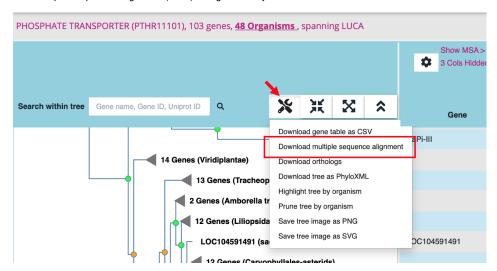# Multiple sequence alignment

The Multiple Sequence Alignment (MSA) of a gene family can be downloaded as a FASTA file.

The default MSA file contains amino acid sequences of all members in the PhyloGenes gene family. When you prune the tree (remove genes of certain organisms), then download MSA, the MSA will exclude those pruned genes. Read more about the MSA

The sequence FASTA header is formatted as:

>UniProt ID|Organism full name|Gene ID

For example:

>A8J0U2|Chlamydomonas reinhardtii|CHLREDRAFT_196438