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The figure displays three panels of protein analysis tracks for different regions of a protein. Each panel shows the sequence, secondary structure, SS confidence, disorder, and disorder confidence.

Panel 1 (Residues 1-60):

- Sequence:** MNVI RTEI EDVLI LEPRVF GDDRGF FYESF NQSAFEHIL GYPVSVF VQDNHSRSSKNVLRG
- Secondary structure:** Blue arrows indicate alpha-helices and loops. A green helix is visible between residues 30 and 40.
- SS confidence:** A bar chart showing confidence levels for secondary structure elements.
- Disorder:** A bar chart showing disorder levels, with some regions marked with question marks.
- Disorder confidence:** A bar chart showing confidence levels for disorder predictions.

Panel 2 (Residues 70-120):

- Sequence:** LHFQRGEYA QDKLV RCTHGAVF DVAVDIR PNSVSFGKWWGVLLSADNKQQLWI PKGF A H G
- Secondary structure:** Blue arrows indicate alpha-helices and loops.
- SS confidence:** A bar chart showing confidence levels for secondary structure elements.
- Disorder:** A bar chart showing disorder levels.
- Disorder confidence:** A bar chart showing confidence levels for disorder predictions.


Panel 3 (Residues 130-180):

- Sequence:** FLVLS DIAEFQYKTTNYYHPESDCGICWNDERIAI DWPQTSGLLI LSPKDERLFTLDELI R
- Secondary structure:** Blue arrows indicate alpha-helices and loops. Green helices are visible between residues 150-160 and 170-180.
- SS confidence:** A bar chart showing confidence levels for secondary structure elements.
- Disorder:** A bar chart showing disorder levels, with some regions marked with question marks.
- Disorder confidence:** A bar chart showing confidence levels for disorder predictions.


Panel 4 (Short Sequence):


- Sequence:** L K L I A
- Secondary structure:** A single blue arrow indicates an alpha-helix.
- SS confidence:** A bar chart showing confidence levels for secondary structure elements.
- Disorder:** A bar chart showing disorder levels, with all regions marked with question marks.
- Disorder confidence:** A bar chart showing confidence levels for disorder predictions.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand