

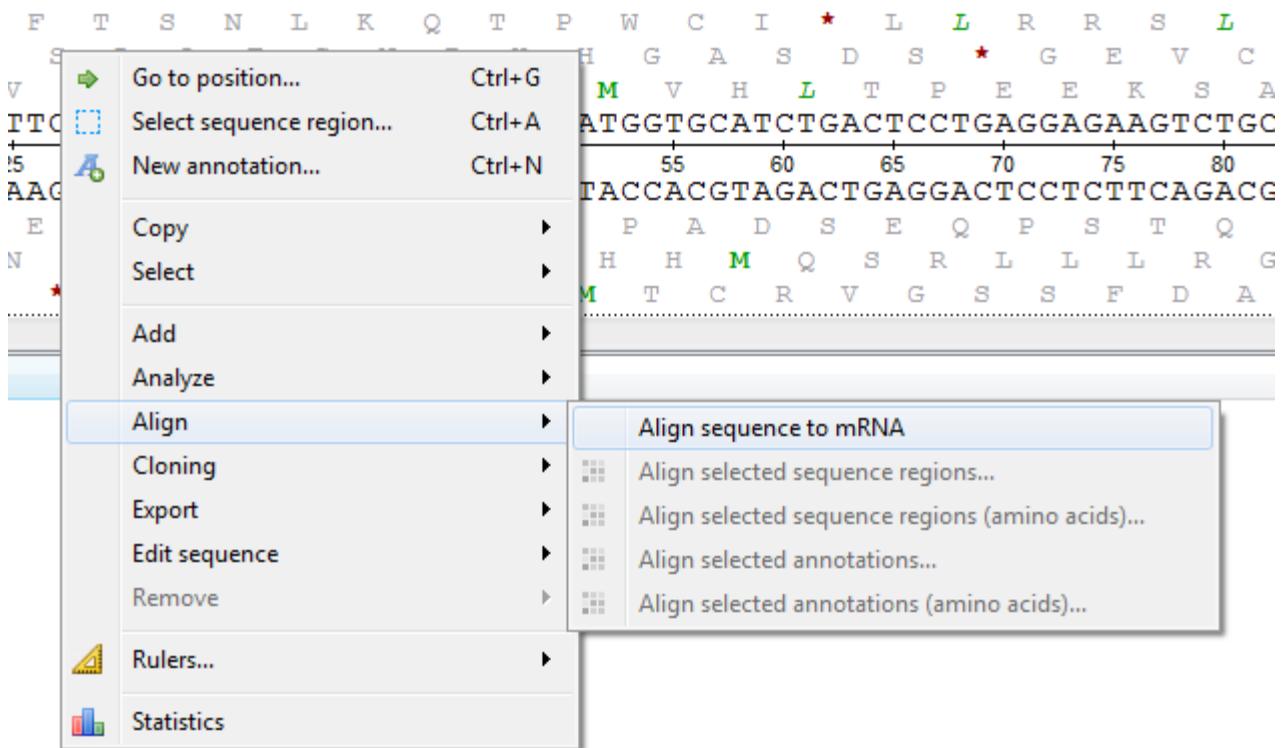
Spliced Alignment (mRNA to genomic)

UGENE allows to align spliced mRNA/cDNA sequence to genomic sequences.

The default underlying algorithm which is used for the alignment is an external tool called [Spidey](#).

Before running the alignment make sure that Spidey is available and validated in the list of [External Tools](#).

To perform the alignment of a mRNA sequence to a genomic sequence open the the genomic sequence in the *Sequence View*. Next activate context menu item *Align -> Align to sequence to mRNA*.



In the list of sequences select the corresponding mRNA sequence and click OK. The resulting alignment will be saved as an annotation with name "exon":

U -* UGENE - [dna [s] dna]

File Actions Settings Tools Window Help

Project 1: Project

Annotations [MyDocument.gb]*

- Annotations [MyDocument.gb]*
- exon (0, 1)
 - exon join(1..142,273..495,1346..1608)
- Auto-annotations [dna.txt | dna]

1 100 200 300 400 500 600 700 800 900 1k 1.1k 1.2k 1.3k 1.4k 1.5k 1.608

1 [142 bp] → 142 273 ← [223 bp] → 495

III

H V H T S Y L P P T A P G Q R A G L C A G
M F I P L I F L P Q L L G N V L V C V L A
S C S Y L L S S S H S S W A T C W S V C W
CATGTTCATACCTCTTATCTTCCTCCACAC CTCCCTGGCAACCTGGCTGCCTCTGAGCTGGC
1315 1320 1325 1330 1335 1340 1345 1350 1355 1360 1365 1370 1377
GTACAAGTATGGAGAATAGAAGGAGGGTGTCAAGGACCCGTTGACGACCAGACACAGACCG
M N M G R I K R G C S K P L Y S T Q T S A
* T * V E * R G G V A G P C R A P R H A P
H E Y R K D E E W L E Q A V H Q D T H Q G

2: Tasks 3: Log No active tasks