Aligning Sequences

The *Alignment Editor* integrates several popular multiple sequence alignment algorithms. Below is the list of available algorithms and links to the documentation:

- Port of the popular *MUSCLE3* algorithm.
- KAlign plugin: effective work with huge alignments.
- ClustalW and MAFFT: these algorithms appeared in the version 1.7.2 of UGENE with the *External Tools* plugin.
- T-Coffee: this alignment algorithm is available since version 1.8.1 of UGENE with the *External Tools* plugin.

To align sequences choose a preferred alignment method in the *Actions* main menu, in the context menu or by *Align* main toolbar button .

Also you may find useful the following video tutorials devoted to the multiple sequence alignment:

- Making a multiple sequence alignment from FASTA file
- Working with large alignments in UGENE
- Performing profile-to-profile and profile-to-sequence MUSCLE alignments
- Running remote MUSCLE task