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The figure displays protein structure and disorder analysis for two segments of a protein. The top segment covers residues 1 to 60, and the bottom segment covers residues 70 to 100. Each segment is analyzed for its sequence, secondary structure (SS), confidence, and disorder.

Top Segment (Residues 1-60):

- Sequence:** MEKKHIYLFCSAGMSTSLLVSKMRAQAEKYEVPIIEAFPETLAGEKGGQNADVLLGPQI
- Secondary structure:** The structure is shown as a blue ribbon diagram. It features a long alpha-helix (residues 10-25) and a long beta-strand (residues 30-45). There are also several short alpha-helices and beta-strands.
- SS confidence:** A bar chart showing the confidence of the secondary structure prediction. The confidence is generally high, with some lower values in the middle of the protein.
- Disorder:** A bar chart showing the disorder of the protein. The protein is mostly ordered, with some disordered regions indicated by red bars.
- Disorder confidence:** A bar chart showing the confidence of the disorder prediction. The confidence is generally high, with some lower values in the middle of the protein.

Bottom Segment (Residues 70-100):

- Sequence:** AYMLPEIQRLPNKPVEVDSLLYGKVDGLGVLKAAVAAIKKAAAN
- Secondary structure:** The structure is shown as a blue ribbon diagram. It features a long alpha-helix (residues 70-85) and a long beta-strand (residues 90-100). There are also several short alpha-helices and beta-strands.
- SS confidence:** A bar chart showing the confidence of the secondary structure prediction. The confidence is generally high, with some lower values in the middle of the protein.
- Disorder:** A bar chart showing the disorder of the protein. The protein is mostly ordered, with some disordered regions indicated by red bars.
- Disorder confidence:** A bar chart showing the confidence of the disorder prediction. The confidence is generally high, with some lower values in the middle of the protein.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand