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Description	P06966
Date	Thu Jan 5 10:59:34 GMT 2012
Unique Job ID	5f85b005d04d0e18

Protein structure and disorder analysis for the protein sequence: METKNLTIGERIRYRRLKHTQRS LAKALKISHVSVSQWVERGDSEPTGKNL FALSKVLQCSPTWILFGDEDKQPTTPVEKPVALSPKELELLELFNALPESEQDTQLAEMRARKNFKLFEE LLKARQRTNKR.

The analysis includes secondary structure predictions (alpha-helices and beta-strands), solvent accessibility (SS), confidence scores, and disorder predictions for the full sequence and three fragments.

Fragment 1 (Residues 1-60):

- Sequence: METKNLTIGERIRYRRLKHTQRS LAKALKISHVSVSQWVERGDSEPTGKNL FALSKVLQ
- Secondary structure: Multiple alpha-helices and beta-strands.
- SS: High solvent accessibility across the fragment.
- confidence: High confidence scores.
- Disorder: Disordered regions are indicated by question marks.
- Disorder confidence: High confidence scores.


Fragment 2 (Residues 61-120):

- Sequence: CSPTWILFGDEDKQPTTPVEKPVALSPKELELLELFNALPESEQDTQLAEMRARKNFK
- Secondary structure: Multiple alpha-helices and beta-strands.
- SS: High solvent accessibility across the fragment.
- confidence: High confidence scores.
- Disorder: Disordered regions are indicated by question marks.
- Disorder confidence: High confidence scores.


Fragment 3 (Residues 121-130):


- Sequence: LFEEL LKARQRTNKR
- Secondary structure: Multiple alpha-helices and beta-strands.
- SS: High solvent accessibility across the fragment.
- confidence: High confidence scores.
- Disorder: Disordered regions are indicated by question marks.
- Disorder confidence: High confidence scores.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand