

Smith-Waterman Algorithm Element

The *element* uses the Smith-Waterman algorithm to search in the input sequence for regions similar to the specified pattern.

Parameters in GUI

Parameter	Description	Default value
Annotate As	Name of the result annotations.	misc_feature
Direction	See the description here .	Any
Algorithm	Algorithm version. Depending on the computer configuration the following values may be available: <ul style="list-style-type: none">• Classic 2• SSE2• CUDA	Classic 2
Filter results	Results filtering strategy. The values available are: <ul style="list-style-type: none">• filter-intersections• none	filter-intersections
Gap ext score	Gap extension score.	-1.00
Gap open score	Gap open score.	-10.00
Scoring matrix	Specifies the scoring matrix to use.	Auto
Min score	Percentage of matching between the pattern and the searched sequence region.	90%
Pattern	The pattern to search for.	You must specify a value!
Search in translation	Translates the nucleotide sequence supplied to a protein sequence and searches in the translated sequence.	False

Parameters in Schema File

Type: ssearch

Parameter	Parameter in the GUI	Type
key	Annotate As	<i>string</i>
algorithm	Algorithm	<i>string</i> Depending on the computer configuration the values available are: <ul style="list-style-type: none">• "Classic 2"• SSE2• CUDA
filter	Filter results	<i>string</i> The values available are: <ul style="list-style-type: none">• filter-intersections• none
gap-ext-score	Gap ext score	<i>numeric</i>
gap-open-score	Gap open score	<i>numeric</i>
matrix	Scoring matrix	<i>string</i>
min-score	Min score	<i>numeric</i>
pattern	Pattern	<i>string</i>

strand	Direction	<i>string</i> Available values are: <ul style="list-style-type: none">• complement• direct• both
translate	Search in translation	<i>boolean</i>