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Description	P0AAR3
Date	Thu Jan 5 11:13:33 GMT 2012
Unique Job ID	94ed0c89ef5a7a40

Panel 1 (Residues 1-60):

Sequence	Secondary structure	SS	Disorder	Disorder confidence
MT PAVKLL EKNKI S FQI HTY E H D P A E T N F G D E V V K K L G L N P D Q V Y K T L L V A V N G D M K H L A	Alpha helix (1-10), Alpha helix (20-30), Alpha helix (35-45), Alpha helix (50-60)	Low	High	High


Panel 2 (Residues 70-120):

Sequence	Secondary structure	SS	Disorder	Disorder confidence
V A V T P V A G Q L D L K K V A K A L G A K K V E M A D P M V A Q R S T G L V G G I S P L G Q K K R L P T I I D A P A	Alpha helix (75-85), Alpha helix (90-100), Alpha helix (115-120)	Low	High	High


Panel 3 (Residues 130-150):


Sequence	Secondary structure	SS	Disorder	Disorder confidence
Q E F A T I Y V S G G K R G L D I E L A A G D L A K I L D A K F A D I A R R D	Alpha helix (135-145), Alpha helix (150-155)	Low	High	High

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand