

Email	l.a.kelley@imperial.ac.uk
Description	P0AFG0
Date	Thu Jan 5 11:26:08 GMT 2012
Unique Job ID	9040530b4566a8b7

Figure 1 displays the protein structure and disorder analysis for the protein sequence MS EAPKKR WY VV QAF S G F E G R V A T S L R E H I K L H N M E D L F G E V M V P T E E V V E I R G G Q R R K S. The protein is a single-chain protein with a total length of 180 residues. The structure is composed of several alpha-helices and beta-strands. The disorder analysis shows regions of high and low disorder confidence.


The figure is divided into three panels, each showing a different segment of the protein sequence and its corresponding structural and disorder analysis.

Panel 1 (Top): Shows the sequence from residue 1 to 60. The secondary structure (SS) is represented by blue arrows (alpha-helices) and green cylinders (beta-strands). The disorder confidence is shown as a red bar, indicating regions of high disorder confidence. The disorder analysis shows regions of high and low disorder confidence.


Panel 2 (Middle): Shows the sequence from residue 70 to 120. The secondary structure (SS) is represented by blue arrows (alpha-helices) and green cylinders (beta-strands). The disorder confidence is shown as a red bar, indicating regions of high disorder confidence. The disorder analysis shows regions of high and low disorder confidence.


Panel 3 (Bottom): Shows the sequence from residue 130 to 180. The secondary structure (SS) is represented by blue arrows (alpha-helices) and green cylinders (beta-strands). The disorder confidence is shown as a red bar, indicating regions of high disorder confidence. The disorder analysis shows regions of high and low disorder confidence.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand