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Description	P03959
Date	Thu Jan 5 10:58:06 GMT 2012
Unique Job ID	4f8be31d5e6e1b2c

Protein structure analysis of the full-length protein (1-420). The analysis includes sequence, secondary structure, and disorder confidence across the entire protein length.

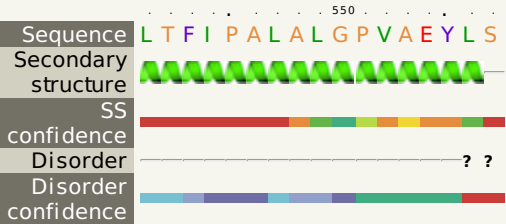
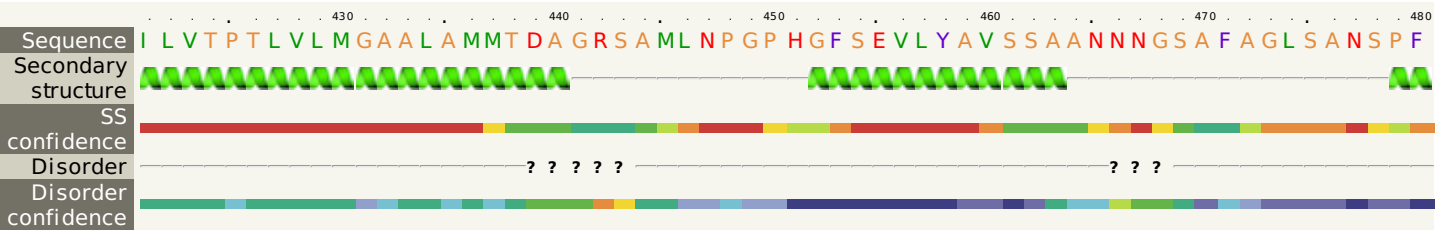
**Sequence:** MAAQQGFLLIATFLLVLMVLARPLGSGLARLI<sup>1</sup>NDIPLPGTTGVERVLFRALGVSDREMN<sup>60</sup>WK  
 QYLCAILGLNMLGLAVLFFMLLGQHYLP<sup>70</sup>LNPPQLPGLSWDLALNTAVSFVTNTNWQSY<sup>120</sup>SG  
 ETTLSYFSQMAGLTVQNFLSAASGIAVIFALIRAFTRQSMSTLGN<sup>130</sup>AVD<sup>140</sup>LLRITLWVLVP<sup>180</sup>  
 VALLIALFFIQQGALQNFLPYQAVNTVEGAQQLLPMGPVVASQEAI<sup>190</sup>KMLGTNGGGFFNANS<sup>240</sup>  
 SHPFENPTALTNFVQMLAIFLIP<sup>250</sup>TALCFAG<sup>260</sup>EVMGDRRQGRMLLWAMSVIFVICGVVMW<sup>300</sup>  
 AEVQGNPHLLALGTDSSINMEGKESRFGVLVSSLFAVVTTAASC<sup>310</sup>GAVI<sup>320</sup>AMHDSFTALGGM<sup>360</sup>  
 VPMWLMQIGEVVFGGVGSGLYGMMLFVLLAVFIAGLMI<sup>370</sup>GRTPEYLGKKI<sup>400</sup>DVREM<sup>410</sup>KL<sup>420</sup>TALA

**Secondary structure:** The protein structure is shown as a ribbon diagram. It features several alpha-helices (green) and beta-strands (blue). Two blue arrows indicate a region of uncertainty or a specific structural feature between residues 210 and 230.

**SS confidence:** The confidence of the secondary structure prediction is shown as a bar chart. It ranges from 0 (red) to 1 (green).

**Disorder:** The disorder prediction is shown as a bar chart. It ranges from 0 (blue) to 1 (red).

**Disorder confidence:** The confidence of the disorder prediction is shown as a bar chart. It ranges from 0 (blue) to 1 (red).



Confidence Key

High(9) Low (0)

? Disordered

Alpha helix

Beta strand