

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

SettingsOutput

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

1. The Standard Genetic Code

Start codonsATG

Alternative start codonsTTG CTG

Stop codonsTAA TAG TGA

RegionWhole sequence

1 - 199950

Region

Strand

Length

0 results found.

Help

Cancel

OK

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. To show or hide the table use *Ctrl+T* shortcut or click the *Show codon table* toolbar button menu:



The codon table will appear:

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.