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Protein structure prediction results for a protein of length 180. The image shows three segments of the protein. Each segment displays the amino acid sequence, secondary structure (alpha helices and beta strands), solvent accessibility (SS), confidence scores, and disorder predictions. The protein is composed of several alpha helices and beta strands, with some regions of high confidence and others of lower confidence or disorder.

**Segment 1 (Residues 1-60):**

- Sequence: MNLMTTITGVVLAGGKARRMGGVDKGLLELNGKPLWQHVADALMTQLSHVVVNANRHQEI
- Secondary structure: Alpha helices at residues 10-15, 25-30, 35-40, 45-50, 55-60.
- SS: High confidence (red) for helices, lower confidence (yellow/green) for loops.
- Disorder: High confidence (red) for helices, lower confidence (yellow/green) for loops.

**Segment 2 (Residues 61-120):**

- Sequence: YQASGLKVIEDSLADYPGPLAGMLSVMQQEAGEWFLFCPCDTPYIPPDLAARLNHQRKDA
- Secondary structure: Alpha helices at residues 65-70, 75-80, 85-90, 95-100, 105-110, 115-120.
- SS: High confidence (red) for helices, lower confidence (yellow/green) for loops.
- Disorder: High confidence (red) for helices, lower confidence (yellow/green) for loops.


**Segment 3 (Residues 121-180):**

- Sequence: PVVWVHDGERDHPTIALVNRAIEPLLLEYLQAGERRMVMFMRLAGGHAVDFS DHKDAFVN
- Secondary structure: Alpha helices at residues 125-130, 135-140, 145-150, 155-160, 165-170, 175-180.
- SS: High confidence (red) for helices, lower confidence (yellow/green) for loops.
- Disorder: High confidence (red) for helices, lower confidence (yellow/green) for loops.


**Segment 4 (Residues 181-200):**


- Sequence: VNTPEELARWQEK R
- Secondary structure: Alpha helices at residues 185-190.
- SS: High confidence (red) for helices, lower confidence (yellow/green) for loops.
- Disorder: High confidence (red) for helices, lower confidence (yellow/green) for loops.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand