

### Protein View: FNRR1\_ARATH

Ferredoxin--NADP reductase, root isozyme 1, chloroplastic OS=Arabidopsis thaliana GN=RFNR1 PE=2 SV=2

**Database:** SwissProt  
**Score:** 68  
**Expect:** 0.0049  
**Nominal mass (M<sub>r</sub>):** 42712  
**Calculated pI:** 8.77  
**Taxonomy:** Arabidopsis thaliana

Sequence similarity is available as [an NCBI BLAST search of FNRR1\\_ARATH against nr.](#)

#### Search parameters

**Enzyme:** Trypsin: cuts C-term side of KR unless next residue is P.  
**Fixed modifications:** Carbamidomethyl (C)  
**Variable modifications:** Oxidation (M)  
**Mass values searched:** 6  
**Mass values matched:** 6

#### Protein sequence coverage: 22%

Matched peptides shown in **bold red**.

```

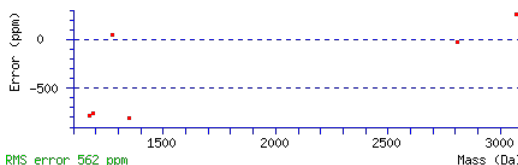
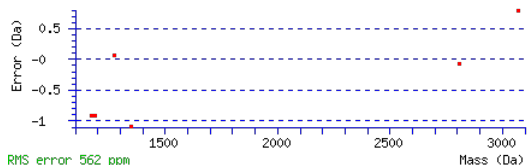
1 MALSTTPSQM SVALPTRIDG SSRSMIKVSQ ISFTDKSWGPF LLRLDLSKSR
51 SLGVKKRSTI CMSLQSSKS KVLVTPLELE DPKETPLNLF RPKEPYTATI
101 VSVVERIVGPG APGETCHIVI DHGDNVPYWE GQSYGVIPPG ENPKKPGAPH
151 NVRLYSIAST RYGDSFDGKT ASLCVRRALY YDPETGKEDP SKAGVCSNFL
201 CNAKPGDKVK ITGPSGKVML LPEDDPKATH IMIATGTGVA PYRGYLRRMF
251 MENVFNPKFD GLAWLFLGVA NSDSLLYDEE FAGYRKDYFE NFRYDKALSR
301 EEKNNKGGKM YVQDKIEEYS DEIFKLLDNG AHIYFCGLKG MMPGIQDTLK
351 RVAEERGESW EQKLTQLRKN KQWHVEVY
    
```

Unformatted sequence string: **378 residues** (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
72 - 83	1351.6816	1350.6744	1351.7599	-1.0855 0	<b>K.VLVTPLELEDPK.E</b>
218 - 227	1171.6773	1170.6701	1171.5795	-0.9094 0	<b>K.VMLLPEDEPK.A + Oxidation (M)</b>
259 - 285	3069.2635	3068.2562	3067.4603	0.7959 0	<b>K.FDGLAWLFLGVANSDSLlyDEEFAGYR.K</b>
316 - 325	1272.6581	1271.6508	1271.5921	0.0587 0	<b>K.IEEYSDEIFK.L</b>
326 - 350	2808.3089	2807.3016	2807.3809	-0.0792 1	<b>K.LLDNGAHIYFCGLKGMPGIQDTLK.R + Oxidation (M)</b>
340 - 350	1189.6841	1188.6768	1189.5835	-0.9067 0	<b>K.GMPGIQDTLK.R</b>



## Protein View: PSBO\_HELAN

Oxygen-evolving enhancer protein 1, chloroplastic OS=Helianthus annuus GN=PSBO PE=1 SV=1

Database: SwissProt  
 Score: 64  
 Expect: 0.014  
 Nominal mass (M<sub>r</sub>): 34487  
 Calculated pI: 5.40  
 Taxonomy: [Helianthus annuus](#)

Sequence similarity is available as [an NCBI BLAST search of PSBO\\_HELAN against nr.](#)

### Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.  
 Fixed modifications: [Carbamidomethyl \(C\)](#)  
 Variable modifications: [Oxidation \(M\)](#)  
 Mass values searched: 8  
 Mass values matched: 6

### Protein sequence coverage: 31%

Matched peptides shown in **bold red**.

```

1 MAASLQAAAT FMTPTSRVQL KSSPSICKAF GIESTGSKVS CSLQADLKDF
51 AQRCTDAAKI AGFALATSAL VVSGASAEGS PKRLTYDEIQ SKTYMEVKGT
101 GTANQCPTIE GGVNGFAVKP GKYNAQKFCL EPTSFTVKA E GISKNSAPEF
151 QKTKLMTRLT YTLDEIEGPL EVSSDGTIKF EEKDGIDYAA VTVQLPGGER
201 VPFLFTIKEL VATGKPESFG GNFLVPSYRG SSFLDPKGRG GSTGYDNAVA
251 LPAGGRGDEE ELLKENIKNT AAGKGEITFS VTSSKPETGE VIGVFESIQP
301 SDTDLGAKAP KDVKIQGVVY AQLW
    
```

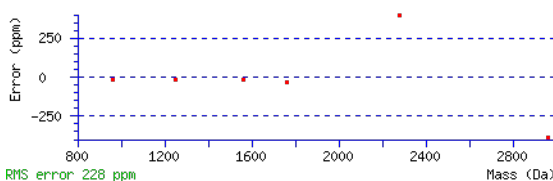
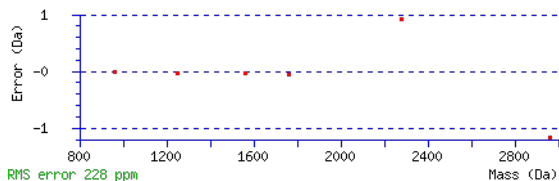
Unformatted sequence string: [324 residues](#) (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	M	Peptide
83 - 92	1252.6314	1251.6241	1251.6459	-0.0218	1	<b>K.RLTYDEIQSK.T</b>
99 - 127	2963.3067	2962.2994	2963.4560	-1.1566	1	<b>K.GGTANQCPTIEGGVNGFAVKPGKYNAQK.F</b>
159 - 179	2281.0610	2280.0537	2279.1420	0.9117	0	<b>R.LTYTLDEIEGPLEVSSDGTIK.F</b>
184 - 200	1760.8255	1759.8183	1759.8741	-0.0558	0	<b>K.DGIDYAAVTVQLP</b> GGER.V
201 - 208	964.5680	963.5608	963.5793	-0.0186	0	<b>R.VPFLFTIK.E</b>
240 - 256	1562.7286	1561.7213	1561.7485	-0.0272	0	<b>R.GGSTGYDNAVALPAGGR.G</b>

No match to: 2808.2181, 3347.5928



## Protein View: PSBO\_POPEU

**Oxygen-evolving enhancer protein 1, chloroplastic (Fragments) OS=Populus euphratica  
GN=PSBO PE=1 SV=1**

**Database:** SwissProt  
**Score:** 67  
**Expect:** 0.0062  
**Nominal mass (M<sub>r</sub>):** 10664  
**Calculated pI:** 5.36  
**Taxonomy:** Populus euphratica

Sequence similarity is available as [an NCBI BLAST search of PSBO\\_POPEU against nr.](#)

### Search parameters

**Enzyme:** Trypsin: cuts C-term side of KR unless next residue is P.  
**Fixed modifications:** Carbamidomethyl (C)  
**Variable modifications:** Oxidation (M)  
**Mass values searched:** 4  
**Mass values matched:** 4

### Protein sequence coverage: 52%

Matched peptides shown in **bold red**.

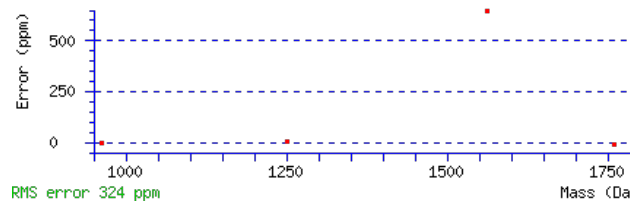
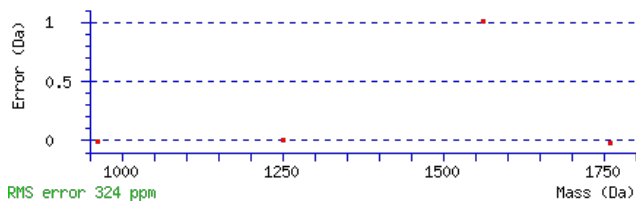
1 **RLTYDEIQSK** AEGINKNSPP DFQKTKLMTR **DGIDYAAVTV QLPGGERVVF**  
 51 **LFTIKGGSTG YDNAVALPAG** GRSKPETGEI IGVFESLQPS DTDLGAKTPK

Unformatted sequence string: **100 residues** (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	M	Peptide
1 - 10	1252.6591	1251.6518	1251.6459	0.0059	1	<b>-.RLTYDEIQSK.A</b>
31 - 47	1760.8608	1759.8536	1759.8741	-0.0205	0	<b>R.DGIDYAAVTVQLPGER.V</b>
48 - 55	964.5832	963.5759	963.5793	-0.0035	0	<b>R.VPFLFTIK.G</b>
56 - 72	1563.7691	1562.7618	1561.7485	1.0133	0	<b>K.GGSTGYDNAVALPAGGR.S</b>



## Protein View: NDHJ\_DIOEL

**NAD(P)H-quinone oxidoreductase subunit J, chloroplastic OS=Dioscorea elephantipes GN=ndhJ PE=3 SV=1**

**Database:** SwissProt  
**Score:** 76  
**Expect:** 0.00087  
**Nominal mass (M<sub>r</sub>):** 18820  
**Calculated pI:** 6.19  
**Taxonomy:** Dioscorea elephantipes

Sequence similarity is available as [an NCBI BLAST search of NDHJ\\_DIOEL against nr.](#)

### Search parameters

**Enzyme:** Trypsin: cuts C-term side of KR unless next residue is P.  
**Fixed modifications:** Carbamidomethyl (C)  
**Variable modifications:** Oxidation (M)  
**Mass values searched:** 6  
**Mass values matched:** 6

### Protein sequence coverage: 41%

Matched peptides shown in **bold red**.

```

1  MQSRLSDWLK KHELVHRSLG FDYQGIETLQ IKTEDWDSIA VISIYGYNY
51  LRSQCAYDVA PGGFLASVYH LTRIYQYGIK VEEVCLKV FV SRNNPRIPSV
101 FWIWKSASADFK ERESYDMLGI SYANHPHLKR IILMPESWIGW PLRKDYITPN
151 FYEIQDAR

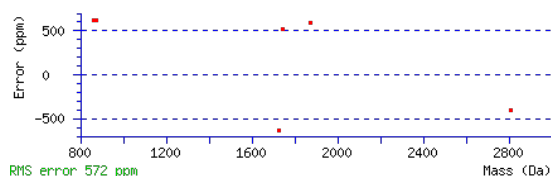
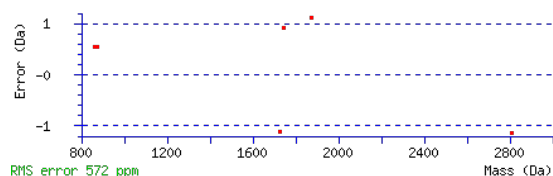
```

Unformatted sequence string: **158 residues** (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
5 - 11	861.0230	860.0157	859.4803	0.5354 0	<b>R.LSDWLVK.H</b>
81 - 87	876.9961	875.9888	875.4422	0.5466 0	<b>K.VEEVCLK.V</b>
106 - 129	2807.1723	2806.1650	2807.2973	-1.1323 1	<b>K.SADFKERESYDMLGISYANHPHLK.R</b>
131 - 144	1724.8474	1723.8401	1724.9436	-1.1035 1	<b>R.IILMPESWIGWPLRK.D</b>
131 - 144	1742.8585	1741.8512	1740.9385	0.9127 1	<b>R.IILMPESWIGWPLRK.D + Oxidation (M)</b>
144 - 158	1874.0140	1873.0067	1871.9054	1.1014 1	<b>R.KDYITPNFYEQDAR.-</b>



## Protein View: NDHJ\_DIOEL

**NAD(P)H-quinone oxidoreductase subunit J, chloroplastic OS=Dioscorea elephantipes GN=ndhJ PE=3 SV=1**

**Database:** SwissProt  
**Score:** 75  
**Expect:** 0.0011  
**Nominal mass (M<sub>r</sub>):** 18820  
**Calculated pI:** 6.19  
**Taxonomy:** Dioscorea elephantipes

Sequence similarity is available as [an NCBI BLAST search of NDHJ\\_DIOEL against nr.](#)

### Search parameters

**Enzyme:** Trypsin: cuts C-term side of KR unless next residue is P.  
**Fixed modifications:** Carbamidomethyl (C)  
**Variable modifications:** Oxidation (M)  
**Mass values searched:** 5  
**Mass values matched:** 5

### Protein sequence coverage: 35%

Matched peptides shown in **bold red**.

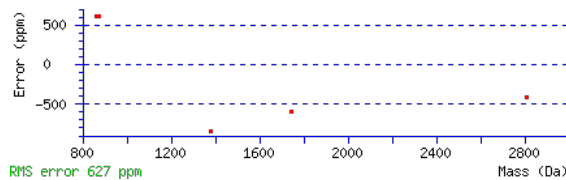
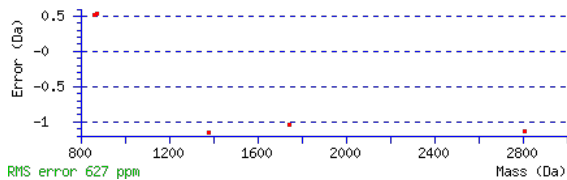
1 **M**Q**S**R**L**S**D**W**L**V **K**HELVHRS**L**G FDYQGI**T**LQ IK**T**EDWDS**I**A VISI**Y**IGY**N**Y  
 51 LRSQ**C**AYD**V**A PGGFLAS**V**YH L**T**RIQ**Y**GID**K** **V**EV**C**L**K**V**F**V SRNN**P**RIP**S**V  
 101 FWI**W****S**AD**F**Q **E**RES**Y**D**L**GI **S**Y**A**N**H**PH**L**K**R** IL**M**PE**S**WIG**W** PL**R**K**D**Y**I**T**P**N  
 151 **F**Y**E**I**Q**D**A**R

Unformatted sequence string: **158 residues** (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	M	Peptide
1 - 11	1377.5544	1376.5471	1377.7075	-1.1603	1	<b>-.M</b> <u>Q</u> <b>S</b> <u>R</u> <b>L</b> <u>S</u> <b>D</b> <u>W</u> <b>L</b> <u>V</u> <b>K</b> <b>.H</b> + Oxidation (M)
5 - 11	861.0104	860.0032	859.4803	0.5228	0	<b>R</b> <b>.L</b> <u>S</u> <b>D</b> <u>W</u> <b>L</b> <u>V</u> <b>K</b> <b>.H</b>
81 - 87	876.9842	875.9769	875.4422	0.5347	0	<b>K</b> <b>.V</b> EV <b>C</b> L <b>K</b> <b>.V</b>
106 - 129	2807.1607	2806.1534	2807.2973	-1.1439	1	<b>K</b> <b>.S</b> AD <b>F</b> Q <b>E</b> RES <b>Y</b> D <b>L</b> GI <b>S</b> Y <b>A</b> N <b>H</b> PH <b>L</b> K <b>.R</b>
145 - 158	1743.7824	1742.7752	1743.8104	-1.0352	0	<b>K</b> <b>.D</b> Y <b>I</b> T <b>P</b> N <b>F</b> Y <b>E</b> I <b>Q</b> D <b>A</b> R <b>.-</b>



## Protein View: NAK\_ARATH

Probable serine/threonine-protein kinase NAK OS=Arabidopsis thaliana GN=NAK PE=2 SV=2

Database: SwissProt  
 Score: 66  
 Expect: 0.0089  
 Nominal mass (M<sub>r</sub>): 43734  
 Calculated pI: 9.28  
 Taxonomy: Arabidopsis thaliana

Sequence similarity is available as [an NCBI BLAST search of NAK\\_ARATH against nr.](#)

### Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.  
 Fixed modifications: Carbamidomethyl (C)  
 Variable modifications: Oxidation (M)  
 Mass values searched: 6  
 Mass values matched: 6

### Protein sequence coverage: 19%

Matched peptides shown in **bold red**.

```

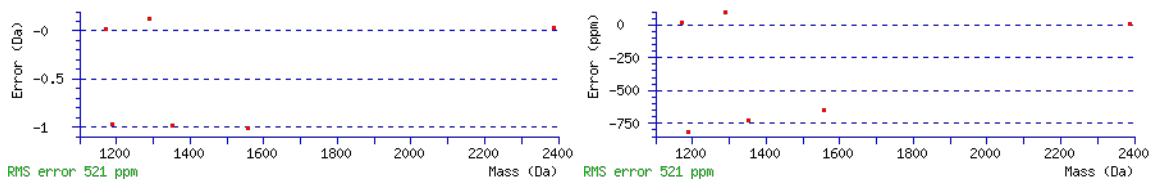
1  MGGCFSNRIK TDIASSTWLS SKFLSRDGSK GSSTASFSYM PRTEGEILQN
51 ANLKNFSLSE LKSATRNFRP DSVVGEGGFG CVFKGWIDES SLAPSKPGTG
101 IVIAVKRLNQ EGFQGHREW L AEINYLGGQLD HPNLVKLIGY CLEEEHRLLV
151 YEFMTRGSLE NHLFRRGTFY QPLSWNTRVR MALGAARGLA FLHNAQPQVI
201 YRDFKASNIL LDSNYNAKLS DFGLARDGPM GDNSHVSTRV MGTQGYAAPE
251 YLATGHLSVK SDVYSFGVVL LELLSGRRAI DKNQPVGEHN LVDWARPYLT
301 NKRLLLRVMD PRLQGGYSLT RALKI AVLAL DCISIDAKSR PTMNEIVKTM
351 EELHIQKEAS KEQQNPQISI DNIINKSPQA VNYPRPSIM
    
```

Unformatted sequence string: **389 residues** (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
31 - 42	1290.7072	1289.6999	1289.5710	0.1289 0	<b>K.GSSTASFSYMPR.T</b>
55 - 66	1351.7304	1350.7231	1351.7095	-0.9864 1	<b>K.NFSLSELKSATR.N</b>
63 - 84	2387.1820	2386.1747	2386.1488	0.0259 1	<b>K.SATRNFPRDSVVGEGGFGCVFK.G</b>
148 - 156	1171.6422	1170.6350	1170.6107	0.0243 0	<b>R.LLVYEFMTR.G</b>
339 - 348	1189.6494	1188.6422	1189.6125	-0.9703 0	<b>K.SRPTMNEIVK.T + Oxidation (M)</b>
349 - 361	1558.7590	1557.7518	1558.7661	-1.0143 1	<b>K.TMEELHIQKEASK.E + Oxidation (M)</b>



## Protein View: IPT8\_ARATH

Adenylate isopentenyltransferase 8, chloroplastic OS=Arabidopsis thaliana GN=IPT8 PE=2 SV=1

Database: SwissProt  
 Score: 74  
 Expect: 0.0012  
 Nominal mass (M<sub>r</sub>): 37583  
 Calculated pI: 8.18  
 Taxonomy: [Arabidopsis thaliana](#)

Sequence similarity is available as [an NCBI BLAST search of IPT8\\_ARATH against nr.](#)

### Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.  
 Fixed modifications: [Carbamidomethyl \(C\)](#)  
 Variable modifications: [Oxidation \(M\)](#)  
 Mass values searched: 6  
 Mass values matched: 6

### Protein sequence coverage: 29%

Matched peptides shown in **bold red**.

```

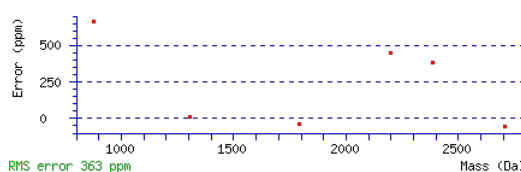
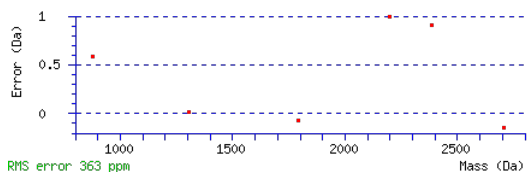
1  MQNLTSTFVS  PSMIPITSPR  LRLPPPRSVV  PMTTVCMEQS  YKQKVVVIMG
51  ATGSGKSCLS  IDLATRFSGE  IVNSDKIQFY  DGLKVTTNQM  SILERCQVPH
101 HLGELPPDD  SELTSEFRS  LASRSISEIT  ARGNLPPIAG  GSNSFIHALL
151  VDRFDPKTYP  FSSETSISSG  LRYECCFLWV  DVSVSVLF EY  LSKRVDQMME
201  SGMFEELAGF  YDPRYSGSAT  RAHGIHKTIG  IPEFDRYFSL  YPPERKQKMS
251  EWDQARKGAY  DEAVQEIKEN  TWRLAKKQIE  RIMKLGSSGW  DIQRLDATPS
301  FGRSSREIWD  NTVLDESIVK  VKRFLVKDKV
    
```

Unformatted sequence string: **330 residues** (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	M	Peptide
<b>28 - 42</b>	<b>1791.7308</b>	<b>1790.7235</b>	<b>1790.7889</b>	<b>-0.0654</b>	<b>0</b>	<b>R.SVVPMTTVCMEQSYK.Q + 2 Oxidation (M)</b>
<b>85 - 95</b>	<b>1307.6730</b>	<b>1306.6657</b>	<b>1306.6551</b>	<b>0.0106</b>	<b>0</b>	<b>K.VTTNQMSILER.C + Oxidation (M)</b>
<b>96 - 119</b>	<b>2706.1347</b>	<b>2705.1275</b>	<b>2705.2755</b>	<b>-0.1481</b>	<b>0</b>	<b>R.CGVPHLLGELPPDDSELTSEFR.S</b>
<b>125 - 132</b>	<b>877.0592</b>	<b>876.0519</b>	<b>875.4712</b>	<b>0.5807</b>	<b>0</b>	<b>R.SISEITAR.G</b>
<b>195 - 214</b>	<b>2384.8911</b>	<b>2383.8838</b>	<b>2382.9807</b>	<b>0.9032</b>	<b>0</b>	<b>R.VDQMMESGMFEELAGFYDPR.Y + 2 Oxidation (M)</b>
<b>228 - 245</b>	<b>2201.1019</b>	<b>2200.0947</b>	<b>2199.1000</b>	<b>0.9946</b>	<b>1</b>	<b>K.TIGIPEFDRYFSLYPPER.K</b>



## Protein View: LIAS\_MEDTR

Lipoyl synthase, mitochondrial OS=Medicago truncatula GN=LIP1 PE=2 SV=1

**Database:** SwissProt  
**Score:** 99  
**Expect:** 4.1e-006  
**Nominal mass (M<sub>r</sub>):** 42342  
**Calculated pI:** 8.75  
**Taxonomy:** Medicago truncatula

Sequence similarity is available as [an NCBI BLAST search of LIAS\\_MEDTR against nr.](#)

### Search parameters

**Enzyme:** Trypsin: cuts C-term side of KR unless next residue is P.  
**Fixed modifications:** Carbamidomethyl (C)  
**Variable modifications:** Oxidation (M)  
**Mass values searched:** 10  
**Mass values matched:** 10

### Protein sequence coverage: 32%

Matched peptides shown in **bold red**.

```

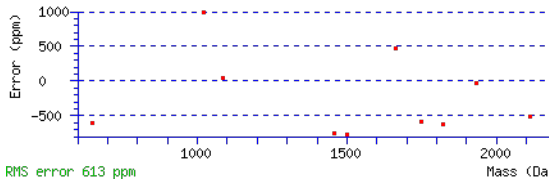
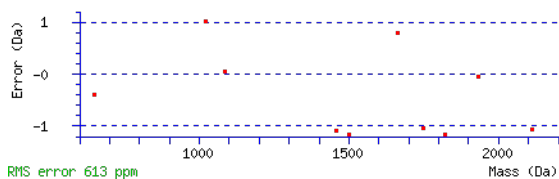
1  MMYSRFRTVA KNLKSTTKPF SFTTATTTTT VSSSEFPQNL TELRARLARE
51 SPSLSDFISL KSNNAYSVEV GTKKNPLPKP KWMESIPGG WKYVQIKKKL
101 RELKLHTVCE EAKCPNMGEC WSGGETGTAT ATIMILGDTC TRGCRFCNVK
151 TSTRTPPPDP DEPTNVAEAI ASWGLDYVVI TSVGRDDLDP QGSSHFTETV
201 QKLKILKPSI LIEALVPDFR GNAECVEKVS KSLGLDVFAHN IETVEELQSA
251 VRDHRANFNQ SLDVLRMAKD YAPAGTLTKT SIMLGCGETP DQIVKTMEKV
301 RAAGVDVMTF QYMRPSKRH MPVSEYITPE AFEKYQLGM EMGFRYVASG
351 PMVRSSYKAG EFYIKSMIDS DRAVSSQS
    
```

Unformatted sequence string: **378 residues** (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	M	Peptide
1 - 7	1023.4691	1022.4619	1021.4473	1.0145	1	<b>-.MMYSRFR.T + 2 Oxidation (M)</b>
47 - 61	1663.6923	1662.6850	1661.8988	0.7862	1	<b>R.LARESPLSDFISLK.S</b>
85 - 97	1503.6427	1502.6355	1503.8085	-1.1731	1	<b>K.ESIPGGWKYVQIK.K</b>
93 - 97	649.9932	648.9859	649.3799	-0.3939	0	<b>K.YVQIK.K</b>
105 - 113	1086.5785	1085.5712	1085.5175	0.0536	0	<b>K.LHTVCEAK.C</b>
205 - 220	1822.9480	1821.9407	1823.0920	-1.1513	0	<b>K.ILKPSILIEALVPDFR.G</b>
280 - 295	1747.8230	1746.8157	1747.8485	-1.0328	0	<b>K.TSIMLGCGETPDQIVK.T</b>
300 - 318	2111.9953	2110.9880	2112.0609	-1.0728	1	<b>K.VRAAGVDVMTFFGQYMRPSK.R</b>
319 - 334	1933.8961	1932.8889	1932.9404	-0.0515	1	<b>K.RHMPVSEYITPEAFEK.Y</b>
346 - 358	1459.6253	1458.6180	1459.7129	-1.0950	1	<b>R.YVASGPMVRSSYK.A + Oxidation (M)</b>





## Protein View: LISC\_RICCO

Lipoyl synthase, chloroplastic OS=Ricinus communis GN=LIP1P PE=3 SV=1

Database: SwissProt  
 Score: 63  
 Expect: 0.018  
 Nominal mass (M<sub>r</sub>): 40734  
 Calculated pI: 7.59  
 Taxonomy: Ricinus communis

Sequence similarity is available as [an NCBI BLAST search of LISC\\_RICCO against nr.](#)

### Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.  
 Fixed modifications: Carbamidomethyl (C)  
 Variable modifications: Oxidation (M)  
 Mass values searched: 5  
 Mass values matched: 5

### Protein sequence coverage: 25%

Matched peptides shown in **bold red**.

```

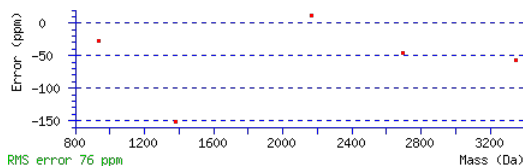
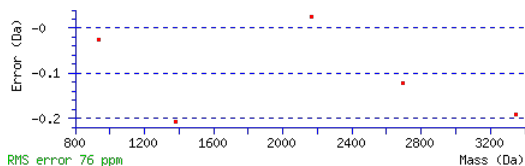
1  MEQTLFNPSI SMPKSFYHKH ITISSRIQQQ LSTNSPSSNT KTTTVVPSK
51  KTMGPYTG RD PNVKKEWLR QRAPQGERFQ EVKHSLSLKL LNTVCEEAQC
101 PNIGECWNGG GDGIATATIM LLGDTCTGRG RFCAVKTSRN PSPDPLEPQ
151 NTALAIASWG VDYIVLTSVD RDDLPDGGSG HFSETVQAMK KKKPEIMVEC
201 LTSDFRGDLE AVETLVHSGL DVFAHNIETV KRLQRIVRDP RAGYEQSLSV
251 LKHAKHSKEG MITKSSIMLG LGETDDELKE AMADLRAIDV DILTLGQYLQ
301 PTPHLHLTVKE YVTPEKFAFW KEYGESIGFR YVASGPMVRS SYRAGELFVK
351 TMVKERSNSNS AAKP
    
```

Unformatted sequence string: **364 residues** (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	M	Peptide
2 - 19	2170.0882	2169.0809	2169.0565	0.0245	1	<b>M.EQTLFNPSISMPKSFYHK.H + Oxidation (M)</b>
42 - 50	933.4996	932.4923	932.5179	-0.0256	0	<b>K.TTTTVVPSK.K</b>
60 - 70	1381.5494	1380.5421	1380.7514	-0.2092	1	<b>R.DPNVKKPEWLR.Q</b>
207 - 231	2693.2559	2692.2487	2692.3708	-0.1222	0	<b>R.GDLEAVETLVHSGLDVFAHNIETVK.R</b>
280 - 309	3350.6123	3349.6050	3349.7955	-0.1905	1	<b>K.EAMADLRAIDVDILTLGQYLQPTPLHLTVK.E + Oxidation (M)</b>



## Protein View: ATPB\_NICBI

ATP synthase subunit beta, chloroplastic OS=Nicotiana bigelovii GN=atpB PE=3 SV=1

**Database:** SwissProt  
**Score:** 87  
**Expect:** 6.9e-005  
**Nominal mass (M<sub>r</sub>):** 53549  
**Calculated pI:** 5.09  
**Taxonomy:** Nicotiana quadrivalvis var. bigelovii

Sequence similarity is available as [an NCBI BLAST search of ATPB\\_NICBI against nr.](#)

### Search parameters

**Enzyme:** Trypsin: cuts C-term side of KR unless next residue is P.  
**Fixed modifications:** Carbamidomethyl (C)  
**Variable modifications:** Oxidation (M)  
**Mass values searched:** 19  
**Mass values matched:** 11

### Protein sequence coverage: 37%

Matched peptides shown in **bold red**.

```

1 MRINPTTSGS GVSTLEKKNP GRVVQIIGPV LDVAFPPGKM FNIYNALVVQ
51 GRDSVGGPIN VACEVQQLG NNRVRVAVMS ATDGLTRGME VIDTGAPISV
101 PVGGATLGRI FNVLGEPVDN LGPVDTSTTS PIHRSAPAFI QLDTKLSIFE
151 TGIKVVDDLLA PYRRGGKIGL FGGAGVGKTV LIMELINNIA KAHGGVSVFVG
201 GVGERTREGN DLYMEMKESG VINEENIAES KVALVYQGMN EPPGARMRVG
251 LTALTMAEYF RDVNEQDVLL FIDNIFRFVQ AGSEVSALLG RMPSAVGYQP
301 TLSTEMGSLQ ERITSTKEGS ITSIQAVYVF ADDLTDPAFA TTFAHLDTATT
351 VLSRGLAAGK IYPAVDPLDS TSTMLQPRIV GEEHYETAQR VKQTLQRYKE
401 LQDIITAILGL DELSEEDRLL VARARKIERF LSQPFVFAEV FTGSPGKYVG
451 LAETIRGFQL ILSGELDGLP EQAFYLVGNI DEATAKAMNL EMESNLKK
    
```

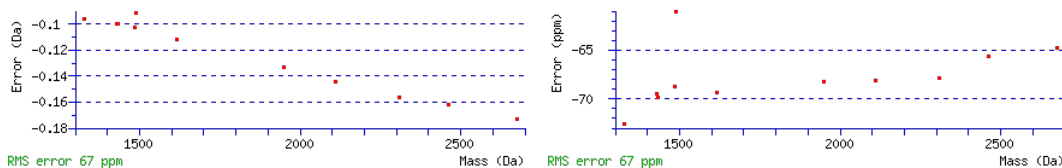
Unformatted sequence string: **498 residues** (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	M	Peptide
3 - 17	1490.6787	1489.6714	1489.7624	-0.0910	0	<b>R. INPTTSGSGVSTLEK.K</b>
53 - 73	2310.9892	2309.9820	2310.1386	-0.1567	0	<b>R. DSVGGPINVACEVQQLGNNR.V</b>
88 - 109	2112.9519	2111.9446	2112.0885	-0.1439	0	<b>R. GMEVIDTGAPISVPVGGATLGR.I + Oxidation (M)</b>
110 - 134	2678.2050	2677.1977	2677.3712	-0.1735	0	<b>R. IFNVLGEPVDNLGPDVDTSTTSPIHR.S</b>
192 - 205	1328.5743	1327.5670	1327.6633	-0.0963	0	<b>K. AHGGVSVFVGGVGER.T</b>
232 - 246	1617.6932	1616.6859	1616.7981	-0.1121	0	<b>K. VALVYQGMNEPPGAR.M + Oxidation (M)</b>
249 - 261	1487.6541	1486.6468	1486.7490	-0.1022	0	<b>R. VGLTALTMAEYFR.D + Oxidation (M)</b>
262 - 277	1949.8638	1948.8566	1948.9894	-0.1329	0	<b>R. DVNEQDVLFFIDNIFR.F</b>
278 - 291	1433.6746	1432.6673	1432.7674	-0.1001	0	<b>R. FVQAGSEVSALLGR.M</b>
379 - 390	1431.5868	1430.5795	1430.6790	-0.0995	0	<b>R. IVGEEHYETAQR.V</b>
398 - 418	2462.1044	2461.0972	2461.2587	-0.1616	1	<b>R. YKELQDIITAILGLDELSEDR.L</b>

No match to: 1390.5866, 1399.6678, 1864.8168, 2185.9971, 2239.0369, 2269.0675, 2329.9661, 2988.4009





# MASCOT Search Results

## Protein View: ATPE\_ATRBE

ATP synthase epsilon chain, chloroplastic OS=Atropa belladonna GN=atpE PE=3 SV=1

Database: SwissProt

Score: 82

Expect: 0.00023

Monoisotopic mass ( $M_r$ ): 14588

Calculated pI: 5.18

Taxonomy: [Atropa belladonna](#)

Sequence similarity is available as [an NCBI BLAST search of ATPE\\_ATRBE against nr](#).

### Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.

Fixed modifications: [Carbamidomethyl \(C\)](#)

Variable modifications: [Oxidation \(M\)](#)

Mass values searched: 5

Mass values matched: 5

### Protein sequence coverage: 45%

Matched peptides shown in **bold red**.

1 MTLNLSVLTP NRIVWDSEVE EIVLSTNSGQ IGILSNHAPI ATAVDIGILR  
51 IRLNDQWLTM ALMGGFARIG NNEITVLVND AEKGSDDIDPQ EAQQTLEIAE  
101 ANVKKAEGRR QKIEANLALR RARTRVEAIN PIS

Unformatted sequence string: [133 residues](#) (for pasting into other applications).

Sort by  residue number  increasing mass  decreasing mass

Show  matched peptides only  predicted peptides also

Start	End	Observed	Mr(expt)	Mr(calc)	Delta	M	Peptide
53	68	1855.8178	1854.8105	1854.8757	-0.0652	0	R.LNDQWLTMALMGGFAR.I + 2 Oxidation (M)
69	83	1629.7796	1628.7723	1627.8417	0.9306	0	R.IGNNEITVLVNDAEK.G
84	104	2256.9879	2255.9806	2255.0917	0.8889	0	K.GSDIDPQEAQQTLEIAEANVK.K
84	105	2384.8405	2383.8333	2383.1867	0.6466	1	K.GSDIDPQEAQQTLEIAEANVKK.A
113	120	899.4946	898.4873	898.5236	-0.0363	0	K.IEANLALR.R

# Protein View: STAD2\_ARATH

**Stearoyl-[acyl-carrier-protein] 9-desaturase 2, chloroplastic**  
**OS=Arabidopsis thaliana GN=S-ACP-DES2 PE=1 SV=1**

**Database:** SwissProt  
**Score:** 84  
**Expect:** 0.00015  
**Monoisotopic mass (M<sub>r</sub>):** 47149  
**Calculated pI:** 5.87  
**Taxonomy:** [Arabidopsis thaliana](#)

Sequence similarity is available as [an NCBI BLAST search of STAD2\\_ARATH against nr.](#)

## Search parameters

**Enzyme:** Trypsin: cuts C-term side of KR unless next residue is P.  
**Fixed modifications:** [Carbamidomethyl \(C\)](#)  
**Variable modifications:** [Oxidation \(M\)](#)  
**Mass values searched:** 8  
**Mass values matched:** 8

## Protein sequence coverage: 25%

Matched peptides shown in **bold red**.

```
1 MALLLNSTIT VAMKQNPLVA VSPRTTCLG SSFSPPRLLR VSCVATNPSK
51 TSEETDKKKF RPIKEVPNQV THTITQEKLE IFKSMENWAQ ENLLSYLKPV
101 EASWQPQDFL PETNDEDRFY EQVKELRDRT KEIPDDYFVV LVGDMITEEA
151 LPTYQTTLNT LDGVKDETGG SLTPWAVWVR AWTAEENRHG DLLNKYLYLS
201 GRVDMRHVEK TIQYLIGSGM DSKFENNPYN GFIYTSFQER ATFISHGNTA
251 KLATTYGDTT LAKICGTIAA DEKRHETAYT RIVEKLFEID PDGTVQALAS
301 MMRKRITMPA HLMHDGRDDD LFDHYAAVAQ RIGVYTATDY AGILEFLLRR
351 WEVEKLGMGL SGEGRRAQDY LCTLPQRIRR LEERANDRVK LASKSKPSVS
401 FSWIYGREVE L
```

Unformatted sequence string: [411 residues](#) (for pasting into other applications).

Sort by  residue number  increasing mass  decreasing mass  
Show  matched peptides only  predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	M	Peptide
2 - 25	2600.2805	2599.2732	2598.4567	0.8165	1	M.A <b>LLLNSTITVAMKQNPLVA</b> V <b>SPR</b> .T + Oxidation (M)
26 - 40	1690.7341	1689.7269	1690.8825	-1.1556	1	R.T <b>TCLGSS</b> F <b>SP</b> PRLLR.V
79 - 83	650.0027	648.9954	648.3846	0.6108	0	K.L <b>E</b> IFK.S
125 - 129	687.9616	686.9543	687.3664	-0.4121	1	K.E <b>L</b> RDR.T
275 - 281	876.9872	875.9800	876.4090	-0.4290	0	R.H <b>E</b> TAYTR.I
286 - 303	1994.8447	1993.8374	1992.9649	0.8725	0	K.L <b>F</b> EID <b>PDGTVQALAS</b> MMR.K
351 - 365	1663.7252	1662.7180	1662.8035	-0.0856	1	R.W <b>E</b> VEK <b>LGMGLS</b> GEGR.R + Oxidation (M)
391 - 407	1913.9026	1912.8953	1912.0207	0.8747	1	K.L <b>A</b> SKSKPSV <b>S</b> F <b>S</b> WIYGR.E

**Protein View: KCS14\_ARATH**

**Probable 3-ketoacyl-CoA synthase 14 OS=Arabidopsis thaliana GN=KCS14 PE=2 SV=1**

**Database:** SwissProt  
**Score:** 66  
**Expect:** 0.0095  
**Monoisotopic mass (M<sub>r</sub>):** 52163  
**Calculated pI:** 9.18  
**Taxonomy:** Arabidopsis thaliana

Sequence similarity is available as [an NCBI BLAST search of KCS14 ARATH against nr.](#)

**Search parameters**

**Enzyme:** Trypsin: cuts C-term side of KR unless next residue is P.  
**Fixed modifications:** Carbamidomethyl (C)  
**Variable modifications:** Oxidation (M)  
**Mass values searched:** 6  
**Mass values matched:** 6

**Protein sequence coverage: 19%**

Matched peptides shown in **bold red**.

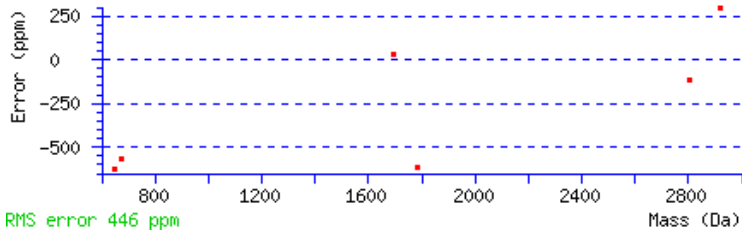
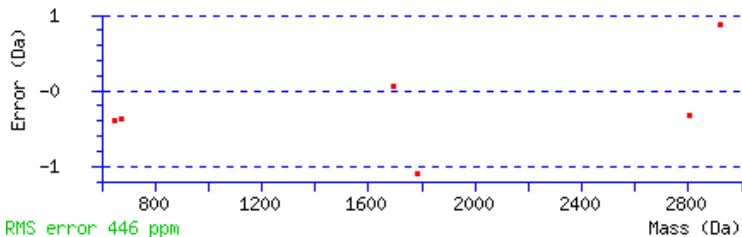
```

1 MFIAMADFKL LLLILILLSL FELDLLHFHH DFFSPFPVKI GLLLISIFFY
51 AYSTTRSKPV YLVDFSCHQP TDSCKISSET FFNMAKGAQL YTEETIQFMT
101 RILNRSGLGD DTYSRPCMLT SPPTPSMYEA RHESELVIFG ALNSLFKKTG
151 IEPREVGIFI VNCSLFNPNP SLSSMIVNRY KLKTDVKTYN LSGISVDLAT
201 NLLKANPNTY AVIVSTENMT LSMYRGNDRS MLVPNCLEFRV GGAAVMLSNR
251 SQDRVRSKYE LTHIVRTHKG SSDKHYTCAE QKEDSKGIVG VALSKELTVV
301 AGDTLKTNLT ALGPLVLPLS EKLRFILFLV KSKLFRLKVS PYVPDFKLCF
351 KHFCIHAGGR ALLDAVEKGL GLSEFDLEPS RMTLHRFGNT SSSSLWYELA
401 YVEAKCRVKR GDRVWQLAFG SGFKCNSIVW RALRTIPANE SLVGNPWGDS
451 VHKEYPVHVT
  
```

Unformatted sequence string: **459 residues** (for pasting into other applications).

Sort by  residue number     increasing mass     decreasing mass  
 Show  matched peptides only     predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	M	Peptide
87 - 101	1786.7644	1785.7571	1786.8560	-1.0989	0	<b>K.GAQLYTEETIQFMTR.I</b>
106 - 131	2922.1500	2921.1427	2920.2677	0.8750	1	R.SGLGDD <b>TYSPRCMLTSPPTPSMYEAR.H</b> + 2 Oxidation (M)
149 - 154	671.9854	670.9781	671.3602	-0.3821	0	<b>K.TGIEPR.E</b>
155 - 179	2807.0928	2806.0855	2806.4146	-0.3291	0	R.EVGIFIV <b>VNCSLFNPNP</b> SLSSMIVNR.Y
226 - 239	1694.8586	1693.8513	1693.8028	0.0485	1	R. <b>GNDRSMLVPNCLEFR.V</b> + Oxidation (M)
332 - 336	649.9925	648.9853	649.3911	-0.4059	1	<b>K.SKLEFR.L</b>




---

ID KCS14\_ARATH Reviewed; 459 AA.  
AC Q9SS39;  
DT 05-SEP-2006, integrated into UniProtKB/Swiss-Prot.  
DT 01-MAY-2000, sequence version 1.  
DT 15-FEB-2017, entry version 102.  
DE RecName: Full=Probable 3-ketoacyl-CoA synthase 14 {ECO:0000303|PubMed:18465198};  
DE Short=KCS-14 {ECO:0000303|PubMed:18465198};  
DE EC=2.3.1.199 {ECO:0000305};  
DE AltName: Full=Very long-chain fatty acid condensing enzyme 14 {ECO:0000303|PubMed:18465198};  
DE Short=VLCFA condensing enzyme 14 {ECO:0000303|PubMed:18465198};  
DE Flags: Precursor;  
GN Name=KCS14 {ECO:0000303|PubMed:18465198};  
GN OrderedLocusNames=At3g10280 {ECO:0000312|Araport:AT3G10280};  
GN ORFNames=F14P13.12 {ECO:0000312|EMBL:AAF02814.1};  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;  
OC Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Camelineae;  
OC Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=cv. Columbia;  
RX PubMed=11130713; DOI=10.1038/35048706;  
RA Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,  
RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,  
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,  
RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,  
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,  
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,  
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,  
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,  
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,  
RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,  
RA Reichelt J., Scharfe M., Schoen O., Barges M., Terol J., Climent J.,  
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,  
RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,  
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,  
RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,  
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,  
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,  
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,  
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,  
RA Pal G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,  
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,  
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,  
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,  
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,  
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;  
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis  
thaliana."  
RL Nature 408:820-822 (2000).  
RN [2]  
RP GENOME REANNOTATION.  
RC STRAIN=cv. Columbia;  
RG The Arabidopsis Information Resource (TAIR);  
RL Submitted (APR-2011) to the EMBL/GenBank/DBJ databases.

RN [3]  
RP INDUCTION, AND GENE FAMILY.  
RX PubMed=12916765; DOI=10.1002/ps.714;  
RA Lechelt-Kunze C., Meissner R.C., Drewes M., Tietjen K.;  
RT "Flufenacet herbicide treatment phenocopies the fiddlehead mutant in  
RT Arabidopsis thaliana.";  
RL Pest Manag. Sci. 59:847-856(2003).  
RN [4]  
RP GENE FAMILY, NOMENCLATURE, 3D-STRUCTURE MODELING, AND TISSUE  
RP SPECIFICITY.  
RX PubMed=18465198; DOI=10.1007/s11103-008-9339-z;  
RA Joubes J., Raffaele S., Bourdenx B., Garcia C., Laroche-Traineau J.,  
RA Moreau P., Domergue F., Lessire R.;  
RT "The VLCFA elongase gene family in Arabidopsis thaliana: phylogenetic  
RT analysis, 3D modelling and expression profiling.";  
RL Plant Mol. Biol. 67:547-566(2008).  
CC -!- CATALYTIC ACTIVITY: A very-long-chain acyl-CoA + malonyl-CoA = CoA  
CC + a very-long-chain 3-oxoacyl-CoA + CO(2). {ECO:0000305}.  
CC -!- PATHWAY: Lipid metabolism; fatty acid biosynthesis.  
CC -!- SUBCELLULAR LOCATION: Membrane {ECO:0000255}; Single-pass membrane  
CC protein {ECO:0000255}.  
CC -!- TISSUE SPECIFICITY: Expressed in siliques.  
CC {ECO:0000269|PubMed:18465198}.  
CC -!- INDUCTION: Repressed by herbicides such as flufenacet and  
CC benfuresate. {ECO:0000269|PubMed:12916765}.  
CC -!- SIMILARITY: Belongs to the chalcone/stilbene synthases family.  
CC {ECO:0000305}.  
DR EMBL; AC009400; AAF02814.1; -; Genomic\_DNA.  
DR EMBL; CP002686; AEE74883.1; -; Genomic\_DNA.  
DR RefSeq; NP\_187639.1; NM\_111863.2.  
DR UniGene; At.36468; -.  
DR UniGene; At.50165; -.  
DR ProteinModelPortal; Q9SS39; -.  
DR STRING; 3702.AT3G10280.1; -.  
DR PaxDb; Q9SS39; -.  
DR EnsemblPlants; AT3G10280.1; AT3G10280.1; AT3G10280.  
DR GeneID; 820190; -.  
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DR KEGG; ath:AT3G10280; -.  
DR Araport; AT3G10280; -.  
DR TAIR; locus:2076254; AT3G10280.  
DR eggNOG; ENOG410JWTH; Eukaryota.  
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DR HOGENOM; HOG000238893; -.  
DR InParanoid; Q9SS39; -.  
DR KO; K15397; -.  
DR OrthoDB; EOG093606UZ; -.  
DR PhylomeDB; Q9SS39; -.  
DR UniPathway; UPA00094; -.  
DR PRO; PR:Q9SS39; -.  
DR Proteomes; UP000006548; Chromosome 3.  
DR Genevisible; Q9SS39; AT.  
DR GO; GO:0016021; C:integral component of membrane; IEA:UniProtKB-KW.  
DR GO; GO:0102336; F:3-oxo-arachidoyl-CoA synthase activity; IEA:UniProtKB-EC.  
DR GO; GO:0102337; F:3-oxo-cerotoyl-CoA synthase activity; IEA:UniProtKB-EC.  
DR GO; GO:0102338; F:3-oxo-lignoceroaryl-CoA synthase activity; IEA:UniProtKB-EC.  
DR GO; GO:0006633; P:fatty acid biosynthetic process; IEA:UniProtKB-UniPathway.  
DR Gene3D; 3.40.47.10; -; 2.  
DR InterPro; IPR012392; 3-ktacl-CoA\_syn.  
DR InterPro; IPR013747; ACP\_syn\_III\_C.  
DR InterPro; IPR013601; FAEL\_typ3\_polyketide\_synth.  
DR InterPro; IPR016039; Thiolase-like.  
DR PANTHER; PTHR31561; PTHR31561; 1.  
DR Pfam; PF08541; ACP\_syn\_III\_C; 1.  
DR Pfam; PF08392; FAEL\_CUT1\_RppA; 1.  
DR PIRSF; PIRSF036417; 3-ktacl-CoA\_syn; 1.  
DR SUPFAM; SSF53901; SSF53901; 2.  
PE 2: Evidence at transcript level;  
KW Acyltransferase; Complete proteome; Membrane; Reference proteome;  
KW Signal; Transferase; Transmembrane; Transmembrane helix.  
FT SIGNAL 1 25 {ECO:0000255}.  
FT CHAIN 26 459 Probable 3-ketoacyl-CoA synthase 14.  
FT /FTid=PRO\_0000249106.  
FT TRANSMEM 32 52 Helical. {ECO:0000255}.  
FT DOMAIN 52 334 FAE. {ECO:0000255}.  
FT ACT\_SITE 268 268 {ECO:0000250|UniProtKB:Q38860}.  
FT ACT\_SITE 352 352 {ECO:0000250|UniProtKB:Q38860}.  
FT ACT\_SITE 356 356 {ECO:0000250|UniProtKB:Q38860}.  
FT ACT\_SITE 385 385 {ECO:0000250|UniProtKB:Q38860}.  
FT ACT\_SITE 389 389 {ECO:0000250|UniProtKB:Q38860}.  
SQ SEQUENCE 459 AA; 51626 MW; 1307C2E49C34C509 CRC64;  
MFIAMADFKL LLLLILLLSL FELDLLHFHH DFFSFPVKI GLLLLISIFFY AYSTTRSKPV

YLVDFSCHQP TDSCKISSET FFNMAKGAQL YTEETIQFMT RILNRSLGSD DTYSRCMLT  
SPPTPSMYEA RHESELVIFG ALNSLFKKTG IEPREVGIFI VNCSLFNPNP SLSSMIVNRY  
KLKTDVKTYN LSGISVDLAT NLLKANPNTY AVIVSTENMT LSMYRGNDRS MLVENCLEFRV  
GGAAVMLSNR SQDRVRSKYE LTHIVRTHKG SSDKHYTCAE QKEDSKGIVG VALSKELTVV  
AGDTLKTNLT ALGPLVLPLS EKLRFILFLV KSKLFRLKVS PYVPDFKLCF KHFCIHAGGR  
ALLDAVEKGL GLSEFDLEPS RMTLHRFGNT SSSSLWYELA YVEAKCRVKR GDRVWQLAFG  
SGFKCNSIVW RALRTIPANE SLVGNPWGDS VHLYPVHVT

**Mascot: <http://www.matrixscience.com/>**



## Protein View: K6PF4\_ARATH

6-phosphofructokinase 4, chloroplastic OS=Arabidopsis thaliana GN=PFK4 PE=1 SV=1

Database: SwissProt  
 Score: 70  
 Expect: 0.0038  
 Nominal mass (M<sub>r</sub>): 58886  
 Calculated pI: 8.46  
 Taxonomy: [Arabidopsis thaliana](#)

Sequence similarity is available as [an NCBI BLAST search of K6PF4\\_ARATH against nr.](#)

### Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.  
 Fixed modifications: [Carbamidomethyl \(C\)](#)  
 Variable modifications: [Oxidation \(M\)](#)  
 Mass values searched: 6  
 Mass values matched: 6

### Protein sequence coverage: 22%

Matched peptides shown in **bold red**.

```

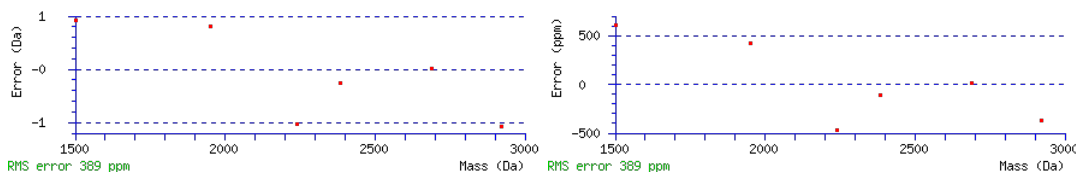
1  MEASISFLGS TKNPISLFPN SSNVLPPRDF PLPALKLKKV SVLPRLHQK
51 RLIRAQCSGDG FKPEEDDGFV LEDVPHLTKF LPDLPSYPNP LKESQAYAIV
101 KRTEFVSSQDV VAQNIVVQKG SKRGVHFERRA GPRERVYFRS DEVKACIVTC
151 GGLCPGINTV IREIVCGLNN MYGVNINLGI QGGYRGFYSK NTMNLTPKVV
201 NDIHKRGGTF LQTSRGGHDT AKIVDNIQDR GINQVYIIGG GGTQKGAEKI
251 YEEVERRGLQ VAVSGIPKTI DNDIAVIDKS FGFDTAVEEA QRAINAAHVE
301 VESVENGVGI VKLMGRYSGF IAMIATLANR DVDCLIPES PFFLEGGKGL
351 FEFIEERLKE NRHMVIVIAE GAGQDYVAQS MRASETKDAS GNRLLLDVGL
401 WLTQQIKDHF TNVRKMMINM KYIDPTYMIR AIPSNASDNV YCTLLAQSAV
451 HGAMAGYSGF TVGPNNSRHA YIPISQVTEV TNTVKLTDRM WARLLASTNQ
501 PSFLTGEAL QNVIDMETQE KIDNMKISSI
    
```

Unformatted sequence string: [530 residues](#) (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
<b>1 - 27</b>	<b>2921.4328</b>	<b>2920.4255</b>	<b>2921.4957</b>	<b>-1.0701 0</b>	<b>-.MEASISFLGSTKPNISLFPNSSNVLP.R + Oxidation (M)</b>
<b>80 - 92</b>	<b>1501.7287</b>	<b>1500.7214</b>	<b>1499.8024</b>	<b>0.9190 0</b>	<b>K.FLPDLPSYPNPLK.E</b>
<b>363 - 387</b>	<b>2691.3465</b>	<b>2690.3392</b>	<b>2690.3156</b>	<b>0.0236 1</b>	<b>R.HMVIVIAEGAGQDYVAQSMRASET.K.D</b>
<b>388 - 407</b>	<b>2239.2031</b>	<b>2238.1958</b>	<b>2239.2325</b>	<b>-1.0367 1</b>	<b>K.DASGNRLLLDVGLWLTQQIK.D</b>
<b>416 - 430</b>	<b>1952.7327</b>	<b>1951.7255</b>	<b>1950.9075</b>	<b>0.8179 1</b>	<b>K.MMINMKYIDPTYMIR.A + 2 Oxidation (M)</b>
<b>469 - 489</b>	<b>2385.0147</b>	<b>2384.0074</b>	<b>2384.2700</b>	<b>-0.2626 1</b>	<b>R.HAYIPISQVTEVTNTVKLTDR.M</b>



## Actin-54 (Fragment) OS=Nicotiana tabacum PE=3 SV=1

Database: SwissProt

Score: 59

Expect: 0.05

Nominal mass ( $M_r$ ): 37521

Calculated pI: 5.66

Taxonomy: [Nicotiana tabacum](#)

Sequence similarity is available as [an NCBI BLAST search of ACT3\\_TOBAC against nr](#).

### Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.

Fixed modifications: [Carbamidomethyl \(C\)](#)

Variable modifications: [Oxidation \(M\)](#)

Mass values searched: 4

Mass values matched: 4

### Protein sequence coverage: 15%

Matched peptides shown in *bold red*.

1 AGFAGDDAPR AVFPSIVGRP RHTGVMVGMG QKDAYVGDEA QSKRGILTLK  
51 YPIEHGIASN WDDMEKI**WHH TFYNELRVAP** EEHPVLLTEA PLNPKANREK  
101 MTQIMFETFS VPAMYVAIQV VLSLYASGRT TGTGIVLDSG DGVSHHVPIY  
151 EGYALPHAIL RLDLAGRDLT **DSL**MKILTER **GYMFTTTAER** EIVRDMKEKL  
201 AYVALDYEQE LETARSSSI EKNYEL**PDGQ VITIGAERFR** CPEVLFQPSM  
251 IGMEAAGIHE TTYNSIMKRD VDIRKDLYGN IVLSGGSTMF PGIADRMSKE  
301 ITALAPSSMK IKVVAPPERK YSVWIGGSIL ASLSTLQQV

Unformatted sequence string: [339 residues](#) (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start	End	Observed $M_r$ (expt)	$M_r$ (calc)	Delta	M	Peptide	
67	-77	1515.6662	1514.6589	1514.7419	-0.0829	0	K.IWHHTFYNELR.V
162	-175	1547.6545	1546.6473	1546.8025	-0.1552	1	R.LDLAGRDLTDSL <b>MK.I</b>
181	-190	1192.4647	1191.4574	1191.5230	-0.0656	0	R.GYMFTTTAER.E + Oxidation (M)
223	-238	1774.8044	1773.7971	1773.8897	-0.0926	0	K.NYELPDGQ <b>VITIGAER.F</b>

## Protein View: EXB13\_ORYSJ

Expansin-B13 OS=*Oryza sativa* subsp. *japonica* GN=EXPB13 PE=3 SV=2

Database: SwissProt  
 Score: 83  
 Expect: 0.00016  
 Nominal mass (M<sub>r</sub>): 24653  
 Calculated pI: 5.55  
 Taxonomy: [Oryza sativa Japonica Group](#)

Sequence similarity is available as [an NCBI BLAST search of EXB13\\_ORYSJ against nr.](#)

### Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.  
 Fixed modifications: [Carbamidomethyl \(C\)](#)  
 Variable modifications: [Oxidation \(M\)](#)  
 Mass values searched: 6  
 Mass values matched: 6

### Protein sequence coverage: 39%

Matched peptides shown in **bold red**.

```

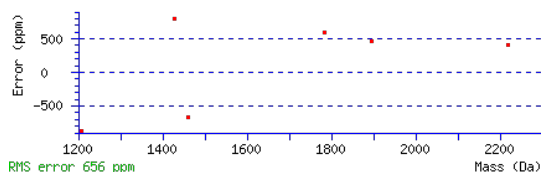
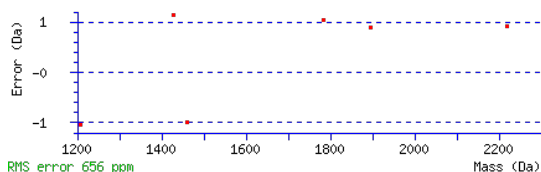
1 MASSSLLLAS VVVAAMVSAV SCGPPKVPPG PNITASYGDK WLEARATWYG
51 AARGAGRKDN SGACGYKDVD KAPFLGMNSC GNDPIFKDGK GCGSCFEIKC
101 SKPKACSDKP VLIHVTDMDN EPIAAYHFDL FGLAFGAMAK DGKDEELLYK
151 VAGDGDVVEV EIKEKGSEEW KALKESWGAI WRIDTPKPLK GPFSVRVTTE
201 GGEKIIAEDA IPDGWKADSV YKSNVQAK
    
```

Unformatted sequence string: **228 residues** (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	M	Peptide
<b>46 - 57</b>	<b>1207.5688</b>	<b>1206.5615</b>	<b>1207.6098</b>	<b>-1.0483</b>	<b>1</b>	<b>R.ATWYGAAKGAGR.K</b>
<b>59 - 71</b>	<b>1429.7513</b>	<b>1428.7441</b>	<b>1427.5987</b>	<b>1.1454</b>	<b>1</b>	<b>K.DNSGACGYKDVDK.A</b>
<b>72 - 87</b>	<b>1784.8570</b>	<b>1783.8497</b>	<b>1782.8069</b>	<b>1.0428</b>	<b>0</b>	<b>K.APFLGMNSCGNDPIFK.D + Oxidation (M)</b>
<b>144 - 163</b>	<b>2221.0446</b>	<b>2220.0374</b>	<b>2219.1209</b>	<b>0.9165</b>	<b>1</b>	<b>K.DEELLYKVVAGDGDVVEVEIK.E</b>
<b>175 - 190</b>	<b>1897.9271</b>	<b>1896.9198</b>	<b>1896.0257</b>	<b>0.8941</b>	<b>1</b>	<b>K.ESWGAIWRIDTPKPLK.G</b>
<b>191 - 204</b>	<b>1462.7648</b>	<b>1461.7575</b>	<b>1462.7416</b>	<b>-0.9841</b>	<b>1</b>	<b>K.GPFSVRVTTEGGEK.I</b>



## Protein View: VPS36\_ARATH

Vacuolar protein sorting-associated protein 36 OS=Arabidopsis thaliana GN=VPS36 PE=1 SV=1

Database: SwissProt  
 Score: 69  
 Expect: 0.0047  
 Nominal mass (M<sub>r</sub>): 49231  
 Calculated pI: 5.54  
 Taxonomy: [Arabidopsis thaliana](#)

Sequence similarity is available as [an NCBI BLAST search of VPS36\\_ARATH against nr.](#)

### Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.  
 Fixed modifications: [Carbamidomethyl \(C\)](#)  
 Variable modifications: [Oxidation \(M\)](#)  
 Mass values searched: 6  
 Mass values matched: 6

### Protein sequence coverage: 27%

Matched peptides shown in **bold red**.

```

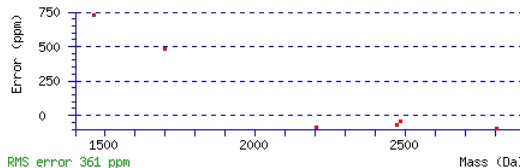
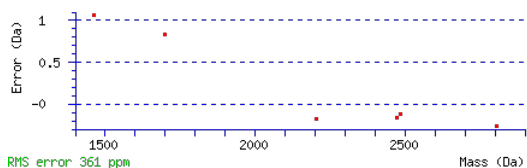
1  MASGSSSIAI GGLFENAEVT TSGRPVLRRN EVECFLSSI DIDSDDPPR
51 FTALRSGNLI LTTRLIWIP SQSNESVPSS IPLSAVTHIY SHKKSIKSMF
101 HSPRIRFQAD PGSIVVTIVF RKGKDFDGFL SKLWECWRGR AWEEEEKSES
151 ETSKSGSGTV AQGLYNDGT VRMVGLAGIL RKEQEQWEST DKSLQDAFQD
201 LNALMSKAKE MVSLAEKMRQ KLLSAPSSQN GSTDDEEMGS KEEMQQWMLS
251 VGIISPVTKE SAGALYHQEL SRQLADFVRI PLEKAGGMIS LTDMYHFNR
301 ARGTELISPD DLWQACTLWE KFDVFVMLRK FDSGVMVIQN KSHSDEEVMS
351 RIRMLVTKTE TLRVGVTASD AALTLKIAPA MAKEHLLSAE TKGLLCDRMS
401 PDGLRFYFNL FPEIDPTNLH IVKEFGTYGE WIKATSLLSV
    
```

Unformatted sequence string: **440 residues** (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
<b>1 - 28</b>	<b>2807.1753</b>	<b>2806.1680</b>	<b>2806.4283</b>	<b>-0.2603 0</b>	<b>-.MASGSSSIAIGGLFENA<b>EV</b>TTSGRPVLR.R</b>
<b>51 - 65</b>	<b>1700.7863</b>	<b>1699.7790</b>	<b>1698.9529</b>	<b>0.8261 1</b>	<b>R.FTALRSGNLI<b>L</b>TT<b>HR</b>.L</b>
<b>148 - 172</b>	<b>2487.0437</b>	<b>2486.0365</b>	<b>2486.1521</b>	<b>-0.1157 1</b>	<b>K.SESETSKSGSGTVA<b>QGLY</b>NDG<b>T</b>VR.M</b>
<b>280 - 300</b>	<b>2472.0419</b>	<b>2471.0346</b>	<b>2471.1977</b>	<b>-0.1631 1</b>	<b>R.I<b>P</b>LEKAGGMIS<b>L</b>TDMY<b>HFN</b>R.A + Oxidation (M)</b>
<b>342 - 353</b>	<b>1462.7361</b>	<b>1461.7289</b>	<b>1460.6678</b>	<b>1.0611 1</b>	<b>K.SHSDEE<b>VMS</b>R<b>IR</b>.M + Oxidation (M)</b>
<b>406 - 423</b>	<b>2206.9699</b>	<b>2205.9626</b>	<b>2206.1463</b>	<b>-0.1837 0</b>	<b>R.FYFNL<b>FPEID</b>PTNL<b>HIVK</b>.E</b>



## Protein View: KRP1\_ARATH

Cyclin-dependent kinase inhibitor 1 OS=Arabidopsis thaliana GN=KRP1 PE=1 SV=2

Database: SwissProt  
 Score: 66  
 Expect: 0.0077  
 Nominal mass (M<sub>r</sub>): 22497  
 Calculated pI: 5.29  
 Taxonomy: [Arabidopsis thaliana](#)

Sequence similarity is available as [an NCBI BLAST search of KRP1\\_ARATH against nr.](#)

### Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.  
 Fixed modifications: [Carbamidomethyl \(C\)](#)  
 Variable modifications: [Oxidation \(M\)](#)  
 Mass values searched: 5  
 Mass values matched: 5

### Protein sequence coverage: 36%

Matched peptides shown in **bold red**.

```

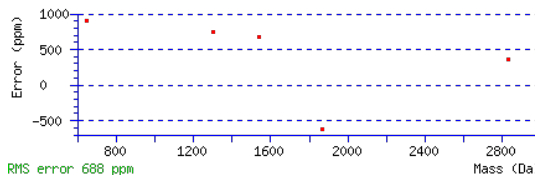
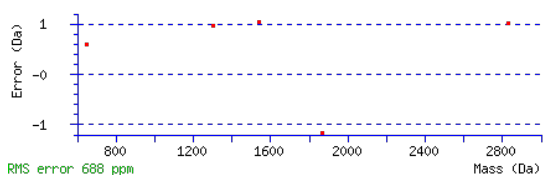
1 MVRKYRKAKG IVEAGVSSTY MQLRSRRIVY VRSEKSSSVS VVDNGVSSS
51 CSGSNEYKKK ELIHLEEDK DGDTETSTYR RGTKRKLFEN LREEEKEELS
101 KSMENYSSEF ESAVKESLDC CCSGRKTMEE TVTAEEEEKA KLMTEMPTES
151 EIEDFFVEAE KQLKEKFKKK YNFDFEKEKP LEGRYEWVKL E
    
```

Unformatted sequence string: **191 residues** (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	M	Peptide
<b>10 - 26</b>	<b>1868.7747</b>	<b>1867.7675</b>	<b>1868.9414</b>	<b>-1.1740</b>	<b>1</b>	<b>K.GIVEAGVSSTY<b>M</b>QLRSR.R + Oxidation (M)</b>
<b>28 - 32</b>	<b>649.9947</b>	<b>648.9874</b>	<b>648.3959</b>	<b>0.5915</b>	<b>0</b>	<b>R.IVYVR.S</b>
<b>71 - 81</b>	<b>1301.5511</b>	<b>1300.5439</b>	<b>1299.5691</b>	<b>0.9747</b>	<b>1</b>	<b>K.DGDTETSTYRR.G</b>
<b>102 - 125</b>	<b>2833.1430</b>	<b>2832.1357</b>	<b>2831.1143</b>	<b>1.0215</b>	<b>1</b>	<b>K.SMENYSSEFESAVKESLDCCCSGR.K</b>
<b>127 - 139</b>	<b>1542.6883</b>	<b>1541.6811</b>	<b>1540.6450</b>	<b>1.0361</b>	<b>0</b>	<b>K.TMEETVTAEEEEK.A + Oxidation (M)</b>



## Protein View: CSPL9\_MAIZE

CASP-like protein 9 OS=Zea mays PE=2 SV=1

Database: SwissProt  
 Score: 65  
 Expect: 0.01  
 Nominal mass (M<sub>r</sub>): 19804  
 Calculated pI: 9.41  
 Taxonomy: [Zea mays](#)

Sequence similarity is available as [an NCBI BLAST search of CSPL9\\_MAIZE against nr.](#)

### Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.  
 Fixed modifications: [Carbamidomethyl \(C\)](#)  
 Variable modifications: [Oxidation \(M\)](#)  
 Mass values searched: 4  
 Mass values matched: 4

### Protein sequence coverage: 38%

Matched peptides shown in **bold red**.

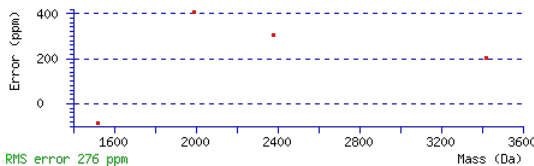
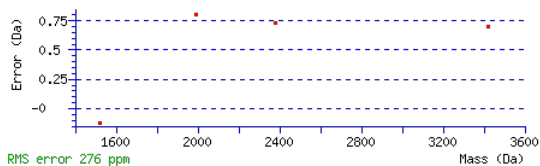
1 MAAGPPSSVR AER**VLRAACA AMAA**GALLL **G**FSAQTKTVL FIQKKAVPKD  
 51 VQALWVLIVA AAAAAAYHVA QLARCFCMER LAITGGGGG RRL**GRAVACA**  
 101 **SFLLDK**GCAIY MVFATTVAAL QACFVGLLGV DALQWSKLCN IYTR**FCEQAA**  
 151 **AGMVC**LLAA **AGMAVLSAFS ARDLFR**RPCS PEYR

Unformatted sequence string: **184 residues** (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
14 - 37	2378.9959	2377.9886	2377.2610	0.7276 1	<b>R.VLRAACA</b> MAAAGALLLG <b>FSAQTK</b> .T + Oxidation (M)
17 - 37	1994.8252	1993.8179	1993.0125	0.8054 0	<b>R.AACA</b> MAAAGALLLG <b>FSAQTK</b> .T
93 - 106	1520.6973	1519.6900	1519.8181	-0.1280 1	<b>R.LGRAVACASFLDK</b> .G
145 - 176	3424.3318	3423.3245	3422.6243	0.7002 1	<b>R.FCEQA</b> AGMVC <b>SLLAAAGMAVLSAFSARDLFR</b> .R + 2 Oxid



## Protein View: PROF3\_CORAV

Profilin-3 OS=Corylus avellana PE=1 SV=1

Database: SwlssProt  
 Score: 44  
 Expect: 1.5  
 Nominal mass (M<sub>r</sub>): 14294  
 Calculated pI: 4.89  
 Taxonomy: Corylus avellana

Sequence similarity is available as [an NCBI BLAST search of PROF3\\_CORAV against nr.](#)

### Search parameters

MS data file: peaklist.xml  
 Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.  
 Fixed modifications: Carbamidomethyl (C)  
 Variable modifications: Oxidation (M)  
 Mass values searched: 18  
 Mass values matched: 4

Protein sequence coverage: 57%

Matched peptides shown in **bold red**.

1 MSWQAYVDEH LMCIDIDGQGQ QLAASAIVGH DGSVWAQSS FPQLKPEEIT  
 51 GIMK**DFDEPG HLAPTGLHLG GTKYMQGE AGAVIRGKKG SGGITIKKTG**  
 101 **QALVFGIYEE PVTPGQCNMV VERLGDYLVE QGL**

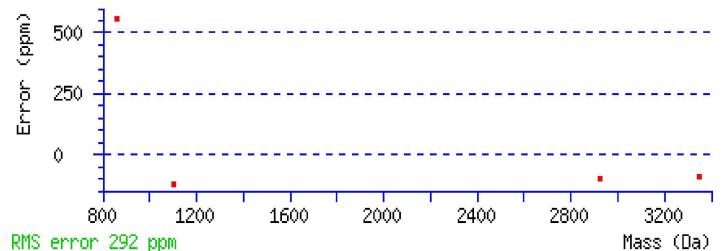
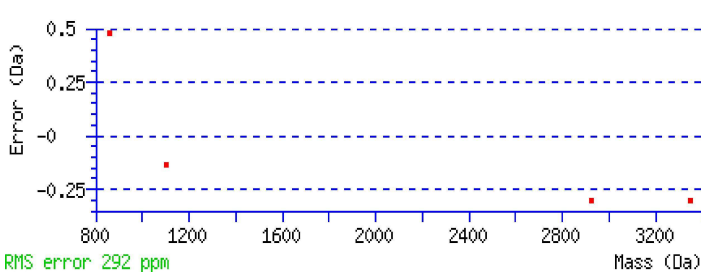
Unformatted sequence string: **133 residues** (for pasting into other applications).

Sort peptides by:  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
55 - 86	3349.3948	3348.3875	3348.6925	-0.3050 1	<b>K.DFDEPGHLAPTGLHLGGTKYMQGEAGAVIR.G</b>
90 - 98	860.9985	859.9912	859.5127	0.4785 1	<b>K.GSGGITIKK.T</b>
98 - 123	2922.1497	2921.1424	2921.4416	-0.2992 1	<b>K.KTGQALVFGIYEEPVTPGQCNMVVER.L</b>
124 - 133	1106.4408	1105.4335	1105.5655	-0.1320 0	<b>R.LGDYLVEQGL.-</b>

No match to: 1065.9856, 1194.0992, 1234.5907, 1365.5361, 1404.5507, 1602.6366, 1691.7271, 1791.5986, 2239.9558, 2384.7822, 2563.9907, 2692.1018, 2807.1182, 3332.3794



## Protein View: PR19A\_ARATH

Pre-mRNA-processing factor 19 homolog 1 OS=Arabidopsis thaliana GN=PRP19A PE=1 SV=1

Database: SwissProt  
 Score: 71  
 Expect: 0.0029  
 Nominal mass (M<sub>r</sub>): 57230  
 Calculated pI: 6.16  
 Taxonomy: [Arabidopsis thaliana](#)

Sequence similarity is available as [an NCBI BLAST search of PR19A\\_ARATH against nr.](#)

### Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.  
 Fixed modifications: [Carbamidomethyl \(C\)](#)  
 Variable modifications: [Oxidation \(M\)](#)  
 Mass values searched: 6  
 Mass values matched: 6

### Protein sequence coverage: 23%

Matched peptides shown in **bold red**.

```

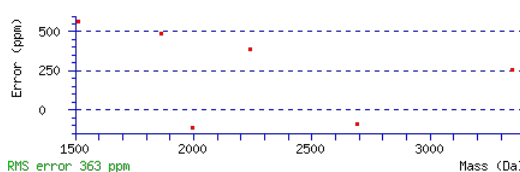
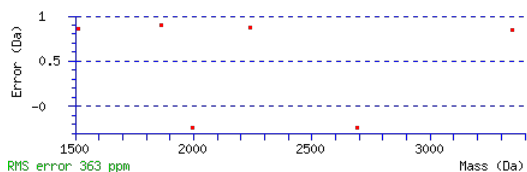
1  MNCAISGEVP EEPVVSKKSG LLYEKRLIQT HISDYGKCFV TGEPTLDDI
51 VPIKTGKIVK PKPLHTASIP GLLGTFQTEW DSLMLSNFAL EQLHTARQE
101 LSHALYQHDA ACRVIARLKK ERDESRQLLA EAERQLPAAP EVATSNAALS
151 NGKRGIDDGE QGPNAKMRL GISAEVITEL TDCNAALSQQ RKKRQIPKTL
201 ASVDALEKFT QLSSHPLHKT NKPGIFSMDI LHSKDVIATG GIDTTAVLFD
251 RPSGQILSTL TGHSKKVTSI KFGVGDLVL TASSDKTVRI WGCSEDGNYT
301 SRHTLKDHSA EVRAVTVHAT NKYFVSASLD STWCFYDLSS GLCLAQVTDA
351 SENDVNYTAA AFHPDGLILG TGTAQSIVKI WDVKSQANVA KFGGHNGEIT
401 SISFSENGYF LATAALDGVR LWDLRKLKNF RTFDFPDANS VEFDHSGSYL
451 GIAASDIRVF QAASVKAewn PIKTLPLSG TGKATSVKFG LSKYIAVGS
501 MDRNLRIFGL PDDNTEDSA QDS
    
```

Unformatted sequence string: **523 residues** (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
1 - 17	1862.7694	1861.7621	1860.8597	0.9024 0	<b>-.MNCAISGEVPEEPVVS<b>K</b>.K + Oxidation (M)</b>
99 - 117	2238.9934	2237.9861	2237.1123	0.8738 1	<b>R.QELSHALYQHDAACRVIAR.L</b>
135 - 154	1994.8283	1993.8210	1994.0545	-0.2335 1	<b>R.QLPAAPEVATSNAALSNGKR.G</b>
168 - 191	2692.1019	2691.0947	2691.3320	-0.2373 1	<b>K.MRLGISAEVITELTDCNAALSQQR.K + Oxidation (M)</b>
195 - 208	1513.7159	1512.7087	1511.8559	0.8528 1	<b>R.QIPKTLASVDALEK.F</b>
429 - 458	3349.4069	3348.3997	3347.5483	0.8513 1	<b>K.NFRTFDFPDANSVEFDHSGSYLGIAASDIR.V</b>





## Protein View: RGA3\_SOLBU

Putative disease resistance protein RGA3 OS=Solanum bulbocastanum GN=RGA3 PE=2 SV=2

Database: SwissProt  
 Score: 74  
 Expect: 0.0014  
 Nominal mass (M<sub>r</sub>): 114864  
 Calculated pI: 6.03  
 Taxonomy: Solanum bulbocastanum

Sequence similarity is available as [an NCBI BLAST search of RGA3\\_SOLBU against nr.](#)

### Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.  
 Fixed modifications: Carbamidomethyl (C)  
 Variable modifications: Oxidation (M)  
 Mass values searched: 10  
 Mass values matched: 10

### Protein sequence coverage: 13%

Matched peptides shown in **bold red**.

```

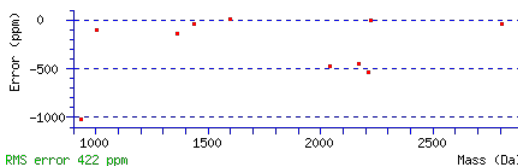
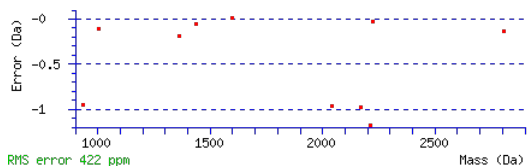
1 MAEAFLLQVLL DNLTFIFIQGE LGLVFGFEKE FKKLSSMFSM IQAVLEDAQE
51 KQLKYKAIKN WLQKLNVAAY EVDDILDCC TEAARFKQAV LGRYHPRTIT
101 FCYKVGKRMK EMMEKLDAIA EERRNPHLDE RIIERQAARR QTGFVLTEPK
151 VYGREKEEDE IVKILINNVV YSEEVVPLPI LGMGGLGKTT LAQMVFNDQR
201 ITEHFNLKIW VCVSDDFDEK RLIKAIVESI EGKSLGMDL APLQKLQEL
251 LNGKRYFLVL DDVWNEDEK WDNLRAVLKI GASGASILIT TRLEKIGSIM
301 GTLQLYQLSN LSQEDCWLLF KQRAFCHQTE TSPKLMIEIG EIVKCKGGVP
351 LAAKTLGGLL RFKREESEWE HVRDSEIWNL PQDENSVLPA LRLSYHHLPL
401 DLRQCFAYCA VFPKDKIEK EYLIALWMAH SFLLSKGNME LEDVGNVWNN
451 ELYLRSFFQE IEVKSGETYF KMHDLIHDLA TSMFASASASS RSIRQINVKD
501 DEDMMFIVTN YKDMSIGFS EVVSSYSPL FKRFVSLRVL NLSNSEFQEL
551 PSSVGDVLVHL RYLDLSGNKI CSLPKRLCKL QNLQTLDLYN CQSLSCLPKQ
601 TSKLCSLRNL VLDHCPITSM PPRIGLLTCL KTLGYFVVG E RKGYQLGELR
651 NLNLRGAISI THLERVKNDM EAKEANLSAK ANLHSLMSW DRPNRYESE
701 VKVLEALKPH PNLKYLEIID FCGFCLPDM NHSVLKNVVS ILISGCENCS
751 CLPPFGELPC LESLELDQGS VEVEYVEDSG FLTRRRFPPL RKLHIGGFEN
801 LKGLQRMKGA EQFPVLEEMK ISDCPMFVFP TLSSVKKLEI WGEADAGGLS
851 SISNLSLTLS LKIFSNHTVT SLLEEMFKNL ENLIYLSVSF LENLKLPTLS
901 LASLNKLKCL DIRICYALES LPPEGLEGLS SLTELFVEHC NMLKCLPEGL
951 QHLTTLTSLK IRGCPQLIKR CEKGIGEDWH KISHIPVNI YI
    
```

Unformatted sequence string: **992 residues** (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
33 - 51	2170.0869	2169.0796	2170.0650	-0.9853	<b>K.KLSSMFSMIQAVLEDAQE.K + Oxidation (M)</b>
34 - 51	2042.0170	2041.0097	2041.9700	-0.9603	<b>K.LSSMFSMIQAVLEDAQE.K + Oxidation (M)</b>
111 - 123	1596.7328	1595.7255	1595.7171	0.0085	<b>K.EMMEKLDIAEER.R + 2 Oxidation (M)</b>
189 - 200	1439.6387	1438.6314	1438.6875	-0.0560	<b>K.TTLAQMVFNDQR.I + Oxidation (M)</b>
225 - 245	2212.9888	2211.9815	2213.1613	-1.1798	<b>K.AIVESIEGKSLGMDLAPLQK.K</b>
355 - 363	1004.5207	1003.5134	1003.6178	-0.1045	<b>K.TLGGLLRFK.R</b>
393 - 403	1363.5565	1362.5493	1362.7408	-0.1915	<b>R.LSYHHLPLDLR.Q</b>
513 - 532	2227.0063	2225.9990	2226.0225	-0.0234	<b>K.DMSIGFSEVVSSYSPLFK.R + Oxidation (M)</b>
577 - 599	2809.2717	2808.2644	2808.3972	-0.1328	<b>R.LCKLQNLQTLDLYNQSLSCLPK.Q</b>
666 - 673	933.5141	932.5068	933.4589	-0.9521	<b>R.VKNDMEAK.E</b>



# Protein View: RBOHJ\_ARATH

Putative respiratory burst oxidase homolog protein J OS=Arabidopsis thaliana GN=RBOHJ PE=3 SV=2

**Database:** SwissProt  
**Score:** 60  
**Expect:** 0.04  
**Monoisotopic mass (M<sub>r</sub>):** 103498  
**Calculated pI:** 9.48  
**Taxonomy:** [Arabidopsis thaliana](#)

Sequence similarity is available as [an NCBI BLAST search of RBOHJ\\_ARATH against nr.](#)

## Search parameters

**Enzyme:** Trypsin: cuts C-term side of KR unless next residue is P.  
**Fixed modifications:** [Carbamidomethyl \(C\)](#)  
**Variable modifications:** [Oxidation \(M\)](#)  
**Mass values searched:** 7  
**Mass values matched:** 7

## Protein sequence coverage: 9%

Matched peptides shown in **bold red**.

```
1  MKNNKKVGTG DSTKWMLESV EIDPKGDSVV KQPESTINSN NPESGAGGG
51  ILKNVSKNLA VGSIIIRSMSV NKWRKSGNLG SPSTRKSGNL GPPLPVSQVK
101 RPGPQVERT TSSAARGLQS LRFLDRTVTG RERDSWRSIE NRFNQFAVDG
151 RLPKDKFGVC IGMGDTLEFA AKVYEALGRR RQIKTENGID KEQLKLFWED
201 MIKKDLDCRL QIFFDMCDKD GDGKLTEEEV KEVIVLSASA NRLVNLKKNA
251 ASYASLIMEE LDPNEQGYIE MWQLEVLTLG IVSNADSHKV VRKSQQLTRA
301 MIPKRYRTPT SKYVVVTAEL MYEHWKKIWV VTLWLAVNVV LFMWKYEEFT
351 TSPLYNITGR CLCAAKGTAE ILKLNMALIL VPVLRRRTLTF LRSTFLNHLI
401 PFDDNINFHK LIAVAIAVIS LLHTALHMLC NYPRLSSCPY NFYSDYAGNL
451 LGAKQPTYLG LMLTPVSVTG VLMIIFMGIS FTLAMHYFRR NIVKLPIPFN
501 RLAGFNSFWY AHLLVIAYA LLIHGYILI IEKPWYQKTT WMYVAIPMVL
551 YASERLFSRV QEHNHRVHII KAIVYSGNVL ALYMTKPQGF KYKSGMYMFV
601 KCPDISKFEW HPFSITSAPG DEYLSVHIRA LGDWTSELRN RFAETCEPHQ
651 KSKPSPNDLI RMETRARGAN PHVEEQALF PRIFIKGPYG APAQSYQKFD
701 ILLLIGLGIG ATPFISILKD MLNNLKPPIP KTGQKYEGSV GGESLGGSSV
751 YGGSSVNGGG SVNGGGSVSG GGRKFPQRAY FYWVTREQAS FEWFKGVMD
801 IAVYDKTNVI EMHNYLTSMY EAGDARSALI AMVQKLQHAK NGVDIVSESR
851 IRTHFARPWV RKVFSELSNK HETSRIGVFY CGSPTLVRPL KSLCQEFSL
901 SSTRFTFHKE NF
```

Unformatted sequence string: [912 residues](#) (for pasting into other applications).

Sort by  residue number  increasing mass  decreasing mass  
Show  matched peptides only  predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	M	Peptide
1 - 5	649.9890	648.9817	649.3217	-0.3400	1	-.MKNNK.K + Oxidation (M)
67 - 72	665.9642	664.9569	664.3214	0.6356	0	R.SMSVNK.W
293 - 299	861.0069	859.9996	859.4875	0.5120	1	R.KSQQLTR.A
328 - 345	2233.0188	2232.0115	2232.2533	-0.2418	0	K.IWVVTLWLAVNVVLFMWK.Y + Oxidation (M)
374 - 385	1352.6350	1351.6277	1350.8421	0.7856	0	K.LNMALILVPVLR.R
567 - 591	2807.1404	2806.1331	2805.5615	0.5716	1	R.VHIKAIIVYSGNVLALYMTKPGFK.Y + Oxidation (M)
630 - 641	1417.6929	1416.6856	1416.7110	-0.0254	1	R.ALGDWTSELRNR.F

# Protein View: GSTF2\_ARATH

Glutathione S-transferase F2 OS=Arabidopsis thaliana GN=GSTF2 PE=1 SV=3

Database: SwissProt

Score: 57

Expect: 0.082

Monoisotopic mass ( $M_r$ ): 24114

Calculated pI: 5.92

Taxonomy: [Arabidopsis thaliana](#)

Sequence similarity is available as [an NCBI BLAST search of GSTF2\\_ARATH against nr](#).

## Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.

Fixed modifications: [Carbamidomethyl \(C\)](#)

Variable modifications: [Oxidation \(M\)](#)

Mass values searched: 4

Mass values matched: 4

## Protein sequence coverage: 23%

Matched peptides shown in *bold red*.

1 MAGIKVFGHP ASIATRRVLI ALHEKNLDFE LVHVELKDGE HKKEPFLSRN  
51 PFGQVPAFED GDLKLFESRA ITQYIAHRYE NQGTNLLQTD SKNISQYAIM  
**101 AIGMQVEDHQ FDPVASKLAF** EQIFKSIYGL TTDEAVVAEE EAKLAKVLDV  
151 YEARLKEFKY LAGETFTLTD LHHIPAIQYL LGTPTKKLFT **ERPRVNEWVA**  
201 EITKRPASEK VQ

Unformatted sequence string: [212 residues](#) (for pasting into other applications).

Sort by  residue number  increasing mass  decreasing mass

Show  matched peptides only  predicted peptides also

Start	End	Observed	Mr(expt)	Mr(calc)	Delta	M	Peptide
43	-49	877.0433	876.0361	875.4865	0.5496	1	K.KEPFLSR.N
93	-117	2807.3358	2806.3285	2807.3258	-0.9973	0	K.NISQYAIMAIGMQVEDHQQFDPVASK.L + Oxidation (M)
187	-194	1045.5375	1044.5302	1045.6032	-1.0731	1	K.KLFTERPR.V
195	-204	1187.6630	1186.6557	1187.6186	-0.9629	0	R.VNEWVAEITK.R

## Protein View: PALY\_VITVI

Phenylalanine ammonia-lyase (Fragment) OS=Vitis vinifera GN=PAL PE=2 SV=1

Database: SwissProt  
 Score: 73  
 Expect: 0.0017  
 Nominal mass (M<sub>r</sub>): 46443  
 Calculated pI: 6.12  
 Taxonomy: Vitis vinifera

Sequence similarity is available as [an NCBI BLAST search of PALY\\_VITVI against nr.](#)

### Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.  
 Fixed modifications: Carbamidomethyl (C)  
 Variable modifications: Oxidation (M)  
 Mass values searched: 8  
 Mass values matched: 7

Protein sequence coverage: 28%

Matched peptides shown in **bold red**.

```

1 TDHLTHK LKH HPGQIEAAAI MEHILDGSSY VKEAKKLHEM DPLQKPKQDR
51 YALRTSPQWL GPHIEVIRAS TKSIEREINS VNDNPLIDVS RNKALHGGNF
101 QGTPIGVSM NTRLAIAAIG KLMFAQFSEL VNDFYNNGLP SNLSGSRNPS
151 LDYGFKGAEI AMASYCSELQ FLANPVTNHV ESAEQHNQDV NSLGLISSRK
201 TAEAVDILKL MSTTYLVALC QAIDLRHLEE NLKSTVKKTV SHVAKKTLTI
251 GANGLHPSR FCEKDLLKVV DREHVFAYID DPCSATYPLM QKVRQVLVEH
301 ALNNGESEKN GSTSIFQKIG AFEEELKAVL PKEVESARDG VESGNPSIPN
351 RIKECRSYPL YKFVREELGT GLLTGEKVR PGEDFDKVFT AMCEGKIIDP
401 LLDCLSAWNG APLPIC
    
```

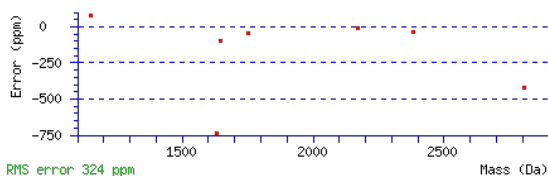
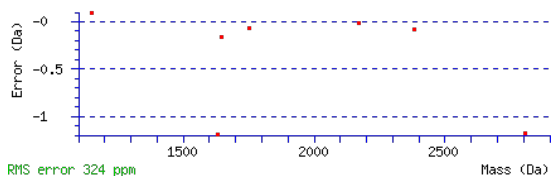
Unformatted sequence string: **416 residues** (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	M	Peptide
37 - 50	1750.8183	1749.8110	1749.8832	-0.0722	1	<b>K.LHEMDPLQKPKQDR.Y + Oxidation (M)</b>
55 - 68	1631.6873	1630.6800	1631.8784	-1.1984	0	<b>R.TSPQWLGPHIEVIR.A</b>
73 - 91	2170.0937	2169.0864	2169.1025	-0.0161	1	<b>K.SIEREINSVNDNPLIDVSR.N</b>
94 - 121	2808.2997	2807.2924	2808.4705	-1.1781	1	<b>K.ALHGGNFQGTPIGVSMNTRLAIAAIGK.L</b>
273 - 292	2385.0064	2383.9991	2384.0817	-0.0825	0	<b>R.EHVFAYIDDPKSATYPLMQK.V</b>
363 - 377	1648.7257	1647.7184	1647.8832	-0.1648	1	<b>K.FVREELGTGLLTGEK.V</b>
378 - 387	1149.6462	1148.6390	1148.5462	0.0928	1	<b>K.VRSPGEDFDK.V</b>

No match to: 2807.3021



# Protein View: CAMT1\_POPTR

Caffeoyl-CoA O-methyltransferase 1 OS=Populus trichocarpa  
GN=CCOAOMT1 PE=2 SV=1

**Database:** SwissProt  
**Score:** 73  
**Expect:** 0.0021  
**Monoisotopic mass (M<sub>r</sub>):** 28017  
**Calculated pI:** 5.30  
**Taxonomy:** [Populus trichocarpa](#)

Sequence similarity is available as [an NCBI BLAST search of CAMT1\\_POPTR against nr.](#)

## Search parameters

**Enzyme:** Trypsin: cuts C-term side of KR unless next residue is P.  
**Fixed modifications:** [Carbamidomethyl \(C\)](#)  
**Variable modifications:** [Oxidation \(M\)](#)  
**Mass values searched:** 5  
**Mass values matched:** 5

**Protein sequence coverage: 34%**

Matched peptides shown in **bold red**.

1 **MATNGEEQQS QAGRHOEVGH** KSLQLQSDALY QYILETSVYP REPECMKELR  
51 EVTAK**HPWNI MTTSADGQF LNMLLKLVNA** KNTMEIGVYT GYSLLATALA  
101 IPEDGKILAM DINRENYELG LPVIQKAGVA HKIDFK**EGPA LPVLDQMIED**  
151 **GKCHGSFDFI FVDADKDYI NYHKRLIELV** KVGGLIGYDN TLWNGSVVAP  
201 PDAPMRKYVR YYRDFVLELN KALAADPRIE ICMLPVGDI TLCRRIQ

Unformatted sequence string: [247 residues](#) (for pasting into other applications).

Sort by  residue number  increasing mass  decreasing mass  
Show  matched peptides only  predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
1 - 14	1507.6841	1506.6769	1505.6528	1.0240 0	<b>-.MATNGEEQQSQAGR.H</b>
2 - 21	2191.9534	2190.9461	2190.0162	0.9299 1	<b>M.ATNGEEQQSQAGRHOEVGHK.S</b>
56 - 81	2970.3391	2969.3318	2970.5095	-1.1777 1	<b>K.HPWNIMTTSADGQFLNMLLKLVNAK.N</b>
137 - 166	3349.5132	3348.5059	3349.5635	-1.0576 1	<b>K.EGPALPVLDQMIEDGKCHGSFDFIFVDADK.D</b>
167 - 174	1066.0276	1065.0203	1065.4879	-0.4676 0	<b>K.DNYINYHK.R</b>

## Protein View: AGO1B\_ORYSJ

Protein argonaute 1B OS=Oryza sativa subsp. japonica GN=AGO1B PE=2 SV=3

Database: SwissProt  
 Score: 58  
 Expect: 0.055  
 Nominal mass (M<sub>r</sub>): 124427  
 Calculated pI: 9.55  
 Taxonomy: Oryza sativa Japonica Group

Sequence similarity is available as [an NCBI BLAST search of AGO1B\\_ORYSJ against nr.](#)

### Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.  
 Fixed modifications: Carbamidomethyl (C)  
 Variable modifications: Oxidation (M)  
 Mass values searched: 8  
 Mass values matched: 8

### Protein sequence coverage: 9%

Matched peptides shown in **bold red**.

```

1  MALQLENGRP HHHQVPIMVK KKRTGSGSTG ESSGEAPGAP GHGSSQRAER
51  GPQQHGGGRG WVPQHGGRRG GQYQGRGGHY QGRGGQSSH PGGPPEYQG
101 RGGPGSHHPG GPPDYQGRG GSGSHHPGGG PPEYQPRDYQ GRGGPRFRGG
151 MPQPYYGGPR GSGGRSVPSG SSRTVPELHQ APHVQYQAPM VSPTPSGAGS
201 SSQPAAEVSS GQVQQQFQQL ATRDQSSTSQ AIQIAPPSSK SVRFPLRPGK
251 GTYGDRCIVK ANHFFAELPD KDLHQYDVSI TPEVTSRGNV RAVMFELVTL
301 YRYSHLGGRL PAYDGRKSLY TAGPLPFASR TFEITLQDEE DSLGGGQGTQ
351 RRERLFRVVI KFAARADLHH LAMFLAGRQA DAPQEALQVL DIVLRELPTT
401 RYSPVGRSFI SPNLGRRQQL GEGLESWRGF YQSIRPTQMG LSLNIDMSST
451 AFIEPLPVID FVAQLLNRI SVRPLSDSDR VKIKKALRGV KVEVTHRGNM
501 RRKYRISGLT SQATRELSFP VDDRGTVKTV VQYFLETYGF SIQHTTLPCL
551 QVGNQQRPNY LPMEVCKIVE GQRYSKRLNE KQITALLKVT CQRPQERELD
601 ILRTVSHNAY HEDQYAQEFQ IKIDERLASV EARVLPPPERL KYHDSGREKD
651 VLPRVGQWNM MNKKMVNGGR VNNWACINFS RNVQDSAARG FCHELAIMCQ
701 ISGMDFALEP VLPPLTARPE HVERALKARY QDAMMLRPQ GRELDLIVI
751 LPDNNGLYGL DLKRICETDL GLVSQCCLTK HVFKMSKQYL ANVALKINVK
801 VGGRTNVLVD ALTRRIPLVS DRPTIIFGAD VTHPHPGEDS SPSIAAVVAS
851 QDWPEVTKYA GLVSAQHRQ ELIQDLFKVW QDPHRGTVTG GMIKELLISF
901 KRATGQKPQR IIFYRDGVSE GQFYQVLLYE LDAIRKACAS LEPNYQPPVT
951 FVVVQKRHHT RLFANNHNDQ RTVDRSGNIL PGTVVDSKIC HPTEFDYFYL
1001 SHAGIQGTSR PAHYHVLWDE NKFTADELQT LTNNLCYTYA RCTRSVSIVP
1051 PYYAHLAAF RARFYMEPET SDSGSMASGA ATSRGLPPGV RSARVAGNVA
1101 VRPLPALKEN VKRVMFYC
    
```

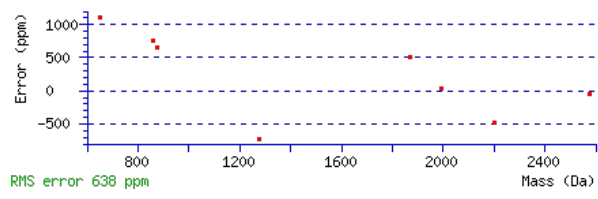
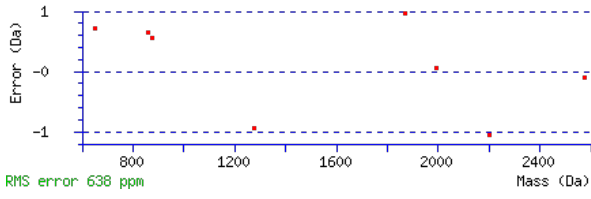
Unformatted sequence string: **1118 residues** (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
2 - 20	2203.1298	2202.1225	2203.1796	-1.0571 0	M.ALQLENGRPHHHQVPIMVK.K
51 - 68	1868.8823	1867.8750	1866.9099	0.9651 1	R.GPQQHGGGRGWVPQHGGRR.G
149 - 160	1278.6486	1277.6413	1278.5815	-0.9403 0	R.GGMPQPYYGGPR.G
379 - 401	2576.2931	2575.2858	2575.3969	-0.1112 1	R.QADAPQEALQVLDIVLRELPTTR.Y
498 - 502	650.0395	649.0322	648.3126	0.7197 1	R.GNMRR.K + Oxidation (M)
665 - 681	1995.0070	1993.9997	1993.9363	0.0634 1	K.MVNGGRVNNWACINFSR.N
682 - 689	861.0694	860.0622	859.4148	0.6474 0	R.NVQDSAARG.G

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
781 - 787	877.0429	876.0357	875.4687	0.5669 1	K.HVFKMSK.Q





# MASCOT Search Results

## Protein View: ARP\_ARATH

DNA-(apurinic or apyrimidinic site) lyase, chloroplastic OS=Arabidopsis thaliana  
GN=ARP PE=1 SV=2

Database: SwissProt

Score: 54

Expect: 0.16

Monoisotopic mass ( $M_r$ ): 60622

Calculated pI: 9.11

Taxonomy: [Arabidopsis thaliana](#)

Sequence similarity is available as [an NCBI BLAST search of ARP\\_ARATH against nr](#).

### Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.

Fixed modifications: [Carbamidomethyl \(C\)](#)

Variable modifications: [Oxidation \(M\)](#)

Mass values searched: 5

Mass values matched: 5

### Protein sequence coverage: 12%

Matched peptides shown in *bold red*.

1 MNVLQFGLQ **SSAIYVAKFL** VVPLRSLRVG SSFVGVGVGT RSFNKRLMSN  
51 ATAFSINNSK RKEIKIPGAA IDQNCHQMGS DTDREMGTL QDDRKEIEAM  
101 **TVQELRSTLR** KLGVPVKGRK QELISTLRLH MDSNLPDQKE TSSSTRSDSV  
151 TIKRKISNRE EPTDECTNS EAYDIEHGEK RVKQSTENL KAKVSAKAI  
201 KEQKSLMRTG KQIQSKEET SSTISSELLK TEEIISPSQ SEPWTVLAHK  
251 KPQKDWKAYN PKTMRPPPLP EGTKCVKVMT WVNGLRGLL KFESFSALQL  
301 AQRENFILC LQETKLQVKD **VEEIKKTLID** GYDHSFWSCS VSKLGYSGTA  
351 IISRIKPLSV RYGTGLSGHD TEGRIVTAEF DSFYLIINTYV PNSGDGLKRL  
401 SYRIEWDRT LSNHIKELEK SKPVVLTGDL NCAHEEIDIF NPAGNKRSAG  
451 FTIEERQSGF ANLLDKGFVD TFRK**QHPGVV** GYTYWGYRHG GRKTNKGWRL  
501 DYFLVSQSIA ANVHDSYILP DINGSDHCPI GLILKL

Unformatted sequence string: [536 residues](#) (for pasting into other applications).

Sort by  residue number  increasing mass  decreasing mass

Show  matched peptides only  predicted peptides also

Start – End Observed  $M_r$ (expt)  $M_r$ (calc) Delta M Peptide

1 -25 2807.1453 2806.1381 2806.5568 -0.4187 1 -.MNNVLQFGLQSSAIYVAKFLVVPLR.S  
96 -110 1776.7130 1775.7057 1774.9247 0.7810 1 K.EIEAMTVQELRSTLR.K  
320 -326 861.0047 859.9974 859.4651 0.5324 1 K.DVEEIKK.T  
474 -488 1809.7996 1808.7924 1809.8951 -1.1027 1 R.KQHPGVVGYTYWGYR.H  
475 -492 2089.0374 2088.0301 2089.0031 -0.9730 1 K.QHPGVVGYTYWGYRHGGR.K



# MASCOT Search Results

Protein View: PP292\_ARATH

Pentatricopeptide repeatcontaining protein At3g61520, mitochondrial  
OS=Arabidopsis thaliana GN=At3g61520 PE=2 SV=1

Database: SwissProt  
Score: 40  
Expect: 4.1  
Nominal mass (M<sub>r</sub>): 87762  
Calculated pI: 6.86  
Taxonomy: [Arabidopsisthaliana](#)

Sequence similarity is available as [anNCBI BLAST search of PP292\\_ARATH against nr](#).

## Search parameters

MS data file: peaklist.xml  
Enzyme: Trypsin: cuts Cterm side of KR unless next residue is P.  
Fixed modifications: [Carbamidomethyl\(C\)](#)  
Variable modifications: [Oxidation\(M\)](#)  
Mass values searched: 15  
Mass values matched: 9

Protein sequence coverage: 16%

Matched peptides shown in **bold red**.

```
1 MSIMLSISRR RNSYILLNHS RFLRRFSYDV DPRPEIKLES QEFVVVKFVK
51 TLQKTPQHDW ASSESLSALV VSSSSASPLV FSQITRRLGS YSLAISFFEY
101 LDAKSQSLKR REESLSLALQ SVIEFAGSEP DPRDKLLRLY EIAKEKNIPL
151 TVVATNLLIR WFGRMGMVNQ SVLVYERLDS NMKNSQVRNV VVDVLLRNGL
201 VDDAFKVLDE MLQKESVFPP NRITADIVLH EVWKGRLLTE EKIIALISRF
251 SSHGVSPNSV WLTRFISSLC KNARANAAWD ILSDLMKNKT PLEAPPFNAL
301 LSCLGRNMDI SRMNDLVLM DEVKIRPDVV TLGILINTLC KSRRVDEALE
351 VFEKMRGKRT DDGNVIKADS IHFNTLIDGL CKVGRLKEAE ELLVRMKLEE
401 RCAPNAVTYN CLIDGYCRAG KLETAKEVVS RMKEDEIKPN VVTVNTIVGG
451 MCRHHGLNMA VVFFMDMEKE GVKGNVTYM TLIHACSVS NVEKAMYWYE
501 KMLEAGCSPD AKIYYALISG LCQVRRDHDA IRVVEKLKEG GFSLDLLAYN
551 MLIGLFCDKN NTEKVYEMLT DMEKEGKKPD SITYNTLISF FGKHKDFESV
601 ERMMEQMRED GLDPTVTTYG AVIDAYCSVG ELDEALKLFK DMGLHSKVNP
651 NTVIYNILIN AFSKLGNFGQ ALSLKEEMKM KMVRPNVETY NALFKCLNEK
701 TQGETLLKLM DEMVEQSCEP NQITMEILME RLSGSDELVK LRKFMQGYSV
751 ASPTEKASPF DVFSLG
```

Unformatted sequence string: [766 residues](#) (for pasting into other applications).

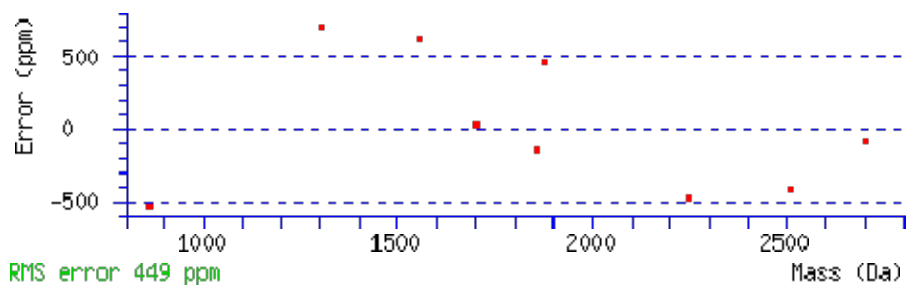
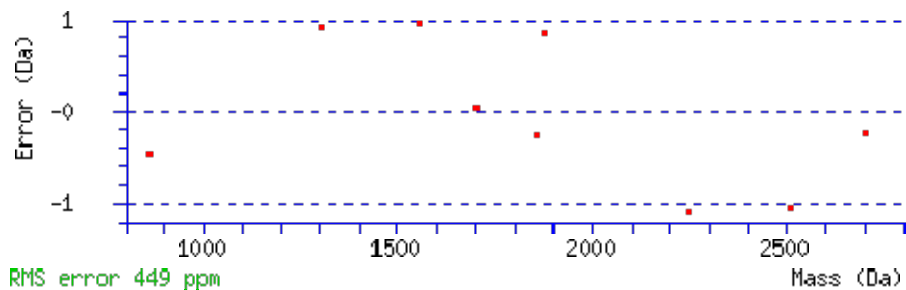
Sort peptides by

● Residue Number ● Increasing Mass ● Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	M	Peptide
165 - 177	1558.7158	1557.7085	1556.7327	0.9758	0	R.MGMVNVQSVLVYER.L + 2 Oxidation (M)
165 - 183	2244.9744	2243.9671	2245.0541	1.0870	1	R.MGMVNVQSVLVYERLDSNMK.N + 2 Oxidation (M)
178 - 188	1308.5549	1307.5477	1306.6299	0.9177	1	R.LDSNMKNSQVR.N + Oxidation (M)
250 - 271	2508.2163	2507.2090	2508.2584	1.0493	1	R.FSSHGVSPNSVWLTRFISSLCK.N
290 - 306	1855.7063	1854.6990	1854.9662	0.2672	0	K.TPLEAPPFNALLSCLGR.N
360 - 367	860.9733	859.9661	860.4240	0.4579	0	R.TDDGNVIK.A
560 - 574	1877.6882	1876.6810	1875.8230	0.8580	1	K.NNTEKVYEMLTDMEK.E + 2 Oxidation (M)
596 - 608	1703.7587	1702.7514	1702.7113	0.0401	1	K.DFESVERMMEQMR.E + Oxidation (M)
641 - 664	2704.1660	2703.1587	2703.4054	0.2467	1	K.DMGLHSKVNPNTVIYNILINAFSK.L + Oxidation (M)

No match to: 1065.9686, 1278.5675, 1514.7343, 1721.7703, 2672.1465, 2808.1155



## Protein View: MGN\_ORYSJ

Protein mago nashi homolog OS=*Oryza sativa* subsp. *japonica* GN=Os12g0287200 PE=2 SV=2

Database: SwissProt  
 Score: 60  
 Expect: 0.037  
 Nominal mass (M<sub>r</sub>): 18475  
 Calculated pI: 5.84  
 Taxonomy: [Oryza sativa Japonica Group](#)

Sequence similarity is available as [an NCBI BLAST search of MGN\\_ORYSJ against nr.](#)

### Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.  
 Fixed modifications: [Carbamidomethyl \(C\)](#)  
 Variable modifications: [Oxidation \(M\)](#)  
 Mass values searched: 4  
 Mass values matched: 4

### Protein sequence coverage: 26%

Matched peptides shown in **bold red**.

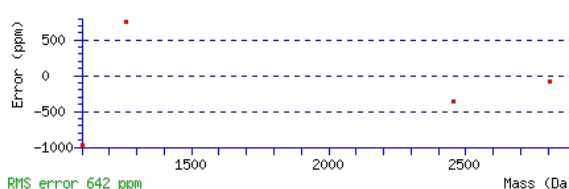
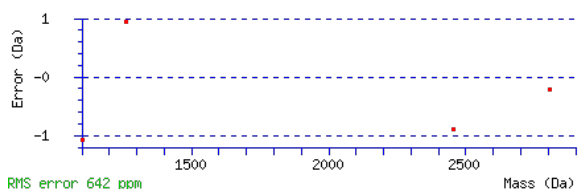
1 MATGGAAGED VPGGGEFYLR YYVGHKGFK HEFLEFEFRP DGKLRYSNS  
 51 NYKNDTMIRK EVFVSPSVLR **EAR**R**IIQ**E**SE **IM**KEDD**N**NP **EP**DRVGRQEL**  
 101 EIVMGNEHIS FTTSKIGSLV DVQTSKDPEG **LR**I**F**Y**Y**L**VQ**D** **L**K**C**F**V**F**SL**I**N**  
 151 **L**H**F**K****IKPIQS**

Unformatted sequence string: [160 residues](#) (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	M	Peptide
<b>74 - 83</b>	<b>1263.6218</b>	<b>1262.6145</b>	<b>1261.6700</b>	<b>0.9445</b>	<b>1</b>	<b>R.RIIQ<b>E</b>SEIM<b>K</b>.E + Oxidation (M)</b>
<b>75 - 83</b>	<b>1105.4960</b>	<b>1104.4887</b>	<b>1105.5689</b>	<b>-1.0802</b>	<b>0</b>	<b>R.IIQ<b>E</b>SEIM<b>K</b>.E + Oxidation (M)</b>
<b>75 - 94</b>	<b>2457.2313</b>	<b>2456.2240</b>	<b>2457.1118</b>	<b>-0.8878</b>	<b>1</b>	<b>R.IIQ<b>E</b>SEIM<b>K</b>EDD<b>N</b>NP<b>E</b>PD<b>R</b>.V</b>
<b>133 - 154</b>	<b>2807.2901</b>	<b>2806.2828</b>	<b>2806.4920</b>	<b>-0.2092</b>	<b>1</b>	<b>R.IF<b>Y</b>Y<b>L</b>VQ<b>D</b>L<b>K</b>C<b>F</b>V<b>F</b>SL<b>I</b>N<b>L</b>H<b>F</b>K.I</b>



## Protein View: LBD26\_ARATH

LOB domain-containing protein 26 OS=Arabidopsis thaliana GN=LBD26 PE=2 SV=2

Database: SwissProt  
 Score: 66  
 Expect: 0.0076  
 Nominal mass (M<sub>r</sub>): 17931  
 Calculated pI: 9.39  
 Taxonomy: [Arabidopsis thaliana](#)

Sequence similarity is available as [an NCBI BLAST search of LBD26\\_ARATH against nr.](#)

### Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.  
 Fixed modifications: [Carbamidomethyl \(C\)](#)  
 Variable modifications: [Oxidation \(M\)](#)  
 Mass values searched: 4  
 Mass values matched: 4

### Protein sequence coverage: 50%

Matched peptides shown in **bold red**.

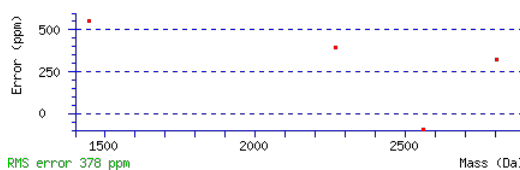
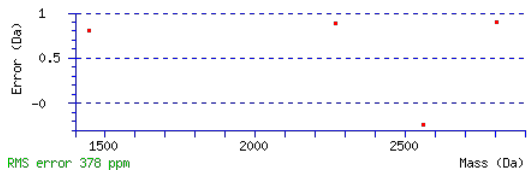
1 MNANPCEVCR **FQNKQCVNNC MFALLFPSSD LEK**FDVNNRI FGLETTLTFYL  
 51 **KDLS**PMERID TTR**TLYEAK PCFLNPPKNP** SKFLEALLNY PYQKAEVSK  
 101 **TKKLLASYSR PCVVLALPAP KYTQSK**SKPS VLRKRKRRTK SSDESAIRVV  
 151 EDS

Unformatted sequence string: **153 residues** (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
11 - 33	2807.2033	2806.1961	2805.2924	0.9036 1	<b>R.FQNKQCVNNCMFALLFPSSDLEK.F + Oxidation (M)</b>
40 - 51	1445.6099	1444.6026	1443.8013	0.8013 0	<b>R.IFGLETTLTFYLYK.D</b>
64 - 82	2268.0405	2267.0332	2266.1456	0.8876 1	<b>R.TLYYEAKPCFLNPPKNPSK.F</b>
104 - 126	2562.1655	2561.1582	2561.4039	-0.2457 1	<b>K.LLASYSRPCVVLALPAPKYTQSK.S</b>



**Protein View: SNL6\_ARATH**

Paired amphipathic helix protein Sin3-like 6 OS=Arabidopsis thaliana GN=SNL6 PE=3 SV=2

Database: SwissProt  
 Score: 71  
 Expect: 0.0031  
 Monoisotopic mass (M<sub>r</sub>): 134332  
 Calculated pI: 7.17  
 Taxonomy: **Arabidopsis thaliana**

Sequence similarity is available as [an NCBI BLAST search of SNL6\\_ARATH against nr.](#)

**Search parameters**

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.  
 Mass values searched: 7  
 Mass values matched: 7

**Protein sequence coverage: 12%**

Matched peptides shown in **bold red**.

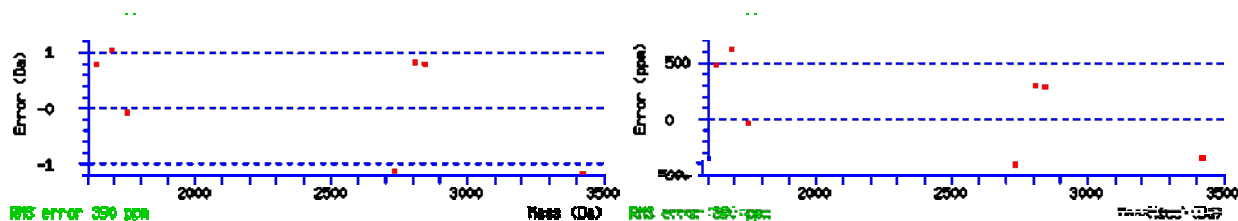
```

1 MRDLLLGTII PSYFSWLGFL PRFLVWFGFL KASFFCSSRN QSAGESGRRL
51 KMKRAREDVH TDTQKRKPEV SSRGETNKLPT RTIDALTYLK AVKDIHFHDNK
101 EKYESFLELM KEFKAQTIDT NGVIERIKVL FKGYRDLGGL FNTFLPKGYK
151 ITLLPEEEKP KIRVDFKDAI GFVTKIKTRF GDDEHAYKRF LDILNLRYKE
201 KKSISEVYEE VTMLFKGHED LLMEFVNFLL NCPEAPSTK NAVPRHKGTA
251 TTAMHSDKRR KQRCKLEDYS GHSDQREDGD ENLVTCASDS PVGEGQPGYF
301 RDIENREDTE TDTADRTEKS AAGSQDIGN HKSTTKYVGT PINELDLSEC
351 TQCTPSYRLL PKDYAVEIPS YRNTLGGKTL NDHLVSVTSG SEDYSFSHMR
401 KNQYEEELFR CEDDRYEMDM LLGSVSSAIK QVEILLEKMN NNTISVDSTI
451 CIEKHLSAMN LRCIERLYGD NGLDVMDDLK KNMHSALPVI LTRLKQKQEE
501 WARCHSDFQK VWAQVYAKNH HKSLDHRSEY FKQDQSKNLS TKCLVAEVKD
551 ISEKHKQEDL LQAIIVRVMP LFTPDLEFNY CDTQIHEDLY LLIKYYCEEI
601 CATEQSDKVM KLWITFLEPI FGIILSRSDN LALEDVSKLK NNRELQDACL
651 AVKETASGSN RKHPISEPKRL SKDNTKMQGS SSREDSVANI KVKTAQPDKL
701 QDDAAMTNEV IQSSKFVSPK NDQIMEDEGN HMVNAASVEK HELEEGELSP
751 TASREQSNFE VNGQNAFKPL QKVTDNVRSN KDKQSCDKKG AKNKTRAEDD
801 KQENCHKLSE NNKTASEMLV SGTKVSCHEE NNRVMNCNGR GSVAGEMANG
851 NQGEDGSFAF SERFLOTVKP VAKHLSWPLQ ASETCSQNSD QVFGNDSYY
901 VLFRLHQMLY ERIQTAKKHS EKKWKAADNT TPDSYPRFMD ALYNLLDGSII
951 DNTKFEDECR AIFGAQSYVL FTLDKLVQKF VKHLHSVAD ETDTKLLQLH
1001 AYENYRKPGK FFDLVYHENA CALLHEANIY RIRYSSEGTR LSIQLMNSGN
1051 NQLEVMGVAM EPAFADYLQN KCLKSVNDEE NHGLFLNRNK KKFTSLDESR
1101 GMPVAMERLN IINEMECRMA CSSSKVKYVA NTSDDLRYRSK QGKPNRSVSE
1151 ILKQRRISRF HIMLNCRLLCA LPL
    
```

Unformatted sequence string: **1173 residues** (for pasting into other applications).

Sort by  residue number  increasing mass  decreasing mass  
 Show  matched peptides only  predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
320 - 336	1689.8578	1688.8505	1687.8125	1.0380	<b>K.SAAGSQDIGNHKSTTK.Y</b>
431 - 454	2733.2749	2732.2676	2733.3928	-1.1252	<b>K.QVEILLEKMNNTISVDSTICIEK.H</b>
700 - 715	1749.7694	1748.7621	1748.8251	-0.0629	<b>K.LQDDAAMTNEVIQSSK.F</b>
905 - 917	1631.6671	1630.6598	1629.8661	0.7937	<b>R.LHQMLYERIQTAK.K</b>
983 - 1006	2841.1968	2840.1895	2839.3889	0.8007	<b>K.HLHSVASDETDTKLLQLHAYENYR.K</b>
1011 - 1033	2808.2332	2807.2259	2806.4013	0.8246	<b>K.FFDLVYHENACALLHEANIYRIR.Y</b>
1041 - 1071	3424.4870	3423.4798	3424.6465	-1.1667	<b>R.LSIQLMNSGNQLEVMGVAMEPAFADYLQNK.C</b>



# Protein View: 1433D\_TOBAC

## 14-3-3-like protein D OS=Nicotiana tabacum PE=2 SV=1

**Database:** SwissProt  
**Score:** 53  
**Expect:** 0.19  
**Monoisotopic mass (M<sub>r</sub>):** 28410  
**Calculated pI:** 4.76  
**Taxonomy:** [Nicotiana tabacum](#)

Sequence similarity is available as [an NCBI BLAST search of 1433D\\_TOBAC against nr.](#)

### Search parameters

**Enzyme:** Trypsin: cuts C-term side of KR unless next residue is P.  
**Fixed modifications:** [Carbamidomethyl \(C\)](#)  
**Variable modifications:** [Oxidation \(M\)](#)  
**Mass values searched:** 4  
**Mass values matched:** 4

### Protein sequence coverage: 21%

Matched peptides shown in **bold red**.

1 MAVPENLTRE QCLYLAKLAE QAERYEEMVK FMDRLVAVSA SSELTV EERN  
51 LLSVAYKNVI GSLRAAWRIV SSIEQKEEGR KNEEHVVLVK DYRSKVESEL  
101 SDVCAGILKI LDQYLIPSAAGESK**VFYLK MKGDYYR**YLA EFKVGNERKE  
151 AAEDTMLAYK AAQDIALAEL APTHPIRLGL ALNYSVFYIE ILNASEK**ACS**  
201 **MAKQAFEEAI AELDTLGEES YK**DSTLIMQL LRD**NLTLWTS DMQEQMDEA**

Unformatted sequence string: [249 residues](#) (for pasting into other applications).

Sort by  residue number  increasing mass  decreasing mass  
Show  matched peptides only  predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	M	Peptide
126 - 132	928.3375	927.3302	927.5252	-0.1949	1	<b>K.VFYLKMK.G</b>
131 - 137	933.4345	932.4272	931.4222	1.0051	1	<b>K.MKGDYYR.Y</b>
198 - 222	2807.1607	2806.1534	2806.2677	-0.1143	1	<b>K.ACSMAKQAFEEAIAELDTLGEESYK.D</b> + Oxidation (M)
233 - 249	2026.9215	2025.9142	2025.8296	0.0847	0	<b>R.DNLTLWTS</b> <b>DMQEQMDEA.-</b>



## Protein View: FB332\_ARATH

Probable F-box protein At5g36000 OS=Arabidopsis thaliana GN=At5g36000 PE=2 SV=2

**Database:** SwissProt  
**Score:** 60  
**Expect:** 0.032  
**Nominal mass (M<sub>r</sub>):** 40170  
**Calculated pI:** 8.51  
**Taxonomy:** Arabidopsis thaliana

Sequence similarity is available as [an NCBI BLAST search of FB332\\_ARATH against nr.](#)

### Search parameters

**Enzyme:** Trypsin: cuts C-term side of KR unless next residue is P.  
**Fixed modifications:** Carbamidomethyl (C)  
**Variable modifications:** Oxidation (M)  
**Mass values searched:** 21  
**Mass values matched:** 10

### Protein sequence coverage: 36%

Matched peptides shown in **bold red**.

```

1  MNTRSGDAEG DIRGKMIAPV RDGNGGQKRK LVQSNDIQRD EDGGAKRRII
51 QSSDQKNGKI LRGIHGCVSP RCSAPTYQSR PSWVEQDIWT YITRFLDGKS
101 LVKLGATNKW FYKIAMEDTV WRFACLRDLQ VPETFPVSST WIKIYASAFD
151 GSHSYLFHQK EKHIDWMLRG AFVLDSRTSF LTESLSGRLK VPTEGTIEQM
201 LQSSGSCLIN DIKSGIWIAD LQLLRCPLCD LSTCDGTMQT LDVRHIEFLF
251 SEGYKDGSD YNLIGSHKLE KDASAACGAI FDLKHLKKS SSGILNLKSW
301 TGEADDSQPK AVIAPHAVAV HTRLQQNEGI LVKYHTMKAG TDGDIVSIRI
351 SQQLL
    
```

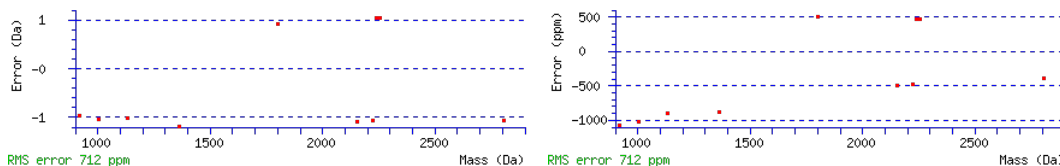
Unformatted sequence string: **355 residues** (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
49 - 56	917.5124	916.5051	917.4818	-0.9767 0	<b>R.IIQSSDQK.N</b>
60 - 71	1363.5619	1362.5547	1363.7507	-1.1960 1	<b>K.ILRGIHGCVSP.R.C</b>
144 - 162	2227.0113	2226.0041	2227.0698	-1.0657 1	<b>K.IYASAFDGS</b> HSHSYLFHQEK.H
169 - 188	2155.0537	2154.0464	2155.1273	-1.0809 1	<b>R.LGAFVLD</b> SRTSFLTESLSGR.L
226 - 244	2242.9970	2241.9897	2240.9534	1.0363 0	<b>R.CPLCDL</b> STCDGTMQTLDVR.H
226 - 244	2258.9956	2257.9883	2256.9484	1.0399 0	<b>R.CPLCDL</b> STCDGTMQTLDVR.H + Oxidation (M)
245 - 268	2807.2922	2806.2849	2807.3555	-1.0706 1	<b>R.HIEFL</b> FLSEGYKDGSDYNLIGSHK.L
288 - 298	1132.6264	1131.6191	1132.6452	-1.0261 1	<b>K.KSSSSGILNLK.S</b>
289 - 298	1004.5295	1003.5223	1004.5502	-1.0279 0	<b>K.SSSSGILNLK.S</b>
324 - 338	1802.8683	1801.8611	1800.9556	0.9055 1	<b>R.LQQNEGI</b> LVKYHTMK.A

No match to: 735.2685, 933.5123, 1020.5193, 1036.5148, 1381.5753, 1841.9519, 2027.0030, 2121.9908, 2212.9940, 2230.9829, 2244.9918



## Protein View: FB169\_ARATH

Putative F-box protein At3g20705 OS=Arabidopsis thaliana GN=At3g20705 PE=4 SV=1

Database: SwissProt  
 Score: 69  
 Expect: 0.0046  
 Nominal mass (M<sub>r</sub>): 26223  
 Calculated pI: 9.19  
 Taxonomy: [Arabidopsis thaliana](#)

Sequence similarity is available as [an NCBI BLAST search of FB169\\_ARATH against nr.](#)

### Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.  
 Fixed modifications: [Carbamidomethyl \(C\)](#)  
 Variable modifications: [Oxidation \(M\)](#)  
 Mass values searched: 6  
 Mass values matched: 6

### Protein sequence coverage: 18%

Matched peptides shown in **bold red**.

```

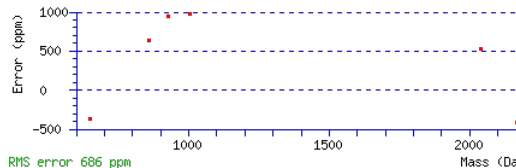
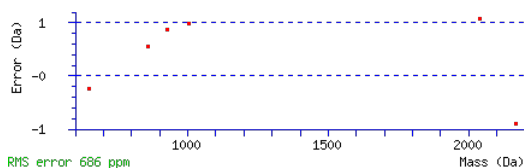
1  MMMSNLPND LVEEILSRVT VTFMRTVRSI CKKWNALTKD RSFTNKYIRN
51 IAALGEREFL MIKEFSIYLV GVNHLGIQNN NFDLSIELKG KLISMDNTIR
101 RFCISQIFHC NGLFLCVSQK DMDNRLVWVN PYCSKPRWIK PSYNYRTVDR
151 FALGYDKSCG SHKILRLFGD NLNNLEIYDL SSNSWRVPNV TLERDIVYMQ
201 PGVSLKEKTY WYARDKESEN
    
```

Unformatted sequence string: **220 residues** (for pasting into other applications).

Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
<b>1 - 18</b>	<b>2170.0873</b>	<b>2169.0801</b>	<b>2169.9778</b>	<b>-0.8977 0</b>	<b>-.<u>MMMSNLPNDLVEEILSR</u>.V + 3 Oxidation (M)</b>
<b>2 - 18</b>	<b>2041.0089</b>	<b>2040.0016</b>	<b>2038.9373</b>	<b>1.0643 0</b>	<b>M.<u>MMMSNLPNDLVEEILSR</u>.V + 3 Oxidation (M)</b>
<b>33 - 39</b>	<b>861.0520</b>	<b>860.0447</b>	<b>859.4916</b>	<b>0.5532 1</b>	<b>K.<u>KWNALTK</u>.D</b>
<b>34 - 41</b>	<b>1004.5153</b>	<b>1003.5080</b>	<b>1002.5247</b>	<b>0.9833 1</b>	<b>K.<u>WNALTKDR</u>.S</b>
<b>121 - 125</b>	<b>650.0219</b>	<b>649.0146</b>	<b>649.2490</b>	<b>-0.2344 0</b>	<b>K.<u>DMDNR</u>.L</b>
<b>187 - 194</b>	<b>928.3969</b>	<b>927.3896</b>	<b>926.5185</b>	<b>0.8711 0</b>	<b>R.<u>VPNVTLER</u>.D</b>





# MASCOT Search Results

## Protein View: CRR27\_ARATH

Putative cysteine-rich repeat secretory protein 27 OS=Arabidopsis thaliana  
GN=CRRSP27 PE=5 SV=2

Database: SwissProt  
Score: 51  
Expect: 0.29  
Nominal mass (M<sub>r</sub>): 29384  
Calculated pI: 8.66  
Taxonomy: [Arabidopsisthaliana](#)

Sequence similarity is available as [anNCBIBLAST searchofCRR27\\_ARATHagainstnr.](#)

### Search parameters

MS data file: peaklist.xml  
Enzyme: Trypsin: cuts Cterm side of KR unless next residue is P.  
Fixed modifications: [Carbamidomethyl\(C\)](#)  
Variable modifications: [Oxidation\(M\)](#)  
Mass values searched: 29  
Mass values matched: 8

Protein sequence coverage: 38%

Matched peptides shown in **bold red**.

```
1 MISKFGSVHI LAVVAIQLLI IPSVSSLNLT NAYLHHKCNN TEGKYSHGSA
51 FEKYINLALR AIDSDNYLNG FAYIERGEDP NKVFVMYQCR GDSYGSKCKS
101 CISAAISGLR RRCPKSKGAV IWYDQCLFEI STINSFNKID YENDFYLSNP
151 NDVNDKELFN KETSALLEEL TNKATDKNNM IGNKFVLYAA GDKRIGTKNV
201 YAMVQCTKDL VTTTSAACFE WIFKMFskCC EGKQGGRVLG TSCNFRYELY
251 PFLRN
```

Unformatted sequence string: [255 residues](#) (for pasting into other applications).

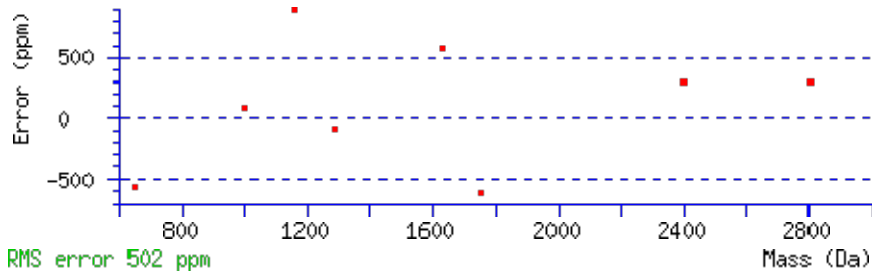
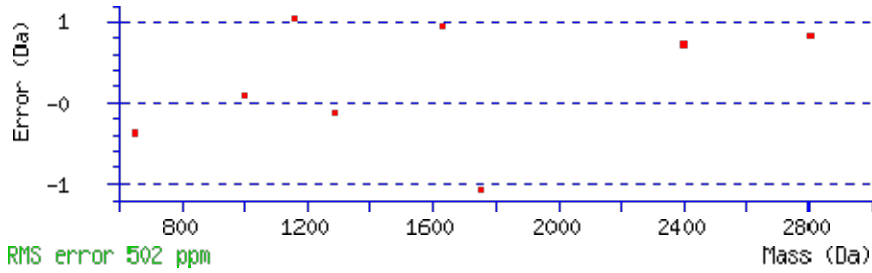
Sort peptides by  Residue Number  Increasing Mass  Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr(expt)	Mr(calc)	Delta M	Peptide
91 - 99	1001.5255	1000.5182	1000.4284	0.0898 1	<b>R.GDSYGSKCK.S</b> K.SCISAAISGLRR.R
100 - 111	1290.5815	1289.5743	1289.6874	0.1131 1	K.IDYENDFYLSNPNDVNDKELFNK.E
139 - 161	2807.1108	2806.1036	2805.2769	0.8266 1	K.ELFNK.E
157 - 161	649.9872	648.9800	649.3435	0.3635 0	K.NNMIGNKFVLYAAGDK.R
178 - 193	1753.8175	1752.8102	1753.8821	1.0719 1	R.IGTKNVYAMVQCTK.D + Oxidation
195 - 208	1629.7625	1628.7552	1627.8062	0.9490 1	..... (M)
209 - 228	2398.8660	2397.8587	2397.1385	0.7202 1	K.DLVTTTSAACFEWIFKMFsk.C + ..... Oxidation (M)

225 - 233 1163.5079 1162.5007 1161.4617 1.0390 1 K.MFSKCCEGK.Q + Oxidation (M)

No match to: 861.0013, 876.9765, 1066.0323, 1272.5970, 1415.5723, 1493.6204, 1558.6411, 1838.8251, 1915.8922, 1916.8766, 1994.8561, 2051.9375, 2101.8428, 2239.9797, 2270.0422, 2691.1355, 2841.1145, 2922.1902, 3026.3208, 3059.3765, 3349.4243



# Protein View: Y4498\_ARATH

Uncharacterized protein At4g04980 OS=Arabidopsis thaliana  
GN=At4g04980 PE=2 SV=1

Database: SwissProt  
Score: 60  
Expect: 0.043  
Monoisotopic mass ( $M_r$ ): 82314  
Calculated pI: 5.01  
Taxonomy: [Arabidopsis thaliana](#)

Sequence similarity is available as [an NCBI BLAST search of Y4498\\_ARATH against nr.](#)

## Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.  
Fixed modifications: [Carbamidomethyl \(C\)](#)  
Variable modifications: [Oxidation \(M\)](#)  
Mass values searched: 7  
Mass values matched: 7

## Protein sequence coverage: 12%

Matched peptides shown in **bold red**.

```
1 MKDLQKLSPE IVTINQSFEM EGADMDKMLI FFYEDLRAIG DSWIMSDDWI
51 YRSKYKNSGV GKNKSDRLVE HVLAALDGLI KTTREERFGMM DLESEGRKSF
101 TTPKGVSSEA RRSFTRSASY SESNNSFYPS PLTPRSVLPG TMMSSNSTS
151 PSLWNLRAQA LDRLSPVDLK RFAMQILSQR DSESVSETKI GIEEENESE
201 ILAEEKEEED NDFSVLETEG TEQEIKTEHH RESSGTEHET EAKDHSEGFE
251 TEHHRIECFE TEHEIDADDH IEDFETEHHH IEGLETEHEI DANDHIEDFE
301 TEHHHIEGFE TEHENETEDH SETTTSETDS TESSPKEDVP PPPPLTSPQT
351 PSPTVSTFNT KSSLRSQPPP PPPSPEHKAP APPPPPPMSK ASESGEFCQF
401 SKTHSTNGDN APSMPAPPAP PGSGRSLKKA TSKLRRSAQI ANLYWALKGK
451 LEGRGVEGKT KKASKGQNSV AEKSPVKVAR SGMADALAEM TKRSSFYQQI
501 EEDVQKYAKS IEELKSSIHS FQTKDMKELL EFHSKVESIL EKLTDDETQVL
551 ARFEGFPEKK LEVIRTAGAL YKKLDGILVE LKNWKIEPPL NDLLDKIERY
601 FNKFKGEIET VERTKDEDK MFKRYNINID FEVLVQVKET MVDVSSNCME
651 LALKERREAN EEAKNGEESK MKEERAKRLW RAFQFAFKVY TFAGGHDERA
701 DCLTRQLAHE IQTDPDQSES SIMS
```

Unformatted sequence string: [724 residues](#) (for pasting into other applications).

Sort by  residue number  increasing mass  decreasing mass  
Show  matched peptides only  predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
105 - 112	861.0502	860.0429	860.4464	-0.4035 1	<b>K.GVSS</b> EARR.S
136 - 157	2444.1979	2443.1907	2443.1182	0.0725 0	R.SVLPG <b>TMMSSNSTS</b> PSLWNL.R.A + 3 Oxidation (M)
164 - 171	928.4443	927.4370	926.5549	0.8821 1	R.LSPVDLKR.F

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
171 - 180	1248.7468	1247.7395	1248.6761	-0.9366 1	K.RFAMQILSQR.D
474 - 480	756.3628	755.3555	755.4654	-0.1098 1	K.SPVKVAR.S
574 - 585	1428.5873	1427.5800	1426.8184	0.7616 1	K.LDGILVELKNWK.I
700 - 724	2833.1854	2832.1782	2831.2702	0.9080 1	R.ADCLTRQLAHEIQTDPDQSESSIMS.-

# Protein View: M1010\_ARATH

Uncharacterized mitochondrial protein AtMg01010 OS=Arabidopsis thaliana GN=AtMg01010 PE=4 SV=1

**Database:** SwissProt  
**Score:** 59  
**Expect:** 0.05  
**Monoisotopic mass (M<sub>r</sub>):** 13161  
**Calculated pI:** 4.59  
**Taxonomy:** [Arabidopsis thaliana](#)

Sequence similarity is available as [an NCBI BLAST search of M1010\\_ARATH against nr.](#)

## Search parameters

**Enzyme:** Trypsin: cuts C-term side of KR unless next residue is P.  
**Fixed modifications:** [Carbamidomethyl \(C\)](#)  
**Variable modifications:** [Oxidation \(M\)](#)  
**Mass values searched:** 4  
**Mass values matched:** 4

## Protein sequence coverage: 30%

Matched peptides shown in **bold red**.

1 **MIGGDSVEAI** ERLLAKYPE GSPSAEIIEM ARIEAEDLFE IKAQIIQR**MA**  
51 **LYDPTGDWMA** **RGAR**ALDNPR TTSGEESLER LYDIWKDLQE TGPLSDEF SR  
101 **LQEKVFLK**KG GPGGDPIA

Unformatted sequence string: [118 residues](#) (for pasting into other applications).

Sort by  residue number  increasing mass  decreasing mass  
Show  matched peptides only  predicted peptides also

Start - End	Observed	Mr(expt)	Mr(calc)	Delta M	Peptide
1 - 12	1277.1298	1276.1226	1275.6129	0.5097 0	<b>-.MIGGDSVEAIER.R</b>
49 - 61	1527.3106	1526.3033	1525.6694	0.6340 0	<b>R.MALYDPTGDWMAR.G</b>
49 - 64	1841.9581	1840.9508	1841.8189	-0.8680 1	<b>R.MALYDPTGDWMARGAR.A + 2 Oxidation (M)</b>
101 - 108	1004.5477	1003.5404	1003.6066	-0.0662 1	<b>R.LQEKVFLK.K</b>