

Email	l.a.kelley@imperial.ac.uk
Description	P37195
Date	Thu Jan 5 11:55:01 GMT 2012
Unique Job ID	9087ec53ff1b4d77


Figure 1 displays the protein structure and disorder analysis of the human protein. The figure is divided into three panels, each showing a different segment of the protein. Each panel includes the amino acid sequence, secondary structure (SS), confidence scores, and disorder predictions.

**Panel 1 (Top):** Shows residues 1 to 60. The sequence is MFLIIITRDTMFFTAMKNI LSKGNVVHI QNEEEI DVMLHQNAFV I I DTL MNNVFHSNFLTQ. The secondary structure (SS) is shown as a blue arrow (helix) at residues 10-15 and a green helix at residues 20-25. The confidence scores are shown as red and green bars. The disorder predictions are shown as red and green bars, with red indicating high confidence and green indicating low confidence.


**Panel 2 (Middle):** Shows residues 70 to 120. The sequence is IERLKPVHVI I FSPFNI KRCLGKVPVTFVPRTI T I I D FVALI NGSYCSVP EAAVSL SRKQ. The secondary structure (SS) is shown as a blue arrow (helix) at residues 75-80 and a green helix at residues 85-90. The confidence scores are shown as red and green bars. The disorder predictions are shown as red and green bars, with red indicating high confidence and green indicating low confidence.


**Panel 3 (Bottom):** Shows residues 130 to 170. The sequence is HQVLSCI ANQMTTEDI LEKLKISLKT FYCHKHNI MMI LNLKRI NELVRHQHI DYLV. The secondary structure (SS) is shown as a green helix at residues 135-140 and a green helix at residues 155-160. The confidence scores are shown as red and green bars. The disorder predictions are shown as red and green bars, with red indicating high confidence and green indicating low confidence.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand