

1. Record Nr.	UNINA9910144273403321
Titolo	Pharmacophores and pharmacophore searches [[electronic resource] /] / edited by Thierry Langer and Rmy D. Hoffmann
Pubbl/distr/stampa	Weinheim, : Wiley-VCH [Chichester, : John Wiley, distributor], c2006
ISBN	1-280-72275-4 9786610722754 3-527-60916-4 3-527-60872-9
Descrizione fisica	1 online resource (397 p.)
Collana	Methods and principles in medicinal chemistry ; ; v. 32
Altri autori (Persone)	HoffmannRmy D LangerThierry
Disciplina	615.1901
Soggetti	Drugs - Research - Methodology Drug development Electronic books.
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 and index.
Nota di contenuto	Pharmacophores and Pharmacophore Searches; Contents; Preface; A Personal Foreword; List of Contributors; Part I Introduction; 1 Pharmacophores: Historical Perspective and Viewpoint from a Medicinal Chemist; 1.1 Definitions; 1.1.1 Functional Groups Considered as Pharmacophores: the Privileged Structure Concept; 1.2 Historical Perspective; 1.2.1 Early Considerations About Structure-Activity Relationships; 1.2.2 Early Considerations About the Concept of Receptors; 1.2.3 Ehrlich's "Magic Bullet"; 1.2.4 Fischer's "Lock and Key"; 1.3 Pharmacophores: the Viewpoint of a Medicinal Chemist 1.3.1 Two-dimensional Pharmacophores1.3.1.1 Sulfonamides and PABA; 1.3.1.2 Estrogens; 1.3.2 An Early Three-dimensional Approach: the Three-point Contact Model; 1.3.2.1 Clonidine and Its Interaction with the -Adrenergic Receptor; 1.3.3 Criteria for a Satisfactory Pharmacophore Model [32]; 1.3.4 Combination of Pharmacophores; 1.4 Conclusion; References; Part II Pharmacophore Approaches; 2 Pharmacophore Model Generation Software Tools; 2.1 Introduction; 2.2

Molecular Alignments; 2.2.1 Handling Flexibility; 2.2.2 Alignment Techniques; 2.2.3 Scoring and Optimization; 2.3 Pharmacophore Modeling  
2.3.1 Compound Structures and Conformations 2.3.2 Representation of Interactions in the Pharmacophore Models; 2.3.3 Conformational Expansion; 2.3.4 Comparison; 2.3.5 Pharmacophores, Validation and Usage; 2.4 Automated Pharmacophore Generation Methods; 2.4.1 Methods Using Pharmacophore Features and Geometric Constraints; 2.4.1.1 DISCO, GASP and GALAHAD; 2.4.1.2 Catalyst; 2.4.1.3 Phase; 2.4.1.4 Pharmacophores in MOE; 2.4.2 Field-based Methods; 2.4.2.1 CoMFA; 2.4.2.2 XED; 2.4.3 Pharmacophore Fingerprints; 2.4.3.1 ChemX/ChemDiverse, PharmPrint, OSPPREYS, 3D Keys, Tuples; 2.5 Other Methods  
2.5.1 SCAMPI 2.5.2 THINK; 2.5.3 Feature Trees; 2.5.4 ILP; 2.6 Conclusions; References; 3 Alignment-free Pharmacophore Patterns - A Correlation-vector Approach; 3.1 Introduction; 3.2 The Correlation-vector Approach; 3.2.1 The Concept; 3.2.2 Comparison of Molecular Topology: CATS; 3.2.3 Comparison of Molecular Conformation: CATS3D; 3.2.4 Comparison of Molecular Surfaces: SURFCATS; 3.3 Applications; 3.3.1 Retrospective Screening Studies; 3.3.2 Scaffold-hopping Potential; 3.3.3 Prospective Virtual Screening; 3.4 New Methods Influenced by the Correlation-vector Approach  
3.4.1 "Fuzzy" Pharmacophores: SQUID 3.4.2 Feature Point Pharmacophores: FEPOPS; 3.5 Conclusions; Acknowledgments; Abbreviations; References; 4 Feature Trees: Theory and Applications from Large-scale Virtual Screening to Data Analysis; 4.1 Introduction: from Linear to Non-linear Molecular Descriptors; 4.2 Creating Feature Trees from Molecules; 4.3 Algorithms for Pairwise Comparison of Feature Trees; 4.3.1 Recursive Division: the Split-search Algorithm; 4.3.2 Subsequently Growing Matchings: the Match-search Algorithm; 4.3.3 Match-Search with Gaps: the Dynamic Match-search Algorithm 4.3.4 Building Multiple Feature Tree Models

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## Sommario/riassunto

This handbook is the first to address the practical aspects of this novel method. It provides a complete overview of the field and progresses from general considerations to real life scenarios in drug discovery research. Starting with an introductory historical overview, the authors move on to discuss ligand-based approaches, including 3D pharmacophores and 4D QSAR, as well as the concept and application of pseudoreceptors. The next section on structure-based approaches includes pharmacophores from ligand-protein complexes, FLIP and 3D protein-ligand binding interactions. The whole is rounded

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