

Email	l.a.kelley@imperial.ac.uk
Description	C3UPD1
Date	Thu Jan 5 10:56:22 GMT 2012
Unique Job ID	9481017d6fde861c

Sequence: GSATIALNKRARHEYFIEEFEEAGLALQGWEVKSLRAGKANISDSYVLLRDGEAFLFGAN

Secondary structure: [Alpha-helix from residue 31 to 60]

SS confidence: [Confidence scores for secondary structure]

Disorder: [Disorder prediction]

Disorder confidence: [Confidence scores for disorder]

Sequence: ITPMAVASTHVVCDPTRTRKLLLNQRELDLSLYGRVNRREGYTVALSLYWKNAWCKVKIGV

Secondary structure: [Alpha-helix from residue 70 to 100]

SS confidence: [Confidence scores for secondary structure]

Disorder: [Disorder prediction]

Disorder confidence: [Confidence scores for disorder]

Sequence: AKGKKQHDKRSDIKEREWQVDKARI MKNHR


Secondary structure: [Alpha-helix from residue 130 to 140]

SS confidence: [Confidence scores for secondary structure]


Disorder: [Disorder prediction]


Disorder confidence: [Confidence scores for disorder]

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand