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Nota di contenuto	Not All Scale Free Networks Are Born Equal: The Role of the Seed Graph in PPI Network Emulation -- Probabilistic Paths for Protein Complex Inference -- Markov Additive Chains and Applications to Fragment Statistics for Peptide Mass Fingerprinting -- A Context-Specific Network of Protein-DNA and Protein-Protein Interactions Reveals New Regulatory Motifs in Human B Cells -- Identification and Evaluation of Functional Modules in Gene Co-expression Networks -- A Linear Discrete Dynamic System Model for Temporal Gene Interaction and Regulatory Network Influence in Response to Bioethanol Conversion Inhibitor HMF for Ethanologenic Yeast -- A Computational Approach for the Identification of Site-Specific Protein Glycosylations Through Ion-Trap Mass Spectrometry -- De Novo Signaling Pathway Predictions Based on Protein-Protein Interaction, Targeted Therapy and Protein Microarray Analysis -- Alignment of Mass Spectrometry Data by Clique Finding and Optimization.

