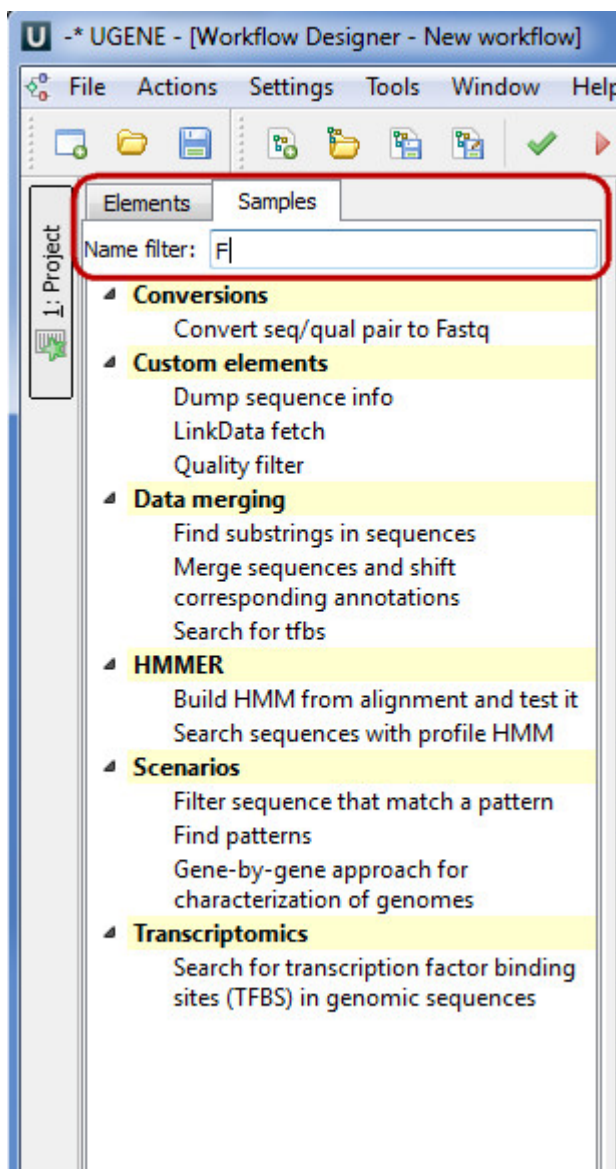


Workflow Samples

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
 - Call Variants with SAMtools
 - ChIP-seq Analysis with Cistrome Tools
 - Extract Consensus
 - Extract transcript sequences
 - RNA-seq Analysis with Tuxedo Tools
- Scenarios
 - Filter sequence that match a pattern
 - Find patterns
 - Gene-by-gene approach for characterization of genomes
 - Merge sequences and annotations
- Transcriptomics
 - Search for transcription factor binding sites (TFBS) in genomic sequences