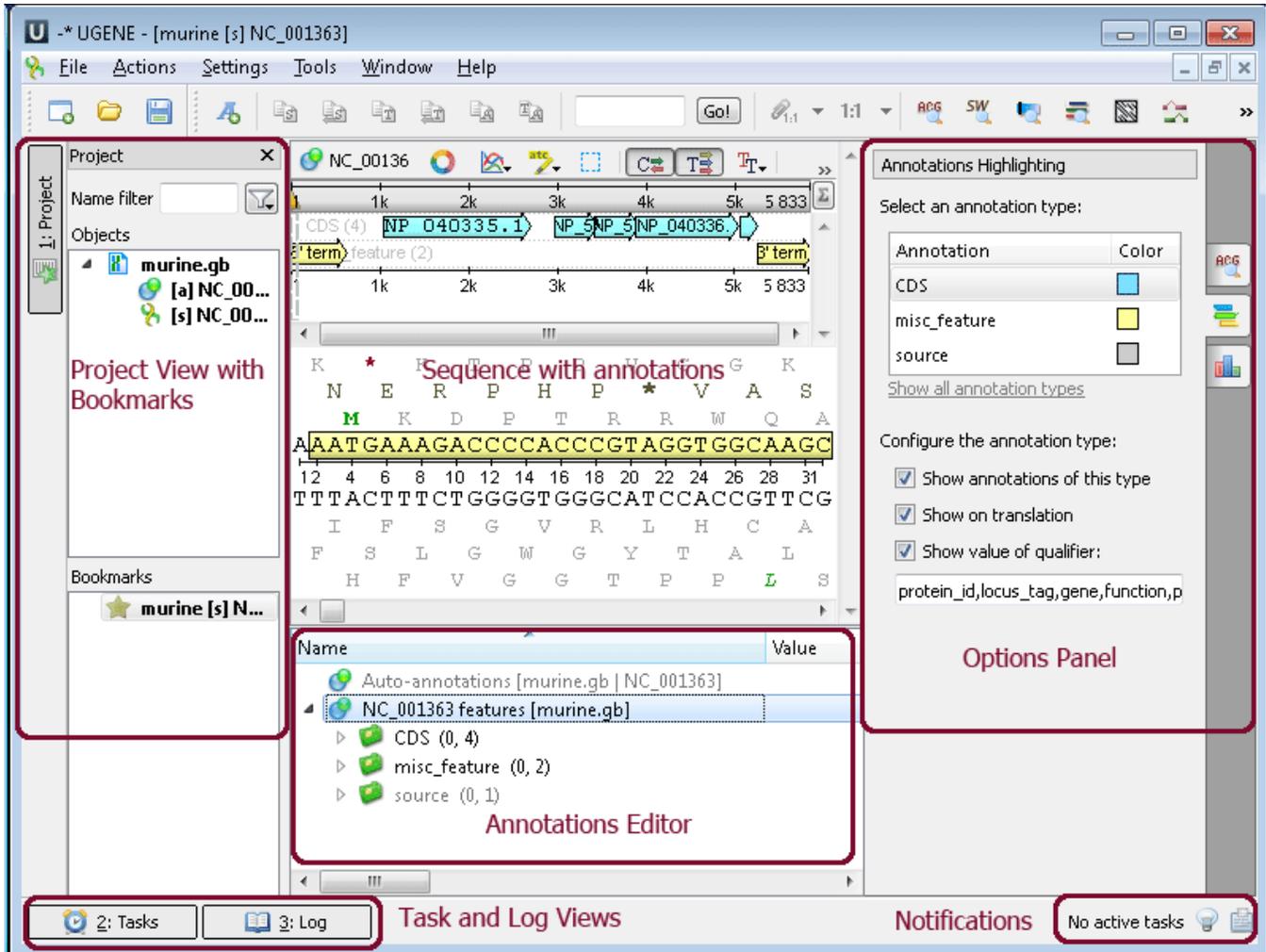


View, edit and annotate DNA, RNA and protein sequences

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:



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 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 "TTCCGAGGGACTAGGCTGACTCCATC" 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_597 NP_597 NP_040336.1 N

5' terminus (2) 5' terminus

pattern_1 (1)

1 500 1k 1.5k 2k 2.5k 3k 3.5k 4k 4.5k 5k 5 833

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 I R A S

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

TCAAGGC **TTCCGAGGGACACTAGGCTGACTCCATC** GAGCCAG

4 971 4975 4980 4985 4990 4995 5000 5005 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