

Multiple sequence alignment

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

The screenshot shows the PhyloGenes web interface for the gene family PHOSPHATE TRANSPORTER (PTHR11101). The header indicates 103 genes from 48 organisms. A search bar is present. A phylogenetic tree is displayed with a dropdown menu open, showing options for downloading the MSA. The option 'Download multiple sequence alignment' is highlighted with a red box. Other options include 'Download gene table as CSV', 'Download orthologs', 'Download tree as PhyloXML', 'Highlight tree by organism', 'Prune tree by organism', 'Save tree image as PNG', and 'Save tree image as SVG'. The tree shows clades such as 14 Genes (Viridiplantae), 13 Genes (Tracheophytes), 2 Genes (Amborella trichomanes), 12 Genes (Liliopsida), and 12 Genes (Carophyllales-asterids).

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