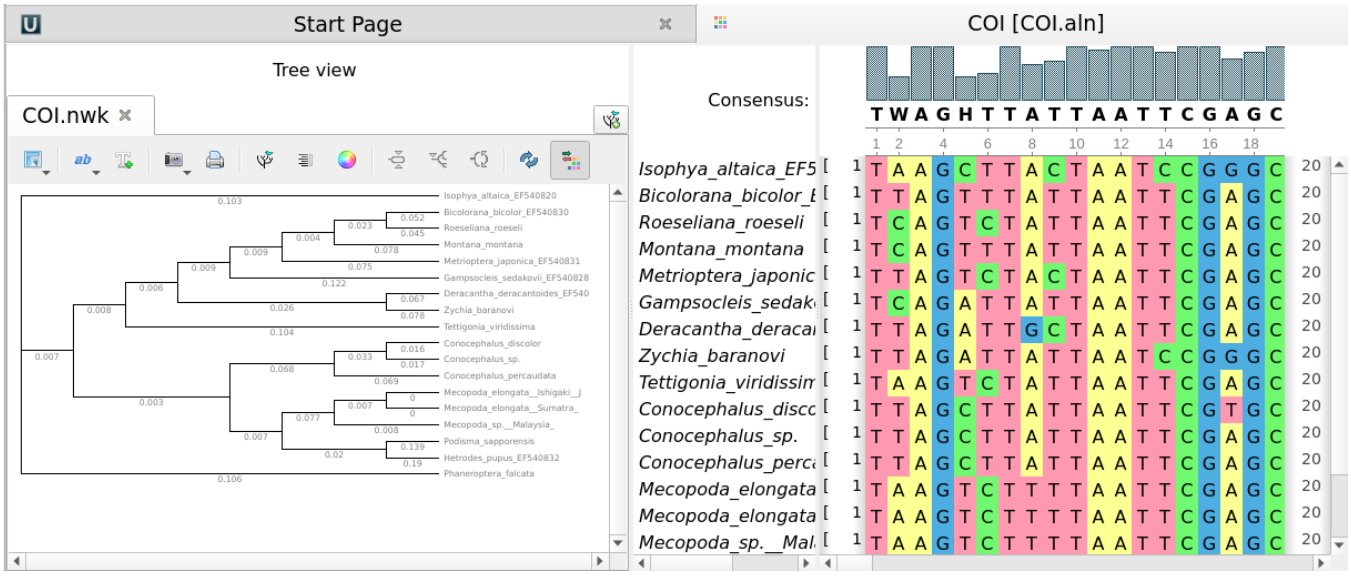
Phylogenetic Tree Viewer

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