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Information Criterion.; Akaike Information Criterion; Pedro Larranaga and Concha Bielza; Algorithm; Matthew He; Alignment (Domain Alignment, Repeats Alignment); Jaap Heringa; Alignment Score; Laszlo Patthy; Allele-Sharing Methods (Non-parametric Linkage Analysis) Mark McCarthy, Steven Wiltshire and Andrew Collins; Allelic Association; Mark McCarthy, Steven Wiltshire and Andrew Collins; Allen Brain Atlas; Dan Bolser; Allopatric Evolution (Allopatric Speciation); A.R. Hoelzel; Allopatric Speciation, see Allopatric Evolution.; AlogP; Bissan Al-Lazikani; Alpha carbon, see C (C-Alpha).; Alpha Helix; Roman Laskowski and Tjaart de Beer; Alternative Splicing; Enrique Blanco and Josep F. Abril; Alternative Splicing Gene Prediction, see Gene Prediction, alternative splicing.; Amide Bond (Peptide Bond); Roman Laskowski and Tjaart de Beer; Amino Acid (Residue) Roman Laskowski, Jeremy Baum and Tjaart de Beer; Amino Acid Abbreviations, see IUPAC-IUB Codes.; Amino Acid Composition; Jeremy Baum; Amino Acid Exchange Matrix (Dayhoff Matrix, Log Odds Score, PAM (Matrix), BLOSUM Matrix); Jaap Heringa; AMINO Acid Substitution Matrix, see Amino Acid Exchange Matrix.; Amino-terminus, see N-terminus.; Amphipathic; Roman Laskowski and Tjaart de Beer; Analog (Analogue); Dov Greenbaum; Ancestral Lineage, see Offspring Lineage.; Ancestral State Reconstruction; Sudhir Kumar and Alan Filipiski; Anchor Points; Roland Dunbrack; Annotation Refinement Pipelines, see Gene Prediction; Annotation Transfer (Guilt by Association Annotation); Dov Greenbaum; APBIONET (Asia-Pacific Bioinformatics Network); Pedro Fernandes; Apomorphy; A. R. Hoelzel; APOLLO, see Gene Annotation, visualization tools.; Arc, see Branch (of a Phylogenetic Tree).; Are We There Yet?, see AWTY.; Aromatic; Roman Laskowski and Tjaart de Beer; Array, see Data Structure.; Artificial Neural Networks, see Neural Networks.; ASBCB (The African Society for Bioinformatics and Computational Biology); Pedro Fernandes; Association Analysis (Linkage Disequilibrium Analysis)

Sommario/riassunto

Concise Encyclopaedia of Bioinformatics and Computational Biology, 2nd Edition is a fully revised and updated version of this acclaimed resource. The book provides definitions and often explanations of over 1000 words, phrases and concepts relating to this fast-moving and exciting field, offering a convenient, one-stop summary of the core knowledge in the area. This second edition is an invaluable resource for students, researchers and academics.
