

**AP[®] BIOLOGY
2013 SCORING GUIDELINES**

Question 5

The table below shows the amino acid sequence of the carboxyl-terminal segment of a conserved polypeptide from four different, but related, species. Each amino acid is represented by a three-letter abbreviation, and the amino acid residues in the polypeptide chains are numbered from the amino end to the carboxyl end. Empty cells indicate no amino acid is present.

	Relative Amino Acid Position									
Species	1	2	3	4	5	6	7	8	9	10
I	Val	His	Leu	Val	Glu	Glu	His	Val	Glu	His
II	Val	His	Leu	Lys	Glu	Glu	His	Val	Glu	His
III	Val	His	Leu	Val	Glu	Glu	His	Val		
IV	Val	His	Leu	Val	Arg	Tyr	Ala	Cys	Met	Asp

- (a) Assuming that species I is the ancestral species of the group, **explain** the most likely genetic change that produced the polypeptide in species II and the most likely genetic change that produced the polypeptide in species III. **(2 points maximum)**

Explanation: **1 point per row**

NOTE: Specific names of mutation types are not required.

Species	Genetic Change in DNA / Bases	Result of Change to Polypeptide / Protein
II	mutation / substitution / point mutation / missense mutation	an amino acid change only at position 4 (Val to Lys)
III	mutation (e.g., substitution / insertion / deletion / point mutation / frameshift mutation / nonsense mutation) that introduces a stop codon after the codon for Val	termination of the polypeptide after the Val at position 8

- (b) **Predict** the effects of the mutation on the structure and function of the resulting protein in species IV. **Justify** your prediction. **(2 points maximum)**

Predicted Change (1 point maximum)	Justification of Prediction (1 point maximum)
Protein may have a different structure and a change in function.	Change in amino acid sequence of the protein starting at position 5 could alter the overall structure or local structural regions, interfering with function of the protein.
Protein may have a different structure and no change in function.	Change in amino acid sequence alters the shape / conformation / folding / binding region / regulatory region of the protein, but does not affect the critical functional region(s) of the protein.
Protein structure and function may not be affected.	Change in amino acid sequence does not alter the protein shape / conformation / folding and does not alter function.

Ap Biology 2008 Scoring Guidelines

Holger Gohlke



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Guide to College Majors 2008 Princeton Review, Princeton Review Publishing Staff, 2005-02 Provides information on over three hundred common college majors from accounting to zoology including related fields prior high school subjects possible courses of study and career and salary prospects for graduates

Developing Assessments for the Next Generation

Science Standards National Research Council, Division of Behavioral and Social Sciences and Education, Board on Science Education, Board on Testing and Assessment, Committee on Developing Assessments of Science Proficiency in

K-12, 2014-05-29 Assessments understood as tools for tracking what and how well students have learned play a critical role in the classroom Developing Assessments for the Next Generation Science Standards develops an approach to science assessment to meet the vision of science education for the future as it has been elaborated in A Framework for K 12 Science Education Framework and Next Generation Science Standards NGSS These documents are brand new and the changes they call for are barely under way but the new assessments will be needed as soon as states and districts begin the process of implementing the NGSS and changing their approach to science education The new Framework and the NGSS are designed to guide educators in significantly altering the way K 12 science is taught The Framework is aimed at making science education more closely resemble the way scientists actually work and think and making instruction reflect research on learning that demonstrates the importance of building coherent understandings over time It structures science education around three dimensions the practices through which scientists and engineers do their work the key crosscutting concepts that cut across disciplines and the core ideas of the disciplines and argues that they should be interwoven in every aspect of science education building in sophistication as students progress through grades K 12 Developing Assessments for the Next Generation Science Standards recommends strategies for developing assessments that yield valid measures of student proficiency in science as described in the new Framework This report reviews recent and current work in science assessment to determine which aspects of the Framework s vision can be assessed with available techniques and what additional research and development will be needed to support an assessment system that fully meets that vision The report offers a systems approach to science assessment in which a range of assessment strategies are designed to answer different kinds of questions with appropriate degrees of specificity and provide results that complement one another Developing Assessments for the Next Generation Science Standards makes the case that a science assessment system that meets the Framework s vision should consist of assessments designed to support classroom instruction assessments designed to monitor science learning on a broader scale and indicators designed to track opportunity to learn New standards for science education make clear that new modes of assessment designed to measure the integrated learning they promote are essential The recommendations of this report will be key to making sure that the dramatic changes in curriculum and instruction signaled by Framework and the NGSS reduce inequities in science education and raise the level of science education for all students

A Comprehensive Guide to Toxicology in Nonclinical Drug Development Ali S. Faqi, 2024-02-11 Selected for 2025 Doody's Core Titles in Toxicology A Comprehensive Guide to Toxicology in Nonclinical Drug Development Third Edition is a valuable reference providing a complete understanding of all aspects of nonclinical toxicology in pharmaceutical research. This updated edition has been expanded and redeveloped covering a wide range of toxicological issues in small molecules and biologics. Topics include ADME in drug discovery, pharmacokinetics, toxicokinetics, formulations, and genetic toxicology testing. The book has been thoroughly updated throughout to reflect the latest scientific advances and includes new information on antiviral drugs, anti-diabetic drugs, immunotherapy, and a discussion on post-pandemic drug development challenges and opportunities. This is an essential and practical resource for all toxicologists involved in nonclinical testing in industry, academic, and regulatory settings. Provides updated, unique content not covered in one comprehensive resource including chapters on stem cells, antiviral drugs, anti-diabetic drugs, and immunotherapy. Includes the latest international guidelines for nonclinical toxicology in both small and large molecules. Incorporates practical examples in order to illustrate day-to-day activities and expectations associated with working in nonclinical toxicology. Serpin Structure and Evolution, 2011-11-07 Serpins are a group of proteins with similar structures that were first identified as a set of proteins able to inhibit proteases. This volume in the Methods in Enzymology series comprehensively covers this topic. With an international board of authors, this volume covers subjects such as Crystallography of serpins and serpin complexes, Serpins as hormone transporters, and Production of serpins using cell-free systems. This volume in the Methods in Enzymology series comprehensively covers the topic of serpins. With an international board of authors, this volume covers subjects such as Crystallography of serpins and serpin complexes, Serpins as hormone transporters, and Production of serpins using cell-free systems. **Virtual Screening** Christoph Sotriffer, 2011-03-31 Drug discovery is all about finding small molecules that interact in a desired way with larger molecules, namely proteins and other macromolecules in the human body. If the three-dimensional structures of both the small and large molecule are known, their interaction can be tested by computer simulation with a reasonable degree of accuracy. Alternatively, if active ligands are already available, molecular similarity searches can be used to find new molecules. This virtual screening can even be applied to compounds that have yet to be synthesized, as opposed to real screening that requires cost and labor-intensive laboratory testing with previously synthesized drug compounds. Unique in its focus on the end user, this is a real how-to book that does not presuppose prior experience in virtual screening or a background in computational chemistry. It is both a desktop reference and practical guide to virtual screening applications in drug discovery, offering a comprehensive and up-to-date overview. Clearly divided into four major sections, the first provides a detailed description of the methods required for and applied in virtual screening, while the second discusses the most important challenges in order to improve the impact and success of this technique. The third and fourth practical parts contain practical guidelines and several case studies covering the most important scenarios for new

drug discovery accompanied by general guidelines for the entire workflow of virtual screening studies Throughout the text medicinal chemists from academia as well as from large and small pharmaceutical companies report on their experience and pass on priceless practical advice on how to make best use of these powerful methods

A Comprehensive Guide to Toxicology in Preclinical Drug Development Ali S. Faqi,2012-11-02 A Comprehensive Guide to Toxicology in Preclinical Drug Development is designed for toxicologists who need a thorough understanding of the drug development process This multi contributed reference will provide a detailed picture of the complex and highly interrelated activities of preclinical toxicology in both small molecules and biologics

Critical Care Study Guide Gerard J. Criner,Rodger E. Barnette,Gilbert E. D'Alonzo,2010-06-27 Critical care medicine is a dynamic and exciting arena where complex pathophysiologic states require extensive knowledge and up to date clinical information An extensive knowledge of basic pathophysiology as well as awareness of the appropriate diagnostic tests and treatments that are used to optimize care in the critically ill is essential Since our first edition 7 years ago new information crucial to the care and understanding of the critically ill patient has rapidly accumulated Because this knowledge base crosses many different disciplines a comprehensive multidisciplinary approach presenting the information is essential similar to the multidisciplinary approach that is used to care for the critically ill patient We have strived to provide this content in an easily digestible format that uses a variety of teaching tools to facilitate understanding of the presented concepts and to enhance information retention To meet the demand to provide comprehensive and diverse education in order to understand the pathogenesis and optimum care of a variety of critical illnesses we have substantially revised the prior topics in the first edition with updated information We have also markedly expanded the number of topics covered to include acute lung injury and the acute respiratory distress syndrome an expanded discussion of the physiology and operation of mechanical ventilation obstetrical care in the ICU neurosurgical emergencies acute coronary syndromes cardiac arrhythmias role of whole body rehabilitation in the ICU ethical conduct of human research in the ICU and nursing care of the ICU patient

Tuberculosis Drug Discovery and Development 2019 Giovanna Riccardi,Claudia Sala,2020-11-24 Tuberculosis TB is an infectious disease caused by Mycobacterium tuberculosis and still represents one of the global health threats to mankind The World Health Organization estimated more than 10 million new cases and reported more than 1.5 million deaths in 2019 thus ranking TB among the main causes of death due to a single pathogen Standard anti TB therapy includes four first line antibiotics that should be administered for at least six months However in the case of multi and extensively drug resistant TB second line medications must be used and these frequently cause severe side effects resulting in poor compliance Developing new anti TB drug candidates is therefore of utmost importance In this Special Issue dedicated to Tuberculosis Drug Discovery and Development we present the main and latest achievements in the fields of drug and target discovery host directed therapy anti virulence drugs and describe the development of two advanced compounds macozinone and delpazolid In addition this Special Issue provides an historical

perspective focused on Carlo Forlanini the inventor of pneumothorax for TB treatment and includes an overview of the state of the art technologies which are being exploited nowadays in TB drug development Finally a summary of TB vaccines that are either approved or undergoing clinical trials concludes the Special Issue Structural Biology in Drug Discovery Jean-Paul Renaud, 2020-02-05 With the most comprehensive and up to date overview of structure based drug discovery covering both experimental and computational approaches Structural Biology in Drug Discovery Methods Techniques and Practices describes principles methods applications and emerging paradigms of structural biology as a tool for more efficient drug development Coverage includes successful examples academic and industry insights novel concepts and advances in a rapidly evolving field The combined chapters by authors writing from the frontlines of structural biology and drug discovery give readers a valuable reference and resource that Presents the benefits limitations and potentiality of major techniques in the field such as X ray crystallography NMR neutron crystallography cryo EM mass spectrometry and other biophysical techniques and computational structural biology Includes detailed chapters on druggability allostery complementary use of thermodynamic and kinetic information and powerful approaches such as structural chemogenomics and fragment based drug design Emphasizes the need for the in depth biophysical characterization of protein targets as well as of therapeutic proteins and for a thorough quality assessment of experimental structures Illustrates advances in the field of established therapeutic targets like kinases serine proteinases GPCRs and epigenetic proteins and of more challenging ones like protein protein interactions and intrinsically disordered proteins **Protein-Ligand Interactions** Holger Gohlke, 2012-04-06 Innovative and forward looking this volume focuses on recent achievements in this rapidly progressing field and looks at future potential for development The first part provides a basic understanding of the factors governing protein ligand interactions followed by a comparison of key experimental methods calorimetry surface plasmon resonance NMR used in generating interaction data The second half of the book is devoted to insilico methods of modeling and predicting molecular recognition and binding ranging from first principles based to approximate ones Here as elsewhere in the book emphasis is placed on novel approaches and recent improvements to established methods The final part looks at unresolved challenges and the strategies to address them With the content relevant for all drug classes and therapeutic fields this is an inspiring and often consulted guide to the complexity of protein ligand interaction modeling and analysis for both novices and experts

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