## **ORF Marker**

From this chapter you can learn how to search for Open Reading Frames (ORF) in a DNA sequence. The ORFs found are stored as automatic annotations. This means that if the automatic annotations highlighting has been enabled then ORFs are searched and highlighted for each sequence opened. Refer *Automatic Annotations Highlighting* to learn more.

To open the ORF Marker dialog, select the Analyze Find ORFs item in the context menu.

% ORF Marker	<b>१</b> ×						
Settings Output							
Strand	Search Settings Preview						
e Both	Image: Min length, bp:       100         Image: Must terminate within region       Clear results						
O Direct	Must start with init codon  Allow overlaps  Allow alternative init codons						
Complement	<ul> <li>☑ Include stop codon</li> <li>☑ Max result</li> <li>☑ 200000</li> </ul>						
11. The Bacterial and Plant Plastid Code							
Start codons     ATG       Alternative start codons     TTG CTG ATT ATC       Stop codons     TAA TAG TGA	ATA GTG						
Region Whole sequence 🔻	1 - 140426						
Region Strand	Length						
0 results found.	OK Cancel Help						

The following search settings are available:

Min length - ORFs with length lower than Min length value will not be found.

Must terminate within region — this option ignores boundary ORFs located beyond the search region.

Must start with init codon — item switches the ORF Marker algorithm to the mode when any non-stop amino acid code is interpreted as region start position.

Allow overlaps — alternative (downstream) initiators, when another start codon is located within a longer ORF, i.e. all possible ORFs will be found, not only the longest ones.

Allow alternative init codon — option includes ORFs starting with alternative initiation codons, accordingly to the current translation table.

Include stop codon — includes stop codons into resulting annotations.

The other available parameters are:

DNA-to-Amino translation table defines the way start, alternative start and stop codons are encoded.

Strand — where to search the ORFs: in the direct strand, in the complement strand or in both strands.

Preview — allow to preview the regions, strands and lengths of the found ORFs.

Clear results - becomes available when some results have been found, clears these results.

To set the saving parameters go to the Output tab of the dialog.

Here you can modify the annotations saving parameters (Group name, Description and a file to save the annotation to).

Results:

When the search parameters has been selected and the OK button has been pressed in the dialog, the *auto-annotating* becomes enabled. In the Annotation ns editor the ORFs annotations can be found in the Auto-annotations\orf group.

After the search has been finished you can browse the results, sort them by length, strand or start position and save as annotations to the original sequence in the Genbank format.

For more information about codons use the codon table. It depends on the translation code selected for the sequence. To show or hide the table use *Ctrl+T* shortcut or click the *Show codon table* submenu of the *Amino translation* toolbar button menu:

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	✓	Show codon table Ctrl+T									
·		Translation frames									
	۲	1. The Standard Genetic Code									
4		2. The Vertebrate Mitochondrial Code									
		3. The Yeast Mitochondrial Code									
		The Mold, Protozoan, and Coelenterate Mitochondria and the Mycoplasma Code									
		5. The Invertebrate Mitochondrial Code									
•		6. The Ciliate, Dasycladacean and Hexamita Nuclear Code									
		9. The Echinoderm and Flatworm Mitochondrial Code									
		10. The Euplotid Nuclear Code									
1		11. The Bacterial and Plant Plastid Code									
		12. The Alternative Yeast Nuclear Code									
		13. The Ascidian Mitochondrial Code									
		14. The Alternative Flatworm Mitochondrial Code									
		15. Blepharisma Nuclear Code									
1		16. Chlorophycean Mitochondrial Code									
		21. Trematode Mitochondrial Code									
		22. Scenedesmus obliquus Mitochondrial Code									
		23. Thraustochytrium Mitochondrial Code									

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Project		000	Phenylalanine (Phe. F)	UCU	•	UAU	<u>Tyrosine (Tyr, Y)</u>	UGU	Cysteine (Cys, C)	U		
- E	U	UUC		UCC		UAC		UGC	Cysteme (Cys, C)	С		
		UUA		UCA UCG	UAA	Stop codon (*)	UGA	Stop codon (*)	A		ACG	
<b>W</b>		UUG			UAG		UGG	Tryptophan (Trp, W)	G			
		CUU	Leucine (Leu, L)		CCU CCC CCA Proline (Pro, P) CCG	CAU		CGU	Arginine (Arg, R)	U		2
	с	CUC				CAC	HISTIDINE (HIS, H)	CGC		c		
		CUA				CAA	Glutamine (Gln. O)	CGA		A		
		CUG				CAG		CGG		G	=	
		AUU		ACU	J C A <u>Threonine (Thr, T)</u>	AAU	Asparagine (Asp. N)	AGU	Serine (Ser. S)	Ŭ		
	A	AUC	Isoleucine (Ile, I)	ACC		AAC		AGC		c		
		AUA		ACA		AAA	Lysine (Lys. K)	AGA		A		
		AUG		ACG		AAG		AGG	<u>Arginine (Arg, R)</u>	G		
		GUU	<u>meanerine (meaning</u>	GCU	U C <u>Alanine (Ala, A)</u> A	GALL	Aspartic acid (Asp, D)	GGU	Glycine (Gly. G)	U		
		GUC				GAC		GGC		c		
	G	GUA	valine (val. v)				Glutamic acid (Glu, F)			-	-	
				GCA		GAA		GGA		A		
		GUG		GCG		GAG		GGG		G	Ŧ	

Clicking on a codon name redirects you to Wikipedia to give you a brief description of the corresponding amino acid. Cells of the table are colored according to classes of amino acids.