

Aligning with MUSCLE

Task Name: align

Performs multiple sequence alignment with MUSCLE algorithm and saves the resulting alignment to file. Source data can be of any format containing sequences or alignments.

Parameters:

in - Input alignment [Url datasets]

max-iterations - Maximum number of iterations (using '2' by default) [Number]

mode - Selector of preset configurations, that give you the choice of optimizing accuracy, speed, or some compromise between the two. The default favors accuracy (using 'MUSCLE default' by default) [Number]

range - Whole alignment or column range e.g. 1..100 (using 'Whole alignment' by default) [String]

stable - Do not rearrange aligned sequences (using 'True' by default) [Boolean]

format - Document format of output alignment (using 'clustal' by default) [String]

out - Output alignment [String]

Example:

```
ugene align --in=test.aln --out=test_out.aln --format=clustal
```