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Description	P0ADA1
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Protein structure analysis of the full-length protein (1-180) and its fragments. The analysis includes sequence, secondary structure, solvent accessibility (SS), confidence, disorder, and disorder confidence for each segment.

Full-length protein (1-180):

- Sequence:** MMNFNNVFRWHL PFLFLVLLTFR A AADTL LILGDSL SAGYRMSASAA WPALLNDKWQSK
- Secondary structure:** [Alpha-helices and beta-strands]
- SS:** [Solvent accessibility values]
- confidence:** [Confidence scores]
- Disorder:** [Disorder prediction]
- Disorder confidence:** [Disorder confidence scores]

Fragment 1 (1-60):

- Sequence:** MMNFNNVFRWHL PFLFLVLLTFR A AADTL LILGDSL SAGYRMSASAA WPALLNDKWQSK
- Secondary structure:** [Alpha-helices and beta-strands]
- SS:** [Solvent accessibility values]
- confidence:** [Confidence scores]
- Disorder:** [Disorder prediction]
- Disorder confidence:** [Disorder confidence scores]

Fragment 2 (61-120):

- Sequence:** TSVVNASISGDT SQQLARLPALLKQHQP RVVLVELGGNDGLRGFPQQTEQTLRQILQD
- Secondary structure:** [Alpha-helices and beta-strands]
- SS:** [Solvent accessibility values]
- confidence:** [Confidence scores]
- Disorder:** [Disorder prediction]
- Disorder confidence:** [Disorder confidence scores]


Fragment 3 (121-180):

- Sequence:** VKAANAEP LLMQIRLPANYGRRYNEAFSAIYPKLAK EFDVPLL PFFMEEVYLKPKQWMQDD
- Secondary structure:** [Alpha-helices and beta-strands]
- SS:** [Solvent accessibility values]
- confidence:** [Confidence scores]
- Disorder:** [Disorder prediction]
- Disorder confidence:** [Disorder confidence scores]


Fragment 4 (181-240):


- Sequence:** GIHPNRDAQPF IADWMAKQLQPLVNHDS
- Secondary structure:** [Alpha-helices and beta-strands]
- SS:** [Solvent accessibility values]
- confidence:** [Confidence scores]
- Disorder:** [Disorder prediction]
- Disorder confidence:** [Disorder confidence scores]

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand