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Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	VStrains: De Novo Reconstruction of Viral Strains via Iterative Path Extraction From Assembly Graphs -- Spectrum preserving tilings enable sparse and modular reference indexing -- Statistically Consistent Rooting of Species Trees under the Multispecies Coalescent Model -- Sequence to graph alignment using gap-sensitive co-linear chaining -- DM-Net: A Dual-Model Network for Automated Biomedical Image Diagnosis -- MTGL-ADMET: A Novel Multi-Task Graph Learning Framework for ADMET Prediction Enhanced by Status-Theory and Maximum Flow -- CDGCN: Conditional de novo Drug generative model using Graph Convolution Networks -- Percolate: an exponential family JIVE model to design DNA-based predictors of drug response -- Translation rate prediction and regulatory motif discovery with multi-task learning -- Computing shortest hyperpaths for pathway inference in cellular reaction networks -- T-Cell Receptor Optimization with Reinforcement Learning and Mutation Polices for Precision Immunotherapy.
Sommario/riassunto	This book constitutes the refereed proceedings of the 27th Annual International Conference on Research in Computational Molecular Biology, RECOMB 2023, held in Istanbul, Turkey, during April 16–19, 2023. The 11 regular and 33 short papers presented in this book were carefully reviewed and selected from 188 submissions. The papers

report on original research in all areas of computational molecular  
biology and bioinformatics.

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