

# **Comparative Proteomics of Phytase-transgenic Maize Seed Indicates Environmental Influence is More Important than that of Gene**

## **Insertion**

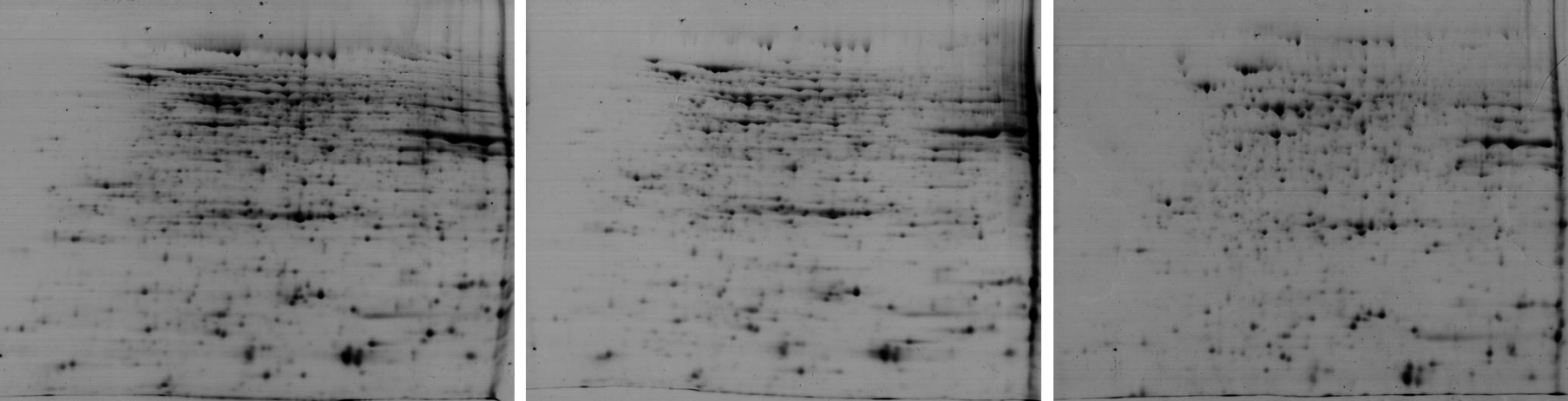
**Authors:** Yanhua Tan, Jiaming Zhang, Yong Sun, Zheng Tong, Cunzhi Peng, Lili Chang, Anping Guo, Xuchu Wang

Supplementary Figure S1: 2D gels of maize seed's proteins in different growth environments.

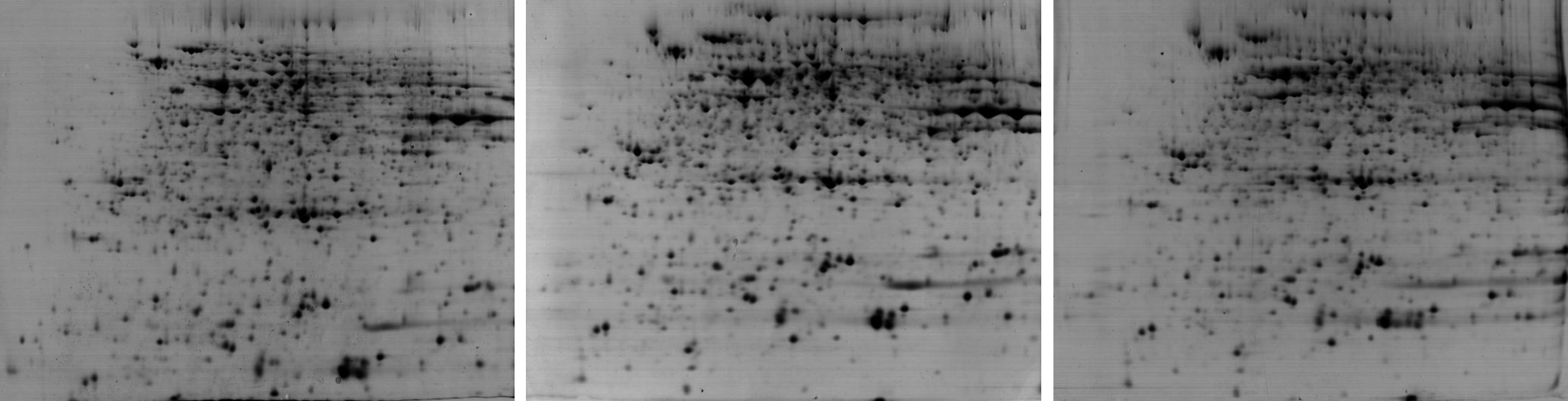
Supplementary Figure S2: Supplemental spectra and MALDI TOF/TOF MS/MS identification of the differentially expressed proteins.

**Supplementary Figure S1: 2D gels of maize seed's proteins in different growth environments.**

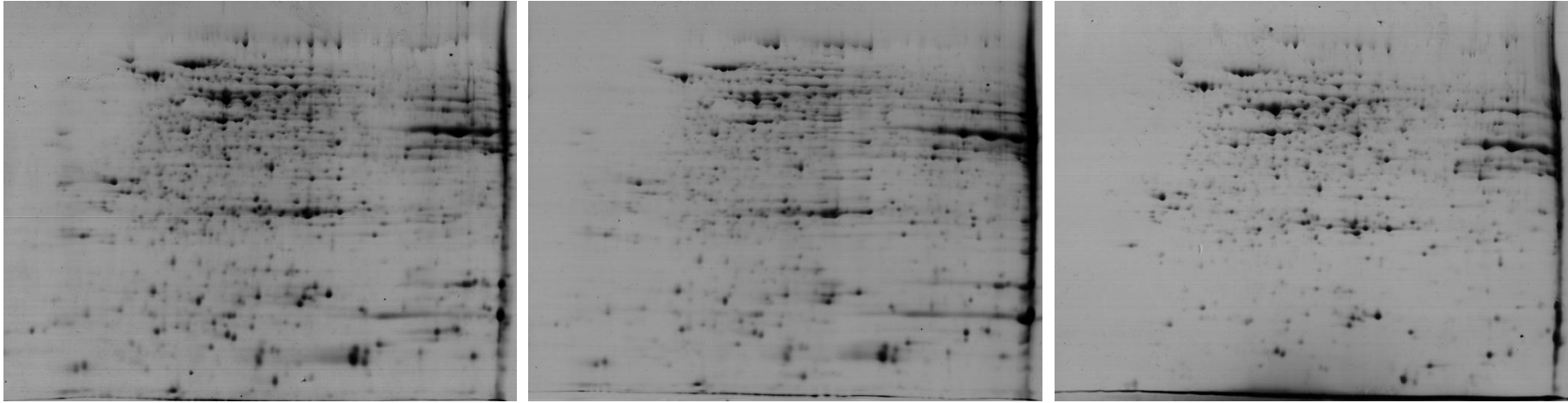
(1): 3 repeated 2D gels of NT maize seeds grown in greenhouse.



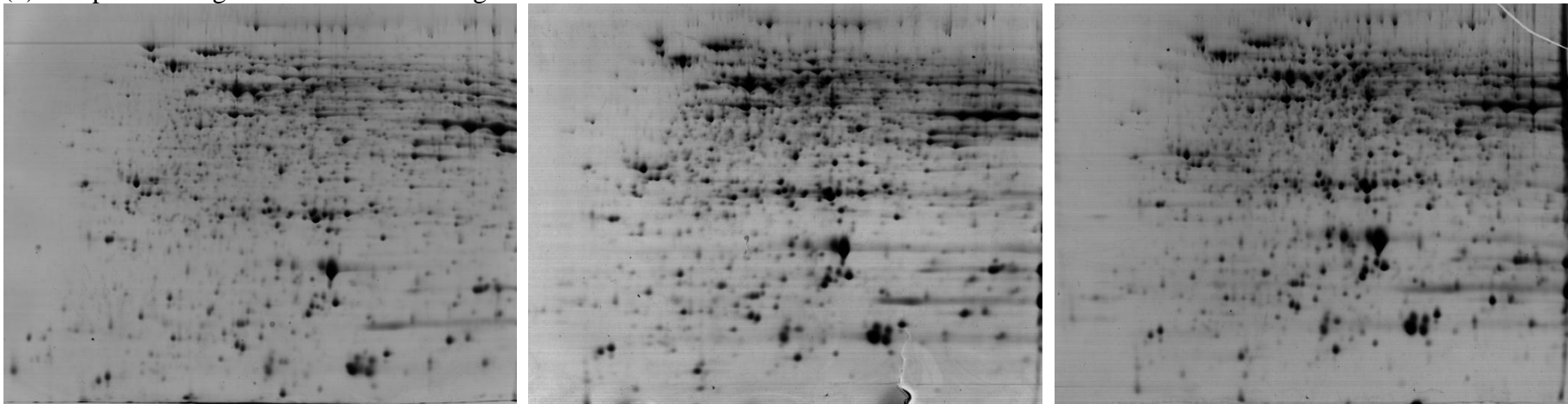
(2): 3 repeated 2D gels of NT maize seeds grown in field.



(3): 3 repeated 2D gels of PT maize seeds grown in greenhouse.



(4): 3 repeated 2D gels of PT maize seeds grown in field.



**Supplementary Figure S2: Supplemental spectra and MALDI TOF/TOF MS/MS identification of the differentially expressed proteins.**

**Annotated spectra for Table 1: 30 proteins identified by PFF.**

Spot numbers of the 30 proteins correspond to the proteins that listed in Table 1.

**CID:** collision induced dissociation

**MALDI TOF:** matrix assisted laser desorption/ionization time of flight

**MS:** mass spectrometry

**PFF:** peptide fragment fingerprinting

Spot No.: **1**

NCBI accession No.: [gi|195630027](#)

Plant species: **Zea mays**

Protein name: **ruBisCO large subunit-binding protein subunit beta**

Peptide sequences: **R.DLITILEDAIR.S; K.NQIEATEQEYER.E;**  
**K.AAVEEGIVVGGGCTLLR.L; R.SGYPIIVAEDIEQEALATLVVNR.L**

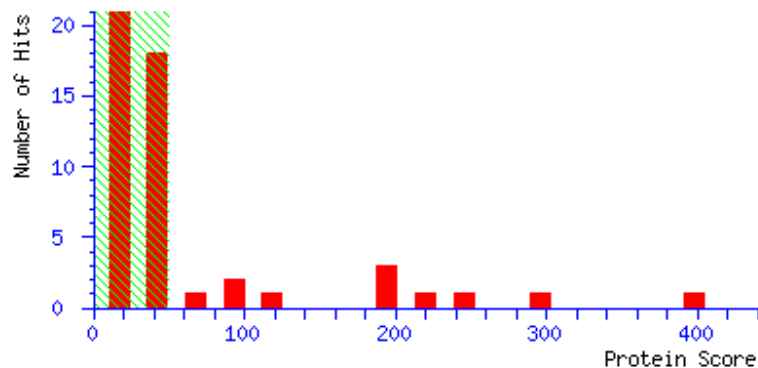
PFF Mascot score: **[398]** Sequence coverage %: **[10]**

Matched peptides No.: **[4]** p value: **1.1e-09**

Calculated Mr: **64688** Calculated pI: **5.81**

PFF Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where  $P$  is the probability that the observed match is a random event. Individual ions scores  $> 50$  indicate identity or extensive homology ( $p < 0.05$ ). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences shown in **Bold Red**

1 MASAFGTAST CGIKHAPAGV ALAAPMKHLS LVSPSLVSLP RKMRPRRKYN  
51 FRVNAAKELH FNKDGSAIRK MQNGVNKLAD LVGVTLGPKG RNVVLESKYG  
101 SPKIVNDGVT VAKEVELEDP VENIGAKLVR QAAAKTNDLA GDGTTTSSVVL  
151 AQQMITEGVK VVAAGANPVQ ITRGIEKTAK ALVSELQKMS KEVEDSELAD  
201 VAAVSAGNNY EIGNMITEAM KKVGRQGVVT LEEGKSAENN LYSVEGMQFD  
251 RGYISPYFVT DSEKMTVEYE NCKLLLVDKK INNARDLITI LEDAIRSGYP  
301 ILIVAEDIEQ EALATLVVNR LRGALKIAAI KAPGFGERKS QYLDDIATLT  
351 GGTVIREEVG LSLDKADNAV LGTAAKVVVT KDSTTIVGDG TTQEEVNKRV  
401 TQIKNQIEAT EQEYEREKLN ERIAKLSGGV AVIQVGAQTE TELKEKKLRV  
451 EDALNATKAA VEEGIVVGGG CTLLRLASKF DAI IETLEND EQKVGAEIVR  
501 KLSYPLKLI AKNAGVNGSV VTEKVLANEN FRYGYNAATG EYEDLMAAGI  
551 IDPTKVVRCC LEHAASVAKT FITSDAVVVD AKVAEQAPSS PANPMAMGGG  
601 SGFGF

Spot No.: **2**

NCBI accession No: [gi|189027076](#)

Plant species: **Zea mays**

Protein name: **glucose-1-phosphate adenylyltransferase large subunit 1**

Peptide sequences: **K.TPFFTAPR.C; R.ATPAVPVGGCYR.L; K.YAFISDGCLLR.E; R.SCEGDGIDRLEK.L; K.YTQLHDFGSEILPR.A; K.GIQEADHPEEGYYIR.S; K.HVEDDADITISCAPVDES.R.A; R.VAATTQCILTSDACPETLHSQTQSSR.K**

PFM Mascot score: **[231]** Sequence coverage %: **[22]**

Matched peptides No.: **[8]** p value: **1.6e-04**

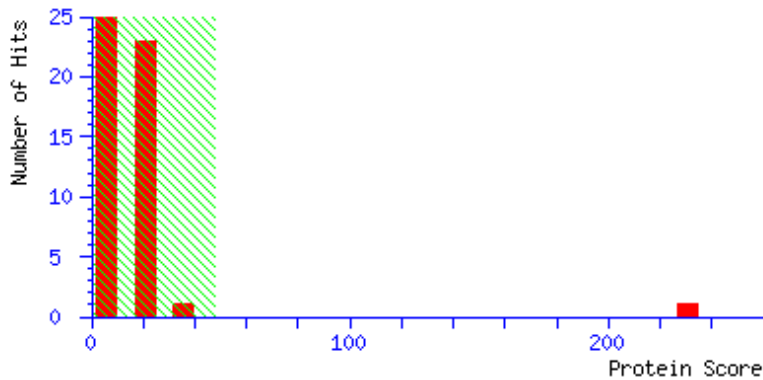
Calculated Mr: **57890** Calculated pI: **6.16**

PFM Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.

Individual ions scores  $> 48$  indicate identity or extensive homology ( $p < 0.05$ ).

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



Matched peptide sequences shown in **Bold Red**

```
1  MQFALALDTN  SGPHQIRSCE  GDGIDRLEKL  SIGGRKQEKA  LRNRCFGGRV
51  AATTQCILTS  DACPETLHSQ  TQSSRKNYAD  ANRVSAIILG  GGTGSQLFPL
101 TSTRATPAVP  VGGCYRLIDI  PMSNCFNSGI  NKIFVMSQFN  STSLNRHIHR
151 TYLEGGINF  A  DGSVQVLAAT  QMPEEPAGWF  QGTADSIRKF  IWVLEDYYSH
201 KSIDNIVILS  GDQLYRMNYM  ELVQKHVEDD  ADITISCAPV  DESRASKNGL
251 VKIDHTGRVL  QFFEKPKGAD  LNSMRVETNF  LSYAIDDAQK  YPYLASMGIY
301 VFKKDALLDL  LKSKYTQLHD  FGSEILPRAV  LDHSVQACIF  TGYWEDVGTI
351 KSFFDANLAL  TEQPSKFDY  DPKTPFFTAP  RCLPPTQLDK  CKMKYAFISD
401 GCLLRECNIE  HSVIGVCSR  V  SSGCELKDSV  MMGADTYETE  EEASKLLLAG
451 KVPVIGIRNT  KIRNCIIDMN  ARIGKNVVIT  NSKGIQEADH  PEEGYYIRSG
501 IVVILKNATI  NDGSVI
```

Spot No.: **3**

NCBI accession No: **gi|226503399**

Plant species: **Zea mays**

Protein name: **Elongation factor 2**

Peptide sequences: **K.DLQEDFMGGAEIIVSPPVVSFR.E; R.PLEEGLAEAI DDGR.I; R.GGGQVIPTAR.R; K.AFLPVIESFGFSSQLR.A**

PFM Mascot score: **[254]** Sequence coverage %: **[7]**

Matched peptides No.: **[4]** p value: **4.5e-07**

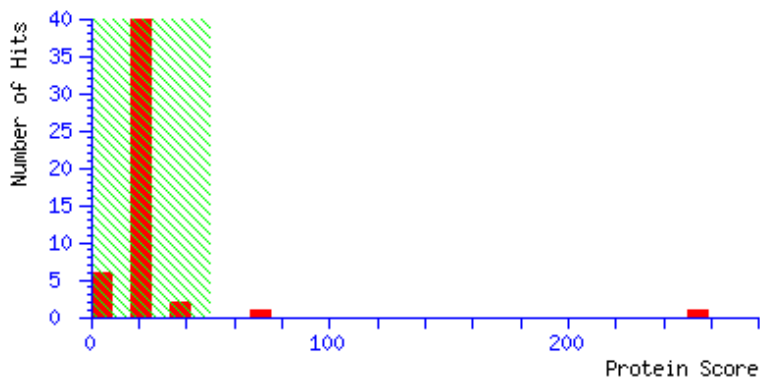
Calculated Mr: **94888** Calculated pI: **6.0**

PFM Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.

Individual ions scores  $> 50$  indicate identity or extensive homology ( $p < 0.05$ ).

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



Matched peptide sequences shown in **Bold Red**



1 MVKFTAELR AIMDKNNIR NMSVIAHVDH GKSTLTDSLVAAGIIAQEV  
51 AGDVRMTDTR ADEAERGITI KSTGISLYYE MTDESLKNYK GERDGNQYLI  
101 NLIDSPGHVD FSSEVTAALR ITDGALVVVD CIEGVCVQTE TVLRQALGER  
151 IRPVLTVNKM DRCFLELQVE GEEAYQTFSR VIENANVIMA TYEDKLLGDV  
201 QVYPEKGTVA FSAGLHGWAF TLTNFAKMYA SKFGVDETKM MERLWGENFF  
251 DPATKKWITK NTGSPTCKRG FVQFCYEPIK QIIKTCMNDQ KEKLWPMLQK  
301 LNVTMKADEK ELIGKALMKR VMQTLWPAST ALLEMMIFHL PSPAKAQKYR  
351 VENLYEGPLD DVYATAIRNC DPEGPLMLYV SKMIPASDKG RFFAFGRVFS  
401 GKVATGMKVR IMGPNYVPGQ KKDLYVKSQVQ RTVIWMGKKQ ESVEDVPCGN  
451 TVAMVGLDQF ITKNATLTNE KETDACPIRA MKFSVSPVVR VAVQCKVASD  
501 LPKLVEGLKR LAKSDPMVLC TMEESGEHII AGAGELHLEI CLKDLQEDFM  
551 GGAEIIVSPP VVSFRETVLE KSCRTVMSKS PNKHNRLYME ARPLEEGLAE  
601 AIDDGRIGPR DDPKQRSQIL SQEFGWDKDL AKKIWCFGPE TTGPNMVVDM  
651 CKGVQYLNEI KDSVVAGFQW ASKEGALAE NMRGICFEVC DVVLHADAIH  
701 RGGGQVIPTA RRVIYASQLT AKPRLLEPVY LVEIQAPENA LGGIYGVNLQ  
751 KRGHVFEEMQ RPGTPLYNIK AFLPVIESFG FSSQLRAATS GQAFPQCVFD  
801 HWDMMGSDPL EAGSQAAQLV LDIRKRKGLK EQMTPLSEFE DKL

Spot No.: **4**

NCBI accession No: [gi|413949327](#)

Plant species: **Zea mays**

Protein name: **pyruvate, phosphate dikinase 2**

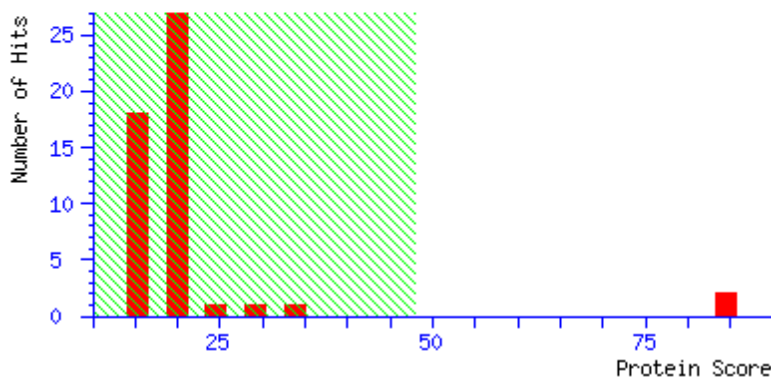
Peptide sequences: **R.SDFEGIFR.A**; **R.TEHMFFASDER.I**;  
**K.LYGEFLVNAQGEDVVAGIR.T**; **R.LLDPPLHEFLPEGNVEEIVR.E**

PFF Mascot score: **[84]**      Sequence coverage %: **[6]**

Matched peptides No.: **[4]**      p value: **1.7**  
Calculated Mr: **103777**      Calculated pI: **6.04**

PFF Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event  
Individual ions scores > 48 indicate identity or extensive homology ( $p < 0.05$ ).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences shown in Bold Red

1 MAASVTSRV ICLQKPGPEG SSRGAREVAP FTRQSVAAPR RPHGANASVI  
51 IGSDSGAGRG QHSPPLRAVV DAGPVQTTKK RVFHFQKGS EGNKNMKELL  
101 GGKGANLAEM ASIGLSVPPG FTVSTEACQQ YQEAGRALPP GLWAEVLDGL  
151 RWVEEYMGAA LGDPRRPLLL SVRSGAAVSM PGMMDTVLNL GLNDQVAAGL  
201 AAKSGDRFAY DSFRRFLDMF GNVVMDIPHA LFEEKLEAMK KAKGLKNDTD  
251 LTATDLKELV SQYKNVYVEA KGEPFSPDPK RQLELAVLAV FDSWESPRAK  
301 KYRSINQITG LRGTAVNVQC MVFGNMGNTS GTGVLFTRNP NTGEKKLYGE  
351 FLVNAQGEDV VAGIRTPEDL DAMKDVMPQA YKELVENCRI LESHYKEMQD  
401 IEFTVQESRL WMLQCRTGKR TGKSAVKIAV DMVNEGLVER RAAIKMVEPG  
451 HLDQLLHPQF ENPSAYKDQV IATGLPASPG AAVGQVVFTA EDAETWHSQG  
501 KSVILVRAET SPEDVGGMHA AAGILTERGG MTSHAAVVAR GWGKCCVSGC  
551 SGIRVNDAEK VVKIGGNVLR EGEWLSLNGS TGEVILGKQP LSPPALSGDL  
601 GTFMSWDDV RKLKVLANAD TPEDALAARN NGAEGIGLCR TEHMFFASDE  
651 RIKAVRQMIM APTVELRQQA LDRLLPYQRS DFEGIFRAMD GLSVTIRLLD  
701 PPLHEFLPEG NVEEIVRELC SETGANQEDA LARIEKLSEV NPMLGFRGCR  
751 LGISYPELTE MQARAI FEAA IAMTNQGVQV FPEIMVPLVG TPQELGHQVA  
801 LIRQVANKVF TSMGKTIGYK IGTMIPIRA ALVADEIAEQ AEFFSFGTND  
851 LTQMTFGYSR DDVGKFIPIY LAQGILQHDP FEVLDQRGVG ELVKLATERG  
901 RKARP NLKVG ICGEHGGEPS SVAFFAKTGL DYVSCSPFRV PIARLAAAQV  
951 LV

Spot No.: **5**

NCBI accession No: **gi|413933276**

Plant species: **Zea mays**

Protein name: **phosphoglucomutase, cytoplasmic 1**

Peptide sequences: **K.SSSNVEPPEFGAAADGDADR.N ; R.YLFGDGSRL.L ; R.VYIEQYER.D**

PFM Mascot score: **[85]** Sequence coverage %: **[5]**

Matched peptides No.: **[3]** p value: **0.026**

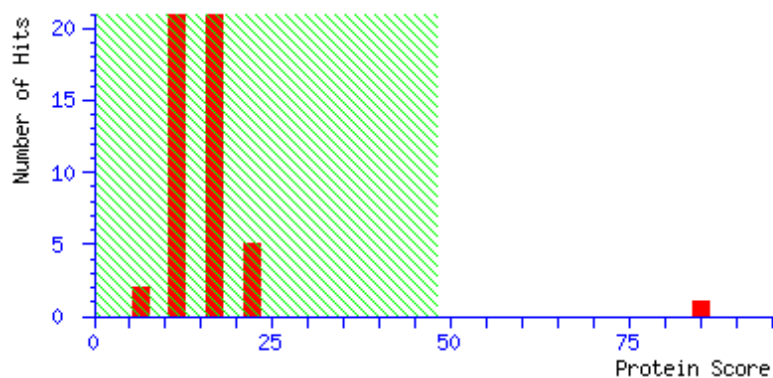
Calculated Mr: **70977** Calculated pI: **7.29**

PFM Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.

Individual ions scores  $> 48$  indicate identity or extensive homology ( $p < 0.05$ ).

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



Matched peptide sequences shown in **Bold Red**

```
1 MIQHRPLVLS LPSPAIIPPR PRRHRHHTT PSLPSHSRSL LHHRFLRVTH
51 LVVASRGDQR RTLRGATMGL FIVIKKATIP FDGQKPGTSG LRKKVTVFQQ
101 PHYLQNFVQS TFNALPVDQV RGATIVVSGD GRYFSKDAVQ IITKMAAANG
151 VRRVWVGQNS LMSTPAVSAV IRERVGADGS KATGAFILTA SHNPGGPKED
201 FGIKYNMGNG GPAPESVTDK IFSNTTISE YLISEDLPDV DISVVGVTSE
251 SGPEGPFVDV VFDSSVDYIK LMKTIFDFEA IKKLLTSPKF TFCYDALHGV
301 AGAYAKHIFV EELGADESSL LNCVPKEDFG GGHPDPNLTY AKELVERMGL
351 GKSSSNVEPP EFGAAADGDA DRNMILGKRF FVTPSDSVAI IAANAVQSIP
401 YFASGLKGVA RSMPTSAALD VVAKNLNLKF FEVPTGWKFF GNLMDAGMCS
451 ICGEESFGTG SDHIREKDG I WAVLAWLSII AFKNKDNLGG DKLVTVEDIV
501 RQHWATYGRH YYTRYDYENV DAGAAKELMA NLVSMQSSLS DVNKLVEKIR
551 SDVSEVVAAD EFYKDPVDG SVSKHQGIRY LFGDGSRLVF RLSGTGSVGA
601 TIRVYIEQYE RDSSKTGRDS QDALAPLVDV ALKLSKMQEY TGRSAPTUIT
```

Spot No.: **6**

NCBI accession No: [gi|212275400](#)

Plant species: **Zea mays**

Protein name: **uncharacterized protein LOC100191408**

Peptide sequences: **K.AVITVPAYFNDAQR.Q; K.SQVFSTAADNQTQVGIR.V**

PFF Mascot score: **[63]** Sequence coverage %: **[4]**

Matched peptides No.: **[2]** p value: **0.9**

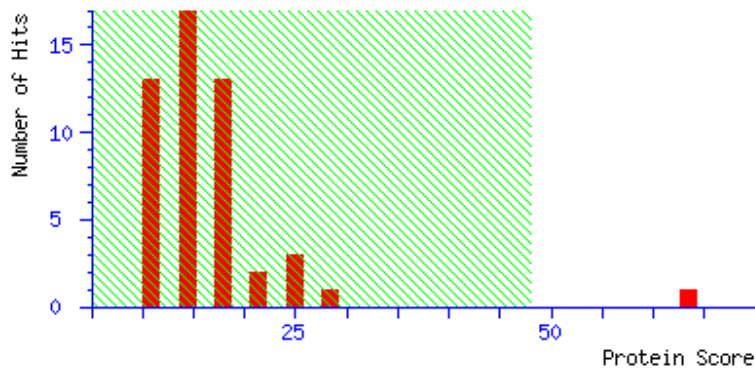
Calculated Mr: **72903** Calculated pI: **5.54**

PFF Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.

Individual ions scores  $> 48$  indicate identity or extensive homology ( $p < 0.05$ ).

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



Matched peptide sequences shown in Bold Red

```
1 MAASLLLRV RRRELASPLG SLGANLQSTC AANICKWGN FARPFSAKAA
51 GNEVIGIDLG TTNSCVAVME GKNPKVIENA EGARTTPSVV AFTQKGERLV
101 GTPAKRQAVT NPQNTFFGTK RMIGRRFDDP QTQKEMKMVP YKIVKAPNGD
151 AWWETTDGKQ YSPSQVGAFV LTKMKETAES YLGKSVSKAV ITVPAYFNDA
201 QRQATKDAGR IAGLDVERII NEPTAAALSY GMNNKEGLIA VFDLGGGTFD
251 ISILEISNGV FEVKATNGDT FLGGEDFDNT LLEFLVSDFK KTEGIDLSKD
301 RLALQRLREA AEKAKVELSS TSQTEINLPF ITADASGAKH LNITLRSKF
351 ESLVHNLIER TRDPCKNCLK DAGISTKEVD EVLLVGGMTR VPKVQEVVSE
401 IFGKSPSKGV NPDEAVAMGA AIQGGILRGD VKELLLLDVT PLSLGIETLG
451 GIFTRLINRN TTIPTKKSSQV FSTAADNQTQ VGIRVLQGER EMAADNKLLG
501 EFDLVGIPPA PRGLPQIEVA FDIDANGIVT VAAKDKATGK EQNITIRSSG
551 GLSEADIQKM VQEAELHAQK DQERKALIDI RNTADTTIYS IEKSLGEYRD
601 KIPAEVASEI EAAIADLRQE MASDDIEKIK AKLEAANKAV SKIGQHMSGG
651 GSGDSQSGSG PQGGGDQAPE AEYEEVKK
```

Spot No.: **7**

NCBI accession No: [gi|226509912](#)

Plant species: **Zea mays**

Protein name: **ubiquitin carboxyl-terminal hydrolase 6**

Peptide sequences: **R.YLTVQFVR.F; K.WIEFDDNPNI.R.K**

PFF Mascot score: **[99]** Sequence coverage %: **[4]**

Matched peptides No.: **[2]** p value: **0.0044**

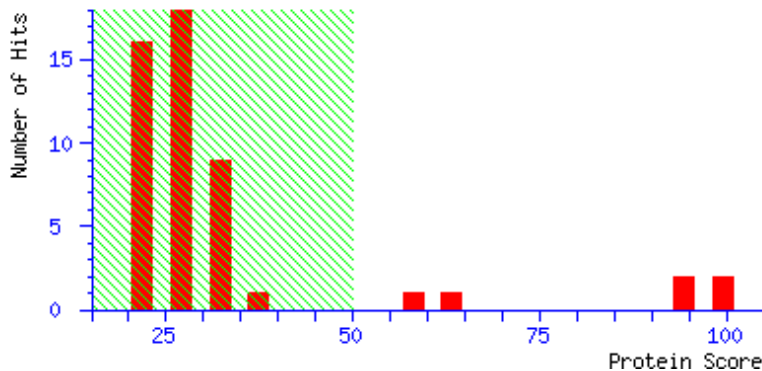
Calculated Mr:**53978** Calculated pI: **5.73**

PFF Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.

Individual ions scores  $> 50$  indicate identity or extensive homology ( $p < 0.05$ ).

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



Matched peptide sequences shown in Bold Red

```
1  MPTVSVKWQK  ELFPGIEIDT  SQPPIVFKTQ  LYTLTGVPPE  RQKIMVKGGI
51  LKDDADWSTL  GVKDQQKLMM  IGTADEIVKA  PEKGPVFVED  LPEEEQVIAL
101 GHSAGLYNLG  NTCYMNSTLQ  CLHSVPELKS  ALLSYSDTVR  GNGIDQASHN
151 LTVATRNTFG  DLDQSVRPVA  PLQFLQTLRK  KYPQFAQQHN  NVYMQQDAEE
201 CWIQLVYTLS  QTLTSDSSES  AALPMKQLFG  IDLVS RVHCA  ESGEESMETE
251 SVYSLKCHIS  QDVNHLHEGI  KHGLKTELEK  ASPTLGRTAV  YTRESRINEL
301 PRYLTVQFVR  FFWKRESNQK  AKILRKVDYP  LELDVYEFCS  DELKQKLQAP
351 RQMLRDAENA  KFGLKAQGKA  SGFKENEGSS  SSAGESSSMD  IDKAESSLPK
401 KQLTGVDLV  AVLTHKGRSA  DSGHYVGWVK  QDDGKWIEFD  DDNPNIRKEE
451 DILKLSGGGD  WHMAYICLYK  ARMAELKS
```

Spot No.: **8**

NCBI accession No: **gi|189027076**

Plant species: **Zea mays**

Protein name: **glucose-1-phosphate adenylyltransferase large subunit 1**

Peptide sequences: **R.VAATTQCILTSDACPETLHSQTQSSR.K;**  
**R.VSAILGGGTGSQFLPLTSTR.A; R.ATPAVPVGGCYR.L ;**  
**K.SIDNIVILSGDQLYR.M; K.HVEDDADITISCAPVDESR.A; K.TPFFTAPR.C;**  
**K.GIQEADHPEEGYYIR.S**

PFM Mascot score: **[424]** Sequence coverage %: **[22]**

Matched peptides No.: **[7]** p value: **7.2e-08**

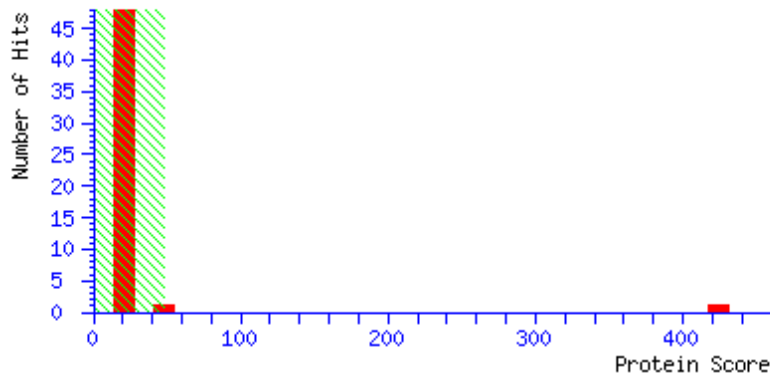
Calculated Mr: **57890** Calculated pI: **6.16**

PFM Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.

Individual ions scores  $> 48$  indicate identity or extensive homology ( $p < 0.05$ ).

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



Matched peptide sequences shown in **Bold Red**

```
1  MQFALALDTN  SGPHQIRSCE  GDGIDRLEKL  SIGGRKQEKA  LRNRCFGGRV
51  AATTQCILTS  DACPETLHSQ  TQSSRKNYAD  ANRVSAIILG  GGTGSQFLPL
101 TSTRATPAVP  VGGCYRLIDI  PMSNCFNSGI  NKIFVMSQFN  STSLNRHIHR
151 TYLEGGINF A DGSVQVLAAT QMPEEPAGWF QGTADSIRKF IWVLEDYYSH
201 KSIDNIVILS  GDQLYRMNYM  ELVQKHVEDD  ADITISCAPV  DESRASKNGL
251 VKIDHTGRVL QFFEKPKGAD LNSMRVETNF LSYAIDDAQK YPYLASMGIY
301 VFKKDALLDL LKSKYTQLHD FGSEILPRAV LDHSVQACIF TGYWEDVGTI
351 KSFFDANLAL TEQPSKFDYF DPKTPFFTAP RCLPPTQLDK CKMKYAFISD
401 GCLLRECNIE HSVIGVCSRV SSGCELKDSV MMGADTYETE EEASKLLLAG
451 KVPVGIGRNT KIRNCIIDMN ARIGKNVVIT NSKGIQEADH PEEGYIRSG
501 IVVILKNATI NDGSVI
```

Spot No.: **9**

NCBI accession No: [gi|413956739](#)

Plant species: **Zea mays**

Protein name: **myo-inositol phosphate synthase**

Peptide sequences: **-MFIESFR.V; R.YGPTEIESEYR.Y; K.DKVQQANYGSLTQASTIR.V; K.VVVLWTANTER.Y**

PFF Mascot score: **[204]** Sequence coverage %: **[10]**

Matched peptides No.: **[4]** p value: **4e-08**

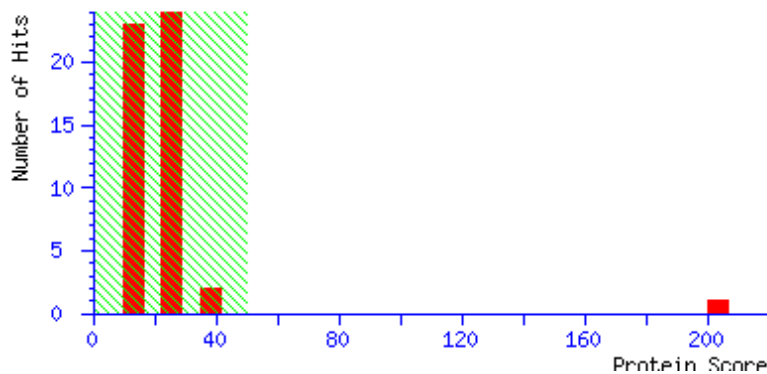
Calculated Mr: **50215** Calculated pI: **5.46**

PFF Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.

Individual ions scores > 50 indicate identity or extensive homology ( $p < 0.05$ ).

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



Matched peptide sequences shown in Bold Red

```
1 MFIESFRVES PHVRYGPTEI ESEYRYDTTE LVHEAKDGAS RWVVRPKSVK
51 YNFRTSTAVP KLGVMLVGWG GNGSTLTAG VIANREGISW ATKDKVQQAN
101 YGSLTQAST IRVGSYNGEE IYAPFKSLLP MVNPDDLVFG GWDISSMNLA
151 DAMTRAKVLD IDLQQLRPY MESMVPLPGV YDPDFIAANQ GSRANVIKG
201 TKKEQVEQII KDIREFKEKN KVDKVVVLWT ANTERYSNVC AGLNDTMENL
251 LASVDKNEAE ISPSTLYAIA CVTEGVPFIN GSPQNTFVPG LIDLAIKNNC
301 LIGGDDFKSG QTKMKSVLVD FLVGAGIKPT SIVSYNHLGN NDGMNLSAPQ
351 TFRSKEISKS NVVDDMVSSN AILYGPGEHP DHVVVIKYVP YVGDSKRAMD
401 EYTSEIFMGG KSTIVLHNTC EDSLLAAPII LDLVLLAEELS TRIQLKPEGT
451 VRAHE
```



Spot No.: **10**

NCBI accession No: **gi|162460991**

Plant species: **Zea mays**

Protein name: **indole-3-acetate beta-glucosyltransferase**

Peptide sequences: **R.NVELAWGAGVR.A; R.NLDEFVQFVR.A;**

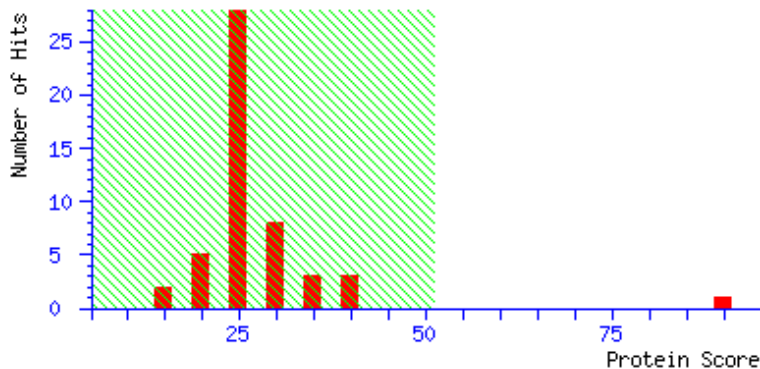
PFM Mascot score: **[90]** Sequence coverage %: **[4]**

Matched peptides No.: **[2]** p value: **0.091**

Calculated Mr: **50135** Calculated pI: **5.75**

PFM Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores  $> 51$  indicate identity or extensive homology ( $p < 0.05$ ). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences shown in **Bold Red**

```
1  MAPHVLVVPF  PGQGHMNPV  QFAKRLASKG  VATTLVTTTRF  IQRTADVDAH
51  PAMVEAISDG  HDEGGFASAA  GVAEYLEKQA  AAASASLASL  VEARASSADA
101  FTCVVYDSYE  DWVLPVARRM  GLPAVPFSTQ  SCAVSAVYYH  FSQGR LAVPP
151  GAAADGSDGG  AGAAALSEAF  LGLPEMERSE  LPSFVFDHGP  YPTIAMQAIK
201  QFAHAGKDDW  VLFNSFEELE  TEVLAGLTKY  LKARAIGPCV  PLPTAGRTAG
251  ANGRITYGAN  LVKPEDACTK  WLDTKPDRSV  AYVSFGSLAS  LGNAQKEELA
301  RGLLAAGKPF  LWVVRASDEH  QVPRYLLAEA  TATGAAMVVP  WCPQLDVLAH
351  PAVGCFVTHC  GWNSTLEALS  FGVPMVAMAL  WTDQPTNARN  VELAWGAGVR
401  ARRDAGAGVF  LRGEVERCVR  AVMDGGEAAS  AARKAAGEWR  DRARAAVAPG
451  GSSDRNLDEF  VQFVRAGATE  K
```

Spot No.: **11**

NCBI accession No: **gi|2500522**

Plant species: **Zea mays**

Protein name: **eukaryotic initiation factor 4A (eIF4A)**

Peptide sequences: **R.GIYAYGFEEKPSAIQQR.G;**  
**K.TATFCSGILQLDYLVEECQALVLAPTR.E; R.ILASGVHVVVGTPGR.V;**  
**K.IQGVVFSATMPPEALEITR.K; K.LDTLCLDYETLAITQSVIFVNTR.R;**  
**R.GIDVQQVSLVINYLPTQPENYLHR.I**

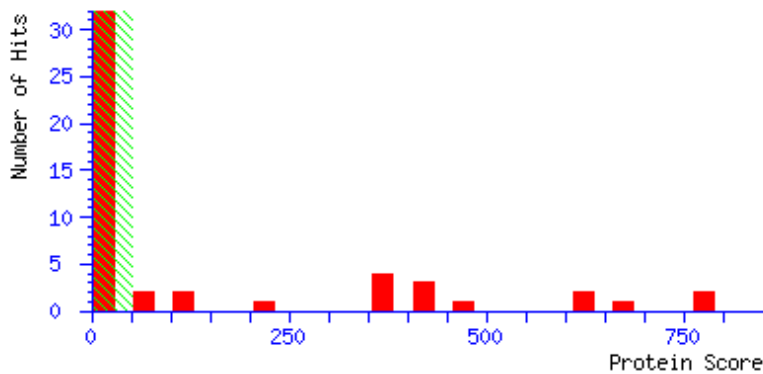
PFF Mascot score: **[773]** Sequence coverage %: **[30]**

Matched peptides No.: **[6]** p value: **1.5e-13**

Calculated Mr:**46849** Calculated pI: **5.28**

PFF Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.  
Individual ions scores  $> 50$  indicate identity or extensive homology ( $p < 0.05$ ).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences shown in **Bold Red**

```
1  MAGLAPEGSQ FDDKQYDKKM QEILTEDFFT SYDDVCESEFD SMGLQENLLR
51  GIYAYGFEEK SAIQQRGIVP FCKGLDVIQQ AQSGTGKTAT FCSGILQLD
101 YGLVEECQALV LAPTRELAQQ IEKVMRALGD YLGVKVHACV GGTSVREDQR
151 ILASGVHVVV GTPGRVFDFML RRQSLRPDNI KMFVLDEADE MLSRGFKDQI
201 YDIFQLLPSK IQGVVFSATM PPEALEITRK FMNKPVRILV KRDELTLEGI
251 KQFYVNIDKE DWKLDLCLDL YETLAITQSV IFVNTRRKVD WLTDKMRSRD
301 HTVSATHGDM DQNTARDIIMR EFRSGSSRVL ITDLLLARGI DVQQVSLVIN
351 YDLPTQPENY LHRIGRSGRF GRKGVAINFV TRDDERIVFD VQRFYNTVTE
401 ELPANVADLL
```

Spot No.: **12**

NCBI accession No: **gi|226529884**

Plant species: **Zea mays**

Protein name: **10-deacetylbaaccatin III 10-O-acetyltransferase**

Peptide sequences: **K.ALVPYYPVAGR.I; R.GLPAPSVAPVWDR.D; K.EELLPRPPPEEK.L**

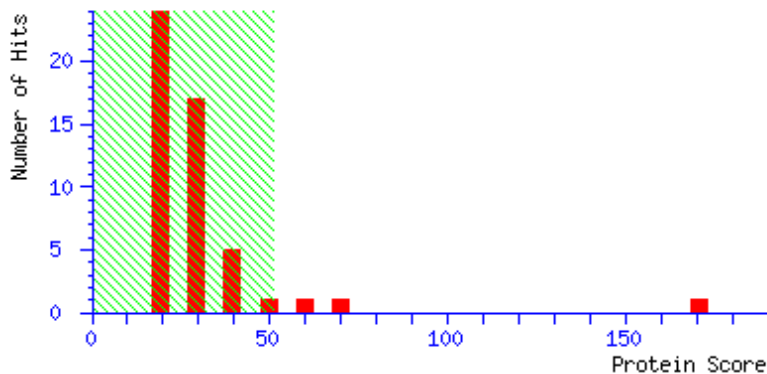
PFM Mascot score: **[171]** Sequence coverage %: **[8]**

Matched peptides No.: **[3]** p value: **1.9e-03**

Calculated Mr: **45911** Calculated pI: **5.03**

PFM Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores  $> 51$  indicate identity or extensive homology ( $p < 0.05$ ). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences shown in **Bold Red**

```
1 MSTVAAAPT V KSAPELVAP VGTPGGTLP LSSIDKTA AV RVSVDFIQVF
51 PPAVGAGGDK DAAVAAMRDG FAKALVPYYP VAGRIADASP GEPVVECTGQ
101 GVWFVEAAAS CALADVNYLE RPLLIPKEEL LPRPPPEEKL EDLVLMAQVT
151 KFACGGFAVG ICFSHLVFDG QGAAQFLKAA GEMARGLPAP SVAPVWDRDA
201 IPDPPKLPRG PPSFTAFA SF VIQVVEISPE SIARIKDDFK DATGQTCSTF
251 DAVTAVVFKC RALAMALPDD AEVRLGFAAS TRHLLHGVL P SVDGYYGNCV
301 YPVGITRTSK AIREASLPEV VGV MREAKEA LTTRFTDWMR GGAKDDHYNV
351 PLDYGTVTVS DWSRVGFNEV DYGFGE PGYV FTLNDDVNIV ASVIYLKPPA
401 PKRGIRLMLR CVEEPHAAAF AEELAKFA
```

Spot No.: **13**

NCBI accession No: [gi|413950795](#)

Plant species: **Zea mays**

Protein name: **Isocitrate dehydrogenase [NADP]**

Peptide sequences: **R.HAFGDQYR.A; K.YYDLGILHR.E; K.DLAILVHGSSSVTR.S; K.SKFEAAGIWYEHR.L; R.SHYLNTEEFIDAVATELR.S**

PFF Mascot score: **[270]** Sequence coverage %: **[15]**

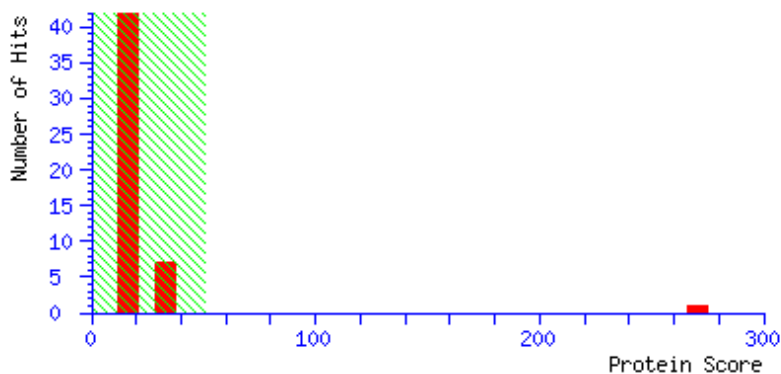
Matched peptides No.: **[5]** p value: **3.1e-09**

Calculated Mr:**46510** Calculated pI: **6.11**

PFF Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores  $> 51$  indicate identity or extensive homology ( $p < 0.05$ ).

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



Matched peptide sequences shown in Bold Red

```
1 MAFEKIKVSN PIVEMDGDEM TRVFWQSIKD KLILPFLDLLD IKYYDLGILH
51 REATDDKVTV EAAEATLKYN VAIKCATITP DETRVKEFNL KHMWKSPNGT
101 IRNIINGTVF REPIICKNVP RLVPGWTKPI CIGRHAFGDQ YRATDAVLKG
151 PGKLKLVFEG KEEQIDLEVF NFTGAGGVAL SMYNTDESIR AFAEASMTTA
201 YEKKWPLYLS TKNTILKKYD GRFKDIFQEV YEADWKSKFE AAGIWYEHRL
251 IDDMVAYALK SEGGYVWACK NYDGDVQSDF LAQGFGSLGL MTSVLVCPDG
301 KTIEAEEAHG TVTRHFRVHQ KGGETSTNSI ASIFAWTRGL AHRAKLDDNA
351 RLLDFALKLE AACVETVESG KMTKDLAILV HGSSSVTRSH YLNTEEFIDA
401 VATELRSRLG AN
```

Spot No. : 14

NCBI accession No: [gi|195627248](#)

Plant species: *Zea mays*

Protein name: **sorbitol dehydrogenase**

Peptide sequences: **K.LPPVGPYDVR.V; K.AVGICGSDVHYLR.E;  
R.AGVGPETGVLVVGAGPIGLVSLAAR.A;  
K.EPMVIGHECAGVVEEVGAGVTHLSVGDR.V**

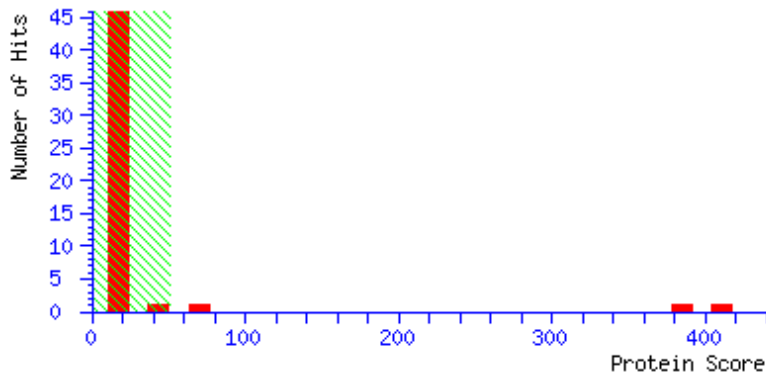
PFF Mascot score: [413] Sequence coverage %: [21]

Matched peptides No.: [4] p value: **4.5e-15**

Calculated Mr:**39528** Calculated pI: **6.27**

PFF Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores  $> 51$  indicate identity or extensive homology ( $p < 0.05$ ). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences shown in Bold Red

```
1  MGKGAQGSDA AAAGGEVEEN MAAWLVAKNT LKIMPFKLLPP VGPYDVRVRM
51  KAVGICGSDV HYLREMRIAH FVVKEPMVIG HECAGVVEEV GAGVTHLSVG
101 DRVVALEPGVS CWRCRHCKGG RYNLCEDMKF FATPPVHGSL ANQVVHPADL
151 CFKLPDGVSL EEGAMCEPLS VGVHACRRAG VGPETGVLVV GAGPIGLVSL
201 LAARAFGAPR VVVVDVDDHR LAVARSLGAD AAVRVSPRAE DLADEVERIR
251 AAMGSDIDVS LDCAGFSKIM STALEATRPG GKVCLVGMGH NEMTLPLTAA
301 AAREVDVVGF RYKDTWPLCI DFLRSGKVDV KPLITHRFGF SQRDVEEAFE
351 VSARGRDAIK VMFNL
```

Spot No. : 15

NCBI accession No: [gi|670397371](#)

Plant species: *Zea mays*

Protein name: **PREDICTED: adenosine kinase 2-like**

Peptide sequences: **K.NAQAAGVTAHYEDETAPTGTCAVCVVGGER.S;**  
**K.RPENWALVEK.A; K.LVDTNGAGDAFVGGFLSR.L**

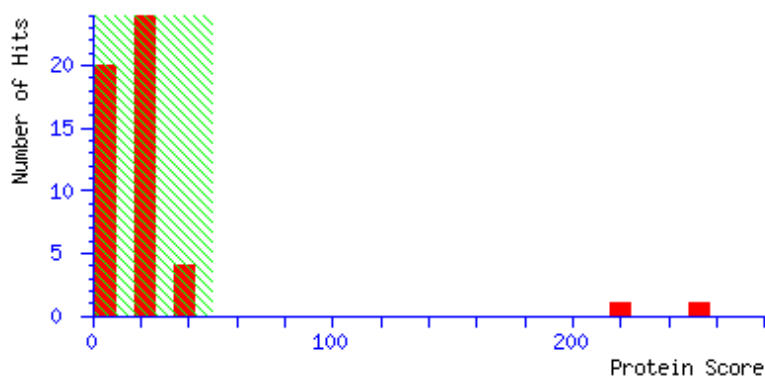
PFF Mascot score: [252] Sequence coverage %: [17]

Matched peptides No.: [3] p value: **3.8e-08**

Calculated Mr: **37436** Calculated pI: **5.00**

PFF Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores  $> 50$  indicate identity or extensive homology ( $p < 0.05$ ). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences shown in Bold Red

```
1 MAASEGVLLG MGNPLLDISA VVDDAFLAKY DIKLNNAILA EEKHSPMYDE
51 LASNSNVEYI AGGATQNSIR VAQWMLQTPG ATSYMGCIGK DKFGEEMKKN
101 AQAAGVTAHY YEDETAPTGT CAVCVVGGER SLIANLSAAN CYKSEHLKRP
151 ENWALVEKAK YIYIAGFFLT VSPDSIQLVA EHAAAANNKVF LMNLSAPFIC
201 EFFYDAQEKV LPYADFIFGN ETEAKIFAKV RGWETENVEE IALKISQLPL
251 ASGKQKRIAV ITQGADPVVV AEDGKVKTFP VILLPKEKLV DTNGAGDAFV
301 GGFLSRLVQG KSIEDCVTAG CYAANVVIQR PGCTYPEKPD FN
```

Spot No.: **16**

NCBI accession No: [gi|195644252](#)

Plant species: **Zea mays**

Protein name: **aspartate-semialdehyde dehydrogenase**

Peptide sequences: **R.GLDIFVCGDQIR.K; R.FPTPLEVSDKDDVAVGR.I; K.YGPAAVASGAVVVDNSSAFR.M; R.KYGPAAVASGAVVVDNSSAFR.M; R.EYTVQDLAAPGAFDGVDIALFSAGGSVSR.K**

PFF Mascot score: **[413]** Sequence coverage %: **[21]**

Matched peptides No.: **[5]** p value: **1.7e-11**

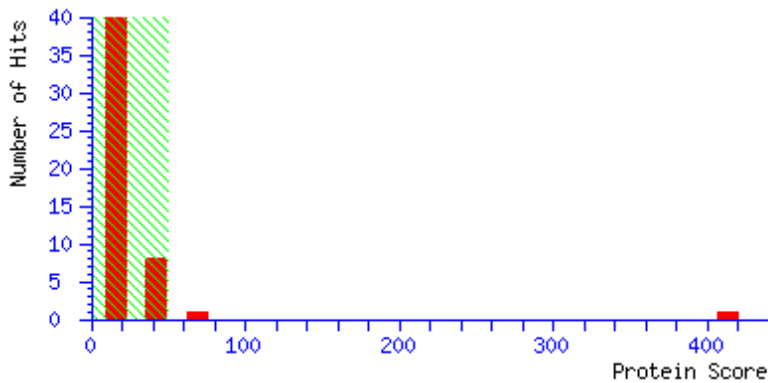
Calculated Mr:**40833** Calculated pI: **6.62**

PFF Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.

Individual ions scores > 50 indicate identity or extensive homology ( $p < 0.05$ ).

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



Matched peptide sequences shown in Bold Red

```
1  MQAAAAVRHP  RLFPPSPGSS  AQHRRAPSTV  RMALREDGPS  VAIVGATGAV
51  GQEFRLVITD  RDFPYRGLRL  LASERSAGKR  LAFEDREYTV  QDLAAPGAFD
101 GVDIALFSAG GSVSRKYGPA AVASGAVVVD NSSAFRMEPE  VPLVIPEVNP
151  EAMANVRLGQ  GAIVANPNCS  TIICLMAATP  LHRHAKVLRM  VVSTYQAASG
201  AGAAAMEELK  LQTQEVLEGK  APTCNIFKQQ  YAFNIFSHNA  PVLENGYNEE
251  EMKMVKETRK  IWNDKAVKVT  ATCIRVPVMR  AHAESVNLQF  EKPLDEDAR
301  EILRAAPGVT  IIDDRASNRF  PTPLEVSDKD DVAVGRIRQD  LSLDDNRGLD
351  IFVCGDQIRK  GAALNAVQIA  EMLLK
```

Spot No.: **17**

NCBI accession No: [gi|162464283](#)

Plant species: **Zea mays**

Protein name: **homocysteine S-methyltransferase 3**

Peptide sequences: **K.SVQIALEAR.E; R.FIHGLILSIR.K; K.CLLSSPHLIR.K; K.VGAVGINCTPPR.F**

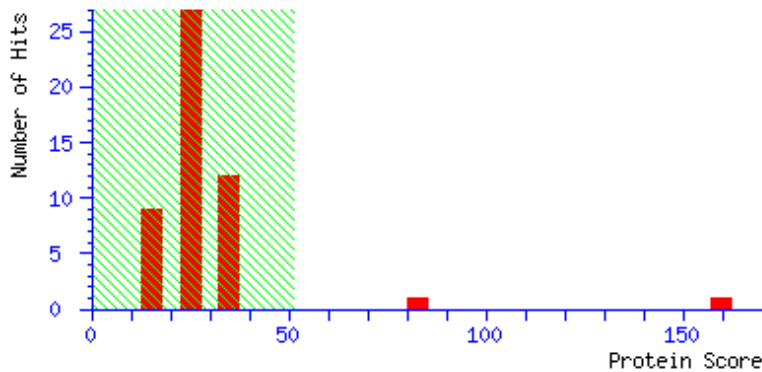
PFM Mascot score: **[159]** Sequence coverage %: **[12]**

Matched peptides No.: **[4]** p value: **0.13**

Calculated Mr:**37247** Calculated pI: **5.53**

PFM Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores  $> 51$  indicate identity or extensive homology ( $p < 0.05$ ). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences shown in Bold Red

```
1  MVGTAEGGAE  RAVRRWVDAA  GGRLVLDGGL  ATELEANGAD  LNDPLWSAKC
51  LLSSPHLIRK  VHMDYLEAGA  NIIITASYQA  TIQGFESKGF  SKEQSENLLT
101 KSVQIALEAR  EMFLKEHLEK  STPIQHPILV  AAALGSYGAY  LADGSEYSGD
151 YGEAGTKEFL  KDFHRRRLQV  LAEAGPDLIA  FETIPNKLEA  QAYVELLEEC
201 NINIPSWLSF  NSKDGHVHVS  GDSLIECATI  ADKCAKVGAV  GINCTPPRFI
251 HGLILSIRKV  TDKPILYIPN  SGERYDGEKK  EWVESTGVSD  GDFVSYVNEW
301 CKDGAALIGG  CCRTTPNTIR  AIHRTLQGC  HKHQLPVA
```



Spot No.: **18**

NCBI accession No: [gi|195628698](#)

Plant species: [Zea mays](#)

Protein name: [hypothetical protein](#)

Peptide sequences: [R.YPPALELPIPR.L](#); [R.SLQITLVGGSIAER.S](#);  
[K.TLTAGQSPTVVDTDVGR.I](#); [R.AADNQLFVATCAPAR.D](#)

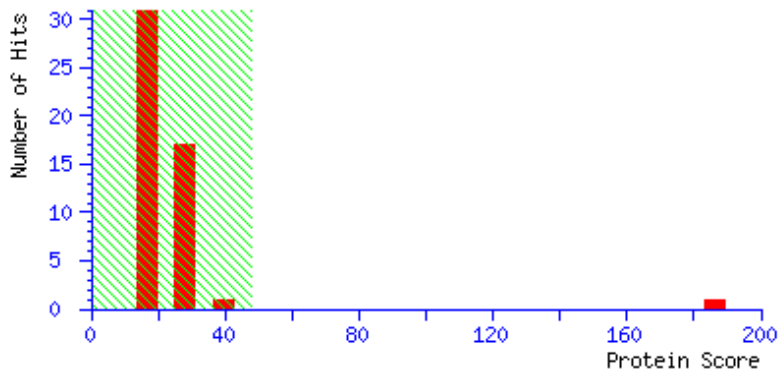
PFM Mascot score: [\[186\]](#) Sequence coverage %: [\[18\]](#)

Matched peptides No.: [\[4\]](#) p value: [1.3e-06](#)

Calculated Mr:[34244](#) Calculated pI: [5.92](#)

PFM Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores  $> 48$  indicate identity or extensive homology ( $p < 0.05$ ). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences shown in Bold Red

```
1 MASAPNSSFR PEEARYYPPAL ELPIPRLSKF KVALCQLSVT ADKSRNIAHA
51 RAAIEKAASD GAKLVVLPEI WNGPYSNDSF PEYAEDIEAG GDAAPSFMSL
101 SEVARSLQIT LVGGSIAERS GNNLYNTCCV FGSDGQLK GK HRKIHLFDID
151 IPGKITFKES KTLTAGQSPT VVDTDVGRIG IGICYDIRFQ ELAML YAARG
201 AHLLCYPGAF NMTTGPLHWE LLQRARAAADN QLFVATCAPA RDTSAGYVAW
251 GHSTLVGPPFG EVIATTEHEE ATIIADIDYS LIEQRRQFLP VQHQRGDLY
301 QLVDVQRLGS Q
```

Spot No.: **19**

NCBI accession No: [gi|806638661](#)

Plant species: **Zea mays**

Protein name: **cysteine synthase**

Peptide sequences: **K.LFVVVFPSFGER.Y; K.EGLLVGISSGAAAAAAVRL**

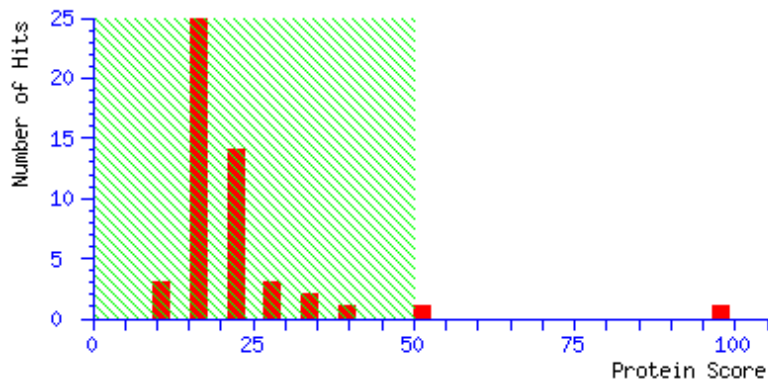
PFF Mascot score: **[98]** Sequence coverage %: **[9]**

Matched peptides No.: **[2]** p value: **4.4e-007**

Calculated Mr:**34266** Calculated pI: **5.67**

PFF Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores  $> 50$  indicate identity or extensive homology ( $p < 0.05$ ). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences shown in Bold Red

```
1 MGEASPSIAK DVTELIGNTP LVYLNKVTDG CVGRVAAKLE SMEPCSSVKD
51 RIGYSMITDA EEKGLITPGV SVLIEPTSGN TGIGLAFMAA AKGYKLTLTM
101 PASMSMERRI ILKAFGAELV LTDPLLGMKG AVKKAEEIQA KTPNSYILQQ
151 FENPANPKIH YETTGPPIWK ATAGKIDGLV SGIGTGGTIT GTGRYLREQN
201 PNVKLYGVPEP VESAVLNGGK PGPHKIQGIG AGFIPGVLDV DLLDETLQVS
251 SDEAIETAKA LALKEEGLLVG ISSGAAAAAA VRLAKRPENA GKLFVVVFPS
301 FGERYLSSVL FQSIKKEAES MVVEP
```

Spot No.: **20**

NCBI accession No: [gi|162460029](#)

Plant species: **Zea mays**

Protein name: **glutathione transferase41**

Peptide sequences: **R.LVDADAFPR.F; R.DFEALDEVRE.E; R.QVHENLALIESELR.D; K.LGPAVGAVFASTGEGQEAAVR.Q**

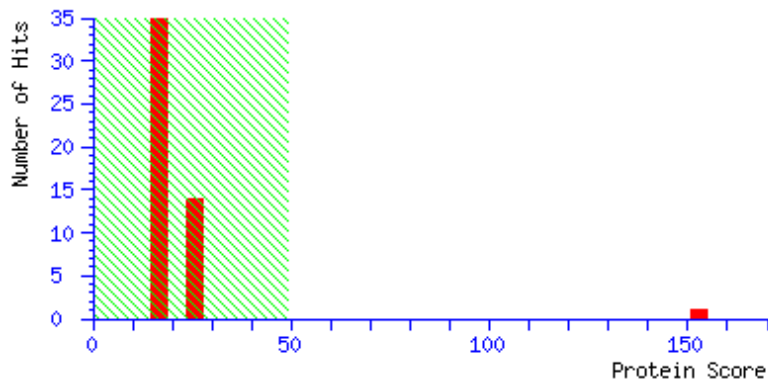
PFM Mascot score: **[153]** Sequence coverage %: **[19]**

Matched peptides No.: **[4]** p value: **0.024**

Calculated Mr: **29093** Calculated pI: **4.85**

PFM Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores  $> 49$  indicate identity or extensive homology ( $p < 0.05$ ). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences shown in Bold Red

```
1 MEKTSESAIP PAASPLMLFG SWASSYTHR V QLALRLKGLE FDYVEEDLGN
51 KSDELLRHNP VHKKVPVLVH GGRALPESVI ILQYLDDAWP ETRPLLPADA
101 FDRALARFWC HFADDKLGPA VGAVFASTGE GQEAAVRQVH ENLALIESEL
151 RDGAFRGRRF FGGDEVGLLD VVLGCGSYWL AVFEEVTGVR LVDADAFPRF
201 HAWLRDFEAL DEVRETIPAV DRLLEYARGL RHMLLGLAGA GAGAGADAPS
251 TDAPAAPPSS ADIAVDI
```

Spot No.: **21**

NCBI accession No: [gi|226495167](#)

Plant species: [Zea mays](#)

Protein name: **desiccation-related protein PCC13-62 precursor**

Peptide sequences: **R.DVATQFCYQEVGHLR.A; R.VPSYAGGVAEITAR.I**

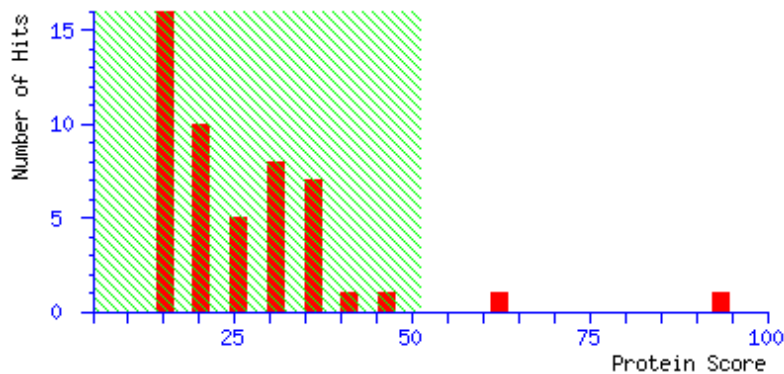
PFF Mascot score: **[93]** Sequence coverage %: **[9]**

Matched peptides No.: **[2]** p value: **0.02**

Calculated Mr:**34238** Calculated pI: **4.82**

PFF Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores  $> 51$  indicate identity or extensive homology ( $p < 0.05$ ). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences shown in Bold Red

```
1  MGAPALSSVV VVATAAVVCL CGAFAQAQDM DSEWARPAYR GFFGAPAGSL
51  LPQSDVDLLE FPLNLEYLET EFFCWSALGY GLDAIDANLT GGGPPSIGGQ
101 SASLTPFIRD VATQFCYQEV GHLRAIKQTV RGFPRPLLDI SAANFGKIIE
151 QALNATLDPP FDPYENSLNF LVASYIIPYV GLTGYVGANP RLLTPQARKL
201 LAGLLAVESA QDAVIRTLTY ERGMARVPSY AGGVAEITAR ISDLRNSLGR
251 RGVKDEGLVV APELGPGLT VGNIIAGDHL SLAYDRTPEE ILGIVYGTGN
301 SAQHGGFFPQ GADGRIARGL LA
```

Spot No.: **22**

NCBI accession No: [gi|226493460](#)

Plant species: **Zea mays**

Protein name: **stem-specific protein TSJT1**

Peptide sequences: **K.DEVFCLEFEGVLDNLGR.L; R.SFAAKDEVFCLEFEGVLDNLGR.L**

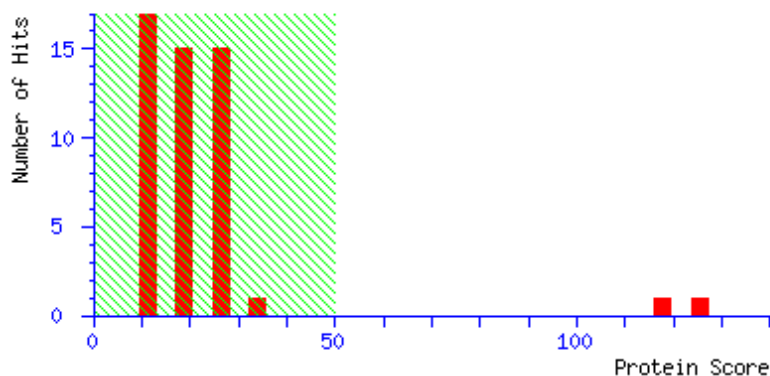
PFM Mascot score: **[125]** Sequence coverage %: **[8]**

Matched peptides No.: **[2]** p value: **5.0e-05**

Calculated Mr:**25050** Calculated pI: **5.23**

PFM Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores  $> 50$  indicate identity or extensive homology ( $p < 0.05$ ). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences shown in Bold Red

```
1 MLAVFSGEVV EVPAELVAAG SRTPSPKTKA SELVARFLGT SCPAAVSVRL
51 ADLGHLAYSH ANQALLRPRS FAAKDEVFCL FEGVLDNLGR LSQQYGLSKG
101 ANEVLLVIEA YKALRDAPY PASLMLAQLA GAYAFVLFDA STNSLLVASG
151 GDVPLFWGVT ADGCVAFSDD IDVLKGSCGK SLAPFPQGCF YSNALGGLKC
201 YENPKNKVTA VPANEEEICG ATFQVEGATV LTALH
```

Spot No.: **23**

NCBI accession No: [gi|226499536](#)

Plant species: **Zea mays**

Protein name: **NADH-ubiquinone oxidoreductase 23 kDa subunit**

Peptide sequences: **K.DWNAVFER.S; R.SINTLFLTEMVR.G; K.LCEAICPAQAITIEAER.E**

PFF Mascot score: **[210]** Sequence coverage %: **[17]**

Matched peptides No.: **[3]** p value: **5.8e-08**

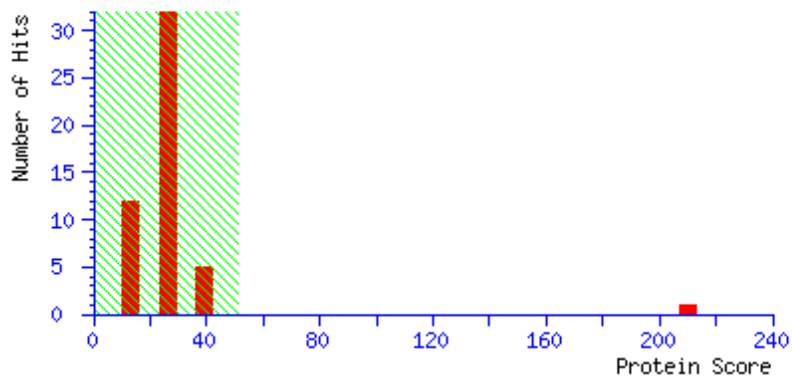
Calculated Mr:**26093** Calculated pI: **5.24**

PFF Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.

Individual ions scores  $> 51$  indicate identity or extensive homology ( $p < 0.05$ ).

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



Matched peptide sequences shown in Bold Red

```
1 MASLLARQAA QALRRARQTAQ LGPAASAMQG HLRTYMNAGI PKRFKEDEEK
51 EQLAKDVAKD WNAVFERSIN TLFLTEMVRG LMLTLKYFFD RNVTINYPFE
101 KGPLSPRFRG EHALRRYESG EERCIACKLC EAICPAQAIT IEAEEREDGS
151 RRTTRYDIDM TKCIYCGFCQ EACPVD AIVE GPNFEFATET HEELLYDKEK
201 LLENGDRWET EIAENLRSES LYR
```

Spot No.: **24**

NCBI accession No: [gi|32330695](#)

Plant species: **Zea mays**

Protein name: **SKP1/ASK1-like protein**

Peptide sequences: **K.SSDGEEFEVVEAVAMESQTIR.H; K.NDFTPEEEEEIR.R; K.NDFTPEEEEEIRR.E**

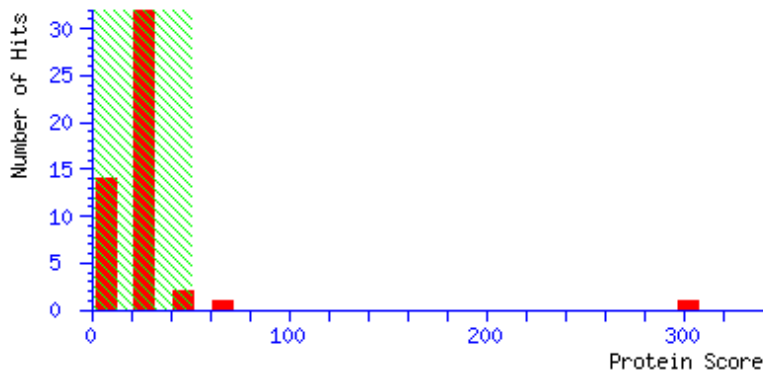
PFF Mascot score: **[301]** Sequence coverage %: **[19]**

Matched peptides No.: **[3]** p value: **4e-12**

Calculated Mr: **19202** Calculated pI: **4.48**

PFF Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores  $> 50$  indicate identity or extensive homology ( $p < 0.05$ ). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences shown in Bold Red

```
1 MAAAGDAGEK KMITLKSSDG EEFVVEEAVA MESQTIRHMI EDDCADNGIP
51 LPNVNSKILS KVIEYCNKHV QAKPADGAAA GAGAGASDAA PAAPAEDLKN
101 WDAEFVKVDQ ATLFDLILAA NYLNIKGLPD LTCQTVADMI KGKTPEEIRK
151 TFNIKNDFTP EEEEEIRREN QWAFE
```

Spot No.: **25**

NCBI accession No: [gi|195636212](#)

Plant species: **Zea mays**

Protein name: **rhicadhesin receptor precursor**

Peptide sequences: **R.NPGNTNNPAGSVVTAANVEK.F; K.FPGVNTLGVSMAR.I; R.IDYAPGGQNPPHTPR.A; K.GDVVFVFP.R; R.GLVHFQQNR.G**

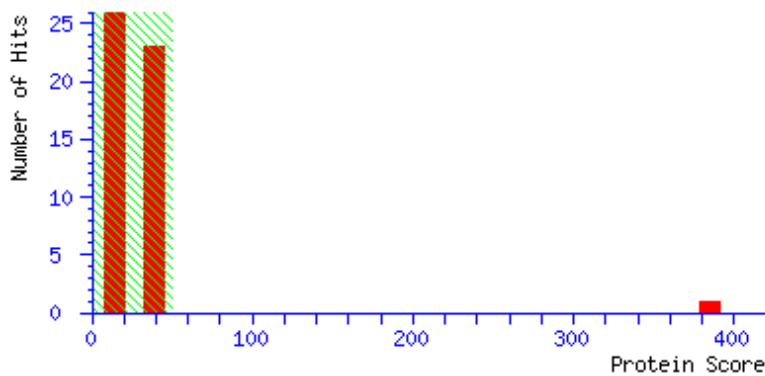
PFM Mascot score: **[385]** Sequence coverage %: **[30]**

Matched peptides No.: **[5]** p value: **2.2e-08**

Calculated Mr:**22948** Calculated pI: **6.58**

PFM Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores  $> 50$  indicate identity or extensive homology ( $p < 0.05$ ). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences shown in Bold Red

```
1  MAKVHLYVAA  ACAVVLALAA  PALAGDPDML  QDVCPADYAS  PVKLNCFACK
51  ANFSADDFFF  DGLRNPGNTN  NPAGSVVTA  NVEKFPGVNT  LGVSMARIDY
101 APGGQNPPHT  HPRATEIIFV  LEGTLEVGFI  TTANALFTKT  VTKGDVVFVP
151 RGLVHFQQNR  GHGPAAVVAA  FNSQLQGTQA  IAMTLFGAVP  PVPSDILAKA
201  FRISSGEVDH  IKANFAPK
```



Spot No.: **26**

NCBI accession No: [gi|195640298](#)

Plant species: [Zea mays](#)

Protein name: [glycine-rich RNA-binding protein 7](#)

Peptide sequences: [K.LFVGGLSYGTDDHSLR.D](#); [K.LFVGGLSYGTDDHSLRDEFAK.Y](#)

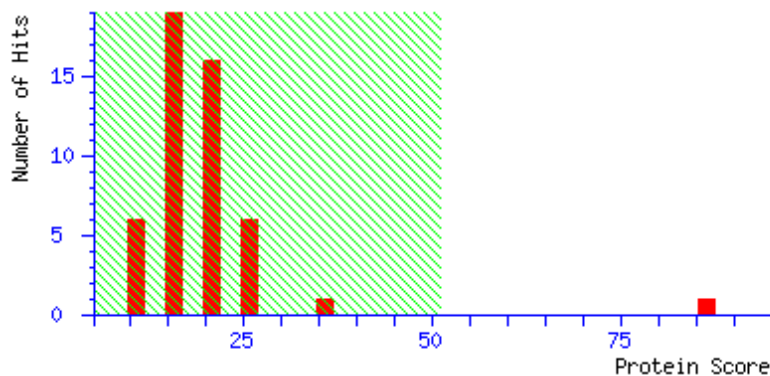
PFF Mascot score: **[86]** Sequence coverage %: **[8]**

Matched peptides No.: **[2]** p value: **0.068**

Calculated Mr:**25155** Calculated pI: **4.87**

PFF Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores  $> 51$  indicate identity or extensive homology ( $p < 0.05$ ). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences shown in Bold Red

```
1 MMLANKLGG LKNATSSKSS NMSVYQAI RC M S S S K L F V G G L S Y G T D D H S L
51 R D E F A K Y G Q V I E A K I I L D R E S G R S R G F G F I T Y T S S E E A S A A I T A M D G K T L
101 D G R N I R V N H A N E R T G G F R S S G G G Y G G G G Y G G Y G G G G S G D Y G G
151 G S G G Y G G N Y G N R A G G G Y G G G G D Y G V A G G A E G S F A A G G S D S F G S S N F A D S G
201 F G E N P A G S F G A T G G S S G A D G F S A G T P G D G N K N D E I M D D L F K D D E P D S Y A N
251 K R S
```

Spot No.: 27

NCBI accession No: gi|162457809

Plant species: Zea mays

Protein name: ubiquitin-conjugating enzyme protein E2

Peptide sequences: R.FTSEMWHPNVYPDGR.V; R.VCISILHPPGEDPNGYELASER.W

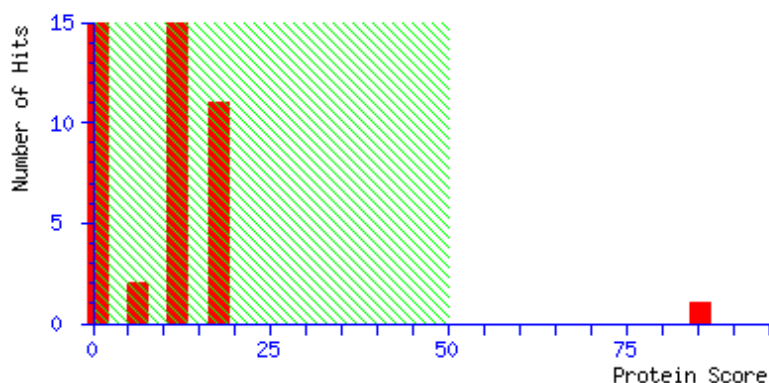
PFF Mascot score: [85] Sequence coverage %: [21]

Matched peptides No.: [2] p value: 0.12

Calculated Mr: 19072 Calculated pI: 5.04

PFF Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores  $> 50$  indicate identity or extensive homology ( $p < 0.05$ ). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences shown in Bold Red

```
1 MASSASQASL LLQQLKDLA KNPVDGFSAG LVDDSNIFEW QVTIIGPPDT
51 LYDGGYFNAI MTFPQNYNS PPSVRFTSEM WHPNVYPDGR VCISILHPPG
101 EDPNGYELAS ERWTPVHIVE SIVLSIISML SSPNDESPAN IEAAKDWREK
151 RDEFKKKVQRQ CVRKSQEML
```

Spot No.: **28**

NCBI accession No: [gi|238009876](#)

Plant species: [Zea mays](#)

Protein name: **protease Pr1C candidate 1**

Peptide sequences: **K.SPLEVFVSFR.G; K.EAVLSGVALEDEQR.E**

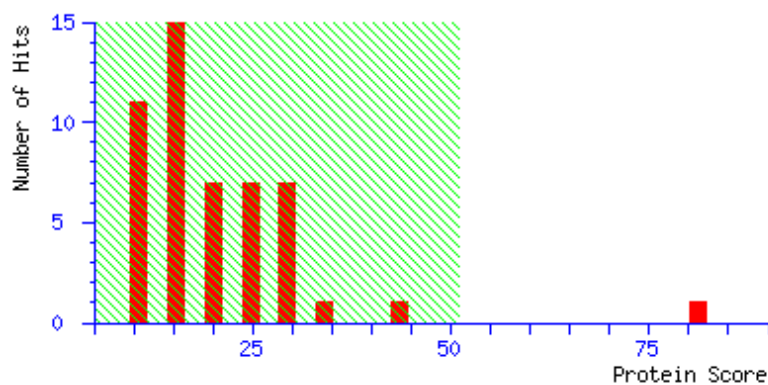
PFF Mascot score: **[81]** Sequence coverage %: **[3]**

Matched peptides No.: **[2]** p value: **0.34**

Calculated Mr:**88301** Calculated pI: **5.82**

PFF Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores  $> 51$  indicate identity or extensive homology ( $p < 0.05$ ). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences shown in Bold Red

1 MGPPRVGVGV GVGGGSGIGV AMVFLIVSAS SFLIRLPLVA RARLPNPTSS  
51 SYTSRSRSRA LLLLPASSPL RAFCPASRRP SPATCSAAYA SSSMATDDNP  
101 LLADFDFFPF DRVEPIHVRP AVRTLLARLE GELTDLEKGV QPTWGKLVPEP  
151 LERIVDSLEV VWGTVDHLKA VKDSSDLRAA VEDVQPKVK FQLRLGQSKP  
201 IYQAFNAIRN SSDWETLSEA RKRIVEAQIK **EAVLSGVALE** **DEQREKFNQI**  
251 EQELEKLTQK FSENVLDATK KFEKLITDKN EIDGLPATAL GLAAQTAASK  
301 GHENASAENG PWIITLDAPS YIAVMQHARN RALREEVYRA YLTRASSGDL  
351 DNTNIISQIL KLRLEKAKLL GYKNYAEVSM AQKMATVDRV EELLEKLRAA  
401 SWDHAVKDME DLKAFAKESA SPEANDLAHW DLSFWSERLR ESKYDINEED  
451 LRPYFALPKV MDGLFSLANR LFGVSVEPAD GLAPVWNSDV KFYCVKDSSN  
501 SPVAYFYFDP YSRPSEKRGG AWMNVVFSRS RVLARNGSPV RFPVAHMVCN  
551 QTPPVGDKPS LMTFREVEVTV FHEFGHALQH MLTKQDEGFV SGIRGVEWDA  
601 VELPSQFMEN WCYHKNTLLS IAKHYETGEL LPEEIIYAKLV AAKNFRAGTF  
651 SLRQIRFASV DMELHTTYDP NGSLSIYDVD RRVAERTQVL APLPEDKFLC  
701 SFSHIFAGGY AAGYYSYKWA EVLSADAFSA FEDVGLDNEK AIEETGRRFR  
751 ETVLALGGGK **SPLEVFVSR** GREPSPEALL RHNGLLPVAA L

Spot No.: **29**

NCBI accession No: [gi|413949328](#)

Plant species: **Zea mays**

Protein name: **pyruvate, phosphate dikinase 3, Precursor**

Peptide sequences: **R.FAYDSFR.R; K.VLANADTPEDALAAR.N; R.SDFEGIFR.A; R.LLDPPLHEFLPEGNVEEIVR.E**

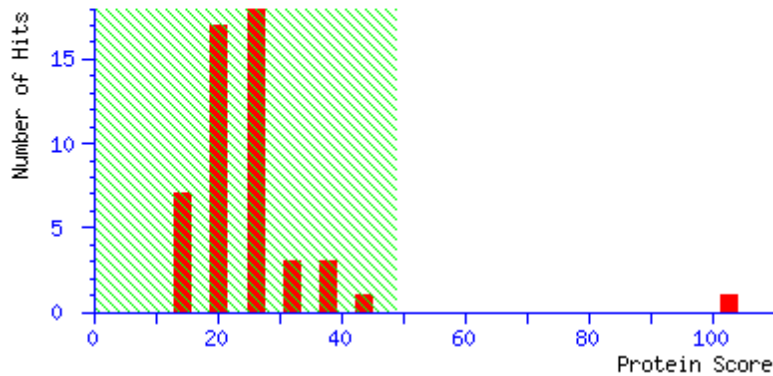
PFM Mascot score: **[103]** Sequence coverage %: **[5]**

Matched peptides No.: **[4]** p value: **1.7**

Calculated Mr: **103777** Calculated pI: **6.04**

PFM Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores  $> 49$  indicate identity or extensive homology ( $p < 0.05$ ). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences shown in Bold Red

1 MAASVSTSRV ICLQKPGPEG SSRGAREVAP FTRQSVAAPR RPHGANASVI  
51 IGSDSGAGRG QHSPPLRAVV DAGPVQTTKK RVFHFQKGGKS EGNKNMKELL  
101 GKGANLAEM ASIGLSVPPG FTVSTEACQQ YQEAGRALPP GLWAEVLDGL  
151 RWVEEYMGAA LGDPRRPLLL SVRSGAAVSM PGMMDTVLNL GLNDQVAAAGL  
201 AAKSGDRFAY DSFRRFLDMF GNVVMDIPHA LFEEKLEAMK KAKGLKNDTD  
251 LTATDLKELV SQYKNVYVEA KGEFFPSDPK RQLELAVLAV FDSWESPRAK  
301 KYRSINQITG LRGTAVNVQC MVFGNMGNTS GTGVLFTRNP NTGEKKLYGE  
351 FLVNAQGEDV VAGIRTPEDL DAMKDVMPQA YKELVENCRI LESHYKEMQD  
401 IEFTVQESRL WMLQCRIGKR TGKSAVKIAV DMVNEGLVER RAAIKMVEPG  
451 HLDQLLHPQF ENPSAYKDQV IATGLPASPG AAVGQVVFTA EDAETWHSQG  
501 KSVILVRAET SPEDVGGMHA AAGILTERGG MTSAAVVAR GWGKCCVSGC  
551 SGIRVNDAEK VVKIGNVLR EGEWLSLNGS TGEVILGKQP LSPPALSGDL  
601 GTFMSWDDV RKLKVLANAD TPEDALAARN NGAEGIGLCR TEHMFFASDE  
651 RIKAVRQMIM APTVELRQQA LDRLLPYQRS DFEGIFRAMD GLSVTIRLLD  
701 PPLHEFLPEG NVEEIVRELC SETGANQEDA LARIEKLSEV NPMLGFRGCR  
751 LGISYPELTE MQARAIFEAA IAMTNQGVQV FPEIMVPLVG TPQELGHQVA  
801 LIRQVANKVF TSMGKTIGYK IGTMIPIRA ALVADEIAEQ AEFFSFGTND  
851 LTQMTFGYSR DDVGKFIPIY LAQGILQHDP FEVLDQRGVG ELVKLATERG  
901 RKARP NLKVG ICGEHGGEPS SVAFFAKTGL DYVSCSPFRV PIARLAAAQV  
951 LV

Spot No.: **30**

NCBI accession No: [gi|48374986](#)

Plant species: **Zea mays**

Protein name: **hypothetical protein Z477F24.14**

Peptide sequences: **R.LAAFYEAVLGFER.I**

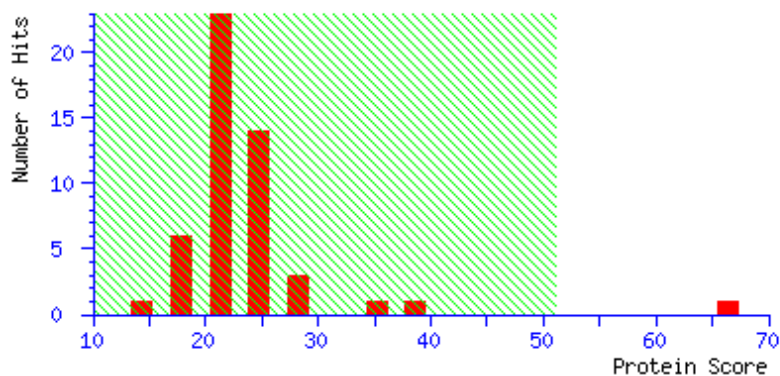
PFF Mascot score: **[66]** Sequence coverage %: **[9]**

Matched peptides No.: **[1]** p value: **0.0014**

Calculated Mr: **15597** Calculated pI: **4.94**

PFF Searched Score:

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores  $> 51$  indicate identity or extensive homology ( $p < 0.05$ ). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Matched peptide sequences shown in Bold Red

```
1  MATLQLNHIA  RETSDVARLA AFYEAVLGFE  RIPSPTYSGF  QVAWLRLPSS
51 PDVALHLIER  DPAAAPVAVG  PGAEGAPPSQ  LPRRHHLAFS  VADYDGFVTG
101 LKARGTDVFE  KSQPDGRTRQ  VFFFDPDDEE  DLVFTKLGLD  VPS
```