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Description	P0A8A8
Date	Thu Jan 5 11:07:21 GMT 2012
Unique Job ID	76229b761e96e134

Protein structure and disorder analysis of the N-terminal region (residues 1-150). The analysis is divided into three segments: residues 1-60, 70-120, and 130-150. Each segment displays the amino acid sequence, secondary structure (alpha-helices in green, beta-strands in blue), solvent accessibility (SS) as a color bar, and disorder predictions with confidence scores.

**Segment 1: Residues 1-60**

Sequence: MSTLEQKLTEMITAPVEALGFELVGI E F I RGR TSTLR I Y I DSE DGINVDDCADVSHQVSA

Secondary structure: [Alpha-helices and beta-strands]

SS: [Solvent accessibility bar]

Disorder: [Disorder prediction bar]

Disorder confidence: [Disorder confidence bar]

**Segment 2: Residues 70-120**

Sequence: VLDVEDPI TVAYNLEVS SPGLDRPLFTA EHYARFVGEEVTLVLRMAVQNR RKVQGV I KAV

Secondary structure: [Alpha-helices and beta-strands]

SS: [Solvent accessibility bar]

Disorder: [Disorder prediction bar]

Disorder confidence: [Disorder confidence bar]

**Segment 3: Residues 130-150**

Sequence: DGE MI T V T V E G K D E V F A L S N I Q K A N L V P H F


Secondary structure: [Alpha-helices and beta-strands]

SS: [Solvent accessibility bar]


Disorder: [Disorder prediction bar]


Disorder confidence: [Disorder confidence bar]

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand