

User Manual

- [About Unipro](#)
- [About UGENE](#)
 - [Key Features](#)
 - [User Interface](#)
 - [Cooperation](#)
- [Download and Installation](#)
 - [System Requirements](#)
 - [Installation on Windows](#)
 - [Installation on macOS](#)
 - [Installation on Linux](#)
 - [Data Analysis Tools](#)
- [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 Amino Acid Translation](#)
 - [Export Sequences Associated with Annotation](#)
 - [Using Bookmarks](#)
 - [Exporting Project](#)
 - [Search in Project](#)
 - [Saving 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](#)
- [Sequence View](#)
 - [Sequence View Components](#)
 - [Global Actions](#)
 - [Sequence Toolbars](#)
 - [Sequence Overview](#)
 - [Zoom View](#)
 - [Details View](#)
 - [Information about Sequence](#)
 - [Melting temperature](#)
 - [Manipulating Sequence](#)
 - [Show and 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
 - Insert subsequence
 - Remove subsequence
 - Replace subsequence
- 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
 - Automatic Annotations Highlighting
 - db_xref Qualifier
 - The comment Annotation
 - Transform into a primer pair
- 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
 - Alignment Entropy Calculation
 - 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
 - Export Highlighting to File
 - Zooming and Fonts
 - Consensus
 - Export Consensus
 - Alignment Overview
- Working with Alignment
 - Selecting Alignment Region
 - Moving Subalignment
 - Copying and Pasting Subalignment
 - Searching in Alignment
 - Showing Alignment in Multiple Lines
 - Editing Alignment
 - Converting 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
 - Adding Sequence(s) to Alignment
 - Pairwise Alignment
 - Working with Sequences List
 - Adding New Sequences
 - Renaming Sequences
 - Sorting Sequences
 - Shifting Sequences
 - Collapsing Rows
 - Copying Sequences
 - Exclude list
 - Exporting in Alignment
 - Extracting Selected as MSA
 - Exporting Sequence from Alignment
 - Exporting Alignment as Image
 - Exporting in Amino Translation
 - Moving Sequences from Alignment
 - Importing APR and ACE Files
 - Realigning sequence(s) to other sequences
- Statistics
 - Distance Matrix
 - Grid Profile
- Advanced Functions
 - Building HMM Profile
- Building Phylogenetic Tree
 - IQ-TREE
 - PHYLIP Neighbor-Joining
 - MrBayes
 - PhyML Maximum Likelihood
 - FastTree
- 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
 - Adjusting Tree nodes
 - 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
- Sanger Reads Settings
- Assembly Browser
 - Import BAM and SAM Files
 - Browsing and Zooming Assembly
 - Opening Assembly 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 Acid Translation 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: Mapping 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: 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 Map 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
 - Find Group of Annotated Regions
 - Plasmid Auto Annotation
 - DNA Flexibility
 - Configuring Dialog Settings
 - Result Annotations
 - DNA Statistics
 - DNA Generator
 - ORF Marker
 - Remote BLAST
 - Primer-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
- PCR Primer Design for DNA Assembly
 - Backbone details
- 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
 - Building Index for UGENE Genome Aligner
 - Converting UGENE Assembly Database to SAM Format
 - Map NGS Reads with UGENE Genome Aligner
- CAP3
- SPAdes
- Weight Matrix
 - Searching JASPAR Database
 - Building New Matrix
- Primer3
 - Primer3 (no target sequence)
 - Posterior Actions
 - RTPCR Primer Design
- Spliced Alignment mRNA and cDNA
- External Tools Plugin
 - Configuring External Tool
- ClustalO
- Kalign Aligning
- GeneCut desktop
- mfold
- 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