Proteomics-2013
3rd International Conference on
Proteomics & Bioinformatics
July 15-17, 2013 Courtyard by Marriott Philadelphia Downtown, USA

Regularity in the amino acid sequences of proteins

Chanchal Das Gupta
Jadavpur University, India

Abstract

The transit of proteins from linear to tertiary states should be exactly tractable because the tertiary states have unambiguous crystalline forms. Since the amino acids interact in the water environment, the solution for the folding problem should give due consideration to the hydrophobic / hydrophilic indices of the amino acids, as mentioned in many studies. Representing amino acids by these indices, we find two different kinds of regularity in amino acid sequence of cytosolic and membrane proteins. If we take the mean hydrophobicity for every few percent of amino acids in proteins and plot them in a cumulative fashion from the N to the C termini, we get two different kind of smooth graphs for cytosolic and membrane proteins. More than 100 cytosolic proteins and 30 membrane proteins of widely varying number of amino acids and structures could be represented in two such smooth graphs with small standard errors. What we know so far, for cytosolic proteins, is that this regularity comes from a simple working principle which can be based on our observation on the kinetics of folding of a number of proteins starting from the N-termini and extending to the C-termini through a sequential interaction with the same set of nucleotides in the peptidyl transferase center (PTC) of the ribosome.

Biography

Chanchal Das Gupta completed his Ph.D. (Biophysics) from Calcutta University and he did Post doctoral research on the role of RecA protein in recombination at Yale University, USA (1978-82). He worked as Professor, Calcutta University and IISER-Kolkata till 2012. Now he is working as Senior Fellow (Indian National Science Academy) at Jadavpur University, kolkata.