Alignment Editor Features

The *Alignment Editor* is a powerful tool for visualization and editing DNA, RNA or protein multiple sequence alignments. The editor supports different multiple sequence alignment (MSA) formats, such as ClustalW, MSF and Stockholm. The full list of file formats supported in UGENE is *here*.

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 profiles;
- Build Hidden Markov Model profiles to use with HMM2/HMM3 tools.