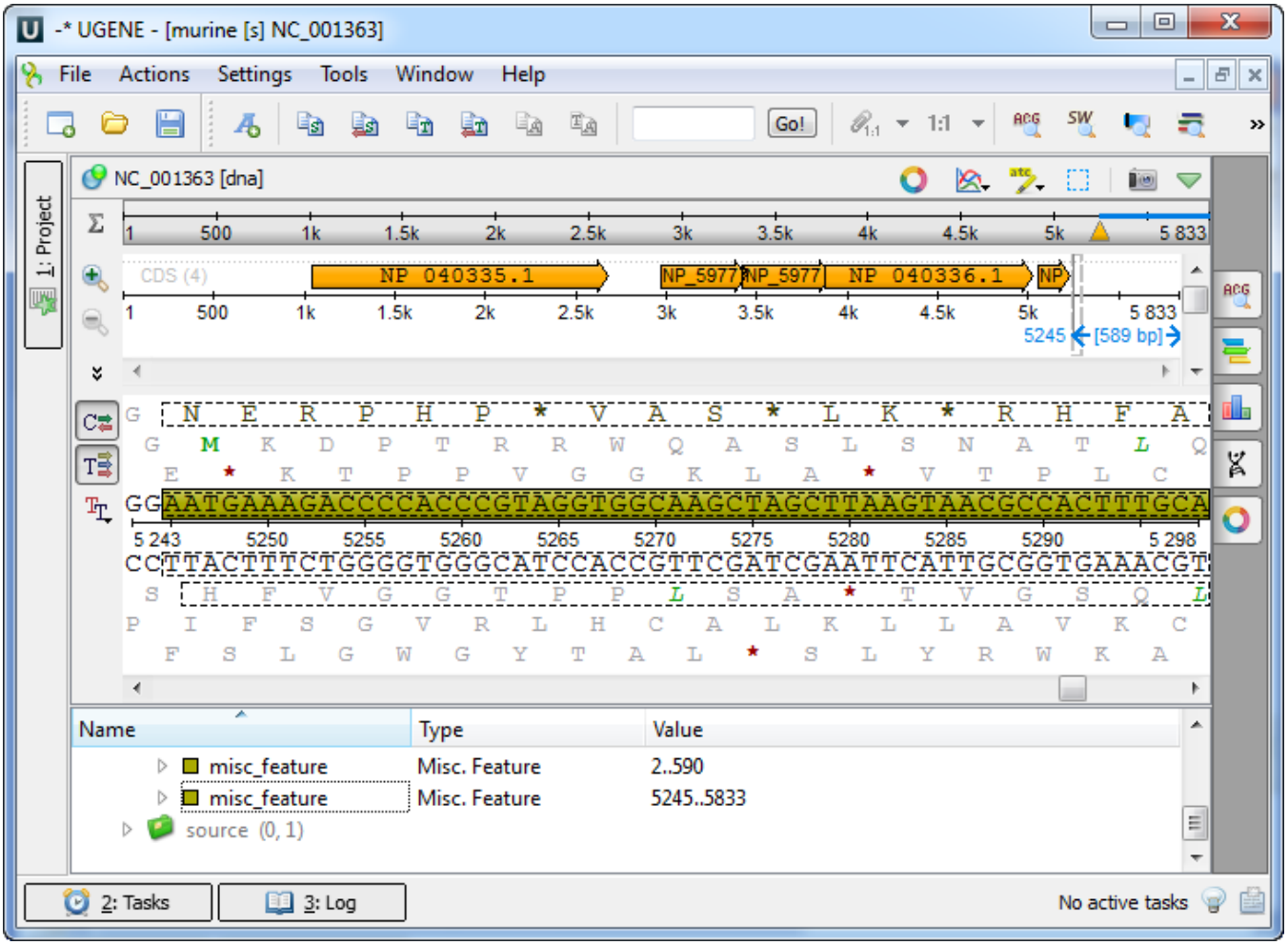
Sequence View Components

The *Sequence View* is one of the major *Object Views* in UGENE aimed to visualize and edit DNA, RNA or protein sequences along with their properties like annotations, chromatograms, 3D models, statistical data, etc.

For each file UGENE analyzes the file content and automatically opens the most appropriate view.

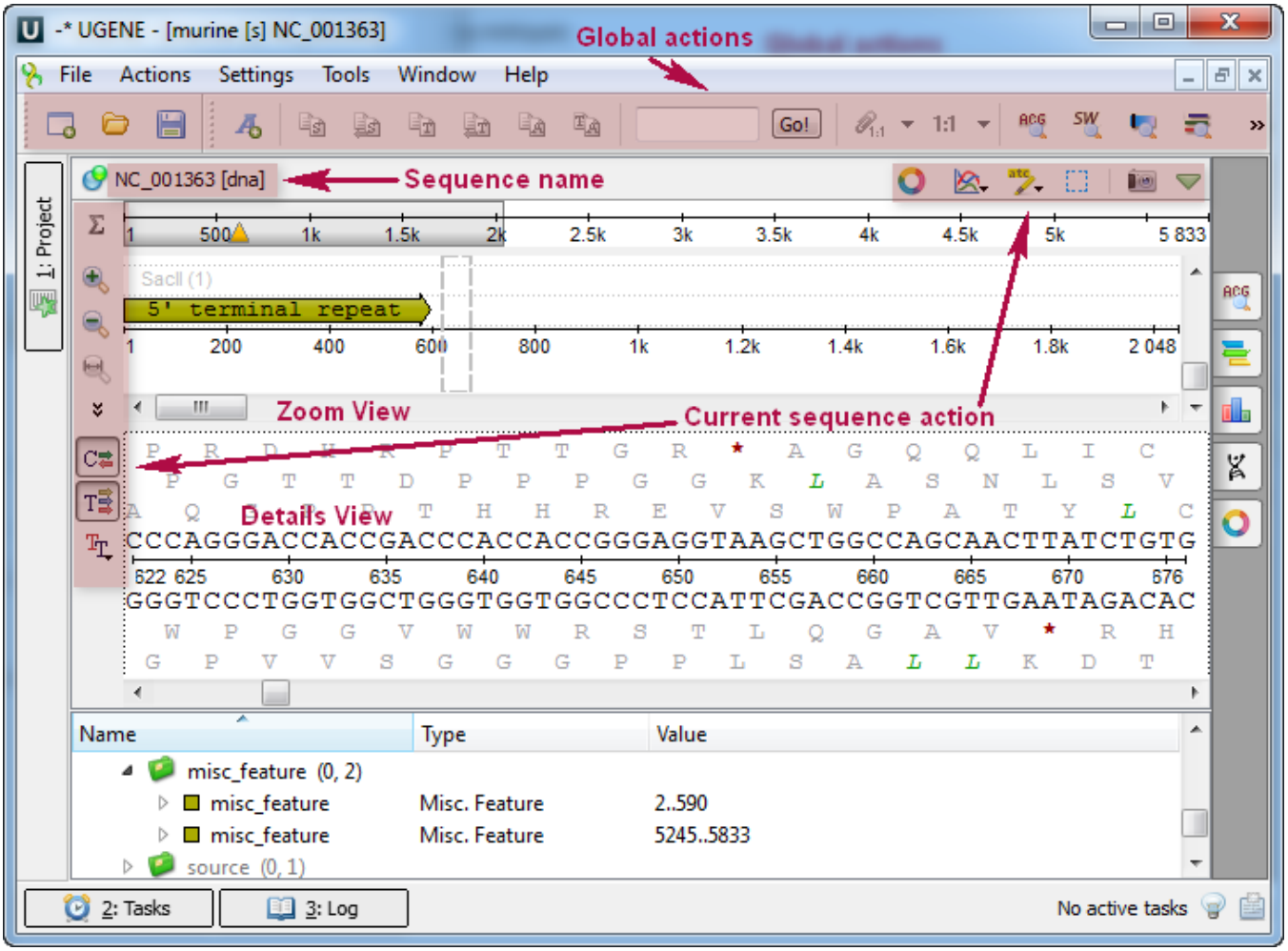
To activate the *Sequence View* open any file with at least one sequence. For example you can use the $UGENE/data/samples/EMBL/AF177870.emb file provided with UGENE.

After opening the file in UGENE the *Sequence View* window appears:



After the view is opened you can see a set of new buttons in the toolbar area. The actions provided by these buttons are available for all sequences opened in the view. In the picture below these buttons are pointed by the “Global actions” arrow.

Below the toolbar there is an area for a single or several sequences. For each sequence a smaller toolbar with actions for the sequence and the following areas are available:



An example of the *Sequence View* with several sequences:

You can change the focus by clicking on the corresponding sequence area. All sequences that are not in focus have the sequence name and icon disabled.

The bottom area of the *Sequence View* is the *Annotations Editor*. It contains a tree-like structure of all annotations available for all sequences shown in the *Sequence View* and can be used to perform various actions on annotations: create a new annotation, modify the existing one, group, sort, etc.