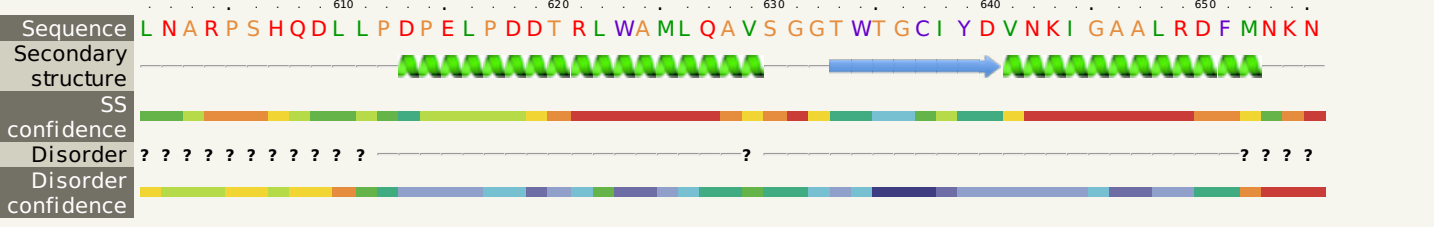
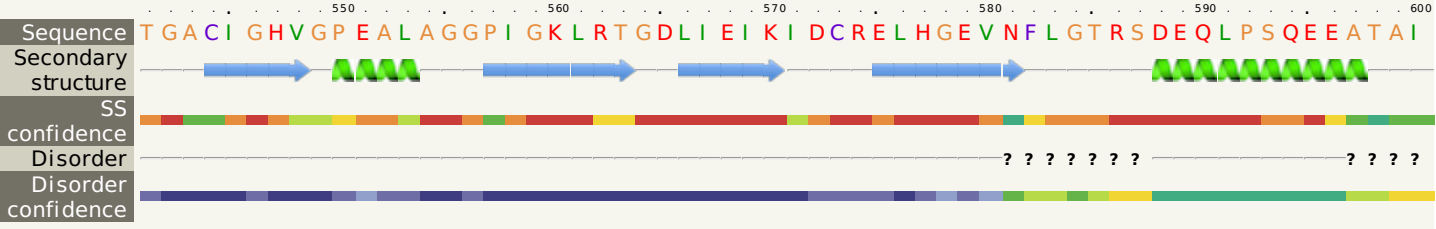
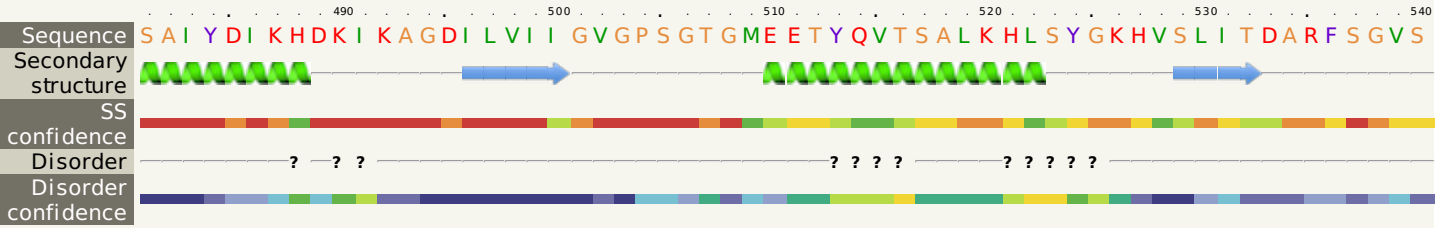
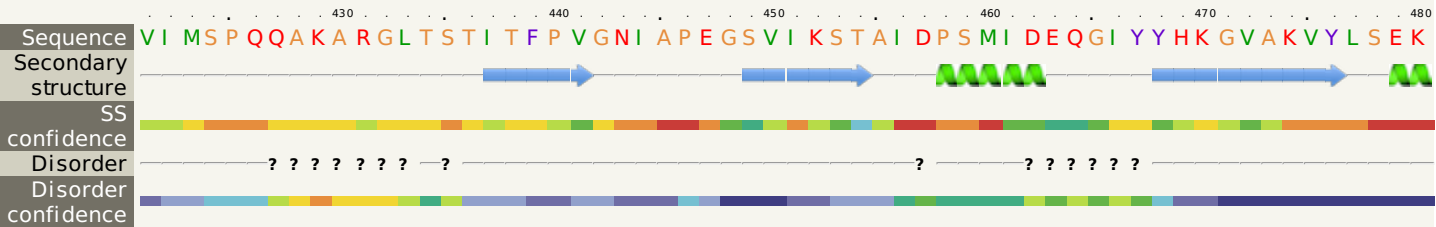


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Description	P39358
Date	Thu Jan 5 11:59:48 GMT 2012
Unique Job ID	8d313280ba75998e

Protein structure prediction and disorder analysis for the protein sequence MSVRNIFADESHDIYTVRTHADGPDGELPLTAEMLINRPSGDLFGMTMNA G MGWSPDELD RDGILLSTLGGRLRGADGKPVALLAHQGHYELDIQMKA AA EVI KANHALPYAVYVSDPCD GRTQGT TGMFDSL PYRNDAS MVMRRLIRSLPDAKAVIGVASC DKGLPATMMALAAQHNI A TVLV PGGATLPAKDGEDNGKVQTI GARFANGELSLQDARRAGCKACASSGGGCQFLGTAG TSQVVAEGLGLAI PHSALAPSGEPVWREIARASARAALNLSQKGI TTREI LTKAI ENAM TVHAAF GGSTNLLLHI PAIAHQAGCHI PTVD DWIRI NKRV PRLVSVLPNGP VYHPTVNAF MAGGVPEVMLHLRSLGLLHE DVMVT VTGSTLKENLDWWEHSERRQRFKQLLLDQEQI NADE.

The figure displays the sequence, secondary structure (SS), confidence, disorder, and disorder confidence for each residue. Blue arrows indicate predicted alpha-helices, and green cylinders indicate predicted beta-strands. The sequence is color-coded by residue type: A (green), C (blue), D (red), E (yellow), F (purple), G (orange), H (brown), I (pink), L (light green), M (dark green), N (light blue), P (dark blue), Q (light purple), R (dark red), S (light yellow), T (light green), V (dark green), W (dark blue), Y (light purple).



Confidence Key
High(9) [Color scale] Low (0)
? Disordered
Alpha helix
Beta strand