

# Unipro UGENE User Manual

- [About Unipro](#)
- [About UGENE](#)
  - [Key Features](#)
  - [User Interface](#)
  - [High Performance Computing](#)
  - [Cooperation](#)
- [Download and Installation](#)
  - [System Requirements](#)
  - [Installation on Windows](#)
  - [Installation on macOS](#)
  - [Installation on Linux](#)
  - [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
  - 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

- Consensus
    - Export Consensus
  - Alignment Overview
- Working with Alignment
  - Selecting Alignment Region
  - Moving Subalignment
  - Copying and Pasting Subalignment
  - Searching in Alignment
  - 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
- 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
- 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
- Workflow Designer
  - About the Workflow Designer
  - Introduction
    - Launching Workflow Designer
    - Workflow Designer Window Components
    - Workflow Elements and Connections
    - Managing Parameters
    - UGENE Components and Workflow Designer
      - Task View, Notifications and Log View
      - Actions Menu
      - Toolbar
      - Context Menus
      - Application Settings
    - How to Create and Run Workflow
    - How to Use Sample Workflows
  - Manipulating Element
    - Adding Element
    - Copying Element
    - Pasting Element
    - Cutting Element
    - Deleting Element
    - Selecting All Elements on Scene
  - Manipulating Workflow
    - Creating New Workflow
    - Loading Workflow
    - Saving Workflow
    - Exporting Workflow as Image
    - Validating Workflow
    - Running Workflow
    - Dashboard
      - Dashboard Window Components
      - Using Dashboard
    - Stopping and Pausing Workflow
  - Changing Appearance
  - Custom Elements with Scripts
    - Functions Supported for Multiple Alignment Data
    - Functions Supported for Sequence Data
    - Functions Supported for Set of Annotations Data

- Functions Supported for Files
  - Common Function
- Custom Elements with External Tools
  - Creating Element
  - Editing Element
  - Adding Existent Element
  - Removing Element
- Using Script to Set Parameter Value
- Running Workflow from the Command Line
- Running Workflow in Debugging Mode
  - Creating Breakpoints
  - Manipulating Breakpoints
- Workflow File Format
  - Header
  - Body
    - Elements
    - Dataflow
    - Metainformation
- Workflow Elements
  - Data Readers
    - Read Alignment Element
    - Read Annotations Element
    - Read FASTQ File with SE Reads Element
    - Read FASTQ Files with PE Reads Element
    - Read File URL(s) Element
    - Read NGS Reads Assembly Element
    - Read Plain Text Element
    - Read Sequence Element
    - Read Sequence from Remote Database Element
    - Read Variants Element
  - Data Writers
    - Write Alignment Element
    - Write Annotations Element
    - Write FASTA Element
    - Write NGS Reads Assembly Element
    - Write Plain Text Element
    - Write Sequence Element
    - Write Variants Element
  - Data Flow
    - Filter Element
    - Grouper Element
    - Multiplexer Element
    - Sequence Marker Element
  - Basic Analysis
    - Amino Translations Element
    - Annotate with UQL Element
    - CD-Search Element
    - Collocation Search Element
    - Export PHRED Qualities Element
    - Fetch Sequences by ID From Annotation Element
    - Filter Annotation by Name Element
    - Filter Annotations by Qualifier
    - Find Correct Primer Pairs Element
    - Find Pattern Element
    - Find Repeats Element
    - Gene-by-gene approach report
    - Get Sequences by Annotations Element
    - Group Primer Pairs Element
    - Import PHRED Qualities Element
    - Intersect Annotations Element
    - Local BLAST+ Search Element
    - Merge Annotations Element
    - ORF Marker Element
    - Remote BLAST Element
    - Sequence Quality Trimmer Element
    - Smith-Waterman Search Element
  - Data Converters
    - Convert bedGraph Files to bigWig Element
    - Convert Text to Sequence Element
    - File Format Conversion Element
    - Reverse Complement Element
    - Split Assembly into Sequences Element
  - DNA Assembly
    - Assembly Sequences with CAP3
  - HMMER2 Tools
    - HMM2 Build Element
    - HMM2 Search Element
    - Read HMM2 Profile Element
    - Write HMM2 Profile Element

- HMMER3 Tools
  - HMM3 Build Element
  - HMM3 Search Element
  - Read HMM3 Profile
  - Write HMM3 Profile
- Multiple Sequence Alignment
  - Align Profile to Profile with MUSCLE Element
  - Align with ClustalO Element
  - Align with ClustalW Element
  - Align with Kalign Element
  - Align with MAFFT Element
  - Align with MUSCLE Element
  - Align with T-Coffee Element
  - Extract Consensus from Alignment as Sequence
  - Extract Consensus from Alignment as Text
  - In Silico PCR Element
  - Join Sequences into Alignment Element
  - Map to Reference Element
  - Split Alignment into Sequences Element
- NGS: Basic Functions
  - CASAVA FASTQ Filter Element
  - Cut Adapter Element
  - Extract Consensus from Assembly Element
  - Extract Coverage from Assembly Element
  - FASTQ Merger Element
  - FASTQ Quality Trimmer Element
  - FastQC Quality Control Element
  - Filter BAM/SAM Files Element
  - Genome Coverage Element
  - Improve Reads with Trimmomatic Element
  - Merge BAM Files Element
  - Remove Duplicates in BAM Files Element
  - Slopbed Element
  - Sort BAM Files Element
- NGS: ChIP-Seq Analysis
  - Annotate Peaks with peak2gene Element
  - Build Conservation Plot Element
  - Collect Motifs with SeqPos Element
  - Conduct GO Element
  - Create CEAS Report Element
  - Find Peaks with MACS Element
- NGS: Map/Assemble Reads
  - Assemble Reads with SPAdes Element
  - Map Reads with Bowtie Element
  - Map Reads with Bowtie2 Element
  - Map Reads with BWA Element
  - Map Reads with BWA-MEM Element
  - Map Reads with UGENE Genome Aligner Element
  - Map RNA-Seq Reads with TopHat Element
- NGS: Metagenomics Classification
  - Build CLARK Database
  - Build DIAMOND Database Element
  - Build Kraken Database Element
  - Classification Report Element
  - Classify Sequences with CLARK Element
  - Classify Sequences with DIAMOND Element
  - Classify Sequences with Kraken Element
  - Classify Sequences with MetaPhlAn2 Element
  - Ensemble Classification Data Element
  - Filter by Classification Element
  - Improve Classification with WEVOTE Element
- NGS: RNA-Seq Analysis
  - Assemble Transcripts with StringTie Element
  - Assembly Transcripts with Cufflinks Element
  - Extract Transcript Sequences with gffread Element
  - Merge Assemblies with Cuffmerge Element
  - StringTie Gene Abundance Report Element
  - Test for Diff. Expression with Cuffdiff Element
- NGS: Variant Analysis
  - Call Variants with SAMtools Element
  - Change Chromosome Notation for VCF Element
  - Convert SnpEff Variations to Annotations Element
  - Create VCF Consensus Element
  - SnpEff Annotation and Filtration Element
- Transcription Factor
  - Build Frequency Matrix Element
  - Build SITECON Model Element
  - Build Weight Matrix Element
  - Convert Frequency Matrix Element

- Read Frequency Matrix Element
  - Read SITECON Model Element
  - Read Weight Matrix Element
  - Search for TFBS with SITECON Element
  - Search for TFBS with Weight Matrix Element
  - Write Frequency Matrix Element
  - Write SITECON Model Element
  - Write Weight Matrix Element
- Utils
  - DNA Statistics Element
  - Generate DNA Element
- Workflow Samples
  - Alignment
    - Align Sequences with MUSCLE
    - Extract Consensus as Sequence
    - Extract Consensus as Text
  - Conversions
    - Convert "seq/qual" Pair to FASTQ
    - Convert Alignments to ClustalW
    - Convert UQL Schema Results to Alignment
    - Convert Sequence to Genbank
  - Custom Elements
    - CASAVA FASTQ Filter
    - FASTQ Trimmer
    - Dump Sequence Info
    - LinkData Fetch
    - Quality Filter
  - Data Marking
    - Marking by Annotation Number
    - Marking by Length
  - Data Merging
    - Find Substrings in Sequences
    - Merge Sequences and Shift Corresponding Annotations
    - Search for TFBS
  - HMMER
    - Build HMM from Alignment and test it
    - Search Sequences with Profile HMM
  - NGS
    - ChIP-Seq Coverage
    - ChIP-seq Analysis with Cistrome Tools
    - Extract Consensus from Assembly
    - Extract Coverage from Assembly
    - Extract Transcript Sequences
    - Quality Control by FastQC
    - De novo Assemble Illumina PE Reads
    - De novo Assemble Illumina PE and Nanopore Reads
    - De novo Assemble Illumina SE Reads
    - De Novo Assembly and Contigs Classification
    - Parallel NGS Reads Classification
    - Serial NGS Reads Classification
    - RNA-Seq Analysis with TopHat and StringTie
    - RNA-seq Analysis with Tuxedo Tools
    - Variation Annotation with SnpEff
    - Call Variants with SAMtools
    - Variant Calling and Effect Prediction
    - Raw ChIP-Seq Data Processing
    - Raw DNA-Seq Data Processing
    - Raw RNA-Seq Data Processing
    - Get Unmapped Reads
  - Sanger Sequencing
    - Trim and Align Sanger Reads
  - Scenarios
    - Filter Sequence That Match a Pattern
    - Search for Inverted Repeats
    - Find Patterns
    - Gene-by-gene Approach for Characterization of Genomes
    - Group Primer Pairs
    - Intersect Annotations
    - Filter out Short Sequences
    - Merge Sequences and Annotations
    - In Silico PCR Sample
    - Remote BLASTing
    - Get Amino Translations of a Sequence
  - Transcriptomics
    - Search for Transcription Factor Binding Sites (TFBS) in Genomic Sequences
- Query Designer
  - About the Query Designer
  - Query Designer Introduction
    - Launching the Query Designer

- Terminology
    - Query Designer Window Components
    - Schema Elements
  - How to Create and Run Schema
- Manipulating Query Designer Element
  - Adding Algorithm Element
  - Adding Constraint Element
  - Renaming Algorithm Element
  - Resizing and Moving Algorithm Element
  - Managing of Elements Parameters
  - Changing Algorithm Element Appearance
  - Deleting Query Designer Element
- Manipulating Schema
  - Creating New Schema
  - Loading Schema
  - Saving Schema
  - Changing Schema Appearance
  - Setting Order of Algorithms Execution
  - Managing Strands
    - Element Direction in Schema
    - Querying Sequence Strands
  - Running Schema from the Query Designer
- Running Schema from the Sequence View
- Query Designer Schema File Format
  - Header Query Designer Element
  - Body Query Designer Element
    - Element Description
      - Algorithm Element Description
      - Constraint Element Description
    - Metainformation Query Designer Element
- Query Elements
  - Algorithm Elements
    - CDD Algorithm Element
    - Base Content Algorithm Element
    - Gc Content Algorithm Element
    - HMM3 Algorithm Element
    - ORF Algorithm Element
    - Primer Algorithm Element
    - Repeats Algorithm Element
    - Restriction Sites Algorithm Element
    - Pattern Algorithm Element
    - SITECON Algorithm Element
    - Smith-Waterman Algorithm Element
    - Tandem Repeats Algorithm Element
    - Weight Matrix Algorithm Element
    - HMM2 Algorithm Element
  - Constraint Elements
    - End-Start Constraint Element
    - Start-End Constraint Element
    - End-End Constraint Element
    - Start-Start Constraint Element
- Extensions
  - 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+
    - 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
- 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
  - 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