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The Protein Folding Problem and Tertiary Structure Prediction

The Protein Folding Problem - :-- and Tertiary Structure Prediction Kenneth M. Merz, Jr., Scott M. Le Grand Editors Birkhauser Boston Basel Berlin , Kenneth M. Merz, Jr. Department of Chemistry The Pennsylvania State University 152 Davey Laboratory University Park, PA 16802-6300 Scott M. Le Grand Department Chemistry The State University 152 Davey University PA 16802-6300 Library of

The protein folding problem and tertiary structure prediction

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The Protein Folding Problem - PubMed Central (PMC)

The protein folding problem is the question of how a protein's amino acid sequence dictates its three-dimensional atomic structure. The notion of a folding problem first emerged around 1960, with the appearance of the first atomic-resolution protein structures. Some form of internal crystalline regularity was previously expected

The Protein Folding Problem and Tertiary Structure Prediction

A solution to the protein folding problem has eluded researchers for more than 30 years. The stakes are high. Such a solution will make 40,000 more tertiary structures available for immediate study by translating the DNA sequence information in the sequence databases into three-dimensional protein structures.

The Protein folding problem and tertiary structure prediction

The Protein folding problem and tertiary structure prediction. [Kenneth M Merz; Scott M Le Grand;] The genetic algorithm and protein tertiary structure prediction / Scott M. Le Grand and Kenneth M. Merz, Jr. -- Conformational search and protein folding / Robert E. Bruccoleri -- Building protein folds using distance geometry : towards a general modeling and prediction method / William R

Structural Biochemistry/Proteins/Protein Folding Problem ...

The Protein Folding Problem is the obstacle that scientists confront when they try to predict 3D structure of proteins based on their amino acid sequence. Although it is known that a given sequence of amino acids almost always folds into a 3D structure with certain functions, it is impossible to predict, with high precision, the exact folding pattern.

Understanding the speed of proteins

PROTINFO: secondary and tertiary protein structure prediction

Information about the secondary and tertiary structure of a protein sequence can greatly assist biologists in the generation and testing of hypotheses, as well as design of experiments. The PROTINFO server enables users to submit a protein sequence and request a prediction of the three-dimensional (tertiary) structure based on comparative modeling, fold generation and de novo methods developed

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Protein structure prediction - Wikipedia

Protein structure prediction is the inference of the three-dimensional structure of a protein from its amino acid sequence that is, the prediction of its folding and its secondary and tertiary structure from its primary structure.

Protein folding - Wikipedia

Protein folding is the physical process by which a protein chain acquires its native 3-dimensional structure, a conformation that is usually biologically functional, in an expeditious and reproducible manner.

The Protein Folding Problem and Tertiary Structure ...

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Prediction: Kenneth M., Jr. Merz, S. Le- Grand;

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