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: • Classic 2 • SSE2 • CUDA	Classic 2
Filter results	Results filtering strategy. The values available are: • 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**	*string*
algorithm	**Algorithm**	*string* Depending on the computer configuration the values available are: • “Classic 2” • SSE2 • CUDA
filter	**Filter results**	*string* The values available are: • filter-intersections • none
gap-ext-score	**Gap ext score**	*numeric*
gap-open-score	**Gap open score**	*numeric*
matrix	**Scoring matrix**	*string*
min-score	**Min score**	*numeric*
pattern	**Pattern**	*string*
strand	**Direction**	*string* Available values are: • complement • direct • both
translate	**Search in translation**	*boolean*