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	3.2 Cellular Investments in Ribosome-mediated Protein Synthesis3.3 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 Code4.2 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 Engineering4.8.1 Genome Size, Composition, Complexity and Codon Reassignments; 4.8.2 Stop Codon Takeover, Codon Capture and Codon Ambiguity; References; 5 Reprograming 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