

# Finding Repeats

**Task Name:** find-repeats

Searches for repeats in sequences and saves the regions found as annotations.

**Parameters:**

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

*out* — output file with the annotations. [String, Required]

*name* — name of the annotated regions. [String, Optional, Default: "repeat\_unit"]

*min-length* — minimum length of the repeats. [Number, Optional, Default: 5]

*identity* — percent identity between repeats. [Number, Optional, Default: 100]

*min-distance* — minimum distance between the repeats. [Number, Optional, Default: 0]

*max-distance* — maximum distance between the repeats. [Number, Optional, Default: 5000]

*inverted* — if *true*, searches for the inverted repeats. [Boolean, Optional, Default: false]

**Example:**

```
ugene find-repeats --in=murine.gb --out=murine_repeats.gb --identity=99
```