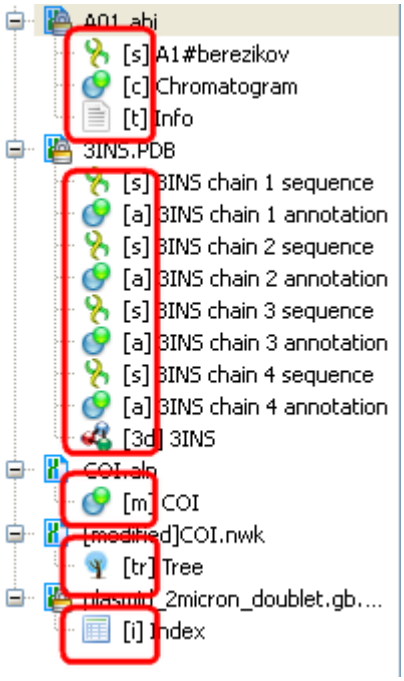
Using Objects and Object Views

The document always contains one or more *objects*. An *object* is a structured biological data that can be visualized by different *Object Views*.

A single *Object View* can visualize one or several objects of different types. For example a single view can show a sequence, annotations for the sequence, 3D model for the part of the sequence or its chromatogram simultaneously.

The type of an object is indicated by the symbol in the square brackets and the icon near the object:



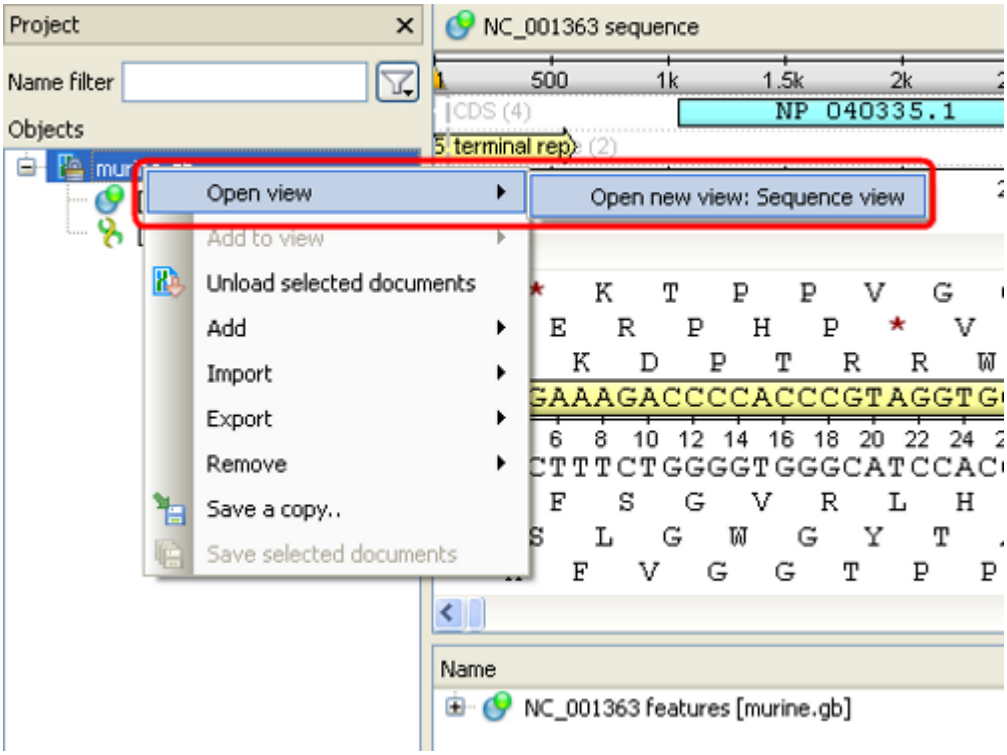
Below is the list of object types supported by the current version of UGENE.

Object types:

Symbol	Icon	Description
[3d]		A 3D model.
[a]		Annotations for DNA sequence regions.
[as]		An assembly.
[c]		Chromatogram data.
[i]		A file with index information for a set of other, usually large files.
[m]		A multiple sequence alignment.
[s]		A nucleic, protein or raw sequence.
[t]		A plain text.
[tr]		A phylogenetic tree.

You can edit names of particular objects, such as sequence objects, by selecting them in the *Project View* and then pressing F2. To be able to do so, the document containing the target object must be unlocked.

To see the list of all available views for a given object select the object and activate the context menu inside the *Project View* window and select the *Open view* submenu:



The picture above illustrates an option to visualize the selected DNA sequence object using the *Sequence View* — a complex and extensible *Object View* t hat focuses on visualization of sequence objects in combination with different kinds of related data: sequence annotations, graphs, chromatograms, sequence analysis algorithms. Note, that the *Sequence View* is described in more details in the separate *documentation section*.