PROTEIN FOLDING - SEEING IS DECEIVING

Bioinformatics Institute
BII

01 October 2021

09.30AM - 11.30AM

Zoom Details
Meeting ID: **985 8190 0216**
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SCAN ME

ABSTRACT

This year marks the 50th anniversary of the Protein Data Bank (PDB). Current ideas about protein structure formation emerged with the advent of solved structures, of which there are now 182,000 PDB entries. Globular proteins are complex, closely-packed, macromolecular assemblies, held together by an abundance of weak intramolecular interactions. This picture anchors a plausible intuition that the constellation of weak interactions, evident in all folded structures, is responsible for selecting that structure from the presumably vast unfolded population. I shall attempt to raise questions about this conventional interpretation of protein folding.

ABOUT SPEAKER



Dr. George Rose

Krieger-Eisenhower Professor Emeritus,
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George Rose is the Krieger-Eisenhower Professor of Biophysics, Emeritus and an Academy Professor in the Jenkins Department of Biophysics, Johns Hopkins University, Baltimore, Maryland 21218 USA. His research is focused primarily on protein folding, the spontaneous disorder to order transition that occurs under physiological conditions. Prior to joining Johns Hopkins, Dr. Rose was Alumni Endowed Professor of Biochemistry and Molecular Biophysics at Washington University School of Medicine in St. Louis, MO. He had earlier held professorship in the Department of Biochemistry and Biophysics at the University of North Carolina, Chapel Hill and from 1980-91 he was a distinguished professor in the Department of Biological Chemistry at the M.S. Hershey Medical Center of The Pennsylvania State University. His contributions were honored by the award of the prestigious Humboldt Research Award (Forschungspreise) and election as Honorary Hans Fischer Senior Fellow at the Institute for Advanced Study, Technische Universität München.