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Description	P19319
Date	Thu Jan 5 11:37:17 GMT 2012
Unique Job ID	33da466fca931e3b

Protein structure prediction results for the protein sequence MSKLLDRFRYFKQKGETFADGHGQVMHSNRDWEDSYRQRWQFDKI VRSTHGVNCTGSCSW. The figure displays the sequence, secondary structure, SS confidence, disorder, and disorder confidence across the entire length of the protein (1-480 residues).

**Sequence:** MSKLLDRFRYFKQKGETFADGHGQVMHSNRDWEDSYRQRWQFDKI VRSTHGVNCTGSCSW

**Secondary structure:** [Alpha-helices and loops represented by green cylinders and blue arrows]

**SS confidence:** [Confidence scores for secondary structure prediction]

**Disorder:** [Disordered regions indicated by question marks]

**Disorder confidence:** [Confidence scores for disorder prediction]

**Sequence:** KIYVKNGLVTEIQQTDYPRTRPDLPNHEPRGCPRGASYSWYLYSANRLKYPLIRKRLIE

**Secondary structure:** [Alpha-helices and loops represented by green cylinders and blue arrows]

**SS confidence:** [Confidence scores for secondary structure prediction]

**Disorder:** [Disordered regions indicated by question marks]

**Disorder confidence:** [Confidence scores for disorder prediction]

**Sequence:** LWREALKQHS DPVLAWASIMNDPQKCLSYKQVRGRGGFIRSNWQELNQLIAAANVWTIKT

**Secondary structure:** [Alpha-helices and loops represented by green cylinders and blue arrows]

**SS confidence:** [Confidence scores for secondary structure prediction]

**Disorder:** [Disordered regions indicated by question marks]

**Disorder confidence:** [Confidence scores for disorder prediction]

**Sequence:** YGPDRAVAGFSPIPAMSMVSYAAGTRYLSLLGGTCLSFYDWYCDLPPASPMTWGEQTDVPE

**Secondary structure:** [Alpha-helices and loops represented by green cylinders and blue arrows]

**SS confidence:** [Confidence scores for secondary structure prediction]

**Disorder:** [Disordered regions indicated by question marks]

**Disorder confidence:** [Confidence scores for disorder prediction]

**Sequence:** SADWYNSSYIIAWGSNVPQTRTPDAHFFTEVRYKGTKTIATIPDYSEVAKLCDQWLAPKQ

**Secondary structure:** [Alpha-helices and loops represented by green cylinders and blue arrows]

**SS confidence:** [Confidence scores for secondary structure prediction]

**Disorder:** [Disordered regions indicated by question marks]

**Disorder confidence:** [Confidence scores for disorder prediction]

**Sequence:** GTDSALAMAMGHVILKEFHLDNPSDYFINYCRRYSDMPMLVMLEPRDDGSYVPGRMIRAS

**Secondary structure:** [Alpha-helices and loops represented by green cylinders and blue arrows]

**SS confidence:** [Confidence scores for secondary structure prediction]

**Disorder:** [Disordered regions indicated by question marks]

**Disorder confidence:** [Confidence scores for disorder prediction]

**Sequence:** DLVDGLGESNNPQWKTVAVNTAGELVVPNGSIGFRWGEKGKWNLESI AAGTETELSLTL

**Secondary structure:** [Alpha-helices and loops represented by green cylinders and blue arrows]

**SS confidence:** [Confidence scores for secondary structure prediction]

**Disorder:** [Disordered regions indicated by question marks]

**Disorder confidence:** [Confidence scores for disorder prediction]

**Sequence:** GOHDAVAGVAFPYFGGIENPHFRSVKHNPLVLRQLPVKNLLTLVDGNTCPV VSVYDLVLAN

**Secondary structure:** [Alpha-helices and loops represented by green cylinders and blue arrows]

**SS confidence:** [Confidence scores for secondary structure prediction]

**Disorder:** [Disordered regions indicated by question marks]

**Disorder confidence:** [Confidence scores for disorder prediction]





Confidence Key  
High(9) Low (0)  
? Disordered  
Alpha helix  
Beta strand