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The figure displays protein structure analysis for two protein constructs. The top construct is the full-length protein (1-120), and the bottom construct is a truncated fragment (1-5).

Full-length protein (1-120):

- Sequence:** MNKQSGMTL L EVLL AMSI F TAVALT L MSS MQGQRNAI E RMRNET L A L W I A D N Q L Q S Q D S F
- Secondary structure:** A green alpha-helix is shown from residue 10 to 60. Blue arrows indicate beta-strands from residue 70 to 120.
- SS confidence:** A red bar indicates high confidence for the alpha-helix and the first part of the beta-strands. A yellow bar indicates lower confidence for the later beta-strands.
- Disorder:** A bar with question marks indicates regions of predicted disorder, primarily in the N-terminal region (residues 1-10) and the C-terminal region (residues 110-120).
- Disorder confidence:** A bar with various colors (red, orange, yellow, green, blue) indicates the confidence of the disorder prediction across the sequence.

Truncated protein (1-5):

- Sequence:** QAQDD
- Secondary structure:** No secondary structure is shown for this short fragment.
- SS confidence:** A red bar indicates high confidence for the short sequence.
- Disorder:** A bar with question marks indicates predicted disorder for the entire fragment.
- Disorder confidence:** A red bar indicates high confidence for the disorder prediction.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand