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Description	P76156
Date	Thu Jan 5 12:19:48 GMT 2012
Unique Job ID	4a402311fca61ba6

**Panel 1: Residues 1-60**

Sequence	Secondary structure	SS	confidence	Disorder	Disorder confidence
MDQVVI F KQI F DKVRNDL NYQWF YSELKRHNVS HYI YYLATENVH I VLKNDNTVLL KGLK	Helices (1-33), Strands (34-60)	Color-coded accessibility	Color-coded confidence	Disorder prediction (e.g., ? ? at start, ? ? ? ? at end)	Disorder confidence


**Panel 2: Residues 70-120**

Sequence	Secondary structure	SS	confidence	Disorder	Disorder confidence
NI VSVKF S KDRHLI E TTSNKLKSREI TFQEYRRNLAKAGVFRWVTNI HEQKRYYYTF DNS	Strands (70-87), Helices (88-105), Strand (106-120)	Color-coded accessibility	Color-coded confidence	Disorder prediction (e.g., ? ? at start, ? ? ? ? ? ? in middle)	Disorder confidence


**Panel 3: Residues 130-138**


Sequence	Secondary structure	SS	confidence	Disorder	Disorder confidence
LLFTESI QKTTQILPR	Strand (130-138)	Color-coded accessibility	Color-coded confidence	Disorder prediction (e.g., ? ? ? ? ? ? in middle)	Disorder confidence

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand