

Email	l.a.kelley@imperial.ac.uk
Description	P46846
Date	Thu Jan 5 12:04:19 GMT 2012
Unique Job ID	2eb9ad68543e1b0c

Sequence: MLTVPGLCWLCRMPALALGHWGISVCSRATRTDKTLCPCQCGLPATHSHLP CGRCLQKPP

Secondary structure: [Helices at residues 25-30, 35-40, 50-55]

SS: [Solvent accessibility bar]

Disorder: [Disorder prediction bar]

Disorder confidence: [Disorder confidence bar]

Sequence: WQRLVTVADYAPPLSPLIHQLKFSRRSEIASALSRLLEVLHARRTTGLQLPDRI VSV

Secondary structure: [Helices at residues 75-85, 90-100, 105-115]

SS: [Solvent accessibility bar]

Disorder: [Disorder prediction bar]

Disorder confidence: [Disorder confidence bar]

Sequence: LWQRRHWRRGFNQSDLLCQPLSRWLHCQWDSEAVTRTRATATQHFLSARLRKRNLKNAPFR

Secondary structure: [Helices at residues 135-145, 150-160, 165-175]

SS: [Solvent accessibility bar]

Disorder: [Disorder prediction bar]

Disorder confidence: [Disorder confidence bar]

Sequence: LELPVQGRHMMVI VDDVVTTGSTVAEIAQLLLRNGAAAVQVWCLCRTL


Secondary structure: [Helices at residues 200-210]

SS: [Solvent accessibility bar]


Disorder: [Disorder prediction bar]


Disorder confidence: [Disorder confidence bar]

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand