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Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Intro -- Preface -- Organization -- Contents -- Applied Bioinformatics and Computational Biology -- Comparative Transcriptome Profiling of <i>Maytenus ilicifolia</i> Root and Leaf -- 1 Introduction -- 2 Methods -- 2.1 Plant Material and Total RNA Isolation -- 2.2 Library Preparation and Sequencing -- 2.3 Quality Control and de novo Assembly -- 2.4 Functional Annotation -- 2.5 Differential Expression Analysis -- 2.6 Gene Ontology Enrichment and KEGG Analysis -- 3 Results and

Discussion -- 3.1 De novo Assembly and Functional Annotation of *M. ilicifolia* -- 3.2 Identification of Differentially Expressed Transcripts in Both Tissues -- References -- Hypusine Plays a Role in the Translation of Short mRNAs and Mediates the Polyamine and Autophagy Pathways in *Saccharomyces Cerevisiae* -- 1 Introduction -- 2 Materials and Methods -- 2.1 RNA-seq Data Analysis -- 2.2 Strain and Growth Conditions -- 2.3 RNA Isolation and qRT-PCR -- 2.4 Protein Extraction and Western Blot Analysis -- 3 Results and Discussion -- 3.1 Translation of Short ORFs is Impaired in *dys1-1* Mutant -- 3.2 Hypusination Modulates Autophagy -- References -- Topological Characterization of Cancer Driver Genes Using Reactome Super Pathways Networks -- 1 Introduction -- 2 Method -- 2.1 Reactome Functional Iteration -- 2.2 Super Pathways as Reactome FI Sub-networks -- 2.3 Super Pathways Sub-networks Enriched with Drivers Information -- 3 Results -- 3.1 Centrality Measures -- 3.2 Network Attack -- 4 Discussion and Conclusion -- References -- Bioinformatics and Computational Biology -- CellHeap: A Workflow for Optimizing COVID-19 Single-Cell RNA-Seq Data Processing in the Santos Dumont Supercomputer -- 1 Introduction -- 2 Description of the CellHeap Workflow -- 3 Results -- 3.1 Input Data and Experiment Setup -- 3.2 Environmental Setup -- 3.3 Results Discussion -- 4 Conclusion -- References.

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Sommario/riassunto

This book constitutes the refereed proceedings of the Brazilian Symposium on Bioinformatics, BSB 2021, held in November 2021. Due to COVID-19 pandemic the conference was held virtually The 10 revised full papers and 5 short papers were carefully reviewed and selected from 28 submissions. The papers address a broad range of current topics in computational biology and bioinformatics.
