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The figure displays protein structure prediction results for a protein of 600 residues, organized into four segments (1-60, 61-120, 121-180, 181-240) and a final segment (241-300). Each segment shows the following tracks:

- Sequence:** Amino acid sequence with residue numbers indicated above.
- Secondary structure:** Alpha-helices (green cylinders) and beta-strands (blue arrows).
- SS confidence:** A bar chart showing the confidence of the secondary structure prediction, with colors representing different confidence levels (red for high, yellow for medium, green for low).
- Disorder:** A bar chart showing the predicted disorder of the protein, with colors representing different confidence levels (red for high, yellow for medium, green for low).
- Disorder confidence:** A bar chart showing the confidence of the disorder prediction, with colors representing different confidence levels (red for high, yellow for medium, green for low).

The protein structure is highly disordered, with no significant alpha-helices or beta-strands predicted. The disorder prediction is consistently high across the entire sequence, with a confidence of 1.0 (red) for most of the protein.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand