

# Aligning with Kalign

**Task Name:** align-kalign

Multiple sequence alignment with Kalign.

**Parameters:**

*in* — semicolon-separated list of input files. [String, Required]

*out* — output file in the ClustalW format. [String, Required]

**Example:**

```
ugene align-kalign --in=COI.aln --out=COI_aligned.aln
```