

1. Record Nr.	UNINA9910841396003321
Titolo	Reviews in computational chemistry . 9 [[electronic resource] /] / edited by Kenny B. Lipkowitz and Donald B. Boyd
Pubbl/distr/stampa	New York, : Wiley-VCH, 1996
ISBN	1-282-30837-8 9786612308376 0-470-12586-1 0-470-12613-2
Descrizione fisica	1 online resource (318 p.)
Collana	Reviews in computational chemistry ; ; 9
Altri autori (Persone)	LipkowitzKenny B BoydDonald B
Disciplina	542.85 542/.8
Soggetti	Chemistry - Data processing Chemistry - Mathematics
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 indexes.
Nota di contenuto	Reviews in Computational Chemistry 9; Contents; Peptide Mimetic Design with the Aid of Computational Chemistry; Introduction; Peptide Mimetic Design Considerations; Case Studies in Peptide Mimetic Design; Human Leukocyte Elastase; The Renin-Angiotensin System; Renin; Angiotensin-Converting Enzyme; Angiotensin II; Combined Angiotensin-Converting Enzyme and Neutral Endopeptidase; Human Immunodeficiency Virus Protease; CD4; Thermolysin; Collagenase; α -Amylase; Fibrinogen; Thrombin; Endothelin-1; Somatostatin; Growth Hormone; Oxytocin; Neurotensin; Enkephalin; Dopamine Receptor Modulating Peptide Thyrotropin-Releasing HormoneSubstance P; R-Loop of Interleukin 1 α ; Bradykinin; Complementarity-Determining Regions; Gramicidin-S; Hypertrehalosemic Hormone; Erabutoxin B; Jaspamide; Taste Molecules; Other Mimetics; Summary of Computational Chemistry Techniques Applied to Peptide Mimetic Design; Nomenclature; Acknowledgment; References; Free Energy by Molecular Simulation; Introduction; Classical Statistical Thermodynamical Background; Computer Simulation

Methods; Hamiltonian; Monte Carlo Simulations; Molecular Dynamics Simulations; Thermodynamic Perturbation; Thermodynamic Integration Thermodynamic Cycles Potentials of Mean Force; Free Energy Evaluations in Practice; Hamiltonian Coupling; Creation and Annihilation of Atoms; Constraints; Conformational Isomeric States; Long-Range Interactions; Boundary Conditions; Error Analysis; Sensitivity of Calculated Free Energies to Force Field Parameters; Electronic Polarization; Atomic Replacement Calculations; Recommendations; Free Energy Methodology; Choice of Pathway; Standard Protocol; Analysis of Results; Conclusion; Acknowledgment; References

The Application of Molecular Modeling Techniques to the Determination of Oligosaccharide Solution Conformations Introduction; Carbohydrate Conformational Analysis: The Motivation and the Challenge; Electronic Effects and Carbohydrate Conformation; Carbohydrate Force Fields: An Overview; Hard Sphere Exo-Anomeric (HSEA) and Monte Carlo Methods; MM2/MM3; Macromolecular Force Fields and Molecular Dynamics Simulations; Role of Water-Sugar Interactions; Conclusions; References; Molecular Mechanics Calculated Conformational Energies of Organic Molecules: A Comparison of Force Fields; Introduction

The Principles of Molecular Mechanics Forms of Potential Energy Functions; Bond Stretching/Compression Functions; Bond Angle Bending Functions; Torsional Functions; Van der Waals Functions; Electrostatic Functions; Cross-Terms; Conjugated Systems; Parameterization; Comparisons of Calculated Conformational Energies; Reproducibility of Conformational Energies; Summary and Conclusions; Acknowledgments; References; Molecular Shape Descriptors; Introduction; Hierarchical Levels of Molecular Shape and Shape Descriptors; Some Notions Regarding Molecular Shape and Scaling Classification of Molecular Models and Shape Descriptors

Sommario/riassunto

A select group of scientists from around the world join in this volume to create unique chapters aimed at both the novice molecular modeler and the expert computational chemist. Chapter 1 shows how molecular modeling of peptidomimetics plays a key role in drug discovery. Specific examples of successful computer-aided drug design are spelled out. Chapter 2 is a definitive exposition on thermodynamic perturbation and thermodynamic integration approaches in molecular dynamics simulations. Three additional chapters elucidate molecular modeling of carbohydrates, the best empirical force fields to u
