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| 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 <i>M. ilicifolia</i> -- 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 <i>Saccharomyces Cerevisiae</i> -- 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 <i>dys1-1</i> 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- |

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