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Nota di bibliografia	Includes bibliographical references at the end of each chapters and index
Nota di contenuto	Protein Engineering Handbook; Contents; Preface; List of Contributors; Volume 1; 1 Guidelines for the Functional Analysis of Engineered and Mutant Enzymes; 1.1 Introduction; 1.2 Steady-State Kinetics; 1.3 Enzyme Assays and the Acquisition of Initial Velocity Data; 1.3.1 Biological Sample Appropriate for Assay; 1.3.2 Enzymatic Assays; 1.3.3 Analysis of Initial Rate Data; 1.3.4 Determination of Functional Catalytic Site Concentrations; 1.4 Steady-State Kinetic Parameters and Their Interpretation; 1.4.1 pH-Dependence of Steady-State Kinetic Parameters; 1.4.2 Analysis of Two-Substrate Enzymes 1.5 Concluding RemarksReferences; 2 Engineering Enantioselectivity in Enzyme-Catalyzed Reactions; 2.1 Introduction; 2.2 Molecular Basis for Enantioselectivity; 2.2.1 Enzymes Stabilize Transition States for Fast-Reacting Enantiomers Better than Slow-Reacting Enantiomers; 2.2.2 The Slow-Reacting Enantiomer Fits by Exchanging Two Substituents; 2.2.3 The Slow Enantiomer Fits by an Umbrella-Like Inversion; 2.3 Qualitative Predictions of Enantioselectivity; 2.3.1 Comparing Substrate

Structures Leads to Empirical Rules and Box Models; 2.3.2 Computer Modeling Based on X-Ray Structures of Enzymes
2.3.3 What Is Missing from Current Computer Modeling?2.4 Protein Engineering to Increase or Reverse Enantioselectivity; 2.4.1 Mutations Closer to the Active Site Increase Enantioselectivity More Effectively than Mutations Far from the Active Site; 2.4.2 Reversing Enantioselectivity by Exchanging Locations of Binding Sites or a Catalytic Group; 2.5 Concluding Remarks; References; 3 Mechanism and Catalytic Promiscuity: Emerging Mechanistic Principles for Identifi cation and Manipulation of Catalytically Promiscuous Enzymes; 3.1 Introduction; 3.2 Calculation of Rate Accelerations
3.3 Catalytic Features and Their Propensity for Promiscuity3.3.1 Metal Ions; 3.3.2 Recognition of Transition State Charges: Analysis of the Nature of the Transition State; 3.3.3 Catalytic Dyads and Triads; 3.3.4 General Acid/Base Catalysts in Promiscuous Functional Motifs in Catalytic Superfamilies; 3.4 Steric Effects and Structural Constriction in the Active Site: Product Promiscuity; 3.5 Medium Effects in Enzyme Active Sites; 3.6 Conclusions; References; 4 -Value Analysis of Protein Folding Transition States; 4.1 Introduction; 4.2 Theoretical Principles of Protein Engineering
4.2.1 Overview4.2.2 Basic Concepts; 4.2.3 Theory of -Value Analysis; 4.2.4 Relationship between and Leffler ; 4.2.5 Linear Free-Energy Relationships and Denaturant Concentration; 4.3 Guidelines for the Determination of Accurate -Values; 4.3.1 Buffer Preparation and Selection; 4.3.2 Optimization of Experimental Conditions; 4.3.3 Equilibrium Denaturation Experiments; 4.3.3.1 Practical Considerations; 4.3.3.2 Curve-Fitting; 4.3.4 Kinetic Measurements; 4.3.4.1 Practical Considerations; 4.3.4.2 Curve Fitting; 4.3.4.3 Error Analysis for Chevron Plots; 4.4 Conclusions; Acknowledgments
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Sommario/riassunto

Unparalleled in size and scope, this new major reference integrates academic and industrial knowledge into a single resource, allowing for a unique overview of the entire field. Adopting a systematic and practice-oriented approach, and including a wide range of technical and methodological information, this highly accessible handbook is an invaluable 'toolbox' for any bioengineer. In two massive volumes, it covers the full spectrum of current concepts, methods and application areas