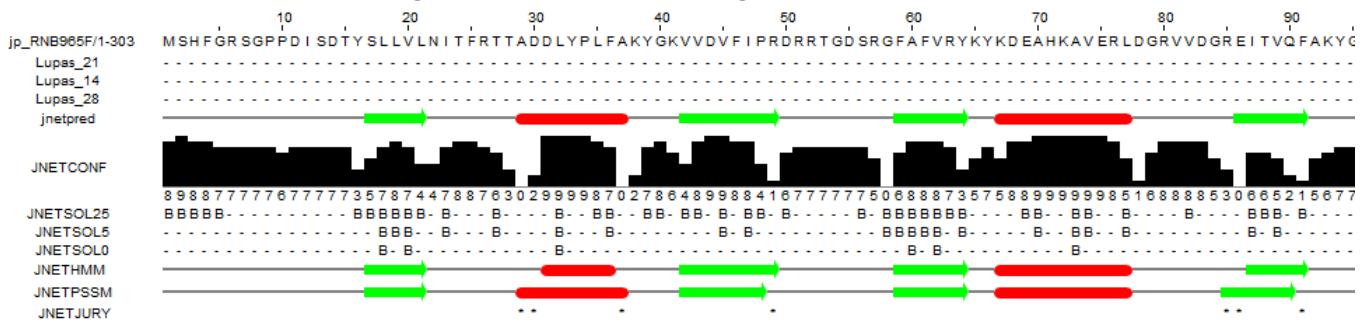


A

NUMR-1



SRSF2 serine and arginine rich splicing factor 2



The annotation bars below the alignment are as follows:

- Lupas_21, Lupas_14, Lupas_28

Coiled-coil predictions for the sequence. These are binary predictions for each location.

- JNetPRED

The consensus prediction - helices are marked as red tubes, and sheets as dark green arrows.

- JNetCONF

The confidence estimate for the prediction. High values mean high confidence. prediction - helices are marked as red tubes, and sheets as dark green arrows.

- JNetHMM

HMM profile based prediction - helices are marked as red tubes, and sheets as dark green arrows.

- JNETPSSM

PSSM based prediction - helices are marked as red tubes, and sheets as dark green arrows.

- JNETJURY

A "" in this annotation indicates that the JNETJURY was invoked to rationalize significantly different primary predictions.

