

Extensions

- Workflow Designer
- DNA Annotator
- DNA Flexibility
 - Configuring Dialog Settings
 - Result Annotations
- DNA Statistics
- DNA Generator
- ORF Marker
- Remote BLAST
 - Exporting BLAST Results to Alignment
 - Fetching Sequences from Remote Database
- BLAST/BLAST+
 - Creating Database
 - Making Request to Database
 - Fetching Sequences from Local BLAST Database
- Repeat Finder
 - Repeats Finding
 - Tandem Repeats Finding
 - Tandem Repeats Search Result
- Restriction Analysis
 - Selecting Restriction Enzymes
 - Using Custom File with Enzymes
 - Filtering by Number of Hits
 - Excluding Region
 - Circular Molecule
 - Results
- Molecular Cloning in silico
 - Digesting into Fragments
 - Creating Fragment
 - Constructing Molecule
 - Available Fragments
 - Fragments of the New Molecule
 - Changing Fragments Order in the New Molecule
 - Removing Fragment from the New Molecule
 - Editing Fragment Overhangs
 - Reverse Complement a Fragment
 - Other Constuction Options
 - Output
 - Creating PCR Product
- In Silico PCR
 - Primers Details
 - Primer Library
- Secondary Structure Prediction
- SITECON
 - SITECON Searching Transcription Factors Binding Sites
 - Types of SITECON Models
 - Eukaryotic
 - Prokaryotic
 - Building SITECON Model
- Smith-Waterman Search
- HMM2
 - Building HMM Model (HMM Build)
 - Calibrating HMM Model (HMM Calibrate)
 - Searching Sequence Using HMM Profile (HMM Search)
- HMM3
 - Building HMM Model (HMM3 Build)
 - Searching Sequence Using HMM Profile (HMM3 Search)
 - Searching Sequence Against Sequence Database (Phmmer Search)
- uMUSCLE
 - MUSCLE Aligning
 - Aligning Profile to Profile with MUSCLE
 - Aligning Sequences to Profile with MUSCLE
- ClustalW
- MAFFT
- T-Coffee
- Bowtie
 - Bowtie Aligning Short Reads
 - Building Index for Bowtie
- Bowtie 2
 - Bowtie 2 Aligning Short Reads
 - Building Index for Bowtie 2
- BWA
 - Aligning Short Reads with BWA
 - Building Index for BWA
- BWA-SW
 - Aligning Short Reads with BWA-SW
 - Building Index for BWA-SW
- BWA-MEM

- [Aligning Short Reads with BWA-MEM](#)
 - [Building Index for BWA-MEM](#)
- [UGENE Genome Aligner](#)
 - [Aligning Short Reads with UGENE Genome Aligner](#)
 - [Building Index for UGENE Genome Aligner](#)
 - [Converting UGENE Assembly Database to SAM Format](#)
- [CAP3](#)
- [SPAdes](#)
- [Weight Matrix](#)
 - [Searching JASPAR Database](#)
 - [Building New Matrix](#)
- [Primer3](#)
 - [RT-PCR Primer Design](#)
- [Spliced Alignment \(mRNA to genomic\)](#)
- [External Tools](#)
 - [Configuring External Tool](#)
- [Query Designer](#)
- [Plasmid Auto Annotation](#)
- [ClustalO](#)
- [Kalign Aligning](#)
- [DAS Annotating](#)
- [Expert Discovery](#)
 - [Loading Sequences](#)
 - [Mapping Sequences](#)
 - [Markup Sequences](#)
 - [Creating Signals](#)
 - [Generating Signals](#)
 - [Complex Signals Recognition on a Sequence](#)