

# Searching HMM Signals Using HMMER2

**Task Name:** hmm2-search

Searches each input sequence for the significantly similar sequence that matches to all specified profile HMM using the HMMER2 tool.

**Parameters:**

*seq* — semicolon-separated list of the input sequence files. [String, Required]

*hmm* — semicolon-separated list of the input HMM files. [String, Required]

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

*name* — name of the result annotations. [String, Optional, Default: "hmm\_signal"]

*e-val* — e-value that can be used to exclude low-probability hits from the result. [Number, Optional, Default: 1e-1]

*score* — score based filtering which is an alternative to e-value filtering to exclude low-probability hits from the result. [Number, Optional, Default: -1000000000]

**Example:**

```
ugene hmm2-search --seq=CBS_seq.fa --hmm=CBS.hmm --out=CBS_hmm.gb
```