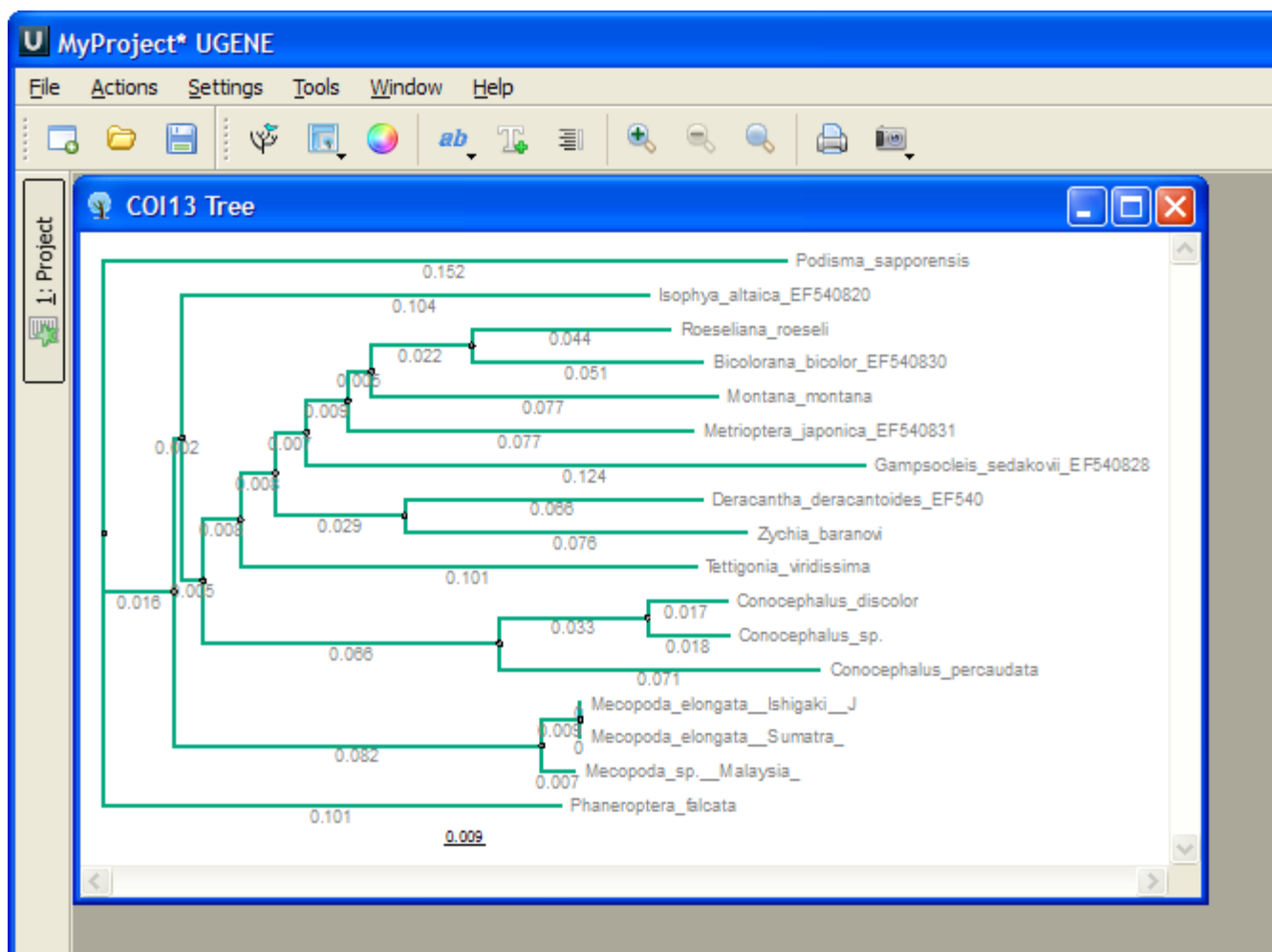


Phylogenetic Tree Viewer

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