

# Finding Pattern Using Smith-Waterman Algorithm

**Task Name:** find-sw

Searches for a pattern in a nucleotide or protein sequence using the Smith-Waterman algorithm and saves the regions found as annotations.

**Parameters:**

*in* — input sequence file. [String, Required]

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

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

*ptrn* — subsequence pattern to search for (e.g. AGGCCCT). [String, Required]

*score* — percent identity between the pattern and a subsequence. [Number, Optional, Default: 90]

*matrix* — scoring matrix. [String, Optional, Default: "Auto"]

Among others the following values are available:

- blosum62
- dna
- ma
- dayhoff
- gonnet
- pam250
- etc.

The matrices available are stored in the \$UGENE\data\weight\_matrix directory.

*filter* — results filtering strategy. [String, Optional, Default: "filter-intersections"]

The following values are available:

- filter-intersections
- none

**Example:**

```
ugene find-sw --in=human_T1.fa --out=sw.gb --ptrn=TGCT --filter=none
```