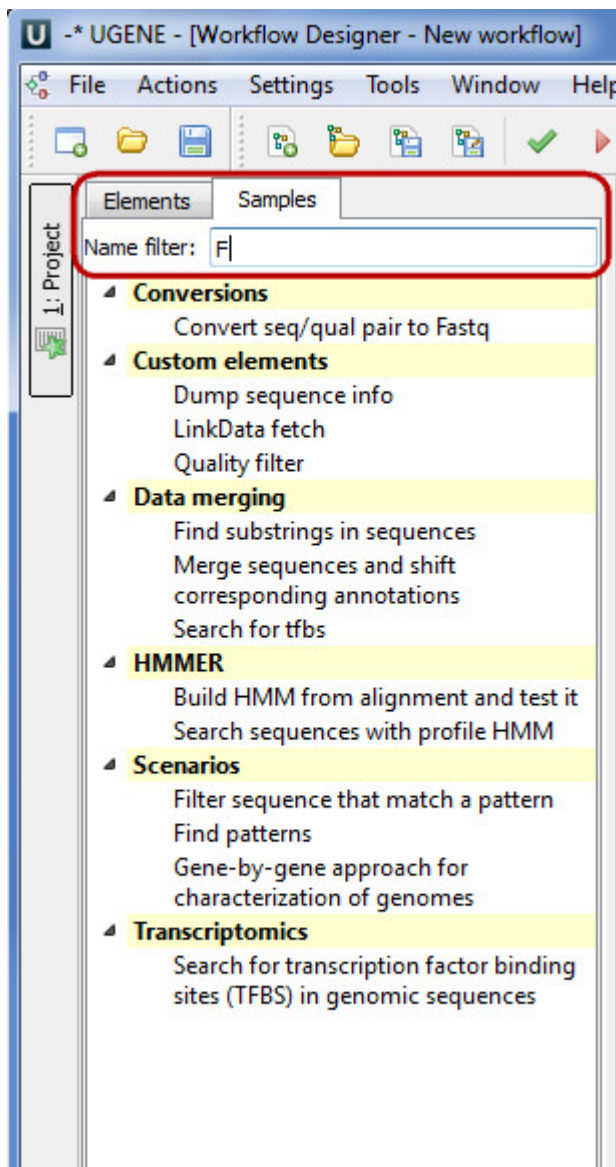


Workflow Samples

This section contains detailed description of workflow samples presented in the Workflow Designer. To search a sample use the name filter or press the *Ctrl+F* shortcut that moves you to the name filter also:



- Alignment
 - Align Sequences with MUSCLE
- 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 Sequences by Annotation Number
 - Marking Sequences by Length
- Data Merging
 - Find Substrings at Sequences
 - Merge Sequences and Shift Corresponding Annotations
 - Search for TFBS
- HMMER
 - Build HMM from Alignment and Test It
 - Search Sequences with Profile HMM
- NGS
 - Assembly with Spades
 - Call Variants with SAMtools
 - ChIP-Seq Coverage
 - ChIP-seq Analysis with Cistrome Tools
 - Extract Consensus from Assembly
 - Extract Coverage from Assembly
 - Extract Transcript Sequences
 - Raw Chip-Seq Processing
 - Raw DNA-Seq Processing
 - Raw RNA-Seq Processing
 - RNA-seq Analysis with Tuxedo Tools
- Scenarios
 - Extract Consensus
 - Filter Sequence That Match a Pattern
 - Search for Inverted Repeats
 - Find Patterns
 - Gene-by-gene Approach for Characterization of Genomes
 - Merge Sequences and Annotations
 - Remote BLASTing
 - Get Amino Translations of a Sequence
 - Group Primer Pairs
- Transcriptomics
 - Search for Transcription Factor Binding Sites (TFBS) in Genomic Sequences