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Panel 1: Full Protein (1-60 residues)

Sequence	Secondary structure	SS confidence	Disorder	Disorder confidence
M K I D A S R R G I L T G R W R K A S N G I R P P W S G D E S H F L T H C T R C D A C I N A C E N N I L Q R G A G G Y P	Alpha-helices (green) at residues 10-18, 28-34, 42-48; Beta-strand (blue) at 52-54; Loop (blue arrow) at 58-60.	Confidence scale from 0.0 (red) to 1.0 (green).	Disorder scale from 0.0 (red) to 1.0 (blue).	Confidence scale from 0.0 (red) to 1.0 (green).

Panel 2: Fragment 1 (1-60 residues)

Sequence	Secondary structure	SS confidence	Disorder	Disorder confidence
S V N F K N N E C S F C Y A C A Q A C P E S L F S P R H T R A W D L Q F T I G D A C L A Y Q S V E C R R C Q D S C E P M	Beta-strand (blue) at 10-12; Alpha-helices (green) at 28-34, 52-58.	Confidence scale from 0.0 (red) to 1.0 (green).	Disorder scale from 0.0 (red) to 1.0 (blue).	Confidence scale from 0.0 (red) to 1.0 (green).

Panel 3: Fragment 2 (130-180 residues)

Sequence	Secondary structure	SS confidence	Disorder	Disorder confidence
A I I F R P T L S G I Y Q P Q L N S Q L C N G C G A C A A S C P V S A I T A E Y L H A H	Beta-strand (blue) at 132-138; Alpha-helices (green) at 142-148, 152-158; Beta-strand (blue) at 162-168.	Confidence scale from 0.0 (red) to 1.0 (green).	Disorder scale from 0.0 (red) to 1.0 (blue).	Confidence scale from 0.0 (red) to 1.0 (green).

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand