

Email	l.a.kelley@imperial.ac.uk
Description	Q2EES0
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Protein structure and analysis for the full-length protein (1-60) and a fragment (1-20). The full-length protein is shown with its sequence, secondary structure (SS), disorder, and disorder confidence. The fragment (1-20) is also shown with its sequence, secondary structure, disorder, and disorder confidence.


Full-length protein (1-60):

- Sequence: M S T K N R T R R T T T R N I R F P N Q M I E Q I N I A L E Q K G S G N F S A W V I E A C R R R L C S E K R V S S E A N
- Secondary structure: Alpha helix (residues 10-15), Alpha helix (residues 18-28), Alpha helix (residues 35-45), Alpha helix (residues 50-55), Alpha helix (residues 58-60).
- SS confidence: High confidence (red) for most regions, lower confidence (yellow/green) for some regions.
- Disorder: Disordered regions (blue) are present at the N-terminus (residues 1-9), between helices (residues 16-17, 29-34, 46-49), and at the C-terminus (residues 56-60).
- Disorder confidence: High confidence (red) for disordered regions, lower confidence (yellow/green) for some regions.


Fragment (1-20):


- Sequence: K E K S D I T E L L R K Q V R P D
- Secondary structure: Alpha helix (residues 1-10), Alpha helix (residues 13-15), Alpha helix (residues 18-20).
- SS confidence: High confidence (red) for most regions, lower confidence (yellow/green) for some regions.
- Disorder: Disordered regions (blue) are present at the N-terminus (residues 1-2) and between helices (residues 11-12, 16-17).
- Disorder confidence: High confidence (red) for disordered regions, lower confidence (yellow/green) for some regions.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand