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Sequence - Evolution - Function is an introduction to the computational approaches that play a critical role in the emerging new branch of biology known as functional genomics.

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The book provides the reader with an understanding of the principles and approaches of functional genomics and of the potential and limitations of computational and experimental approaches to genome analysis.

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This book is intended to serve as an introduction to the computational approaches that play a critical role in this emerging new branch of biology, which deals with genome analysis, linking sequence to function, and has been referred to as genomics, or, more specifically, functional genomics.

Sequence - evolution - function sequence - evolution ...

Identifying protein-coding genes in the genome sequence and predicting the cellular functions of these proteins can be accomplished only by combining powerful computational tools with a variety of experimental approaches from the arsenals of biochemistry, molecular biology, genetics and cell biology.

Sequence - evolution - function sequence - evolution ...

computational approaches, it is usually possible to reliably predict the protein-coding regions in the DNA sequence with

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reasonable (albeit varying) confidence and to get at least some insight into the possible functions of the encoded proteins. Such an analysis proves

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Prev Next > Problems. We included only 20 problems but most of them are large, include multiple questions, and ...

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Comparative genomics is a field of biological research in which the genomic features of different organisms are compared. The genomic features may include the DNA sequence, genes, gene order, regulatory sequences, and other genomic structural landmarks. In this branch of genomics, whole or large parts of genomes resulting from genome projects are compared to study basic biological similarities ...

Comparative genomics - Wikipedia

Study of biological functions of individual proteins, complexes, pathways, etc. based on or at least facilitated by analysis of genome sequences. Gap A space introduced into an alignment to

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compensate for an insertion or deletion in one aligned sequence relative to the other(s); typically designated by a dash.

Glossary - Sequence - Evolution - Function - NCBI Bookshelf

Directed evolution makes it possible to identify undiscovered protein sequences which have novel functions. This ability is contingent on the proteins ability to tolerant amino acid residue substitutions without compromising folding or stability. Directed evolution methods can be broadly categorized into two strategies, asexual and sexual methods.

Protein engineering - Wikipedia

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principles and approaches of functional genomics and of the potential and limitations of computational and experimental approaches to genome analysis.

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