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Figure 1 displays the protein structure and disorder analysis of the human protein. The figure is divided into three horizontal panels, each showing a different segment of the protein sequence (residues 1-60, 70-120, and 130-160). Each panel displays the amino acid sequence, secondary structure (alpha-helices and beta-strands), solvent accessibility (SS), confidence scores, and disorder predictions.

Panel 1 (Residues 1-60):

- Sequence:** MLVSKSNGFNASAVLGSGSYENKSSKHMELLAHSILKLICKEAASETYRGALETLQKMM
- Secondary structure:** Shows a long alpha-helix starting around residue 25 and ending around residue 55.
- SS:** Solvent accessibility plot showing high accessibility in the N-terminal region and lower accessibility in the helical region.
- confidence:** Confidence scores for the secondary structure prediction, with higher values (red/orange) in the helical region.
- Disorder:** Disorder prediction plot showing high disorder (red) in the N-terminal region and lower disorder (blue) in the helical region.
- Disorder confidence:** Confidence scores for the disorder prediction, with higher values (red/orange) in the N-terminal region.


Panel 2 (Residues 70-120):

- Sequence:** SECITYQEGNAFVIMGAGEQLKRIKYEVGENNLLKVFNVHFNNNHVELVSSGEPDVICLSKQV
- Secondary structure:** Shows several alpha-helices and beta-strands, including a long helix from residue 75 to 95 and another from 105 to 120.
- SS:** Solvent accessibility plot showing high accessibility in the N-terminal region and lower accessibility in the helical regions.
- confidence:** Confidence scores for the secondary structure prediction, with higher values (red/orange) in the helical regions.
- Disorder:** Disorder prediction plot showing high disorder (red) in the N-terminal region and lower disorder (blue) in the helical regions.
- Disorder confidence:** Confidence scores for the disorder prediction, with higher values (red/orange) in the N-terminal region.


Panel 3 (Residues 130-160):


- Sequence:** WENLLIKLKLENNENVFSETKKLSNKNNA DQFF ECAKRNE
- Secondary structure:** Shows several alpha-helices and beta-strands, including a long helix from residue 135 to 155.
- SS:** Solvent accessibility plot showing high accessibility in the N-terminal region and lower accessibility in the helical region.
- confidence:** Confidence scores for the secondary structure prediction, with higher values (red/orange) in the helical region.
- Disorder:** Disorder prediction plot showing high disorder (red) in the N-terminal region and lower disorder (blue) in the helical region.
- Disorder confidence:** Confidence scores for the disorder prediction, with higher values (red/orange) in the N-terminal region.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand