

# Searching for TFBS with Weight Matrices

**Task Name:** pwm-search

Searches for transcription factor binding sites (TFBS) with position weight matrices (PWM) and saves the regions found as annotations.

**Parameters:**

*seq* — semicolon-separated list of input sequence files to search TFBS in. [String, Required]

*matrix* — semicolon-separated list of the input PWM. [String, Required]

*out* — output Genbank file.

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

*min-score* — minimum percentage score to detect TFBS. [Number, Optional, Default: 85]

*strand* — strands to search in. [Number, Optional, Default: 0]

The following values are available:

- 0 (both strands)
- 1 (direct strand)
- -1 (complement strand)

**Example:**

```
ugene pwm-search --seq=input.fa --matrix=Aro80.pwm;Aft1.pwm --out=res.gb
```