



Email	l.a.kelley@imperial.ac.uk
Description	P0ACV4
Date	Thu Jan 5 11:19:09 GMT 2012
Unique Job ID	ae0d29a2fdbae0b


Protein structure and sequence analysis of the first two domains of the protein. The top panel shows the first 60 residues (MKYLLIFLLVLAIFVIVSVTLGAQNDQQVTFNYLLAQGEYRISTLLAVLFAAGFAIGWLI) with a secondary structure prediction (green helices) and a confidence score (red bar). The bottom panel shows residues 70-100 (GLFVLRVRVSLARAERKIKRLENQLSPATDVAVVPHSSAAKE) with a secondary structure prediction (green helices) and a confidence score (red bar).

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand