

Selecting Amino Translation

The default value for the genetic code is read by UGENE from the sequence file when it is available. You can also select the genetic code for the sequence using the *Amino translation* menu button on the sequence toolbar.



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

- ☒ 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

The numbering of the genetic codes corresponds the NCBI Genbank database numbering.