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Protein structure analysis of the full-length protein (1-300) and its fragments. The analysis includes sequence, secondary structure, SS confidence, disorder, and disorder confidence for each segment.

Full-length protein (1-300):

- Sequence: MGKEVVMGKKENEMAEKERPAGSQSLFRGLMLIEILSNYPNGCPLAHLSELAGLNKSTVH
- Secondary structure: [Alpha-helices and loops]
- SS confidence: [Confidence scores]
- Disorder: [Disorder scores]
- Disorder confidence: [Disorder confidence scores]

Fragment 1 (70-120):

- Sequence: RLLQGLQSCGYVTTAPAGSYRLTTKFI AVGQKALSSLNIIHIAAPHLEALNIATGETIN
- Secondary structure: [Alpha-helices and loops]
- SS confidence: [Confidence scores]
- Disorder: [Disorder scores]
- Disorder confidence: [Disorder confidence scores]

Fragment 2 (130-180):

- Sequence: FSSREDDHAILIYKLEPTTGMLRTRAYIGQHMPLYCSAMGKIYMAFGHPDYVKSYWESHQ
- Secondary structure: [Alpha-helices and loops]
- SS confidence: [Confidence scores]
- Disorder: [Disorder scores]
- Disorder confidence: [Disorder confidence scores]


Fragment 3 (190-240):

- Sequence: HEIQPLTRNTITELPAMFDELAHIRESGAAMDREENELGVSCIAVPVFDIHGRVPYAVSI
- Secondary structure: [Alpha-helices and loops]
- SS confidence: [Confidence scores]
- Disorder: [Disorder scores]
- Disorder confidence: [Disorder confidence scores]


Fragment 4 (250-300):


- Sequence: SLSTSRLKQVGKENLLKPLRETAQAISNELGFTVRDDLGAIT
- Secondary structure: [Alpha-helices and loops]
- SS confidence: [Confidence scores]
- Disorder: [Disorder scores]
- Disorder confidence: [Disorder confidence scores]

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand