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Development of an Algorithm to Calculate Torsional Angles of Polypeptide Structures

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Development of an Algorithm to Calculate Torsional Angles of Polypeptide Structures *Krish Tejas Bharat*

Mentor: Rohit Pappu

Dihedral angles ϕ (phi) and ψ (psi) are important structural factors that determine local conformations of peptides. As a part of an effort to assess ϕ - ψ angle distributions within amino acid motifs known as short linear motifs (SLiMs) found in intrinsically disordered regions (IDRs) that are implicated in diseases such as Alzheimer's disease and Mad Cow disease, this study reports the development of a tool to calculate torsional angles of given polypeptide structures. From a trajectory file generated by a molecular simulation software, the algorithm generates ϕ - ψ angle distributions at different time points along the length of a simulation. To illustrate its application, we used OpenMM, a molecular simulation package, to run molecular dynamics simulations on various dipeptide chains, and parsed dihedral angles to obtain ϕ - ψ distributions for different systems.