

Email	l.a.kelley@imperial.ac.uk
Description	P08839
Date	Thu Jan 5 11:01:38 GMT 2012
Unique Job ID	3546c154e9a788ac

Protein structure prediction results for the protein sequence: MI SGI LASPGI AFGKALLL KEDEI VI DRKKI SADQVDQEV ERFLSGRAKASA QLETI KTK.

The figure displays the sequence, secondary structure, SS confidence, disorder, and disorder confidence across the entire length of the protein (1-420 residues).

Sequence: MI SGI LASPGI AFGKALLL KEDEI VI DRKKI SADQVDQEV ERFLSGRAKASA QLETI KTK

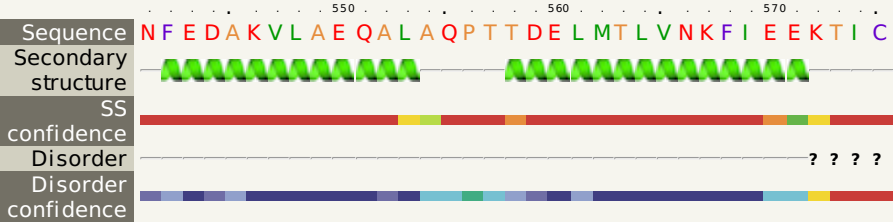
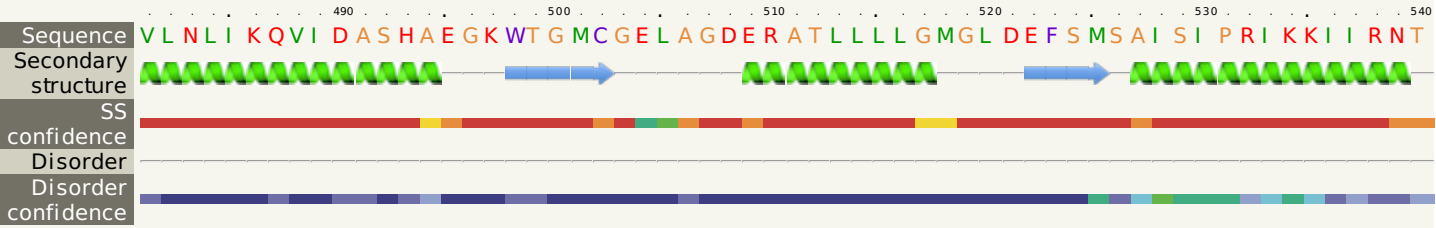
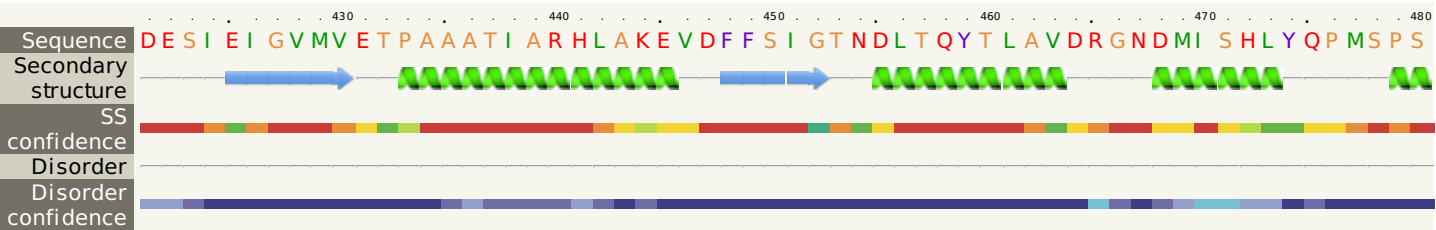
Secondary structure: [Blue arrows indicate predicted secondary structure elements, including alpha-helices and beta-strands.]

SS confidence: [Color scale from red (low confidence) to green (high confidence).]

Disorder: [Blue arrows indicate predicted disordered regions.]

Disorder confidence: [Color scale from red (low confidence) to green (high confidence).]

Residue positions are marked at intervals of 10 (1, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420).



Confidence Key

High(9) Low (0)

? Disordered

Alpha helix

Beta strand