

# ORF Marker Element

Finds Open Reading Frames (ORFs) in each supplied nucleotide sequence, stores found regions as annotations.

**Element type:** orf-search

## Parameters in GUI

| Parameter                       | Description  | Default value             | Parameter in Workflow File      | Type  |
|---------------------------------|--|---------------------------|---------------------------------|---|
| <b>Annotate as</b> (required)   | Name of the result annotations.  | ORF                       | <b>result-name</b>              | <i>string</i>   |
| <b>Search in</b>                | Specifies which strands should be searched: direct, complement 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>Min length</b>               | Ignores ORFs shorter than the specified length.  | 100                       | <b>min-length</b>               | <i>numeric</i>  |
| <b>Genetic code</b>             | Specifies which genetic code should be used for translating the input nucleotide sequence.             | The Standard Genetic Code | <b>genetic-code</b>             | <i>string</i><br><br>Available values are: <ul style="list-style-type: none"><li>• NCBI-GenBank #1</li><li>• NCBI-GenBank #2</li><li>• etc.</li></ul>   |
| <b>Require init codon</b>       | Allows or not ORFs starting with any codon other than terminator.                                      | True                      | <b>require-init-codon</b>       | <i>boolean</i>  |
| <b>Require stop codon</b>       | Ignores boundary ORFs which last beyond the search region (i.e. have no stop codon within the range).  | False                     | <b>require-stop-codon</b>       | <i>boolean</i>  |
| <b>Allow alternative codons</b> | Allows ORFs starting with alternative initiation codons, accordingly to the current translation table. | False                     | <b>allow-alternative-codons</b> | <i>boolean</i>  |

## Input/Output Ports

The element has 1 *input port*.

**Name in GUI:** *Input sequence*

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

**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:** *ORF 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> |