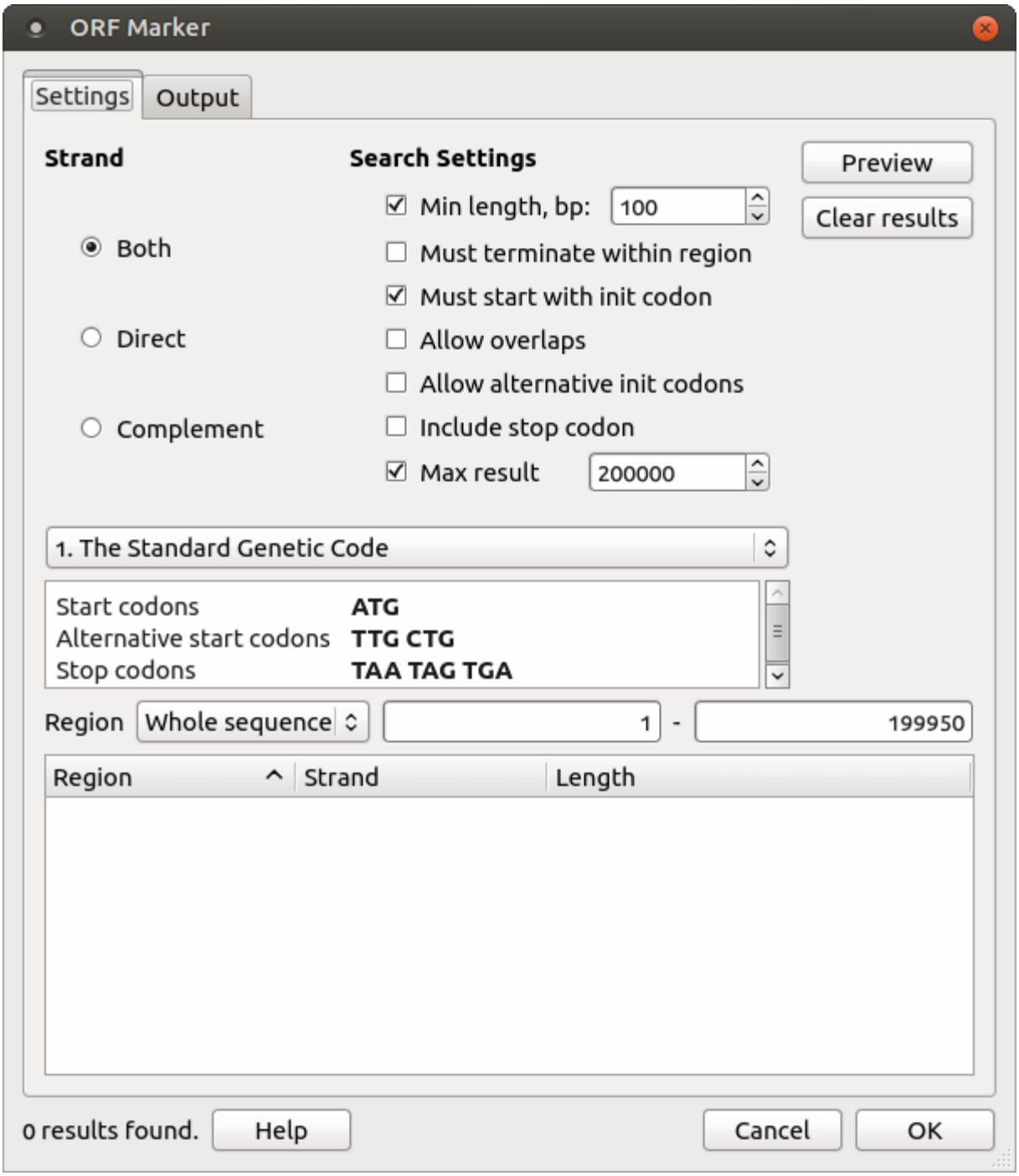
ORF Marker

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.



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).

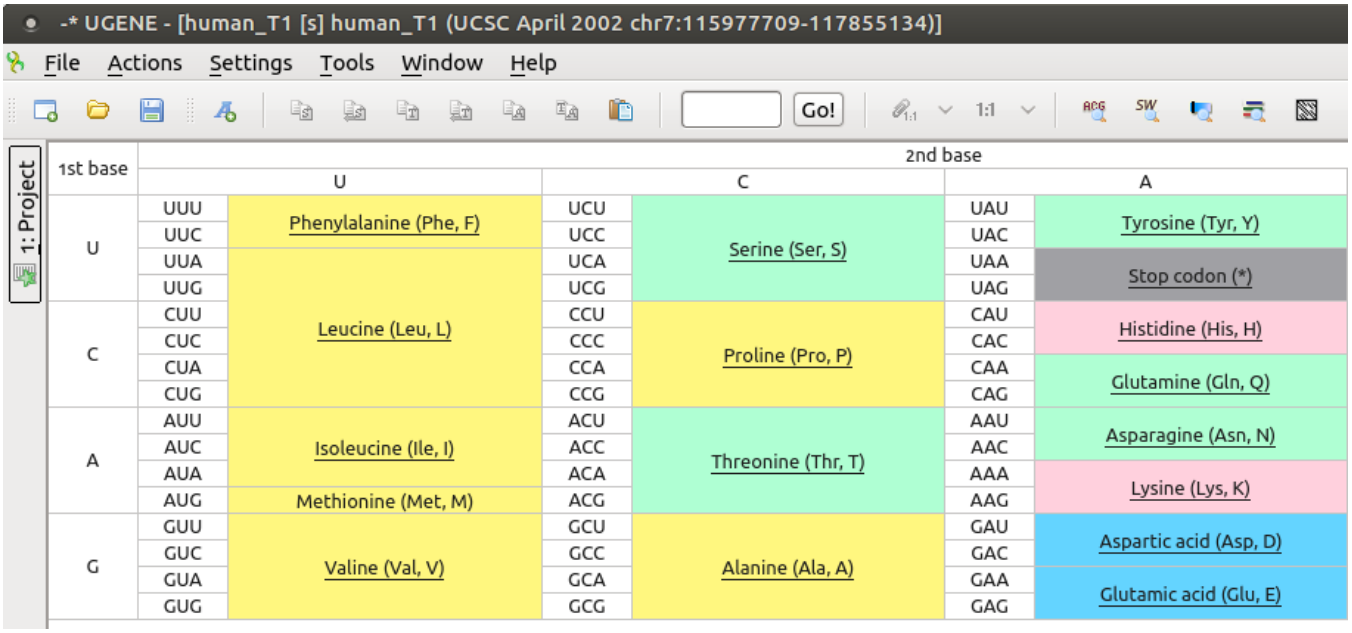
Results:

When the search parameters has been selected and the *OK* button has been pressed in the dialog, the *auto-annotating* becomes enabled. In the *Annotatio 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. To show or hide the table use *Ctrl+T* shortcut or click the *Show codon table* toolbar button menu:

The codon table will appear:



1st base	2nd base U		2nd base C		2nd base A	
U	UUU	Phenylalanine (Phe, F)	UCU	Serine (Ser, S)	UAU	Tyrosine (Tyr, Y)
	UUC		UCC		UAC	
	UUA	Leucine (Leu, L)	UCA		UAA	Stop codon (*)
	UUG		UCG		UAG	
C	CUU		CCU	Proline (Pro, P)	CAU	Histidine (His, H)
	CUC		CCC		CAC	
	CUA		CCA		CAA	Glutamine (Gln, Q)
	CUG		CCG		CAG	
A	AUU	Isoleucine (Ile, I)	ACU	Threonine (Thr, T)	AAU	Asparagine (Asn, N)
	AUC		ACC		AAC	
	AUA		ACA		AAA	Lysine (Lys, K)
	AUG	Methionine (Met, M)	ACG		AAG	
G	GUU	Valine (Val, V)	GCU	Alanine (Ala, A)	GAU	Aspartic acid (Asp, D)
	GUC		GCC		GAC	
	GUA		GCA		GAA	Glutamic acid (Glu, E)
	GUG		GCG		GAG	

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.