

Mass spectrometry data of 88 differentially abundant proteins

Spot No.: **OL1**

NCBI accession No.: **AAL09820.1**

Plant species: ***Arabidopsis thaliana***

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

Peptide sequences: **UK.ALEYEDFDKFDR.V ;
UR.YLVSPPEIDR.T**

PFF Mascot score: **[105]** Sequence coverage %: **[3]**

Matched peptides No.: **[2]**

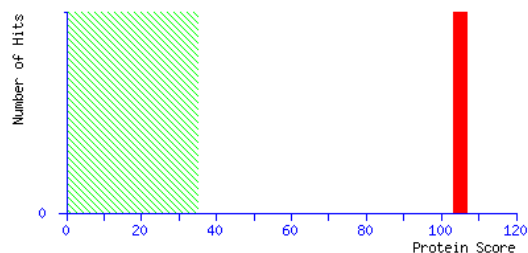
Calculated Mr: **60671** Calculated pI: **5.27**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```

1 MATSSAWKLD DHPKLPKGKT IAVIVLDGWG ESAPDQYNCI HNAPTPAMDS
51 LKHGAPDTWT LIKAHGTAVG LPSEDDMGNS EVGHNALGAG RIFAQGAKLC
101 DQALASGKIF EGEQFKYVSE SFETNTLHLV GLLSDGGVHS RLDQLQLLIK
151 GSAERGAKRI RVHILTDGRD VLDGSSVGFV ETLEADLVAL RENGVDQAIA
201 SGGGRMYVTL DRYENDWEVV KRGWDAQVLG EAPHKFKNAV EAVKTLRKEP
251 GANDQYLPPF VIVDESGKAV GPIVDGDAVV TFNFRADRMV MHAKALEYED
301 FDKFDRVRYP KIRYAGMLQY DGELKLPSRY LVSPPEIDRT SGEYLTHNGV
351 STFACSSSCL LIIGLYYALH FCQYETVKFG HVIFFWNGNR SGYFNEKLEE
401 YVEIPSDSGI SFNVQPKMKA LEIGEKARDA ILSGKFDQVR VNIPNGDMVG
451 HTGDIEATVV ACEAADLAVK MIFDAIEQVK GIYVVTADHG NAEDMVKRDK
501 SGKPALDKEG KLQILTSHL KPVPIAIGGP GLAQGVFRK DLETPLGLANV
551 AATVMNLHGF VAPSDYEPTL IEVVE

```

Spot No.: **OL2**

NCBI accession No.: **AAL09820.1**

Plant species: ***Arabidopsis thaliana***

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

Peptide sequences: **K.ALEYEDFDKFDR.V; R.YLVSPPEIDR.T**

PFF Mascot score: **[150]** Sequence coverage %: **[3]**

Matched peptides No.: **[2]**

Calculated Mr: **60671**

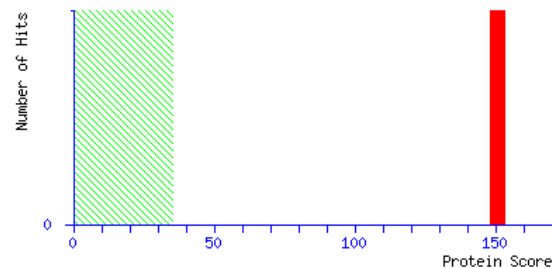
Calculated pI: **5.27**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1 MATSSAWKLD DHPKLPKGKT IAVIVLDGWG ESAPDQYNCI HNAPTPAMDS
51 LKHGAPDTWT LIKAHGTA VG LPSEDDMGNS EVGHNALGAG RIFAQGAKLC
101 DQALASGKIF EGE GFKYVSE SFETNTLHLV GLLSDGGVHS RLDQLQLLIK
151 GSAERGAKRI RVHILTDGRD VLDGSSVG FV ETLEADLVAL RENGVD AQIA
201 SGGGRMYVTL DRYENDWEVV KRGWDAQVLG EAPHKFKNAV EAVKTLRKEP
251 GANDQYLPFF VIVDESGKAV GPIVDGDAVV TFNFRADRMV MHAKALEYED
301 FDKFDRVRYP KIRYAGMLQY DGELKLPSRY LVSPPEIDRT SGEYLTHNGV
351 STFACSSSCL LIIGLYYALH FCQYETVKFG HVTFFWNGNR SGYFNEKLEE
401 YVEIPSDSGI SFNVQPKMKA LEIGEKARDA ILSGKFDQVR VNIPNGDMVG
451 HTGDIEATVV ACEAADLAVK MIFDAIEQVK GIYVVTADHG NAEDMVKRDK
501 SGKPALDKEG KQILTSTHTL KVPPIAIGGP GLAQGVFRK DLETPLANV
551 AATVMNLHGF VAPSDYEPTL IEVVE
```

Spot No.: **OL4**

NCBI accession No.: **NP_051044.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **ATP synthase CF1 alpha subunit**

Peptide sequences:**K.IAQIPVSEAYLGR.V; R.VINALANPIDGR.G;**

R.EAYPGDVFYLSR.L

PFF Mascot score: **[200]**

Sequence coverage %: **[7]**

Matched peptides No.: **[3]**

Calculated Mr: **55351**

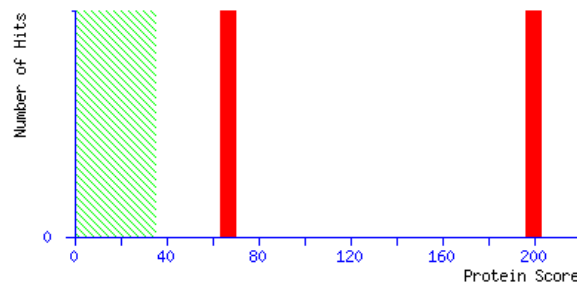
Calculated pI: **5.19**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

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

Spot No.: **OL5**

NCBI accession No.: **CAC81058.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **mitochondrial F1 ATP synthase beta subunit**

Peptide sequences: **R.TIAMDGTEGLVR.G;**

R.VCQVIGAIVDVR.F; K.VVDLLAPYQR.G;

R.VGLTGLTVAEYFR.D; R.FTQANSEVSALLGR.I

PFF Mascot score: **[339]**

Sequence coverage %: **[10]**

Matched peptides No.: **[5]**

Calculated Mr: **63560**

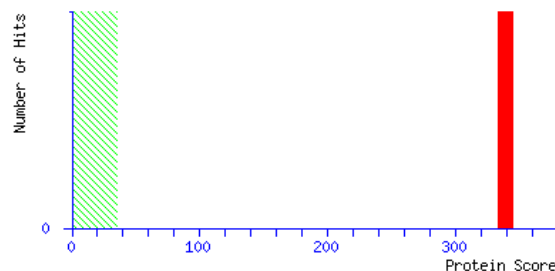
Calculated pI: **6.52**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

| | | | | | |
|-----|--------------------|--------------------|-------------------|-------------------|--------------------|
| 1 | MTMITPSSNT | THYRESWYAC | RYRSGIPGST | HASVASRRVL | SSLLRSSSGR |
| 51 | SAAKLGNRNP | RLPSPSPARH | AAPCSYLLGR | VAEYATSSPA | SSAAPSSAPA |
| 101 | KDEGKKTYDY | GGKGAIGRVC | QVIGAIVDVR | FEDQEGLPPI | MTSLEVQDHP |
| 151 | TRLVLEVSHH | LGQNVVR TIA | MDGTEGLVRG | RKVLNTGAPI | TVPVGRATLG |
| 201 | RIMNVLGEPI | DERGEIKTEH | YLPPIHRDAPA | LVDLATGQEI | LATGIK VVDL |
| 251 | LAPYQR GGKI | GLFGGAGVGK | TVLIMELINN | VAKAHGGFSV | FAGVGERTRE |
| 301 | GNDLYREMIE | SGVIKLGEKQ | SESKCALVYG | QMNEPPGARA | RVGLTGLTVA |
| 351 | EYFR DAEGQD | VLLFIDNIFR | FTQANSEVSA | LLGRIPSAVG | YQPTLASDLG |
| 401 | ALQERITTTK | KGSITSVQAI | YVPADDLTD | APATTFAHLD | ATTVLSRQIS |
| 451 | ELGIYPAVDP | LDSTSRMLSP | HILGEEHYNT | ARGVQKVLQN | YKNLQDIIAI |
| 501 | LGMDELSDD | KLTVARARKI | QRFLSQPFHV | AEIFTGAPGK | YVDLKENINS |
| 551 | FQGLLDGKYD | DLSEQSFYMV | GGIDEVVAKA | EKIAKESAA | |

Spot No.: **OL7**

NCBI accession No.: **AAL08228.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **AT4g23100/F7H19_290**

Peptide sequences:**R.SHIWTDTDKDR.T; K.YIDCTGMTFR.Q;**

K.EAGFLNAVDEVVR.T

PFF Mascot score: **[228]**

Sequence coverage %: **[6]**

Matched peptides No.: **[3]**

Calculated Mr: **58938**

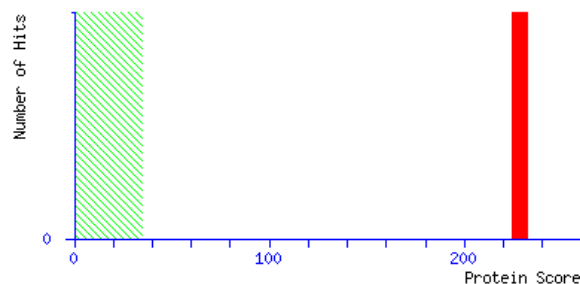
Calculated pI: **6.16**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MALLSQAGGS  YTVVPSGVCS  KTGTKAVVSG  GVRNLDVLRM  KEAFGSSNSR
51  SLSTKSMLLH  SVKRSKRGHQ  LIVAAASPTE  EAVVATEPLT  REDLIAYLAS
101 GCKTKDKYRI  GTEHEKFGFE  VNTLRPMKYD  QIAELLNGIA  ERFWEKVM
151 GDKIIGLKQG  KQSISLEPGG  QFELSGAPLE  TLHQTCAEVN  SHLYQVKAVA
201 EEMGIGFLGI  GFQPKWRRED  IPIMPKGRYD  IMRNYMPKVG  TLGLDMMLRT
251 CTVQVNLDFF  SEADMIRKFR  AGLALQPIAT  ALFANSPFTE  GKPNGFLSMR
301 SHIWTDTDKD RTGMLPFVFD DSFGFEQYVD YALDVPMYFA YRKNKYIDCT
351 GMTFRQFLAG KLPCLPGELP SYNDWENHLT TIFPEVRLKR YLEMRGADGG
401 PWRRLCALPA  FWVGLLYDDD  SLQAILDITA  DWTPAEREML  RNKVPVTGLK
451 TPFRDGLLKH  VAEDVLKLAK  DGLERRGYKE AGFLNAVDEV VRTGVTPAEK
501 LLEMNGEWG  QSVDPVFEEL  LY
```

Spot No.: **OL8**

NCBI accession No.: **BAF01944.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **S-adenosylmethionine synthase like protein**

Peptide sequences: K.ANVDYEQIVR.K;

R.EIGFVSADVGLDADNCK.V; R.FVIGGPHGDAGLTGR.K

PFF Mascot score: **[291]**

Sequence coverage %: **[10]**

Matched peptides No.: **[3]**

Calculated Mr: **43110**

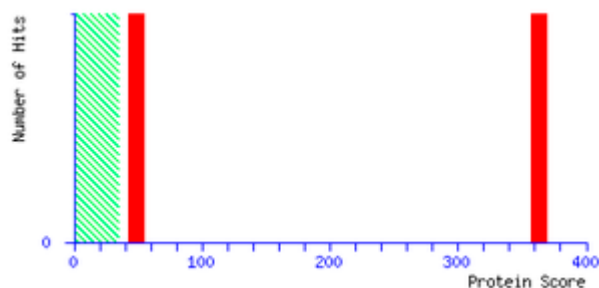
Calculated pI: **5.60**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1 MESFLFTSES VNEGHPDKLC DQISDAILDA CLEQDPESKV ACETCTKTNM
51 VMVFGEITTK ANVDYEQIVR KTCREIGFVS ADVGLDADNC KVLVNIEQQS
101 PDIAQGVHGH LTKKPEEVGA GDQGHMFGYA TDETPELMPL THVLATKLGA
151 KLTEVRKNGT CPWLRPDGKT QVTIEYINES GAMVPVRVHT VLISTQHDET
201 VTNDEIAADL KEHVIKPVIP EKYLDEKTIF HLNPSGRFVI GGPHGDAGLT
251 GRKIIIDTYG GWGAHGGAFA SGKDPTKVDR SGAYIVRQAA KSIVASGLAR
301 RVIVQVSYAI GVPEPLSVFV DSYGTGKIPD KEILEIVKES FDFRPGMISI
351 NLDLKRGGNG RFLKTAAYGH FGRDDADFTW EVVKPLKSNK VQA
```


Spot No.: **OL10**

NCBI accession No.: **AAM61185.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **phosphoglycerate kinase**

Peptide sequences: **R.VTLFLNLANDPTIER.I;**

R.VDLNVPLDDNSNITDDTR.I;K.LVAGLPEGGVLLLENVR.F;R.FY

AEEEKNDPEFAK.K;K.LAALADVYVNDAFGTAHR.A;K.ELDYL

GAVANPK.K;K.AQGLSVGSSLVEEDKLDLAK.S

PFF Mascot score: **[519]**

Sequence coverage %: **[24]**

Matched peptides No.: **[6]**

Calculated Mr: **42178**

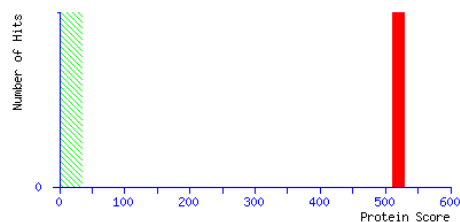
Calculated pl: **5.49**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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  VPRLSSELLGV  EVVMANDSIG
101 EEVQKLVAGL  PEGGVLLLEN  VRFYAEEERN  DPEFAKLAA  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.: **OL11**

NCBI accession No.: **BAE98486.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **glutamine synthetase like protein**

Peptide sequences: **R.HKEHISAYGEGNER.R;**

K.EHISAYGEGNER.R

PFF Mascot score: **[180]**

Sequence coverage %: **[3]**

Matched peptides No.: **[2]**

Calculated Mr: **39323**

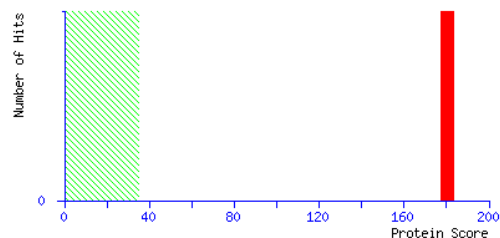
Calculated pI: **5.14**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MSLADLVNL DISDNSEKII AEYIWVGGSG MDMRSKARTL PGPVTDPSKL
51 PKWNYDGSST GQAPGQDSEV ILYPQAIFKD PFRRGNNILV MCDAYTPAGE
101 PIPTNKRHAA AEIFANPDVI AEVPWYGIEQ EYTLLQKDVN WPLGWPIGGF
151 PGPQGPYYCS IGADKSFGRD IVD AHYKASL YAGINISGIN GEVMPGQWEF
201 QVGPSVGISA ADEIWIARYI LERITEIAGV VVSFDPKPIP GDWNGAGAHT
251 NYSTKSMREE GGYEIIKKAI EKLGLRHKEH ISAYGEGNER RLTGHHETAD
301 INTFLWGVAN RGASIRVGRD TEKEGKGYFE DRRPASNMDP YVVTSMIAET
351 TLLWNP
```

Spot No.: **OL13**

NCBI accession No.: **BAH20341.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **AT1G04410, partial**

Peptide sequences: **R.ELVKDDAWLDGEFISTVQQR.G**

PFF Mascot score: **[50]** Sequence coverage %: **[8]**

Matched peptides No.: **[1]**

Calculated Mr: **26347**

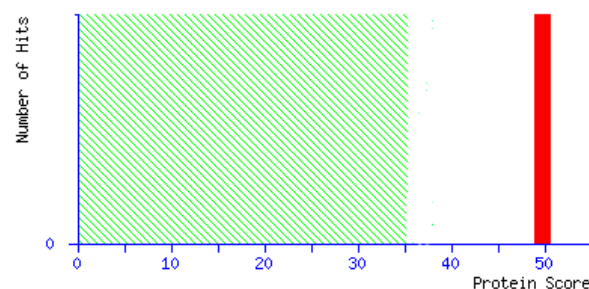
Calculated pI: **6.59**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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 LVPMIARGIM LGADQPVILH MLDIPPAAEA
51  LNGVKMELID AAFPLLKGVV ATTDAVEGCT GVNVAVMVGG FPRKEGMERK
101 DVMSKNVSIY KSQAAALEKH AAPNCKVLVV ANPANTNALI LKEFAPSIPE
151 KNISCLTRLD HNRALGQISE RLSVPVSDVK NVIIWGNHSS SQYPDVNHAK
201 VQTSSGEKPV RELVKDDAWL DGEFISTVQQ RGAAIIKARK LSSALSAASS
251 ACDHIRDWVL GTPEGTFVSM GVYSDGSYSV PSGLIYSFPV TCRNGDWSIV
301 QGLPIDEVSR KKMDLTAEEL KEEKDLAYSC LS
```

Spot No.: **OL14**

NCBI accession No.: **AAC49472.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Annexin-like protein**

Peptide sequences:**K.TLDKELSNDFER.A;**

R.AILLWTLEPGER.D;K.SLEEDVAHHTTGDFR.K;K.HYNDEDVI

R.I;K.AQINATFNR.Y

PFF Mascot score: **[270]**

Sequence coverage %: **[17]**

Matched peptides No.: **[5]**

Calculated Mr: **36322**

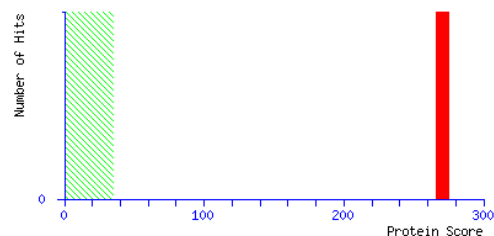
Calculated pI: **5.34**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MATLKVSDSV PAPSDDAEQL RTAFEGWGTN EDLIISILAH RSAEQRKVIR
51 QAYHETYGKD LLKTLDKELS NDFERAILLW TLEPGERDAL LANEATKRWT
101 SSNQVLMEVA CTRTSTQLLH ARQAYHARYK KSLEEDVAHH TTGDFRKLLV
151 SLVTSYRYEG DEVNMTLAKQ EAKLVHEKIK DKHYNDEDVI RILSTRSKAQ
201 INATFNRYQD DHGEEILKSL EEGDDDDKLP CTLRSTIQCL TRPELYFVDV
251 LRSAINKTGT DEGALTRIVT TRAEIDLKVI GEEYQRRNSI PLEKAITKDT
301 RGDYEKMLVA LLGEDDA
```

Spot No.: **OL15**

NCBI accession No.: **CAA67608.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Annexin, partial**

Peptide sequences: K.VSDSVPA PSDDAEQLR.T;

R.AILLWTLEPGER.D; K.SLEEDVAHHTTGDFR.K;

K.SLEEGDDDDKFLALLR.S

PFF Mascot score: **[350]**

Sequence coverage %: **[18]**

Matched peptides No.: **[4]**

Calculated Mr: **35928**

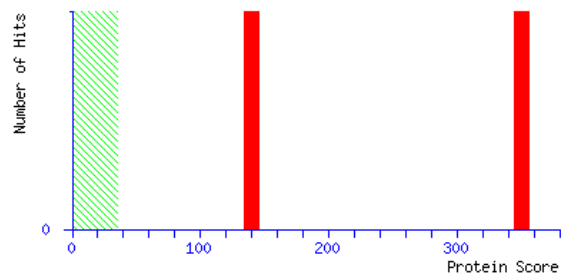
Calculated pI: **5.19**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  TLKVSDSVPA PSDDAEQLRT AFEGWGTNED LIISILAHRS AEQRKVI RQA
51 YHETYGEDLL KTLDKELSND FERAILLWTL EPGERDALLA NEATKRWTSS
101 NQVLMEVACT RTSTQLLHAR QAYHARYKKS LEEDVAHHTT GDFRKLLVSL
151 VTSYRYEGDE VNMTLAKQEA KLVHEKIKDK HYNDEDVIRI LSTISKAQIN
201 ATFNRYQDDH GEEILKSLEE GDDDDKFLAL LRSTIQCLTR PELYFVDVLR
251 SAINKTGTDE GALTRIVTTR AEIDLKVICE EYQRRNSIPL RAITKDNCGD
301 YGKMLVAIFG EDDA
```

Spot No.: **OL16**

NCBI accession No.: **BAH20433.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **AT4G04640, partial**

Peptide sequences: **K.SEPVIHTLLPLSPK.G;**

K.GEICDINGTCVDAAEDEFRR.L; R.ALQESLASELAAR.M

PFF Mascot score: **[299]**

Sequence coverage %: **[31]**

Matched peptides No.: **[3]**

Calculated Mr: **16738**

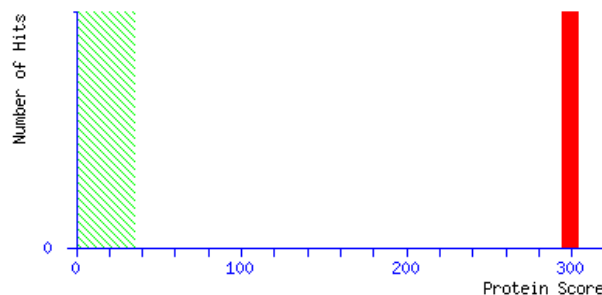
Calculated pI: **5.06**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  YTKFVSLVKS EPVIHTLLPL SPKGEICDIN GTCVDAAEDE FFRLTTKEGK
51 LTVERETFRT PTADFSPILQ FEQDPVQILD ALLPLYLNSQ ILRALQESLA
101 SELAARMSAM SSASDNASDL KKSLSMVYNR KRQAKITGEI LEIVAGANAQ
151 V
```

Spot No.: **OL18**

NCBI accession No.: **AAL16248.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **AT3g44310/T10D17_100**

Peptide sequences: R.KYHASAIHVPGPGEVAR.L;

K.YHASAIHVPGPGEVAR.L; K.LGAAICWENR.M

PFF Mascot score: **[149]**

Sequence coverage %: **[7]**

Matched peptides No.: **[3]**

Calculated Mr: **38553**

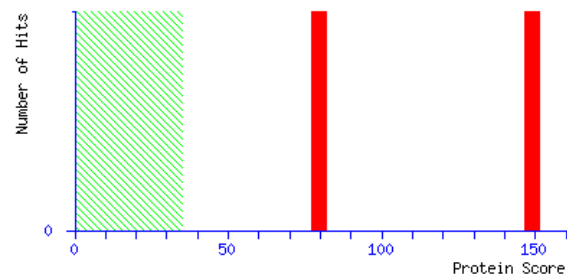
Calculated pI: **5.78**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1 MSSTKDMSTV QNATPFNGVA PSTTVRVTIV QSSTVYNDTP ATIDKAEKYI
51 VEAASKGAEL VLFPEGFIGG YPRGFRFGLA VGVHNEEGRD EFRKYHASAI
101 HVPGPEVARL ADVARKNHVY LVMGAIEKEG YTLYCTVLFF SPQGQFLGKH
151 RKLMPSTLER CIWGQGDGST IPVYDTPIGK LGAAICWENR MPLYRTALYA
201 KGIELYCAPT ADGSKEWQSS MLHIAIEGGC FVLSACQFCQ RKFDPDHPDY
251 LFTDWYDDKE HDSIVSQGGS VIISPLGQVL AGPNFESEGL VTADIDLGDI
301 ARAKLYFDSV GHYSRPDVLH LTVNEYPRKS VTFVTKVEKA EDDSNK
```

Spot No.: **OL19**

NCBI accession No.: **AAL16224.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **AT4g38970/F19H22_70**

Peptide sequences: **R.TAAYYQQGAR.F;**

K.TWGGRPENVNAAQTTLAR.A

PFF Mascot score: **[133]**

Sequence coverage %: **[7]**

Matched peptides No.: **[2]**

Calculated Mr: **43029**

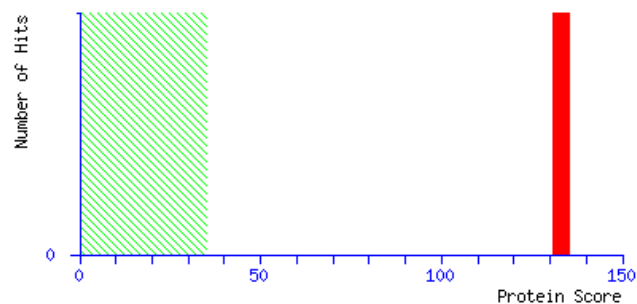
Calculated pI: **6.79**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MASTSLLKAS  PVLDKSEWVK  GQSVLFRQPS  SASVVLNRNA  TSLTVRAASS
51  YADELVKTAK  TIASPGRGIL  AMDESNATCG  KRLDSIGLEN  TEANRQAFRT
101 LLVSAPGLGQ  YVSGAILFEE  TLYQSTTEGK  KMVDVLVEQN  IVPGIKVDKG
151 LVPLVGSNNE  SWGQGLDGLS  SRTAAYYQQG  ARFAKWRTVV  SIPNGPSALA
201 VKEAAWGLAR  YAAISQDSGL  VPIVEPEILL  DGEHDIDRTY  DVAEKVWAEV
251 FFYLAQNNVM  FEGILLKPSM  VTPGAESKDR  ATPEQVAAYT  LKLLRNRVPP
301 AVPGIMFLSG  GQSEVEATLN  LNAMNQAPNP  WHVSFSYARA  LQNTCLKTWG
351 GRPENVNAAQ  TTLARAKAN  SLAQLGKYTG  EGESEEAKEG  MFVKGYTY
```


Spot No.: **OL20**

NCBI accession No.: **BAH56881.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **AT2G21330**

Peptide sequences: **R.LASIGLENTEANR.Q;**

R.TAAYYQQGAR.F

PFF Mascot score: **[111]**

Sequence coverage %: **[6]**

Matched peptides No.: **[2]**

Calculated Mr: **40612**

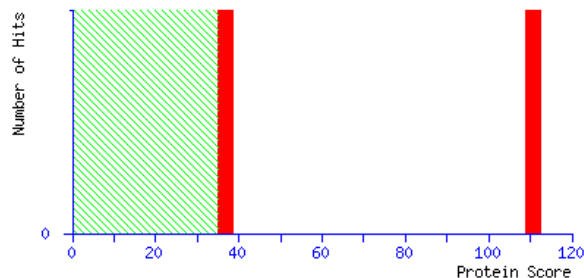
Calculated pI: **6.34**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MASSTATMLK ASPVKSDWVK GQSLLLRQPS SVSAIRSHVA PSALTVRAAS
51 AYADELVKTA KTIASPGHGI MAMDESNATC GKRLLASIGLE NTEANRQAYR
101 TLLVSAPGLG QYISGAILFE ETLYQSTTDG KKMVDVLVEQ NIVPGIKVDK
151 GLVPLVGSYD ESWCQGLDGL ASRTAAYYQQ GARFAKWRTV VSIPNGPSAL
201 AVKEAAWGLA RYAAISQDSG LVPIVEPEIM LDGEHGIDRT YDVAEKVWAE
251 VFFYLAQNNV MFEGILLKPS MVTPGAETD RATPEQVASY TLKLLRNRIIP
301 PAVPGIMFLS GGQSELEATL NLNAMNQAPN TCLAEHLLED MGRQGREREG
351 GSGHSLGQSQ SQFAGSAREI HWRRRV
```

Spot No.: **OL22**

NCBI accession No.: **NP_565203.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **mercaptopyruvate sulfurtransferase 1**

Peptide sequences: **R.NPIQEYQVAHIPR.A;**

R.ALFFDLGISDR.K; K.VWVLDGGLPR.W

PFF Mascot score: **[197]**

Sequence coverage %: **[9]**

Matched peptides No.: **[3]**

Calculated Mr: **42152**

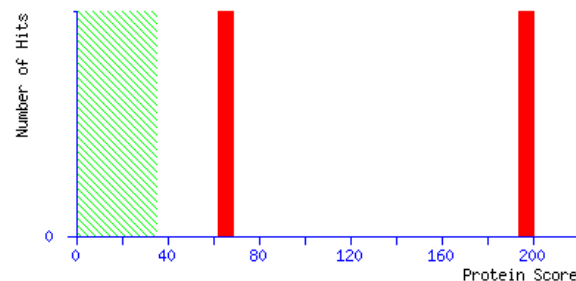
Calculated pI: **5.95**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MASTLFSRTF LAASHRLITP SLPQKIFNPA TFLSRSLHSQ LGSASTAYKS
51 TTWARRAMAS TGVETKAGYS TSSVSTSEPV VSVDWLHANL REPDLKILDA
101 SWYMPDEQRN PIQEYQVAHI PRALFFDLG ISDRKTSSLPH MLPTEEAFAA
151 GCSALGIDNK DEVVVDGKG IFSAARVWWM FRVFGHEKVW VLDGGLPRWR
201 ASGYDVESSA SGDAILKASA ASEAIEKIYQ GQTVSPITFQ TKFQPHLVWT
251 LDQVKNNMED PTYQHIDARS KARFDGTAPE PRKGIRSGHI PGSKCIPFPQ
301 MFDSCNTLLP AEELKKRFDQ EDISLDKPIM ASCGTGVTAC ILAMGLHRLG
351 KTDVPIYDGS WTEWATQPD LPIESVESSS
```

Spot No.: **OL23**

NCBI accession No.: **BAH57171.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **AT3G16420**

Peptide sequences: **K.GANLWDDGSTHDAVTK.I;**

K.QLTAFGSDDGTVWDDGAYVGVK.K;

K.KVYVGQAQDGISAVK.F; K.VYVGQAQDGISAVK.F;

K.FVYDKSPPEEVTGEEHGK.S; K.IGVHVRPLSN.-

PFF Mascot score: **[576]**

Sequence coverage %: **[28]**

Matched peptides No.: **[6]**

Calculated Mr: **29808**

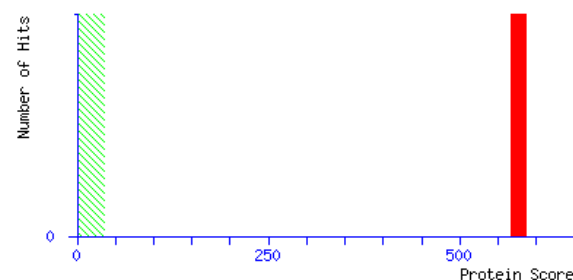
Calculated pI: **5.44**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1 MAQKVEAQGG KGANLWDDGS THDAVTKIQL AAGIDGIQYV QFDYVKNQGP
51 EQAPLRGTKG RVLPAFPFVI NHPDEHLVSV EGWYSPEGTH FTLQVKDKKI
101 IGFHGSAGGN LNSLGAYFAP LTTTTPPLTPA KQLTAFGSDD GTVWDDGAYV
151 GVKRVYVGQA QDGISAVKFV YDKSPPEEVTG EEHGKSTLLG FEEFVLDYPS
201 EYITAVDGTY DKIFGSDGSV ITMLRFKTNK QTSPPFGLA GTVFELKEEG
251 HKIVGFHGRA DVLLHKIGVH VRPLSN
```

Spot No.: **OL24**

NCBI accession No.: **AAA96254.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **GF14chi isoform**

Peptide sequences: **K.AVDKDELTV EER.N; R.GNDDHVS LIR.D;**

R.KDAAEHTLTAYK.A; K.DAAEHTLTAYK.A;

K.AAQDIANSELAPTHPIR.L; K.DSTLIMQLLR.D

PFF Mascot score: **[354]**

Sequence coverage %: **[22]**

Matched peptides No.: **[6]**

Calculated Mr: **29997**

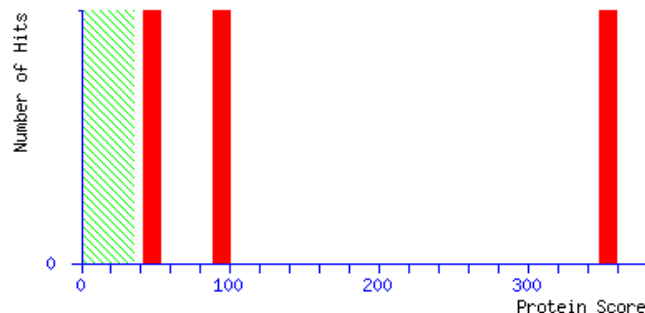
Calculated pI: **4.68**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1 MATPGASSAR DEFVYMAKLA EQAERYEEMV EFMEKVAKAV DKDELTV EER
51 NLLSVAYKNV IGARRASWRI ISSIEQKEES RGNDDHVS LI RDYRSKIETE
101 LSDICDGILK LLDITILVPAA ASGDSKV FYL KMKGDYHRYL AEFKSGQERK
151 DAAEHTLTAY KAAQDIANSE LAPTHPIRLG LALNFSVFYY EILNSPDRAC
201 NLAKQAFDEA IAELDTLGEE SYKDSTLIMQ LLRDNLT LWA SDMQDDVADD
251 IKEAAPAAAK PADEQQS
```

Spot No.: **OL26**

NCBI accession No.: **BAH20249.1**

Plant species: *Arabidopsis thaliana*

Protein name: **AT5G14740, partial**

Peptide sequences: K.YMVFACSDSR.V;

R.VCPSHVLDFHPGDAFVVR.N; K.VLAESSESAFEDQCGR.C;

R.EAVNVSLANLLTYPFVR.E

PFF Mascot score: **[367]**

Sequence coverage %: **[22]**

Matched peptides No.: **[4]**

Calculated Mr: **30867**

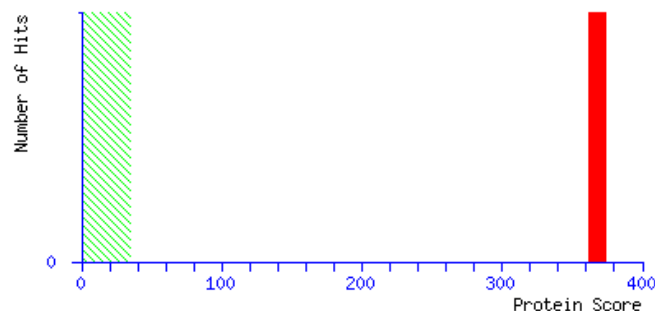
Calculated pI: **5.94**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  CFRCTCFSHF KLELRRMGNE SYEDAIEALK KLLIEKDDLK DVAAAKVKKI
51  TAE LQAASSS DSKSFDPVER IKEGFVTFKK EKYETNPALY GELAKGQSPK
101 YMFACSDSR VCPSHVLDFH PGDAFVVRNI ANMVPPFDKV KYAGVGAAIE
151 YAVLHLKVEN IVVIGHSACG GIKGLMSFPL DGNNSTDFIE DWVKICLPAK
201 SKVLAESESS AFEDQCGRCE REAVNVSLAN LLTPFVREG VVKGTLALKG
251 GYYDFVNGSF ELWELQFGIS FVHSI
```

Spot No.: **OL27**

NCBI accession No.: **AAA03449.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Cytosolic triose phosphate isomerase**

Peptide sequences: **R.AILNESSEFVGDK.V;**

K.VIACVGETLEER.E; K.VASPAQAQEVHDEL.R.K;

K.VASPAQAQEVHDEL.RK.W; K.NVSADVAATTR.I

PFF Mascot score: **[363]**

Sequence coverage %: **[20]**

Matched peptides No.: **[5]**

Calculated Mr: **27366**

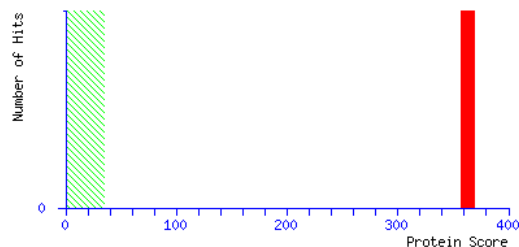
Calculated pI: **5.24**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1 MARKFFVGGN WKCNGTAEV KKIVNTLNEA QVPSQDVVEV VVSPPYVFLP
51 LVKSTLRSDF FVAAQNCWVK KGGFTGEVS AEMLVNLDIP WVILGHSERR
101 AILNESSEFV GDKVAYALAQ GLKVIACVGE TLEREAGST MDVVAAQTKA
151 IADRVTNWSN VVIAYEPVWA IGTGKVASPA QAQEVHDEL R KWLAKNVSAD
201 VAATTRIIYG GSVNGGNCKE LGGQADVDGF LVGGASLKPE FIDIKAAEV
251 NKSA
```

Spot No.: **OL28**

NCBI accession No.: **AAA03449.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Cytosolic triose phosphate isomerase**

Peptide sequences: **R.SDFFVAAQNCWVK.K;**

K.VIACVGETLEER.E; K.VASPAQAQEVHDEL.R.K;

K.VASPAQAQEVHDEL.R.K.W; K.NVSADVAATTR.I

PFF Mascot score: **[513]**

Sequence coverage %: **[20]**

Matched peptides No.: **[5]**

Calculated Mr: **27366**

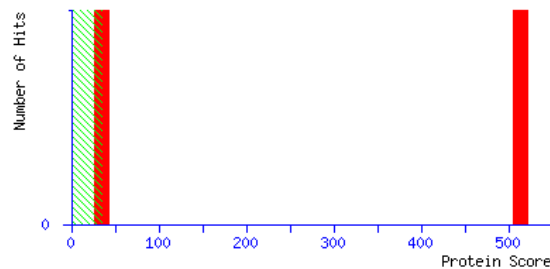
Calculated pI: **5.24**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MARKFFVGGN  WKCNGTAEV  KKIVNTLNEA  QVPSQDVVEV  VVSPPYVFLP
51  LVKSTLRSDF  FVAAQNCWVK  KGGFTGEVS  AEMLVNLDIP  WVILGHSERR
101 AILNESSEFV  GDKVAYALAQ  GLKVIACVGE  TLEEREAGST  MDVVAAQTKA
151 IADRVTNWSN  VVIAYEPVWA  IGTGKVASPA  QAQEVHDELR  KWLAKNVSAD
201 VAATTRIIYG  GSVNGGNCKE  LGGQADVDGF  LVGGASLKPE  FIDIKAAEV
251 NKSA
```

Spot No.: **OL29**

NCBI accession No.: **BAH56801.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **AT3G01500**

Peptide sequences: **K.AFDPVETIK.Q; K.YETNPALYGELAK.G;**

K.YMVFACSDSR.V; R.VCPSHVLDFQPGDAFVVR.N;

K.VISELGDSAFEDQCGR.C

PFF Mascot score: **[388]**

Sequence coverage %: **[22]**

Matched peptides No.: **[5]**

Calculated Mr: **31727**

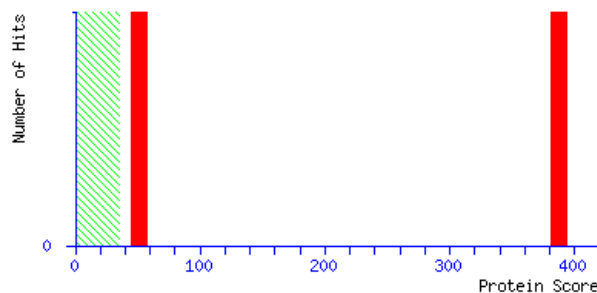
Calculated pI: **6.14**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MSTAPLSGFF  LTSLSPSQSS  LQKLSLRTSS  TVACLPPASS  SSSSSSSSSS
51  RSVPTLIRNE  PVFAAPAPII  APYWSEEMGT  EAYDEAIEAL  KKLLIEKEEL
101 KTVAAAKVEQ  ITAALQTGTS  SDKKAFDPVE  TIKQGFIKFK  KEYETNPAL
151 YGELAKGQSP  KYMFACSDS  RVCPSHVLDF  QPGDAFVVRN  IANMVPPFDK
201 VKYGGVGAAI  EYAVLHLKVE  NIVVIGHSAC  GGIKGLMSFP  LDGNNSTDFI
251 EDWVKICLPA  KSKVISELGD  SAFEDQCGRC  ERVYKHMLDR
```


Spot No.: **OL30**

NCBI accession No.: **BAH56801.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **AT3G01500**

Peptide sequences: **K.AFDPVETIK.Q; K.YETNPALYGELAK.G;**

K.YMVFACSDSR.V; R.VCPSHVLDFQPGDAFVVR.N;

K.VISELGDSAFEDQCGR.C

PFF Mascot score: **[344]**

Sequence coverage %: **[22]**

Matched peptides No.: **[5]**

Calculated Mr: **31727**

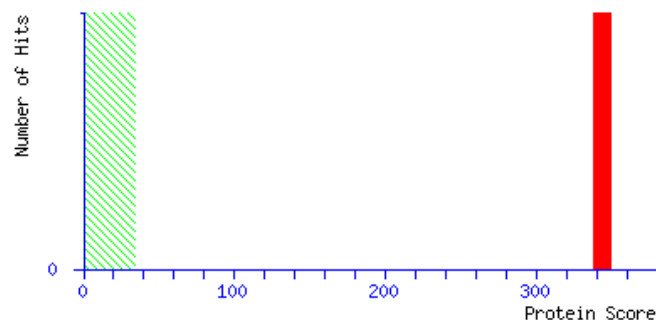
Calculated pI: **6.14**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MSTAPLSGFF  LTSLSPSQSS  LQKLSLRTSS  TVACLPPASS  SSSSSSSSSS
51  RSVPTLIRNE  PVFAAPAPII  APYWSEEMGT  EAYDEAIEAL  KKLLIEKEEL
101 KTVAALKVEQ  ITAALQTGTS  SDKKAAFDPVE  TIKQGFIKFK  KEKEYETNPAL
151 YGELAKGQSP  KYMFACSDS  RVCPSHVLDF  QPGDAFVVRN  IANMVPPFDK
201 VKYGGVGAAI  EYAVLHLKVE  NIVVIGHSAC  GGIKGLMSFP  LDGNNSTDFI
251 EDWVKICLPA  KSKVISELGD  SAFEDQCGRC  ERVYKHMLDR
```

Spot No.: **OL31**

NCBI accession No.: **BAH56768.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **AT5G54270**

Peptide sequences: **R.VDFKEPVWFK.A; R.VDFKEPVWFK.A**

PFF Mascot score: **[63]** Sequence coverage %: **[6]**

Matched peptides No.: **[2]**

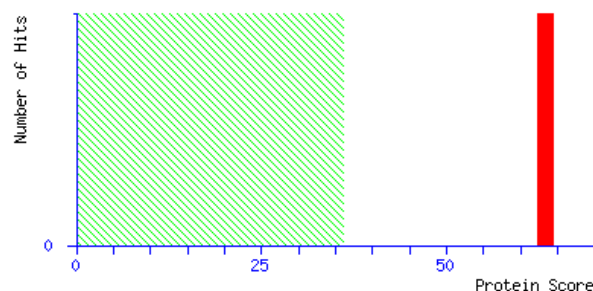
Calculated Mr: **17583** Calculated pI: **4.76**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MLGAFGCITP  EVLQKWVRVD  FKEPVWFKAG  SQIFSEGGLD  YLGNPNLVHA
51  QSILAVLGFQ  VILMGLVEGF  RINGLDGVGE  GNDLYPGGQY  FDPLGLADDP
101 VTFAELKVKE  IKNGRLAMFS  MFGFFVQAIV  TGKGPLENLL  DHLDPVANN
151 AWAFA TKFAP  GA
```

Spot No.: **OL32**

NCBI accession No.: **CAA72973.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Glutathione transferase**

Peptide sequences: K.HVSAWWDDISSR.P

PFF Mascot score: **[68]** Sequence coverage %: **[5]**

Matched peptides No.: **[1]**

Calculated Mr: **24148**

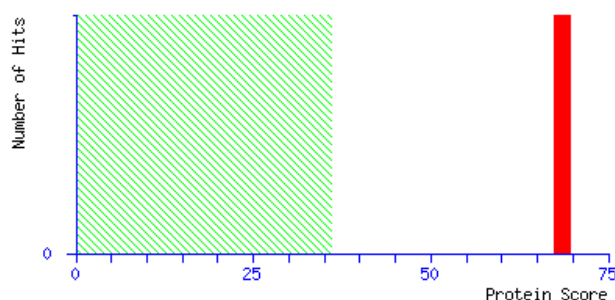
Calculated pI: **7.03**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MVLKVYGP HF ASPKRALVTL IEKGVA FETI PVDLMKGEHK QPAYLALQPF
51 GTVPAVVDGD YKIFESRAVM RYVAEKYRSQ GPDLLGKTVE DRGQVEQWLD
101 VEATTYHPPL LNLTLHIMFA SVMGFPSDEK LIKESEEKLA GVLDVYKAQR
151 AKSKYLAGDF VSLADLAHLP FTDYLVGPIG KAYMIKDRKH VSAWWDDISS
201 RPAWKETVAK YSFPA
```

Spot No.: **OL33**

NCBI accession No.: **BAD94306.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **ferretin 1 precursor, partial**

Peptide sequences: **K.ISDYITQLR.M**

PFF Mascot score: **[78]** Sequence coverage %: **[18]**

Matched peptides No.: **[1]**

Calculated Mr: **5787**

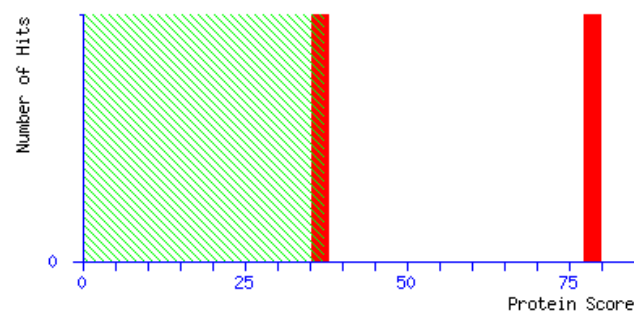
Calculated pI: **4.74**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

1 NNDPQLADFV ESEFLGEQIE AIKK**ISDYIT** QLRMIGKGHG VWHFDQMLLN

Spot No.: **OL34**

NCBI accession No.: **AAG30126.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Glutathione S-transferase**

Peptide sequences: **K.VFGHPASTATR.R; R.RVLIALHEK.N;**
K.VPAFEDGDFK.L; K.VLDVYEHR.L

PFF Mascot score: **[297]**

Sequence coverage %: **[18]**

Matched peptides No.: **[4]**

Calculated Mr: **23539**

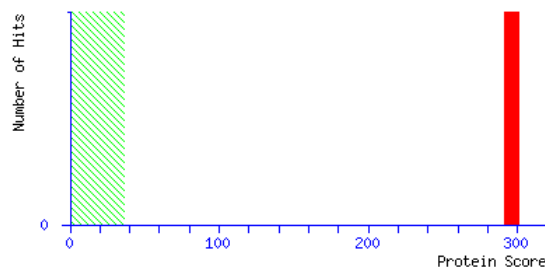
Calculated pI: **6.31**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MAGIKVFGHP ASTATRRVLI ALHEKNLDFE FVHIELKDGE HKKEPFIFRN
51 PFGKVPAFED GDFKLFESRA ITQYIAHFYS DKG NQLVSLG SKDIAGIAMG
101 IEIESHEFDP VGSKLVWEQV LKPLYGMTTD KTVVEEEEAK LAKVLDVYEH
151 RLGESKYLAS DKFTLVDLHT IPVIQYLLGT PTKKLFAERP HVSAWVADIT
201 SRPSAKKVL
```

Spot No.: **OL35**

NCBI accession No.: **AAM61077.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Ferretin 1 precursor**

Peptide sequences: **K.FFKESSEEER.G; K.ISDYITQLR.M**

PFF Mascot score: **[107]** Sequence coverage %: **[7]**

Matched peptides No.: **[2]**

Calculated Mr: **28156**

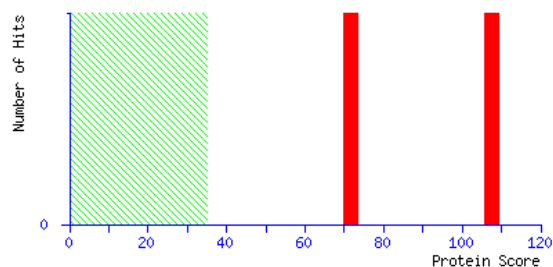
Calculated pI: **5.73**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MASNALSSFT  AANPALSPKP  LLPHGSASPS  VSLGFSRKVG  GSRAVVVAAA
51  TVDTNNMPMT  GVVVFQPLEEV  KKADLAIPIT  SHASLARQRF  ADASEAVINE
101 QINVEYNVSY  VYHSMYAYFD  RDNVAMKGLA  KFFKESSEE  RGHAEKFMEY
151 QNQRGGRVKL  HPIVSPISEF  EHAEKGDALY  AMELALSLEK  LTNEKLLNVH
201 KVASENNDPQ  LADFVESEFL  GEQIEAIKKI  SDYITQLRMI  GKGHGVWHFD
251 QMLLN
```

Spot No.: **OL36**

NCBI accession No.: **AAA32791.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Fe-superoxide dismutase, partial**

Peptide sequences: **K.QTLEFWGK.H; K.PSGELLALLER.D;**

K.TFMTNLVSWEAVSAR.L

PFF Mascot score: **[159]**

Sequence coverage %: **[15]**

Matched peptides No.: **[3]**

Calculated Mr: **25409**

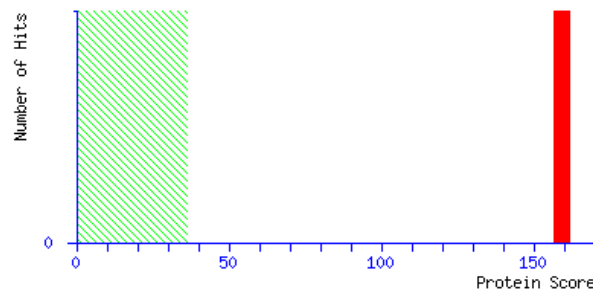
Calculated pI: **6.30**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  SLHSSLKLEL QLQRMAASSA VTANYVLKPP PFALDALEPH MSKQTLEFW
51 GKHHRAYVDN LKKQVLGTEL EGKPLEHIIH STYNNGDLLP AFNNAAQAWN
101 HEFFWESMKP GGGGKPSGEL LALLERDFTS YEKFYEEFNA AAATQFGAGW
151 AWLAYSNEKL KVVKTPNAVN PLVLGSFPLL TIDVWEHAYY LDFQNRDPDY
201 IKTFMTNLVS WEAVSARLEA AKAASA
```

Spot No.: **OL37**

NCBI accession No.: **AAM66134.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Translationally controlled tumor protein**

Peptide sequences: **K.VVDIVDTFR.L; R.LQEQTPTYDKK.G**

PFF Mascot score: **[115]** Sequence coverage %: **[11]**

Matched peptides No.: **[2]**

Calculated Mr: **18926**

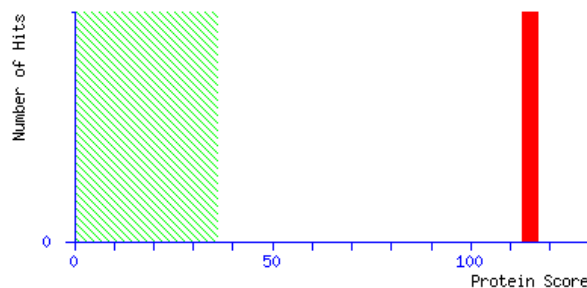
Calculated pI: **4.52**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MLVYQDLLTG  DELLSDSFPY  KEIENGILWE  VEGKWVTVGA  VDVNIGANPS
51  AEEGGEDEGV  DDSAQKVVDI VDTFRLQEQP TYDKKGFIAY  IKKYIKLLTP
101 KLSEEDQAVF  KKGIEGATKF  LLPRLSDFQF  FVGEGMHDDS  TLVFAYYKEG
151 STNPTFLYFA  HGLKEVKC
```


Spot No.: **OL39**

NCBI accession No.: **NP_173813.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **MLP-like protein 423**

Peptide sequences: **K.TIQVLAGDGNAPGSIR.L;**

R.LITYGEGSPLVK.I; K.TAHEIDDPHVIKDFAVK.N

PFF Mascot score: **[281]**

Sequence coverage %: **[29]**

Matched peptides No.: **[3]**

Calculated Mr: **17044**

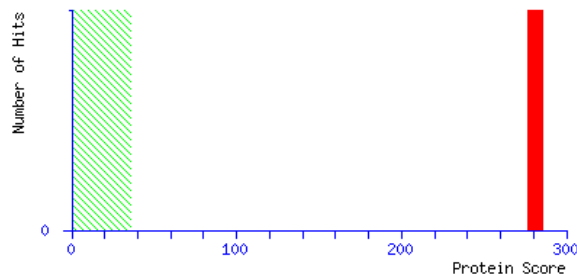
Calculated pI: **5.1**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MGLSGVLHVE VEVKSPAETF WVALGDGINL FPKAFPNDYK TIQVLAGDGN
51 APGSIRLITY GEGSPLVKIS AERIEAVDLE NKSMYSYIIG GEMLEYKTF
101 KGTITVIPKN GGSLLKWSGE FETAHEIDD PHVIKDFAVK NFKEIDEYLL
151 KQTSA
```

Spot No.: **OL40**

NCBI accession No.: **CAA32701.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Ribulose biphosphate carboxylase**

Peptide sequences: **R.EHGNTPGYYDGR.Y;**

K.LPLFGCTDSAQVLK.E; K.KEYPGA FIR.I

PFF Mascot score: **[261]**

Sequence coverage %: **[19]**

Matched peptides No.: **[3]**

Calculated Mr: **20588**

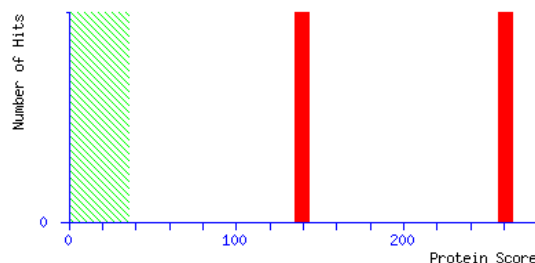
Calculated pI: **7.59**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MASSMLSSSTA VVTSPAQATM VAPFTGLKSS ASFPVTRKAN NDITSITSNG
51  GRVSCMKVWP PIGKKKFETL SYLPDLS DVE LAKEVDYLLR NKWIPCVEFE
101 LEHGFVYREH GNTPGYYDGR YWTMWKLPLF GCTDSAQVLK EVEECKKEYP
151 GAFIRIIIGFD NTRQVQCISF IAYKPPSFTE A
```

Spot No.: **OL41**

NCBI accession No.: **CAA32701.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Ribulose biphosphate carboxylase**

Peptide sequences: **R.EHGNTPGYYDGR.Y;**

K.LPLFGCTDSAQVLK.E

PFF Mascot score: **[133]**

Sequence coverage %: **[14]**

Matched peptides No.: **[2]**

Calculated Mr: **20588**

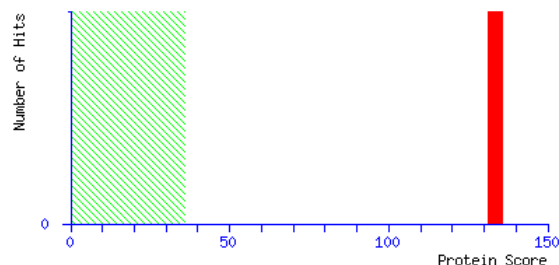
Calculated pI: **7.59**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MASSMLSSSTA VVTSPAQATM VAPFTGLKSS ASFPVTRKAN NDITSITSNG
51 GRVSCMKVWP PIGKKKFETL SYLPDLS DVE LAKEVDYLLR NKWIPCVEFE
101 LEHGFVYREH GNTPGYYDGR YWTMWKLPLF GCTDSAQVLK EVEECKKEYP
151 GAFIRIIGFD NTRQVQCISF IAYKPPSFTE A
```

Spot No.: **OL42**

NCBI accession No.: **CAA32701.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Ribulose biphosphate carboxylase**

Peptide sequences: **R.EHGNTPGYYDGR.Y;**

K.LPLFGCTDSAQVLK.E

PFF Mascot score: **[197]**

Sequence coverage %: **[14]**

Matched peptides No.: **[2]**

Calculated Mr: **20588**

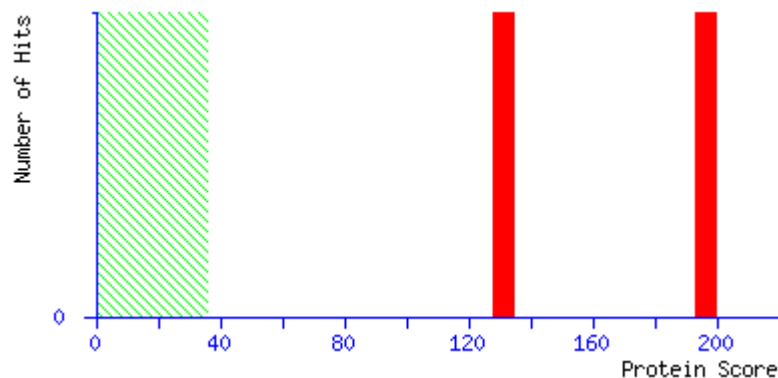
Calculated pI: **7.59**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1 MASSMLSSSTA VVTSPAQATM VAPFTGLKSS ASFPVTRKAN NDITSITSNG
51 GRVSCMKVWP PIGKKKFETL SYLPDLS DVE LAKEVDYLLR NKWIPCVEFE
101 LEHGFVYREH GNTPGYYDGR YWTMWKLPLF GCTDSAQVLK EVEECKKEYP
151 GAFIRIIGFD NTRQVQCISF IAYKPPSFTE A
```

Spot No.: **OL43**

NCBI accession No.: **CAA32701.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Ribulose biphosphate carboxylase**

Peptide sequences: **R.EHGNTPGYYDGR.Y**

PFF Mascot score: **[68]** Sequence coverage %: **[6]**

Matched peptides No.: **[1]**

Calculated Mr: **20588**

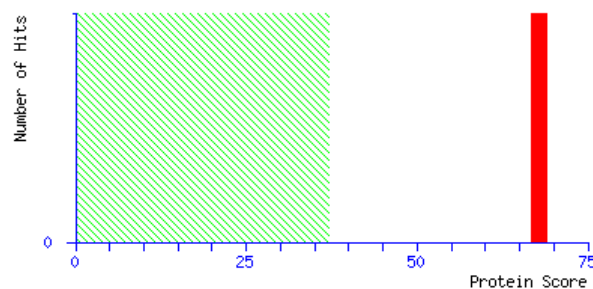
Calculated pI: **7.59**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1 MASSMLSSTA VVTSPAQATM VAPFTGLKSS ASFPVTRKAN NDITSITSNG
51 GRVSCMKVWP PIGKKKFETL SYLPDLSDVE LAKEVDYLLR NKWIPCVEFE
101 LEHGFVYREH GNTPGYYDGR YWTMWKLPLF GCTDSAQVLK EVEECKKEYP
151 GAFIRIIGFD NTRQVQCISF IAYKPPSFTE A
```

Spot No.: **OL44**

NCBI accession No.: **CAA31948.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Ribulose biphosphate carboxylase**

Peptide sequences: **R.EHGNSPGYYDGR.Y;**

K.LPLFGCTDSAQVLK.E; K.KEYPNAFIR.I; K.EYPNAFIR.I

PFF Mascot score: **[303]**

Sequence coverage %: **[19]**

Matched peptides No.: **[4]**

Calculated Mr: **20733**

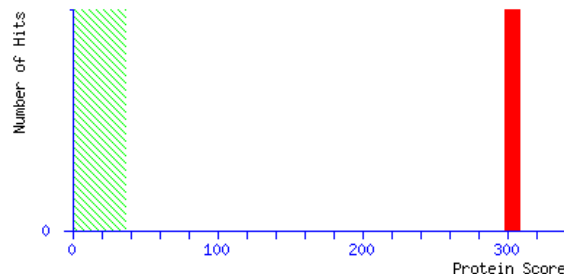
Calculated pI: **7.59**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1 MASSMLSSAT MVASPAQATM VAPFNGLKSS AAFPATRKAN NDITSITSNG
51 GRVNCMQMQV WPPIGKKKFE TLSYLPDLTD SELAKEVDYL IRNKWI PCVE
101 FELEHGFVYR EHGNSPGYYD GRYWIMWKLP LFGCTDSAQV LKEVEECKKE
151 YPNAFIRIIG FDNIRQVQCI SFVAYKPPSF TG
```

Spot No.: **OL45**

NCBI accession No.: **CAA31948.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **ribulose biphosphate carboxylase**

Peptide sequences: **R.EHGNSPGYYDGR.Y;**
K.LPLFGCTDSAQVLK.E; K.KEYPNAFIR.I; K.EYPNAFIR.I

PFF Mascot score: **[324]** Sequence coverage %: **[19]**

Matched peptides No.: **[4]**

Calculated Mr: **20733**

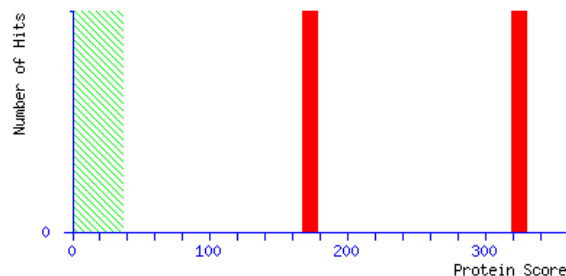
Calculated pI: **7.59**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1 MASSMLSSAT MVASPAQATM VAPFNGLKSS AAFPATRKAN NDITSITSNG
51 GRVNCMQMQV WPPIGKKKFE TLSYLPDLTD SELAKEVDYL IRNKWIPCVE
101 FELEHGFEVYR EHGNSPGYYD GRYWTMWKLP LFGCTDSAQV LKEVEECKKE
151 Y PNAFIRIIG FDNTRQVQCI SFVAYKPPSF TG
```

Spot No.: **OR1**

NCBI accession No.: **NP_199996.1**

Plant species: ***Arabidopsis thaliana***

Protein name: ***PfkB-like carbohydrate kinase family protein***

Peptide sequences: **K.KAPGGAPANVAVGVSR.L;**

K.IFHYGSISLIEEPCR.S; K.AAGSLLSYDPNLR.L;

R.LPLWPSEEAAR.K

PFF Mascot score: **[343]**

Sequence coverage %: **[16]**

Matched peptides No.: **[4]**

Calculated Mr: **37233**

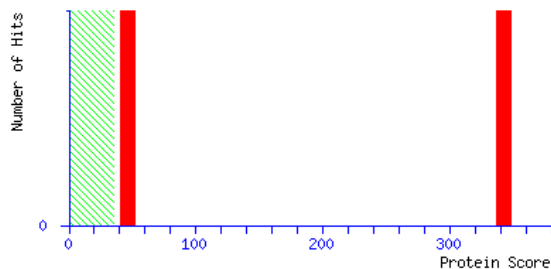
Calculated pI: **4.99**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in **bold red**.

```
1  MGEDAISGNL  KNLTIDTRDS  ETLVVCFGEM  LIDFVPTVGG  VSLAEAPAFK
51  KAPGGAPANV  AVGVSRLGGS  SAFIGKVGDD  EFGRMLADIL  RLNNVDNSGM
101 RFDHNARTAL  AFVTLRGDGE  REFLFFRHPS  ADMLLLESEL  DKNLIQKAKI
151 FHYGSISLIE EPCRSTQLVA  MKIAKAAGSL  LSYDPNLRLP  LWPSEEAARK
201 EIMSIWNLAD  VIKISEDEIT  FLTGGDDPYD  DDVVLQKLFH  PNLKLLVNSE
251 GPNGCRYYTQ  EFKGRVGGVK  VKPVDTTGAG  DAFVSGLLNS  LASDLTLLKD
301 EKKLREALLF  ANACGAITVT  ERGAIPAMPS  MDAVQDLLSS  TRS
```


Spot No.: **OR2**

NCBI accession No.: **AAC27484.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **ACC oxidase**

Peptide sequences: **K.GLDNLETEVEDVDWESTFYVR.H;**

R.HLPQSNLNDISDVSDEYR.T; R.VVTQQEGNR.M

PFF Mascot score: **[254]**

Sequence coverage %: **[15]**

Matched peptides No.: **[3]**

Calculated Mr: **36374**

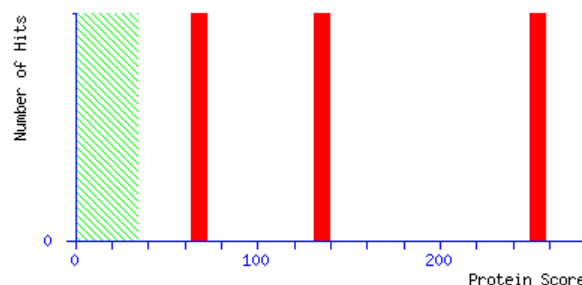
Calculated pI: **4.97**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in bold red.

```
1  MEKNMKFPVV  DLSKLNGEER  DQTMALINEA  CENWGFFEIV  NHGLPHDLMD
51  KIEKMTKDHY  KTCQEQKFND  MLKSKGLDNL  ETEVEDVDWE  STFYVRHLPQ
101 SNLNDISDVS  DEYRTAMKDF  GKRLNLAED  LLDLLCENLG  LEKGYLKKVF
151 HGTKGPTFGT  KVSNYPPCPK  PEMIKGLRAH  TDAGGIILLF  QDDKVSGIQL
201 LKDGDWIDVP  PLNHSIVINL  GDQLEVITNG  KYKSVLHRVV  TQQEGNRMSV
251 ASFYNPGSDA  DISPATSLVE  KDSEYPSFVF  DDYMKLYAGV  KFQPKEPRFA
301 AMKNASAVTE  LNPTAAVETF
```

Spot No.: **OR4**

NCBI accession No.: **AAC14026.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Chaperonin 10**

Peptide sequences: **K.YTSIKPLGDR.V; K.DGSNYIALR.A**

PFF Mascot score: **[111]** Sequence coverage %: **[7]**

Matched peptides No.: **[2]**

Calculated Mr: **26912**

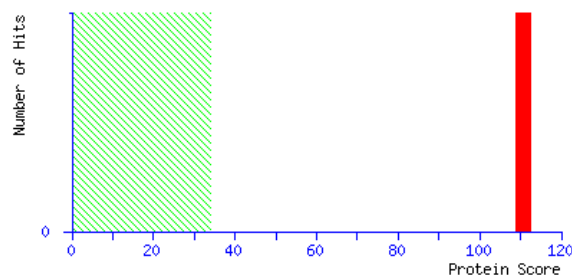
Calculated pI: **8.86**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in bold red.

```
1 MAATQLTASP VTMSARSLAS LDGLRASSVK VSSLKPGTLR QSQFRRLVVK
51 AASVVAPKYT SIKPLGDRVL VKIKEAEEKT LGGILTFHST AQSKPQGGEV
101 VAVGEGRTIG KNKIDITVPT GAQIIYSKYA GTEVEFNDVK HLILKEDDIV
151 GILETEDIKD LKPLNDRVFI KVAEAEKTA GGLLLTETTK EKPSIGTVIA
201 VGPGLDEEG KITPLPVSTG STVLYSKYAG NDFKGDDGSN YIALRASDVM
251 AILS
```

Spot No.: **OR5**

NCBI accession No.: **NP_173387.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Dehydroascorbate reductase**

Peptide sequences: **K.AAVGAPDHLGDCPFSQR.A;**
K.SKDSNDGSEHALLVELEALENHLK.S; K.SHDGPFIAGER.V;
K.SWSVPESFPHVHNYMK.T + Oxidation (M); K.YVISGWAPK.V

PFF Mascot score: **[356]** Sequence coverage %: **[36]**

Matched peptides No.: **[5]**

Calculated Mr: **23740**

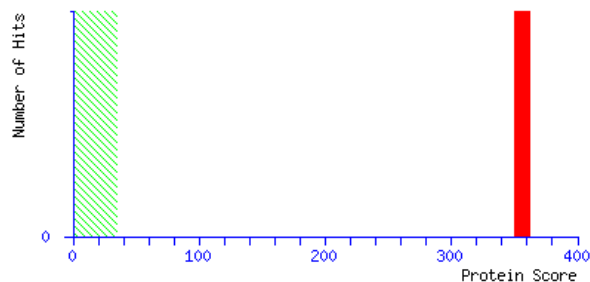
Calculated pI: **5.56**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in bold red.

```
1  MALEICVKAA VGAPDHLGDC PFSQRALLTL  EEKSLTYKIH  LINLSDKPQW
51  FLDISPQGV  PVLKIDDKWV  TDSDVIVGIL  EEKYPDPPLK  TPAEFASVGS
101 NIFGTFGTFL KSKDSNDGSE HALLVELEAL ENHLKSHDGP FIAGERVSAV
151 DLSLAPKLYH LQVALGHFKS WSVPESFPHV HNYMKTLFSL DSFEKTKTEE
201 KYVISGWAPK  VNP
```

Spot No.: **OR6**

NCBI accession No.: **NP_180643.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Glutathione S-transferase PHI 9**

Peptide sequences: **K.VYGPHFASPK.R;**

K.GVAFETIPVDLMK.G; K.GVAFETIPVDLMK.G + Oxidation (M);

K.LAGVLDVYEAHLSK.S; R.KHVSAWWDDISSR.P;

K.HVSAWWDDISSR.P

PFF Mascot score: **[432]**

Sequence coverage %: **[23]**

Matched peptides No.: **[6]**

Calculated Mr: **24131**

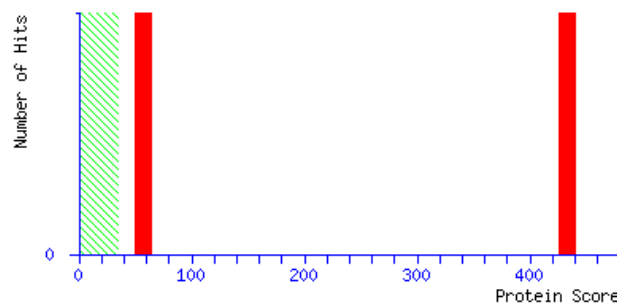
Calculated pI: **6.17**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in bold red.

```
1  MVLKVYGPHF ASPKRALVTL IEKGVAFETI PVDLMKGEHK QPAYLALQPF
51 GTVPAVVDGD YKIFESRAVM RYVAEKYRSQ GPDLLGKTVE DRGQVEQWLD
101 VEATTYHPPL LNLTLHIMFA SVMGFPSDEK LIKESEEKLA GVLDVYEAHL
151 SKSKYLAGDF VSLADLAHLP FTDYLVGPIG KAYMIKDRKH VSAWWDDISS
201 RPAWKETVAK YSPPA
```

Spot No.: **OR7**

NCBI accession No.: **AAC04902.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Mitochondrial chaperonin (HSP60)**

Peptide sequences: **R.NVIEQSWGAPK.V;**

K.QVANATNDVAGDGTTCAVLTR.A; K.LAVDTVVTNLQSR.A;

K.LLEQDNPD LGYDAAK.G

PFF Mascot score: **[260]**

Sequence coverage %: **[11]**

Matched peptides No.: **[4]**

Calculated Mr: **55561**

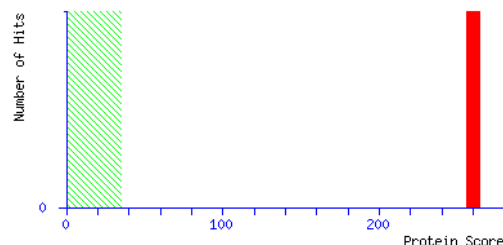
Calculated pI: **5.30**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in **bold red**.

```
1  MGPKGRNVII EQSWGAPKVT KDGVTVAKSI EFKDRIKNVG ASLVKQVANA
51 TNDVAGDGTT CATVLTRAIF TEGCKSVAAG MNAMDLRRGI KLAVDTVVTN
101 LQSRARMIST SEEIAQVGTI SANGDREIGE LIAKAMETVG KEGVITIQDG
151 KTLFNELEV V EGMKIDRGYI SPYFITNPKT QKCELEDPLI LIHEKKISNI
201 NAMVKVLELA LKKQRPLIV AEDVESDALA TLILNKLRAN IKVCAVKAPG
251 FGENRKANLH DLAALTGAQV ITEELGMNLD NIDLSMFGNC KKVTVSKDDT
301 VVLGDGAGDKQ AIGERCEQIR SMVEASTSDY DKEKLQERLA KLSGGVAVLK
351 IGGASETEVS EKKDRVTDAL NATKAAVEEG IVPGGGVALL YASKELEKLS
401 TANFDQKIGV QIIQNALKTP VYTIASNAGV EGAVVVGKLL EQDNPD LGYD
451 AAKGEYVDMI KAGIIDPLKV IRTALVDAAS VSSLLTTEA VVTEIPTKEV
501 ASPGMGGGGM GGMGGMGGMG GGMGF
```

Spot No.: **OR8**

NCBI accession No.: **OAP06349.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **TSA1 (tryptophan synthase beta subunit)**

Peptide sequences: **R.AVGVQGLVVPDVPLEETEMLR.K;**

K.EALNNDIELVLLTTPPTPTER.M

PFF Mascot score: **[219]**

Sequence coverage %: **[13]**

Matched peptides No.: **[2]**

Calculated Mr: **33362**

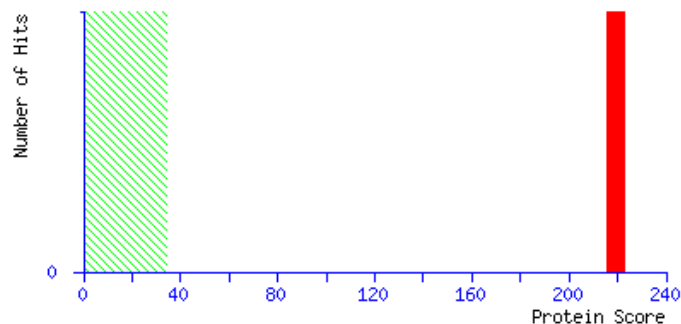
Calculated pI: **7.68**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in **bold red**.

```
1 MAIAFKSGVF FLQSPKSQIG FRHSSPPDSS LSFKRFTPMA SLSTSSPTLG
51 LADTFTQLKK QGKVPFIPYI TAGDPDLSTT AEALKVLDAC GSDIIELGVP
101 YSDPLADGPV IQAAATRSLE RGTNLD SILE MLDKVVPQIS CPISLFTYYN
151 PILKRGLGKF MSSIRAVGVQ GLVVPDVPLE ETEMLRKEAL NNDIELVLLT
201 TPTTPTERMK RIVDASEGFI YLVSSIGVTG ARSSVSGKVQ SLLKDIKEAT
251 DKPVAVGFGI SKPEHVKQIA GWGADGVIVG SAMVKLLGDA KSPTEGLKEL
301 EKLTSLKSA LL
```

Spot No.: **OR9**

NCBI accession No.: **AAN31820.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Putative cysteine proteinase AALP**

Peptide sequences: **K.DWREDGIVSPVK.D;**

K.AYPYTGKDETCK.F; K.NSWGADWGDK.G

PFF Mascot score: **[161]**

Sequence coverage %: **[9]**

Matched peptides No.: **[3]**

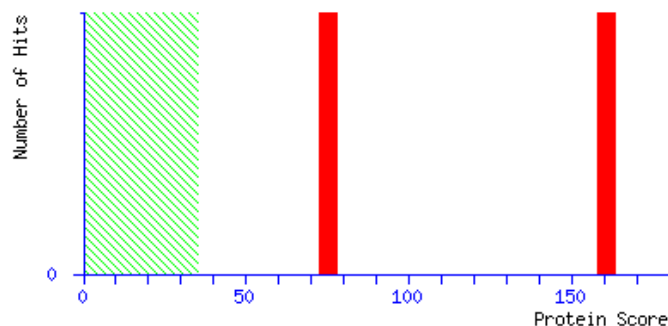
Calculated Mr: **39495**

Calculated pI: **6.26**

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in bold red.

```
1  MSAKTILSSV VLVVLF AASA AANIGFDESN PIRMVSDGLR EVEESVSQIL
51 GQSRHVL SFA RFTHRYGKKY QNVEEMKLRF SIFKENLDLI RSTNKKGLSY
101 KLGVNQFADL TWQEFQRTKL GAAQNCSATL KGSHKVTEAA LPETKDWRED
151 GIVSPVKDQG GCGSCWTFST TGALEAAYHQ AFGKGISLSE QQLVDCAGAF
201 NNYGCNGGLP SQAFEYIKSN GGLDTEKAYP YTGKDETCKF SAENVGVQVL
251 NSVNITLGAE DELKHAVGLV RPSIAFEVI HSFRLYKSGV YTDSHCGSTP
301 MDVNHAVLAV GYGVEDGVPY WLIKNSWGAD WGDKGYFKME MGKNMCGIAT
351 CASYPVVA
```

Spot No.: **OR10**

NCBI accession No.: **AAL07227.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Putative lactoylglutathione lyase**

Peptide sequences: K.DPDGYTFELIQR.G;

**R.GPTPEPFCQVMLR.V; R.GPTPEPFCQVMLR.V + Oxidation
(M); R.EAGPLPGLGTK.I; K.IVSFLDPDGWK.T**

PFF Mascot score: **[292]**

Sequence coverage %: **[16]**

Matched peptides No.: **[5]**

Calculated Mr: **31995**

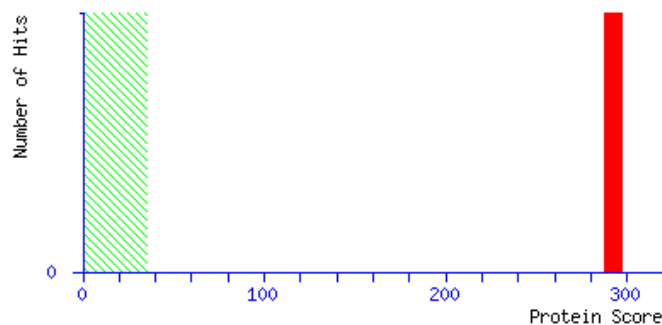
Calculated pI: **5.11**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in bold red.

```
1 MAEASDLLEW PKKDNRRFLH VVYRVGDLDR TIEFYTEVFG MKLLWKRDI
51 EEKYSNAFLG FGPETSNFV ELTYNYGVSS YDIGTGFGHF AISTQDVSKL
101 VENVRAKGGN VTREPGPVKG GGSVIAFVKD PDGYTFELIQ RGPTPEPFCQ
151 VMLRVGDLDR AIKFYEKALG MRLLRKIERP EYKYTIGMMG YAEYESIVL
201 ELTYNYDVTE YTKGNAYAQI AIGTDDVYKS GEVIKIVNQE LGGKITREAG
251 PLPGLGTKIV SFLDPDGWKT VLVDNKDFLK ELE
```


Spot No.: **OR11**

NCBI accession No.: **AAB17995.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Glyoxalase II**

Peptide sequences: **K.VSIGDIYLEVR.A;**

R.ATPGHTAGCVTYVTGEGADQPQPR.M; R.MAFTGDAVLIR.G;

R.MAFTGDAVLIR.G + Oxidation (M);

K.GFEVSTVGEEMQHNPR.L

PFF Mascot score: **[455]**

Sequence coverage %: **[24]**

Matched peptides No.: **[5]**

Calculated Mr: **27941**

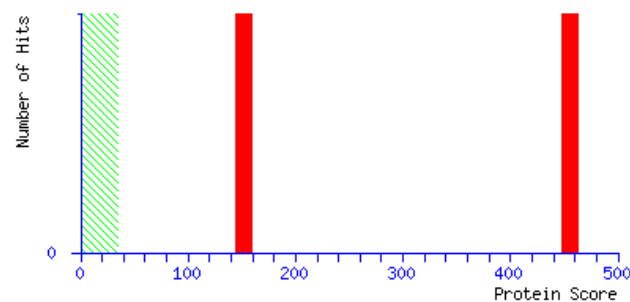
Calculated pI: **5.58**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in bold red.

```
1  MGSSSSFSSS  SSKLLFRQLF  ENESSTFTYL  LADVSHDPKP  ALLIDFVDKT
51  VDRDLKLIDE  LGLKLIYAMN  THVHADHVTG  TGLLKTKLPG  VKSVISKASG
101 SKADLFLEPG  DKVSIGDIYL  EVRATPGHTA  GCVTYVTGEG  ADQPQPRMAF
151 TGDAVLIRGC  GRTDFQGGSS  DQLYESVHSQ  IFSLPKDTLI  YPAHDYKGFE
201 VSTVGEEMQH  NPRLTKDKET  FKTIMSNLNL  SYPRMIDVAV  PANMVCGLQD
251 VPSQAN
```

Spot No.: **OR12**

NCBI accession No.: **NP_565203.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Mercaptopyruvate sulfurtransferase 1**

Peptide sequences: **K.ILDASWYMPDEQR.N;**

R.NPIQEYQVAHIPR.A; R.ALFFDLGISDR.K;

K.VWVLDGGLPR.W

PFF Mascot score: **[343]**

Sequence coverage %: **[12]**

Matched peptides No.: **[4]**

Calculated Mr: **42152**

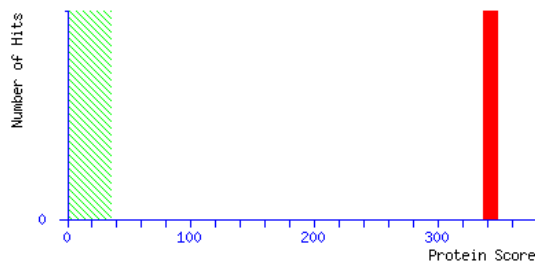
Calculated pI: **5.95**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in bold red.

```
1  MASTLFSRTF LAASHRLITP SLPQKIFNPA TFLSRSLHSQ LGSASTAYKS
51 TTWARRAMAS TGVETKAGYS TSSVSTSEPV VSVDWLHANL REPDLKILDA
101 SWYMPDEQRN PIQEYQVAHI PRALFFDLDG ISDRKTSLPH MLPTEEAFAA
151 GCSALGIDNK DEVVVDGKG IFSAARVWWM FRVFGHEKVW VLDGGLPRWR
201 ASGYDVESSA SGDAILKASA ASEAIEKIYQ GQTVSPITFQ TKFQPHLVWT
251 LDQVKNNMED PTYQHIDARS KARFDGTAPE PRKGIRSGHI PGSKCIPFPQ
301 MFDSCNTLLP AEELKKRFDQ EDISLDKPIM ASCGTGVTAC ILAMGLHRLG
351 KTDVPIYDGS WTEWATQPD LPIESVESSS
```

Spot No.: **OR13**

NCBI accession No.: **NP_199898.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Transketolase family protein**

Peptide sequences: **K.VFVMGEEVGQYQGAYK.I;**

K.VLAPYSAEDAR.G; K.LAEEGISAEVINLR.S;

R.IAGADVPMPLYAANLER.L; R.LALPQIEDIVR.A

PFF Mascot score: **[409]**

Sequence coverage %: **[18]**

Matched peptides No.: **[5]**

Calculated Mr: **39436**

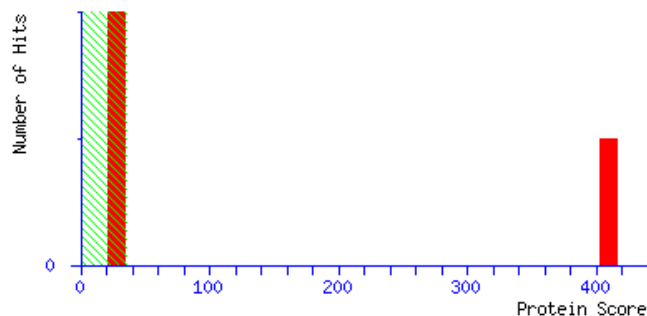
Calculated pI: **5.67**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in bold red.

```
1  MLGILRQRAI  DGASTLRRTR  FALVSARSYA  AGAKEMTVRD  ALNSAIDEEM
51  SADPKVFVMG EEVGQYQGAY KITKGLLEKY GPERVYDTPI  TEAGFTGIGV
101 GAAYAGLKPV  VEFMTFNFSM  QAIDHIINSA  AKSNYMSAGQ  INVPIVFRGP
151 NGAAAGVGAQ  HSQCYAAWYA  SVPGLKVLAP YSAEDARGLL KAAIRDPDPV
201 VFLENELLYG  ESFPISSEAL  DSSFCLPIGK  AKIEREGKDV  TIVTFSKMVG
251 FALKAAEKLA EEGISAEVIN LRSIRPLDRA TINASVRKTS  RLVTVEEGFP
301 QHGVCAEICA  SVVEESFSYL  DAPVERIAGA DVPMPLYAANL ERLALPQIED
351 IVRASKRACY RSK
```

Spot No.: **OR14**

NCBI accession No.: **NP_850976.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **MLP-like protein 34**

Peptide sequences: K.TEAPSLVGKLETEVEIK.A;

R.IEAVEPEKNLITFR.V; R.VIEGDLMKEYK.S;

R.VIEGDLMKEYK.S + Oxidation (M); K.TTETLETEVEIK.A;

K.EIDEHLLAEE.-

PFF Mascot score: **[329]**

Sequence coverage %: **[20]**

Matched peptides No.: **[6]**

Calculated Mr: **35719**

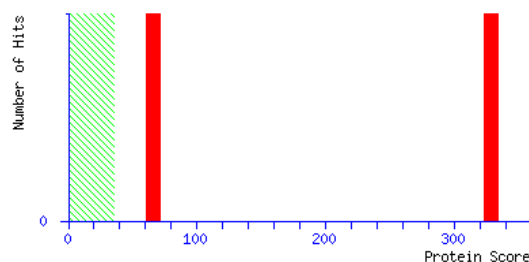
Calculated pI: **5.14**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in bold red.

```
1  MAKTEAPSLV GKLETEVEIK ASAGQFHMF AGKPHHVSKA SPGNIQSCDL
51 HEGDWGTVGS IVFWNYVHDG EAKVAKERIE AVEPEKNLIT FRVIEGDLMK
101 EYKSFLITIQ VTPKHGGPGS IVHWHLEYEK ISDEVAHPET LLQFCVEVSQ
151 EIDEHLLSEE EEVKTTETLE TEVEIKASAE KFHHMFAGKP HHVSKATPGN
201 IQSCDLHEGD WGTVGSIVFW NYVHDGEAKV AKERIEAVDP EKNLITFRVI
251 EGDLMKEYKS FVITIQVTPK HGGSGSVVHW HFHEYKINEE VAHPETLLQF
301 AVEVSKEEIDE HLLAEE
```

Spot No.: **OR15**

NCBI accession No.: **NP_565107.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **NmrA-like negative transcriptional regulator**

Peptide sequences: **K.AGHSTFALVR.E;**

K.DLGVTILHGDLNDHESLVK.A; R.FLPSEFGVDVDR.T;

K.AVINKEEDIAAYTIK.A

PFF Mascot score: **[336]**

Sequence coverage %: **[18]**

Matched peptides No.: **[4]**

Calculated Mr: **33733**

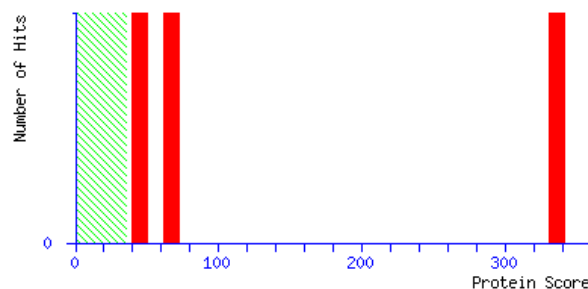
Calculated pI: **5.66**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in bold red.

```
1 MATEKSKILV IGGTGYIGKF LVEASAKAGH STFALVREAT LSDPVKGKTV
51 QSFKDLGVTI LHGDLNDHES LVKAIKQVDV VISTVGSMQI LDQTKIISAI
101 KEAGNVKRFL PSEFGVDVDR TSAVEPAKSA FAGKIQIRRT IEAEGIPYTY
151 AVTGCFGGYY LPTLVQFEPG LTSPPRDKVT ILGDGNAKAV INKEEDIAAY
201 TIKAVDDPRT LNKILYIKPS NNTLSMNEIV TLWEKKIGKS LEKTHLP EEQ
251 LLKSIQESPI PINVVL SINH AVFVNGDTNI SIEPSFGVEA SELYPDVKYT
301 SVDEYLSYFA
```

Spot No.: **OR16**

NCBI accession No.: **OAP16650.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **GSTU26**

Peptide sequences: **R.FWAEFIDKK.F; R.IIEYVYVLR.K**

PFF Mascot score: **[106]** Sequence coverage %: **[8]**

Matched peptides No.: **[2]**

Calculated Mr: **25891**

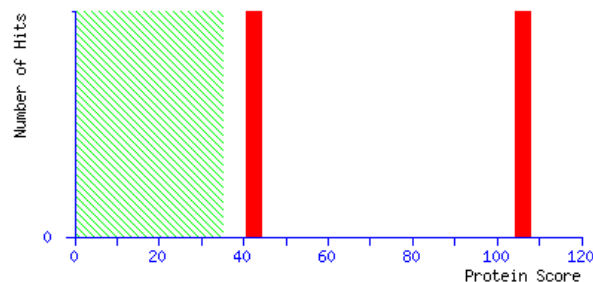
Calculated pI: **5.53**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in **bold red**.

```
1  MANDQVILLD YWPSMFGMRT KMALAEKGVK YEYKETDPWV KTPLLIEMNP
51 IHKKIPVLIH NGKPICESLI QLEYIDEVWS DASPILPSDF YQKSRARFWA
101 EFIDKKFYDP SWKVWATMGE EHAAVKKELL EHFKTLETETL GDKPYYGGEV
151 FGYLDIALMG YYSWFKAMEK FGEFSIETEF PKLTTWTKRC LERESVVKAL
201 ADSDRIIEYV YVLRKQFGAA
```

Spot No.: **OR17**

NCBI accession No.: **CAA52238.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **RCI1B**

Peptide sequences: **K.AAQDIAAADMAPTHPIR.L**

PFF Mascot score: **[58]** Sequence coverage %: **[6]**

Matched peptides No.: **[1]**

Calculated Mr: **28239**

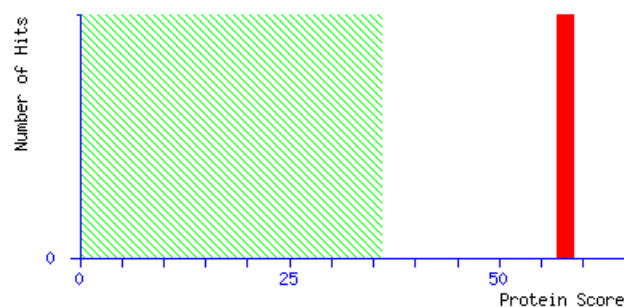
Calculated pI: **4.97**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in bold red.

```
1  MAATLGRDQY VYMAKLAEQA ERYEEMVQFM EQLVTGATPA EELTVEERNL
51 LSVAYKNVIG SLRAAWRIVS SIEQKEESRK NDEHVSIVKD YRSKVESELS
101 SVCSGILKLL DSHLIPSAGA SESKVLYLKM KGDYHRYMAE FKSGDERKTA
151 AEDTMLAYKA AQDIAAADMA PTHPIRLGLA LNFSVFYYEI LNSSDKACNM
201 AKQAFEEAIA ELDTLGEESY KDSTLIMQLL RDNLTLTWSD YAGADGRGLR
251 I
```

Spot No.: **OR18**

NCBI accession No.: **NP_188267.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Mannose-binding lectin superfamily protein**

Peptide sequences: **K.SGFQISAPEATGK.Q;**

K.IYASYGGEGIQYVK.F; K.VYVGQQQDGVAAVK.F;

K.TAGPFGIVSGTK.F; K.LEGAGSEAGTLWDDGAFDGVR.K;

K.FGVHVAPITK.-

PFF Mascot score: **[560]**

Sequence coverage %: **[11]**

Matched peptides No.: **[6]**

Calculated Mr: **72430**

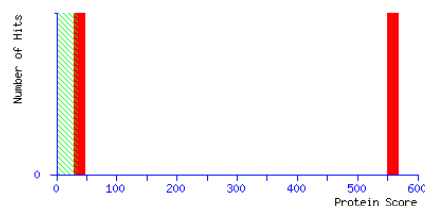
Calculated pI: **5.31**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in **bold red**.

```
1 MSWDDGSHAK VKKVQLTFDE IIYSIQVTYD GATALQSQLR GSVGPKSAEF
51 TLAPDEYITA LSAYGKSLST QEVITALIFT TNKTSYGFYV TKSGFQISAP
101 EATGKQISGF LGTSGNVLNT IDVHYSIPT GGTGTGGTGT GTGTGTGTGT
151 GTGTGTGTGT GTGTGTGGTG TGTGTGTGGT GTGTGTGGTG TGTGTGTGTG
201 TGTGTGTGTG TGGTGTGTGT GGTGTGTGTG TGTGTGTGGT GTGTGTGTGS
251 GAQKLEAQGN STGGSWDDG SDYDGVTKIY ASYGGEGIQY VKFDYVKGGV
301 IKQGVLHGKQ QSRQNPREFV INHPDEYLVV VEGWYETVML GIQFKTNLNT
351 YEVSIYPFEP STDTKFTLQV QDKKIIGFHG FAGNHVNSIG AYFVPKSSST
401 PVPSTPLKLT AEGGETGAVW DGS HDDVKK VYVGQQQDGVA AAVKFEYKNG
451 SQVVFQDERG TRILLGFEEF ELESDEYITS VEGYYEKNFG VDIIVVITLIF
501 KTSKNTAGP FGIVSGTKFE FKKEGYKITG FHGRAGEYVN AIGAYLAPSG
551 ITPLTPATQS QKLEGAGSEA GTLWDDGAFD GVRKVSVGQA QDGIGAVSFV
601 YDKAGQVVEG KEHGKPTLLG FEEFELDYPG EYITAVDGTY DAIFGNEPIV
651 NMLAFTTNKR VSIPFGIGAG TAFEKKKDGQ KIVGFHGRAG DLLHKFGVHV
701 APITK
```


Spot No.: **OR19**

NCBI accession No.: **AAF19535.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **F23N19.3**

Peptide sequences: R.TAFHFQPEK.N; K.DFRDPTTAWK.T;

R.TGISLIYDTTDFK.T; K.GWSSVQGIPR.T; K.NLVQWPVEEIK.S

PFF Mascot score: **[334]**

Sequence coverage %: **[7]**

Matched peptides No.: **[5]**

Calculated Mr: **81758**

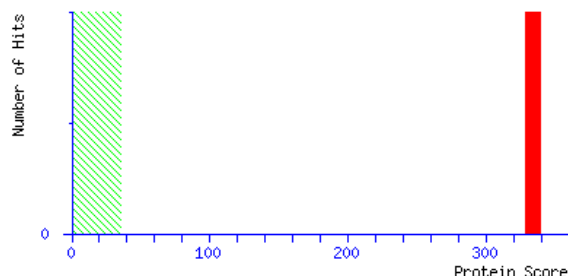
Calculated pI: **7.26**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in bold red.

```
1  MASTEALLPV  TSLQDPLSES  RSDQIPETRR  RRPIKVHLAV  YSGLLLIALY
51  VTLIVTHDGS  KAEIATESRP  RMAGVSEKSN  DGVWISSDDG  KVEAFFWNNT
101 ILSWQRTAFH  FQPEKNWMNG  TNIKCP LFYK  GWYHFFYQYN  PNAAVWGDIV
151 WGHAVSKDLI  HWLYLPIAMV  PDQWYDANGV  WTGSATFLDD  GSIVMLYTGS
201 TDEFVQVQNL  AYPEDPSDPL  LLKWVKFSGN  PVLVPPPGIG  AKDFRDPTTA
251 WKTSSGKWRI  TIGSKINRTG  ISLIYDTTDF  KTYEKHETLL  HQVPNTGMWE
301 CVDFYPVSKT  QLNLGLDTSVN  GPDVKHVIKA  SMDDTRIDHY  AIGTYDDSNA
351 TWVPDNPSID  VGISTGLRYD  YGKYASKTF  YDQNKGRRL  WGWIGESDSE
401 AADVQKGWSS  VQGIPTTVL  DTRTHKNLVQ  WPVEEIKSLR  LSSKKFDMTI
451 GPGTVVPVDV  GSATQLDIEA  EFEIKTDDLK  LFFDDDSVEA  DNKFSCETNG
501 GSTARGALGP  FGFSVLADeg  LSEQTPVYFY  VTKGKHSKLN  TVFCTDTSRS
551 TLANDVVKPI  YGSFVPVLKG  EKLTMRLVD  HSIVEGFAQG  GRSCITSRVY
601 PTKAIYGATK  LFLFNNAIDA  TVIASFTVWQ  MNNAFIHPYS  SDDLGGILSL
651 TYLRTQSRAS  SNAAFYFISY  KTTKTVVTMT  QYELKSLAVH  KTITKQKSLS
701 FVKKKEGEKQ  KQSHPRARKI  SIRNLKSA
```

Spot No.: **OR20**

NCBI accession No.: **OAP11759.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **GSTF8**

Peptide sequences: **K.VHGVPMSTATMR.V;**

K.VHGVPMSTATMR.V + Oxidation (M); K.DLQFELIPVDMR.A;

K.DLQFELIPVDMR.A + Oxidation (M);

R.AITQYLAEYSEKGEK.L; K.ATTNVWLQVEGQQFDPNASK.L

PFF Mascot score: **[341]**

Sequence coverage %: **[22]**

Matched peptides No.: **[6]**

Calculated Mr: **29357**

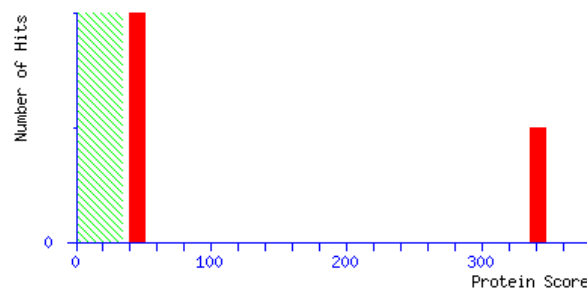
Calculated pI: **8.50**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in bold red.

```
1  MGAIQARLPL  FLSPPSIKHH  TFLHSSSSNS  NFKIRSNKSS  SSSSSSSIIM
51  ASIKVHGVPM  STATMRVLAT  LYEKDLQFEL  IPVDMRAGAH  KQEAHLALNP
101 FGQIPALEDG  DLTLFESRAI  TQYLAEYSE  KGEKLISQDC  KKVKATTNVW
151 LQVEGQQFDP  NASKLAFERV  FKGMFGMTTD  PAAVQELEGK  LQKVLDVYEA
201 RLAKSEFLAG  DSFTLADLHH  LPAIHLLGT  DSKVLFDSRP  KVSEWIKKIS
251 ARPAAKVID  LQKQ
```

Spot No.: **OR21**

NCBI accession No.: **AAM61077.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Ferretin 1 precursor**

Peptide sequences: **K.KADLAIPITSHASLAR.Q;**

K.ADLAIPITSHASLAR.Q; K.FFKESSEEER.G; K.KISDYITQLR.M;

K.ISDYITQLR.M

PFF Mascot score: **[384]**

Sequence coverage %: **[14]**

Matched peptides No.: **[5]**

Calculated Mr: **28156**

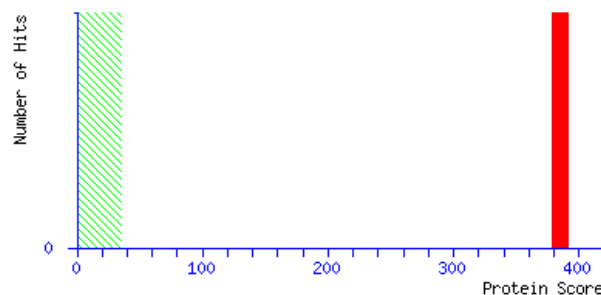
Calculated pI: **5.73**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in bold red.

```
1  MASNALSSFT  AANPALSPKP  LLPHGSASPS  VSLGFSRKVG  GSRAVVVAAA
51  TVDTNNMPMT  GVVFQPLEEV  KKADLAIPIT  SHASLARQRF  ADASEAVINE
101 QINVEYNVSY  VYHSMYAYFD  RDNVAMKGLA  KFFKESSEEE  RGHAЕКFMEY
151 QNQRGGRVKL  HPIVSPISEF  EHAЕКGDALY  AMELALSLEK  LTNEKLLNVH
201 KVAENNDPQ   LADFVESEFL  GEQIEAIKKI  SDYITQLRMI  GKGHGVWHFD
251 QMLLN
```

Spot No.: **OR22**

NCBI accession No.: **AAM63854.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Atpm24.1 glutathione S-transferase**

Peptide sequences: **K.VFGHPASIATR.R;**

R.NPFGQVPAFEDGDLK.L; R.AITQYIAHR.Y;

R.YENQGTNLLQTDSK.N; K.SIYGLTTDEAVVAEEEEAK.L;

R.VNEWVAEITK.R

PFF Mascot score: **[526]**

Sequence coverage %: **[36]**

Matched peptides No.: **[6]**

Calculated Mr: **24036**

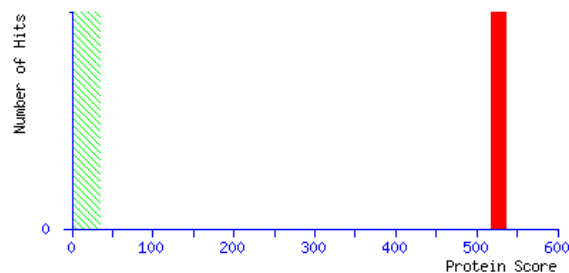
Calculated pI: **6.08**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in bold red.

```
1  MAGIKVFGHP ASIATRRVLI  ALHEKNLDFE  LVHVELKDGE  HKKEPFLSRN
51 PFGQVPAFED GDLKLFESRA ITQYIAHRYE NQGTNLLQTD SKNISQYAIM
101 AIGMQVEDHQ  FDPVASKLAF  EQISKSIYGL TTDEAVVAXE EAKLAKVLDV
151 YEARKLKEFKY  LAGETFTLTD  LHHIPAIQYL  LGTPTKKLFT  ERPRVNEWVA
201 EITKRPASEK  VQ
```

Spot No.: **OR23**

NCBI accession No.: **NP_195637.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Cold, circadian rhythm, and RNA binding 1**
(Glycine-rich RNA-binding protein 8)

Peptide sequences: **R.CFVGGLAWATNDEDLQR.T;**
R.GFGFVTFKDEK.A; R.VITVNEAQSR.G;
R.SGGGGGGYSGGGGGGGYSGGGGGGGYER.R

PFF Mascot score: **[528]** Sequence coverage %: **[37]**

Matched peptides No.: **[4]**

Calculated Mr: **16626**

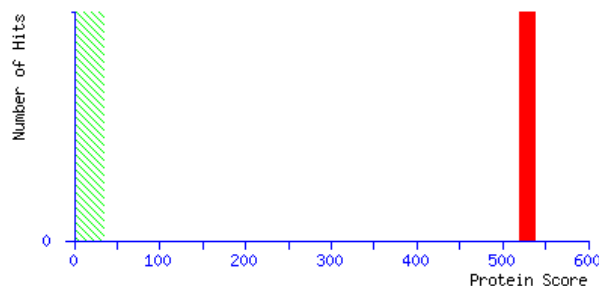
Calculated pI: **5.58**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in **bold red**.

```
1  MSEVEYRCFV GGLAWATNDE DLQRTFSQFG DVIDSKIIND RESGRSRGFG
51 FVTFKDEKAM RDAIEEMNGK ELDGRVITVN EAQSRGSGGG GGGRGGSGGG
101 YRSGGGGGYS GGGGGGYSGG GGGGYERRSG GYGSGGGGGG RYGGGGGRRE
151 GGGYGGGDGG SYGGGGGGW
```

Spot No.: **ML1**

NCBI accession No.: **AAL06896.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **AT5g26000/T1N24_7**

**Peptide sequences: K.LFNSGNFEK.G; R.GYALGTDAPGR.C;
R.EYVGDRLPEFSETEAALVK.G**

PFF Mascot score: **[238]**

Sequence coverage %: **[7]**

Matched peptides No.: **[3]**

Calculated Mr: **61704**

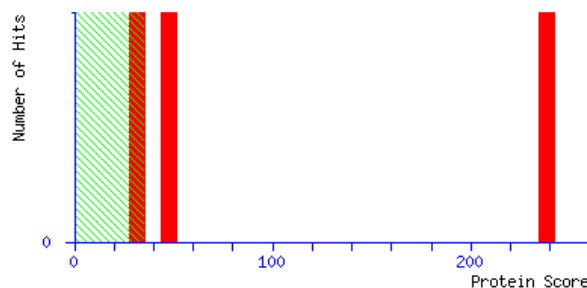
Calculated pI: **5.67**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



Matched peptides shown in bold red.

```
1  MKLLMLAFVF LLALATCKGD EFVCEENEPEF TCNQTKLFNS GNFEKGFIFG
51 VASSAYQVEG GRGRGLNVWD SFTHRFPEKG GADLGNGDTT CDSYTLWQKD
101 IDVMDELNST GYRFSIAWSR LLPKGKRSRG VNPGAIIYYN GLIDGLVAKN
151 MTPFVTLFWH DLPQTLQDEY NGFLNKTIVD DFKDYADLCF ELFGDRVKNW
201 ITINQLYTVP TRGYALGTDA PGRCSPKIDV RCPGGSNSTE PYIVAHNQLL
251 AHAAAVDVYR TKYKDDQKGM IGPVMITRWF LPFDHSQESK DATERAKIFF
301 HGWFMGPLTE GKYPDIMEY VGDRLPEFSE TEAALVKGSY DFLGLNYYVT
351 QYAQNNQTIIV PSDVHTALMD SRTTLTSKNA TGHAGPPFN AASYYPKGI
401 YYVMDYFKTT YGDPLIYVTE NGFSTPGDED FEKATADYKR IDYLCSHLCF
451 LSKVIKEKNV NVKGYFAWSL GDNYEFCNGF TVRFGLSYVD FANITGDRDL
501 KASGKWFQKF INVTDSDTN QDLLRSSVSS KNRDRKSLAD A
```

Spot No.: **ML3**

NCBI accession No.: **CAA61592.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Thioglucoside glucohydrolase**

Peptide sequences: **R.GPALWDIYCR.R;**

K.DFLSQGVRPSALK.K; R.CNNDNGDVAVDFFHR.Y

PFF Mascot score: **[183]**

Sequence coverage %: **[7]**

Matched peptides No.: **[3]**

Calculated Mr: **60222**

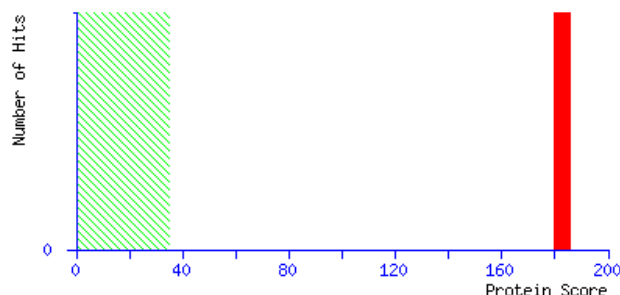
Calculated pI: **6.45**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1 MVLQKLPLIG LLLLLTIVAS PANADGPVCP PSNKLSRAS FEGFLFGTAT
51 AAYQVEGAIN ETCRGPALWD IYCRRYPERC NNDNGDVAVD FFHRYKEDIQ
101 LMKNLNTDAF RMSIAWPRIF PHGRKEKGVS QAGVQFYHDL IDELIKNGIT
151 PFVTVFHWDT PQDLEDEYGG FLSEIRIVKDF REYADFVFQE YGGKVKHWIT
201 FNEPWVFSHA GYDVGKKAPG RCSSYVNAKC QDGRSGYEAY LVTHNLLISH
251 AEAVEAYRKC EKCKGGKIGI AHSPAWEAH DLADSQDGAS IDRALDFILG
301 WHLDTTTFGD YPQIMKDIVG HRLPKFTTEQ KAKLKASTDF VGLNYYTSVF
351 SNHLEKPDPS KPRWMQDSLI TWESKNAQNY AIGSKPLTAA LNVYSRGFRS
401 LLKYIKDKYA NPEIMIMENG YGEELGASDS VAVGTADHNR KYYLQRHLLS
451 MQEAVCIDEV NVTGYFVWSL LDNFEWQDGY KNRFGLYYVD FKNNLTRYEK
501 ESGKYYKDFL SQGVRPSALK KDEL
```

Spot No.: **ML4**

NCBI accession No.: **NP_051044.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **ATP synthase CF1 alpha subunit**

Peptide sequences: **R.ADEISNIIR.E; K.IAQIPVSEAYLGR.V;**

R.VINALANPIDGR.G; R.EQHTLIYDDLSK.Q;

R.EAYPGDVFYLHSR.L; K.EGIQEQLER.F

PFF Mascot score: **[506]**

Sequence coverage %: **[13]**

Matched peptides No.: **[6]**

Calculated Mr: **55351**

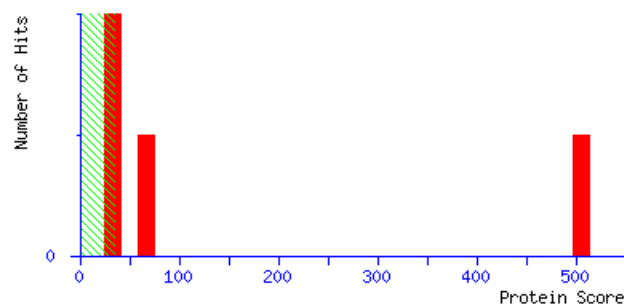
Calculated pI: **5.19**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1 MVTIRADEIS NIIRERIEQY NREVTIVNTG TVLQVGDGIA RIYGLDEVMA
51 GELVEFEETG IGIALNLESN NVGVVLMGDG LMIQEGSSVK ATGKIAQIPV
101 SEAYLGRVIN ALANPIDGRG KISASESRLI ESPAPGIISR RSVYEPLQTG
151 LIAIDSMIPI GRGQRELIIG DRQTGKTAVA TDTILNQGGQ NVICVYVAIG
201 QKASSVAQVV TSLQERGAME YTIVVAETAD SPATLQYLAP YTGAALAEYF
251 MYREQHTLII YDDLSKQAQA YRQMSLLLR PPGREAYPGD VFYLHSRLLE
301 RAAKLSSQLG EGSMIALPIV ETQSGDVSAY IPTNVISITD GQIFLSADLF
351 NAGIRPAINV GISVSRVGS A QIKAMKQVA GKLKLELAQF AELEAFSQFS
401 SDDLKATQNG LARGQRLREL LKQSQSAPLT VEEQIMTIYT GTNGYLDGLE
451 IGQVRKFLVQ LRTYLKTNKP QFQEIIASTK TLTAEAESFL KEGIQEQLER
501 FLLQEKV
```


Spot No.: **ML5**

NCBI accession No.: **OAP04789.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **HCEF1 (fructose 1,6-bisphosphatase)**

Peptide sequences: **U R.YIGSLVGDFHR.T;**

R.TLLYGGIYGYP.R.D; R.VLDIQPTEIHQR.V

PFF Mascot score: **[214]**

Sequence coverage %: **[8]**

Matched peptides No.: **[3]**

Calculated Mr: **45592**

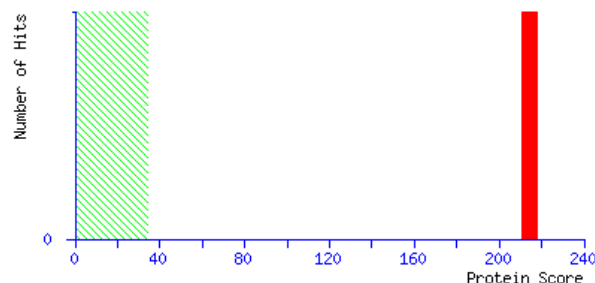
Calculated pI: **5.25**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1 MAASAATTTT SHLLLSSSRH VASSSQPSIL SPRSLFSNNG KRPTGVRNH
51 QYASGVRCMA VAADASETKT AARKKSGYEL QTLTGWLLRQ EMKGEIDAEI
101 TIVMSSISLA CKQIASLVQR AGISNLTGVQ GAVNIQGEDQ KKLDVISNEV
151 FSNCLRSSGR TGIIASEEED VPAVEESYS GNYVVVFDPL DGSSNIDAAV
201 STGSIFGIYS PNDECIVDDS DDISALGSEE QRCIVNVCQP GNNLLAAGYC
251 MYSSSVIFVL TLGKGVFSFT LDPMYGEFVL TQENIEIPKA GRIYSFNEGN
301 YQMWDDKLKK YIDDLKDPGP TGKPYSARYI GSLVGDFHRT LLYGGIYGYP
351 RNAKSKNGKL RLLYECAPMS FIVEQAGGKG SDGHSRVLDI QPTTEIHQRVP
401 LYIGSTEEVE KLEKYLA
```

Spot No.: **ML6**

NCBI accession No.: **AAN18180.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **At2g39730/T5I7.3**

Peptide sequences: **R.GLAYDTSDDQQDITR.G;**

U.R.YREAADLIK.K; R.VPIICTGNDFSTLYAPLIR.D;

R.EGPPVFEQPEMTYEK.L;R.VQLAETILSQAALGDANADAIGR.

G; K.GAQQVNLPVPEGCTDPVAENFDPTAR

PFF Mascot score: **[517]**

Sequence coverage %: **[22]**

Matched peptides No.: **[6]**

Calculated Mr: **52371**

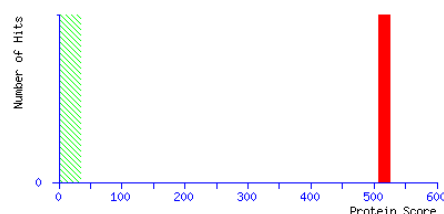
Calculated pI: **5.69**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MAAAVSTVGA  INRAPLSLNG  SGSGAVSAPA  STFLGKKVVT  VSRFAQSNKK
51  SNGSFKVLAV  KEDKQTDGDR  WRGLAYDTSDDQQDITR  GKG  MVDSVFQAPM
101 GTGTHHAVLS  SYEYVSQGLR  QYNLDNMMDG  FYIAPAFMDK  LVVHITKNFL
151 TLPNIKVPLI  LGIWGGKGQG  KSFQCELVMA  KMGINPIMMS  AGELESGNAG
201 EPAKLIRQRY  REAADLIKK  KMCCLLINDL  DAGAGRMGGT  TQYTVNNQMV
251 NATLMNIADN  PTNVQLPGMY  NKEENARVPI  ICTGNDFSTL  YAPLIRDGRM
301 EKFYWAPTRE  DRIGVCKGIF  RTDKIKDEDI  VTLVDQFPDQ  SIDFFGALRA
351 RVDDEVRKF  VESLGVEKIG  KRLVNSREGP  PVFEQPEMTY  EKLMEYGNML
401 VMEQENVKRV  QLAETILSQA  ALGDANADAI  GRGTFYKGGA  QQVNLPVPEG
451 CTDPVAENFD  PTARSDDGTC  VYNF
```

Spot No.: **ML7**

NCBI accession No.: **AAO19414.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Ribulose-1,5-bisphosphate carboxylase**

Peptide sequences: **K.DTDILAAFR.V; K.TFQGPPHGIQVER.D;**
R.DNGLLLHIHR.A; R.ESTLGFVDLLR.D; R.VALEACVQAR.N;
R.DLAVEGNEIR.-

PFF Mascot score: **[488]**

Sequence coverage %: **[14]**

Matched peptides No.: **[6]**

Calculated Mr: **47920**

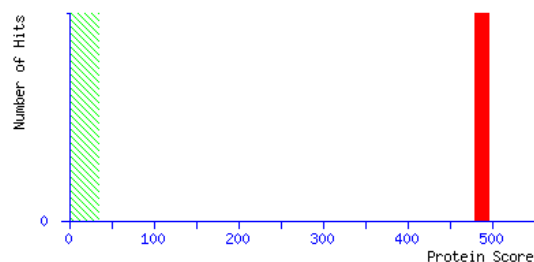
Calculated pI: **6.12**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

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

Spot No.: **ML9**

NCBI accession No.: **AAN18180.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **At2g39730/T5I7.3**

Peptide sequences: **R.GLAYDTSDDQQDITR.G;**

K.SFQCELVMAK.M; R.VQLAETYLSQAALGDANADAIGR.G

PFF Mascot score: **[214]**

Sequence coverage %: **[10]**

Matched peptides No.: **[3]**

Calculated Mr: **52371**

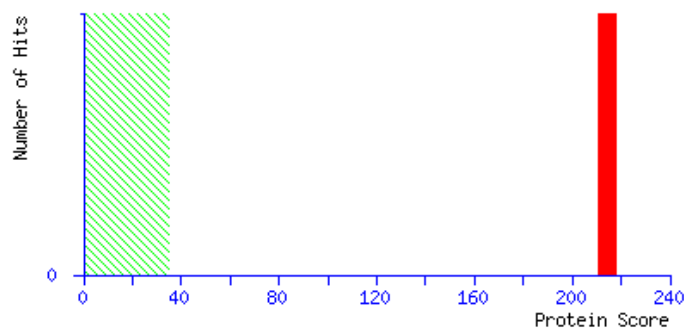
Calculated pI: **5.69**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MAAAVSTVGA  INRAPLSLNG  SGSGAVSAPA  STFLGKKVVT  VSRFAQSNKK
51  SNGSFKVLAV  KEDKQTDGDR  WRGLAYDTS  DQQDITRGKG  MVDSVFQAPM
101 GTGTHHAVLS  SYEYVSQGLR  QYNLDNMMDG  FYIAPAFMDK  LVVHITKNFL
151 TLPNIKVPLI  LGIWGGKGQG  KSFQCELVMA  KMGINPIMMS  AGELESGNAG
201 EPAKLIRQRY  REAADLIKKG  KMCCLLINDL  DAGAGRMGGT  TQYTVNNQMV
251 NATLMNIADN  PTNVQLPGMY  NKEENARVPI  ICTGNDFSTL  YAPLIRDGRM
301 EKFYWAPTRE  DRIGVCKGIF  RTDKIKDEDI  VTLVDQFPDQ  SIDFFGALRA
351 RVDYDEVKRF  VESLGVEKIG  KRLVNSREGP  PVFEQPEMTY  EKLMEYGNML
401 VMEQENVKRV  QLAETYLSQA  ALGDANADAI  GRGTFYKGKA  QQVNLPVPEG
451 CTDPAENFD  PTARSDDGTC  VYNF
```

Spot No.: **ML14**

NCBI accession No.: **NP_566728.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Plastid-lipid associated protein PAP / fibrillin family protein**

Peptide sequences: **R.GLVASVDDLER.A; R.LLYSSAFSSR.S; K.TSGNLSQIPPFDIR.L**

PFF Mascot score: **[216]**

Sequence coverage %: **[12]**

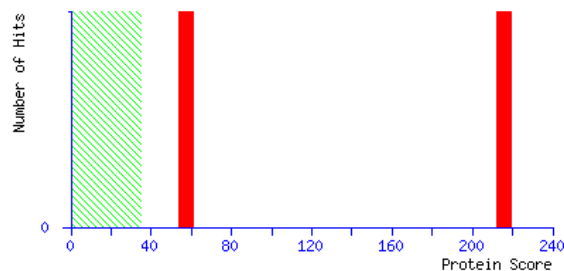
Matched peptides No.: **[3]**

Calculated Mr: **30493**

Calculated pI: **5.82**

Annotated PFF spectra:

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

```
1  MATSSTFSSL LPSPPALLSD HRSPPPSIRY SFSPLTPKS SRLGFTVPEK
51 RNLAANSSLV EVSIGGESDP PPSSSGSGGD DKQIALLKLK LLSVVSGLNR
101 GLVASVDDLE RAEVAAKELE TAGGPVDLTD DLDKLQGWK LLYSSAFSSR
151 SLGGSRPGLP TGRLLPVTLG QVFQRINVFS KDFDNIAEVE LGAPWPFPPPL
201 EATATLAHKF ELLGTCKIKI TFEKTTVKTS GNLSQIPPF IPRLPDSFRP
251 SSNPGTGDFE VTYVDDTMRI TRGDRGELRV FVIA
```

Spot No.: **ML15**

NCBI accession No.: **AAL07227.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Putative lactoylglutathione lyase**

Peptide sequences: **K.DPDGYTFELIQR.G;**

R.GPTPEPFCQVMLR.V; R.EAGPLPGLGTK.I

PFF Mascot score: **[217]**

Sequence coverage %: **[12]**

Matched peptides No.: **[3]**

Calculated Mr: **31995**

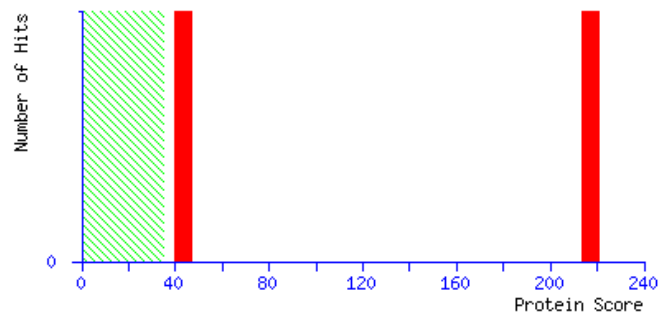
Calculated pI: **5.11**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1 MAEASDLLEW PKKDNRRFLH VVYRVGDLDR TIEFYTEVFG MKLLWKRDIP
51 EEKYSNAFLG FGPETSNFVV ELTYNYGVSS YDIGTGFGHF AISTQDVSKL
101 VENVRAKGGN VTREPGPVKG GGSVIAFVKD PDGYTFELIQ RGPTPEPFCQ
151 VMLRVGDLDR AIKFYEKALG MRLLRKIERP EYKYTIGMMG YAEYESIVL
201 ELTYNYDVTE YTKGNAYAQI AIGTDDVYKS GEVIKIVNQE LGGKITREAG
251 PLPGLGTKIV SFLDPDGWKT VLVDNKDFLK ELE
```

Spot No.: **ML17**

NCBI accession No.: **CAA63909.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **2-Cys peroxiredoxin bas1**

Peptide sequences: K.SFGVLIHDQGIALR.G

PFF Mascot score: **[97]** Sequence coverage %: **[5]**

Matched peptides No.: **[1]**

Calculated Mr: **28966**

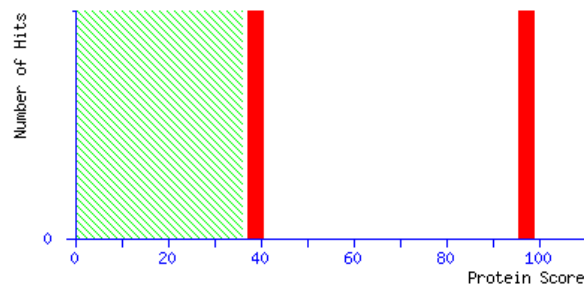
Calculated pI: **8.76**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MASVASSTTL ISSPSSRVFP AKSSLSPSPV SFLRTLSSPS ASASLRSGFA
51  RRSSLSTSR RSFAVKAQAD DLPLVGNKAP DFKAQAVFDQ EFIKVKLSY
101 NGKKYVILFF YPLDFTFVCP TEITAFSDRH SEFEKLNTEV LGVSVDSVFS
151 HLAHVQTDRK SGGGLGDLNYP LISDVTKSIS KSFGVLIHDQ GIALRGLFII
201 DKEGVIQHST INNLGIGRSV DETMRTLQAL QYTGNPDEV C PAGWKSGEKS
251 MKPDPKLSKE YFSAI
```

Spot No.: **ML18**

NCBI accession No.: AAM63854.1

Plant species: *Arabidopsis thaliana*

Protein name: **Atpm24.1 glutathione S transferase**

Peptide sequences: K.VFGHPASIATR.R;

R.NPFGQVPAFEDGDLK.L; R.YENQGTNLLQTDSK.N

PFF Mascot score: **[218]**

Sequence coverage %: **[18]**

Matched peptides No.: **[3]**

Calculated Mr: **24036**

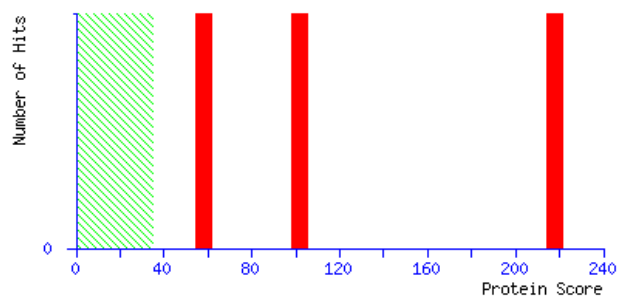
Calculated pI: **6.08**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MAGIKVFGHP ASIATRRVLI  ALHEKNLDFE  LVHVELKDGE  HKKEPFLSRN
51  PFGQVPAFED GDLKLFESRA  ITQYIAHRYE  NQGTNLLQTD SKNISQYAIM
101 AIGMQVEDHQ  FDPVASKLAF  EQISKSIYGL  TTDEAVVAXE  EAKLAKVLDV
151 YEARKLKFYK  LAGETFTLTD  LHHIPAIQYL  LGTPTKKLFT  ERPRVNEWVA
201 EITKRPASEK  VQ
```


Spot No.: **ML19**

NCBI accession No.: **AAM64537.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Putative 2-cys peroxiredoxin BAS1 precursor**

Peptide sequences: **K.APDFEAEAVFDQEFIK.V;**

K.SFGVLIHDQGIALR.G; K.SFGVLIHDQGIALR.G

PFF Mascot score: **[164]**

Sequence coverage %: **[11]**

Matched peptides No.: **[3]**

Calculated Mr: **29256**

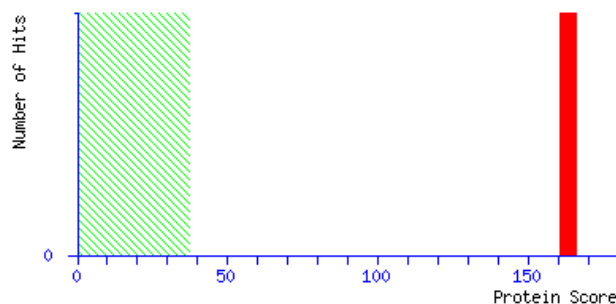
Calculated pI: **6.91**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1 MASVASSTTL ISSPSSRVFP AKSSLSSPSV SFLRTLSSPS ASASLRSGFA
51 RRSSLSTSR RSFAVKAQAD DLPLVGNKAP DFEAEAVFDQ EFIKVKLSDY
101 IGKKYVILFF YPLDFTFVCP TEITAFSDRH SEFEKLNTEV LGVSVDSVFS
151 HLAWVQTRK SGGLGDLNYP LISYFTKSIS KSFGVLIHDQ GIALRGLFII
201 DKEGVQHST INNLGIGQSV DETMRTLQAL QYIQENPDEV CPAGWKPGKEK
251 SMKPDPKLSK EYFSAI
```

Spot No.: **ML20**

NCBI accession No.: **AAM64537.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **putative 2-cys peroxiredoxin BAS1 precursor**

Peptide sequences: **K.APDFEAEAVFDQEFIK.V;**

K.SFGVLIHDQGIALR.G; K.SFGVLIHDQGIALR.G

PFF Mascot score: **[164]**

Sequence coverage %: **[11]**

Matched peptides No.: **[3]**

Calculated Mr: **29256**

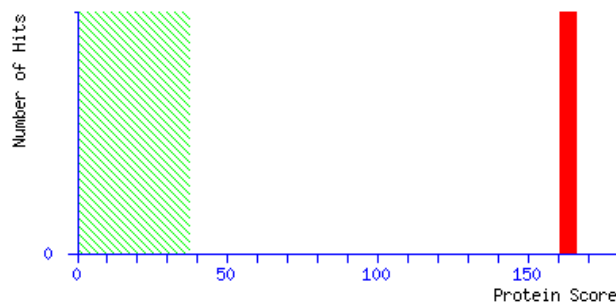
Calculated pI: **6.91**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1 MASVASSTTL ISSPSSRVFP AKSSLSSPSV SFLRTLSSPS ASASLRSGFA
51 RRSSLSTSR RSFAVKAQAD DLPLVGNKAP DFEAEAVFDQ EFIKVKLSDY
101 IGKKYVILFF YPLDFTFVCP TEITAFSDRH SEFEKLNTEV LGVSVDVSFS
151 HLAWVQTRK SGGLGDLNYP LISYFTKSIS KSFGVLIHDQ GIALRGLFII
201 DKEGVIQHST INNLGIGQSV DETMRTLQAL QYIQENPDEV CPAGWKPGEK
251 SMKPDPKLSK EYFSAI
```

Spot No.: **ML21**

NCBI accession No.: **OAP02726.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **PBPI (PYK10-binding protein 1)**

**Peptide sequences: K.GANLWDDGSTHDAVTK.I;
K.VYVGQAQDGISAVK.F; K.FVYDKSPEEVTGEEHGK.S;
K.IGVHVRPLSN.-**

PFF Mascot score: **[208]** Sequence coverage %: **[19]**

Matched peptides No.: **[4]**

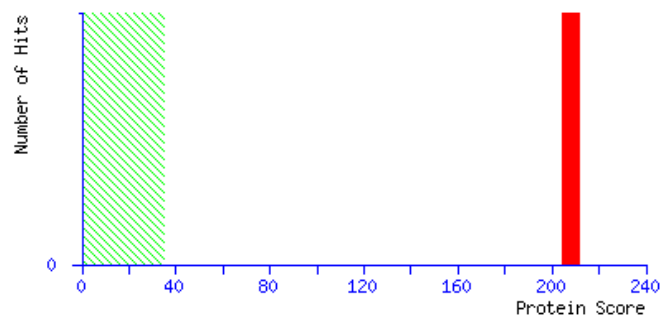
Calculated Mr: **32110** Calculated pI: **5.46**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1 MAQKVEAQGG KGANLWDDGS THDAVTKIQL AAGIDGIQYV QFDYVKNQGP
51 EQAPLRGTKG RVLPA DPFVI NHPDEHLVSV EGWYSPEGII QGIKFISNKK
101 TSDVIGSDEG THFTLQVKDK KIIGFHGSAG GNLNSLGAYF APLTTTTPLT
151 PAKQLTAFGS DDGTAWDDGA YVGVKVYVG QAQDGISAVK FVYDKSPEEV
201 TGEEHGKSTL LGFEFVLDY PSEYITAVDG TYDKIFGSDG SVITMLRFKT
251 NKQTSPPFGL EAGTVFELKE EGHKIVGFHG RADVLLHKIG VHVRPLSN
```

Spot No.: **ML22**

NCBI accession No.: **CAA31948.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Ribulose biphosphate carboxylase**

Peptide sequences: **R.EHGNSPGYYDGR.Y; K.EYPNAFIR.I**

PFF Mascot score: **[80]** Sequence coverage %: **[10]**

Matched peptides No.: **[2]**

Calculated Mr: **20733**

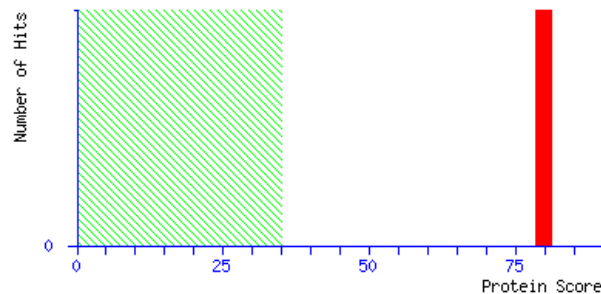
Calculated pI: **7.59**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MASSMLSSAT  MVASPAQATM  VAPFENGLKSS  AAFPATRKAN  NDITSITSNG
51  GRVNCMQMQV  WPPIGKKKFE  TLSYLPDLTD  SELAKEVDYL  IRNKWIPCVE
101 FELEHGFVYR  EHGNSPGYYD  GRYWTMWKLP  LFGCTDSAQV  LKEVEECKE
151 YPNAFIRIIIG  FDNTRQVQCI  SFVAYKPPSF  TG
```

Spot No.: **ML23**

NCBI accession No.: **CAA36675.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **33 kDa oxygen-evolving protein**

Peptide sequences: **K.RLTYDEIQSK.T; K.NAPPEFQNTK.L;**
K.QLDASGKPDSFTGK.F

PFF Mascot score: **[140]**

Sequence coverage %: **[10]**

Matched peptides No.: **[3]**

Calculated Mr: **35285**

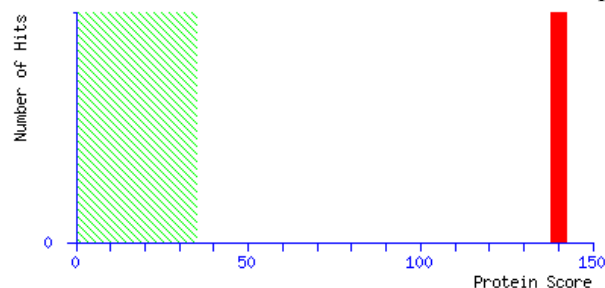
Calculated pI: **5.68**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MAASLQSTAT  FLQSAKIATA  PSRGSSHLRS  TQAVGKSFGL  ETSSARLTCS
51  FQSDFKDFTG  KCSDAVKIAG  FALASSALVV  SGASAEGAPK  RLTYDEIQSK
101 TYMEVKGITG  ANQCPTIDGG  SETFSFKPGK  YAGKKFCFEP  TSFTVKADSV
151 SKNAPPEFQN  TKLMTRLTYT  LDEIEGPFEV  ASDGSVNFKE  EDGIDYAAVT
201 VQLPGGERVP  FLFTVKQLDA  SGKPDSFTGK  FLVPSYRGSS  FLDPKGRGGS
251 TGYDNAVALP  AGGRGDEEEL  VKENVKNTAA  SVGEITLKVT  KSKPETGEVI
301 GVFESLQPSD  TDLGAKVPKD  VKIQGVWYGQ  LE
```

Spot No.: **ML24**

NCBI accession No.: **AAG30126.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Glutathione S-transferase**

Peptide sequences: **K.VFGHPASTATR.R; K.VPAFEDGDFK.L;**
K.VLDVYEHR.L

PFF Mascot score: **[206]**

Sequence coverage %: **[13]**

Matched peptides No.: **[3]**

Calculated Mr: **23539**

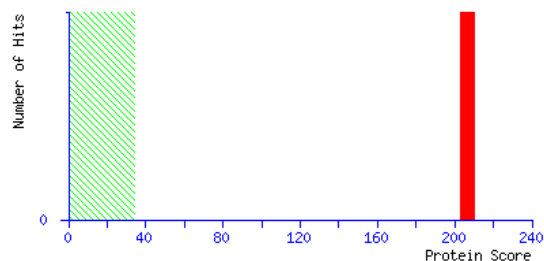
Calculated pI: **6.31**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MAGIKVFGHP ASTATRRVL I ALHEKNLDFE FVHIELKDGE HKKEPFIFRN
51  PFGKVPAFED GDFKLFESRA ITQYIAHFYS DKG NQLVSLG SKDIAGIAMG
101 IEIESHEFDP VGSKLVWEQV LKPLYGMTTD KTVVEEEEAK LAKVLDVYEH
151 RLGESKYLAS DKFTLVDLHT IPVIQYLLGT PTKKLFAERP HVSAWVADIT
201 SRPSAKKVL
```

Spot No.: **MR1**

NCBI accession No.: **OAP03586.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Hypothetical protein AXX17_AT3G17230 (plant invertase/pectin methylesterase inhibitor)**

Peptide sequences: **K.HLYVFDLETR.T; K.LLTPVEEGPTPR.S; R.LDKFGGEEETPSSR.G**

PFF Mascot score: **[180]** Sequence coverage %: **[7]**

Matched peptides No.: **[3]**

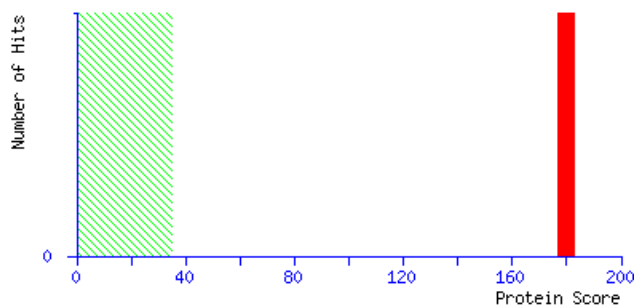
Calculated Mr: **51810** Calculated pI: **5.37**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

1 MAQKLEAKGG EMGDVWDDGV YENVRKVYVG QAQYGIQFVK FEYVNGSQVV
 51 VGDEHGKKTE LGVEEFEIDA DDYIVYVEGY REKVNDMTSE MITFLSIKTF
 101 KGKTSHPLEK RPKVKFVLHG GKIIGFHGRS TDVLHSLGAY VSLSSSTKLL
 151 GKWIKVEQKG EGPGLRCSHG IAQVGNKIYS FGGEFTPNQP IDKHLVFDL
 201 ETRTWSISPA TGDVPHLSCL GVRMVSVGST LYVFGGRDAS RQYNGFYSFD
 251 TTTNEWKLLT PVEEGTPRS FHSMAADEEN VYVFGGVSAT ARLNTLDSYN
 301 IVDKKWFHCS TPGDSLARG GAGLEVVGK VVVYGFNGC EVDDVHYYP
 351 VQDKWTQVET FGVRPSERSV FASAALGKHI VIFGGEIAMD PLAHVGPGL
 401 TDGTFALDTE TLQWERLDKF GGEEETPSSR GWTASTTATI GGKKGLVMHG
 451 GKAPTNDRFD DLFFYGIDSA

Spot No.: **MR2**

NCBI accession No.: **OAP09497.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **JAL22 (Jacalin-related lectin 22)**

Peptide sequences: **R.KLALCGGEGGQEWDDDVYEGVR.K;**
R.KVYVGQDLNR.I; K.VYVGQDLNR.I; R.VWDDGSYDGIK.T;
R.ITYLEVEYEKDGAEK.T; K.GDTPSEFVLGYDEYIK.S;
R.TSFFGYNVGK.K; K.LPAIGGNEGVTWDDGVYDGVR.K;
K.ILVGQGNDGVSFVK.F

PFF Mascot score: **[624]**

Sequence coverage %: **[26]**

Matched peptides No.: **[9]**

Calculated Mr: **50604**

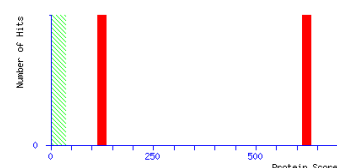
Calculated pI: **5.15**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MAKMYRKLAL CGGEGGQEWDDDVYEGVRKV YVGQDLNRIT YIKFEYVQED
51  GEVVITEYGT  TNQHPKEFVI  QYPDEHIIAV  EGSYHQVALI  ATEVITSLIF
101 KTSKGRKSPL  FGNLLGITT  GTKFVFEDEG  KKIVGFHGRA  GDAVDALGVY
151 FVLDTTPFPL  YKLDAQGGTD  GRVWDDGSYD GIKTLRIDQD NSRITYLEVE
201 YEKDGAEKTF NHGGKGDTPS EFVLGYPDEY IKSVEATYQK  PNIFSNTAIT
251 SLKFLTSKGR  TSFFGYNVGK KFVLEQKGHR  LVGFHGKEDA  AIDALGAYFG
301 PVPTPTPLIP  SKKLPAIGGN EGVTWDDGVY DGVRKILVGQ GNDGVSFVKF
351 EYSKGDLPV  GDDHGKKTLL  GAEEFVLEDG  EYLMNIDGY  DKIFGVVEPI
401 IVCLQFKTNK  RESMPFGMDS  GKKFSLGEEG  HKIVGFHGQA  SDVVHSIGVT
451 IVPITTE
```

Spot No.: **MR3**

NCBI accession No.: **OAP06341.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **JR 1 (JA-responsive protein 1)**

**Peptide sequences: R.GGEEWDDGGAYENVK.K;
K.VYVGQGDSGVVYVK.F; K.TSQPFGLTSGEEAELGGGK.I;
R.GGDVWDDGGAYDNVK.K**

PFF Mascot score: **[426]**

Sequence coverage %: **[13]**

Matched peptides No.: **[4]**

Calculated Mr: **48548**

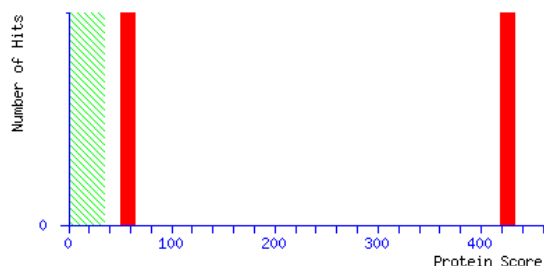
Calculated pI: **5.17**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MAKKLEAQGG  RGGEWDDGG  AYENVKKVYV  GQGDSGVVYV  KFDYEKDGKI
51  VSHEHGKQTL  LGTEEFVVDP  EDYITSVKIY  YEKLFGSPIE  IVTALIFKTF
101 KGKTSQPFGL  TSGEEAELGG  GKIVGFHGSS  SDLIHSGVGY  IIPSTTPLTP
151  PVSGLTKLE   AQQGRGGDVW  DDGGAYDNVK  KVVYVGQDSG  VVYVKFDYEK
201  DGKIVSHEHG  KQTLLGTEEF  EIDPEDYITY  VKVYYEKLFG  SPIEIVTALI
251  FKTFKGKTSQ  PFGLTSGEEA  ELGGGKIVGF  HGTSSDLIHS  LGAYIIPSST
301  PLTPSSNTIP  AQQGDGGVAW  DDGVHDSVKK  IYVGQGDSCV  TYFKADYEKA
351  SKPVLGSDHG  KKTLLGAEEF  VLGPDYVTA  VSGYYDKIFS  VDAPAIVSLK
401  FKTNKRISIP  YGLEGGTEFV  LEKKDHKIVG  FYGQAGEYLY  KLGNVAPIA
451  K
```

Spot No.: **MR4**

NCBI accession No.: **OAP06341.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **JR 1 (JA-responsive protein 1)**

Peptide sequences: **R.GGEEWDDGGAYENVK.K;**

K.VYVGQGDSGVVYVK.F; K.FDYEKDGK.I;

K.TSQPFGLTSGEEAELGGGK.I; R.GGDVWDDGGAYDNVK.K;

K.ASKPVLGSDHKG.K; R.TSIPYGLEGGTEFVLEK.K

PFF Mascot score: **[561]**

Sequence coverage %: **[22]**

Matched peptides No.: **[7]**

Calculated Mr: **48548**

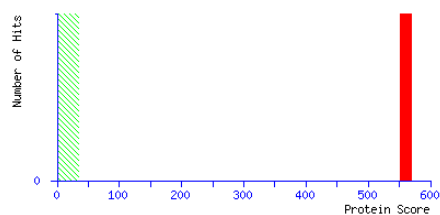
Calculated pI: **5.17**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MAKKLEAQQG  RGGEEWDDGG  AYENVKKVYV  GQGDSGVVYV  KFDYEKDGKI
51  V SHEHGKQTL  LGTEEFVVDP  EDYITSVKIY  YEKLFGSPIE  IVTALIFKTF
101 KGKTSQPFGL  TSGEEAELGG  GKIVGFHGSS  SDLIHSGVGY  IIPSTTPLTP
151  PVSGGLTKLE  AQGGRGGDVW  DDGGAYDNVK  KVYVGQGD SG  VVYVKFDYEK
201  DGKIVSHEHG  KQTLLGTEEF  EIDPEDYITY  VKVYVEKLFG  SPIEIVTALI
251  FKTFKGKTSQ  PFGLTSGEEA  ELGGGKIVGF  HGTSSDLIHS  LGAYIIP SST
301  PLTPSSNTIP  AQGGDGGVAV  DDGVHDSVKK  IYVGQGDSCV  TYFKADYEKA
351  SKPVLGSDHG  KKILLGAEEF  VLGPD EYVTA  VSGYYDKIFS  VDAPAI VSLK
401  FKTNKRTSIP  YGLEGGTEFV  LEKKDHKIVG  FYGQAGEYLY  KLG VNVAPIA
451  K
```

Spot No.: **MR5**

NCBI accession No.: **BAE98486.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Glutamine synthetase like protein**

Peptide sequences: **R.TLPGPVTDP SKLPK.W;**

R.HKEHISAYGEGNER.R; K.EHISAYGEGNER.R

PFF Mascot score: **[229]**

Sequence coverage %: **[7]**

Matched peptides No.: **[3]**

Calculated Mr: **39323**

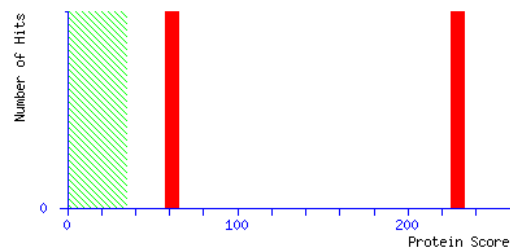
Calculated pI: **5.14**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MSLLADLVNL  DISDNSEKII  AEYIWVGSG  MDMRSKARTL  PGPVTDP SKL
51 PKWNYDGSST  GQAPGQDSEV  ILYPQAIFKD  PFRRGNNILV  MCDAYTPAGE
101 PIPTNKRHAA  AEIFANPDVI  AEPWPYGIEQ  EYTLLQKDVN  WPLGWPIGGF
151 PGPQGPYYCS  IGADKSFGRD  IVD AHYKASL  YAGINISGIN  GEVMPGQWEF
201 QVGPSVGISA  ADEIWIPRYI  LERITEIAGV  VVSFDPKPIP  GDWNGAGAHT
251 NYSTKSMREE  GGYEIIKKAI  EKLGLRHKEH  ISAYGEGNER  RLTGHHETAD
301 INTFLWGVAN  RGASIRVGRD  TEKEGKGYFE  DRRPASNMDP  YVVTSMIAET
351 TLLWNP
```

Spot No.: **MR7**

NCBI accession No.: **NP_188266.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Mannose-binding lectin superfamily protein**

Peptide sequences: **K.VEAGGGAGGASWDDGVHDGVR.K;**

K.TSPPYGLETQK.K; K.LSAIGGDEGTAWDDGAYDGVK.K;

K.VYVGQGQDGISAVK.F; K.QTSAPFGLEAGTAFELK.E

PFF Mascot score: **[425]**

Sequence coverage %: **[28]**

Matched peptides No.: **[5]**

Calculated Mr: **32003**

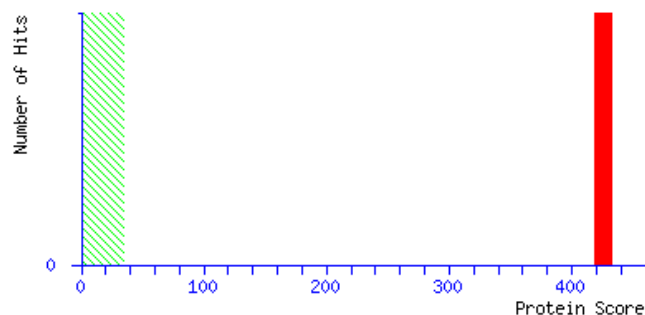
Calculated pI: **5.06**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1 MAQKVEAGGG AGGASWDDGV HDGVRKVHVG QGQDGVSSIN VVYAKDSQDV
51 EGGEHGKCTL LGFETFEVDA DDYIVAVQVT YDNVFGQDSD IITSITFNTF
101 KGKTSPPYGL ETQKKFVLKD KNGGKLVGFH GRAGEALYAL GAYFATTTTP
151 VTPAKKLSAI GGDEGTAWDD GAYDGVKKVY VGQGQDGISA VKFEYNKGAE
201 NIVGGEHGKP TLLGFEEFEI DYPSEYITAV EGTYDKIFGS DGLIITMLRF
251 KTNKQTSAPF GLEAGTAFEL KEEGHKIVGF HGKASELLHQ FGVHVMPLTN
```

Spot No.: **MR8**

NCBI accession No.: **AAM66134.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Translationally-controlled tumor protein-like protein**

Peptide sequences: **K.VVDIVDTFR.L**

PFF Mascot score: **[74]** Sequence coverage %: **[5]**

Matched peptides No.: **[1]**

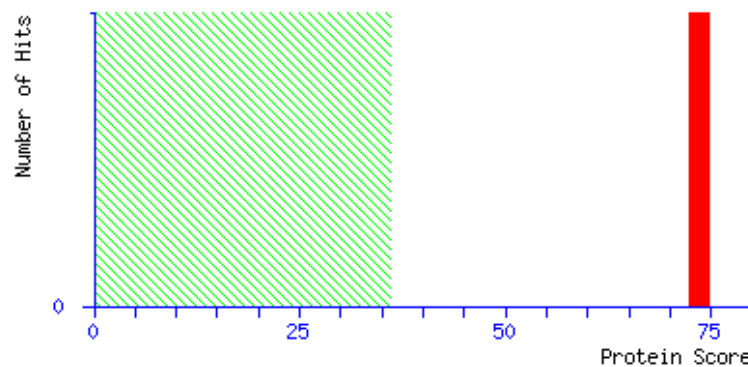
Calculated Mr: **18925** Calculated pI: **4.52**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MLVYQDLLTG  DELLSDSFPY  KEIENGILWE  VEGKWVTVGA  VDVNIGANPS
51  AEEGGEDEGV  DDSAQKVVDI VDTFRLQEQP  TYDKKGFIAY  IKKYIKLLTP
101 KLSEEDQAVF  KKGIEGATKF  LLPRLSDFQF  FVGEGMHDDS  TLVFAYYKEG
151 STNPTFLYFA  HGLKEVKC
```

Spot No.: **MR9**

NCBI accession No.: **NP_180766.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Ribosomal protein L7Ae/L30e/S12e/Gadd45
family protein**

Peptide sequences: **R.NAQLCVLAEDCNQPDYVK.L;
K.ALCADHSIK.L; K.TLGEWAGLCK.I**

PFF Mascot score: **[227]** Sequence coverage %: **[25]**

Matched peptides No.: **[3]**

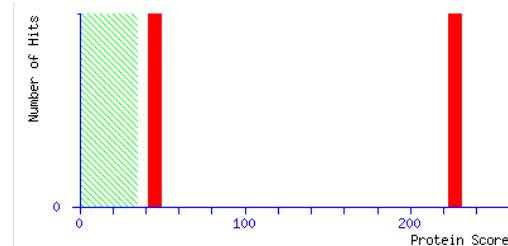
Calculated Mr: **15661**

Calculated pI: **5.62**

Annotated PFF spectra:

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MSGDEAVAAP  VVPPVAEAAV  IPEDMDVSTA  LETVRKSRA  YGGVVRGLHE
51  SAKLIEKRNA  QLCVLAEDCN  QPDYVKLVKA  LCADHSIKLL  TVPSAKTLGE
101 WAGLCKIDSE  GNARKVVGCS  CLVIKDFGEE  TTALNIVKKH  LDSN
```

Spot No.: **MR10**

NCBI accession No.: **AAM66134.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Translationally controlled tumor protein-like protein**

Peptide sequences: **K.VVDIVDTFR.L**

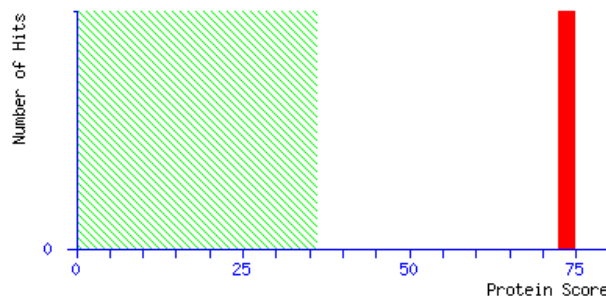
PFF Mascot score: **[74]** Sequence coverage %: **[5]**

Matched peptides No.: **[1]**

Calculated Mr: **18925** Calculated pI: **4.52**

Annotated PFF spectra:

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



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

```
1 MLVYQDLLTG DELLSDSPFY KEIENGILWE VEGKWVTVGA VDVNIGANPS
51 AEEGGEDEGV DDSAQKVVDI VDTFRLQEQP TYDKKGFIAY IKKYIKLLTP
101 KLSEEDQAVF KKGIEGATKF LLPRLSDFQF FVGEGMHDDS TLVFAYYKEG
151 STNPFLYFA HGLKEVKC
```


Spot No.: **MR12**

NCBI accession No.: **NP_565265.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **MLP-like protein 329**

Peptide sequences: **K.EIDDENMVITFR.G + Oxidation (M)**

PFF Mascot score: **[66]** Sequence coverage %: **[7]**

Matched peptides No.: **[1]**

Calculated Mr: **17705**

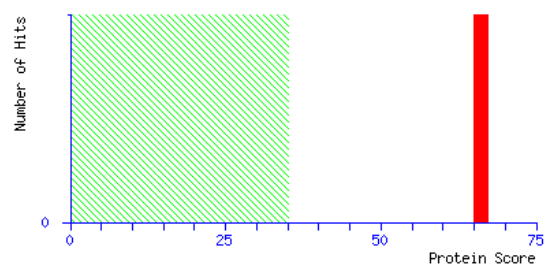
Calculated pI: **5.30**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1 MATSGTYVTE VPLKGSADKH YKRWRDENHL FPDAIGHHIQ GVTVHDGEWD
51 SHEAIKIWNV TCDGKPEVFK ERK.EIDDENM VITFRGLEGH VMEQLKVYDL
101 IYQFSQKSPD DIVCKITMIW EKRTDDSEPE SNYMKFLKSV VADMDEHVLK
151 A
```

Spot No.: **MR13**

NCBI accession No.: **NP_194098.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **Polyketide cyclase/dehydrase and lipid transport superfamily protein**

Peptide sequences: **R.SWDYTYDGK.K; R.SWDYTYDGKK.E;**
R.GLDGHVMEHLK.V; K.ITMIWEKR.N; K.RNDDFPEPSGYMK.F;
R.NDDFPEPSGYMK.F; K.QMVVDIEGHVNKA.-

PFF Mascot score: **[414]**

Sequence coverage %: **[35]**

Matched peptides No.: **[7]**

Calculated Mr: **17621**

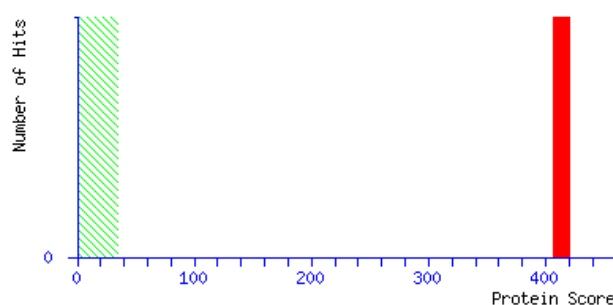
Calculated pI: **5.91**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1  MATSGTYVTE VPLKGSAEKH YKSWKSENHV FADAIGHHIQ NVVVHEGEHD
51  SHGSIRSWDY TYDGKKEMFK EKREIDDENK TLTKRGLDGH VMEHLKVFDI
101 IYEFIPKSED SCVCKITMIW EKRNDDFPEP SGYMKFVKQM VVDIEGHVNK
151 A
```

Spot No.: **MR14**

NCBI accession No.: **NP_565264.1**

Plant species: ***Arabidopsis thaliana***

Protein name: **MLP-like protein 328**

Peptide sequences: **K.IWNYTCDGKPEVFK.E;**

R.REIDDENMAVTFR.G; R.EIDDENMAVTFR.G;

R.EIDDENMAVTFR.G + Oxidation(M); R.GLEGHVMEQLK.V;

R.GLEGHVMEQLK.V + Oxidation (M)

PFF Mascot score: **[369]**

Sequence coverage %: **[25]**

Matched peptides No.: **[6]**

Calculated Mr: **17616**

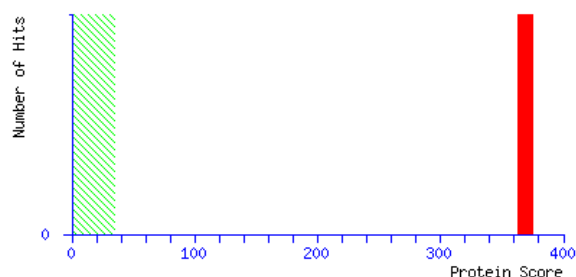
Calculated pI: **5.42**

Annotated PFF spectra:

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

Individual ions scores > 35 indicate identity or extensive homology ($p < 0.05$).

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



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

```
1 MATSGTYVTE VPLKGSAEKH YKRWSENHL FPDIGHHHIQ GVTIHDGEWD
51 SHGAIKIWNY TCDGKPEVFK ERREIDDENM AVTFRGLEGH VMEQLKVYDV
101 IFQFIQKSPD DIICKITMIW EKQNDMPPEP SNYMKFVKSL AADMDDHVLK
151 A
```