

Aligning Sequences

UGENE integrates several popular tools for aligning a set of sequences. Some of the tools are embedded as external into UGENE, so to have all the tools available out-of-the-box, it is recommended to install a [UGENE full package](#). The list of the tools with the links to the corresponding documentation chapters can be found below:

- [MUSCLE](#)
- [ClustalW](#)
- [ClustalO](#)
- [MAFFT](#)
- [T-Coffee](#)
- [KAlign](#)

The sequences can be aligned in the [UGENE Alignment Editor](#). To align sequences in it, do one of the following:

- Open the *Align* menu in the Alignment Editor context menu
- Select *Actions > Align* item in the main menu
- Select the following button on the Alignment Editor toolbar:



And then, in the appeared menu, select one of the items that corresponds to a tool that you want to use to align your sequences, for example, *Align with MUSCLE*. After that, follow the documentation of the selected tool to set up the parameters and align the sequences.



To align any sequences opened in UGENE, you should first open them in the Alignment Editor. To do that, for example, select the corresponding sequence objects in the [Project View](#) and [export the sequences as alignment](#).

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](#)