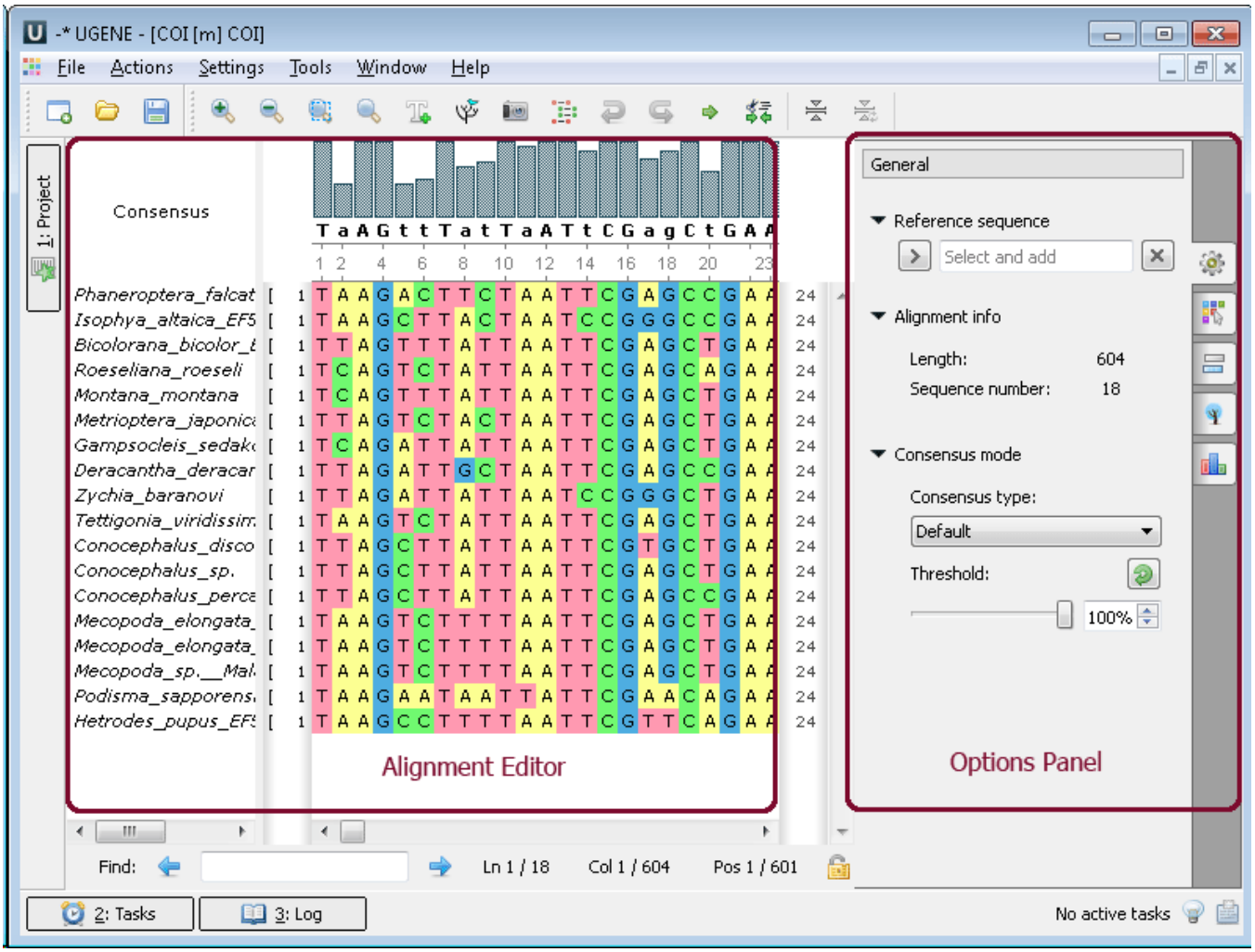
View, edit and align multiple sequence alignments

Multiple sequence alignment (*MSA Editor*). The *Alignment Editor* is a powerful tool for visualization and editing DNA, RNA or protein multiple sequence a lignments. To activate the *Alignment Editor* open any alignment le. For example you can use the $*ugene/data/samples/CLUSTALW/COI.aln* le provided with UGENE. After opening the le in UGENE the *Alignment Editor* window appears:



The editor supports dierent multiple sequence alignment (MSA) formats, such as ClustalW, MSF and Stockholm. The editor provides interactive visual representation which includes:

- Navigation through an alignment;
- Optional coloring schemes (for example Clustal, Jalview like, etc.);
- Flexible zooming for large alignments;
- Export publication-ready images of alignment;
- Several consensus calculation algorithms.

Using the *Alignment Editor* you can:

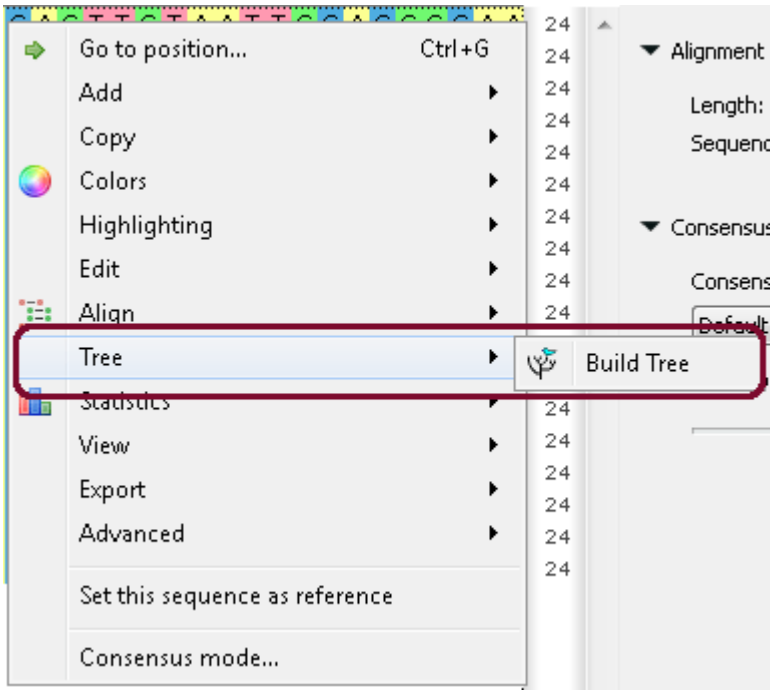
- Perform multiple sequence alignment using integrated MUSCLE and KAlign algorithms;
- Edit an alignment: delete/copy/paste symbols, sequences and subalignments;
- Build phylogenetic trees;
- Generate grid proles;
- Build Hidden Markov Model proles to use with HMM2/HMM3 tools.

Example 2: Build a tree from your alignment. You can do this by three different ways:

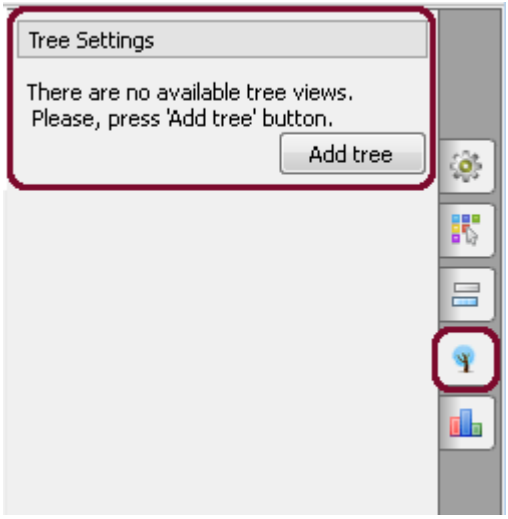
a. From the toolbar. Click to the tree icon:



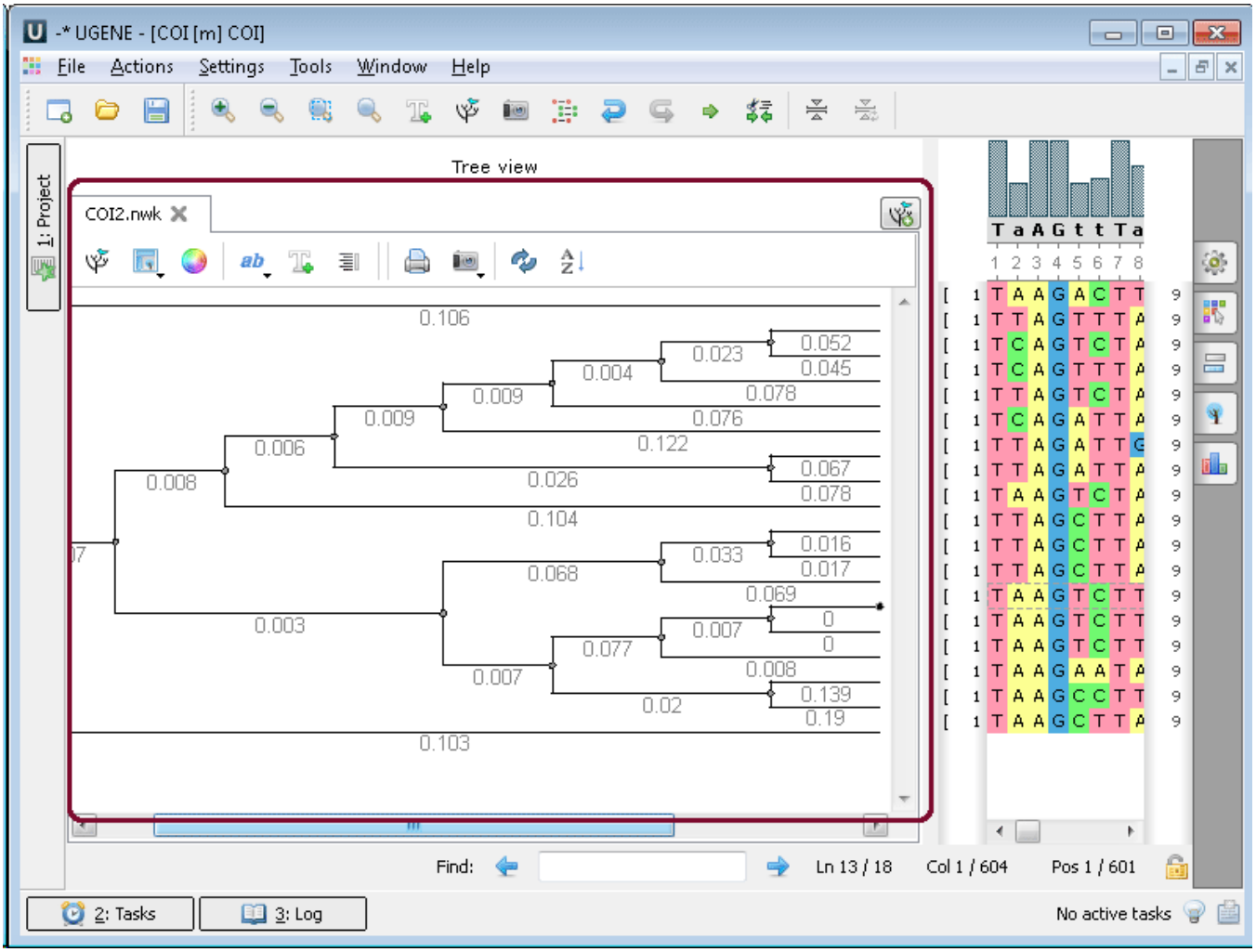
b. From the context menu:



c. From the Options Panel:



After calculation the tree appears in the MSA Editor in a separate window:


-* UGENE - [COI [m] COI]
File
Actions
Settings
Tools
Window
Help
1: Project
Tree view
COI2.nwk
0.106
0.023
0.052
0.004
0.045
0.009
0.078
0.009
0.076
0.122
0.006
0.008
0.067
0.026
0.078
0.104
0.033
0.016
0.068
0.017
0.069
0.003
0.007
0
0.077
0
0.008
0.007
0.139
0.02
0.19
0.103
Find:
Ln 13 / 18
Col 1 / 604
Pos 1 / 601
2: Tasks
3: Log
No active tasks