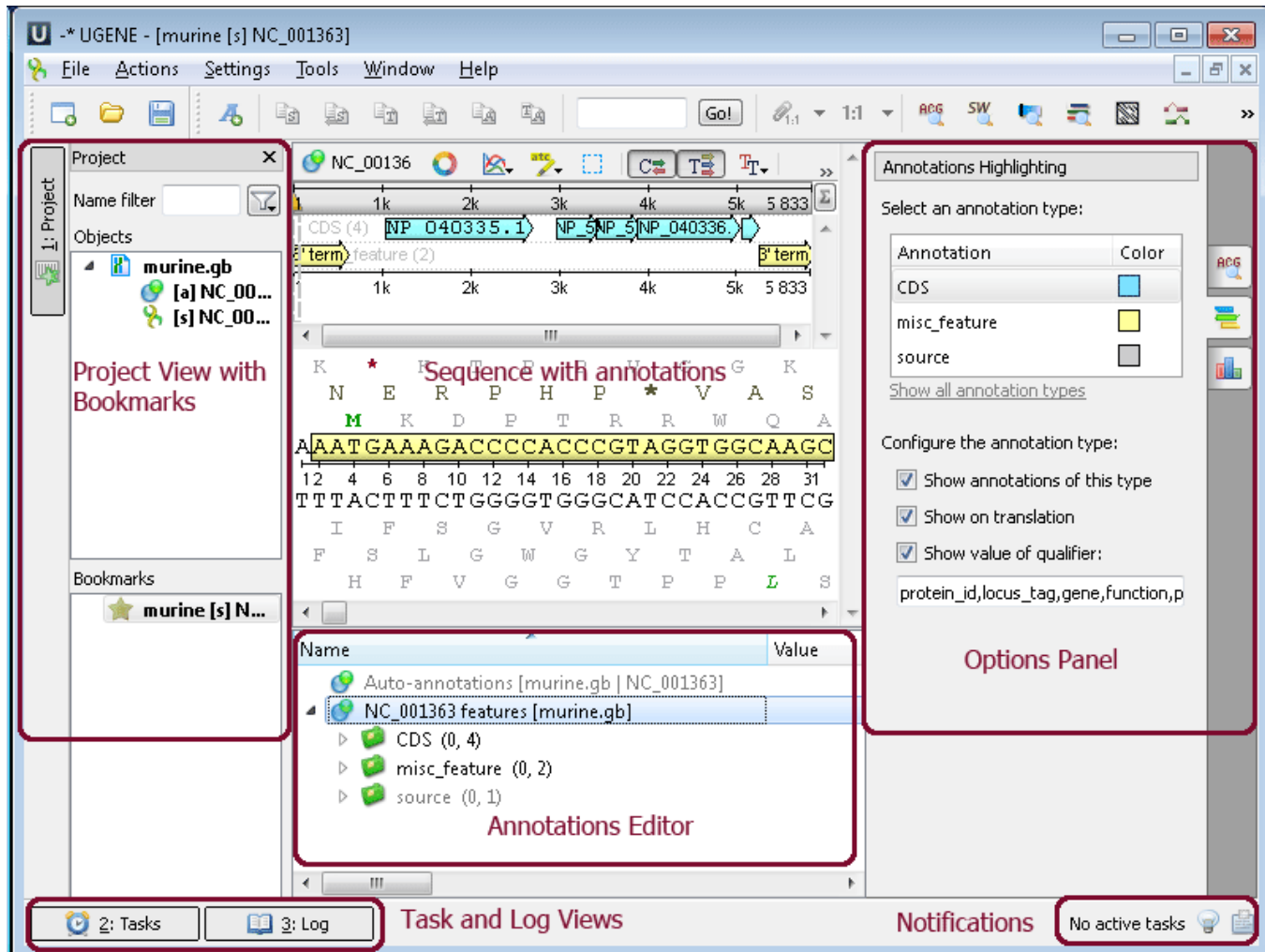


View, edit and annotate DNA, RNA and protein sequences

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 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/Genbank/murine.gb` file provided with UGENE. After opening the file in UGENE the *Sequence View* window appears:



Sequence 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 different 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 are 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 *Search for:* field and choose annotation parameters. For example as in the picture below:

Search in Sequence

Search for:

TCCGAGGGACACTAGGCTGACTCCA
TC

Search algorithm

Algorithm Exact

Search in

Strand Both

Search in Sequence

Region Whole sequence

Other settings

☐ Remove overlapped results

☐ Limit results number to:

100000

Save annotation(s) to

☒ Existing table

NC_001363 feat

☐ Create new table

algaer/MyDocument.gb

Annotation parameters

Group name:

patterns

Annotation name:

pattern_1

☐ Use pattern name

☐ Load patterns from file

Path:

Search [Show less options](#)

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

U -* UGENE - [murine [s] NC_001363]

File Actions Settings Tools Window Help

NC_00136

1 500 1k 1.5k 2k 2.5k 3k 3.5k 4k 4.5k 5k 5.833

CDS (4) NP_040335.1 NP_59 NP_597 NP_040336.1 N

5' terminus (2) 5' terminus

pattern_1 (1) 4979..5006 [28 bp]

Q G F P R D T R L T P S S Q

L K A F R G T L G * L H R A S

S R T S E S H A D S I E P

TCAAGGC TTCCGAGGGACACTAGGCTGACTCCATC GAGCCAG

4 971 4975 4980 4985 4990 4995 5000 5005 5010 5013

AGTTCCGAAAGGCTCCCTGTGATCCGACTGAGGTAGCTCGGTC

E L S E S P C * A S E M S G T

L A K R P V S P Q S W R A L

* P K G L S V L S V G D L W

Name Value

- NC_001363 features [murine.gb] *
 - CDS (0, 4)
 - misc feature (0, 2)
 - patterns (0, 1)
 - pattern_1 4979..5006
 - source (0, 1)

Search in Sequence

Search for: TTCCGAGGGACACTAGGCTGACTCCA TC

Search algorithm

Algorithm Exact

Search in

Strand Both

Search in Sequence

Region Whole sequence

Other settings

☐ Remove overlapped results

☐ Limit results number to: 100000

2: Tasks 3: Log No active tasks