

# 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><br><br>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> |