

Email	l.a.kelley@imperial.ac.uk
Description	P76345
Date	Thu Jan 5 12:22:07 GMT 2012
Unique Job ID	de3bd159abd8154a

Sequence: MNRFSKTQIYLHWITLLFVAITYAAMELRGWFPKGSSTYLLMRETHYNAGIFVWVLMFSR

Secondary structure: [Helices at positions 10-30, 35-55, 70-85, 95-115, 125-140]

SS confidence: [High confidence (red) for most of the sequence, with some lower confidence (green/yellow) regions]

Disorder: [Disorder prediction (red/green bars)]

Disorder confidence: [Disorder confidence (red/green bars)]

Sequence: LI IKHRYSDPSIVPPPAWQMKAAASLMHIMLYITFLALPLLGI ALMAYSGKKSWSFLGFNV

Secondary structure: [Helices at positions 75-85, 95-115, 125-140]

SS confidence: [High confidence (red) for most of the sequence, with some lower confidence (green/yellow) regions]

Disorder: [Disorder prediction (red/green bars)]

Disorder confidence: [Disorder confidence (red/green bars)]

Sequence: SPFVTPNSEI KALIKNIHETWANI GYFLIAAHAGAA LFHHYIQKDNTLLRMMPPRRK


Secondary structure: [Helices at positions 135-145, 155-175, 185-200]

SS confidence: [High confidence (red) for most of the sequence, with some lower confidence (green/yellow) regions]


Disorder: [Disorder prediction (red/green bars)]


Disorder confidence: [Disorder confidence (red/green bars)]

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand