

# ORF Algorithm Element

The *element* searches for open reading frames (ORFs) in the supplied sequence.

## Parameters in GUI

Parameter	Description	Default value
Annotate As	Name of the result annotations.	ORF
Direction	See the description <a href="#">here</a> .	Any
Allow alternative codons	Allows / disallows ORFs starting with alternative initiation codons, accordingly to the current translation table.	False
Require init codons	Allows / disallows ORFs starting with any codon other than terminator.	True
Require stop codons	Ignores or takes into account boundary ORFs which last beyond the search region.	False
Min length	Ignores ORFs shorter than the specified length.	100bp
Max length	Maximum length of annotation allowed.	10000bp
Genetic code	Genetic code that should be used to translate the input nucleotide sequence.	The standard genetic code

## Parameters in Schema File

Type: orf

Parameter	Parameter in the GUI	Type
key	Annotate As	<i>string</i>
strand	Direction	<i>string</i> Available values are: <ul style="list-style-type: none"><li>• complement</li><li>• direct</li><li>• both</li></ul>
alt-start	Allow alternative codons	<i>boolean</i>
starts-with-init	Require init codons	<i>boolean</i>
ends-with-stop	Require stop codons	<i>boolean</i>
min-length	Min length	<i>numeric</i>
max-length	Max length	<i>numeric</i>
trans-id	Genetic code	<i>string</i> Available values are: <ul style="list-style-type: none"><li>• "NCBI-GenBank #1"</li><li>• "NCBI-GenBank #2"</li><li>• etc.</li></ul>