

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
- 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
 - RTPCR 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