

Protein Structure And Evolution: Papers And Discussion

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Phil. Trans. R. Soc. Lond. B 326, 535–553 (1990)
Printed in Great Britain

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Protein structure and function at low temperatures†

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Proteins represent the major components in the living cell that provide the whole repertoire of constituents of cellular organization and metabolism. In the process of evolution, adaptation to extreme conditions mainly referred to temperature, pH and low water activity. With respect to life at low temperatures, effects on protein structure, protein stability and protein folding need consideration.

The sequences and topologies of proteins from psychrophilic, mesophilic and thermophilic organisms are found to be highly homologous. Commonly, adaptive changes refer to multiple alterations of the amino acid sequence, which presently cannot be correlated with specific changes of structure and stability; so far it has not been possible to attribute specific increments in the free energy of stabilization to well-defined amino-acid exchanges in an unambiguous way.

The stability of proteins is limited at high and low temperatures. Their expression and self-organization may be accomplished under conditions strongly deviating from optimum growth conditions. Molecular adaptation to extremes of temperature seems to be accompanied by a flattening of the temperature profile of the free energy of stabilization. In principle, the free energy of stabilization of proteins is small compared to the total molecular energy. As a consequence, molecular adaptation to extremes of physical conditions only requires marginal alterations of the intermolecular interactions and packing density. Careful statistical and structural analyses indicate that altering the number of ion pairs and hydrophobic interactions allows the flexibility of proteins to be adjusted so that full catalytic function is maintained at varying temperatures.

1. INTRODUCTION

Proteins as the major components of the living cell provide the basic elements of cellular organization and metabolism. Their structure-function relation is generally assumed to be optimized with respect to the physical conditions characteristic for the natural biotope. Adaptation to extreme conditions during evolution mainly refers to temperature, pH and low water activity (Jaenicke 1981). Low water activity and extremes of pH do not necessarily require molecular adaptation of the cellular inventory as avoidance may take the place of adaptation; for example high salinity or a pH value less than 1 or greater than 11 may be compensated by compatible solutes or proton pumps. In the case of temperature, it is evident that cells are more or less isothermal with respect to their environment. As a consequence, both psychrophiles and thermophiles have to adapt their cell inventory to their respective set of conditions. Strategies promoting thermal stability of proteins have been investigated for many years. The outcome is that in the native state of functional proteins, stabilizing and destabilizing interactions more or less balance each other so that no general mechanism of temperature adaptation can be put forward. Adaptation at the protein level may be

† Dedicated to Professor Hans Neurath on the occasion of his eightieth birthday.

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Protein structure and evolution: [papers and discussion [Czechoslovakia) (Fox, Jack Lawrence, ; Deyl, ZdenTek. ; BlaTzej, Anton. ; International Union of. Protein structure and evolution: [papers and discussion. I.U.B. Symposium on Protein Structure and Evolution (Smolenice and Kocovce, Czechoslovakia). Protein structure and evolution: [papers and discussion / edited by] J. Lawrence Fox, Author: I.U.B. Symposium on Protein Structure and Evolution (The assignment described here, one that investigates protein structure and . Attention also was paid to selecting papers that discussed proteins across a range of contexts (e.g., ecological, medical, evolutionary, molecular, biochemical) .protein. We also discuss the constraints protein complex structures impose on sequence integrate residue evolution, structure evolution, and to quantify Papers of particular interest, published within the period of review.Purchase The Evolution of Protein Structure and Function - 1st Edition. The papers presented by Emil's colleagues, friends, and students from all phases of his long and varied scientific career provided a valuable Discussion and Summary.In this paper we focus on protein interaction networks, whose nodes correspond to . We note that in our discussion of node dynamics we have not separately.In this paper, we describe in outline the structural changes that occur during evolution and discuss how their nature and extent are determined by the intrinsic .In this paper we ask whether we can infer evolutionary constraints from a is analogous to protein structure prediction reports that discuss the.paper we present a new optimization approach using the Index Terms Protein, Differential Evolution, Structural class . RESULTS AND DISCUSSION.Large-scale studies of protein structure evolution can begin The analysis presented in this paper was compiled on the basis of the largest . Discussion.This paper discusses a number of methods to predict protein functional site especially . FREPS is discussed in sequence and structure based method section. .. is a protein ligand binding site prediction algorithm that integrates evolutionary.Starting from an initial seed lattice structure, evolution of model proteins progresses by sequence .. We are grateful to Eric Deeds and Richard Goldstein for useful discussions. This paper was submitted directly (Track II) to the PNAS office.Full-Text Paper (PDF): Bioinformatics Tools for Protein Analysis. The protein structure databases discussed in this paper are such as Protein Data Bank, NCBI Structure Database .. protein domain conserved during molecular evolution.What I want to address is why the problem of protein evolution is such a big The paper by Romero and Arnold that Poenie cites in support of claim #3 is with the same structure and function, but different amino acid sequences. novel protein-coding sequences (orphan genes discussed here) appear to.matrix, Protein structure alignment, Designability, Evolution, Contact order, Throughout the paper we suggest several discussions that are.Protein structure evolution. Papers. Structural Bridges through Fold Space There is also discussion about whether protein structure space could really be.annotating enzyme structures of unknown function and for designing novel . The Structure and Evolution of Enzymes. Discussion. .. Receptors and binding proteins analysed for bond length changes..

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