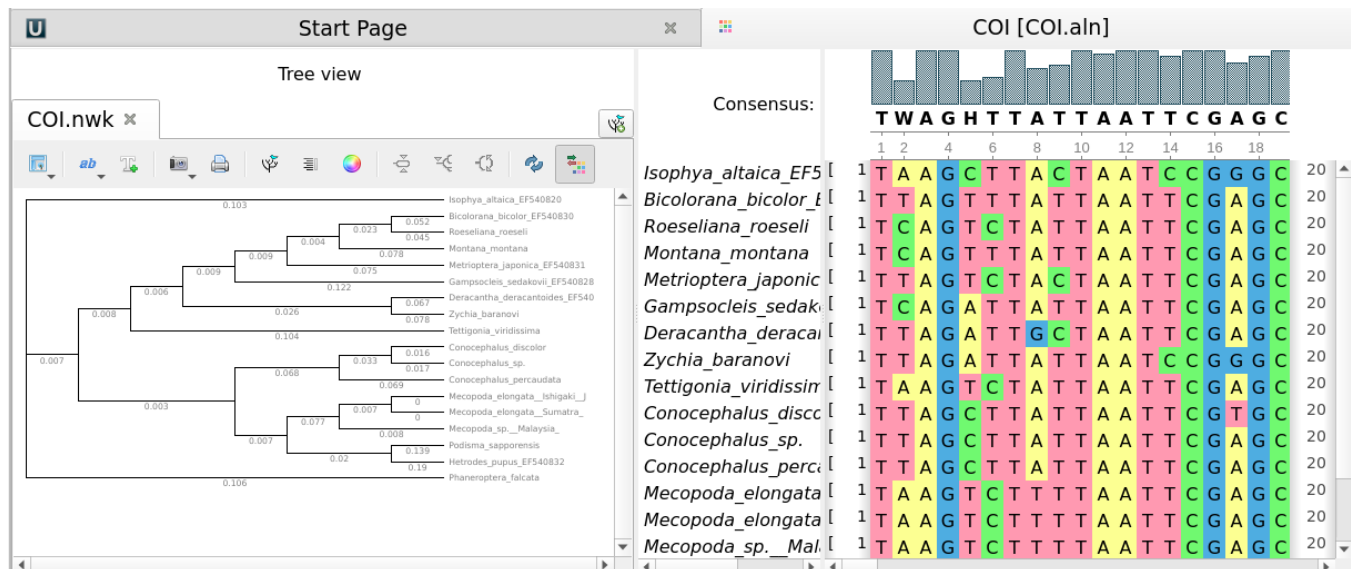


# Phylogenetic Tree Viewer

The *Phylogenetic Tree Viewer* is intended to display a phylogenetic tree built from an alignment or loaded from a file (e.g. a Newick file).



By default, a phylogenetic tree is synchronized with the corresponding alignment.



To disable/enable synchronization use the *Tree and Alignment synchronization* button.

To load a tree from a file follow the instruction described in the [Opening Document](#) paragraph or use the *Tree settings* tab of the *Options Panel*. For example, you may open the \$UGENE\data\samples\Newick\COI.nwk sample file provided within UGENE package.

To build a tree from a multiple sequence alignment see the [Building Phylogenetic Tree](#) paragraph.

To learn what you can do with a tree using UGENE Phylogenetic Tree Viewer read the documentation below.

- [Tree Settings](#)
  - [Selecting Tree Layout and View](#)
  - [Modifying Labels Appearance](#)
    - [Showing and Hiding Labels](#)
    - [Aligning Labels](#)
    - [Changing Labels Formatting](#)
  - [Adjusting Branch Settings](#)
  - [Adjusting Tree nodes](#)
- [Zooming Tree](#)
- [Working with Clade](#)
  - [Selecting Clade](#)
  - [Collapsing and Expanding Branches](#)
  - [Swapping Siblings](#)
  - [Zooming Clade](#)
  - [Adjusting Clade Settings](#)
  - [Changing Root](#)
- [Exporting Tree Image](#)
- [Printing Tree](#)