

# CLI Predefined Tasks

Using current version of UGENE you can perform the following tasks by running a simple command:

- [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](#)