

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