

# UGENE Command Line Interface

UGENE command line interface (CLI) was developed keeping in mind the following principles:

- To make it as easy as popular shell commands.
- To include all significant UGENE features.
- To allow users to add their own commands.

To use UGENE CLI make sure to add the path to the UGENE executable to your **%PATH%** environment variable.

The general syntax is the following:

```
ugene [--task=]task_name] [--task_parameter=value ...] [-task_parameter value ...] [--option[=value]] [-option  
[ value]]
```

Here:

**task\_name** — task to execute, it can be one of the [predefined tasks](#) or [a task you have created](#).

**task\_parameter** — parameter of the specified task. Some parameters of a task are required, like *in* and *out* parameters of some tasks.

**option** — one of the [CLI options](#).

See the example below:

```
ugene align --in=COI.aln -out result.aln -log-level-details
```

- 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
  - 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
  - Annotating with DAS
  - Gene-by-Gene Report
  - Reverse-Complement Converting Sequences
  - Variants Calling
  - Generating DNA Sequence
- Creating Custom CLI Tasks