

Email	l.a.kelley@imperial.ac.uk
Description	P31663
Date	Thu Jan 5 11:48:25 GMT 2012
Unique Job ID	25831ce7ca6f560f

This section provides a detailed view of the protein structure prediction results for the full-length protein, showing sequence, secondary structure, and disorder confidence across the entire length (1-280 residues).

Sequence: MLI IETLPLL RQQI RRLRME GKRVALVPTMGNL HDG HMKLVDEAKARADV VVVSIFVNP M

Secondary structure: The structure is primarily composed of alpha-helices (green cylinders) and loops (blue arrows). Key features include a long alpha-helix from residue 10 to 20, a loop from 25 to 30, another long alpha-helix from 35 to 45, a loop from 50 to 55, and a final alpha-helix from 60 to 65.

SS confidence: The confidence is generally high, indicated by the green color in the bar chart, with some lower confidence regions (yellow and red) around residues 25-30 and 50-55.

Disorder: The protein is mostly ordered, with some regions of low confidence (yellow and red) indicating potential disorder, particularly around residues 25-30 and 50-55.

Disorder confidence: The confidence is generally high, indicated by the green color in the bar chart, with some lower confidence regions (yellow and red) around residues 25-30 and 50-55.

Sequence: QFDRPEDLARY PRTLQEDCEKLNKRKVDLV APSVKEIYPNGTETHTYVDVPGLSTMLEG

Secondary structure: The structure continues with alpha-helices (green cylinders) and loops (blue arrows). Key features include a long alpha-helix from residue 70 to 80, a loop from 85 to 90, another long alpha-helix from 95 to 105, a loop from 110 to 115, and a final alpha-helix from 120 to 125.

SS confidence: The confidence is generally high, indicated by the green color in the bar chart, with some lower confidence regions (yellow and red) around residues 85-90 and 110-115.

Disorder: The protein is mostly ordered, with some regions of low confidence (yellow and red) indicating potential disorder, particularly around residues 85-90 and 110-115.

Disorder confidence: The confidence is generally high, indicated by the green color in the bar chart, with some lower confidence regions (yellow and red) around residues 85-90 and 110-115.

Sequence: ASRPGHFRGVSTI VSKLFNLVQPDIA CFGEKDFQQLALIRKMVADMGFDEI VGVPI MRA

Secondary structure: The structure continues with alpha-helices (green cylinders) and loops (blue arrows). Key features include a long alpha-helix from residue 130 to 140, a loop from 145 to 150, another long alpha-helix from 155 to 165, a loop from 170 to 175, and a final alpha-helix from 180 to 185.

SS confidence: The confidence is generally high, indicated by the green color in the bar chart, with some lower confidence regions (yellow and red) around residues 145-150 and 170-175.

Disorder: The protein is mostly ordered, with some regions of low confidence (yellow and red) indicating potential disorder, particularly around residues 145-150 and 170-175.

Disorder confidence: The confidence is generally high, indicated by the green color in the bar chart, with some lower confidence regions (yellow and red) around residues 145-150 and 170-175.

Sequence: KDGLALSSRNGYLTAEQRKI APGLYKVLSSIADKLQAGERDLDEIITITAGQELNEKGFRA

Secondary structure: The structure continues with alpha-helices (green cylinders) and loops (blue arrows). Key features include a long alpha-helix from residue 190 to 200, a loop from 205 to 210, another long alpha-helix from 215 to 225, a loop from 230 to 235, and a final alpha-helix from 240 to 245.

SS confidence: The confidence is generally high, indicated by the green color in the bar chart, with some lower confidence regions (yellow and red) around residues 205-210 and 230-235.

Disorder: The protein is mostly ordered, with some regions of low confidence (yellow and red) indicating potential disorder, particularly around residues 205-210 and 230-235.

Disorder confidence: The confidence is generally high, indicated by the green color in the bar chart, with some lower confidence regions (yellow and red) around residues 205-210 and 230-235.

Sequence: DDIQIRDADTLLLEVSETSKRAVILVA A WLGDARLIDNKMV ELA


Secondary structure: The structure continues with alpha-helices (green cylinders) and loops (blue arrows). Key features include a long alpha-helix from residue 250 to 260, a loop from 265 to 270, another long alpha-helix from 275 to 285, a loop from 290 to 295, and a final alpha-helix from 300 to 305.

SS confidence: The confidence is generally high, indicated by the green color in the bar chart, with some lower confidence regions (yellow and red) around residues 265-270 and 290-295.


Disorder: The protein is mostly ordered, with some regions of low confidence (yellow and red) indicating potential disorder, particularly around residues 265-270 and 290-295.


Disorder confidence: The confidence is generally high, indicated by the green color in the bar chart, with some lower confidence regions (yellow and red) around residues 265-270 and 290-295.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand