Proteomics-2013
OMICS Group Conferences
Accelerating Scientific Discovery
3rd International Conference on
Proteomics & Bioinformatics
July 15-17, 2013 Courtyard by Marriott Philadelphia Downtown, USA

Scale for nature of hydrophobic interactions in proteins

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Abstract

There exist several work for measurement of hydrophobic interactions in proteins. Many hydrophobic parameters are used to scale the hydrophobicity of proteins. They vary from one another. One could not come to a unified principle of hydrophobic measurement. Most of the attempts were at residue level. Carbon is the element contributes towards this hydrophobic interaction. A study on carbon content in proteome reveal that globular protein exist maximum with 31.45% of carbon. This is taken as a scale of measurement. Using this scale, a program (CARd) has been developed and applied for several biological phenomena that arise due to proteins. It reveals the hydrophobic features clearly. Studies on protein's half life, protein growth, pattern prediction, epitope prediction and disease state of proteins reveal that this new method is proper. This method explains several biological phenomena that take place due to proteins. This gives reason why some regions are disorder in proteins. This also explains the toxicity of proteins. Analyses leading to understand the mutational effect on biological activities are positive and encourage to work further. One can extend this new development for solving genetic disorders. The 3D structure analysis using this scale will give further insight into the existence of different state of protein in different activity. Protein stabilization, active site improvement and reverse transcription in solving disease are given importance as future work.

Biography

E.Rajasekaran has completed his Ph.D from Indian Institute of Technology, Delhi and postdoctoral studies from University of Nebraska. He is working as associate professor in Karunya University, Tamil Nadu. He has published more than 50 papers in bioinformatics journals.