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Harald Tschesche (Ed.)

MODERN METHODS IN PROTEIN- AND NUCLEIC ACID RESEARCH

Modern Methods In Protein And Nucleic Acid Research Review Articles

Harald Tschesche

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in Bioinformatics Raffaele Giancarlo, Sridhar Hannenhalli, 2007-08-24 The refereed proceedings from the 7th International Workshop on Algorithms in Bioinformatics are provided in this volume Papers address current issues in algorithms in bioinformatics ranging from mathematical tools to experimental studies of approximation algorithms to significant computational analyses Biological problems examined include genetic mapping sequence alignment and analysis phylogeny comparative genomics and protein structure In Silico Drug Design Kunal Roy, 2019-02-12 In Silico Drug Design Repurposing Techniques and Methodologies explores the application of computational tools that can be utilized for this approach The book covers theoretical background and methodologies of chem bioinformatic techniques and network modeling and discusses the various applied strategies to systematically retrieve integrate and analyze datasets from diverse sources Other topics include in silico drug design methods 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Computational Methods for Rational Drug Design covers the tools and techniques of drug design with applications to the discovery of small molecule based therapeutics detailing methodologies and practical applications and addressing the challenges of techniques like AI ML and drug design for unknown receptor structures Divided into 23 chapters the contributors address various cutting edge areas of therapeutic importance such as neurodegenerative disorders cancer multi drug resistant bacterial infections inflammatory diseases and viral infections Edited by a highly qualified academic with significant research contributions to the field Computational Methods for Rational Drug Design explores topics including Computer assisted methods and tools for structure and ligand based drug design virtual screening and lead discovery and ADMET and physicochemical assessments In silico and pharmacophore modeling fragment based design de novo drug design and scaffold hopping network based methods and 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