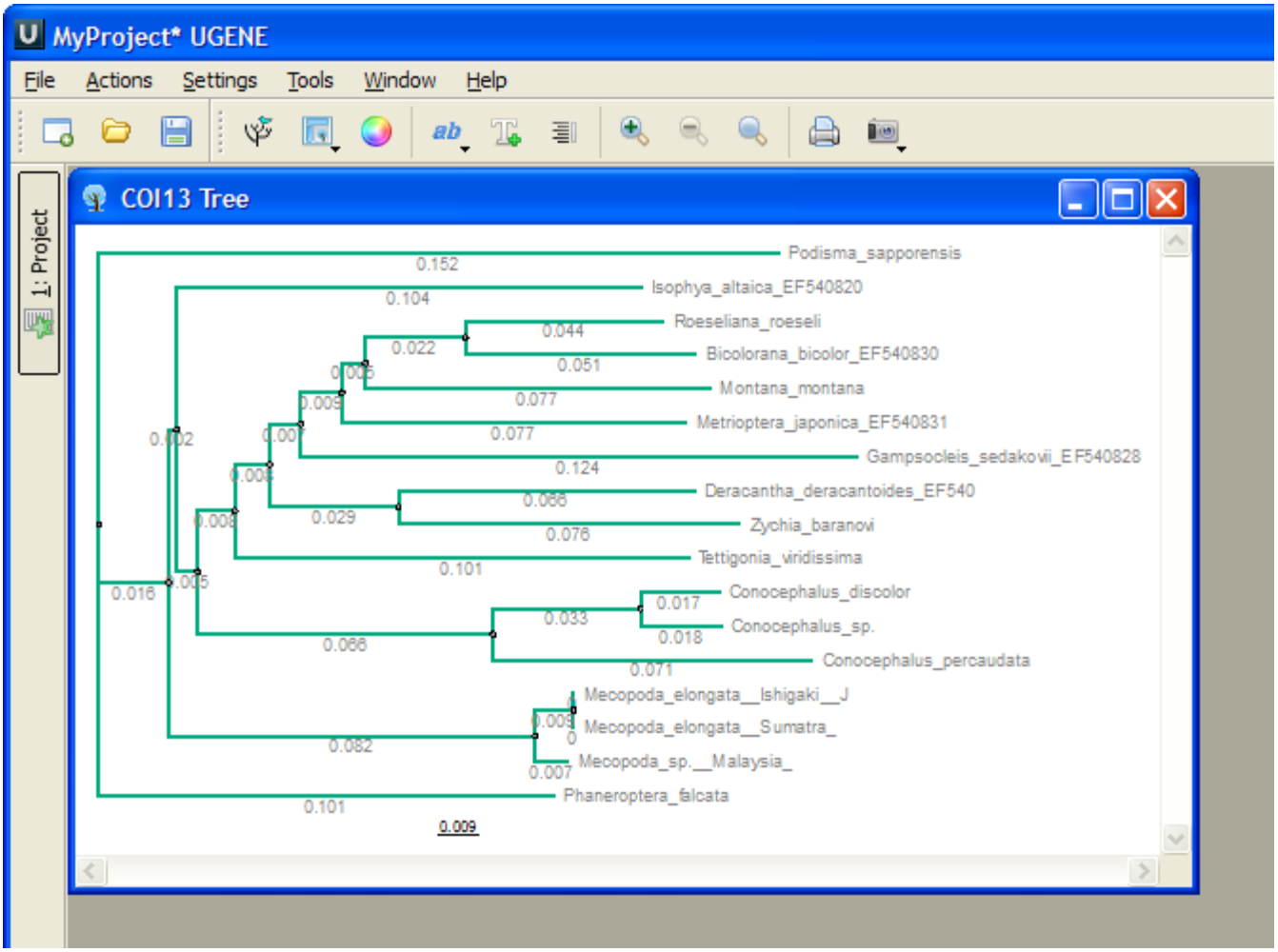
Phylogenetic Tree Viewer

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).



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/Hiding Labels
        - Aligning Labels
        - Changing Labels Formatting
    - Adjusting Branch Settings
- Zooming Tree
- Working with Clade
    - Selecting Clade
    - Collapsing/Expanding Branches
    - Swapping Siblings
    - Zooming Clade
    - Adjusting Clade Settings
    - Changing Root
- Exporting Tree Image
- Printing Tree