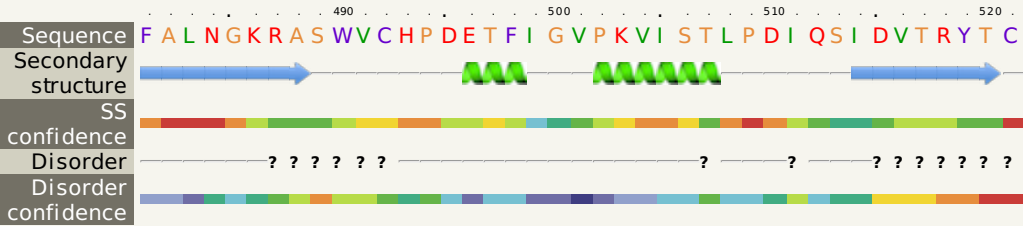
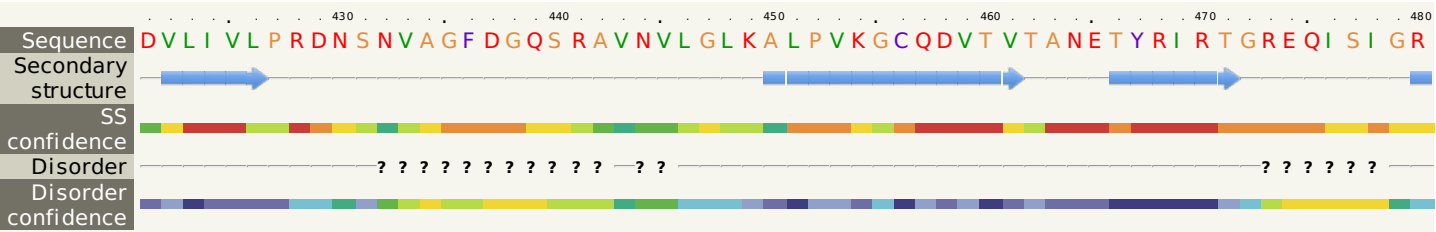


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Description	P39391
Date	Thu Jan 5 12:00:24 GMT 2012
Unique Job ID	ce4165e42eff0a1f

Protein structure prediction results for the protein sequence: MLWGFVFVSFISKELALGQSEYISWVKCTSWLSNFVNLRGLRQPDGRPLYEYHATNDEYTLQLQLLRAVGQSQCNI CNRDF AACFVLFCS EWYRRDYERQCGWTWDPIYKKIGISFTATELGTIVPKGMEDYWL RPI RFY ESERRNFLGT L FSEGGLPFRLLKESDSRFLAVFSRILGQYLEQAKQSGFSALSLARAVIEKSALPTVFSEDT SVELI SHMADNLNSLVLT HNLI NHKEPVQLEKVHPTWRSEFPPI PLDDDETGT HFL NGLL CAASVEAKPRLQKNKSTRCQFYWSEKHPDEL RVI VSLPDEVSFPVTSEPSTTRFELAI CEDGEEVSGLGPAYASLENRQATVRLRKSEVRFGRQNPSAGLSLVARAGGMI VGSIKLDDSEIAI GEVPLTFIVDADQWLLQGQASCSVRSSF.

The figure displays the sequence, secondary structure (SS), confidence, disorder, and disorder confidence for each residue. The protein is predicted to be a monomer with a complex fold, including several alpha-helices and beta-strands. The disorder prediction shows several regions of low confidence, particularly in the N-terminal and C-terminal regions.



Confidence Key

High(9) [Color scale] Low (0)

? Disordered

Alpha helix

Beta strand