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Description	P17854
Date	Thu Jan 5 11:36:21 GMT 2012
Unique Job ID	5ddd77c27b4e85e0

Protein structure and sequence analysis of the protein sequence MSKLDLNALNELPKVDRI LALAETNAELEKLD AEGRVAWALDNLPG EYVLSSSF G IQAAVSLHLVNQIRPDI PVI L TDTGYLFPETYRFI DELTDKLKLN LKVYRATESA AWQEAR YGK LWEQGV EGI EKYNDI NKVE P MNRAL KELNAQT WFA GLRREQS GSRANLPV LAI QRGV FKV LPI I DWDNR TI YQYL QKHGL KYHPL WDEGY LSVGD TH TTRK WEP GMAEEET RFFGL KREC GP L H E G.


The figure displays the protein structure and sequence analysis across the entire length of the protein, showing the following data:


- Sequence:** MSKLDLNALNELPKVDRI LALAETNAELEKLD AEGRVAWALDNLPG EYVLSSSF G IQAAVSLHLVNQIRPDI PVI L TDTGYLFPETYRFI DELTDKLKLN LKVYRATESA AWQEAR YGK LWEQGV EGI EKYNDI NKVE P MNRAL KELNAQT WFA GLRREQS GSRANLPV LAI QRGV FKV LPI I DWDNR TI YQYL QKHGL KYHPL WDEGY LSVGD TH TTRK WEP GMAEEET RFFGL KREC GP L H E G
- Secondary structure:** The structure is shown as a ribbon diagram, with alpha-helices in green and beta-strands in blue. The structure is mostly alpha-helical, with a few beta-strands.
- SS confidence:** The confidence is shown as a bar chart, with values ranging from 0.0 to 1.0. The confidence is generally high, with some lower values in the middle of the protein.
- Disorder:** The disorder is shown as a bar chart, with values ranging from 0.0 to 1.0. The protein is mostly ordered, with some disordered regions.
- Disorder confidence:** The confidence is shown as a bar chart, with values ranging from 0.0 to 1.0. The confidence is generally high, with some lower values in the middle of the protein.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand