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Description	P37750
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Figure 1 displays the protein structure and disorder analysis of the human protein. The protein is composed of 180 amino acids. The figure is divided into three main sections corresponding to different regions of the protein: 1-60, 70-120, and 130-180. Each section provides a detailed view of the sequence, secondary structure (SS), confidence, disorder, and disorder confidence.


Section 1 (1-60): The sequence is MI LKLAKRYGLCGFI RLVRDVL LTRVFYRNCRI I RFP CYI RNDGSI NFGE NFTSGVGLRL. The secondary structure (SS) is shown as a continuous alpha-helix. The confidence is high (red). The disorder is low (blue). The disorder confidence is 1.0 (red).

Section 2 (70-120): The sequence is DAFGRGVI FFS DNQVNDYVHI ASI ESVTI GRDTLI ASKVFI TDH NHGSF KHS DP MSSPN. The secondary structure (SS) is shown as a continuous alpha-helix. The confidence is high (red). The disorder is low (blue). The disorder confidence is 1.0 (red).


Section 3 (130-180): The sequence is IPPDMRTL ESSAVVI GQRVWL GENVTVLPGTI I GNGVVGANSVVRGSI PENTVI AGVPA. The secondary structure (SS) is shown as a continuous alpha-helix. The confidence is high (red). The disorder is low (blue). The disorder confidence is 1.0 (red).


Section 4 (190-200): The sequence is KIIKKYNHETKLWEKA. The secondary structure (SS) is shown as a continuous alpha-helix. The confidence is high (red). The disorder is low (blue). The disorder confidence is 1.0 (red).

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand