

Chapter 16 Lab **Amino Acid Sequences: Indicators of Evolution**

Problem

How can you use proteins to determine how closely organisms are related?

Introduction

Biologists have many ways to study evolution. They can use fossils to learn about ancient species. They can compare the anatomy of modern species. They can observe the order in which cells develop in embryos. All these clues reflect what took place over time at the molecular level. DNA and proteins, the genes and the products of genes, provide powerful evidence for descent with modification.

As DNA changes over time, the proteins that are produced by the DNA change too. The result is that many organisms have similar, but not identical, versions of a given protein. Differences among these homologous proteins provide clues to evolution.

In Part A of this lab, you will compare amino acid sequences of hemoglobin from eight mammals. In Part B, you will analyze data about sequences in a second protein—cytochrome *c*. In Part B, the organisms will be more varied.

Skills Focus

Analyze Data, Graph, Draw Conclusions

Build Vocabulary

Term	Definition
compare	To examine two or more things in order to discover ways in which they are alike, or <i>comparable</i> , and ways in which they are different
sequence	The order in which things are arranged, actions are carried out, or events happen
related	Connected by a common, or shared, origin; descended from a common ancestor
identical	Exactly the same or alike in every way

Big Idea

Molecular biology provides evidence for evolution.

Skills Objectives

Students will be able to

- analyze amino acid sequences of proteins.
- infer the relatedness of species from differences in proteins.

Class Time

40 minutes

Group Size

Individuals

Build Vocabulary

Students will have a more successful lab experience if they understand these terms.

Amino Acid Sequences Indicators Of Evolution

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Amino Acid Sequences Indicators Of Evolution:

The New Foundations of Evolution Jan Sapp, 2009-07-24 This is the story of a profound revolution in the way biologists explore life's history, understand its evolutionary processes, and reveal its diversity. It is about life's smallest entities, deepest diversity, and greatest cellular biomass: the microbiosphere. Jan Sapp introduces us to a new field of evolutionary biology and a new brand of molecular evolutionists who descend to the foundations of evolution on Earth to explore the origins of the genetic system and the primary life forms from which all others have emerged. In so doing, he examines from Lamarck to the present the means of pursuing the evolution of complexity and of depicting the greatest differences among organisms. The *New Foundations of Evolution* takes us into a world that classical evolutionists could never have imagined: a deep phylogeny based on three domains of life and multiple kingdoms, and created by mechanisms very unlike those considered by Darwin and his followers. Evolution by leaps seems to occur regularly in the microbial world where molecular evolutionists have shown the inheritance of acquired genes and genomes are major modes of evolutionary innovation. Revisiting the history of microbiology for the first time from the perspective of evolutionary biology, Sapp shows why classical Darwinian conceptions, centering on questions of the origin of species, were forged without a microbial foundation; why classical microbiologists considered it impossible to know the course of evolution; and why classical molecular biologists considered the evolution of the molecular genetic system to be beyond understanding. In telling this stirring story of scientific iconoclasm, this book elucidates how the new evolutionary biology arose, what methods and assumptions underpin it, and the fiery controversies that continue to shape biologists' understanding of the foundations of evolution today.

[Biotechnology of Microbial Enzymes](#)
Goutam Brahmachari, Arnold L Demain, Jose L Adrio, 2016-07-21 *Biotechnology of Microbial Enzymes: Production, Biocatalysis, and Industrial Applications* provides a complete survey of the latest innovations on microbial enzymes, highlighting biotechnological advances in their production and purification, along with information on successful applications as biocatalysts in several chemical and industrial processes under mild and green conditions. Applications of microbial enzymes in food, feed, and pharmaceutical industries are given particular emphasis. The application of recombinant DNA technology within industrial fermentation and the production of enzymes over the last 20 years have produced a host of useful chemical and biochemical substances. The power of these technologies results in novel transformations, better enzymes, a wide variety of applications, and the unprecedented development of biocatalysts through the ongoing integration of molecular biology methodology, all of which is covered insightfully and in depth within the book. Features research on microbial enzymes from basic science through application in multiple industry sectors for a comprehensive approach. Includes information on metabolic pathway engineering, metagenomic screening, microbial genomes, extremophiles, rational design, directed evolution, and more. Provides a holistic approach to the research of microbial enzymes.

Mammalian Genomics Anatoly Ruvinsky, Jennifer A. Marshall Graves, 2005 Genomics has experienced a dramatic development during the last 15-20 years.

Data from mammalian genomes such as the human mouse and rat have already been published while others such as the dog cattle and chimpanzee will soon follow This book summarizes the current knowledge of mammalian genomics and offers a comparative analysis of genomes known today This analysis includes farm companion and lab animals Topics covered include structural and functional aspects of the mammalian genome mechanisms of genomic changes at the molecular level evolution of DNA sequences comparative chromosome mapping and painting genome databases gene prediction and the use of genomic information to understand inherited diseases Contributors include leading researchers from Europe USA Australia and Japan

Comparative Primate Biology: Systematics, evolution, and anatomy G. Mitchell, Joseph Erwin, Daris Ray Swindler, 1986

The Biology of Pseudomonas L. Nicholas Ornston, 1960

Trends in Comparative Endocrinology and Neurobiology, Volume 1162 Hubert Vaudry, 2009-06-02 This volume is the result of a conference entitled Trends in comparative endocrinology and neurobiology held on September 2 6 2008 in Genoa Italy P v

Hemostasis and Thrombosis, 1968 Monthly with annual cumulation Recurring bibliography from MEDLARS data base Index medicus format Entries arranged under subject review and author sections Subject author indexes

Plant Taxonomy Tod F. Stuessy, 2009-01-01 The field of plant taxonomy has transformed rapidly over the past fifteen years especially with regard to improvements in cladistic analysis and the use of new molecular data The second edition of this popular resource reflects these far reaching and dramatic developments with more than 3 000 new references and many new figures Synthesizing current research and trends Plant Taxonomy now provides the most up to date overview in relation to monographic biodiversity and evolutionary studies and continues to be an essential resource for students and scholars This text is divided into two parts Part 1 explains the principles of taxonomy including the importance of systematics characters concepts of categories and different approaches to biological classification Part 2 outlines the different types of data used in plant taxonomic studies with suggestions on their efficacy and modes of presentation and evaluation This section also lists the equipment and financial resources required for gathering each type of data References throughout the book illuminate the historical development of taxonomic terminology and philosophy while citations offer further study Plant Taxonomy is also a personal story of what it means to be a practicing taxonomist and to view these activities within a meaningful conceptual framework Tod F Stuessy recalls the progression of his own work and shares his belief that the most creative taxonomy is done by those who have a strong conceptual grasp of their own research

The Bacteria: The Biology of pseudomonas, 1960

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in Evolution John J. Marchalonis,1977 Embryos, Genes, and Evolution Rudolf A. Raff,Thomas C. Kaufman,1991
Perspectives on Science and Christian Faith ,1998 *Computer Methods for Macromolecular Sequence Analysis*
Russell F. Doolittle,1996-05-23 This volume supplements Volume 183 in the Methods in Enzymology series and complements
Volume 224 It addresses a variety of areas in which computers are used to manage and manipulate macromolecular
sequence data The manipulations include searching aligning and determining the significance of similarities as well as the
construction of phylogenetic trees that show evolutionary history of related sequences

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