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The figure displays the protein structure and analysis for the full-length protein (1-159) and two fragments (1-60 and 70-120). The protein is shown in a ribbon diagram, with the full-length protein in blue and the fragments in red. The analysis includes sequence, secondary structure, SS confidence, Disorder, and Disorder confidence for each region.

Full-length protein (1-159):

- Sequence:** M L S N D I L R S V R Y I L K A N N N D L V R I L A L G N V E A T A E Q I A V W L R K E D E E G F Q R C P D I V L S S F
- Secondary structure:** Alpha helix (1-10), Alpha helix (11-20), Alpha helix (21-30), Alpha helix (31-40), Alpha helix (41-50), Alpha helix (51-60), Alpha helix (61-70), Alpha helix (71-80), Alpha helix (81-90), Alpha helix (91-100), Alpha helix (101-110), Alpha helix (111-120), Alpha helix (121-130), Alpha helix (131-140), Alpha helix (141-150), Alpha helix (151-159)
- SS confidence:** High confidence (red) for most regions, with some lower confidence (yellow/green) at the N-terminus and C-terminus.
- Disorder:** No disorder predicted for the full-length protein.
- Disorder confidence:** High confidence (red) for most regions, with some lower confidence (yellow/green) at the N-terminus and C-terminus.

Fragment 1 (1-60):

- Sequence:** M L S N D I L R S V R Y I L K A N N N D L V R I L A L G N V E A T A E Q I A V W L R K E D E E G F Q R C P D I V L S S F
- Secondary structure:** Alpha helix (1-10), Alpha helix (11-20), Alpha helix (21-30), Alpha helix (31-40), Alpha helix (41-50), Alpha helix (51-60)
- SS confidence:** High confidence (red) for most regions, with some lower confidence (yellow/green) at the N-terminus and C-terminus.
- Disorder:** No disorder predicted for the fragment.
- Disorder confidence:** High confidence (red) for most regions, with some lower confidence (yellow/green) at the N-terminus and C-terminus.

Fragment 2 (70-120):

- Sequence:** L N G L I Y E K R G K D E S A P A L E P E R R I N N N I V L K K L R I A F S L K T D D I L A I L T E Q Q F R V S M P E I
- Secondary structure:** Alpha helix (71-80), Alpha helix (81-90), Alpha helix (91-100), Alpha helix (101-110), Alpha helix (111-120)
- SS confidence:** High confidence (red) for most regions, with some lower confidence (yellow/green) at the N-terminus and C-terminus.
- Disorder:** No disorder predicted for the fragment.
- Disorder confidence:** High confidence (red) for most regions, with some lower confidence (yellow/green) at the N-terminus and C-terminus.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand