/44	6.05/25.1	85	226897734	*T. flavum*	norcoclaurine 6-O-methyltransferase
113	0.0262	5.38/49	5.53/54.1	[49]	255565071	*R. communis*	conserved hypothetical protein
114	0.0502	5.47/51	5.52/61.0	96	1346735	*R. communis*	Phosphoglyceromutase
115	0.0152	5.51/61	5.87/95.0	141	255565836	*R. communis*	eukaryotic translation elongation factor
116	0.0926	5.02/39	5.0/43.1	147	6707018	*H. brasiliensis*	latex protein allergen Hev b 7
117	0.0363	5.05/39	5.0/43.9	[59]	51315784	*H. brasiliensis*	Esterase
118	0.0152	5.29/21	5.06/19.6	98	38122474	*H. brasiliensis*	rubber elongation factor
119	0.0968	5.34/46	5.41/47.8	[51]	3023685	*A. glutinosa*	Enolase
120	0.0518	5.28/41	4.83/22.0	81	351723039	*G. max*	uncharacterized protein
121	0.0992	5.02/27	7.63/31.6	[55]	255554865	*R. communis*	lactoylglutathione lyase, putative
122	0.139	5.35/26	5.59/18.4	[83]	118485535	*P. trichocarpa*	unknown
123	0.152	5.51/26	5.93/27.6	86	15225839	*A. thaliana*	proteasome subunit alpha type-3
124	0.179	5.49/23	6.06/23.0	81	10862818	*H. brasiliensis*	IgE-binding protein Mn SOD
125	0.153	5.17/24	7.7/25.7	[53]	1737447	*E. globulus*	auxin-induced protein
126	0.104	4.45/15	4.61/12.8	[97]	29170601	*H. brasiliensis*	small rubber particle protein
127	0.119	5.46/13	5.64/20.9	[84]	2832430	*H. brasiliensis*	prohevein
128	0.065	5.55/14	6.82/15.0	[68]	224054224	*P. trichocarpa*	predicted protein
129	0.178	5.31/12	5.89/13.3	[61]	329750601	*H. brasiliensis*	thioredoxin H-type 2

130	0.532	5.01/11	5.45/11.2	81	268321205	*H. brasiliensis*	latex cystatin
131	1.01	5.02/13	5.04/14.7	[539]	132270	*H. brasiliensis*	Rubber elongation factor protein
132	0.105	5.45/13	5.04/14.7	138	132270	*H. brasiliensis*	Rubber elongation factor protein
133	0.117	5.16/15	6.4/8.6	81	242083244	*S. bicolor*	hypothetical protein
134	0.0976	4.94/13	4.61/12.8	[85]	29170601	*H. brasiliensis*	small rubber particle protein
135	0.0865	4.86/15	4.61/12.8	[493]	29170601	*H. brasiliensis*	small rubber particle protein
136	0.448	4.13/13	4.1/16.9	[128]	354318	*T. aestivum*	calmodulin
137	0.0284	4.12/21	4.8/22.3	85	14423933	*H. brasiliensis*	Small rubber particle protein
138	0.0653	4.45/24	4.8/22.3	165	14423933	*H. brasiliensis*	Small rubber particle protein
139	0.0351	5.36/47	5.57/48.0	107	14423688	*H. brasiliensis*	Enolase 1
140	0.149	4.87/19	5.04/14.7	[52]	132270	*H. brasiliensis*	Rubber elongation factor protein
141	0.0517	5.38/45	5.57/48.0	165	14423688	*H. brasiliensis*	Enolase 1
142	0.083	5.43/44	5.92/48.1	[766]	14423687	*H. brasiliensis*	Enolase 2
143	0.115	5.01/26	5.48/25.6	[52]	333690873	*H. brasiliensis*	glutathione-S-transferase tau 1
144	0.0957	5.33/53	8.78/43.5	82	242080619	*S. bicolor*	hypothetical protein
145	0.101	5.09/15	5.95/17.6	[87]	140083605	*R. hybrid*	cytosolic class II small HSP17.5
146	0.0217	4.02/41	5.01/14.6	[88]	37901124	*H. brasiliensis*	latex abundant protein 1
147	0.0256	4.35/40	4.53/38.0	[173]	359806300	*G. max*	uncharacterized protein
148	0.0301	4.28/38	4.53/38.1	[166]	37625031	*V. aestivalis*	ankyrin-repeat protein
149	0.0356	4.39/38	4.45/37.5	[71]	13310811	*N. tabacum*	ankyrin-repeat protein HBP1
150	0.518	5.18/42	5.64/42.2	[180]	129916	*T. aestivum*	Phosphoglycerate kinase
151	0.0258	4.31/36	4.5/25.3	[117]	378464888	*A. mongolicus*	translation elongation factor
152	0.0335	4.43/32	4.5/25.1	[107]	225456295	*V. vinifera*	elongation factor 1-delta-like
153	0.0201	4.83/30	5.26/35.7	[132]	22261807	*S. tuberosum*	Light-induced protein
154	0.0125	4.89/31	4.82/28.9	83	345103803	*G. thurberi*	14-3-3-like protein, partial
155	0.0549	5.08/26	4.76/29.9	[384]	326694865	*H. brasiliensis*	14-3-3 protein 2
156	0.0563	4.78/33	5.02/30.9	[53]	225458231	*V. vinifera*	proteasome subunit alpha
157	0.0338	4.89/31	5.69/32.6	[80]	211906514	*G. hirsutum*	lactoylglutathione lyase
158	0.186	5.02/33	5.5/33.2	80	359483362	*V. vinifera*	lactoylglutathione lyase
159	0.0491	5.12/37	5.08/53.7	80	340033945	*C. maritimum*	ATP synthase CF1 beta subunit
160	0.0565	5.15/36	5.41/49.2	84	4388534	*S. bicolor*	F1-ATP synthase, beta subunit
161	0.0209	5.13/30	5.64/27.4	[136]	147805616	*V. vinifera*	hypothetical protein
162	0.0607	5.06/36	8.89/54.7	83	326492265	*Ho. Vulgare*	predicted protein
163	0.06679	4.89/46	4.99/54.4	[343]	225459744	*V. vinifera*	V-type proton ATPase subunit B
164	0.0157	5.08/46	5.04/54.4	[377]	225428086	*V. vinifera*	V-type proton ATPase subunit B 1
165	0.116	4.78/42	5.28/47.1	[59]	224071449	*P. trichocarpa*	phospholipase A
166	0.0203	4.81/16	5.91/13.4	81	116789736	*P. sitchensis*	unknown
167	0.0414	5.35/17	5.98/51.0	[51]	115392253	*C. betuloides*	polyphenol oxidase
168	0.0691	5.36/19	5.39/18.0	[210]	225430941	*V. vinifera*	regulator of ribonuclease
169	0.179	5.23/16	5.64/20.9	[152]	2832430	*H. brasiliensis*	prohevein
170	0.14	5.18/15	5.92/16.2	[110]	298362843	*H. brasiliensis*	actin-depolymerizing factor
171	0.477	4.81/19	9.23/58.4	[104]	255539441	*R. communis*	actin depolymerizing factor
172	0.125	5.18/18	5.64/20.9	[252]	2832430	*H. brasiliensis*	prohevein
173	0.0849	5.12/23	5.17/24.9	101	255574159	*R. communis*	proteasome subunit beta type

174	0.0317	4.89/31	5.93/34.3	[117]	242059605	*S. bicolor*	hypothetical protein
175	0.0295	5.22/27	6.44/66.4	86	2832654	*A. thaliana*	chloroplast protein cs/ch-42
176	0.0419	5.38/26	5.78/27.5	[487]	27449248	*H. brasiliensis*	ascorbate peroxidase
177	0.0415	5.32/24	6.06/22.6	[369]	357480975	*M. truncatula*	Proteasome subunit beta type
178	0.054	5.35/25	6.08/24.9	[302]	255541320	*R. communis*	proteasome subunit beta type
179	0.19	6.98/15	6.56/9.7	82	350537255	*S. lycopersicum*	small zinc finger-like protein
180	0.0431	5.56/27	8.99/18.9	107	37622210	*H. brasiliensis*	small rubber particle protein
181	0.0442	5.87/38	5.8/61.3	81	168038495	*P. patens*	predicted protein
182	0.18	6.35/33	6.04/61.4	82	164472662	*T. aestivum*	calcium-dependent protein kinase
183	0.145	5.86/45	5.68/51.9	92	32527831	*P. tremula*	UDP-glucose pyrophosphorylase
184	0.0292	5.91/45	6.04/51.8	92	356576773	*G. max*	seryl-tRNA synthetase-like
185	0.0442	5.48/34	8.64/36.3	[51]	357514973	*M. truncatula*	Annexin D4
186	0.0553	5.35/38	6.48/42.1	[63]	1351887	*M. domestica*	Alcohol dehydrogenase
187	0.0362	5.51/37	5.54/41.0	[123]	380468126	*H. brasiliensis*	caffeic acid 3-O-methyltransferase
188	0.0275	5.28/36	5.54/41.0	[117]	380468126	*H. brasiliensis*	caffeic acid 3-O-methyltransferase
189	0.069	5.11/26	5.41/27.5	[159]	284433794	*J. curcas*	glutathione S-transferase omega
190	0.0311	5.56/28	6.09/30.8	[52]	255567721	*R. communis*	carboxymethylenebutenolidase
191	0.0405	5.48/29	10.36/29.7	[59]	125573095	*O. sativa*	hypothetical protein OsJ_04535
192	0.0954	5.44/33	5.5/34.4	82	255542380	*R. communis*	cysteine synthase, putative
193	0.0329	5.23/32	5.56/32.4	[57]	255562276	*R. communis*	pyridoxine kinase, putative
194	0.0813	5.85/33	6.5/32.1	[303]	255552291	*R. communis*	short chain dehydrogenase
195	0.0796	5.17/54	5.27/72.0	102	255543357	*R. communis*	heat shock protein, putative
196	0.0398	5.07/53	7.9/68.9	82	224139936	*P. trichocarpa*	predicted protein
197	0.0121	5.09/72	5.18/90.5	174	351727028	*G. max*	cell division cycle protein 48 homolog
198	0.0331	5.25/48	5.01/46.4	180	4235430	*H. brasiliensis*	latex-abundant protein
199	0.0648	5.51/47	4.96/48.7	[57]	198400319	*Camellia sinensis*	senescence-related protein
200	0.0702	5.15/40	5.6/42.4	[282]	255570457	*R. communis*	protease C56, putative
201	0.0708	5.46/41	5.44/41.9	149	32186896	*G. hirsutum*	actin
202	0.0756	5.41/42	5.49/47.1	109	255560725	*R. communis*	dead box ATP-dependent RNA helicase
203	0.0199	5.35/48	5.57/48.0	[229]	14423688	*H. brasiliensis*	Enolase 1
204	0.0168	5.38/55	5.27/72.0	[311]	186898205	*H. brasiliensis*	heat-shock protein 70
205	0.0392	5.68/58	5.6/65.4	[63]	255537027	*R. communis*	HSP70-interacting protein
206	0.0262	6.32/51	8.96/65.0	81	302853426	*V. carteri*	hypothetical protein
207	0.0208	6.14/67	5.6/65.4	[266]	255537027	*R. communis*	HSP70-interacting protein
208	0.0133	6.35/67	5.6/65.4	[68]	255537027	*R. communis*	HSP70-interacting protein
209	0.0489	5.36/57	5.52/61.0	[161]	1346735	*R. communis*	phosphoglycerate mutase
210	0.0132	5.38/68	5.6/65.4	[69]	255537027	*R. communis*	HSP70-interacting protein
211	0.0415	5.35/72	5.13/90.4	[1185]	255556934	*R. communis*	Transitional endoplasmic reticulum ATPase
212	0.0352	5.36/53	5.79/66.6	[166]	4588474	*B. napus*	phosphoinositide-specific phospholipase C
213	0.0419	5.38/55	5.79/66.6	[116]	4588474	*B. napus*	phosphoinositide-specific phospholipase C
214	0.0365	5.33/52	5.46/63.7	[138]	255568794	*R. communis*	nucleoredoxin, putative
215	0.0159	5.37/51	5.66/53.8	[289]	32967699	*A. thaliana*	S-adenosyl-L-homocystein hydrolase
216	0.0354	5.61/49	5.69/52.8	[327]	336390551	*G. max*	adenosylhomocysteinase

217	0.0327	5.78/48	5.2/51.8	[52]	6136111	*H. vulgare*	glucose-1-phosphate uridylyltransferase
218	0.0876	6.28/38	6.86/51.8	[802]	14916100	*H. brasiliensis*	hydroxymethylglutaryl Co-A synthase
219	0.0746	5.65/34	5.92/34.8	[181]	307707110	*P. armeniaca*	NAD-dependent malate dehydrogenase
220	0.091	5.54/38	5.64/42.2	[357]	357137038	*B. distachyon*	phosphoglycerate kinase, cytosolic-like
221	0.031	5.25/34	8.64/36.3	[99]	357514973	*M. truncatula*	Annexin D4
222	0.0629	5.41/37	5.49/42.2	[314]	21536853	*A. thaliana*	phosphoglycerate kinase, putative
223	0.0416	5.68/39	5.82/41.6	[77]	255547137	*R. communis*	Alpha-1,4-glucan-protein synthase
224	0.0396	5.29/37	5.54/41.0	[922]	380468126	*H. brasiliensis*	caffeic acid 3-O-methyltransferase
225	0.0375	5.25/39	5.6/42.4	[237]	255570457	*R. communis*	protease C56, putative
226	0.0626	5.13/27	5.24/26.2	[172]	224131618	*P. trichocarpa*	predicted protein
227	0.166	5.31/25	5.48/25.6	[386]	333690873	*H. brasiliensis*	glutathione-S-transferase tau 1
228	0.0928	5.38/26	6.0/27.5	[243]	211906460	*G. hirsutum*	triosephosphate isomerase
229	0.0256	5.21/27	5.13/27.5	[93]	255568460	*R. communis*	glutathione-s-transferase omega
230	0.0459	5.15/25	5.62/25.8	[104]	2970051	*V. radiata*	ARG10
231	0.0957	5.23/21	5.64/20.9	[217]	2832430	*H. brasiliensis*	prohevein
232	0.136	5.35/20	5.64/20.9	[112]	2832430	*H. brasiliensis*	prohevein
233	0.0722	4.98/23	4.8/22.3	[384]	14423933	*H. brasiliensis*	Small rubber particle protein
234	0.185	5.01/15	5.04/14.7	[379]	132270	*H. brasiliensis*	Rubber elongation factor protein
235	0.0425	5.56/15	6.32/17.1	[128]	123550	*P. sativum*	heat shock protein, 17.1 kDa class II
236	0.212	5.36/14	5.96/16.5	[272]	312985293	*H. brasiliensis*	nucleoside diphosphate kinase 2
237	0.234	5.67/13	5.04/14.7	[90]	132270	*H. brasiliensis*	Rubber elongation factor protein
238	1.121	5.54/13	5.64/20.9	[344]	2832430	*H. brasiliensis*	prohevein
239	0.0902	5.01/41	5.6/42.4	[193]	255570457	*R. communis*	protease C56, putative
240	0.0535	5.58/46	5.68/47.0	[58]	727357	*A. thaliana*	DnaJ homolog
241	0.0674	5.34/48	5.46/63.7	[100]	255568794	*R. communis*	nucleoredoxin, putative
242	1.13	4.75/51	4.6/41.5	93	37719658	*H. brasiliensis*	50 kDa protein
243	0.354	4.78/49	4.6/41.5	85	37719658	*H. brasiliensis*	50 kDa protein
244	1.05	4.55/50	4.6/41.5	95	37719658	*H. brasiliensis*	50 kDa protein
245	1.02	4.73/47	4.6/41.5	101	37719658	*H. brasiliensis*	50 kDa protein
246	0.121	4.77/47	4.6/41.5	118	37719658	*H. brasiliensis*	50 kDa protein
247	0.215	5.35/13	5.63/22.7	[158]	123062	*H. brasiliensis*	Pro-hevein
248	1.41	6.96/13	5.64.20.9	[446]	2832430	*H. brasiliensis*	prohevein
249	0.428	5.01/13	5.04/14.7	[405]	132270	*H. brasiliensis*	Rubber elongation factor protein
250	0.478	5.24/13	5.04/14.7	[340]	132270	*H. brasiliensis*	Rubber elongation factor protein
251	0.401	5.11/13	5.04/14.7	[470]	132270	*H. brasiliensis*	Rubber elongation factor protein
252	0.788	5.69/14	5.04/14.7	[402]	132270	*H. brasiliensis*	Rubber elongation factor protein
B1	---	---	5.04/14.7	[282]	132270	*H. brasiliensis*	Rubber elongation factor protein
B2	---	---	5.14/90.3	90	225440045	*V. vinifera*	cell division cycle protein 48 homolog
B3	---	---	5.54/92.3	[100]	88193697	*A. hypogaea*	phospholipase D
B4	---	---	5.17/71.4	102	225440324	*V. vinifera*	heat shock cognate 70 protein
B5	---	---	6.77/23.7	95	253760141	*S. bicolor*	hypothetical protein
B6	---	---	4.8/22.3	[348]	14423933	*H. brasiliensis*	Small rubber particle protein
B7	---	---	9.4/41.5	125	124365253	*H. brasiliensis*	beta-1,3-glucanase

B8	---	---	9.46/35.3	187	124365253	*H. brasiliensis*	beta-1,3-glucanase
B9	---	---	7.1/36.9	103	255540341	*R. communis*	glyceraldehyde 3-phosphate dehydrogenase
B10	---	---	4.8/22.3	160	14423933	*H. brasiliensis*	small rubber particle protein
B11	---	---	5.06/19.6	106	38122474	*H. brasiliensis*	rubber elongation factor
B12	---	---	5.0/43.0	87	3288200	*H. brasiliensis*	latex allergen
B13	---	---	5.04/14.9	[271]	334854628	*H. brasiliensis*	rubber elongation factor
B14	---	---	5.57/48.0	117	14423688	*H. brasiliensis*	Enolase 1
B15	---	---	5.27/72.0	85	255543357	*R. communis*	heat shock protein, putative
B16	---	---	5.12/91.0	88	225456951	*V. vinifera*	cell division cycle protein 48 homolog
B17	---	---	5.22/21.0	[67]	66735596	*A. hypogaea*	phospholipase D alpha
B18	---	---	5.02/80.4	90	33326375	*H. brasiliensis*	heat shock protein
B19	---	---	5.11/70.4	107	450880	*A. thaliana*	heat shock cognate 70-1
B20	---	---	7.01/28.4	81	379068234	*R. formosanum*	leucine-rich repeat protein
B21	---	---	5.57/48.0	101	14423688	*H. brasiliensis*	enolase 1
B22	---	---	5.0/43.0	121	3288200	*H. brasiliensis*	latex allergen
B23	---	---	5.64/42.2	[81]	113217	*Daucus carota*	Actin-1
B24	---	---	97.2/6.1	84	147835357	*V. vinifera*	hypothetical protein
B25	---	---	5.67/11.7	81	170525118	*P. mendocina*	geranylgeranyl reductase
B26	---	---	8.11/43.2	83	145346735	*O. lucimarinus*	predicted protein
B27	---	---	4.79/29.0	[101]	37903393	*S. hybrid*	14-3-3-like protein
B28	---	---	9.46/35.5	181	10946499	*H. brasiliensis*	beta-1,3-glucanase
B29	---	---	9.4/41.5	105	124365253	*H. brasiliensis*	beta-1,3-glucanase
B30	---	---	4.8/22.3	130	14423933	*H. brasiliensis*	small rubber particle protein
B31	---	---	7.77/20.7	132	313586569	*H. brasiliensis*	hypothetical protein 19
B32	---	---	6.56/8.5	162	327492451	*M. crystallinum*	N-terminal end of polyubiquitin
B33	---	---	5.73.15.7	87	27449246	*H. brasiliensis*	Cu/Zn superoxide dismutase SOD
B34	---	---	4.61/12.8	84	29170601	*H. brasiliensis*	small rubber particle protein
B35	---	---	5.01/10.3	[118]	242080683	*S. bicolor*	hypothetical protein

Note:

[a] Assigned spot (S1-S252) or band (B1-B35) number as indicated in Fig. 2.

[b] The statistical percent of volue value (Vol%) of the target protein spot in all the proteins in the 2-DE gels produced by ImageMaster.

[c, d] The experimental (c) and theoretical (d) values for the mass (kDa) and *p*I of identified proteins. The theoretical values were retrieved from the protein database, and the experimental values were produced by ImageMaster.

[e] Mascot searched scores (M.S.) against NCBInr for the MS and [MS/MS] searched results.

[f] Database accession (gi|) numbers according to NCBInr. ---, the values were not detected.

Supplementary Table S2 MS identification of the differential latex proteins in DIGE gels

Spot NO.[a]	**Changed**[b] **3 | 5-day**	**Exper.**[c] ***p*****I/M*****r***	**Thero.**[d] ***p*****I/M*****r***	**M.S.**[e] **Score**	**NCBI No.**[f]	**Plant species**	**Protein name**
D1	-1.23/-1.85	5.19/30	4.71/28.6	[278]	255545912	*R. communis*	14-3-3 protein, putative
D2	-1.47/-1.97	4.75/51	4.6/41.5	93	37719658	*H. brasiliensis*	50 kDa protein
D3	-1.51/-2.09	4.78/49	4.6/41.5	85	37719658	*H. brasiliensis*	50 kDa protein
D4	-1.24/-4.02	5.87/62	5.64/27.4	[324]	147805616	*V. vinifera*	hypothetical protein VITISV_028800
D5	-1.24/-1.68	6.33/68	5.3/35.8	[122]	224137430	*P. trichocarpa*	predicted protein
D6	1.31/1.59	5.16/47	5.57/48.0	[229]	14423688	*H. brasiliensis*	Enolase 1
D7	-1.52/-2.74	4.55/50	4.6/41.5	95	37719658	*H. brasiliensis*	50 kDa protein
D8	1.11/1.54	5.45/61	5.87/95.0	123	255565836	*R. communis*	eukaryotic translation elongation factor
D9	1.52/1.34	4.93/41	5.047/54.4	146	225428086	*V. vinifera*	V-type proton ATPase subunit B 1
D10	-1.27/-1.57	6.42/16	5.65/20.9	[446]	2832430	*H. brasiliensis*	Pro-hevein
D11	-1.23/-1.54	6.61/15	5.63/22.7	[158]	123062	*H. brasiliensis*	Pro-hevein
D12	-1.52/1.31	5.87/71	5.42/45.9	[77]	15237159	*A. thaliana*	regulatory particle triple-A ATPase 3
D13	-1.53/1.19	6.0/21	5.63/22.7	[129]	123062	*H. brasiliensis*	Pro-hevein
D14	-1.09/1.56	5.94/54	5.75/35.6	[196]	225446010	*V. vinifera*	glucose-6-phosphate 1-epimerase
D15	1.51/-1.53	5.25/97	5.15/75.5	[338]	1143427	*C. sativus*	heat shock protein 70
D16	-1.43/-1.87	6.23/48	4.94/28.6	[198]	255558037	*R. communis*	nucleic acid binding protein, putative
D17	-1.27/-1.52	6.35/18	5.73/15.7	[105]	27449246	*H. brasiliensis*	Cu/Zn superoxide dismutase
D18	-1.07/-1.55	6.96/14	5.64/20.9	[446]	2832430	*H. brasiliensis*	pro-hevein
D19	-1.57/-1.53	6.6/99	6.08/59.6	[301]	255551408	*R. communis*	chaperonin containing t-complex protein 1
D20	-1.51/-1.82	6.02/55	6.18/35.6	[75]	225438145	*V. vinifera*	malate dehydrogenase, cytoplasmic
D21	1.75/-1.98	5.6/43	5.19/56.6	[116]	224056377	*R. communis*	Aspartic proteinase precursor, putative
D22	1.15/-1.55	5.59/54	7.63/31.6	[145]	255554865	*R. communis*	lactoylglutathione lyase, putative
D23	-1.95/1.55	6.23/64	5.83/27.7	[466]	356517215	*G. max*	uncharacterized protein LOC100817735
D24	1.52/1.14	5.55/98	5.1/71.2	[505]	356569000	*G. max*	heat shock cognate 70 kDa protein
D25	1.54/1.52	5.01/13	5.04/14.7	[405]	132270	*H. brasiliensis*	Rubber elongation factor protein
D26	1.51/-1.11	6.53/42	7.81/31.3	[79]	6624721	*P. sativum*	cysteine protease, putative
D27	1.55/-1.1	5.24/13	5.04/14.7	[340]	132270	*H. brasiliensis*	Rubber elongation factor protein
D28	3.01/1.06	5.96/87	5.47/46.2	[115]	314991144	*G. hirsutum*	mitogen-activated protein kinase
D29	-2.92/1.05	6.01/33	5.59/18.4	[82]	118485535	*P. trichocarpa*	unknown
D30	1.26/1.54	5.11/13	5.04/14.7	[470]	132270	*H. brasiliensis*	Rubber elongation factor protein
D31	1.58/-1.15	6.61/41	6.43/36.7	[80]	470127750	*F. vesca*	uncharacterized protein LOC101300446
D32	1.53/1.19	5.69/14	5.04/14.7	[398]	132270	*H. brasiliensis*	Rubber elongation factor protein
D33	1.67/1.21	6.37/102	5.31/47.9	[106]	351724891	*G. max*	enolase
D34	1.56/1.32	5.27/68	4.65/41.4	[154]	255578278	*R. communis*	hypothetical protein RCOM_0537780
D35	1.53/1.19	6.63/41	5.15/75.5	[378]	1143427	*C. sativus*	heat shock protein 70
D36	1.55/1.54	6.54/82	6.96/41.2	[120]	164604960	*H. brasiliensis*	acetyl-CoA C-acetyltransferase
D37	-1.58/-1.53	6.54/41	8.99/18.9	[77]	37622210	*H. brasiliensis*	small rubber particle protein
D38	-1.49/1.52	5.24/35	4.87/30.8	[109]	255555641	*R. communis*	26S proteasome atpase regulatory subunit
D39	-1.59/-2.53	6.32/31	6.08/24.9	[157]	255541320	*R. communis*	proteasome subunit beta type
D40	-1.55/-1.95	5.21/97	5.35/75.4	[459]	255570990	*R. communis*	heat shock protein, putative
D41	-1.26/-1.55	6.53/24	5.86/22.7	[97]	351726646	*G. max*	uncharacterized protein

D42	1.51/1.87	5.49/72	4.98/54.8	[111]	166627	*A. thaliana*	nucleotide-binding subunit of V-ATPase
D43	-1.51/-1.53	6.21/14	5.04/14.7	[55]	132270	*H. brasiliensis*	Rubber elongation factor protein
D44	1.53/-1.39	6.71/34	5.84/27.5	[366]	255583952	*R. communis*	proteasome subunit alpha type, putative
D45	-1.21/-1.58	5.97/28	5.48/26.3	[189]	356547978	*G. max*	eukaryotic translation initiation factor 3
D46	-1.17/-1.56	6.51/31	6.4/23.7	[78]	310772392	*M. glabra*	dehydroascorbate reductase
D47	1.63/-1.29	5.54/19	5.39/17.9	[370]	255547584	*R. communis*	Regulator of ribonuclease activity A
D48	1.24/-1.55	6.72/85	6.29/35.5	[128]	255568992	*R. communis*	conserved hypothetical protein
D49	-1.52/-1.54	6.24/91	5.78/54.6	[206]	356522666	*G. max*	ubiquitin carboxyl-terminal hydrolase 6
D50	1.54/-1.23	5.51/47	5.84/27.4	[120]	224099853	*P. trichocarpa*	predicted protein
D51	-1.12/1.58	6.13/90	5.46/63.7	[380]	255568794	*R. communis*	nucleoredoxin, putative
D52	1.53/1.58	5.51/31	4.8/22.3	[137]	14423933	*H. brasiliensis*	Small rubber particle protein
D53	-1.01/1.53	5.9/45	5.48/25.6	[132]	333690873	*H. brasiliensis*	glutathione-S-transferase tau 1
D54	-1.27/1.55	6.01/62	5.71/38.4	[105]	356543702	*G. max*	pulegone reductase-like
D55	1.21/1.52	6.4/20	5.82/18.5	[56]	351721881	*G. max*	heat shock protein,18.5 kDa class I
D56	-1.09/1.56	5.61/96	5.02/48.4	[96]	462406561	*P. persica*	hypothetical protein
D57	1.12/1.59	6.64/35	7.6/30.6	[56]	255570177	*R. communis*	proteasome subunit beta type
D58	1.13/-1.54	6.75/16	5.93/18.3	[197]	3834310	*A. thaliana*	Ubiquitin-conjugating enzyme
D59	1.02/1.56	6.7/18	6.2/16.7	[256]	315937232	*J. curcas*	ubiquitin-conjugating family protein
D60	1.27/1.52	5.53/72	5.07/54.1	[271]	226531470	*Z. mays*	vacuolar ATP synthase subunit B
D61	-1.78/-2.65	6.34/22	5.64/20.9	[175]	2832430	*H. brasiliensis*	pro-hevein
D62	1.61/1.31	6.32/56	5.54/40.1	[195]	114199044	*M. domestica*	caffeic acid O-methyltransferase
D63	1.12/1.57	5.74/29	8.33/27.7	[77]	255538084	*R. communis*	Adenine phosphoribosyltransferase
D64	1.52/1.51	5.79/35	5.55/26.0	[94]	255546213	*R. communis*	o-methyltransferase, putative
D65	1.53/1.52	4.88/13	5.04/14.7	95	132270	*H. brasiliensis*	Rubber elongation factor protein
D66	1.57/1.51	4.9/23	4.8/22.3	122	14423933	*H. brasiliensis*	Small rubber particle protein
D67	1.56/1.53	4.82/23	4.8/22.3	135	14423933	*H. brasiliensis*	Small rubber particle protein
D68	1.54/1.51	4.88/26	4.79/29.5	93	388503664	*L. japonicus*	unknown
D69	1.57/1.14	5.05/49	5.01/46.6	96	4235430	*H. brasiliensis*	latex-abundant protein
D70	1.03/-1.52	5.18/15	8.01/11.2	[86]	30575570	*C. paradisi*	HSP19 class II, partial
D71	-1.54/-1.7	5.61/15	8.29/35.1	[60]	37806305	*O. sativa*	hypothetical protein
D72	-1.55/-1.56	5.69/27	8.72/34.1	[56]	3451147	*H. brasiliensis*	chitinase
D73	-1.59/-1.58	6.75/33	7.1/36.9	86	255540341	*R. communis*	glyceraldehyde 3-phosphate dehydrogenase
D74	1.01/-1.55	4.95/40	5.0/43.0	[81]	3288200	*H. brasiliensis*	latex allergen
D75	-1.22/1.53	4.91/39	5.0/43.0	[138]	1916805	*H. brasiliensis*	latex patatin homolog
D76	-1.11/3.13	5.03/40	5.12/43.0	152	41581137	*H. brasiliensis*	latex allergen hev b 7.02
D77	-1.07/2.02	5.06/40	5.12/43.0	142	41581137	*H. brasiliensis*	latex allergen hev b 7.02
D78	-1.27/-1.58	3.65/33	9.45/38.9	156	4469175	*H. brasiliensis*	beta-1,3-glucanase
D79	-1.17/-1.61	5.64/16	6.22/34.3	84	34538473	*H. vulgare*	caleosin 1
D80	1.54/1.16	5.03/49	5.49/47.1	144	255560725	*R. communis*	dead box ATP-dependent RNA helicase
D81	1.52/1.1	4.91/46	4.65/41.4	[76]	255578278	*R. communis*	hypothetical protein RCOM_0537780
D82	-1.04/1.68	5.27/44	5.44/50.1	83	2501850	*N. tabacum*	GDP dissociation inhibitor
D83	-1.06/-1.52	4.9/49	4.72/28.9	[74]	3264769	*P. armeniaca*	late embryogenesis-like protein
D84	1.04/1.55	4.98/27	5.84/27.4	[69]	224099853	*P. trichocarpa*	predicted protein
D85	-1.56/-1.03	5.17/21	5.06/19.6	[410]	38122474	*H. brasiliensis*	rubber elongation factor

D86	-1.52/2.18	5.21/22	5.06/19.6	[226]	38122474	*H. brasiliensis*	rubber elongation factor
D87	1.53/1.52	4.62/19	4.06/15.2	[496]	334854634	*H. brasiliensis*	elicitor-responsive protein
D88	-1.57/-1.62	5.37/16	5.39/18.0	[180]	224144943	*P. trichocarpa*	predicted protein
D89	-1.58/-1.28	6.74/16	5.63/22.7	96	123062	*H. brasiliensis*	Pro-hevein
D90	-1.58/-4	5.42/22	5.06/19.6	99	38122474	*H. brasiliensis*	rubber elongation factor
D91	-1.02/-1.61	5.35/26	6.17/27.5	[49]	1709761	*S. oleracea*	Proteasome subunit alpha type-4
D92	-1.58/1.02	5.22/22	5.06/19.6	125	38122474	*H. brasiliensis*	rubber elongation factor
D93	-1.56/-1.52	5.75/23	8.44/29.9	93	157831407	*H. brasiliensis*	Chain A, Crystal Structures Of Hevamine
D94	1.03/-1.58	5.52/33	5.89/27.9	[89]	3127890	*C. arietinum*	cysteine synthase, O-acetyl-(thiol)-lyase
D95	-1.24/3.05	5.05/39	5.0/43.9	[59]	51315784	*H. brasiliensis*	Esterase
D96	1.39/5.24	5.29/21	5.06/19.6	98	38122474	*H. brasiliensis*	rubber elongation factor
D97	1.04/1.52	5.02/27	7.63/31.6	[55]	255554865	*R. communis*	lactoylglutathione lyase, putative
D98	1.58/1.39	5.51/26	5.93/27.6	86	15225839	*A. thaliana*	proteasome subunit alpha type-3
D99	1.55/1.02	4.45/15	4.61/12.8	[97]	29170601	*H. brasiliensis*	small rubber particle protein
D100	-1.09/-1.63	5.46/13	5.64/20.9	[84]	2832430	*H. brasiliensis*	pro-hevein
D101	-1.67/-1.16	5.55/14	6.82/15.0	[68]	224054224	*P. trichocarpa*	predicted protein
D102	1.13/1.72	5.01/11	5.45/11.2	81	268321205	*H. brasiliensis*	latex cystatin
D103	-1.62/-1.02	5.16/15	6.4/8.6	81	242083244	*S. bicolor*	hypothetical protein
D104	1.57/1.12	4.94/13	4.61/12.8	[85]	29170601	*H. brasiliensis*	small rubber particle protein
D105	-2.51/-3.62	4.13/13	4.1/16.9	[128]	354318	*T. aestivum*	calmodulin
D106	-1.51/-8.05	4.12/21	4.8/22.3	85	14423933	*H. brasiliensis*	Small rubber particle protein
D107	-2.36/1.06	4.45/24	4.8/22.3	165	14423933	*H. brasiliensis*	Small rubber particle protein
D108	-1.62/-1.1	5.36/47	5.57/48.0	107	14423688	*H. brasiliensis*	Enolase 1
D109	1.61/1.65	5.01/26	5.48/25.6	[52]	333690873	*H. brasiliensis*	glutathione-S-transferase tau 1
D110	-1.12/-1.57	5.09/15	5.95/17.6	[87]	140083605	*R. hybrid*	cytosolic class II HSP17.5
D111	-2.32/-11.52	4.02/41	5.01/14.6	[88]	37901124	*H. brasiliensis*	latex abundant protein 1
D112	-1.27/-1.87	4.35/40	4.53/38.0	[173]	359806300	*G. max*	uncharacterized protein
D113	-8.92/-8.16	4.28/38	4.53/38.1	[166]	37625031	*V. aestivalis*	ankyrin-repeat protein
D114	1.02/-1.7	4.39/38	4.45/37.5	[71]	13310811	*N. tabacum*	ankyrin-repeat protein HBP1
D115	-1.64/-1.6	4.31/36	4.5/25.3	[117]	378464888	*A. mongolicus*	translation elongation factor
D116	-1.08/-1.94	4.83/30	5.26/35.7	[132]	22261807	*S. tuberosum*	Light-induced protein, chloroplastic
D117	1.21/1.73	5.13/30	5.64/27.4	[136]	147805616	*V. vinifera*	hypothetical protein VITISV_028800
D118	1.63/1.17	5.08/46	5.04/54.4	[377]	225428086	*V. vinifera*	V-type proton ATPase subunit B 1
D119	1.01/1.56	4.78/42	5.28/47.1	[59]	224071449	*P. trichocarpa*	phospholipase A
D120	-1.57/1.52	4.81/16	5.91/13.4	81	116789736	*P. sitchensis*	unknown
D121	-1.12/-1.65	5.35/17	5.98/51.0	[51]	115392253	*C. betuloides*	polyphenol oxidase
D122	-1.21/-1.9	5.36/19	5.39/18.0	[210]	225430941	*V. vinifera*	regulator of ribonuclease-like protein 2
D123	-1.81/1.07	4.81/19	9.23/58.4	[104]	255539441	*R. communis*	actin depolymerizing factor, putative
D124	-1.1/2.05	5.32/24	6.06/22.6	[369]	357480975	*M. truncatula*	Proteasome subunit beta type
D125	-1.21/1.65	5.51/37	5.54/41.0	[123]	380468126	*H. brasiliensis*	caffeic acid 3-O-methyltransferase
D126	-1.05/1.55	5.28/36	5.54/41.0	[117]	380468126	*H. brasiliensis*	caffeic acid 3-O-methyltransferase
D127	-1.59/1.15	5.11/26	5.41/27.5	[159]	284433794	*J. curcas*	glutathione S-transferase omega
D128	-1.05/-1.64	5.56/28	6.09/30.8	[52]	255567721	*R. communis*	carboxymethylenebutenolidase, putative
D129	-1.74/1.13	5.44/33	5.5/34.4	82	255542380	*R. communis*	cysteine synthase, putative

D130	-1.62/-1.64	5.09/72	5.18/90.5	174	351727028	*G. max*	cell division cycle protein 48 homolog
D131	-1.65/-1.12	6.28/38	6.86/51.8	[802]	14916100	*H. brasiliensis*	hydroxymethylglutaryl CoA synthase
D132	-1.62/-1.01	5.25/34	8.64/36.3	[99]	357514973	*M. truncatula*	Annexin D4
D133	1.62/1.06	5.41/37	5.49/42.2	[314]	21536853	*A. thaliana*	phosphoglycerate kinase, putative
D134	1.71/1.16	5.68/39	5.82/41.6	[77]	255547137	*R. communis*	Alpha-1,4-glucan-protein synthase
D135	-1.02/1.57	5.31/25	5.48/25.6	[386]	333690873	*H. brasiliensis*	glutathione-S-transferase tau 1
D136	1.1/1.72	5.15/25	5.62/25.8	[104]	2970051	*V. radiata*	ARG10
D137	-1.66/1.63	5.23/21	5.64/20.9	[217]	2832430	*H. brasiliensis*	pro-hevein
D138	-1.1/-1.71	4.98/23	4.8/22.3	[384]	14423933	*H. brasiliensis*	Small rubber particle protein
D139	1.63/1.09	5.01/15	5.04/14.7	[379]	132270	*H. brasiliensis*	Rubber elongation factor protein
D140	-1.56/-1.62	5.54/13	5.64/20.9	[344]	2832430	*H. brasiliensis*	pro-hevein
D141	-1.63/-1.54	5.35/13	5.63/22.7	[158]	123062	*H. brasiliensis*	Pro-hevein
D142	1.63/1.51	5.01/13	5.04/14.7	[405]	132270	*H. brasiliensis*	Rubber elongation factor protein
D143	1.61/1.64	5.11/13	5.04/14.7	[470]	132270	*H. brasiliensis*	Rubber elongation factor protein

Note:

[a] Assigned spot number (D1-D143) as indicated in Fig. 3.

[b] The relatively changed ratios of the target protein spots in the 3 and 5 days latex from rubber trees treated by water and ethylene. All the protein spots in the 2-D DIGE gels were analyzed by DeCyder 7.0 software.

[c, d] The experimental (c) and theoretical (d) values for the mass (kDa) and *p*I of identified proteins. The theoretical values were retrieved from the protein database, and the experimental values were produced by ImageMaster.

[e] Mascot searched scores (M.S.) against NCBInr for the MS and [MS/MS] searched results.

[f] Database accession (gi|) numbers according to NCBInr.

Supplementary Table S3 MS information of ethylene responsive latex proteins by iTRAQ

Protein No. I-[a]	**Un[b] Score**	**Cov.[c] 95%**	**Peptides[d] (95%)**	**Ratio [e] E3/D3**	**Ratio [e] E5/D5**	**Accession species[f]**	**Protein name**
2	66.5	67.1	135	0.38	0.57	tr|D1M8S7|D1M8S7_HEVBR	Beta-1,3-glucanase
5	58.21	95.4	66	3.25	1.54	sp|Q39967|ALL5_HEVBR	Major latex allergen Hev b 5
7	54.77	71.6	105	0.33	0.30	tr|Q706V4|Q706V4_HEVBR	Latex allergen hev b 7.02
10	44.55	56.2	49	0.39	0.75	tr|E5FR85|E5FR85_MORAL	Actin
11	43.62	38.3	34	1.58	1.42	tr|Q71EE1|Q71EE1_HEVBR	Heat shock protein
12	42.03	35.4	37	0.46	0.56	tr|Q5VLJ6|Q5VLJ6_HEVBR	50 kDa protein
13	41.88	76	55	0.65	0.45	tr|A9ZMZ4|A9ZMZ4_HEVBR	Acetyl-CoA C-acetyltransferase
15	39.75	45.2	55	0.30	0.37	sp|Q9LEJ0|ENO1_HEVBR	Enolase 1
17	37.25	65.5	49	0.52	0.30	tr|Q9ZSP8|Q9ZSP8_HEVBR	Latex-abundant protein
18	34.69	43.4	22	0.49	0.35	tr|Q944G0|Q944G0_HEVBR	Mevalonate disphosphate decarboxylase
19	32.73	46.6	41	0.50	0.77	sp|P81406|GAPN_PEA	glyceraldehyde-3-phosphate dehydrogenase
22	31.1	42.7	22	0.19	0.44	tr|Q944F8|Q944F8_HEVBR	Hydroxymethylglutaryl CoA synthase
23	30.18	25.5	30	2.17	1.57	tr|B9SI90|B9SI90_RICCO	Methyl transferase
24	30.15	42	36	0.31	0.59	tr|B9RZR0|B9RZR0_RICCO	ATP-citrate synthase
25	29.94	42.5	31	0.34	0.36	tr|B9R8U5|B9R8U5_RICCO	Phosphofructokinase, putative
27	27.55	51.5	17	0.53	0.86	tr|F2YZ43|F2YZ43_HEVBR	14-3-3 protein 2
28	27.3	65.4	20	0.38	0.39	tr|Q40208|Q40208_LOTJA	RAB2A
30	27.13	90	24	0.33	0.40	tr|F8SKC5|F8SKC5_HEVBR	Elicitor-responsive protein
31	27.02	37.6	16	1.60	1.32	tr|C6TEK4|C6TEK4_SOYBN	phospholipase D alpha 1
32	27.02	22.7	28	0.63	0.55	tr|B9RV56|B9RV56_RICCO	Phospholipase D
33	26.07	64.5	48	0.06	0.28	tr|B3FNQ1|B3FNQ1_HEVBR	Peptidyl-prolyl cis-trans isomerase
39	24.89	97.4	54	0.39	0.61	tr|Q84T88|Q84T88_HEVBR	Small rubber particle protein
40	24.28	45.2	40	2.07	1.56	tr|Q8H9B1|Q8H9B1_9ROSI	eukaryotic translation elongation factor 1
42	24.12	36.8	28	1.87	1.11	tr|B9SP64|B9SP64_RICCO	Phosphoglucomutase, putative
43	23.88	22.7	15	0.59	0.70	tr|B9S8D6|B9S8D6_RICCO	Trehalose-6-phosphate synthase
49	22.33	12.4	11	1.84	2.19	tr|B9I8G4|B9I8G4_POPTR	Exportin-1
50	22.29	26	14	1.51	2.20	tr|E9KF95|E9KF95_HEVBR	Invertase 2
53	21.98	15.9	14	0.57	0.62	tr|A9NIV2|A9NIV2_MANES	Sucrose synthase
54	21.97	32.8	19	0.31	0.92	tr|B9NBW3|B9NBW3_POPTR	Malate dehydrogenase
55	21.39	30.8	18	1.51	1.63	tr|B9RSN1|B9RSN1_RICCO	Chaperonin containing t-complex protein 1
57	21.05	24.2	17	3.50	2.24	tr|E4MXI2|E4MXI2_THEHA	Luminal binding protein
58	21.05	22.7	12	0.36	0.70	tr|B9RM60|B9RM60_RICCO	Glu-fructose-6-phosphate aminotransferase
60	20.86	29.1	28	0.29	0.40	tr|B9STR1|B9STR1_RICCO	Leucine aminopeptidase, putative1
61	20.57	41.2	17	0.63	0.39	tr|B9RIY3|B9RIY3_RICCO	Rab GDP dissociation inhibitor
64	19.65	36.3	16	0.60	0.44	tr|B9RLK7|B9RLK7_RICCO	Alpha-1,4-glucan-protein synthase
69	18.74	19.2	18	0.58	0.57	tr|B9RBP6|B9RBP6_RICCO	Heat shock protein 70
70	18.66	38.1	12	0.52	0.45	tr|Q9ZSZ6|Q9ZSZ6_HEVBR	DnaJ protein
71	18.31	33.9	13	0.54	0.63	tr|B9RHY3|B9RHY3_RICCO	Phosphoglycerate kinase
73	18.11	13.1	13	0.63	0.52	tr|B9SYR5|B9SYR5_RICCO	Alanyl-tRNA synthetase, putative
76	17.33	21.8	9	1.72	1.29	tr|B9I5Y4|B9I5Y4_POPTR	T-complex protein 1 subunit theta
77	17.27	42.2	15	2.23	1.96	tr|Q8L3U6|Q8L3U6_HEVBR	Cis-prenyl transferase II

80	16.77	39.6	10	0.47	0.72	tr|B9S943|B9S943_RICCO	GTP-binding protein ras-like protein
83	16.69	7.1	7	0.23	0.66	tr|F6HJZ9|F6HJZ9_VITVI	cullin-associated protein 1
85	16.45	40.7	14	1.71	1.12	tr|B9RR89|B9RR89_RICCO	Proteasome subunit alpha type
86	16.41	37.5	8	2.07	1.87	tr|C6TKI4|C6TKI4_SOYBN	Proteasome subunit alpha type
87	16.33	16.6	10	0.41	0.26	tr|B9R7S8|B9R7S8_RICCO	Glucose-6-phosphate isomerase
89	16.31	19.8	12	2.11	1.37	tr|B9S5K6|B9S5K6_RICCO	26S proteasome regulatory subunit
95	16.17	27.3	13	0.47	0.74	tr|D2D2Z1|D2D2Z1_GOSHI	UDP-D-glucose pyrophosphorylase
98	15.62	14.3	12	0.61	0.59	tr|B9SJV6|B9SJV6_RICCO	Eukaryotic translation initiation factor 2c
99	15.49	11.9	10	1.80	1.49	tr|A5AHP0|A5AHP0_VITVI	Coatomer subunit beta
102	15.18	18.4	15	0.42	0.59	tr|B9SH99|B9SH99_RICCO	Nucleoredoxin, putative
106	14.96	32.3	13	0.44	0.76	tr|B9SIT3|B9SIT3_RICCO	L-lactate dehydrogenase
108	14.87	27.6	10	1.51	1.47	tr|A5BEF3|A5BEF3_VITVI	26S proteasome regulatory subunit 4
109	14.75	17.6	10	0.55	0.72	tr|B9SS36|B9SS36_RICCO	Chaperonin containing t-complex protein 1
112	14.47	30	13	0.08	0.10	tr|B9RXK1|B9RXK1_RICCO	Lactoylglutathione lyase, putative
115	14.31	28.7	9	3.10	1.52	tr|B9SN65|B9SN65_RICCO	Glucose 4-6-dehydratase, putative
117	14.13	42.8	7	0.30	0.37	tr|A9PFQ6|A9PFQ6_POPTR	Regulator of ribonuclease activity A
119	14.02	22.1	8	0.22	0.28	tr|Q547W6|Q547W6_HEVBR	Hydroxymethylglutaryl CoA reductase
122	13.95	13.5	11	0.58	1.19	tr|B9II82|B9II82_POPTR	villin-2
125	13.43	11.8	11	0.17	0.40	tr|F6HTU8|F6HTU8_VITVI	Cysteine synthase
129	13.13	39.2	7	0.52	0.66	tr|C6TGU2|C6TGU2_SOYBN	Proteasome subunit alpha type
131	12.95	31.6	7	2.47	1.62	sp|O22518|RSSA_SOYBN	40S ribosomal protein SA
132	12.91	19.8	9	2.27	1.66	tr|D2D2Z2|D2D2Z2_GOSHI	UDP-D-glucose dehydrogenase
133	12.91	25.4	9	0.56	0.73	tr|Q8L7F4|Q8L7F4_HEVBR	Farnesyl diphosphate synthase
134	12.79	27.6	9	0.21	0.77	tr|F6HPS0|F6HPS0_VITVI	Serine/threonine-protein phosphatase
135	12.78	18.2	12	0.63	1.20	tr|B9RCK2|B9RCK2_RICCO	Calcium-dependent protein kinase
136	12.7	18.5	6	0.64	0.79	tr|D7TKK5|D7TKK5_VITVI	obg-like ATPase 1
138	12.64	19.3	9	0.46	0.69	tr|D7SUQ2|D7SUQ2_VITVI	GTP-binding nuclear protein Ran-3
141	12.36	27	10	0.55	0.47	tr|D7SUD7|D7SUD7_VITVI	Aspartate aminotransferase
145	12.21	34.9	15	0.29	0.38	sp|Q39962|CBPR_HEVBR	Citrate-binding protein
148	12	61.8	41	0.55	0.66	tr|A9ZMZ5|A9ZMZ5_HEVBR	Acetyl-CoA C-acetyltransferase
150	11.87	29.8	10	2.40	1.42	sp|Q39963|PDX1_HEVBR	Pyridoxal biosynthesis protein PDX1
151	11.81	27.5	9	1.75	1.51	tr|B9RC03|B9RC03_RICCO	NAD dependent epimerase/dehydratase
152	11.77	50	23	0.61	0.63	tr|B1NDK1|B1NDK1_9ERIC	Calmodulin
160	11.38	20.7	7	0.44	0.62	tr|B9RAM4|B9RAM4_RICCO	26S proteasome non-atpase
161	11.37	21.3	22	0.31	0.42	tr|Q6XNP8|Q6XNP8_HEVBR	Abscisic acid stress ripening-related protein
167	11.12	18	7	10.47	2.51	tr|C7B9C0|C7B9C0_RICCO	Myo-inositol-1-phosphate synthase
168	10.98	22.2	11	0.45	0.64	tr|B9SZU0|B9SZU0_RICCO	Catalytic, putative
169	10.97	15.2	5	1.53	1.66	tr|B9SWY5|B9SWY5_RICCO	Proliferation-associated 2g4
170	10.95	26.1	12	0.30	0.52	tr|B9SVA7|B9SVA7_RICCO	Aspartic proteinase, putative
175	10.83	33.5	8	0.08	0.59	tr|Q6J6I5|Q6J6I5_HEVBR	Phosphoglyceride transfer protein
182	10.63	15.2	10	1.75	1.24	tr|B9RYE9|B9RYE9_RICCO	Polyadenylate-binding protein,
186	10.47	29	7	1.60	1.41	tr|B9SPS6|B9SPS6_RICCO	Proteasome subunit beta type
187	10.45	42.2	8	0.52	0.70	tr|B9GTP5|B9GTP5_POPTR	ras-related protein RABC1 isoform
188	10.41	17.3	7	7.52	1.63	sp|P29685|ATPBM_HEVBR	ATP synthase subunit beta

191	10.38	7	5	0.58	0.60	tr|B9RUL1|B9RUL1_RICCO	Acid phosphatase, putative
195	10.23	4.2	5	5.50	2.29	tr|B9RN01|B9RN01_RICCO	Putative uncharacterized protein
197	10.18	24.9	10	0.55	0.59	tr|B9SIC4|B9SIC4_RICCO	chitinase Class I, putative
198	10.16	20.1	9	0.52	0.31	tr|B9RTJ4|B9RTJ4_RICCO	Stem-specific protein TSJT1SV=1
204	9.98	21.7	9	1.85	1.56	tr|A9PFJ7|A9PFJ7_POPTR	Pyruvate kinase
205	9.88	66.3	40	0.66	0.75	tr|F8RW92|F8RW92_HEVBR	Peptidyl-prolyl cis-trans isomerase
208	9.79	6.4	6	3.31	2.11	tr|B9T1E9|B9T1E9_RICCO	Importin beta-3, putative
210	9.66	31.3	12	1.67	1.53	tr|Q2XPH2|Q2XPH2_MANIN	Profilin
212	9.6	37.5	7	0.35	0.72	tr|Q8GZP2|Q8GZP2_HEVBR	Superoxide dismutase [Cu-Zn]
213	9.57	13.9	8	0.66	0.53	tr|B9RKX9|B9RKX9_RICCO	Seryl-tRNA synthetase, putative
216	9.47	18.8	21	0.36	0.77	tr|B9GH43|B9GH43_POPTR	Phospholipase D
219	9.44	47.7	12	0.65	0.66	tr|F2YZ44|F2YZ44_HEVBR	14-3-3 protein 3
220	9.44	19.2	6	0.61	0.63	tr|Q14VV8|Q14VV8_BOENI	Caffeic acid O-methyltransferase
221	9.34	35.3	10	0.28	0.53	tr|D2JWP4|D2JWP4_POPDE	Pathogenesis-related thaumatin
224	9.24	32.6	7	0.52	0.61	tr|D2WL72|D2WL72_POPTR	Glutathione transferase
226	9.2	32.7	26	0.57	0.52	tr|E8Z9H3|E8Z9H3_HEVBR	Latex cystatin
227	9.17	40.6	14	0.17	0.40	tr|F2VXU6|F2VXU6_HEVBR	Rab4
230	9.12	14.9	7	0.54	0.62	tr|B9H8X6|B9H8X6_POPTR	6-phosphofructokinase 3
241	8.78	35.9	6	0.40	0.58	tr|D6BR55|D6BR55_9ROSI	Acyl-CoA-binding protein
242	8.71	61.9	13	0.58	0.58	tr|D9I9X9|D9I9X9_HEVBR	Actin-depolymerizing factor
244	8.65	23.3	6	1.61	1.50	tr|B9R7X1|B9R7X1_RICCO	Proteasome subunit alpha type
245	8.65	41.8	7	0.65	0.70	tr|F8RWS9|F8RWS9_HEVBR	ubiquitin-protein ligase 1
246	8.6	12.1	6	1.79	0.69	tr|B9HR67|B9HR67_POPTR	Plant synaptotagmin
247	8.57	6.7	4	2.03	1.66	tr|B9SE11|B9SE11_RICCO	Delta 1-pyrroline-5-carboxylate synthetase
248	8.56	16.7	6	0.34	0.50	tr|F6HNF4|F6HNF4_VITVI	adenosine kinase 2
256	8.36	19.2	6	0.66	0.75	tr|B9HJ73|B9HJ73_POPTR	Fructose-bisphosphate aldolase
261	8.15	14.2	8	0.53	0.96	tr|B9RKG2|B9RKG2_RICCO	Arginyl-tRNA synthetase, putative
262	8.15	10.3	5	0.20	0.65	tr|E2DQG6|E2DQG6_MANES	Carotenoid cleavage dioxygenase 1
264	8.09	43	5	0.28	0.31	tr|B3FNP8|B3FNP8_HEVBR	Glutaredoxin
266	8.05	42	8	0.46	0.58	tr|B9T509|B9T509_RICCO	ras-related protein RABA3
267	8.02	29	6	0.39	0.12	tr|B9RKM9|B9RKM9_RICCO	Peroxiredoxin, putative
268	8	9.3	4	1.53	1.67	tr|B9S6T7|B9S6T7_RICCO	Ubiquilin, putative
269	7.99	7.5	5	0.61	0.57	tr|B9IGY9|B9IGY9_POPTR	2,3-bispho-phosphoglycerate mutase
278	7.82	20.6	10	0.58	0.62	tr|B9SXW5|B9SXW5_RICCO	26S proteasome non-atpase
279	7.78	14.4	7	0.47	0.67	tr|B9GXV5|B9GXV5_POPTR	FAS-associated factor 2
280	7.72	3.6	5	0.34	0.50	tr|B9RRX1|B9RRX1_RICCO	Putative uncharacterized protein
281	7.7	12.3	5	3.25	0.90	tr|B9SR96|B9SR96_RICCO	Glutamate decarboxylase, putative
284	7.66	15	5	0.38	1.00	tr|B2Z6Q5|B2Z6Q5_POPTR	hydroxycinnamoyltransferase
289	7.53	7.3	6	1.50	1.39	tr|B9SCN8|B9SCN8_RICCO	Eukaryotic translation initiation factor 2c
290	7.51	21.9	22	0.66	1.37	tr|O04975|O04975_MESCR	Fructose-bisphosphate aldolase
293	7.44	18.2	5	0.11	0.68	tr|B9S3Y6|B9S3Y6_RICCO	Nuclear protein localization
297	7.32	21.9	5	0.50	0.64	tr|B9S228|B9S228_RICCO	Nucleic acid binding protein
299	7.28	28.7	9	1.57	0.84	tr|B9HUT6|B9HUT6_POPTR	Proteasome subunit beta type
306	7.1	12.1	5	2.78	1.59	tr|B9HIC5|B9HIC5_POPTR	differentiation associated protein

310	7.05	18.2	4	1.51	1.12	tr|B9RIC4|B9RIC4_RICCO	40S ribosomal protein S2, putative
314	6.98	13.9	4	0.47	0.52	tr|A9PEP6|A9PEP6_POPTR	DNA damage-inducible protein
315	6.98	5	4	0.44	0.60	tr|F6H158|F6H158_VITVI	Putative uncharacterized protein
321	6.86	6.5	3	1.80	1.08	tr|B9SG36|B9SG36_RICCO	Ubiquitin-protein ligase, putative
322	6.86	20.2	7	0.44	2.25	tr|B9GXZ6|B9GXZ6_POPTR	alanine aminotransferase
324	6.85	19.6	5	0.51	0.71	tr|A5AQP2|A5AQP2_VITVI	ATP-citrate synthase alpha chain
327	6.81	33.3	36	0.65	0.70	tr|B2MW33|B2MW33_HEVBR	Heat shock protein 70
328	6.77	17.7	5	0.32	2.32	tr|B9SCD6|B9SCD6_RICCO	Esterase D, putative
329	6.77	30.3	6	0.23	0.75	tr|B9H2B8|B9H2B8_POPTR	Predicted protein
335	6.7	24.3	7	0.37	0.53	tr|B9RLJ0|B9RLJ0_RICCO	L-asparaginase, putative
338	6.66	12.1	4	0.61	1.26	tr|B9HLM0|B9HLM0_POPTR	Chorismate synthase
343	6.6	17.6	4	2.09	0.82	tr|B9SKG4|B9SKG4_RICCO	40S ribosomal protein S11, putative
345	6.54	6.8	4	0.33	1.27	tr|E6NU17|E6NU17_9ROSI	JHL07K02.17 protein
348	6.52	7	4	31.33	2.51	tr|B9SUE9|B9SUE9_RICCO	Hydrolase, O-glycosyl compounds
349	6.51	31.9	4	2.42	1.28	tr|B9SWB0|B9SWB0_RICCO	60S ribosomal protein L12, putative
350	6.49	14.7	4	0.48	0.84	tr|B9HG22|B9HG22_POPTR	GTP-binding protein
351	6.48	37.8	14	0.39	0.72	tr|A9ZN23|A9ZN23_HEVBR	Cis-prenyl transferase
355	6.46	22.7	3	2.27	0.86	tr|B9S120|B9S120_RICCO	40S ribosomal protein S14, putative
357	6.44	64	14	0.51	1.17	tr|Q6T708|Q6T708_HEVBR	Rubber elongation factor
364	6.34	13.9	5	0.60	0.62	tr|Q9ZTT8|Q9ZTT8_GOSHI	Chitinase, Class I
366	6.31	67.1	9	2.78	1.56	tr|B3FNP9|B3FNP9_HEVBR	Protease inhibitor protein
369	6.2	51.7	17	2.61	1.12	tr|A9P8X5|A9P8X5_POPTR	Ras-related protein RABB1b
370	6.18	11.2	7	1.64	1.17	tr|F6HGX0|F6HGX0_VITVI	Asparaginyl-tRNA synthetase
371	6.18	17.6	5	0.63	1.25	tr|O24328|O24328_RICCO	S-adenosyl-methionine hyltransferase
372	6.14	8.1	3	2.31	2.14	tr|F6HQV3|F6HQV3_VITVI	60S ribosomal protein L4
373	6.14	13.6	3	0.28	0.31	tr|B9SE47|B9SE47_RICCO	Malate dehydrogenase
374	6.12	18.5	7	0.09	0.29	tr|B9SUZ4|B9SUZ4_RICCO	Alcohol dehydrogenase
375	6.11	17.5	14	0.39	0.51	tr|G3G858|G3G858_CAMSI	Methionine synthase
382	6.03	24.2	4	1.71	1.47	tr|B9SA27|B9SA27_RICCO	Trafficking protein particle complex subunit
383	6.02	9.9	3	0.50	0.58	tr|Q5J3P0|Q5J3P0_MALDO	Sucrose phosphate phosphatase
386	6	19.1	3	2.19	1.74	tr|B9RYZ1|B9RYZ1_RICCO	60S ribosomal protein L9
389	6	6.5	3	6.19	1.20	tr|B9IBL7|B9IBL7_POPTR	Predicted protein
390	5.99	18	7	0.39	0.71	tr|F6I510|F6I510_VITVI	Putative uncharacterized protein
391	5.98	11.8	5	0.54	1.06	tr|B9IER7|B9IER7_POPTR	Carbonic anhydrase
392	5.95	7.6	4	5.06	1.78	tr|B9SN36|B9SN36_RICCO	Protein SEY1;root hair defective 3
395	5.85	17.4	3	1.75	1.46	tr|B9SU88|B9SU88_RICCO	Receptor for activated protein kinase
401	5.79	22.9	4	1.61	3.14	tr|G0YC94|G0YC94_9ROSI	Fumarylacetoacetate hydrolase
408	5.72	65.7	8	1.51	1.34	sp|Q6XNP7|HPI_HEVBR	Protease inhibitor
409	5.7	13.6	8	0.58	0.50	tr|B9T5Y1|B9T5Y1_RICCO	bisphosphate phosphodiesterase
410	5.68	8.9	4	2.29	2.13	tr|B9GU26|B9GU26_POPTR	Protein disulfide isomerase, putative
412	5.65	8.4	4	3.16	1.62	tr|F6HLF4|F6HLF4_VITVI	DEAD-box ATP-dependent RNA helicase
413	5.62	15.1	3	0.64	1.24	tr|B9A9C9|B9A9C9_MORAL	Urease accessory protein ureG
414	5.61	7.9	3	0.41	1.27	tr|B9N3J3|B9N3J3_POPTR	Predicted protein
419	5.57	11.9	2	0.41	0.73	tr|B9IJM2|B9IJM2_POPTR	Predicted protein

422	5.53	43.4	9	0.25	0.39	tr|Q94KV2|Q94KV2_MANES	Aspartic protease
424	5.45	43.5	31	3.02	2.08	tr|B9HV14|B9HV14_POPTR	Vacuolar H+-ATPase catalytic subunit A
426	5.44	42.9	55	0.41	0.51	sp|Q9LEI9|ENO2_HEVBR	Enolase 2
429	5.42	8.3	4	0.43	0.58	tr|C6TFR0|C6TFR0_SOYBN	alpha-galactosidase-like isoform 1
436	5.37	7.2	3	0.65	1.35	tr|Q6S9W9|Q6S9W9_GOSHI	Betaine-aldehyde dehydrogenase
437	5.35	12.4	5	0.45	0.61	tr|B9SPZ1|B9SPZ1_RICCO	2-hydroxyphytanoyl-CoA lyase
439	5.34	9.4	5	2.58	2.14	sp|Q38871|CDPK5_ARATH	Calcium-dependent protein kinase 5
441	5.34	8	6	0.10	0.39	tr|B9SX16|B9SX16_RICCO	acetylglucosamine transferase
447	5.22	16.1	4	0.21	0.17	tr|D7TLU7|D7TLU7_VITVI	Triosephosphate isomerase
448	5.22	17.3	4	9.73	2.08	tr|B9RUZ3|B9RUZ3_RICCO	Serine-threonine kinase receptor
449	5.22	21.7	3	1.56	1.71	tr|A9PGL4|A9PGL4_POPTR	40S ribosomal protein
453	5.19	20.4	5	0.38	0.53	tr|B9MU39|B9MU39_POPTR	quinone oxidoreductase, putative
456	5.16	59.1	79	0.13	0.65	tr|Q7XJ83|Q7XJ83_HEVBR	Beta-1,3-glucanase
459	5.11	38.7	34	0.47	0.54	tr|B9HIN6|B9HIN6_POPTR	ATP-citrate synthase beta chain
467	4.99	7.7	3	1.58	1.11	tr|D7U7I9|D7U7I9_VITVI	COP9 signalosome complex 1
475	4.89	5.6	2	0.60	0.64	tr|B9RF45|B9RF45_RICCO	Amidase, putative
478	4.86	5.2	3	0.52	1.06	tr|B9SBV7|B9SBV7_RICCO	Ligatin, putative
481	4.82	5.9	2	3.40	1.38	tr|B9RMR2|B9RMR2_RICCO	Steroid dehydrogenase, putative
482	4.81	11.6	5	0.61	0.56	tr|B9SGQ4|B9SGQ4_RICCO	Importin alpha-2 subunit, putative
485	4.79	8.8	4	0.58	0.72	tr|B9HRN7|B9HRN7_POPTR	Adenylyl cyclase-associated protein
487	4.74	10.6	2	0.66	0.89	tr|B9RF46|B9RF46_RICCO	Mevalonate kinase, putative
498	4.69	30.4	34	0.10	0.44	tr|B6EBD6|B6EBD6_SOYBN	Heat shock protein 90-2
503	4.65	4.9	2	0.60	0.69	tr|A9PF66|A9PF66_POPTR	isoflavone reductase related protein
504	4.65	13.2	3	0.44	0.57	tr|Q9STB5|Q9STB5_HEVBR	Superoxide dismutase
506	4.63	16.6	7	0.63	0.70	tr|C6TIP9|C6TIP9_SOYBN	Cysteine synthase
510	4.59	15.8	15	1.54	1.43	tr|B9T216|B9T216_RICCO	Fimbrin, putative
511	4.59	5.2	2	0.26	1.11	tr|B9HMM6|B9HMM6_POPTR	Folylpolyglutamate synthase
512	4.58	5.5	6	1.61	1.52	tr|B9S596|B9S596_RICCO	Myosin XI, putative
514	4.58	4.5	3	0.29	0.25	tr|A5C5R6|A5C5R6_VITVI	Cinnamyl alcohol dehydrogenase 1
516	4.57	12.2	5	0.14	0.57	tr|B9S1F8|B9S1F8_RICCO	Acetylornithine deacetylase
520	4.51	5.6	5	0.38	0.57	tr|B9SUT5|B9SUT5_RICCO	Isoleucyl tRNA synthetase, putative
533	4.37	9.8	2	0.31	0.21	tr|D7LDD9|D7LDD9_ARALL	3R-hydroxymyristoyl ACP dehydrase
534	4.35	20	10	0.23	0.36	tr|B9RHV9|B9RHV9_RICCO	Glyceraldehyde 3-phosphate dehydrogenase
536	4.35	12.9	5	0.22	0.55	tr|B5M1W3|B5M1W3_RHEAU	Glutathione-S-transferase
547	4.31	15.8	8	15.42	3.93	tr|Q9M563|Q9M563_VITVI	Beta-1,3-glucanase
549	4.3	17.7	5	0.18	2.47	tr|B9HFG8|B9HFG8_POPTR	annexin1
550	4.3	8.2	3	0.61	0.39	tr|B9SS35|B9SS35_RICCO	Argininosuccinate synthase, putative
552	4.28	9.2	4	0.13	0.25	tr|Q5PYQ3|Q5PYQ3_MANES	Glycerophosphodiester phosphodiesterase
556	4.24	7.6	3	0.61	0.68	tr|B9SL55|B9SL55_RICCO	DNA-binding protein smubp-2
561	4.21	5.1	2	1.67	1.63	tr|B9I337|B9I337_POPTR	transportin, putative
562	4.21	17.7	3	1.60	1.65	tr|B9HYZ8|B9HYZ8_POPTR	vacuolar protein sorting-associated protein
563	4.2	16	7	0.29	0.42	tr|B9SFR8|B9SFR8_RICCO	Aspartic proteinase, putative
567	4.17	50.4	7	0.65	1.98	sp|O65812|PROF1_HEVBR	Profilin-1
572	4.15	7.5	2	7.45	2.63	tr|Q307Z8|Q307Z8_SOLTU	ribosomal protein-like

578	4.13	45.4	5	0.65	0.52	tr|D4P094|D4P094_HEVBR	Copper transport protein ATOX1
580	4.12	10.2	4	0.60	2.02	tr|C6TIG8|C6TIG8_SOYBN	auxin-induced protein PCNT115
584	4.09	14	2	0.64	1.17	tr|B9IPT2|B9IPT2_POPTR	FH protein interacting protein
592	4.05	8.7	2	1.71	1.69	tr|B9MUU5|B9MUU5_POPTR	Vesicle-associated protein 1
596	4.05	12.9	4	0.52	0.30	tr|B9SJL8|B9SJL8_RICCO	Protease C56, putative
602	4.04	7.3	2	2.31	1.96	sp|O04373|ILL4_ARATH	IAA-amino acid hydrolase ILR1-like 4
605	4.03	8.3	4	0.48	0.56	tr|B9SC09|B9SC09_RICCO	Putative uncharacterized protein
606	4.03	4.1	4	0.21	0.39	tr|Q9LUL3|Q9LUL3_ARATH	Lipase class 3 family protein
610	4.02	15.2	6	1.91	1.58	tr|D7SXZ2|D7SXZ2_VITVI	dehydrogenase/reductase
612	4.01	23.6	3	0.52	0.27	sp|O64459|UGPA_PYRPY	UTP-phosphate uridylyltransferase
613	4.01	13.1	12	0.24	0.21	tr|Q7Y237|Q7Y237_EUOEU	Chitinase
618	4	64.6	79	0.60	0.33	tr|Q6JYQ9|Q6JYQ9_HEVBR	HEV1.2
625	4	14.1	6	0.65	1.05	tr|B9ST42|B9ST42_RICCO	Pyruvate kinase
628	4	8.4	3	0.22	0.22	tr|B9GFV7|B9GFV7_POPTR	TBC1 domain family member 13
631	4	29.9	2	3.05	2.04	tr|F4YFE3|F4YFE3_CAMSI	Cytochrome b5
634	4	5.7	2	0.46	1.44	tr|C6TGB0|C6TGB0_SOYBN	Putative uncharacterized protein
643	4	32.8	4	0.30	1.26	tr|D9IZZ6|D9IZZ6_HEVBR	Translation machinery-associated protein 7
648	3.96	10.8	2	0.22	0.59	tr|D7SIZ7|D7SIZ7_VITVI	20 kDa chaperonin, chloroplastic
650	3.95	16.5	3	11.48	2.11	tr|D1ML39|D1ML39_9ROSI	Ribosomal protein
651	3.94	9.3	3	3.40	2.06	tr|B9RDG1|B9RDG1_RICCO	Calcium lipid binding protein
653	3.92	8.3	4	0.13	0.70	sp|Q9FK25|OMT1_ARATH	Quercetin 3-O-methyltransferase 1
666	3.83	44.6	37	0.24	0.99	tr|D7U1A1|D7U1A1_VITVI	glyceraldehyde-3-phosphate dehydrogenase
668	3.82	13.7	9	0.50	1.13	tr|Q8GZD8|Q8GZD8_SOLLC	aminopeptidase preprotein
680	3.74	14.4	4	9.46	2.53	tr|E0CPI5|E0CPI5_VITVI	hydrolase domain-containing protein
683	3.7	26.6	8	3.31	2.04	tr|D7SN69|D7SN69_VITVI	bifunctional polymyxin resistance protein
687	3.68	21.5	2	1.69	1.53	tr|B8Y6I1|B8Y6I1_HEVBR	V-type proton ATPase subunit F
688	3.66	8	3	0.54	0.47	tr|E0CRW7|E0CRW7_VITVI	argininosuccinate lyase
692	3.63	7	3	0.09	0.19	tr|B9RXB8|B9RXB8_RICCO	Homogentisate 1,2-dioxygenase
694	3.61	8.2	2	0.48	0.67	tr|B9SQS5|B9SQS5_RICCO	3-isopropylmalate dehydratase
700	3.54	15.2	5	0.61	0.87	tr|B9RAR0|B9RAR0_RICCO	Protein-L-isoaspartate O-methyltransferase
703	3.53	19.8	3	1.50	1.34	tr|D5JG84|D5JG84_9ROSI	Heat shock protein 17.5 class II
704	3.52	3	2	0.10	0.35	tr|D7T494|D7T494_VITVI	Putative uncharacterized protein
708	3.46	6.5	4	16.00	3.72	tr|B9T139|B9T139_RICCO	Hydrolase
710	3.44	17.3	6	0.55	0.61	tr|B9N432|B9N432_POPTR	ATP-citrate synthase, putative
713	3.44	7.6	2	12.13	2.13	tr|B9RWM3|B9RWM3_RICCO	Potassium channel beta, putative
714	3.43	11.2	3	0.59	0.68	tr|Q5EBY6|Q5EBY6_EUPCH	Aldehyde dehydrogenase family 7
716	3.43	20.1	7	0.23	0.48	tr|B9R7W5|B9R7W5_RICCO	Isoflavone reductase, putative
717	3.42	10.9	7	0.61	0.79	tr|B9GZ19|B9GZ19_POPTR	glycine-tRNA ligase 1
718	3.42	20.4	2	2.07	0.91	tr|B9RH67|B9RH67_RICCO	40S ribosomal protein S25-1
720	3.4	15.1	26	1.63	1.20	tr|A5ACP0|A5ACP0_VITVI	clathrin heavy chain 1
723	3.4	100	4	0.11	0.58	sp|P86104|UP01_VITRO	Unknown protein 1
729	3.37	16.8	19	0.62	1.09	tr|B9RQ33|B9RQ33_RICCO	5-methyl-homocysteine methyltransferase
732	3.37	8.5	2	4.02	11.62	tr|B9T676|B9T676_RICCO	Catalytic, putative

735	3.34	3.4	2	1.71	1.29	tr|D7T8E1|D7T8E1_VITVI	Phagocytic receptor 1b
738	3.33	6.1	2	0.43	0.25	tr|B9RLT7|B9RLT7_RICCO	Dimethylaniline monooxygenase
740	3.31	6.8	6	0.19	0.38	tr|Q8VZH2|Q8VZH2_ARATH	Aminopeptidase M1
743	3.29	2.3	2	2.11	1.19	tr|B9SDH3|B9SDH3_RICCO	Cytochrome P450, putative
744	3.29	6.8	2	1.61	2.01	tr|F6HIY1|F6HIY1_VITVI	cytochrome b5 reductase 1-like
746	3.29	11.3	2	0.62	0.41	tr|Q38HT5|Q38HT5_SOLTU	40S ribosomal protein S23
757	3.24	7.1	2	1.94	2.65	tr|A9PDL9|A9PDL9_POPTR	Very-long-chain enoyl-CoA reductase
758	3.22	6.4	3	0.52	1.67	tr|B9RRB9|B9RRB9_RICCO	Suppression of tumorigenicity
759	3.22	7.1	2	2.49	1.56	tr|B9SEA1|B9SEA1_RICCO	Peroxidase 12, putative
760	3.21	25	21	1.63	1.51	tr|F6H4T7|F6H4T7_VITVI	elongation factor 2-like
763	3.19	5.9	2	0.58	1.02	tr|E9M776|E9M776_HEVBR	Cinnamoyl-CoA reductase
771	3.09	5.7	2	0.58	0.52	tr|B0LUS9|B0LUS9_TOBAC	Multicopy suppressor
772	3.06	5.5	3	0.13	0.57	tr|B9IEZ0|B9IEZ0_POPTR	ubiquitin domain-containing protein
774	3.05	2.5	2	1.96	2.06	tr|B9SYU2|B9SYU2_RICCO	Vacuolar sorting protein
778	3.04	4.2	2	0.19	0.54	tr|A9PEK1|A9PEK1_POPTR	Phosphoglycerate dehydrogenase
779	3.03	8.6	6	0.27	0.32	tr|D7MNN8|D7MNN8_ARALL	Sucrose synthase
780	3.03	2.4	2	2.01	1.67	tr|B9HPP7|B9HPP7_POPTR	Calcium ATPase
782	3.02	6.4	2	0.54	0.27	sp|Q9M9E9|SRK2C_ARATH	Serine/threonine-protein kinase
783	3.02	4.5	2	0.62	0.38	tr|B9T5L2|B9T5L2_RICCO	Nonsense-mediated mRNA decay protein
784	3	15.9	4	1.64	1.77	tr|B9RTH6|B9RTH6_RICCO	ADP-ribosylation factor
789	2.98	10.3	3	0.10	0.14	tr|B9R730|B9R730_RICCO	Putative uncharacterized protein
790	2.98	3.6	3	0.48	1.16	sp|Q2XPU6|CAS1_RICCO	Cycloartenol synthase
794	2.95	23	10	0.24	0.19	tr|F6H7L5|F6H7L5_VITVI	Lactoylglutathione lyase
799	2.93	2.2	2	0.55	2.21	tr|A5BG74|A5BG74_VITVI	protein argonaute 4A-like
801	2.92	26	10	1.60	0.96	sp|Q9AT56|METK1_ELAUM	S-adenosylmethionine synthase 1
807	2.9	13.4	3	1.51	0.33	tr|B9SS61|B9SS61_RICCO	60S ribosomal protein L14
808	2.9	25.2	2	0.08	0.30	tr|B9IJS4|B9IJS4_POPTR	Thioredoxin
813	2.87	19.8	4	1.77	2.51	tr|B9IEB2|B9IEB2_POPTR	Ras-related protein RABA6b
817	2.85	65.7	63	0.62	0.34	sp|P02877|HEVE_HEVBR	Pro-hevein OS=Hevea brasiliensis
819	2.84	14.3	5	1.96	1.18	tr|Q66PF9|Q66PF9_PEA	Monodehydroascorbate reductase I
825	2.81	11.8	6	1.72	1.18	tr|F6HHF5|F6HHF5_VITVI	eukaryotic initiation factor 4A-3
827	2.81	7.7	2	0.31	0.35	tr|B9IAZ4|B9IAZ4_POPTR	Ribosomal protein L5A, 60S
828	2.81	13.3	2	1.75	0.48	tr|C6SZQ3|C6SZQ3_SOYBN	60S ribosomal protein L23A
832	2.78	3.5	2	2.21	1.97	tr|B9GSW4|B9GSW4_POPTR	Long chain acyl-CoA synthetase 1
835	2.77	8.1	2	1.51	1.02	tr|B9T7A3|B9T7A3_RICCO	Ubiquitin carboxyl-terminal hydrolase
838	2.76	6	2	0.63	1.29	tr|D7LLA4|D7LLA4_ARALL	Tubulin beta-7 chain
839	2.75	6.8	4	1.77	0.98	tr|B9RSG5|B9RSG5_RICCO	Dipeptidyl peptidase IV
840	2.75	16.7	3	0.38	1.15	tr|B9S069|B9S069_RICCO	Glutathione-s-transferase theta
844	2.72	16.4	4	0.61	0.51	tr|B9S7R8|B9S7R8_RICCO	Pyridoxine kinase, putative
845	2.72	8.4	5	0.21	0.18	tr|B9H6S4|B9H6S4_POPTR	rhamnogalacturonate lyase
864	2.65	9.4	4	0.62	0.98	tr|B9RZ84|B9RZ84_RICCO	Glutaredoxin, grx, putative
868	2.65	23.5	3	0.54	0.47	tr|D7TK03|D7TK03_VITVI	programmed cell death protein 5
869	2.64	5.7	3	0.30	0.34	tr|A5BDT4|A5BDT4_VITVI	14 kDa zinc-binding protein
870	2.64	7.2	2	0.53	2.38	sp|B9SL58|PURA2_RICCO	Adenylosuccinate synthetase 2

871	2.63	11	3	2.68	0.54	tr|B9SGS2|B9SGS2_RICCO	60S ribosomal protein L4
879	2.61	30.2	23	0.30	1.01	tr|B9H5X2|B9H5X2_POPTR	Phosphofructokinase
885	2.61	15.3	3	1.77	0.79	tr|E9JFW4|E9JFW4_9ROSI	Thioredoxin
886	2.6	8.9	2	0.64	0.97	tr|A5BVN4|A5BVN4_VITVI	Nucleoside diphosphate kinase
888	2.59	10	2	7.31	2.19	tr|B9RTJ5|B9RTJ5_RICCO	Coated vesicle membrane protein
900	2.53	15.9	2	0.47	0.24	tr|B9MT66|B9MT66_POPTR	Glutathione transferase GSTL3
903	2.53	11.9	3	0.46	0.22	tr|Q9S7R3|Q9S7R3_ARATH	177 protein
904	2.53	7.2	2	2.36	1.50	tr|G1ED19|G1ED19_GOSHI	Protein disulfide isomerase
905	2.52	9.1	3	0.35	0.16	tr|O49235|O49235_SOYBN	Glutathione S-transferase
907	2.5	19.1	10	0.59	1.07	tr|B7FKU7|B7FKU7_MEDTR	Cysteine synthase
914	2.48	3.5	2	1.89	1.96	tr|D7KNJ9|D7KNJ9_ARALL	trehalose-phosphate synthase
921	2.45	6.2	3	0.27	0.99	tr|B9SGK0|B9SGK0_RICCO	Adaptin ear-binding coat-associated protein
929	2.41	6.6	2	0.61	0.29	tr|B9T8C2|B9T8C2_RICCO	Putative uncharacterized protein
938	2.37	15.9	2	2.27	2.11	tr|D6BRD9|D6BRD9_9ROSI	Glutathione-s-transferase theta
944	2.35	28.2	20	0.52	0.22	tr|D7LJ40|D7LJ40_ARALL	Fructose-bisphosphate aldolase
945	2.35	5.9	3	0.20	0.47	tr|B9ICR4|B9ICR4_POPTR	coatomer subunit delta
948	2.34	8.2	4	0.40	0.54	tr|B9H0Q2|B9H0Q2_POPTR	Adenylyl cyclase-associated protein
949	2.34	6.7	5	0.09	0.37	sp|P51074|ANX4_FRAAN	Annexin-like protein RJ4
952	2.33	23.5	18	0.47	0.33	tr|Q2WFK8|Q2WFK8_9ASTR	Fructose-bisphosphate aldolase
975	2.28	14.7	2	1.77	2.07	tr|B9H5H4|B9H5H4_POPTR	dolichol-phosphate mannosyltransferase
981	2.26	9.5	3	0.61	1.05	tr|B9H739|B9H739_POPTR	Predicted protein
982	2.25	11.6	13	0.29	0.24	tr|Q533V0|Q533V0_FRAAN	Phospholipase D
990	2.23	7.3	5	0.59	1.25	tr|B9ILT5|B9ILT5_POPTR	Malic enzyme
993	2.23	6.9	2	2.91	0.86	tr|B9RA70|B9RA70_RICCO	Signal recognition particle 68 kDa protein
1002	2.2	5.2	2	6.19	3.09	tr|B9SD61|B9SD61_RICCO	Hydrolase; Leukotriene hydrolase
1008	2.19	5.9	2	5.06	1.54	tr|B7FM77|B7FM77_MEDTR	Alanine aminotransferase
1016	2.18	33.2	7	0.35	1.21	sp|Q40521|RB11B_TOBAC	Ras-related protein Rab11B
1019	2.17	12.2	2	1.67	0.30	tr|A5BV59|A5BV59_VITVI	guanine nucleotide-binding protein
1026	2.15	3.4	2	2.38	1.60	tr|B9T6N8|B9T6N8_RICCO	Indole-3-acetic acid-amido synthetase
1029	2.15	11.9	2	1.66	1.74	tr|B9N7F9|B9N7F9_POPTR	Vesicle transport protein-lik
1030	2.14	10	5	0.27	0.38	tr|A9PCM5|A9PCM5_POPTR	Proteasome subunit alpha type
1037	2.13	18.7	8	0.28	0.22	tr|B9GTA1|B9GTA1_POPTR	Aminoacyl-tRNA synthetase
1044	2.12	6.9	3	0.60	1.09	tr|D7TMA3|D7TMA3_VITVI	Chorismate synthase
1049	2.12	3.8	5	0.47	1.01	tr|F6HLA1|F6HLA1_VITVI	pantothenate kinase
1051	2.11	4.7	4	0.60	0.93	tr|A9Z0V7|A9Z0V7_ROSDA	Carotenoid cleavage dioxygenase 1
1059	2.1	11.6	3	0.56	0.75	tr|B9R8F0|B9R8F0_RICCO	Nucleoredoxin, putative
1062	2.09	11.2	2	0.65	1.15	tr|B9SS56|B9SS56_RICCO	Structural molecule, putative
1065	2.08	8.7	4	1.66	2.75	tr|Q6TKR0|Q6TKR0_TOBAC	Ribosomal protein L3A
1066	2.08	8.1	4	2.21	0.92	tr|Q94KK8|Q94KK8_TOBAC	Glutamate decarboxylase isozyme 3
1067	2.08	4.6	5	0.59	0.41	tr|F8WL79|F8WL79_CITUN	Aminopeptidase
1071	2.07	14.8	13	0.16	0.28	tr|D7SIX7|D7SIX7_VITVI	serine/threonine-protein phosphatase
1072	2.07	6.5	4	0.42	1.36	tr|B3TZ27|B3TZ27_RICCO	Long-chain acyl-CoA synthetase 4
1081	2.06	27.4	19	0.28	0.62	tr|F6HZK0|F6HZK0_VITVI	Malate dehydrogenase
1082	2.06	8	2	2.05	1.06	tr|B9IF79|B9IF79_POPTR	Aspartyl aminopeptidase

1085	2.06	7.6	4	1.58	1.04	tr|Q9M835|Q9M835_ARATH	L-allo-threonine aldolase, putative
1120	2.03	10.2	8	0.60	4.17	tr|D1MAF2|D1MAF2_SOLLC	Exportin-1
1121	2.03	25.7	7	2.13	0.82	tr|B9SR17|B9SR17_RICCO	Glucose 4-6-dehydratase, putative
1130	2.03	23.3	4	0.42	0.88	tr|Q8LCK3|Q8LCK3_ARATH	copper transport protein
1136	2.02	3	2	0.51	1.13	tr|Q9SJT7|Q9SJT7_ARATH	V-type H+-transporting ATPase subunit I
1137	2.02	26.2	8	0.61	0.53	tr|B9IF97|B9IF97_POPTR	Translation elongation factor
1155	2.01	8.5	5	11.07	3.94	tr|B9HA87|B9HA87_POPTR	Galactinol-sucrose galactosyltransferase
1157	2.01	3.8	2	1.60	1.63	tr|D7SS21|D7SS21_VITVI	Pyrophosphate-energized membrane proton
1171	2	33.9	18	0.61	0.22	tr|C0LDX2|C0LDX2_9ROSI	Glyceraldehyde-3-pho- dehydrogenase
1172	2	73.3	18	0.62	1.21	tr|A9P8Q6|A9P8Q6_POPTR	Ras-related protein Rab7
1173	2	40.9	17	3.22	1.02	tr|Q9M5X2|Q9M5X2_EUPES	Heat shock protein 80
1179	2	11.3	10	1.58	0.71	tr|B9HRP1|B9HRP1_POPTR	Coatomer subunit gamma
1180	2	37	8	0.60	0.29	tr|D5K0Z8|D5K0Z8_9FABA	Actin-like protein
1186	2	8.5	8	0.60	0.25	tr|B9I7J3|B9I7J3_POPTR	Luminal-binding protein 5
1188	2	45.1	5	0.65	0.53	tr|B2X0F6|B2X0F6_9ROSI	Glyceraldehyde 3-phosphate dehydrogenase
1191	2	2.9	3	2.58	1.98	tr|F6GZ28|F6GZ28_VITVI	Myosin-Vb-like
1195	2	11.3	3	2.05	1.05	tr|D7U7P5|D7U7P5_VITVI	Fructokinase-5-like
1196	2	5.8	4	0.65	0.53	tr|C9EA44|C9EA44_CARPA	Ripening-reduced arabinofuranosidase
1203	2	16.3	4	1.85	1.08	tr|C6TED4|C6TED4_SOYBN	Ras-related protein RHN1-like
1206	2	6.1	2	0.19	0.23	tr|A9P745|A9P745_HELAN	Enolase
1207	2	11.2	5	1.51	0.72	tr|B9RFA8|B9RFA8_RICCO	Rubber elongation factor protein
1210	2	6.7	2	5.40	1.25	tr|Q8LA96|Q8LA96_ARATH	RNA recognition motif-containing protein
1211	2	5.2	2	0.20	0.51	tr|Q40581|Q40581_TOBAC	GTP-binding protein
1214	2	6.3	4	0.48	1.01	tr|B9GK93|B9GK93_POPTR	FAS-associated factor 2
1225	2	3.7	3	0.66	0.63	tr|A5AEX6|A5AEX6_VITVI	carboxymethylenebutenolidase
1228	2	16.8	2	0.61	0.52	tr|B9H401|B9H401_POPTR	Prefoldin subuni
1231	2	8.2	3	2.29	3.08	tr|D7SZI9|D7SZI9_VITVI	60S ribosomal protein
1236	2	6	2	0.52	0.37	tr|B9HQZ2|B9HQZ2_POPTR	chitinase 1
1247	2	8.2	2	0.34	0.82	tr|B9SYE9|B9SYE9_RICCO	ADP-ribosylation factor, putative
1275	2	9.2	2	0.61	1.16	tr|B9S7V3|B9S7V3_RICCO	V-type proton ATPase subunit F
1278	2	27.6	6	0.39	0.95	tr|A9PBT2|A9PBT2_POPTR	nuclear transport factor 2 isoform 1
1281	2	29.8	6	0.51	1.43	tr|A9PE14|A9PE14_POPTR	nuclear transport factor
1318	2	8.9	5	0.52	0.12	tr|F6HF70|F6HF70_VITVI	Putative uncharacterized protein
1320	2	16.7	2	2.07	1.03	tr|B9T0W0|B9T0W0_RICCO	heat shock factor-binding protein
1336	1.95	11.3	4	1.67	4.33	tr|B9SXV3|B9SXV3_RICCO	Calcium lipid binding protein
1337	1.94	4.5	2	1.96	1.54	tr|F6HCT7|F6HCT7_VITVI	heat shock 70 kDa protein
1341	1.92	11.2	2	0.62	0.58	tr|B9N560|B9N560_POPTR	Predicted protein
1346	1.91	5.7	2	1.71	3.28	tr|B9R7B8|B9R7B8_RICCO	Serine/threonine-protein kinase
1348	1.89	10.3	3	0.33	1.16	tr|B9S119|B9S119_RICCO	Putative uncharacterized protein
1353	1.87	7.1	4	0.45	0.51	tr|Q949H3|Q949H3_HEVBR	Chitinase, class I
1355	1.86	22	19	2.75	0.78	tr|B9H023|B9H023_POPTR	GTP-binding protein
1387	1.77	77.3	20	0.24	0.82	tr|B7FLK9|B7FLK9_MEDTR	ubiquitin 11
1404	1.7	7	2	2.94	3.98	tr|B9RGW6|B9RGW6_RICCO	Conserved hypothetical protein
1407	1.69	1.5	2	0.59	0.56	tr|B9I2G0|B9I2G0_POPTR	Predicted protein

1418	1.65	7.5	3	0.10	0.21	tr|B9HBL6|B9HBL6_POPTR	aspartate-tRNA ligase, cytoplasmic
1426	1.61	8.3	3	0.17	0.93	tr|F6H1I3|F6H1I3_VITVI	random slug protein 5 isoform 2
1434	1.58	32.5	19	0.58	0.73	tr|Q6QLW8|Q6QLW8_HEVBR	HMG-CoA synthase 2
1437	1.57	5.2	2	3.73	7.78	tr|B9IEB9|B9IEB9_POPTR	methyl transferase
1453	1.53	5.9	2	0.64	0.51	tr|Q1W6C5|Q1W6C5_9CARY	chitinase Class Ib
1459	1.51	8.9	4	0.60	0.56	tr|B9SBH8|B9SBH8_RICCO	Dynamin, putative
1464	1.5	7.2	3	0.60	0.94	tr|A8IKE1|A8IKE1_SOYBN	Alanine aminotransferase 1
1467	1.49	20.7	6	0.52	0.24	tr|Q8LBD5|Q8LBD5_ARATH	L-lactate dehydrogenase
1479	1.43	14.7	3	0.64	0.79	tr|C6TB50|C6TB50_SOYBN	S-formylglutathione hydrolase-like
1487	1.4	5.1	2	2.25	1.82	tr|E0CR92|E0CR92_VITVI	Aminotransferase YbdL-like
1494	1.39	6.5	2	0.13	0.29	tr|F6H2P8|F6H2P8_VITVI	Putative uncharacterized protein
1523	1.31	3.1	2	2.11	1.52	tr|C6TNV4|C6TNV4_SOYBN	succinyl-CoA ligase subunit alpha-1

Note:

[a] The protein number (I-) obtained from the iTRAQ experiments.

[b] The Unused Score produced by the ProteinPilot™ Software.

[c] The percent of sequence coverage value for the matched peptides with higher than 95% confidence.

[d] The number of matched matched peptides with higher than 95% confidence.

[e] The changed ration of target protein in the E-3 and D-3 rubber latex identified by iTRAQ.

[f] Accession numbers and plant species in the Swiss-Prot Database.

Supplementary Table S4 MS identification of the 59 phosphorlated latex proteins

Spot	**Changed ratio**[b]	**Thero.**[c]	**M.S.**[d]	**NCBI**	**Plant**	**Protein**
P-.[a]	**E3/D3:E3/D0:D3/D0**	***p*I/M*r***	**Score**	**No.**[e]	**species**	**name**
P1	0.26: 0.36: 2.03	5.11/71.6	97	123650	*P. hybrida*	Heat shock cognate 70 kDa protein
P2	3.75: 7.78: 2.48	5.52/61.4	[54]	249262	*M. esculenta*	linamarase
P3	0.46: 0.56: 0.92	4.54/46.1	[112]	224100473	*P. trichocarpa*	predicted protein
P4	1.31: 0.57: 0.45	5.52/61.4	[56]	249262	*M. esculenta*	linamarase
P5	4.48: 2.82: 0.48	4.61/12.8	[502]	29170601	*H. brasiliensis*	Small rubber particle protein
P6	15.04: 5.74: 0.21	4.61/12.8	[429]	29170601	*H. brasiliensis*	Small rubber particle protein
P7	0.46: 1.01: 1.77	5.28/47.1	[75]	224071449	*P. trichocarpa*	phospholipase A
P8	5.26: 7.09: 2.01	5.31/42.0	[519]	32186890	*G. hirsutum*	actin
P9	0.28: 0.64: 3.21	4.8/22.3	[384]	14423933	*H. brasiliensis*	Small rubber particle protein
P10	0.36: 0.43: 1.30	5.28/47.1	[71]	224071449	*P. trichocarpa*	phospholipase A
P11	1.13: 0.45: 0.62	5.28/47.1	[52]	224071449	*P. trichocarpa*	phospholipase A
P12	0.47: 0.37: 0.46	5.28/47.1	[106]	224071449	*P. trichocarpa*	phospholipase A
P13	1.95: 2.15: 1.10	5.49/50.3	[51]	1550740	*A. thaliana*	GDP-associated inhibitor
P14	0.37: 0.37: 1.67	6.5/32.1	[144]	255552291	*R. communis*	short chain dehydrogenase, putative
P15	0.49: 0.38: 0.87	6.56/39.2	[174]	218157	*O. sativa*	cytoplasmic aldolase
P16	2.47: 0.73: 0.38	6.56/39.2	[125]	218157	*O. sativa*	cytoplasmic aldolase
P17	4.66: 15.17: 4.53	4.8/22.3	[171]	14423933	*H. brasiliensis*	Small rubber particle protein
P18	1.15: 2.32: 3.97	8.42/35.9	[74]	118489480	*P. trichocarpa*	unknown
P19	3.29: 3.33: 1.07	5.04/14.7	[341]	132270	*H. brasiliensis*	Rubber elongation factor protein
P20	2.81: 2.11: 0.71	5.04/14.7	[597]	132270	*H. brasiliensis*	Rubber elongation factor protein
P21	2.33: 1.87: 0.72	5.04/14.7	[672]	132270	*H. brasiliensis*	Rubber elongation factor protein
P22	0.18: 0.41: 2.34	4.94/80.3	[197]	38154482	*N. benthamiana*	Hsp 90-1
P23	1.42: 3.24: 2.76	4.95/81.1	[126]	1708314	*I. nil*	Heat shock protein 83
P24	2.38: 2.65: 1.37	5.07/71.1	[136]	20559	*P. hybrida*	hsp70 (AA 6 - 651)
P25	1.55: 2.67: 2.61	5.08/59.1	[118]	255566038	*R. communis*	Phospholipase C 3 precursor
P26	2.10: 3.98: 1.61	5.01/46.4	[80]	4235430	*H. brasiliensis*	latex-abundant protein
P27	0.61: 3.71: 6.87	5.21/59.4	[53]	297833008	*A. lyrata*	phosphoesterase family protein
P28	2.70: 1.93: 0.37	5.23/62.1	[108]	226530579	*Z. mays*	uncharacterized protein
P29	2.39: 0.75: 0.41	6.75/59.3	[133]	149938954	*A. chinensis*	G6PD1; glucose-6-phosphate dehydrogenase
P30	1.04: 2.15: 3.11	6.26/38.2	[53]	226493285	*Z. mays*	flavonol 4-sulfotransferase
P31	0.51: 0.31: 1.34	5.28/47.1	[104]	224071449	*P. trichocarpa*	phospholipase A
P32	0.93: 1.36: 2.07	5.0/43.0	[219]	1916805	*H. brasiliensis*	latex patatin homolog
P33	0.51: 0.27: 0.41	5.0/43.1	[196]	6707018	*H. brasiliensis*	latex protein allergen Hev b 7
P34	0.46: 0.83: 1.33	5.31/41.9	[392]	32186890	*G. hirsutum*	actin
P35	5.06: 6.54: 0.89	6.5/32.1	[141]	255552291	*R. communis*	short chain dehydrogenase, putative
P36	3.77: 1.01: 0.22	5.06/19.6	[393]	38122474	*H. brasiliensis*	Rubber elongation factor protein
P37	0.14: 0.21: 1.29	4.06/15.2	[288]	334854634	*H. brasiliensis*	elicitor-responsive protein
P38	7.23: 7.56: 2.19	4.8/22.3	[353]	14423933	*H. brasiliensis*	Small rubber particle protein
P39	4.51: 5.10: 1.94	4.8/22.3	[342]	14423933	*H. brasiliensis*	Small rubber particle protein
P40	2.06: 2.04: 1.51	4.61/12.8	[316]	29170601	*H. brasiliensis*	Small rubber particle protein
P41	0.88: 9.80: 10.89	5.64/20.9	[261]	2832430	*H. brasiliensis*	prohevein

P42	2.11: 2.06: 1.12	4.79/29.5	93	388503664	*L. japonicus*	unknown
P43	2.33: 3.97: 2.19	4.76/29.9	[294]	326694865	*H. brasiliensis*	14-3-3 protein 2
P44	1.55: 3.01: 2.80	5.84/27.4	[69]	224099853	*P. trichocarpa*	predicted protein
P45	1.35: 2.18: 1.71	9.4/41.5	[745]	124365253	*H. brasiliensis*	beta-1,3-glucanase
P46	1.63: 2.23: 1.35	6.11/36.1	[347]	224102193	*P. trichocarpa*	malate dehydrogenase
P47	0.67: 0.46: 0.74	4.65/41.4	[75]	*255578278*	*R. communis*	hypothetical protein
P48	2.41: 6.72: 3.69	6.5/32.1	[201]	255552291	*R. communis*	short chain dehydrogenase, putative
P49	1.14: 2.77: 2.94	5.17/30.1	[175]	255581753	*R. communis*	adenosine kinase, putative
P50	1.39: 1.18: 2.23	5.79/66.6	[96]	4588474	*B. napus*	phosphoinositide phospholipase C
P51	1.43: 5.81: 11.34	4.65/41.4	[95]	255578278	*R. communis*	hypothetical protein
P52	5.02: 7.38: 1.33	6.5/32.1	[67]	255552291	*R. communis*	short chain dehydrogenase, putative
P53	1.26: 2.25: 2.17	5.08/36.3	[279]	224057068	*P. trichocarpa*	predicted protein
P54	0.44: 0.43: 0.89	5.64/20.9	[181]	2832430	*H. brasiliensis*	prohevein
P55	0.41: 0.46: 0.95	5.28/47.1	[55]	224071449	*P. trichocarpa*	phospholipase A
P56	0.24: 0.58: 3.23	6.56/39.2	[58]	218157	*O. sativa*	cytoplasmic aldolase
P57	0.40: 0.50: 1.64	5.49/42.2	[120]	15219412	*A. thaliana*	phosphoglycerate kinase
P58	5.28: 1.23: 0.22	5.33/63.7	[121]	356513072	*G. max*	phosphoglucomutase, cytoplasmic
P59	2.65: 1.03: 0.37	5.46/63.7	[95]	255568794	*R. communis*	nucleoredoxin, putative

Note:

[a] Assigned spot number (P1-P59) of the differentially phosphorylated proteins were indicated in Fig. 5.

[b] The relatively changed ratios (E-3/D-3; E-3/D-0; D-3/D-0) of the phosphorylated protein spots among the D-0, D-3 and E-3 latex proteins from the rubber trees treated by water and ethylene. All the protein spots in the 2-DE gels were analyzed by ImageMaster software.

[c] The theoretical values for the *p*I and mass (kDa)of the identified proteins. The theoretical values were retrieved from the protein database.

[d] Mascot searched scores (M.S.) against NCBInr for the MS and [MS/MS] searched results.

[e] Database accession (gi|) numbers according to NCBInr.