

Key Features

- Creating, editing and annotating **nucleic acid** and **protein** sequences
- Search through online databases: **NCBI**, **ENSEMBL**, **PDB**, **SWISS-PROT**, **UniProtKB/Swiss-Prot**, **UniProtKB/TrEMBL**, **UniProt(DAS)**, **Ensembl Human Genes (DAS)**
- Multiple sequence alignment: **ClustalW**, **ClustalO**, **MUSCLE**, **Kalign**, **MAFFT**, **T-Coffee**
- Online and local **BLAST** and **BLAST+** search
- Restriction analysis with integrated **REBASE** restriction enzyme database
- Integrated **Primer3** package for **PCR** primers design
- Search for direct, inverted and **tandem repeats** in DNA sequences
- Constructing **dotplots** for nucleic acid sequences
- Search for transcription factor binding sites (**TFBS**) with **weight matrix** and **SITECON** algorithms
- Aligning short reads with **Bowtie**, **Bowtie 2**, **BWA**, **BWA-SW** and **UGENE Genome Aligner**
- Contig assembly with **CAP3**
- Search for **ORFs**
- **Cloning in silico**
- **3D structure viewer** for files in **PDB** and **MMDB** formats, anaglyph view support
- Protein secondary structure prediction with **GOR IV** and **PSIPRED** algorithms
- **HMMER2** and **HMMER3** packages integration
- Building (using integrated **PHYLP** and **MrBayes** packages) and viewing **phylogenetic trees**
- Local sequence alignment with optimized **Smith-Waterman** algorithm
- Combining various algorithms into custom workflows with **UGENE Workflow Designer**
- Search for a pattern of various algorithms' results in a nucleic acid sequence with **UGENE Query Designer**
- Visualization of **next generation sequencing data** (**BAM** files) using **UGENE Assembly Browser**