



Email	l.a.kelley@imperial.ac.uk
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
Protein structure and disorder analysis for the full-length protein (1-60). The sequence is MT KTVSTSK KPRKQHSPEFRSEALKLAERI GVTAAARELSLYESQLYNWRSKQQNQQTSS. The secondary structure is shown as a green ribbon model. The disorder analysis shows a high confidence disorder region from residue 1 to 30, and a lower confidence disorder region from residue 30 to 60.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand