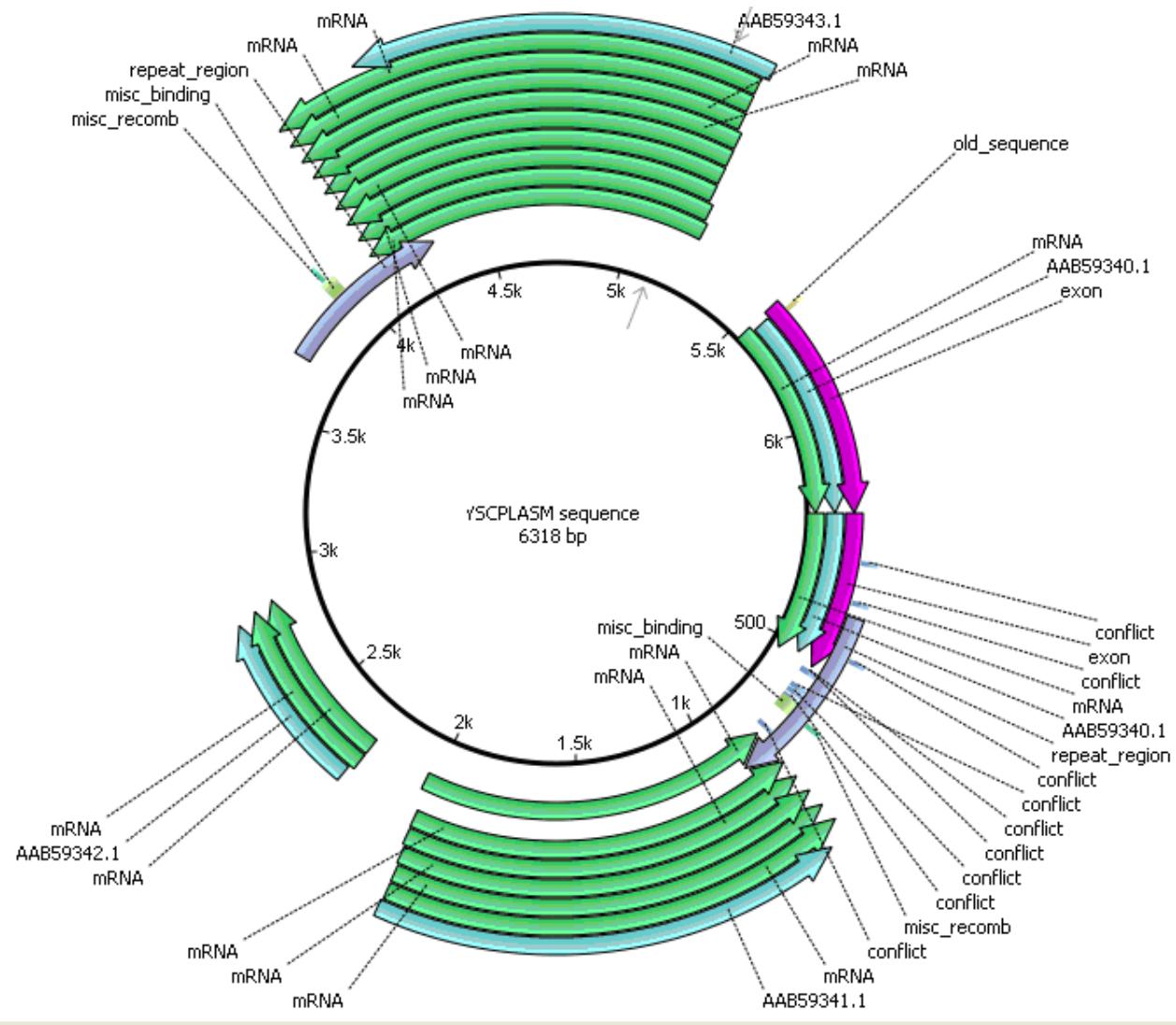


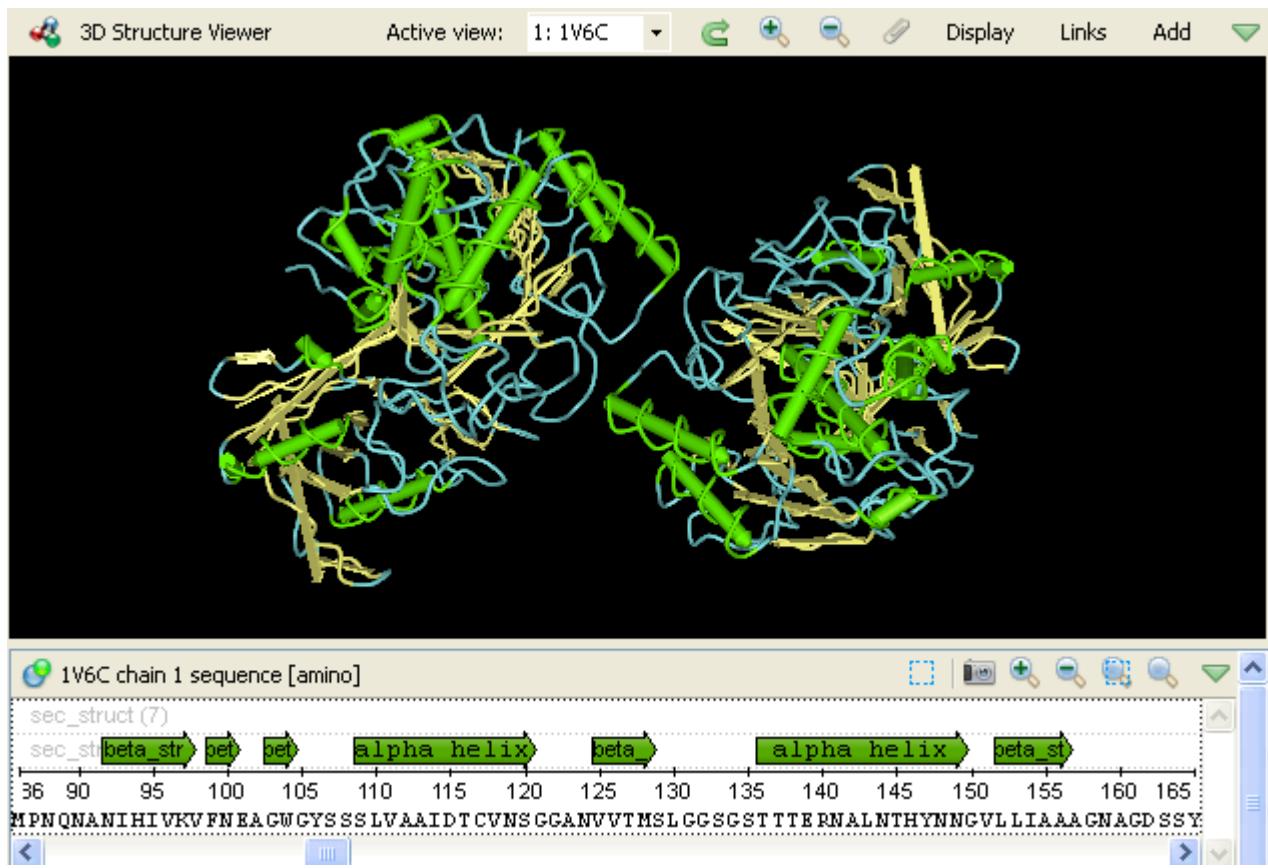
Sequence View Extensions

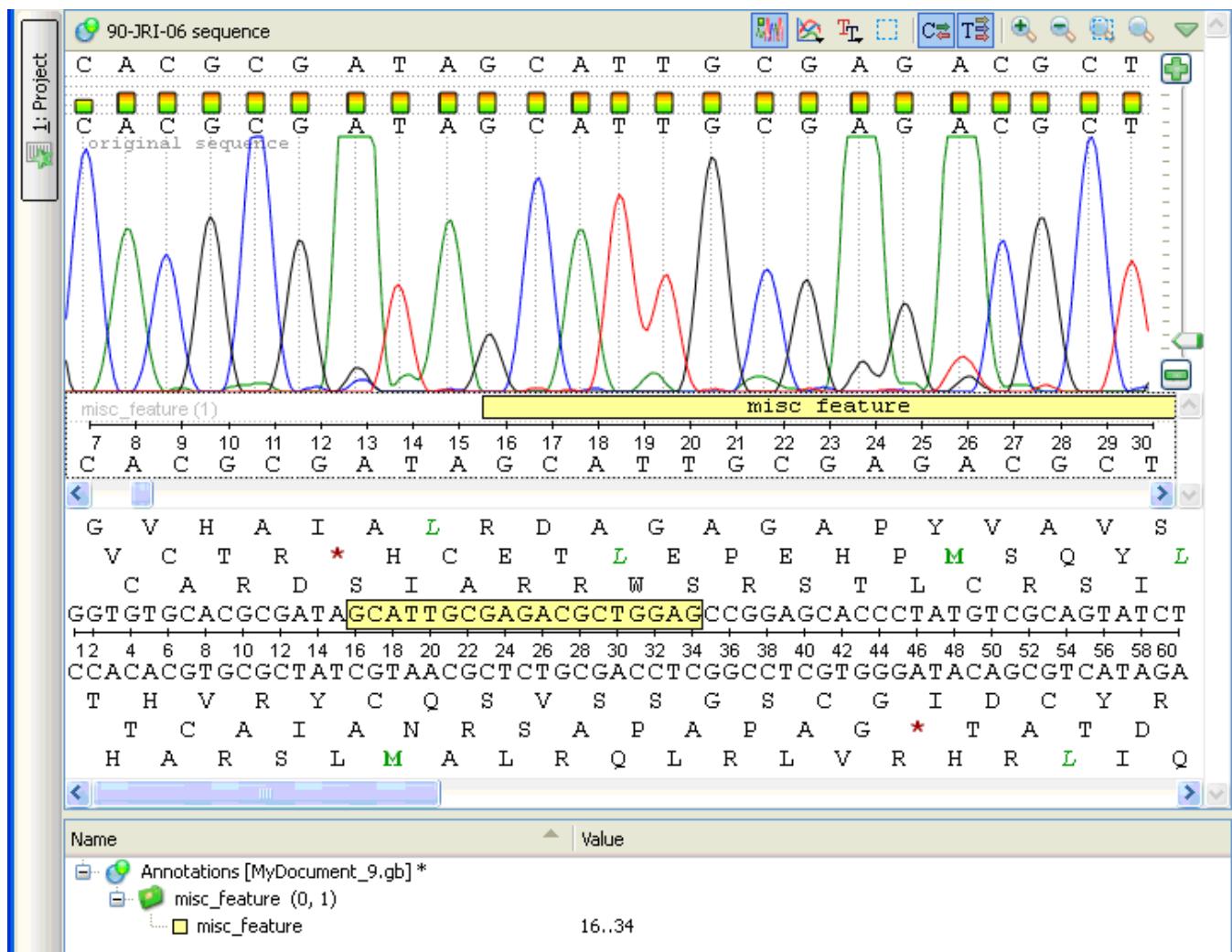
The functionality of the *Sequence View* can be significantly increased with *Sequence View Extensions*. Below is the demonstration its functionality.

The [Circular Viewer](#) shows the circular view of a sequence:

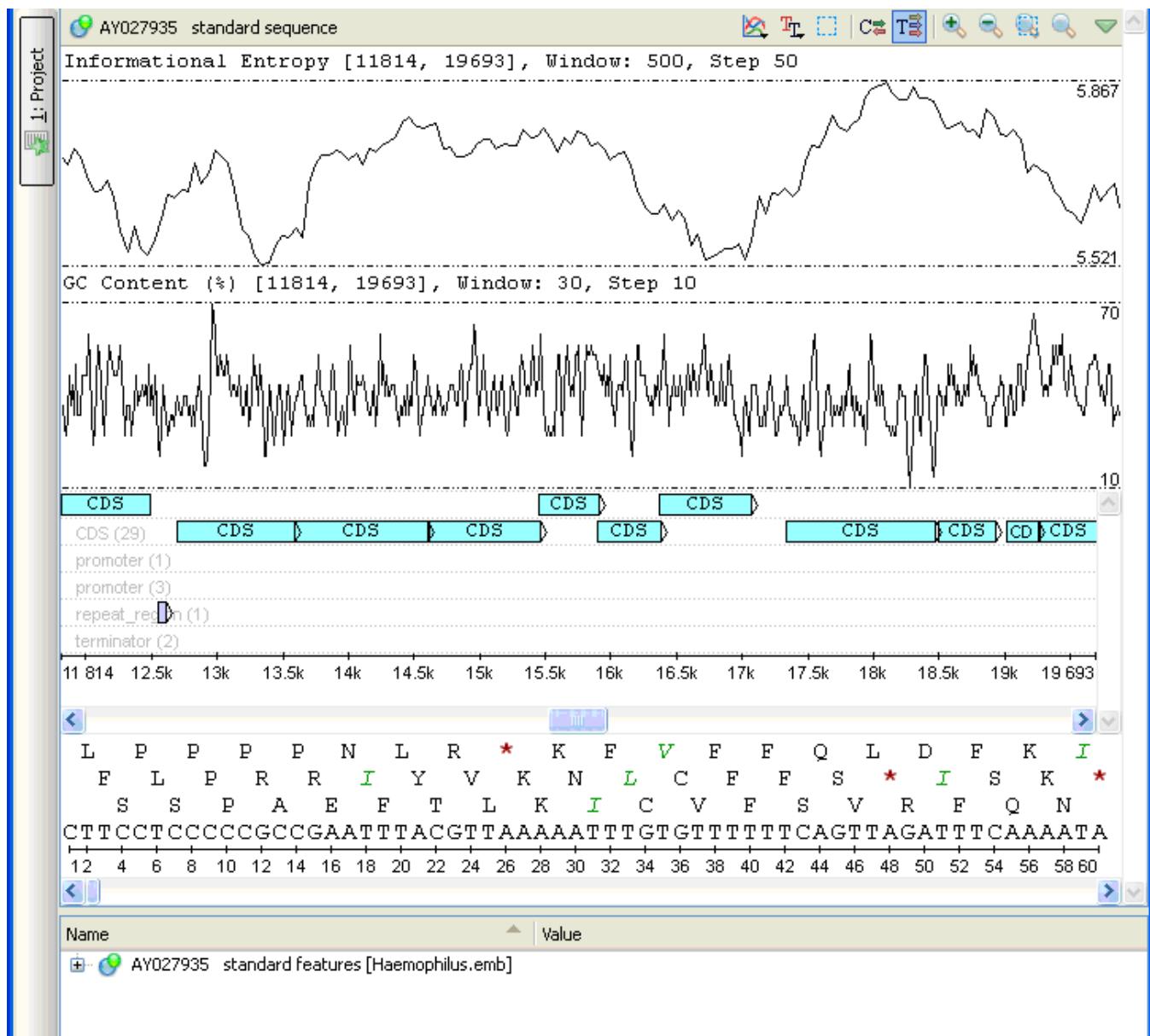


The [3D Structure Viewer](#) adds 3D visualization for PDB and MMDB files:

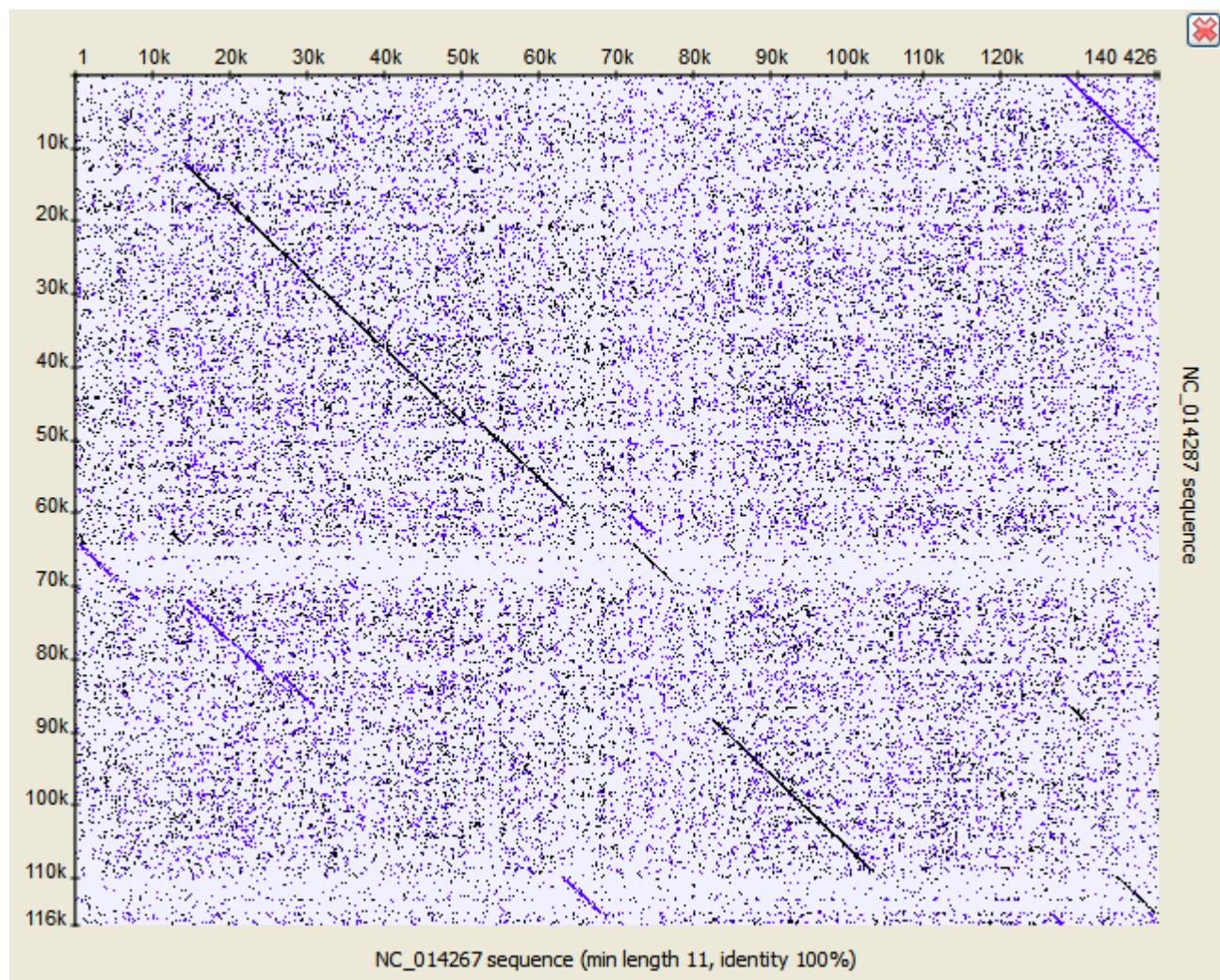




The [DNA Graphs Package](#) shows various graphs for sequences:



The [Dotplot](#) provides a tool to build dotplots for DNA or RNA sequences.



A number of other instruments add graphical interface for popular sequence analysis methods:

U -* UGENE - [murine NC_001363 sequence]

File Actions Settings Tools Window Help

Project

NC_001363 sequence [dna]

D335.1

NP_597742.2

NP_597742.2

2k 2.5k 3k 3.5k 4k

2k 2.5k 3k 3.5k 4k

K N M AAT T T T A I F H

12 4

AAAT

Find pattern... Ctrl+F

Find pattern [Smith-Waterman]... Ctrl+Shift+F

Find ORFs...

Find annotated regions...

Build dotplot...

Find repeats...

Find tandems...

Find query designer pattern...

Find restriction sites...

Query NCBI BLAST database...

Search HMM signals with HMMER3...

Search with HMM model...

Search TFBS with SITECON...

Search TFBS with matrices...

Primer3...

Predict secondary structure...

Query with BLAST...

Query with BLAST+...

Go!

1:1

ACG SW

Project

NC_001363 features [murine.gb]

Name Annotations highlighting...

2: Tasks

3: Log

The screenshot shows the UGENE software interface. The main window displays a DNA sequence named 'NC_001363 sequence [dna]' with a length of 4k. A specific region from approximately 2.5k to 3.5k is highlighted in light blue. A context menu is open over this highlighted region, with the 'Analyze' option selected. The 'Analyze' submenu contains 15 items, each with an icon and a command name. The commands include: Find pattern..., Find pattern [Smith-Waterman]..., Find ORFs..., Find annotated regions..., Build dotplot..., Find repeats..., Find tandems..., Find query designer pattern..., Find restriction sites..., Query NCBI BLAST database..., Search HMM signals with HMMER3..., Search with HMM model..., Search TFBS with SITECON..., Search TFBS with matrices..., Primer3..., Predict secondary structure..., Query with BLAST..., and Query with BLAST+... . The background shows a sequence viewer with a ruler at the top and a sequence editor below it. The left sidebar lists the project and its features.

For details see the next sections of the documentation:

- Circular Viewer
 - Circular View Settings
- 3D Structure Viewer
 - Opening 3D Structure Viewer
 - Changing 3D Structure Appearance
 - Selecting Render Style
 - Selecting Coloring Scheme
 - Calculating Molecular Surface
 - Selecting Background Color
 - Selecting Detail Level
 - Enabling Anaglyph View
 - Moving, Zooming and Spinning 3D Structure
 - Selecting Sequence Region
 - Selecting Models to Display
 - Structural Alignment
 - Exporting 3D Structure Image
 - Working with Several 3D Structures Views
- Chromatogram Viewer
 - Exporting Chromatogram Data
 - Viewing Two Chromatograms Simultaneously
- DNA/RNA Graphs Package
 - Description of Graphs
 - Graph Settings
 - Saving Graph Cutoffs as Annotations
- Dotplot
 - Creating Dotplot
 - Navigating in Dotplot
 - Zooming to Selected Region
 - Selecting Repeat
 - Interpreting Dotplot: Identifying Matches, Mutations, Inversions, etc.
 - Editing Parameters
 - Filtering Results
 - Saving Dotplot as Image
 - Saving and Loading Dotplot
 - Building Dotplot for Currently Opened Sequence
 - Comparing Several Dotplots