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Protein Structure Prediction Report (Residues 1-180)

Section 1: Residues 1-60

Sequence: MVLGKPKQTDP TLEWFLSHCHI HKYPSKSTLI HQGGEKAETLYYI VKGSVAVLI KDEEGKE M

Secondary structure: [Alpha-helices and beta-strands shown]

SS: [Solvent accessibility bar]

confidence: [Confidence scores]

Disorder: [Disorder prediction]

Disorder confidence: [Disorder confidence scores]

Section 2: Residues 70-120

Sequence: ILSYLNQGD F I GELGLFEEGQERSA VWRAKTACEVAEI SYKKFRQLIQVNPDI LMRLSAQ

Secondary structure: [Alpha-helices and beta-strands shown]

SS: [Solvent accessibility bar]

confidence: [Confidence scores]

Disorder: [Disorder prediction]

Disorder confidence: [Disorder confidence scores]

Section 3: Residues 130-180

Sequence: MARRLQVTSEK VGNLAF L DVTGRI AQTLLNLAKQPDAMTHPDGMQI K I TRQEIGQIVGCS

Secondary structure: [Alpha-helices and beta-strands shown]

SS: [Solvent accessibility bar]

confidence: [Confidence scores]

Disorder: [Disorder prediction]

Disorder confidence: [Disorder confidence scores]

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand