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	Туре
Annotate as (req uired)	Name of the result annotations.	ORF	result-name	string
Search in	Specifies which strands should be searched: direct, complement or both.	both strands	strand	numeric 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	numeric
Genetic code	Specifies which genetic code should be used for translating the input nucleotide sequence.	The Standard Genetic Code	genetic-code	string 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	boolean
Require stop codon	Ignores boundary ORFs which last beyound the search region (i.e. have no stop codon within the range).	False	require-stop-codon	boolean
Allow alternative codons	Allows ORFs starting with alternative initiation codons, accordingly to the current translation table.	False	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	Туре
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	Туре
Set of annotations	annotations	annotation-table