

Email	l.a.kelley@imperial.ac.uk
Description	P68066
Date	Thu Jan 5 12:10:55 GMT 2012
Unique Job ID	01b4daeb11285427

Protein structure prediction results for three protein segments. Each segment is shown with its amino acid sequence, secondary structure (alpha helices and beta strands), sequence confidence, disorder, and disorder confidence.

Segment 1 (Residues 1-60):

- Sequence: MI TGI QI TKAANDDLLNSFWLLDSEKGEARCI VAKAGYAEDEVVAVSKLGDI EYREVPVE
- Secondary structure: Multiple alpha helices and beta strands.
- SS confidence: High confidence across the sequence.
- Disorder: No disorder predicted.
- Disorder confidence: High confidence across the sequence.

Segment 2 (Residues 70-120):

- Sequence: VKPEVRVEGGQHLNVNVLRRRETLEDAVKHPEKYPQLTIRVSGYAVRFNSLTPEQQRDVI A
- Secondary structure: Multiple alpha helices and beta strands.
- SS confidence: High confidence across the sequence.
- Disorder: No disorder predicted.
- Disorder confidence: High confidence across the sequence.

Segment 3 (Residues 1-5):

- Sequence: RTFTESL
- Secondary structure: Alpha helix.
- SS confidence: High confidence across the sequence.
- Disorder: No disorder predicted.
- Disorder confidence: High confidence across the sequence.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand