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**	*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	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*