

Email	l.a.kelley@imperial.ac.uk
Description	P0AEC5
Date	Thu Jan 5 11:23:00 GMT 2012
Unique Job ID	d424f9ddcc5b7e54

Protein structure prediction results for the protein sequence MTNYSLRARMMLILAPT... showing sequence, secondary structure, SS confidence, disorder, and disorder confidence across 420 residues.

**Sequence:** MTNYSLRARMMLILAPT... (Residues 1-420)

**Secondary structure:** Alpha helices (green) and beta strands (blue) are shown. Key features include a long alpha helix from residue 10 to 30, a beta strand at residue 70, and a long alpha helix from residue 370 to 420.

**SS confidence:** High confidence (red) is observed for the alpha helices, while lower confidence (yellow/green) is seen for the beta strands and loops.

**Disorder:** Disordered regions are indicated by question marks (?) along the sequence, primarily in the N-terminal region (residues 1-60) and some internal loops.

**Disorder confidence:** High confidence (red) is shown for the disordered regions, indicating a high probability of disorder.



