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Nota di contenuto	 Structure-Based Ligand Design; Preface; List of Contributors; Contents; 1 Rational Design of Bioactive Molecules; 1.1 Introduction; 1.1.1 From Ligand Design to Drug Discovery; 1.2 Source of Structural Information; 1.3 Classes of Therapeutic Agents; 1.4 Protein-Ligand Interaction; 1.4.1 Covalent versus Noncovalent Inhibitors; 1.4.2 Nonbonded Interactions in Protein-Ligand Complexes; 1.4.3 HydrogenBonds; 1.4.4 The Role of Solvent in Polar Protein-Ligand Interactions; 1.4.5 Lipophilic Interactions; 1.4.6 Criteria for Strong Protein-Ligand Interactions 1.5 Approaches to Structure-Based Ligand Design1.5.1 Ligands Derived from Substrate or Natural Ligand; 1.5.2 Structures Derived from 3D Database Searches; 1.5.3 De-Novo Design of Ligands; 1.6 Methods and Toois used in Structure-Based Ligand Design; 1.7 Outlook and Future Developments; References; 2 Examples of Active Areas of Structure- Based-Design; 2.1 Thrombin Inhibitors; 2.2 Design of Orally Active Inhibitors of Elastase; 2.3 Dorzolamide:A Success Story of Structure-

1.

	 Based Drug Design; 2.4 Inhibitors of Serine Esterases; 2.4.1 Human Pancreatic Lipase (hPL) 2.4.2 Model of the Trilaurin Triglyceride Substrate Binding2.4.3 Tetrahydrolipstatin (THL); 2.5 Acetylcholinesterase (AChE); 2.5.1 Model of the Acetylcholine Substrate Binding; 2.5.2 Physostigmine; 2.5.3 Eisai E2020; References; 3 From Renin to HIV-1 Protease; 3.1 Introduction; 3.2 Renin; 3.2.1 Catalytic Site Binding; 3.2.2 Backbone Variations; 3.2.3 Subsite Interdependencies; 3.2.4 Renin Crystal Structure; 3.2.5 Summary - Renin Modeling; 3.3 HIV-1 Protease; 3.3.1 3D Structures of HIV-1 Protease; 3.3.2 HIV-1 Protease Nonpeptide Inhibitors 3.3.3 Docking/Modeling HIV-1 Protease Nonpeptide Inhibitors 3.3.3 Docking/Modeling HIV-1 Protease versus Renin Structure-Based Design; 3.5 Current Limitations/Future Perspective; 3.6 Conclusion; References; 4 Zinc Endoproteases: A Structural Superfamily; 4.1 Introduction; 4.2 Structural Classification of Zinc Endopeptidase Families; 4.2.1 Short Spacer or Metzincins Family; 4.2.2 Long Spacer or Gluzincins Family; 4.3 Overview of Inhibitor Design; 4.4 Current Limitations; 4.5 Future Prospects; References; 5 Structure-Based Design of Potent Beta-Lactamase Inhibitors; 5.1 Introduction 5.2 Structure of Citrobacter freundii Class C Beta-Lactamase5.3 Model of the Mechanism of Action: Cleavage of Penicillin G; 5.4 Structure of the Complex with Aztreonam; 5.5 Design of Inhibitors; 5.6 Kinetics of the Inhibition Reaction; 5.7 Hydrolysis by Class A Beta-Lactamases; 5.8 X-Ray Structure of the Complex with a Bridged Monobactam; 5.9 Structure-Activity Relationship among Bridged Monobactam; 5.9 Structure-Activity Relationship among Bridged Monobactam; 5.10 Conclusion; References; 6 Inhibition of Sialidase; 6.1 Introduction; 6.2 Influenza: Disease and Virus; 6.3 Structure of Sialidase; 6.4 Mechanism of Catalysis 6.5 Binding of Substrate and Transition State Mimics
Sommario/riassunto	Most drugs bind to a clearly defined macromolecular target that is complementary in terms of structure and chemistry. This observation is the basic paradigm of structure-based ligand design. Although this method first emerged in the 1980s, it has already become a powerful tool for pharmaceutical research. Much has been learned, however, since the first attempts to discover drugs on the basis of available biochemical and structural data. Nowadays, structure-based ligand design is an established method for creating drugs with new structural features, for modifying binding activities and pharmaco