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Description	P28307
Date	Thu Jan 5 11:44:55 GMT 2012
Unique Job ID	93244fdeb16ce084

Figure 1 displays the protein structure and disorder analysis of the N-terminal region of the protein, showing three segments of the sequence (residues 1-60, 70-120, and 130-150).

Segment 1 (Residues 1-60):

- Sequence:** MKLLKVAALAAIVSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
- Secondary structure:** Shows a series of alpha-helices and beta-strands.
- SS (Solvent Accessibility):** High accessibility (red) for the first 10 residues, followed by low accessibility (green) for the rest of the segment.
- confidence:** High confidence (green) for the first 10 residues, followed by low confidence (red) for the rest of the segment.
- Disorder:** High disorder (grey) for the first 10 residues, followed by low disorder (blue) for the rest of the segment.
- Disorder confidence:** High disorder confidence (blue) for the first 10 residues, followed by low disorder confidence (red) for the rest of the segment.


Segment 2 (Residues 70-120):

- Sequence:** TDARNSDLTITQHGGNGADVGGQSSDDLTLQRGFNGSATLDQWNGKNSEMTVKQFGG
- Secondary structure:** Shows a series of alpha-helices and beta-strands.
- SS (Solvent Accessibility):** High accessibility (red) for the first 10 residues, followed by low accessibility (green) for the rest of the segment.
- confidence:** High confidence (green) for the first 10 residues, followed by low confidence (red) for the rest of the segment.
- Disorder:** High disorder (grey) for the first 10 residues, followed by low disorder (blue) for the rest of the segment.
- Disorder confidence:** High disorder confidence (blue) for the first 10 residues, followed by low disorder confidence (red) for the rest of the segment.


Segment 3 (Residues 130-150):


- Sequence:** GNGAAVDQTASNSSVNVTVQVGFNNATAHQY
- Secondary structure:** Shows a series of alpha-helices and beta-strands.
- SS (Solvent Accessibility):** High accessibility (red) for the first 10 residues, followed by low accessibility (green) for the rest of the segment.
- confidence:** High confidence (green) for the first 10 residues, followed by low confidence (red) for the rest of the segment.
- Disorder:** High disorder (grey) for the first 10 residues, followed by low disorder (blue) for the rest of the segment.
- Disorder confidence:** High disorder confidence (blue) for the first 10 residues, followed by low disorder confidence (red) for the rest of the segment.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand