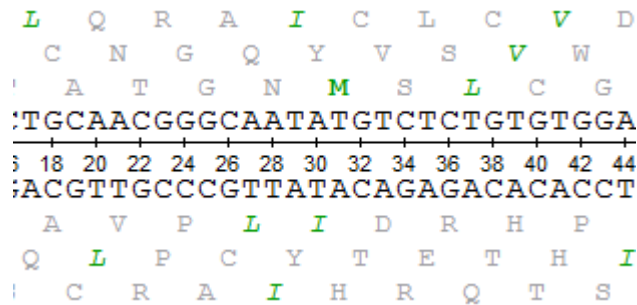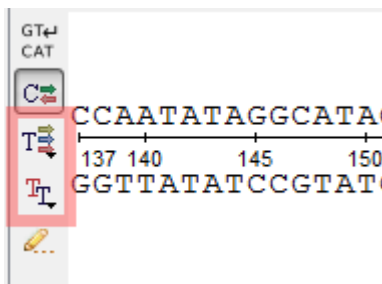# Translating Nucleotide Sequence

When a nucleotide sequence is opened in the *Sequence View*, the sequence and its complementary sequence are shown by default in the *Details View*.
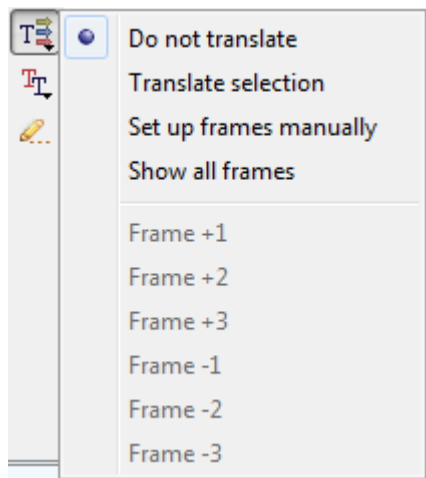
Showing/hiding the amino acid sequences

It is possible to translate them and show also the corresponding amino acid sequences:

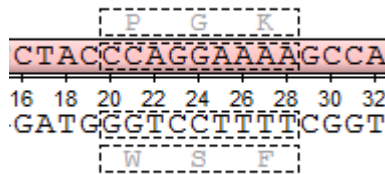The translation settings are available on the left toolbar of the *Details View*:

The *Show/hide amino acid translations* menu allows one to set up the mode of the amino acid sequences visualization:
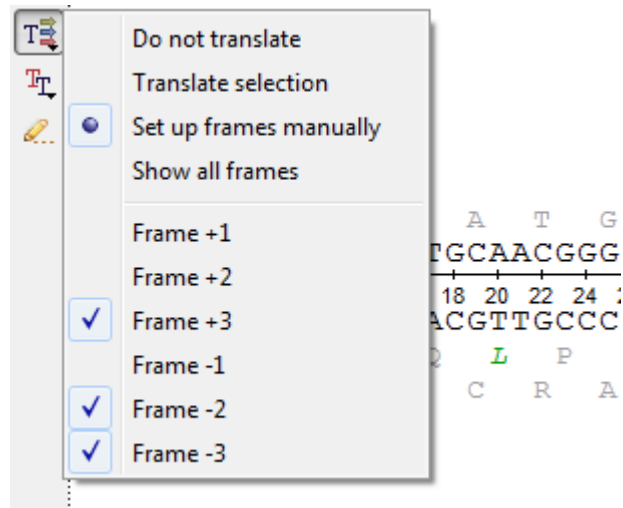

The following options are available:

- *Do not translate*— hide the amino acid sequences.
- *Translate selection* — translate only a selected region of the sequence and the complementary sequence.

- *Set up frames manually* — select the reading frames to show. There are three frames for the sequence ("+1", "+2", "+3") and three frames for the complementary sequence ("-1", "-2", "-3"). Note that the complementary frame items are hidden in the menu, if the complementary sequence is hidden.

- *Show all frames* — show all amino acid sequences.

Setting the genetic code

The default value for the genetic code for a nucleotide sequence translation is read by UGENE from the sequence file when it is available. One can also set up the genetic code for the sequence using the *Select genetic code* menu:

1. The Standard Genetic Code
2. The Vertebrate Mitochondrial Code
3. The Yeast Mitochondrial Code
4. 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
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
16. Chlorophycean Mitochondrial Code
21. Trematode Mitochondrial Code
22. Scenedesmus obliquus Mitochondrial Code
23. Thraustochytrium Mitochondrial Code

ⓘ All analysis routines (like HMMER, ORF finding, etc.) will use this code by default.

Codon table

To refresh the knowledge about the amino acid codes, select the *Show codon table* button [CAG Q] on the *Sequence View* global toolbar. The codon table appears at the upper part of the window:

1st base	2nd base								3rd base
	U		C		A		G		
U	UUU	Phenylalanine (Phe, F)	UCU	Serine (Ser, S)	UAU	Tyrosine (Tyr, Y)	UGU	Cysteine (Cys, C)	U
	UUC		UCC		UAC		UGC		C
	UUA	Leucine (Leu, L)	UCA		UAA	Stop codon (*)	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	Glutamine (Gln, Q)	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	Lysine (Lys, K)	AGA	Arginine (Arg, R)	A
	AUG	Methionine (Met, M)	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	Glutamic acid (Glu, E)	GGA		A
	GUG		GCG		GAG		GGG		G