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Figure 1 displays the protein structure and disorder analysis of the human protein. The protein is 180 residues long. The figure shows three panels of protein data, each corresponding to a different region of the protein.

Panel 1 (Residues 1-60):

- Sequence:** MKPGCTLFLFLLCSALTVTTEAHAQTPTDTATTAPYLLAGAPTFFDLSISQFREDFNSQNPSSL
- Secondary structure:** The structure shows a series of alpha-helices and beta-strands, with a large blue arrow indicating a long-range interaction.
- SS confidence:** The confidence is high (red) for the first 10 residues and then drops to low (green/yellow) for the rest of the region.
- Disorder:** The disorder is high (red) for the first 10 residues and then drops to low (green/yellow) for the rest of the region.
- Disorder confidence:** The confidence is high (red) for the first 10 residues and then drops to low (green/yellow) for the rest of the region.

Panel 2 (Residues 70-120):

- Sequence:** PLNEFRAIDSSDPKANLTRAASKINENLYASTALERGTLKIKSIQMTWLP IQGPEQKA AK
- Secondary structure:** The structure shows a series of alpha-helices and beta-strands, with a large blue arrow indicating a long-range interaction.
- SS confidence:** The confidence is high (red) for the first 10 residues and then drops to low (green/yellow) for the rest of the region.
- Disorder:** The disorder is high (red) for the first 10 residues and then drops to low (green/yellow) for the rest of the region.
- Disorder confidence:** The confidence is high (red) for the first 10 residues and then drops to low (green/yellow) for the rest of the region.

Panel 3 (Residues 130-180):

- Sequence:** AKAQEYMAAVIRTLTPLMTKTSQKKLQSLLTAGKNKRYTETEGALRYVVADNGEKGLT
- Secondary structure:** The structure shows a series of alpha-helices and beta-strands, with a large blue arrow indicating a long-range interaction.
- SS confidence:** The confidence is high (red) for the first 10 residues and then drops to low (green/yellow) for the rest of the region.
- Disorder:** The disorder is high (red) for the first 10 residues and then drops to low (green/yellow) for the rest of the region.
- Disorder confidence:** The confidence is high (red) for the first 10 residues and then drops to low (green/yellow) for the rest of the region.

Panel 4 (Residues 190-200):

- Sequence:** FAVEPIKLALSESLEGLNK
- Secondary structure:** The structure shows a series of alpha-helices and beta-strands, with a large blue arrow indicating a long-range interaction.
- SS confidence:** The confidence is high (red) for the first 10 residues and then drops to low (green/yellow) for the rest of the region.
- Disorder:** The disorder is high (red) for the first 10 residues and then drops to low (green/yellow) for the rest of the region.
- Disorder confidence:** The confidence is high (red) for the first 10 residues and then drops to low (green/yellow) for the rest of the region.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand