

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
Annotate as (required)	Name of the result annotations.	ORF	result-name	<i>string</i>
Search in	Specifies which strands should be searched: direct, complement or both.	both strands	strand	<i>numeric</i> Available values are: • 0 - for searching in both strands • 1 - for searching in direct strand • 2 - for searching in complement strand
Min length	Ignores ORFs shorter than the specified length.	100	min-length	<i>numeric</i>
Genetic code	Specifies which genetic code should be used for translating the input nucleotide sequence.	The Standard Genetic Code	genetic-code	<i>string</i> Available values are: • NCBI-GenBank #1 • NCBI-GenBank #2 • etc.
Require init codon	Allows or not ORFs starting with any codon other than terminator.	True	require-init-codon	<i>boolean</i>
Require stop codon	Ignores boundary ORFs which last beyond the search region (i.e. have no stop codon within the range).	False	require-stop-codon	<i>boolean</i>
Allow alternative codons	Allows ORFs starting with alternative initiation codons, accordingly to the current translation table.	False	allow-alternative-codons	<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
Sequence	sequence	<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
Set of annotations	annotations	<i>annotation-table</i>