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Nota di contenuto	Intro -- Preface -- Organization -- Contents -- Computational Advances in Bio and Medical Sciences -- Single Model Quality Estimation of Protein Structures via Non-negative Tensor Factorization -- 1 Introduction -- 2 Related Works -- 3 Methodology -- 3.1 Stage I: From Structures to Groups -- 3.2 Stage II: Ranking Groups -- 3.3 Stage III: Partitioning Groups into Subgroups -- 3.4 Stage IV: Scoring Each Structure -- 3.5 Experimental Setup -- 3.6 Dataset -- 3.7 Evaluation Metrics -- 4 Results -- 4.1 Comparative Evaluation on Correlation with TM-Score -- 4.2 Loss-Based Comparison -- 4.3 Statistical Significance Analysis -- 5 Conclusion -- References -- Graph Representation Learning for Protein Conformation Sampling -- 1 Introduction -- 1.1 Related Work -- 2 Methods -- 3 Results -- 3.1 Experimental Setup -- 3.2 Evaluation of Models on Fixed-Length Chains -- 3.3 Evaluation of Models on Variable-Length Chains -- 4 Conclusion -- References -- Excerpt: Filtering Mutations Caused by the Clinical Archival Process in Sequencing Data -- 1 Introduction -- 2 Excerpt: A Bayes Classifier Using Mutational Signatures -- 3 Simulation and Evaluation Approach -- 4 Simulation Results -- 4.1 Performance Characteristics Across Different COSMIC Baseline Signatures -- 4.2 Performance Characteristics Across Different Percentages of FFPE -- 5 Conclusions -- References -- Relabeling Metabolic Pathway Data with Groups to Improve Prediction Outcomes -- 1 Introduction -- 2 Method -- 2.1

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