

Email	l.a.kelley@imperial.ac.uk
Description	P76044
Date	Thu Jan 5 12:17:47 GMT 2012
Unique Job ID	9b2484471b241b20

The figure displays a protein structure analysis of the human protein sequence MKIGTQNQAF... The analysis is presented in four segments, each showing the sequence, secondary structure, and disorder predictions.

Segment 1 (Residues 1-60): The sequence is MKIGTQNQAF... The secondary structure shows a blue arrow (coil) from residue 1 to 10, a green helix from 11 to 25, a blue arrow from 26 to 30, a green helix from 31 to 45, and a blue arrow from 46 to 60. The disorder prediction shows a red bar from 1 to 10, a green bar from 11 to 25, a red bar from 26 to 30, a green bar from 31 to 45, and a red bar from 46 to 60.


Segment 2 (Residues 70-120): The sequence is GYDGIW... The secondary structure shows a green helix from residue 70 to 90, a blue arrow from 91 to 100, and a green helix from 120 to 125. The disorder prediction shows a red bar from 70 to 90, a green bar from 91 to 100, and a red bar from 120 to 125.

Segment 3 (Residues 130-180): The sequence is DRKMSV... The secondary structure shows a green helix from residue 130 to 145, a blue arrow from 146 to 155, a green helix from 156 to 165, a green helix from 166 to 175, and a blue arrow from 176 to 180. The disorder prediction shows a red bar from 130 to 145, a green bar from 146 to 155, a red bar from 156 to 165, a green bar from 166 to 175, and a red bar from 176 to 180.


Segment 4 (Residues 190-240): The sequence is YHNI... The secondary structure shows a green helix from residue 190 to 200, a green helix from 201 to 210, a blue arrow from 211 to 220, a green helix from 221 to 230, and a blue arrow from 231 to 240. The disorder prediction shows a red bar from 190 to 200, a green bar from 201 to 210, a red bar from 211 to 220, a green bar from 221 to 230, and a red bar from 231 to 240.


Segment 5 (Residues 250-260): The sequence is GRI... The secondary structure shows a blue arrow from residue 250 to 255 and a green helix from 256 to 260. The disorder prediction shows a red bar from 250 to 255 and a green bar from 256 to 260.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand