Converting MSA

Task Name: convert-msa

Converts a multiple sequence alignment file from one format to another.

Parameters:

in — input multiple sequence alignment file. [String, Required]

out — name of the output file. [String, Required]

format — format of the output file. [String, Optional]

The following values are available:

- clustal (default)
- fasta
- mega
- msf
- nexus
- phylip-interleaved
- phylip-sequential
- stockholm

Example:

```
ugene convert-msa --in=CBS.sto --out=CBS --format=msf
```