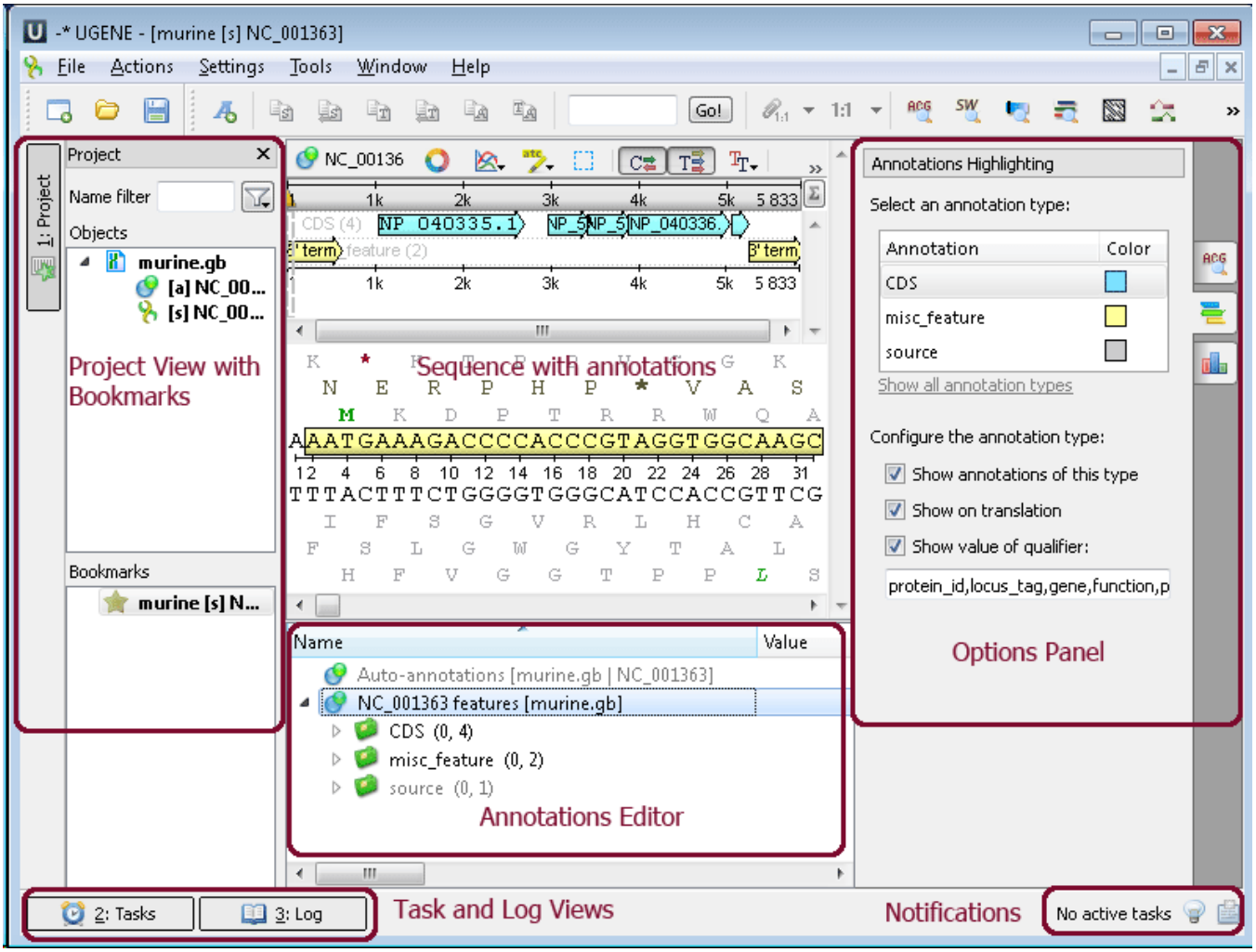
View, edit and annotate DNA, RNA and protein sequences

DNA, RNA or protein sequences (*Sequence View*). 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 le UGENE analyzes the le content and automatically opens the most appropriate view. To activate the *Sequence View* open any le with at least one sequence. For example you can use the $*ugene/data/samples/Genbank/murine.gb* le provided with UGENE. After opening the le in UGENE the *Sequence View* window appears:



Sequece View - an object view aimed to visualize DNA, RNA or protein sequences along with their properties like annotations, chromatograms, 3D models, statistical data, etc.

Project View - a visual component used to manage active project and bookmarks.

Annotations Editor - contains tools to manipulate annotations for a sequence.

Options Panel - it is the panel with dierent information tabs and tabs with settings for Sequence View.

Task View - shows active tasks, for example, algorithms computations.

Log View - shows the program log information.

Notifications - shows notifications for task reports.

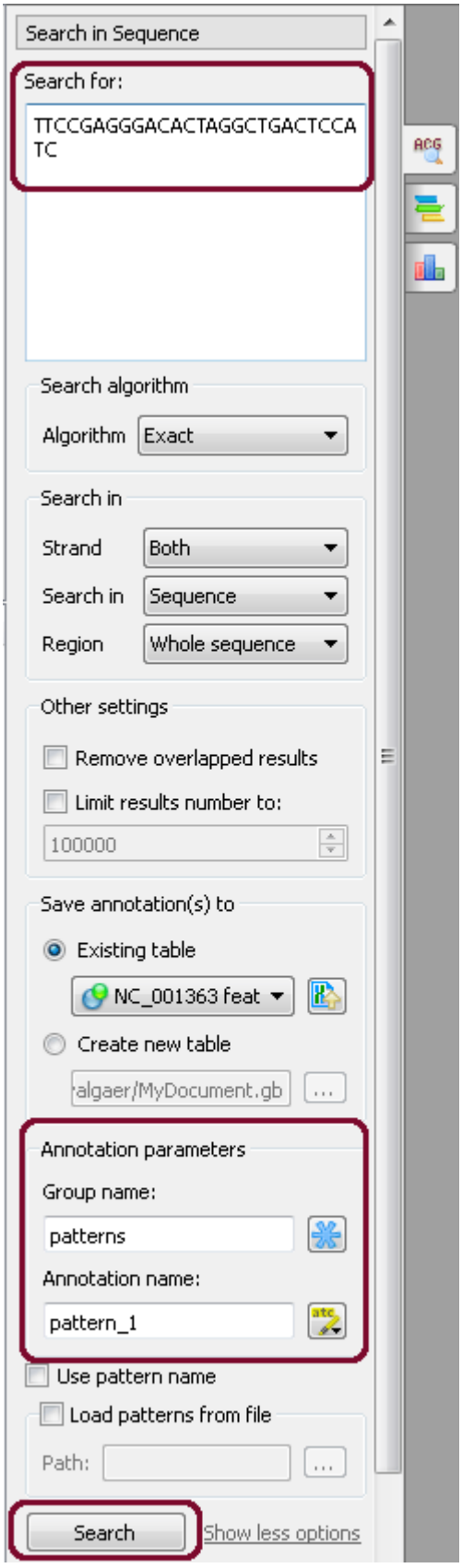
After the view is opened you can see a set of new buttons in the toolbar area. The actions provided by these buttons are available for all sequences opened in the view. These actions also available from the context menu. Many instruments and algorithms are available:

- Find pattern
- Find ORFs
- Find annotated regions
- Build dotplot
- Find repeats
- Find tandems

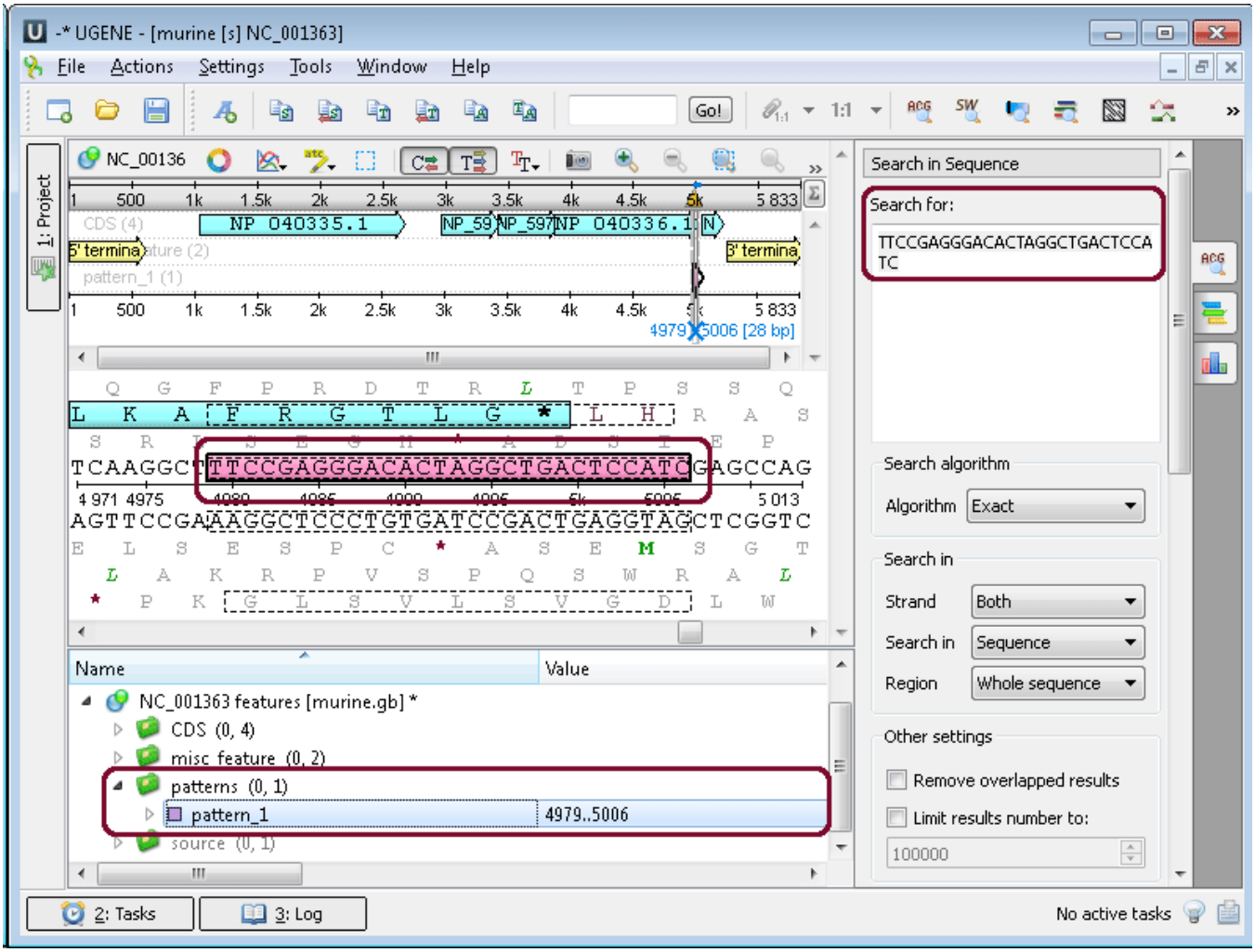
- Find restriction sites
- Primer 3
- Find high DNA flexibility regions
- ...

Example 1: Finding patterns in your sequence. Do the following steps:

Open the *ugene/data/samples/murine.gb* by *File–>Open* menu, for example. Sequence View with murine.gb opens. Select the *Search in Sequence* tab of the *Options Panel*. Click *Show more options* and more options appear. Insert, for example "TTCCGAGGGACACTAGGCTGACTCCATC" pattern into *Searc h for:* field and choose annototation parameters. For example as in the picture below:



After that click the *Search* button. If the pattern there is or there are in the sequence it appears as new annotation(s):


-* UGENE - [murine [s] NC_001363]
File Actions Settings Tools Window Help
Go!
1: Project
NC_00136
CDS (4)
NP_040335.1
NP_597
NP_040336.1
pattern_1 (1)
4979..5006 [28 bp]
TCAAGGCTTTCCGAGGGACACTAGGCTGACTCCATCGAGCCAG
AGTTCCGAAAAGGCTCCCTGTGATCCGACTGAGGTAGCTCGGTC
Search in Sequence
Search for:
TTCCGAGGGACACTAGGCTGACTCCATC
Search algorithm
Algorithm Exact
Search in
Strand Both
Search in Sequence
Region Whole sequence
Other settings
Remove overlapped results
Limit results number to:
100000
Name
Value
NC_001363 features [murine.gb] *
CDS (0, 4)
misc_feature (0, 2)
patterns (0, 1)
pattern_1
4979..5006
source (0, 1)
2: Tasks
3: Log
No active tasks