

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