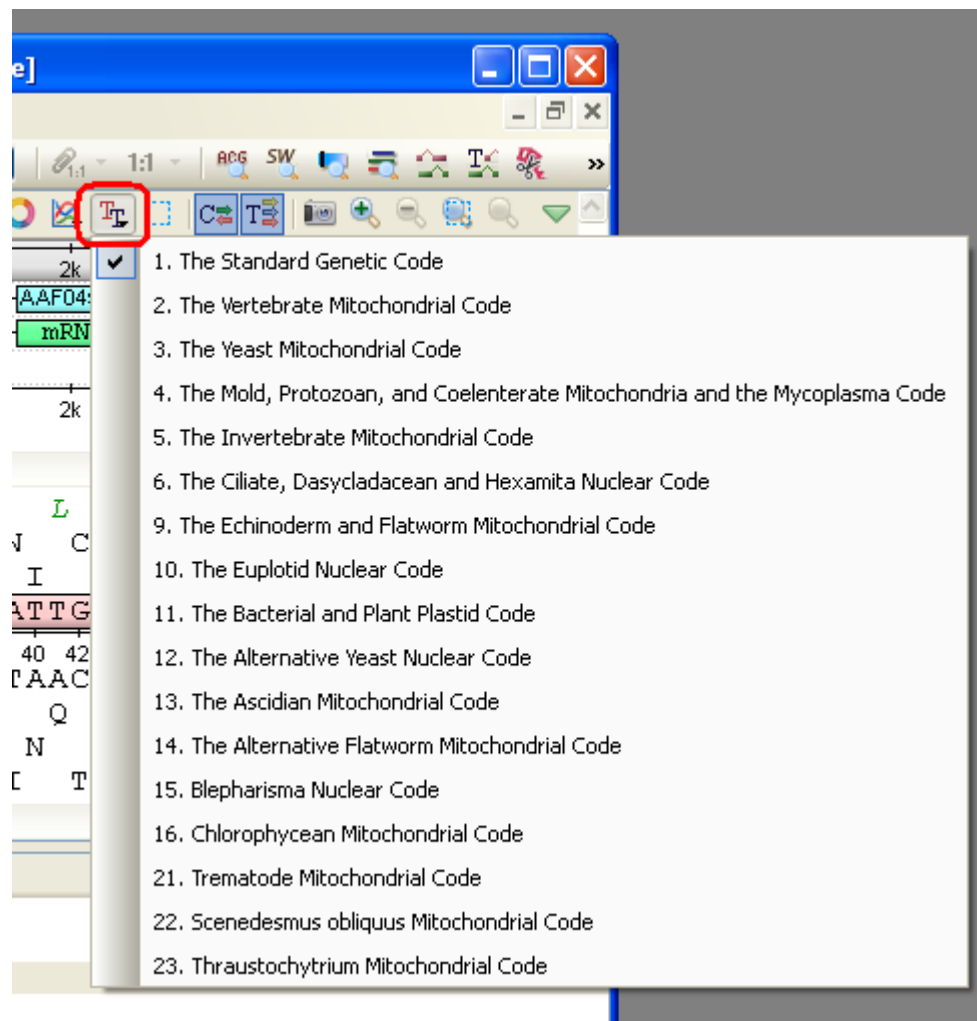# Selecting Amino Translation

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.

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