

# Workflow Designer

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  - Find Correct Primer Pairs Element
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  - Local BLAST Search Element
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  - Assembly Sequences with CAP3
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  - In Silico PCR Element
  - Join Sequences into Alignment Element
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- NGS: Basic Functions
  - CASAVA FASTQ Filter Element
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  - Assemble Reads with SPAdes Element
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- Map Reads with BWA Element
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- NGS: RNA-Seq Analysis
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    - Convert Alignments to ClustalW
    - Convert UQL Schema Results to Alignment
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  - Custom Elements
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    - LinkData Fetch
    - Quality Filter
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    - 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
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    - Quality Control by FastQC
    - De novo Assemble Illumina PE Reads
    - De novo Assemble Illumina PE and Nanopore Reads
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    - 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
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  - 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
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  - Filter out Short Sequences
  - Merge Sequences and Annotations
  - In Silico PCR Sample
  - Remote BLASTing
  - Get Amino Translations of a Sequence
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  - Search for Transcription Factor Binding Sites (TFBS) in Genomic Sequences