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Description	P33937
Date	Thu Jan 5 11:52:56 GMT 2012
Unique Job ID	2233654703a0b717

Protein structure and disorder analysis of the full-length protein (1-420 aa). The figure displays the amino acid sequence, secondary structure, solvent accessibility (SS), confidence scores, and disorder predictions across the entire protein length.

**Sequence:** MKL SRRSF MKANAVAAAAAAGL SVPGVARAVVGQQA I KWDKAPCRFCGTGCGVLVGTQ  
**Secondary structure:** [Alpha-helices and loops represented by green and blue arrows]  
**SS:** [Solvent accessibility scale from 0 to 100]  
**confidence:** [Confidence score scale from 0 to 100]  
**Disorder:** [Disorder prediction scale from 0 to 100]  
**Disorder confidence:** [Disorder confidence scale from 0 to 100]

**Sequence:** QGRVVACQGD PDAPVNRGLNCI KGYFLPKI MYGKDRLTQPLL RMKNGKYDKEGEFTPI TW  
**Secondary structure:** [Alpha-helices and loops represented by green and blue arrows]  
**SS:** [Solvent accessibility scale from 0 to 100]  
**confidence:** [Confidence score scale from 0 to 100]  
**Disorder:** [Disorder prediction scale from 0 to 100]  
**Disorder confidence:** [Disorder confidence scale from 0 to 100]

**Sequence:** DQAFDVMEEKFKTALKEKGPESI GMFGSGQWTI WEGYAASKL FKAGFRSNNI DPNARHCM  
**Secondary structure:** [Alpha-helices and loops represented by green and blue arrows]  
**SS:** [Solvent accessibility scale from 0 to 100]  
**confidence:** [Confidence score scale from 0 to 100]  
**Disorder:** [Disorder prediction scale from 0 to 100]  
**Disorder confidence:** [Disorder confidence scale from 0 to 100]

**Sequence:** ASAVVGF MRTFGMDEPMGCYDDI EQADAFVLWGANAEMHPI LWSRITNRRLSNQNVTV A  
**Secondary structure:** [Alpha-helices and loops represented by green and blue arrows]  
**SS:** [Solvent accessibility scale from 0 to 100]  
**confidence:** [Confidence score scale from 0 to 100]  
**Disorder:** [Disorder prediction scale from 0 to 100]  
**Disorder confidence:** [Disorder confidence scale from 0 to 100]

**Sequence:** VLSTYQHRSE LADNGIIFT PQSDLVILNYI ANYII QNNAI NQDFFSKHVNL RKGATDI G  
**Secondary structure:** [Alpha-helices and loops represented by green and blue arrows]  
**SS:** [Solvent accessibility scale from 0 to 100]  
**confidence:** [Confidence score scale from 0 to 100]  
**Disorder:** [Disorder prediction scale from 0 to 100]  
**Disorder confidence:** [Disorder confidence scale from 0 to 100]

**Sequence:** YGLRPTHPL EKAANKPGSDASEPMS FEDYKAFVAEYTL EKTAEMTGVPK DQLEQLAQLYA  
**Secondary structure:** [Alpha-helices and loops represented by green and blue arrows]  
**SS:** [Solvent accessibility scale from 0 to 100]  
**confidence:** [Confidence score scale from 0 to 100]  
**Disorder:** [Disorder prediction scale from 0 to 100]  
**Disorder confidence:** [Disorder confidence scale from 0 to 100]

**Sequence:** DPNKKVI SYWTMGFNQHTRG VWANNLVYNL HLLTGKI SQPGCGPFS LTGQPSACGTAREV  
**Secondary structure:** [Alpha-helices and loops represented by green and blue arrows]  
**SS:** [Solvent accessibility scale from 0 to 100]  
**confidence:** [Confidence score scale from 0 to 100]  
**Disorder:** [Disorder prediction scale from 0 to 100]  
**Disorder confidence:** [Disorder confidence scale from 0 to 100]



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