

# Smith-Waterman Search Element

Searches regions in a sequence similar to a pattern sequence. Outputs a set of annotations.

Under the hood is the well-known Smith-Waterman algorithm for performing local sequence alignment.

## Parameters in GUI

Parameter	Description	Default value
<b>Substitution Matrix</b>	Describes the rate at which one character in a sequence changes to other character states over time.	Auto
<b>Algorithm</b>	Version of the Smith-Waterman algorithm. You can use the optimized versions of the algorithm (SSE, CUDA and OpenCL) if your hardware supports these capabilities.	OPENCL
<b>Filter Results</b>	Specifies either to filter the intersected results or to return all the results.	filter-intersections
<b>Min Score</b>	Minimal percent similarity between a sequence and a pattern.	90%
<b>Search in</b>	Specifies which strands should be searched: direct, complementary or both.	both strands
<b>Search in Translation</b>	Translates a supplied nucleotide sequence to protein and searches in the translated sequence.	False
<b>Gap Open Score</b>	Penalty for opening a gap.	-10.0
<b>Gap Extension Score</b>	Penalty for extending a gap.	-1.0
<b>Use Pattern Names</b>	Use a pattern name as an annotation name.	True
<b>Annotate as</b>	Name of the result annotations.	misc_feature
<b>Qualifier name for pattern name</b>	Name of qualifier in result annotations which is containing a pattern name.	pattern name

## Parameters in Workflow File

Type: ssearch

Parameter	Parameter in the GUI	Type
<b>matrix</b>	<b>Substitution Matrix</b>	<i>string</i>  Available values are: <ul style="list-style-type: none"><li>• Auto - for auto detecting matrix</li><li>• blosum60</li><li>• dna</li><li>• rna</li><li>• ...</li></ul>
<b>algorithm</b>	<b>Algorithm</b>	<i>string</i>  Available values are: <ul style="list-style-type: none"><li>• Classic 2</li><li>• SSE2</li><li>• OpenCL</li><li>• CUDA</li></ul>
<b>filter-strategy</b>	<b>Filter Results</b>	<i>string</i>  Available values are: <ul style="list-style-type: none"><li>• filter-intersections</li><li>• none</li></ul>
<b>min-score</b>	<b>Min Score</b>	<i>numeric</i>

<b>strand</b>	<b>Search in</b>	<i>numeric</i>  Available values are: <ul style="list-style-type: none"> <li>• 0 - for searching in both strands</li> <li>• 1 - for searching in direct strand</li> <li>• 2 - for searching in complement strand</li> </ul>
<b>amino</b>	<b>Search in Translation</b>	<i>boolean</i>
<b>gap-open-score</b>	<b>Gap Open Score</b>	<i>numeric</i>
<b>gap-ext-score</b>	<b>Gap Extension Score</b>	<i>numeric</i>
<b>use-names</b>	<b>Use Pattern Names</b>	<i>boolean</i>
<b>result-name</b>	<b>Annotate as</b>	<i>string</i>
<b>pattern-name-qual</b>	<b>Qualifier name for pattern name</b>	<i>string</i>

## Input/Output Ports

The element has 2 *input ports*. The first input port:

**Name in GUI:** *Input data*

**Name in Workflow File:** in-sequence

**Slots:**

Slot In GUI	Slot in Workflow File	Type
<b>Sequence</b>	<b>sequence</b>	<i>sequence</i>

The second input port:

**Name in GUI:** *Pattern data*

**Name in Workflow File:** pattern

**Slots:**

Slot In GUI	Slot in Workflow File	Type
<b>Sequence</b>	<b>sequence</b>	<i>sequence</i>

And 1 *output port*:

**Name in GUI:** *Pattern annotations*

**Name in Workflow File:** out-annotations

**Slots:**

Slot In GUI	Slot in Workflow File	Type
<b>Set of annotations</b>	<b>annotations</b>	<i>annotation-table</i>