


Email	l.a.kelley@imperial.ac.uk
Description	P33668
Date	Thu Jan 5 11:52:35 GMT 2012
Unique Job ID	099c4923b0597b91


The figure displays three horizontal tracks representing different protein segments. Each track includes a sequence alignment, secondary structure prediction, solvent accessibility (SS) confidence, disorder prediction, and disorder confidence.


- Top Segment:** The sequence is MKYSSIFSMLSFFILFACNETAVYGSDENIIFMRYVEKLHLDKYSVKNTVKTETMAIQLA. It shows several alpha-helices (green cylinders) and beta-strands (blue arrows). The SS confidence is high across most regions. Disorder is predicted at positions 1-3, 18, 38, and 48.
- Middle Segment:** The sequence is EIVVRYYRGERIAEEKPYLITELPDSVVVEGAKLPYEVAAGGVFIIEINKNGCVLNFLH. It features multiple alpha-helices and beta-strands. The SS confidence is generally high. Disorder is predicted at positions 92-98.
- Bottom Segment:** The sequence is SK. It consists of a single beta-strand. The SS confidence is low. Disorder is predicted at position 1.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand