

1. Record Nr.	UNINA9910830794003321
Titolo	De novo molecular design // edited by Gisbert Schneider ; cover design Mannheim Formgeber
Pubbl/distr/stampa	Weinheim, Germany : , : Wiley-VCH, , 2014 ©2014
ISBN	3-527-67703-8 3-527-67701-1 3-527-67700-3
Descrizione fisica	1 online resource (578 p.)
Altri autori (Persone)	SchneiderGisbert FormgeberMannheim
Disciplina	639.485
Soggetti	Drugs - Design Molecular structure
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references at the end of each chapters and index.
Nota di contenuto	De novo Molecular Design; Title Page; Copyright; Contents; List of Contributors; Foreword; Preface; Chapter 1 De Novo Design: From Models to Molecules; 1.1 Molecular Representation; 1.2 The Molecular Design Cycle; 1.3 Receptor-Ligand Interaction; 1.4 Modeling Fitness Landscapes; 1.4.1 Na ive Bayes Classifier; 1.4.2 Artificial Neural Network; 1.4.3 Support Vector Machine; 1.4.4 Gaussian Process; 1.5 Strategies for Compound Construction; 1.6 Strategies for Compound Scoring; 1.6.1 Receptor-Based Scoring; 1.6.2 Ligand-Based Scoring; 1.7 Flashback Forward: A Brief History of De Novo Drug Design 1.8 ConclusionsAcknowledgments; References; Chapter 2 Coping with Complexity in Molecular Design; 2.1 Introduction; 2.2 A Simple Model of Molecular Interactions; 2.3 Enhancements to the Simple Complexity Model; 2.4 Enumerating and Sampling the Complexity of Chemical Space; 2.5 Validation of the Complexity Model; 2.6 Reductionism and Drug Design; 2.7 Complexity and Information Content as a Factor in De Novo Design; 2.8 Complexity of Thermodynamic Entropy and Drug Design; 2.9 Complex Systems, Emergent Behavior, and Molecular

Design; Acknowledgments; References; Chapter 3 The Human Pocketome  
3.1 Predicted Pockets 3.2 Compilation of the Validated Human Pocketome; 3.3 Diversity and Redundancy of the Human Pocketome; 3.4 Compound Activity Prediction by Ligand-Pocket Docking and Scoring; 3.4.1 Optimizing Pocket Sets for Reliable Docking and Scoring Results; 3.4.2 Difficult Cases: Unusually Large and Multifunctional Pockets; 3.5 Pocketome-Derived 3D Chemical Fields as Activity Prediction Models; 3.6 Clustering the Ligands by Function and Subpockets; 3.7 Conclusions; Acknowledgments; References; Chapter 4 Structure-Based De Novo Drug Design; 4.1 Introduction  
4.2 Current Progress in SBDND Methodologies 4.2.1 Identification of Binding Site; 4.2.2 Design of Molecules; 4.2.2.1 Atom-Based versus Fragment-Based Methods; 4.2.2.2 Pharmacophore-Based Methods; 4.2.3 Searching the Chemical Space; 4.2.3.1 Monte Carlo-Based Methods; 4.2.3.2 Evolutionary Algorithms; 4.2.4 Scoring Methods; 4.2.4.1 Force-Field-Based Scoring Functions; 4.2.4.2 Empirical Scoring Functions; 4.2.4.3 Knowledge-Based Scoring Functions; 4.2.4.4 Consensus Scoring; 4.2.5 Synthetic Accessibility; 4.3 Recent Applications of Structure-Based De Novo Design; 4.4 Perspectives and Conclusion  
Acknowledgment References; Chapter 5 De Novo Design by Fragment Growing and Docking; 5.1 Introduction; 5.2 Case Study I: High-Throughput Screening with Dr Feils; 5.2.1 Target Identification; 5.2.2 Small-Molecule Library Design; 5.2.2.1 Computer Docking; 5.2.2.2 Pharmacophore Searching; 5.2.3 High-Throughput Screening; 5.2.4 Optimization; 5.3 Case Study II: Fragment-Based Drug Design with Dr Goode; 5.3.1 Library Generation; 5.3.1.1 Computational Techniques for Library Refinement; 5.3.2 Detection Methods; 5.3.2.1 Functional/High-Concentration Screening  
5.3.2.2 Fluorescence-Based Thermal Shift Assay (TSA)

---

Sommario/riassunto

Systematically examining current methods and strategies, this ready reference covers a wide range of molecular structures, from organic-chemical drugs to peptides, proteins and nucleic acids, in line with emerging new drug classes derived from biomacromolecules. A leader in the field and one of the pioneers of this young discipline has assembled here the most prominent experts from across the world to provide first-hand knowledge. While most of their methods and examples come from the area of pharmaceutical discovery and development, the approaches are equally applicable for molecular probe

---