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Description	P33361
Date	Thu Jan 5 11:52:03 GMT 2012
Unique Job ID	faac36e4c44a6b0d

Protein structure and disorder analysis of the full-length protein (1-380 aa). The figure displays the amino acid sequence, secondary structure, and disorder predictions across the entire protein. The sequence is color-coded by amino acid type. Secondary structure is shown as green bars. Disorder is indicated by red bars. Confidence scores are shown as a bar chart below the disorder prediction.

Position	Sequence	Secondary structure	Disorder	Disorder confidence
1-60	MTYFRI NPVL ALLLLLTAI AAALPFI SYAPNRLVSGEGRHLWQLWPQTIWMLVGVGC A WL	Alpha-helix	Disordered	0.95
61-120	TACFI PGKKGSI CALILAQFV FVLLVWGAGKAATQLAQNGSALARTSLGSGFWLAAALAL	Alpha-helix	Disordered	0.95
121-180	LACSDAIRRI STHPLWRVLLHMQIAIIPLVLLYSGLTNDLSLMKEYANRQDVDDALAQH	Alpha-helix	Disordered	0.95
181-240	LTLLFGAVLPALVIGVPLGIWCYFSTARQGAI FSLLNVIQTVPSVALFGLLIAPLAALVT	Alpha-helix	Disordered	0.95
241-300	AFPWLGT LGI AGTGMPALI ALVLYALLPLVRGVVGLNQIPRDVLESARAMGMSG AQR F	Alpha-helix	Disordered	0.95
301-360	LHVQLPLALPVFLRSLRVVMVQTVGMAVIAALI GAGGF GALVFQGLLSSAIDLVL L GVI P	Alpha-helix	Disordered	0.95
361-380	VI VLA VLT DALF DLLI ALLKVKRND	Alpha-helix	Disordered	0.95

Confidence Key  
High(9)  Low (0)  
? Disordered  
 Alpha helix  
 Beta strand