

Name: Jack Reddan
PID: A59010543

[Q1] Tell me the name of a protein you are interested in. Include the species and the accession number. This can be a human protein or a protein from any other species as long as it's function is known.

Name: glutathione reductase
Accession: NP_191026
Species: Arabidopsis thaliana
Function: glutathione-disulfide reductase activity

[Q2] Perform a BLAST search against a DNA database, such as a database consisting of genomic DNA or ESTs. The BLAST server can be at NCBI or elsewhere. Include details of the BLAST method used, database searched and any limits applied (e.g. Organism).

Method: NCBI TBLASTN (v2.12.0) searched against all ESTs
Database: Expressed Sequence Tags [est] database
Organism: None
Results:

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Job TitleNP_191026:glutathione reductase [Arabidopsis...

RIDRONEQBNT013

Search expires on 10-22 01:45 am

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Databaseest

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Query IDNP_191026.1

Descriptionglutathione reductase [Arabidopsis thaliana]

Molecule typeamino acid

Query Length565

Other reports?

Filter Results

Organism

only top 20 will appear

Type common name, binomial, taxid or group name

+ Add organism

Percent Identity

to

E value

to

Query Coverage

to

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Alignments

Taxonomy

Sequences producing significant alignments

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select all

100 sequences selected

GenBank

Graphics

| | Description | Scientific Name | Max Score | Total Score | Query Cover | E value | Per. Ident | Acc. Len | Accession |
|-------------------------------------|--|---------------------|-----------|-------------|-------------|---------|------------|----------|------------|
| <input checked="" type="checkbox"/> | chlorokybus_71836.3_lrc301_c Chlorokybus atmophyticus EST library Chlorokybus atmophyticus cDNA 5' mRNA... | Chlorokybus atm... | 578 | 578 | 87% | 0.0 | 58.61% | 4069 | HO413015.1 |
| <input checked="" type="checkbox"/> | CLS_cLiFroots_12a4_1_j12cLibkit5LD_E06 CLS_cLiFroots_plant Festuca arundinacea cDNA clone 12j12 5'... | Lolium arundinac... | 569 | 569 | 59% | 0.0 | 81.66% | 1063 | GT033527.1 |
| <input checked="" type="checkbox"/> | KP1B_113E21F.06011777 KP1B Nicotiana tabacum cDNA clone KP1B_113E21_mRNA sequence | Nicotiana tabacum | 560 | 560 | 54% | 0.0 | 85.39% | 926 | EB682653.1 |
| <input checked="" type="checkbox"/> | CLS_cLiFpEFSpn_24a2_1_a12cLibkit5LD_A06 CLS_cLiFpEFSpn_plant Festuca pratensis cDNA clone 24a12 5'... | Festuca pratensis | 560 | 560 | 58% | 0.0 | 82.07% | 987 | GO853961.1 |
| <input checked="" type="checkbox"/> | GR_Ea44J17.r GR_Ea Gossypium raimondii cDNA clone GR_Ea44J17 3' mRNA sequence | Gossypium raim... | 545 | 545 | 52% | 0.0 | 84.80% | 891 | CO080876.1 |
| <input checked="" type="checkbox"/> | UFL_352_72 Cotton fiber 0-10 day post anthesis Gossypium hirsutum cDNA mRNA sequence | Gossypium hirsu... | 540 | 540 | 54% | 0.0 | 82.79% | 1014 | ES820783.1 |
| <input checked="" type="checkbox"/> | CHTM8760.b1_P06.ab1 CHT(LMS) Jerusalem artichoke Helianthus tuberosus cDNA clone CHTM8760_mRNA s... | Helianthus tuber... | 518 | 518 | 53% | 1e-180 | 80.67% | 901 | EL456095.1 |
| <input checked="" type="checkbox"/> | KT7C.109E11F.051221T7 KT7 Nicotiana tabacum cDNA clone KT7C.109E11_mRNA sequence | Nicotiana tabacum | 516 | 516 | 50% | 3e-180 | 85.21% | 856 | EB450985.1 |
| <input checked="" type="checkbox"/> | SLA_T3_196_C04_20APRIL2006_028.1 SLA (leaves from unfertilized Solanum tuberosum Shepody) Solanum t... | Solanum tuberos... | 521 | 607 | 69% | 7e-180 | 68.80% | 1307 | JG558174.1 |
| <input checked="" type="checkbox"/> | RR4AZ14TF.RR4(PB) Raphanus raphanistrum subsp. landra cDNA 5' mRNA sequence | Raphanus rapha... | 513 | 513 | 46% | 3e-179 | 93.89% | 804 | EV568609.1 |
| <input checked="" type="checkbox"/> | ZO_Eg0004B15.r ZO_Eg Zingiber officinale cDNA clone ZO_Eg0004B15 3' mRNA sequence | Zingiber officinale | 514 | 514 | 52% | 6e-179 | 80.81% | 892 | DY377800.1 |
| <input checked="" type="checkbox"/> | 53COT5_T3_007_E01_19JUL2004_007 Brassica napus 36hr germinating seed library 53COT5 Brassica napus... | Brassica napus | 512 | 512 | 46% | 8e-179 | 94.30% | 803 | DY020544.1 |
| <input checked="" type="checkbox"/> | CLS_cLiFroots_20a1_1_i03cLibkit5LD_E02 CLS_cLiFroots_plant Festuca arundinacea cDNA clone 20i03 5'... | Lolium arundinac... | 511 | 576 | 60% | 3e-177 | 81.31% | 1019 | GT036447.1 |

Chosen match: Accession H0413015.1, 4069 bp *Chlorokybus atmophytus* mRNA sequence, highlighted in purple above. Alignment details are printed below:

Query: glutathione reductase [Arabidopsis thaliana] Query ID: NP_191026.1 Length: 565

>chlorokybus_71836.3_lrc301_c Chlorokybus atmophyticus EST library Chlorokybus atmophyticus cDNA 5', mRNA sequence
Sequence ID: H0413015.1 Length: 4069
Range 1: 2451 to 3941

Score:578 bits(1489), Expect:0.0,
Method:Compositional matrix adjust.,
Identities:296/505(59%), Positives:363/505(71%), Gaps:17/505(3%)

| | | | |
|-------|------|---|------|
| Query | 52 | LRPRIALLSNHRYHYSRRFS-----VCASTDNGAESDRHYDFDLFTIGAGSGGVRA | 102 |
| | | LRP L HSR+ S V AS++ YD+D+ TIGAGSGGVRA | |
| Sbjct | 3941 | LRPS-GLAQGQSRPHSRQQSRTVQRYGLRVIASSNGSG-----YDYDVITIGAGSGGVRA | 3780 |
| Query | 103 | SRFATSGASAAVCELPFSTISSDTAGGVGGTCVLRGCVPKKLLVYASKYSHEFEDSHGF | 162 |
| | | SR A+ GA A E+PF+ ++SDT GGVGGTCVLRGCVPKKLLVY S +S+EF+DS GF | |
| Sbjct | 3779 | SRIASQLGAKVACVEMPFNNVASDTEGGVGGTCVLRGCVPKKLLVYGSIFSNEFDDDSAGF | 3600 |
| Query | 163 | GWKYETEPSHDWTTLIANKNAELQRLTGIYKNILSKANVKLIEGRGKVIDPHTVDVDGKI | 222 |
| | | GWK EP W TL NKN EL RL +Y+NILSKANV+L+EGR ++D HTVD+DGK | |
| Sbjct | 3599 | GWKLPGEPKFTWQTLNENKNKELTRLNNAVYRNILSKANVELLEGRASLVDAHTVDIDGKQ | 3420 |
| Query | 223 | YTTRNIIIAVGGRRPFIPDIPGKEFAIDSDAALDLPSKPKKIAIVGGGYIALEFAGIFNGL | 282 |
| | | T +NI++A GGR F IPG E AIDSD AL L PK+IAI GGGYIALEFA IF+G | |
| Sbjct | 3419 | LTAKNIILATGGRSFALPIPGAHAIDSDKALSLDEVPKRIAIYGGGYIALEFACIFSGF | 3240 |
| Query | 283 | NCEVHVFIHQKKVLRGFDEEDVRDFVGEQMSLRGIEFHTEESPEAIKAGDGSFSLKTSKG | 342 |
| | | +V VF R LRGFDE++R+ + E++ +GI H + + E I K +G ++LKT+ G | |
| Sbjct | 3239 | GAKVDVIFYRAPLPLRGFDEEIRNALVEELGKKGINLHPKCTAEEIRKEANGEYTLKTNCG | 3060 |
| Query | 343 | TVEGFSHVMFATGRKPNTKNLGLENVGVKMAKNGAIEVDEYSQTSVPSIWAVGDVTDRIN | 402 |
| | | + VMFATGR PNTK L L+ VGV + GAI VDEYS+T+VP+I+A+GDVT+RIN | |
| Sbjct | 3059 | EFKA-DLVMFATGRTPNTKYLNLDVAVGVDTEKGAIIVDEYSRTTVPNIFAIGDVTNRIN | 2883 |
| Query | 403 | LTPVALMEGGALAKTLFQNEPTKPDYRAVPCAVFSQPPIGTVGLTEEQAIEQYGDVDVYT | 462 |
| | | LTPVALMEG A+AKT+ Q EPTKPD+ VP AVF+QPPIGT GLTEE+A EQ+ +VDVYT | |
| Sbjct | 2882 | LTPVALMEGTAVAKTI-QGEPTKPDHVNVPASVFTQPPIGTAGLTEEEAKEQFDEVDVYT | 2706 |
| Query | 463 | SNFRPLKATLSGLPDRVFMKLIVCANTNKVLGVHMCGEDSPEIIQGFVAVKAGLTKADF | 522 |
| | | S+FRP+K T+SG +R MK+IV T+KVLG+HM GE SPEI+QGF VA+K G TK | |
| Sbjct | 2705 | SSFRPMKHTISGRDERSLMKIIVDVKTDKVLGIHMLGESSPEILQGFVAVALKCGATKKQL | 2526 |
| Query | 523 | DATVGVHPTAAEEFVTMRAPTRKFR | 547 |
| | | DAT+G+HPTAAEEFVTMR TR+ R | |
| Sbjct | 2525 | DATIGIHPTAAEEFVTMRTVTRQHR | 2451 |

[Q3] Gather information about this “novel” protein. At a minimum, show me the protein sequence of the “novel” protein as displayed in your BLAST results from [Q2] as FASTA format (you can copy and paste the aligned sequence subject lines from your BLAST result page if necessary) or translate your novel DNA sequence using a tool called EMBOSS Transeq at the EBI. Don’t forget to translate all six reading frames; the ORF (open reading frame) is likely to be the longest sequence without a stop codon. It may not start with a methionine if you don’t have the complete coding region. Make sure the sequence you provide includes a header/subject line and is in traditional FASTA format.

Chosen sequence [from EMBOSS Transeq of the TBLASTN result in Q2]:

>2451-3941_6 chlorokybus_71836.3_lrc301_c Chlorokybus atmophyticus EST library
Chlorokybus atmophyticus cDNA 5', mRNA sequence

```
ALLPAPRVAAVATRSSSSRRSELPGLLARPLGVSRFRGFSGLRPSGLAQGQSRPHSRQQ  
SRTVQRYGLRVIASSNGSGYDYDVITIGAGSGGVRASRIASQLGAKVACVEMPFFNNVASD  
TEGGVGGTCVLRGCVPKLLVYGSIFSNEFDDSDAGFGWKLPGEPKFTWQTLNENKNKELT  
RLNNVYRNILSKANVELLEGRASLVDADHTVDIDGKQLTAKNIILATGGRSFALPIPGA  
AIDSDKALSLEVPKRIAIYGGGYIALEFACIFSGFGAKVDVFYRAPLPLRGFDEEIRNA  
LVEELGKKGINLHPKCTAEIRKEANGEYTLKTNCGEFKADLVMFATGRTPNTKYLNLDA  
VGVDTEKGAIVVDEYSRTTPNIFAIGDVTNRINLTPVALMEGTAVAKTIQGEPTKPDH  
VNVPSAVFTQPPIGTAGLTEEEAKEQFDEVDVYTSSFRPMKHTISGRDERSLMKIIIVDK  
TDKVLGIHMLGESSPEILQGFVAALKCGATKKQLDATIGIHPTAAEEFVTMRTVTRQHRK  
EKQQQQEEKEKVAANK*
```

Name (Unofficial): *Chlorokybus* glutathione reductase.

Species: *Chlorokybus atmophyticus*: Cellular organisms;
Eukaryota; Viridiplantae; Streptophyta;
Chlorokybophyceae; Chlorokybales; Chlorokybaceae;
Chlorokybus

[Q4] Prove that this gene, and its corresponding protein, are novel. For the purposes of this project, “novel” is defined as follows. Take the protein sequence (your answer to [Q3]), and use it as a query in a blastp search of the nr database at NCBI.

Conducted a BLASTP search against the NR database using the protein sequences listed in [Q3]:

Method: NCBI BLASTP (v2.12.0) searched all nr protein entries
Database: non-redundant protein sequences [nr] database
Organism: *None*

Results:

BLAST » blastp suite » results for RID-R0R28H65016

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Job Title

2451-3941_6 chlorokybus_71836.3_lrc301_c Chlorokybus...

RID

[R0R28H65016](#) Search expires on 10-22 02:13 am [Download All](#)

Program

BLASTP [Citation](#)

Database

nr [See details](#)

Query ID

lcl|Query_53894

Description

2451-3941_6 chlorokybus_71836.3_lrc301_c Chlorokybus ...

Molecule type

amino acid

Query Length

557

Other reports

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Organism

only top 20 will appear

☐ exclude

Type common name, binomial, taxid or group name

[Add organism](#)

Percent Identity

E value

Query Coverage

to

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Sequences producing significant alignments

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| | Description | Scientific Name | Max Score | Total Score | Query Cover | E value | Per. Ident | Acc. Len | Accession |
|-------------------------------------|--|-------------------------------------|-----------|-------------|-------------|---------|------------|----------|--------------------------------|
| <input checked="" type="checkbox"/> | Glutathione reductase [Klebsormidium nitens] | Klebsormidium n... | 616 | 616 | 86% | 0.0 | 63.04% | 580 | GAQ78357.1 |
| <input checked="" type="checkbox"/> | glutathione reductase [Pyrus ussuriensis x Pyrus communis] | Pyrus ussuriensi... | 603 | 603 | 95% | 0.0 | 56.34% | 559 | KAB2627620.1 |
| <input checked="" type="checkbox"/> | hypothetical protein C1H46_000718 [Malus baccata] | Malus baccata | 602 | 602 | 96% | 0.0 | 56.19% | 560 | TQE13711.1 |
| <input checked="" type="checkbox"/> | hypothetical protein DVH24_010675 [Malus domestica] | Malus domestica | 599 | 599 | 96% | 0.0 | 55.82% | 590 | RXH98350.1 |
| <input checked="" type="checkbox"/> | glutathione reductase_chloroplastic-like [Malus domestica] | Malus domestica | 599 | 599 | 96% | 0.0 | 55.82% | 560 | XP_028958518.1 |
| <input checked="" type="checkbox"/> | PREDICTED: glutathione reductase_chloroplastic [Pyrus x bretschneideri] | Pyrus x bretschn... | 595 | 595 | 95% | 0.0 | 56.05% | 559 | XP_009367745.1 |
| <input checked="" type="checkbox"/> | glutathione reductase [Pyrus ussuriensis x Pyrus communis] | Pyrus ussuriensi... | 595 | 595 | 96% | 0.0 | 55.64% | 560 | KAB2636727.1 |
| <input checked="" type="checkbox"/> | hypothetical protein DVH24_021775 [Malus domestica] | Malus domestica | 595 | 595 | 95% | 0.0 | 55.68% | 600 | RXH86502.1 |
| <input checked="" type="checkbox"/> | glutathione reductase_chloroplastic-like [Malus domestica] | Malus domestica | 595 | 595 | 95% | 0.0 | 55.68% | 560 | XP_008393844.1 |
| <input checked="" type="checkbox"/> | hypothetical protein H5410_047701 [Solanum commersonii] | Solanum comme... | 594 | 594 | 88% | 0.0 | 59.48% | 557 | KAG5587267.1 |
| <input checked="" type="checkbox"/> | PREDICTED: glutathione reductase_chloroplastic-like [Pyrus x bretschneideri] | Pyrus x bretschn... | 593 | 593 | 95% | 0.0 | 55.78% | 560 | XP_009354878.1 |
| <input checked="" type="checkbox"/> | hypothetical protein KY289_036763 [Solanum tuberosum] | Solanum tuberos... | 592 | 592 | 89% | 0.0 | 58.97% | 557 | KAH0636848.1 |

The top result was glutathione reductase in *Klebsormidium nitens* highlighted in purple above. Alignment is printed below:

Query: 2451-3941_6 chlorokybus_71836.3_lrc301_c Chlorokybus atmophyticus EST
Library Chlorokybus atmophyticus cDNA 5', mRNA sequence Query ID: lcl|Query_53894
Length: 557

>Glutathione reductase [Klebsormidium nitens]
Sequence ID: GAQ78357.1 Length: 580
Range 1: 93 to 579

Score:616 bits(1588), Expect:0.0,
Method:Compositional matrix adjust.,
Identities:307/487(63%), Positives:366/487(75%), Gaps:3/487(0%)

| | | | |
|-------|-----|--|-----|
| Query | 73 | ASSNGSGYDYDVITIGAGSGGVRASRIASQLGAKVACVEMPFNNVASDTEGGVGGTCVLR | 132 |
| | | ++ +G +DYD+ TIGAGSGGVRASR ASQ GAKVA E+PF+ ASD +GGVGGTCVLR | |
| Sbjct | 93 | STEDGQQFDYDLFTIGAGSGGVRASRFASQYGAKVAVCELPFSTKASDDKGGVGGTCVLR | 152 |
| Query | 133 | GCVPKKLLVYGSIFSNEFDDSAGFGWKLPG-EPKFTWQTLNENKNKELTRLNNVYRNILS | 191 |

| | | | |
|-------|-----|--|-----|
| Sbjct | 153 | GCVPKKLLVYGS F++ F+DS GFGW PG EP+ W L E KNKEL RLNN Y+ L GCVPKKLLVYGSHFADYFEDSRGFGWSFPGGEPEVDWSHLIEKKNKELDRLNNAYKTTLK | 212 |
| Query | 192 | KANVELLEGRASLVDAHTVDIDGKQLTAKNIILATGGRSFALPIPGAHAIDSDKALS LD A V+L+EG+ ++VD HTVD+DGK+ KNI++ATGGR F PIPGAEH I SD AL L | 251 |
| Sbjct | 213 | NAKVDLIEGKGTIVDRHTVDVDGKRFKVKNIL IATGGRIFVPPIPGAEHVITSDDALDLT | 272 |
| Query | 252 | EVPKRIAIYGGGYIALEFACIFSGFGAKVDVFYRAPLPLRGFDEEIRNALVEELGKKGIN VP +IAI GGGYIALEFA IF+ GA+VD+F R LRGFD+E+R L E+L +GI | 311 |
| Sbjct | 273 | SVPSKIAIVGGGYIALEFAGIFNSAGA EVDIFVRGDKLLRGFDDEVREFLAELQAQGIR | 332 |
| Query | 312 | LHPKCTAEEIRKEANGEYTLKTNCGE-FKADLVMFATGRTPNTKYLNLDAVGVD TTEKGA +H EI K + TLKT G+ ++ VMFATGR PN K L L+ GVD +K A | 370 |
| Sbjct | 333 | IHFGAKPVEIEKRDEDQLTLKTEQGDTWQGSHVMFATGRRPNIKGLGLEEAGVDVDDKTA | 392 |
| Query | 371 | IVVDEYSRTTVPNIFAIGDVTNRINLTPVALMEGTAVAKT-IQGEPTKPDHVNVP SAVFT I VDEYSRT+V NI+A+GDVT+RINLTPVALMEG A AKT Q EPTKPDH NVPSAVFT | 429 |
| Sbjct | 393 | IKVDEYSRTSVDNIWAVGDVTD RINLTPVALMEGMAFAKTAFQDEPTKPDHTNVPSAVFT | 452 |
| Query | 430 | QPPIGTAGLTEEEAKEQFDEVDVYTSSFRPMKHTISGRDERSLMKIIVDVKTDKVLGIHM PPIGT GLTE EA EQ+ +VDV+TS+FRPMK TISG R+ +KI+VD TDKV+G+HM | 489 |
| Sbjct | 453 | NPPIGTVGLTEAEAVEQYGDVDVFTSTFRPMKSTISGNPVRTFVKILVDAATDKVIGLHM | 512 |
| Query | 490 | LGESSPEILQGFAVALKCGATKKQLDATIGIHPTAAEEFVTMRTVTRQHRKEKQQQQQEE GE PEI+QGFAVA++ G TKKQ+D+T+GIHPT+AEE VTMRT TRQ RKE+ Q + E | 549 |
| Sbjct | 513 | CGEDGPEIMQGFAVAVRMGVTKKQMDSTVGIHPTS AEELVTMRTPTRQIRKEEAQNGKGE | 572 |
| Query | 550 | KEKVAAA 556 KE AAA | |
| Sbjct | 573 | KEMAAAA 579 | |

This result matches almost all classification of “novel” for this class project:

- There is no 100% match found in the database for the protein sequence in the original species (*Chlorokybus atmophyticus*).
- The top match reported has less than 100% identity.
- There is no 100% match to a different species (redundant to above).
- x There are no database matches to the original query when no organism is specified, but when you refine the search to the original query (*Arabidopsis thaliana*) there is a database match (see below):

◀ Edit Search

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i Your search is limited to records that include: Arabidopsis thaliana (taxid:3702)

| | |
|---------------|--|
| Job Title | 2451-3941_6 chlorokybus_71836.3_lrc301_c Chlorokybus... |
| RID | R0RYHSJJ013 Search expires on 10-22 02:28 am Download All ▾ |
| Program | BLASTP ? Citation ▾ |
| Database | nr See details ▾ |
| Query ID | Icl Query_77954 |
| Description | 2451-3941_6 chlorokybus_71836.3_lrc301_c Chlorokybus ... |
| Molecule type | amino acid |
| Query Length | 557 |
| Other reports | Distance tree of results Multiple alignment MSA viewer ? |

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Organism only top 20 will appear ☐ exclude

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to

E value

to

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| | Description ▾ | Scientific Name ▾ | Max Score ▾ | Total Score ▾ | Query Cover ▾ | E value ▾ | Per. Ident ▾ | Acc. Len ▾ | Accession |
|-------------------------------------|---|--------------------------------------|-------------|---------------|---------------|-----------|--------------|------------|--------------------------------|
| <input checked="" type="checkbox"/> | Glutathione reductase, chloroplast precursor [Arabidopsis thaliana] | Arabidopsis thaliana | 588 | 588 | 93% | 0.0 | 56.90% | 565 | AAK96868.1 |
| <input checked="" type="checkbox"/> | glutathione reductase [Arabidopsis thaliana] | Arabidopsis thaliana | 586 | 586 | 93% | 0.0 | 56.71% | 565 | NP_191026.1 |
| <input checked="" type="checkbox"/> | GR [Arabidopsis thaliana] | Arabidopsis thaliana | 586 | 586 | 93% | 0.0 | 56.71% | 565 | OAP01378.1 |
| <input checked="" type="checkbox"/> | glutathione-disulfide reductase [Arabidopsis thaliana] | Arabidopsis thaliana | 519 | 519 | 83% | 2e-180 | 53.83% | 499 | NP_001030756.2 |
| <input checked="" type="checkbox"/> | putative glutathione reductase [Arabidopsis thaliana] | Arabidopsis thaliana | 519 | 519 | 83% | 2e-180 | 53.83% | 499 | AAK25938.1 |
| <input checked="" type="checkbox"/> | unnamed protein product [Arabidopsis thaliana] | Arabidopsis thaliana | 493 | 493 | 83% | 2e-159 | 52.77% | 1445 | CAD5323997.1 |
| <input checked="" type="checkbox"/> | glutathione reductase, cytosolic [Arabidopsis thaliana] | Arabidopsis thaliana | 275 | 275 | 41% | 8e-89 | 58.01% | 242 | BAD95212.1 |
| <input checked="" type="checkbox"/> | lipoamide dehydrogenase 1 [Arabidopsis thaliana] | Arabidopsis thaliana | 186 | 186 | 92% | 4e-51 | 30.36% | 570 | NP_566562.1 |
| <input checked="" type="checkbox"/> | unnamed protein product [Arabidopsis thaliana] | Arabidopsis thaliana | 186 | 186 | 92% | 8e-51 | 30.36% | 623 | CAA0382694.1 |
| <input checked="" type="checkbox"/> | lipoamide dehydrogenase 1 [Arabidopsis thaliana] | Arabidopsis thaliana | 186 | 186 | 92% | 1e-50 | 30.36% | 623 | NP_001078165.1 |