Record Nr. UNINA9910734828903321 Autore Kar Supratik **Titolo** Current Trends in Computational Modeling for Drug Discovery // edited by Supratik Kar, Jerzy Leszczynski Cham:,: Springer International Publishing:,: Imprint: Springer,, Pubbl/distr/stampa 2023 3-031-33871-5 **ISBN** Edizione [1st ed. 2023.] Descrizione fisica 1 online resource (311 pages) Collana Challenges and Advances in Computational Chemistry and Physics, , 2542-4483;;35 Altri autori (Persone) LeszczynskiJerzy Disciplina 541.2 615.19 Soggetti Drugs—Design Molecules-Models Chemistry—Data processing Medicinal chemistry Pharmacology Structure-Based Drug Design Molecular Modelling Computational Chemistry Medicinal Chemistry Lingua di pubblicazione Inglese **Formato** Materiale a stampa Livello bibliografico Monografia Nota di contenuto SBDD and its challenges -- In silico discovery of class IIb HDAC inhibitors: The state of art -- Role of computational modelling in drug discovery for Alzheimer's disease -- Computational Modeling in the Development of Antiviral Agents -- Targeted computational approaches to identify potential inhibitors for Nipah virus -- Role of Computational Modelling in Drug Discovery for HIV -- Recent insight of the emerging severe fever with thrombocytopenia syndrome virus: drug discovery, therapeutic options, and limitations -- Computational toxicological aspects in drug design and discovery, screening adverse effects -- Read-Across and RASAR tools from the DTC Laboratory --

Databases for Drug Discovery and Development.

This contributed volume offers a comprehensive discussion on how to

Sommario/riassunto

design and discover pharmaceuticals using computational modeling techniques. The different chapters deal with the classical and most advanced techniques, theories, protocols, databases, and tools employed in computer-aided drug design (CADD) covering diverse therapeutic classes. Multiple components of Structure-Based Drug Discovery (SBDD) along with its workflow and associated challenges are presented while potential leads for Alzheimer's disease (AD), antiviral agents, anti-human immunodeficiency virus (HIV) drugs, and leads for Severe Fever with Thrombocytopenia Syndrome Virus (SFTSV) disease are discussed in detail. Computational toxicological aspects in drug design and discovery, screening adverse effects, and existing or future in silico tools are highlighted, while a novel in silico tool, RASAR, which can be a major technique for small to big datasets when not much experimental data are present, is presented. The book also introduces the reader to the major drug databases covering drug molecules. chemicals, therapeutic targets, metabolomics, and peptides, which are great resources for drug discovery employing drug repurposing, high throughput, and virtual screening. This volume is a great tool for graduates, researchers, academics, and industrial scientists working in the fields of cheminformatics, bioinformatics, computational biology, and chemistry.