

# ORF Algorithm Element

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

## Parameters in GUI

Parameter	Description	Default value
<b>Annotate As</b>	Name of the result annotations.	ORF
<b>Direction</b>	See the description <a href="#">here</a> .	Any
<b>Allow alternative codons</b>	Allows / disallows ORFs starting with alternative initiation codons, accordingly to the current translation table.	False
<b>Require init codons</b>	Allows / disallows ORFs starting with any codon other than terminator.	True
<b>Require stop codons</b>	Ignores or takes into account boundary ORFs which last beyond the search region.	False
<b>Min length</b>	Ignores ORFs shorter than the specified length.	100bp
<b>Max length</b>	Maximum length of annotation allowed.	10000bp
<b>Genetic code</b>	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
<b>key</b>	<b>Annotate As</b>	<i>string</i>
<b>strand</b>	<b>Direction</b>	<i>string</i> Available values are: <ul style="list-style-type: none"><li>• complement</li><li>• direct</li><li>• both</li></ul>
<b>alt-start</b>	<b>Allow alternative codons</b>	<i>boolean</i>
<b>starts-with-init</b>	<b>Require init codons</b>	<i>boolean</i>
<b>ends-with-stop</b>	<b>Require stop codons</b>	<i>boolean</i>
<b>min-length</b>	<b>Min length</b>	<i>numeric</i>
<b>max-length</b>	<b>Max length</b>	<i>numeric</i>
<b>trans-id</b>	<b>Genetic code</b>	<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>