

# Find Pattern Element

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

**Element type:** search

## Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
<b>Annotate as</b>	Name of the result annotation.	misc_feature	<b>result-name</b>	<i>string</i>
<b>Pattern(s)</b>	Semicolon-separated list of patterns to search for.		<b>pattern</b>	<i>string</i>
<b>Pattern file</b>	Load pattern from file in any sequence format or in newline-delimited format.		<b>pattern_file</b>	<i>string</i>
<b>Use pattern name</b>	If patterns are loaded from a file, use names of pattern sequences as annotation names. The name from the parameters is used by default.	False	<b>use-names</b>	<i>boolean</i>
<b>Max Mismatches</b>	Maximum number of mismatches between a substring and a pattern.	0	<b>max-mismatches-num</b>	<i>numeric</i>
<b>Search in</b>	Specifies which strands should be searched: direct, complementary or both.	both strands	<b>strand</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>Allow Insertions /Deletions</b>	Takes into account possibility of insertions/deletions when searching. By default substitutions are only considered.	False	<b>allow-ins-del</b>	<i>boolean</i>
<b>Support ambiguous bases</b>	Performs correct handling of ambiguous bases. When this option is activated insertions and deletions are not considered.	False	<b>ambiguous</b>	<i>boolean</i>
<b>Search in Translation</b>	Translates a supplied nucleotide sequence to protein and searches in the translated sequence.	False	<b>amino</b>	<i>boolean</i>
<b>Qualifier name for pattern name</b>	Name of qualifier in result annotations which is containing a pattern name.	pattern_name	<b>pattern-name-qual</b>	<i>string</i>

## Input/Output Ports

The element has 1 *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>
<b>Plain text</b>	<b>text</b>	<i>string</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>