

# Data panel

In the data panel you will see several columns:

- Gene name (symbol)
- Gene ID (see details in [Search](#))
- UniProt ID
- Organism
- Protein name
- This information was extracted from the ProteinName field of the FASTA header in the UniProt protein FASTA file (<https://www.uniprot.org/help/fasta-headers>).
- Functional annotations (GO aspects Molecular Function (F) and Biological Process (P))
- This information was extracted from GOC (<http://geneontology.org/>). Annotation supported by experimental evidence is indicated by a yellow flask icon. Annotation propagated from ancestral genes (GO evidence code IBA) is indicated by a green tree glyph. Experimental evidence are:
  - IDA: direct assay
  - IMP: mutant phenotype
  - IGI: genetic interaction
  - IPI: physical interaction
  - IEP: expression pattern
  - EXP: experimental evidence

<div>  Show MSA &gt; 3 Cols Hidden         </div>		<div> <div> </div> <div> </div> </div>											
Gene	Organism	arsenate ion trans...	high-affinity inorg...	inorganic phospho...	low-affinity phosph...	sodium:inorganic ...	solute:proton sym...	tellurite transmem...	zinc ion transmem...	arsenate ion trans...	phosphate ion tran...	phosphate ion tran...	sodium ion tran...
Bra034242	Brassica rapa subsp. pekin...												
PHT2-1	Arabidopsis thaliana												
CISIN_1g0120382mg	Citrus sinensis												
CISIN_1q0120383mq	Citrus sinensis												

Uniprot ID: Q38954			
GO term	Evidence description	Reference	More
low-affinity phosphate transmembrane transporter activity	direct assay	1	<a href="#">QuickGO</a>
<div>OK</div>			

Within the Functional annotations, each listed GO term has annotation to **at least one** member of the gene family. A yellow flask or a green tree icon in a gene row underneath a GO term indicates the presence of that particular function in that gene supported either by experimental evidence or phylogenetic inference, respectively. Clicking on any of the icons will open a popup window where details about the functional annotation can be found. The columns in the popup include:

- GO term: Shows the GO term name, which is hyperlinked to the term detail page in GOC.
- Evidence description: Shows the type of evidence that supports the annotation of the GO term to the gene/protein.
- Reference: Shows the publication(s) containing the evidence supporting the GO annotation. We use digits (i.e., 1, 2, etc.) to indicate each distinct reference. Each number is a hyperlink to the PubMed record for the article.
- More: Clicking 'QuickGO' takes you to the complete annotation record of the gene (UniProt protein) in QuickGO. You will likely find annotations with other types of evidence, and annotations to cellular components.
- Subfamily name
- Subfamilies within each family are groups of genes that share a particularly high degree of similarity due to limited divergence from their common ancestor. Subfamilies are, in general, closely-related orthologs. [More about subfamilies](#)

**Tips:** Only seeing partial text in some data cells? Mouse over the '...', a tool tip will popup in a few seconds with the complete text.

### Show/hide and reorder columns in the data panel

Clicking on the configuration icon located at the top left corner of data panel, you will see a popup menu.

The image shows a data panel with a configuration icon (gear) in the top left corner. A red arrow points from this icon to a popup menu titled "Customize gene info table (3 Cols Hidden)". The popup menu allows users to check or uncheck columns and reorder them using up and down arrows. The columns listed are Gene, Organism, and Molecular function. Under Molecular function, several GO terms are listed, some of which are checked. The data table in the background shows columns for Gene, Organism, and several molecular functions. The table has two rows of data: PHO89 from Saccharomyces cerevisiae and OT\_ostta02g02460 from Ostreococcus tauri. The table also shows several columns for molecular functions, some of which are truncated with ellipses. The table has a light blue header and a light gray body. The popup menu has a white background and a gray border. The "Update Table" and "Close" buttons are at the bottom right of the popup menu.

Gene	Organism	high-affinity inorg...	low-affinity phosph...	tellurite transmem...	zinc ion transmem...	arsenate ion trans...	phosphate ion tran...
PHO89	Saccharomyces cerevisiae						
OT_ostta02g02460	Ostreococcus tauri						

Customize gene info table (3 Cols Hidden)

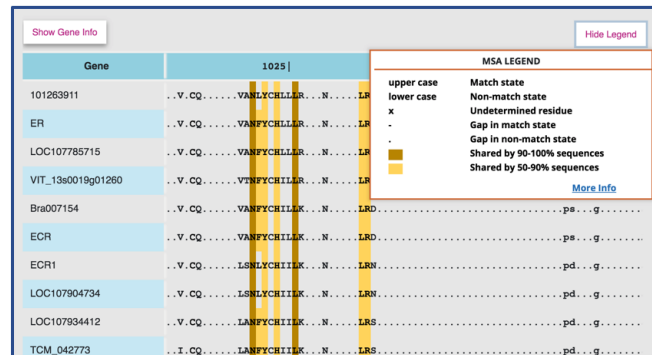
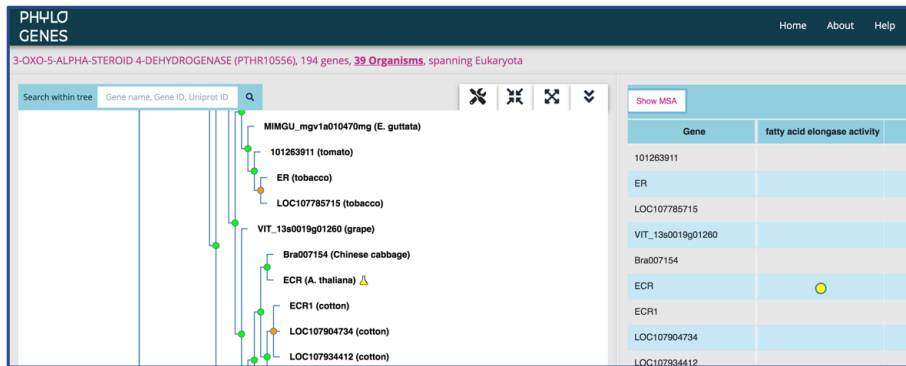
- ☒ Gene
- ☒ Organism
- ☒ Molecular function
  - ☐ arsenate ion transmembrane transporter activity
  - ☒ high-affinity inorganic phosphate:sodium symporter activity
  - ☐ inorganic phosphate transmembrane transporter activity
  - ☒ low-affinity phosphate transmembrane transporter activity
  - ☐ sodium:inorganic phosphate symporter activity

Update Table Close

Within the popup configuration menu you can:

- Check or uncheck a particular column or a particular GO term to see or hide it from the data panel.
- Use the up or down arrow to relocate (reorder) columns or GO terms.

### Toggle to see the multiple sequence alignment (MSA) of a gene family



The MSA is built using the MAFFT software and represents an alignment across the entire length of all protein sequences in a **PANTHER family** (please see [here](#) for difference between a PANTHER family and a PhyloGenes family.) The sequence of an internal node is deduced from all of its child nodes, and is shown in the MSA when the child nodes are collapsed in the gene family tree.

- an uppercase letter: the residue is shared by at least 30% of sequences at the same position. It is considered more conserved (aka match state). Only match state residues are used in constructing PANTHER HMMs. When looking at the sequence of an internal node, the uppercase letter X indicates an undetermined ancestral residue.
- a lowercase letter: less conserved amino acid residue (aka non-match state). The lower case letter x represents an undetermined ancestral residue.
- a dash symbol (-): a gap in a match state site
- a dot symbol (.): a gap in a non-match state site

Higher sequence similarities shared among proteins in a **PhyloGenes family** are indicated with color shadings in MSA.

- a darker shading over an amino acid residue indicates that the residue is shared by 90% or more sequences at the same position.
- a lighter shading indicates a residue shared by more than 50% but less than 90% of sequences.
- the identity is calculated by including all protein sequences in a PhyloGenes family.
- sequence similarity is recalculated when a user chooses to run 'prune tree by organism'. The pruned protein sequences are excluded in recalculating sequence similarity.