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
    - 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