# ORF Marker Element

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

## Parameters in GUI

| Parameter | Description | Default value |
|---|---|---|
| **Annotate as** (required) | Name of the result annotations. | ORF |
| **Search in** | Specifies which strands should be searched: direct, complement or both. | both strands |
| **Min length** | Ignores ORFs shorter than the specified length. | 100 |
| **Genetic code** | Specifies which genetic code should be used for translating the input nucleotide sequence. | The Standard Genetic Code |
| **Require init codon** | Allows or not ORFs starting with any codon other than terminator. | True |
| **Require stop codon** | Ignores boundary ORFs which last beyound the search region (i.e. have no stop codon within the range). | False |
| **Allow alternative codons** | Allows ORFs starting with alternative initiation codons, accordingly to the current translation table. | False |

# Parameters in Workflow File

**Type:** orf-search

| Parameter | Parameter in the GUI | Type |
|---|---|---|
| **result-name** | **Annotate as** | *string* |
| **strand** | **Search in** | *numeric*<br><br>Available values are:<br><br>• 0 - for searching in both strands<br>• 1 - for searching in direct strand<br>• 2 - for searching in complement strand |
| **min-length** | **Min length** | *numeric* |
| **genetic-code** | **Genetic code** | *string*<br><br>Available values are:<br><br>• NCBI-GenBank #1<br>• NCBI-GenBank #2<br>• etc. |
| **require-init-codon** | **Require init codon** | *boolean* |
| **require-stop-codon** | **Require stop codon** | *boolean* |
| **allow-alternative-codons** | **Allow alternative codons** | *boolean* |

# 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 |
|---|---|---|
| **Sequence** | **sequence** | *sequence* |

And 1 *output port*:

**Name in GUI:** *ORF annotations*

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

**Slots:**

| Slot In GUI | Slot in Workflow File | Type |
|---|---|---|
| **Set of annotations** | **annotations** | *annotation-table* |