

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

Settings Output

Strand

☒ Both

☐ Direct

☐ Complement

Search Settings

☒ Min length, bp: 100

☐ Must terminate within region

☒ Must start with init codon

☐ Allow overlaps

☐ Allow alternative init codons

☐ Include stop codon

☒ Max result: 200000

Preview

Clear results

11. The Bacterial and Plant Plastid Code

Start codons	ATG
Alternative start codons	TTG CTG ATT ATC ATA GTG
Stop codons	TAA TAG TGA

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.

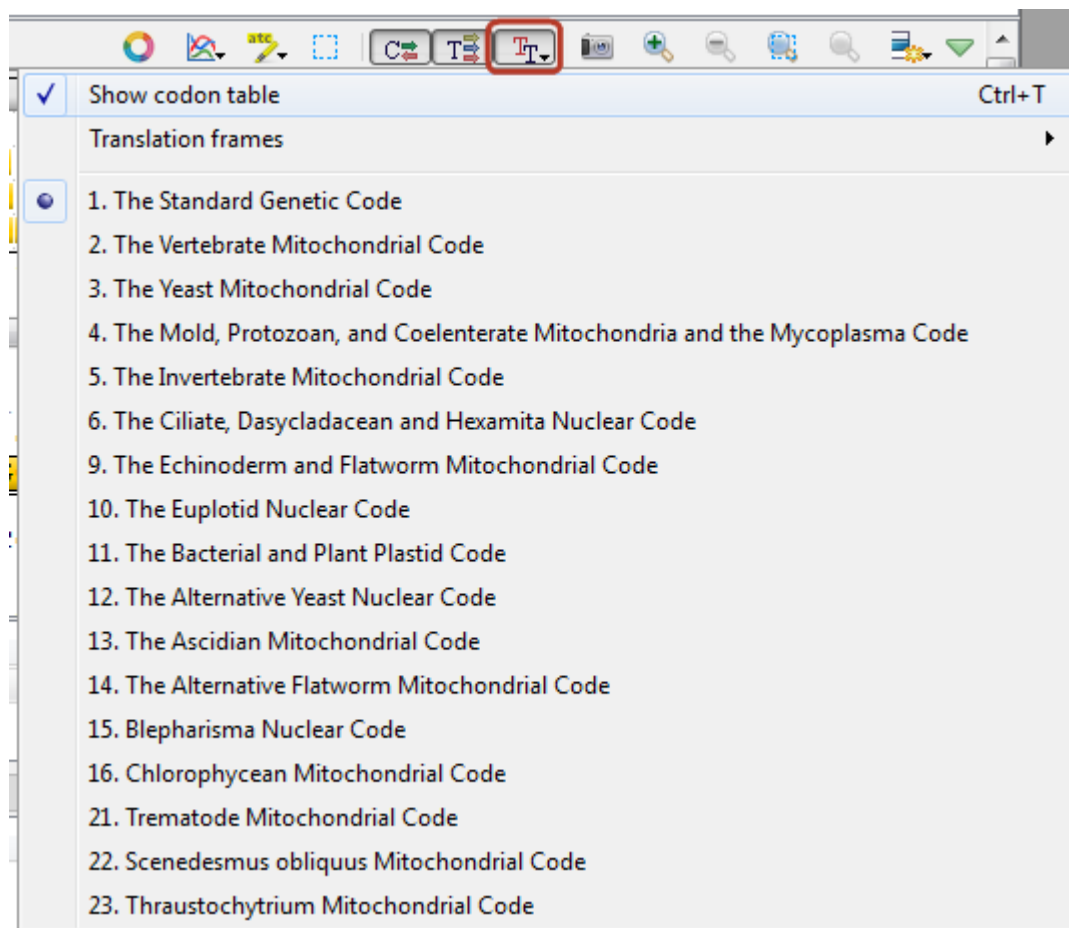
Here you can modify *the annotations saving* parameters (*Group name*, *Description* and a file to save the annotation to).

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 *Annotations 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:



The codon table will appear:

U - * UGENE - [human_T1 [s] human_T1 (UCSC April 2002 chr7:115977709-117855134)]

File Actions Settings Tools Window Help

1st base

2nd base

3rd base

U	UUU	Phenylalanine (Phe, F)	UCU	Serine (Ser, S)	UAU	Tyrosine (Tyr, Y)	UGU	Cysteine (Cys, C)	U
	UUC		UCC		UAC	UGC	C		
	UUA		UCA		UAA	UGA	Stop codon (*)	A	
	UUG		UCG		UAG	UGG	Tryptophan (Trp, W)	G	
C	CUU	Leucine (Leu, L)	CCU	Proline (Pro, P)	CAU	Histidine (His, H)	CGU	Arginine (Arg, R)	U
	CUC		CCC		CAC	CGC	C		
	CUA		CCA		CAA	CGA	A		
	CUG		CCG		CAG	CGG	G		
A	AUU	Isoleucine (Ile, I)	ACU	Threonine (Thr, T)	AAU	Asparagine (Asn, N)	AGU	Serine (Ser, S)	U
	AUC		ACC		AAC	AGC	C		
	AUA		ACA		AAA	AGA	A		
	AUG		ACG		AAG	AGG	G		
G	GUU	Valine (Val, V)	GCU	Alanine (Ala, A)	GAU	Aspartic acid (Asp, D)	GGU	Glycine (Gly, G)	U
	GUC		GCC		GAC	GGC	C		
	GUA		GCA		GAA	GGA	A		
	GUG		GCG		GAG	GGG	G		

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.