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Protein structure analysis of the full-length protein (1-260) and its fragments. The analysis includes sequence, secondary structure, SS confidence, disorder, and disorder confidence for each segment.

Full-length protein (1-260):

- Sequence:** MSWLKEVIGTEKAVIAMCHLRALPGDPSFDAQLGMNVVIDKAWDDLMAHQNGGVDAVMFS
- Secondary structure:** Alpha-helices (green) and beta-strands (blue) are distributed throughout the protein.
- SS confidence:** High confidence (red) is observed in the N-terminal region (1-60) and the C-terminal region (190-260).
- Disorder:** Disordered regions (grey) are present in the N-terminal region (1-60) and the C-terminal region (190-260).
- Disorder confidence:** High confidence (red) is observed in the N-terminal region (1-60) and the C-terminal region (190-260).

Fragment 1 (1-60):

- Sequence:** MSWLKEVIGTEKAVIAMCHLRALPGDPSFDAQLGMNVVIDKAWDDLMAHQNGGVDAVMFS
- Secondary structure:** Alpha-helices (green) and beta-strands (blue) are present.
- SS confidence:** High confidence (red) is observed.
- Disorder:** Disordered regions (grey) are present.
- Disorder confidence:** High confidence (red) is observed.

Fragment 2 (70-120):

- Sequence:** NEFSLPYLTKVRPETTAAMARIIGQLMSDIRIPFGVNVLWDPVASFDLAMATGAKFIREI
- Secondary structure:** Alpha-helices (green) and beta-strands (blue) are present.
- SS confidence:** High confidence (red) is observed.
- Disorder:** Disordered regions (grey) are present.
- Disorder confidence:** High confidence (red) is observed.

Fragment 3 (130-180):

- Sequence:** FTGAYASDFGVWDTNVGETIRHQHRI GAGEVKTLFNI VPEAAVYLGNRDICSIAKSTVFN
- Secondary structure:** Alpha-helices (green) and beta-strands (blue) are present.
- SS confidence:** High confidence (red) is observed.
- Disorder:** Disordered regions (grey) are present.
- Disorder confidence:** High confidence (red) is observed.


Fragment 4 (190-240):

- Sequence:** NHPDALCVSGLTAGTRTDSALLKRVKETVPDVTVLANTGVCLNVVEEQLSADGCVTATT
- Secondary structure:** Alpha-helices (green) and beta-strands (blue) are present.
- SS confidence:** High confidence (red) is observed.
- Disorder:** Disordered regions (grey) are present.
- Disorder confidence:** High confidence (red) is observed.


Fragment 5 (250-260):


- Sequence:** FKKGDFVAFNV DQARVVSQFMEKVHHIRR
- Secondary structure:** Alpha-helices (green) and beta-strands (blue) are present.
- SS confidence:** High confidence (red) is observed.
- Disorder:** Disordered regions (grey) are present.
- Disorder confidence:** High confidence (red) is observed.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand