


Email	l.a.kelley@imperial.ac.uk
Description	P0A964
Date	Thu Jan 5 11:09:28 GMT 2012
Unique Job ID	8a5d789b5b2e6ccd

Panel 1 (Residues 1-60):  
 Sequence: MTGMTNVTKLASEPSGGQFLLVFTLGDDEEYGI DILKVQEIRGYDQVTRIANTPAFIKGVTN  
 Secondary structure: Helices at residues 10-15, 25-30, 35-40, 45-50, 55-60.  
 SS confidence: High confidence (red/yellow) across most of the region.  
 Disorder: Disordered regions at residues 1-9 and 51-54.  
 Disorder confidence: High confidence (red/yellow) for disordered regions.


Panel 2 (Residues 70-120):  
 Sequence: LRGVIVPIVDLRIKFSQVDVDYNDNTVVI VLN LGQRVVGIVVDGVS DVL SLTAEQIRPAP  
 Secondary structure: Helices at residues 75-80, 115-120.  
 SS confidence: High confidence (red/yellow) across most of the region.  
 Disorder: Disordered regions at residues 81-86 and 121-125.  
 Disorder confidence: High confidence (red/yellow) for disordered regions.


Panel 3 (Residues 130-160):  
 Sequence: EFAVTLSTEYLTGLGALGDRMLILVNI EKLLNSEEMALLDSAASEVA  
 Secondary structure: Helices at residues 135-140, 145-150, 155-160.  
 SS confidence: High confidence (red/yellow) across most of the region.  
 Disorder: Disordered regions at residues 131-134 and 161-165.  
 Disorder confidence: High confidence (red/yellow) for disordered regions.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand