

Unipro UGENE Online User Manual

- [About Unipro](#)
- [About UGENE](#)
 - [Key Features](#)
 - [User Interface](#)
 - [High Performance Computing](#)
 - [Cooperation](#)
- [Download and Installation](#)
 - [System Requirements](#)
 - [UGENE Packages](#)
 - [Installation on Windows](#)
 - [Installation on macOS](#)
 - [Installation on Linux](#)
 - [Native Installation on Ubuntu](#)
 - [Native Installation on Fedora](#)
 - [Data Analysis Tools](#)
 - [Reference Data for NGS](#)
 - [Configure Data for Metagenomics Classification](#)
 - [Configure ChIP-Seq Analysis Data](#)
- [Basic Functions](#)
 - [UGENE Terminology](#)
 - [UGENE Window Components](#)
 - [Start Page](#)
 - [Project View](#)
 - [Task View](#)
 - [Log View](#)
 - [Notifications](#)
 - [Main Menu Overview](#)
 - [Creating New Project](#)
 - [Creating Document](#)
 - [Renaming Object](#)
 - [Opening Document](#)
 - [Opening for the First Time](#)
 - [Advanced Dialog Options](#)
 - [Opening Document Present in Project](#)
 - [Opening Several Documents](#)
 - [Opening Unloaded Documents](#)
 - [Opening from Clipboard](#)
 - [Opening Containing Folder](#)
 - [Exporting Documents](#)
 - [Locked Documents](#)
 - [Using Objects and Object Views](#)
 - [Exporting Objects](#)
 - [Exporting Sequences to Sequence Format](#)
 - [Exporting Sequences as Alignment](#)
 - [Exporting Alignment to Sequence Format](#)
 - [Exporting Nucleic Alignment to Amino Translation](#)
 - [Export Sequences Associated with Annotation](#)
 - [Using Bookmarks](#)
 - [Exporting Project](#)
 - [Search in Project](#)
 - [Options Panel](#)
 - [Plugins Viewer](#)
 - [Searching NCBI Genbank](#)
 - [Fetching Data from Remote Database](#)
 - [UGENE Application Settings](#)
 - [General](#)
 - [Resources](#)
 - [Network](#)
 - [File Format](#)
 - [Directories](#)
 - [Logging](#)
 - [Alignment Color Scheme](#)
 - [External Tools](#)
 - [Supported External Tools](#)
 - [Custom External Tools](#)
 - [Workflow Designer Settings](#)
 - [OpenCL](#)
- [Sequence View](#)
 - [Sequence View Components](#)
 - [Global Actions](#)
 - [Sequence Toolbars](#)
 - [Sequence Overview](#)
 - [Zoom View](#)
 - [Details View](#)
 - [Information about Sequence](#)

- Manipulating Sequence
 - Show/Hide Sequence View Components
 - Showing Sequence in Multiple Lines
 - Translating Nucleotide Sequence
 - Zooming Sequence
 - Creating New Ruler
 - Going To Position
 - Selecting Sequence Region
 - Copying and Pasting Sequence
 - Editing Sequence
 - Searching in Sequence
 - Load Patterns from File
 - Search Algorithm
 - Search in
 - Other Settings
 - Annotations Settings
 - Exporting Selected Sequence Region
 - Exporting Sequence of Selected Annotations
 - Exporting Sequence Image
 - Locking and Synchronize Ranges of Several Sequences
 - Multiple Sequence Opening
- Annotations Editor
 - "db_xref" Qualifier
 - Automatic Annotations Highlighting
 - The "comment" Annotation
- Manipulating Annotations
 - Creating Annotation
 - Selecting Annotations
 - Editing Annotation
 - Highlighting Annotations
 - Annotations Color
 - Annotations Visibility
 - Show on Translation
 - Captions on Annotations
 - Creating and Editing Qualifier
 - Adding Column for Qualifier
 - Copying Qualifier Text
 - Finding Qualifier
 - Deleting Annotations and Qualifiers
 - Importing Annotations from CSV
 - Exporting Annotations
- Sequence View Extensions
 - Circular Viewer
 - Circular View Settings
 - 3D Structure Viewer
 - Opening 3D Structure Viewer
 - Changing 3D Structure Appearance
 - Selecting Render Style
 - Selecting Coloring Scheme
 - Calculating Molecular Surface
 - Selecting Background Color
 - Selecting Detail Level
 - Enabling Anaglyph View
 - Moving, Zooming and Spinning 3D Structure
 - Highlight Region on 3D Structure
 - Selecting Models to Display
 - Structural Alignment
 - Exporting 3D Structure Image
 - Working with Several 3D Structures Views
 - Chromatogram Viewer
 - Exporting Chromatogram Data
 - Viewing Two Chromatograms Simultaneously
 - Graphs Package
 - Description of Graphs
 - Graph Settings
 - Saving Graph Cutoffs as Annotations
 - Dotplot
 - Creating Dotplot
 - Navigating in Dotplot
 - Zooming to Selected Region
 - Selecting Repeat
 - Interpreting Dotplot: Identifying Matches, Mutations, Inversions, etc.
 - Editing Parameters
 - Filtering Results
 - Saving Dotplot as Image
 - Saving and Loading Dotplot
 - Building Dotplot for Currently Opened Sequence
 - Comparing Several Dotplots
- Alignment Editor

- Overview
 - Alignment Editor Features
 - Alignment Editor Components
 - Navigation
 - Coloring Schemes
 - Creating Custom Color Scheme
 - Highlighting Alignment
 - Zooming and Fonts
 - Searching for Pattern
 - Consensus
 - Export Consensus
 - Alignment Overview
- Working with Alignment
 - Selecting Alignment Region
 - Moving Subalignment
 - Copying and Pasting Subalignment
 - Editing Alignment
 - Removing Selection
 - Filling Selection with Gaps
 - Replacing Selected Character
 - Replacing with Reverse-Complement
 - Replacing with Reverse
 - Replacing with Complement
 - Removing Columns of Gaps
 - Removing Sequence
 - Removing All Gaps
 - Undo and Redo Framework
 - Saving Alignment
 - Aligning Sequences
 - Aligning Sequence to this Alignment
 - Pairwise Alignment
 - Working with Sequences List
 - Adding New Sequences
 - Renaming Sequences
 - Sorting Sequences
 - Shifting Sequences
 - Collapsing Rows
 - Copying Sequences
 - Exporting in Alignment
 - Extracting Selected as MSA
 - Exporting Sequence from Alignment
 - Exporting Alignment as Image
 - Importing APR and ACE Files
- Statistics
 - Distance Matrix
 - Grid Profile
- Advanced Functions
 - Building HMM Profile
- Building Phylogenetic Tree
 - PHYLIP Neighbor-Joining
 - MrBayes
 - PhyML Maximum Likelihood
- Sanger Reads Editor
 - Sanger Reads Editor Overview
 - Sanger Reads Editor Features
 - Sanger Reads Editor Components
 - Working with Chromatogram
 - Mapping Reads to Reference
 - Alignment Statistics
 - Alignment Appearance
 - Overview and Show and Hide Chromatogram
 - Sanger Reads Consensus
 - Export Chromatogram Consensus
 - Navigation in Sanger Reads Alignment
 - Editing Sanger Reads
 - Inserting Character
 - Replacing Character and Gap
 - Removing Character and Gap
 - Inserting Gap
 - Removing Gap at the Left
 - Removing All Columns of Gaps
 - Trimming Left End
 - Trimming Right End
 - Renaming Read
 - Removing Read
 - Undo and Redo
 - Exporting Alignment without Chromatograms
- Assembly Browser
 - Import BAM and SAM Files

- Browsing and Zooming Assembly
 - Opening Assembler Browser Window
 - Assembly Browser Window
 - Assembly Browser Window Components
 - Reads Area Description
 - Assembly Overview Description
 - Ruler and Coverage Graph Description
 - Go to Position in Assembly
 - Using Bookmarks for Navigation in Assembly Data
- Getting Information About Read
- Short Reads Visualization
 - Reads Highlighting
 - Reads Shadowing
- Associating Reference Sequence
- Associating Variations
- Consensus Sequence
- Exporting
 - Exporting Reads
 - Exporting Visible Reads
 - Exporting Coverage
 - Exporting Consensus
 - Exporting Consensus Variations
 - Exporting Assembly as Image
 - Exporting Assembly Region
- Options Panel in Assembly Browser
 - Navigation in Assembly Browser
 - Assembly Statistics
 - Assembly Browser Settings
- Assembly Browser Hotkeys
 - Assembly Overview Hotkeys
 - Reads Area Hotkeys
- Phylogenetic Tree Viewer
 - Tree Settings
 - Selecting Tree Layout and View
 - Modifying Labels Appearance
 - Showing and Hiding Labels
 - Aligning Labels
 - Changing Labels Formatting
 - Adjusting Branch Settings
 - Zooming Tree
 - Working with Clade
 - Selecting Clade
 - Collapsing and Expanding Branches
 - Swapping Siblings
 - Zooming Clade
 - Adjusting Clade Settings
 - Changing Root
 - Exporting Tree Image
 - Printing Tree
- 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 and 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 HMM2 Model
 - Calibrating HMM2 Model
 - Searching Sequence Using HMM2 Profile
- HMM3
 - Building HMM Model
 - Searching Sequence Using HMM Profile
 - Searching Sequence Against Sequence Database
- 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 and cDNA
- External Tools Plugin
 - Configuring External Tool
- Query Designer
- Plasmid Auto Annotation
- ClustalO
- Kalign Aligning
- Shared Database
 - Configuring Database
 - Connecting to a Shared Database
 - Adding Data to the Database
 - Database in the Project
 - Deleting Data
 - Drag'n'drop in the Database
 - Exporting Objects from the Database
- UGENE Public Storage
- UGENE Command Line Interface

- CLI Options
- CLI Predefined Tasks
 - Format Converting Sequences
 - Converting MSA
 - Extracting Sequence
 - Finding ORFs
 - Finding Repeats
 - Finding Pattern Using Smith-Waterman Algorithm
 - Adding Phred Quality Scores to Sequence
 - Local BLAST Search
 - Local BLAST+ Search
 - Remote NCBI BLAST and CDD Requests
 - Annotating Sequence with UQL Schema
 - Building Profile HMM Using HMMER2
 - Searching HMM Signals Using HMMER2
 - Aligning with MUSCLE
 - Aligning with ClustalW
 - Aligning with ClustalO
 - Aligning with Kalign
 - Aligning with MAFFT
 - Aligning with T-Coffee
 - Building PFM
 - Searching for TFBS with PFM
 - Building PWM
 - Searching for TFBS with Weight Matrices
 - Building Statistical Profile for SITECON
 - Searching for TFBS with SITECON
 - Fetching Sequence from Remote Database
 - Gene-by-Gene Report
 - Reverse-Complement Converting Sequences
 - Variants Calling
 - Generating DNA Sequence
- Creating Custom CLI Tasks
- APPENDIXES
 - Appendix A. Supported File Formats
 - Specific File Formats
 - UGENE Native File Formats
 - Other File Formats
- Tutorials
 - Using BioMart with UGENE
 - Environment requirements
 - Installing UGENE extension on Mozilla Firefox
 - Opening data found using BioMart in UGENE
 - Opening BioMart data in UGENE by ID
 - Opening selected data in UGENE