

Email	l.a.kelley@imperial.ac.uk
Description	P0A8A0
Date	Thu Jan 5 11:07:16 GMT 2012
Unique Job ID	b63b28ce7a127386

Protein structure prediction results for the protein sequence: MAGHSKWANTRHRKAAQDAKRGKIFTKIIRELVTAAKLGGGDPDANPRLRAAVDKALSNNTMTRDTLNRAIARGVGGDDANMETIIYEGYGGGTAIMIECLSDNRRNTVAEVRHAFSKCGGNLGT DGSVAYLF S KKGVI SFEKGDEDTIMEAALEAGAE DVV TYDDGAI DVYTAW EEMG KVRDALEAAGL KADSAEVS MI PSTKADMDAETAPKLMRLI DMLED CDDVQEVYHNGEIS DEVAATL.

The figure displays four segments of the protein, each with the following tracks:

- Sequence:** Amino acid sequence (e.g., MAGHSKWANTRHRKAAQDAKRGKIFTKIIRELVTAAKLGGGDPDANPRLRAAVDKALSNNTMTRDTLNRAIARGVGGDDANMETIIYEGYGGGTAIMIECLSDNRRNTVAEVRHAFSKCGGNLGT DGSVAYLF S KKGVI SFEKGDEDTIMEAALEAGAE DVV TYDDGAI DVYTAW EEMG KVRDALEAAGL KADSAEVS MI PSTKADMDAETAPKLMRLI DMLED CDDVQEVYHNGEIS DEVAATL).
- Secondary structure:** Predicted secondary structure elements (alpha-helices and beta-strands) shown as green cylinders and blue arrows.
- SS confidence:** Confidence scores for the secondary structure prediction, shown as a color-coded bar (red for high confidence, yellow for medium, green for low).
- Disorder:** Predicted disorder regions, shown as a bar with question marks indicating uncertainty.
- Disorder confidence:** Confidence scores for the disorder prediction, shown as a color-coded bar (red for high confidence, yellow for medium, green for low).

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand