

# 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 interface includes a search bar, a phylogenetic tree, and a dropdown menu for downloading the multiple sequence alignment. The dropdown menu is open, showing options such as "Download gene table as CSV", "Download multiple sequence alignment" (highlighted with a red box), "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 14 genes from Viridiplantae, 13 genes from Tracheophytes, 2 genes from Amborella trichomanes, 12 genes from Liliopsida, and 12 genes from Caryophyllales-asterids. The gene LOC104591491 is highlighted in the tree.

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