The annotation bars below the alignment are as follows:

- **Lupas_21, Lupas_14, Lupas_28**
  Colledd-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.

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**B**

RNA recognition-like motif

serine-rich

serine-arginine rich

arginine-rich

histidine-glycine-rich