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* Available values are: • 0 - for searching in both strands • 1 - for searching in direct strand • 2 - for searching in complement strand
min-length	**Min length**	*numeric*
genetic-code	**Genetic code**	*string* Available values are: • NCBI-GenBank #1 • NCBI-GenBank #2 • 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*