

# HMM3 Algorithm Element

Searches a sequence for significantly similar sequence matches with one or more profile HMM and saves the results as annotations.

The search is performed using HMMER3 **hmmsearch** tool integrated into UGENE.

## Parameters in GUI

### General parameters:

Parameter	Description	Default value
<b>Annotate As</b>	Name of the result annotations.	hmm_signal
<b>Profile HMM</b>	Semicolon-separated list of input HMM files.	You must specify a value!
<b>Min Length</b>	Minimum length of a result region.	30
<b>Max Length</b>	Maximum length of a result region.	5000

### Parameters controlling reporting threshold:

Reporting thresholds controls which hits are reported.

Parameter	Description	Default value
<b>Use E-value</b>	Filter by E-value if true. Otherwise, filters by score.	True
<b>Filter by High E-value</b>	Reports domains <= this E-value threshold in output ( <b>hmmsearch-domE</b> option).	1e+1
<b>Filter by Low Score</b>	Reports domains >= this score cutoff in output ( <b>hmmsearch-domT</b> option).	0.01

### Parameters controlling the acceleration pipeline:

HMMER3 searches are accelerated in a three-step filter pipeline: the MSV filter, the Viterbi filter, and the Forward filter. The first filter is the fastest and most approximate; the last is the full Forward scoring algorithm. There is also a bias filter step between MSV and Viterbi.

Parameter	Description	Default value
<b>Max</b>	Turns off all acceleration heuristic filters. This increases sensitivity somewhat, at a large cost in speed.	False
<b>MSV Filter Threshold</b>	P-value threshold for the MSV filter step.	0.02
<b>Viterbi Filter Threshold</b>	P-value threshold for the Viterbi filter step.	0.001
<b>Forward Filter Threshold</b>	P-value threshold for the Forward filter step.	1e-5
<b>No Bias Filter</b>	Turns off composition bias filter. This increases sensitivity somewhat, but can come at a high cost in speed.	False

### Other parameters:

Parameter	Description	Default value
<b>No Null2</b>	Turns off the null2 score corrections for biased composition.	False
<b>Number of Sequences</b>	Specifies number of significant sequences. It is used for domain E-value calculations ( <b>hmmsearch-domZ</b> option).	1 (i.e. one input sequence)
<b>Seed</b>	Random number seed. The default is to use a fixed seed(42), so that results are exactly reproducible. Any other positive integer will give different (but also reproducible) results. A choice of 0 uses a randomly chosen seed.	42

## Parameters in Schema File

Type: hmm3

Parameter	Parameter in the GUI	Type
key	Annotate As	<i>string</i>
min-len	Min Length	<i>string</i>
max-len	Max Length	<i>string</i>
hmm-profile	Profile HMM	<i>string</i>
use-e-val	Use E-value	<i>boolean</i>
e-val	Filter by High E-value	<i>numeric</i>
score	Filter by Low Score	<i>numeric</i>
do-max	Max	<i>boolean</i>
msv-filter-threshold	MSV Filter Threshold	<i>numeric</i>
viterbi-filter-threshold	Viterbi Filter Threshold	<i>numeric</i>
forward-filter-threshold	Forward Filter Threshold	<i>numeric</i>
no-bias-filter	No Bias Filter	<i>boolean</i>
no-score-corrections	No Null2	<i>boolean</i>
seqs-num	Number of Sequences	<i>numeric</i>
random-generator-seed	Seed	<i>numeric</i>