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Protein structure prediction results for the protein sequence MTRAVKPRRF... The figure displays the sequence, secondary structure, SS confidence, disorder, and disorder confidence across the full length of the protein (residues 1 to 410).

**Sequence:** MTRAVKPRRF... (Residues 1 to 410)

**Secondary structure:** The structure is primarily alpha-helical, with several beta-strands and loops. The structure is shown in green, with helices represented by coiled lines and strands by arrows.

**SS confidence:** The confidence is generally high, with some regions of lower confidence (yellow/green) indicating potential uncertainty in the secondary structure prediction.

**Disorder:** The protein is mostly ordered, with some regions of disorder (red) indicated, particularly in the N-terminal and C-terminal regions.

**Disorder confidence:** The confidence is generally high, with some regions of lower confidence (yellow/green) indicating potential uncertainty in the disorder prediction.

Confidence Key  
High(9)  Low (0)  
? Disordered  
 Alpha helix  
 Beta strand