Measurement of the Elastic Properties of Proteins Using a Fast and Robust Molecular Mechanics Approach

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Proteins in living cells are constantly subjected to a wide spectrum of mechanical forces, such as the forces that stem from the lipid bilayer (specific to membrane proteins), other proteins or inetra/extra-cellular ligands [1-3]. Given the key role that mechanical properties of transmembrane helices play in proteins' structural integrity and function [4], it is therefore essential to develop computational tools that are precise and at the same time fast in describing proteins' behaviour under different mechanical loading. We have developed a molecular mechanics (MM) approach that accounts for the atomic as well as molecular interactions in proteins by modelling the bonded and non-bonded interactions as physical springs, while using finite element method for solving the governing differential equations. In this study we have used the helices of a mechanosensitive ion channel MscL as a prototype protein. This method is used to measure the mechanical properties and study the behaviour of different transmembrane helices of MscL under various types of mechanical forces such as stretch, torsion and bending. We compared our results with those estimated using molecular dynamics (MD) simulation. For instance, the Young's modulus of TM1 helix in mycobacterium tuberculosis (MtMscL) has been estimated to be $E = 8.5 \pm 0.1$ GPa using the MM approach, which is in good agreement with that obtained by MD simulation [5]. Compared to techniques such as all-atom MD simulations, by utilizing this approach, excessive computation costs and simulation time can be avoided. Our method has several implications for modelling macro biological molecules such as large membrane proteins complexes and cytoskeletal elements [6].

References

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