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Nota di contenuto	Engineering the Genetic Code; Foreword; Contents; Preface; 1 Introduction; 1.1 Classical Approaches to Protein Modification; 1.2 Peptide Synthesis, Semisynthesis and Chemistry of Total Protein Synthesis; 1.3 Chemoselective Ligations Combined with Biochemical Methods; 1.4 Methods and Approaches of Classical Protein Engineering; 1.5 Genetically Encoded Protein Modifications - Reprogramming Protein Translation; 1.6 Basic Definitions and Taxonomy; References; 2 A Brief History of an Expanded Amino Acid Repertoire; 2.1 The ""Golden Years"" of Molecular Biology and Triplet Code Elucidation 2.2 Early Experiments on the Incorporation of Amino Acid Analogs in Proteins2.3 Test Tube (Cell-free) Synthesis of Proteins and Early Incorporation Experiments; 2.4 Noncanonical Amino Acids as Tools for Studying Cell Metabolism, Physiology, Protein Processing and Turnover; 2.5 Problem of Proofs and Formal Criteria for Noncanonical Amino Acid Incorporation; 2.6 Recent Renaissance - Genetic Code Engineering; References; 3 Basic Features of the Cellular Translation Apparatus; 3.1 Natural Laws, Genetic Information and the ""Central Dogma"" of

Molecular Biology

3.2 Cellular Investments in Ribosome-mediated Protein Synthesis

3.3 Molecular Architecture of AARS; 3.4 Structure and Function of the tRNA Molecule; 3.5 Aminoacylation Reaction; 3.6 AARS:tRNA Interactions - Identity Sets; 3.7 Translational Proofreading; 3.8 Ribosomal Decoding - A Brief Overview; 3.9 Codon Bias and the Fidelity of Protein Synthesis; 3.10 Preprogrammed Context-dependent Recoding: fMet, Sec, Pyl, etc.; 3.11 Beyond Basic Coding - Posttranslational Modifications; References;

4 Amino Acids and Codons - Code Organization and Protein Structure

4.1 Basic Features and Adaptive Nature of the Universal Genetic Code

4.2 Metabolism and Intracellular Uptake of Canonical Amino Acids; 4.3 Physicochemical Properties of Canonical Amino Acids; 4.4 Reasons for the Occurrence of Only 20 Amino Acids in the Genetic Code; 4.5 What Properties of Amino Acids are Best Preserved by the Genetic Code?; 4.6 Evolutionary Legacy: Dual Nature of Conserved Code and Finite Number of Protein Folds; 4.7 Natural Variations in Assignment of Codons of the Universal Genetic Code; 4.7.1 Nucleoside Modifications and Codon Reassignments

4.8 Codon Reassignment Concepts Possibly Relevant to Code

Engineering 4.8.1 Genome Size, Composition, Complexity and Codon Reassignments; 4.8.2 Stop Codon Takeover, Codon Capture and Codon Ambiguity; References; 5 Reprogramming the Cellular Translation

Machinery; 5.1 Enzyme Specificity of Aminoacyl-tRNA Synthetases (AARS) and Code Interpretation; 5.1.1 Living Cells as Platforms for Amino Acid Repertoire Expansion; 5.1.2 Uptake, Toxicity and Metabolic Fate of Noncanonical Amino Acids; 5.1.2.1 General Considerations; 5.1.2.2 Amino Acid Transport

5.1.2.3 Metabolic Conversions and Toxicity of Analogs and Surrogates

Sommario/riassunto

The ability to introduce non-canonical amino acids in vivo has greatly expanded the repertoire of accessible proteins for basic research and biotechnological application. Here, the different methods and strategies to incorporate new or modified amino acids are explained in detail, including a lot of practical advice for first-time users of this powerful technique. Novel applications in protein biochemistry, genomics, biotechnology and biomedicine made possible by the expansion of the genetic code are discussed and numerous examples are given. Essential reading for all molecular life s