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Nota di contenuto	Cover; Title Page; Copyright; Contents; Preface; List of Contributors; Contributors to Previous Volumes; Chapter 1 Free-Energy Calculations with Metadynamics: Theory and Practice; Introduction; Molecular Dynamics and Free-Energy Estimation; Molecular Dynamics; Free-Energy Landscapes; A Toy Model: Alanine Dipeptide; Biased Sampling; Adaptive Biasing with Metadynamics; Reweighting; Well-Tempered Metadynamics; Reweighting; Metadynamics How-To; The Choice of the CV(s); The Width of the Deposited Gaussian Potential; The Deposition Rate of the Gaussian Potential A First Test Run Using Gyration Radius A Better Collective Variable: Dihedral Angle; Well-Tempered Metadynamics Using Gyration Radius; Well-Tempered Metadynamics Using Dihedral Angle ; Advanced Collective Variables; Path-Based Collective Variables; Collective Variables Based on Dimensional Reduction Methods; Template-Based Collective Variables; Potential Energy as a Collective Variable; Improved Variants; Multiple Walkers Metadynamics; Replica Exchange Metadynamics; Bias Exchange Metadynamics; Adaptive Gaussians; Conclusion; Acknowledgments; Appendix A: Metadynamics Input Files with PLUMED References Chapter 2 Polarizable Force Fields for Biomolecular Modeling; Introduction; Modeling Polarization Effects; Induced Dipole

Models; Classic Drude Oscillators; Fluctuating Charges; Recent Developments; AMOEBA; SIBFA; NEMO; CHARMM-Drude; CHARMM-FQ; X-Pol; PFF; Applications; Water Simulations; Ion Solvation; Small Molecules; Proteins; Lipids; Continuum Solvents for Polarizable Biomolecular Solutes; Macromolecular X-ray Crystallography Refinement; Prediction of Organic Crystal Structure, Thermodynamics, and Solubility; Summary; Acknowledgment; References

Chapter 3 Modeling Protein Folding Pathways Introduction; Outline of this Chapter; Protein Simulation Methodology; Force Fields, Models and Solvation Approaches; Unfolding: The Reverse of Folding; Elevated Temperature Unfolding Simulations; Biological Relevance of Forced Unfolding; Biased or Restrained MD; Characterizing Different States; Protein Folding and Refolding; Folding in Families; Conclusions and Outlook; Acknowledgment; References; Chapter 4 Assessing Structural Predictions of Protein-Protein Recognition: The CAPRI Experiment; Introduction; Protein-Protein Docking

A Short History of Protein-Protein Docking Major Current Algorithms; The CAPRI Experiment; Why Do Blind Predictions?; Organizing CAPRI; The CAPRI Targets; Creating a Community; Assessing Docking Predictions; The CAPRI Evaluation Procedure; A Survey of the Results of 12 Years of Blind Predictions on 45 Targets; Recent Developments in Modeling Protein-Protein Interaction; Modeling Multicomponent Assemblies. The Multiscale Approach; Genome-Wide Modeling of Protein-Protein Interaction; Engineering Interactions and Predicting Affinity; Conclusion; Acknowledgments; References

Chapter 5 Kinetic Monte Carlo Simulation of Electrochemical Systems

Sommario/riassunto

The Reviews in Computational Chemistry series brings together leading authorities in the field to teach the newcomer and update the expert on topics centered around molecular modeling, such as computer-assisted molecular design (CAMD), quantum chemistry, molecular mechanics and dynamics, and quantitative structure-activity relationships (QSAR). This volume, like those prior to it, features chapters by experts in various fields of computational chemistry. Topics in Volume 28 include: Free-energy Calculations with Metadynamics Polarizable Force Fields for Biomolecular Modeling Modeling Protei
