

Email	l.a.kelley@imperial.ac.uk
Description	P05707
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
Protein structure prediction results for the protein sequence: MNQVAVVI GGGQTLGAF LCHGLAAEGYRVAVVDI QSDKAANVAQEI NAEYGESMAYGF GA.

The figure displays four segments of the protein, each with the following tracks:


- Sequence:** Amino acid sequence (e.g., MNQVAVVI GGGQTLGAF LCHGLAAEGYRVAVVDI QSDKAANVAQEI NAEYGESMAYGF GA).
- Secondary structure:** Predicted secondary structure elements (alpha-helices and beta-strands) shown as green cylinders and blue arrows.
- SS confidence:** Confidence scores for the secondary structure prediction, shown as a red bar.
- Disorder:** Predicted disorder regions, shown as a blue bar with question marks indicating uncertainty.
- Disorder confidence:** Confidence scores for the disorder prediction, shown as a blue bar.


The protein is shown in four segments, with residue numbers 1-60, 70-120, 130-180, and 190-240 displayed above the sequence. The disorder track indicates regions of predicted disorder with question marks.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand