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A review on structure-function relationship in protein degradation and its importance in pathology

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Structure-function relationship is a key to the understanding of functioning of bioactive molecules, as well as a prerequisite for predictive analysis and design of novel molecules with desirable bioactive properties. The authors group had analysed various in silico methodologies *(Ganguli and Sharma, Computer Society of India Communication, January 2016, pp 26—28)* and the use of open source software packages. Use of open source software and databases permit molecular modeling and predictive design of molecules and of the active site in the protein by homolgy. Stability of a protein molecule *in vivo* determines the effectiveness of its function under physiological conditions. Pathological conditions can be traced to malfunctioning of the proteins due the alteration in primary structure by mutation or by alteration in the post-translational modifications affecting functioning of the molecule. This review catalogues few of the better studied protein structures and describe their characteristic peculiarities with the hope that one would be able to develop predictive heuristics.

Biography

Subrata Ganguli had completed his Ph.D. from the University of Illinois at Chicago, USA after completing his education in the Indian Insitutes of Technologies. He was a recepient of the prestigious JBNSTS Undergraduate Fellowship. He had been active in theIndian Academy press and the internet media authoring on several scientific and publc issues. He has presented more than 10 papers.

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