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Description	P75974
Date	Thu Jan 5 12:16:42 GMT 2012
Unique Job ID	8f84b58747639b26

The figure displays three panels of protein analysis tracks for different regions of a protein. Each panel shows the following tracks:

- Sequence:** Amino acid sequence with residue numbers indicated above.
- Secondary structure:** Representation of alpha-helices (green cylinders) and beta-strands (blue arrows).
- SS confidence:** A bar representing the confidence in the secondary structure prediction, with colors indicating different confidence levels.
- Disorder:** A bar representing the predicted disorder of the protein, with colors indicating different confidence levels.
- Disorder confidence:** A bar representing the confidence in the disorder prediction, with colors indicating different confidence levels.


Panel 1 (Residues 1-60): The sequence is MKTI HDI RRS NARKLRDGV GGNSS FATMI DREPTQTSRF MGDGATKNI GDSMARHI EKCF. The secondary structure shows several alpha-helices. The SS confidence is high (red) for most of the sequence. The disorder confidence is high (red) for most of the sequence.

Panel 2 (Residues 70-120): The sequence is DLPVGWL DQEHQTNTI TKKP DVSI TNKQI TLVPVI S WVQA GAWKEVGY SEVDL STAETYP. The secondary structure shows a beta-strand followed by a loop and then another beta-strand. The SS confidence is high (red) for most of the sequence. The disorder confidence is high (red) for most of the sequence.


Panel 3 (Residues 130-180): The sequence is CPVPCGEMTYI LRVIGDSMI DEYRPGDMI FVDPEVPACHGDDVI ALMHDGETTFKRLIE. The secondary structure shows a beta-strand followed by a loop and then another beta-strand. The SS confidence is high (red) for most of the sequence. The disorder confidence is high (red) for most of the sequence.


Panel 4 (Residues 190-220): The sequence is DGTQRYL KALNPWP EPIYI KINGNC S I GTVI FSGKPRRYKI KA. The secondary structure shows a beta-strand followed by a loop and then another beta-strand. The SS confidence is high (red) for most of the sequence. The disorder confidence is high (red) for most of the sequence.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand