

Walter Sanseverino

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

6,709
citations

201385

27
h-index

128067

60
g-index

65
all docs

65
docs citations

65
times ranked

9275
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | GreNC 2.0: a comprehensive database of plant long non-coding RNAs. <i>Nucleic Acids Research</i> , 2022, 50, D1442-D1447. | 6.5 | 33 |
| 2 | PRGdb 4.0: an updated database dedicated to genes involved in plant disease resistance process. <i>Nucleic Acids Research</i> , 2022, 50, D1483-D1490. | 6.5 | 30 |
| 3 | A longitudinal study of the pulmonary mycobiome in subjects with and without chronic obstructive pulmonary disease. <i>PLoS ONE</i> , 2022, 17, e0267195. | 1.1 | 3 |
| 4 | Next-Generation Probiotics for Inflammatory Bowel Disease. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5466. | 1.8 | 10 |
| 5 | Engineered <i>Lactobacillus paracasei</i> Producing Palmitoylethanolamide (PEA) Prevents Colitis in Mice. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2945. | 1.8 | 16 |
| 6 | The pulmonary mycobiome—A study of subjects with and without chronic obstructive pulmonary disease. <i>PLoS ONE</i> , 2021, 16, e0248967. | 1.1 | 16 |
| 7 | A Palmitoylethanolamide Producing <i>Lactobacillus paracasei</i> Improves <i>Clostridium difficile</i> Toxin A-Induced Colitis. <i>Frontiers in Pharmacology</i> , 2021, 12, 639728. | 1.6 | 6 |
| 8 | The impact of chromosomal fusions on 3D genome folding and recombination in the germ line. <i>Nature Communications</i> , 2021, 12, 2981. | 5.8 | 34 |
| 9 | An anchored chromosome-scale genome assembly of spinach improves annotation and reveals extensive gene rearrangements in euasterids. <i>Plant Genome</i> , 2021, 14, e20101. | 1.6 | 13 |
| 10 | Phytotherapies in COVID19 : Why palmitoylethanolamide?. <i>Phytotherapy Research</i> , 2021, 35, 2514-2522. | 2.8 | 12 |
| 11 | External ear canal mycobiome of some rabbit breeds. <i>Medical Mycology</i> , 2021, 59, 683-693. | 0.3 | 3 |
| 12 | LOXL2-mediated H3K4 oxidation reduces chromatin accessibility in triple-negative breast cancer cells. <i>Oncogene</i> , 2020, 39, 79-121. | 2.6 | 28 |
| 13 | A semi-automated protocol for NGS metabarcoding and fungal analysis in forensic. <i>Forensic Science International</i> , 2020, 306, 110052. | 1.3 | 5 |
| 14 | Complex migration history is revealed by genetic diversity of tomato samples collected in Italy during the eighteenth and nineteenth centuries. <i>Horticulture Research</i> , 2020, 7, 100. | 2.9 | 4 |
| 15 | Daily intake of probiotic strain <i>Bacillus subtilis</i> DE111 supports a healthy microbiome in children attending day-care. <i>Beneficial Microbes</i> , 2020, 11, 611-620. | 1.0 | 17 |
| 16 | Fruit Development in <i>Ficus carica</i> L.: Morphological and Genetic Approaches to Fig Buds for an Evolution From Monoecy Toward Dioecy. <i>Frontiers in Plant Science</i> , 2020, 11, 1208. | 1.7 | 15 |
| 17 | The potential of cannabidiol in the COVID-19 pandemic. <i>British Journal of Pharmacology</i> , 2020, 177, 4967-4970. | 2.7 | 81 |
| 18 | Comprehensive characterization of HBV in tumor and non-tumor liver tissues from patients with HBV related-HCC. <i>Digestive and Liver Disease</i> , 2020, 52, e3-e4. | 0.4 | 1 |

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|----|--|-----|-----------|
| 19 | Can the enteric nervous system be an alternative entrance door in SARS-CoV2 neuroinvasion?. Brain, Behavior, and Immunity, 2020, 87, 93-94. | 2.0 | 84 |
| 20 | Three-Dimensional Genomic Structure and Cohesin Occupancy Correlate with Transcriptional Activity during Spermatogenesis. Cell Reports, 2019, 28, 352-367.e9. | 2.9 | 112 |
| 21 | A de novo transcriptome assembly approach elucidates the dynamics of ovarian maturation in the swordfish (<i>Xiphias gladius</i>). Scientific Reports, 2019, 9, 7375. | 1.6 | 12 |
| 22 | Distribution, Characteristics, and Regulatory Potential of Long Noncoding RNAs in Brown-Rot Fungi. International Journal of Genomics, 2019, 2019, 1-12. | 0.8 | 8 |
| 23 | A Walkthrough to the Use of GreeNC: The Plant lncRNA Database. Methods in Molecular Biology, 2019, 1933, 397-414. | 0.4 | 7 |
| 24 | A study of the airway mycobiome in COPD patients and controls. , 2019, , . | | 1 |
| 25 | Genomic diversity in ochratoxigenic and non ochratoxigenic strains of <i>Aspergillus carbonarius</i> . Scientific Reports, 2018, 8, 5439. | 1.6 | 12 |
| 26 | Whole-genome re-sequencing of two Italian tomato landraces reveals sequence variations in genes associated with stress tolerance, fruit quality and long shelf-life traits. DNA Research, 2018, 25, 149-160. | 1.5 | 68 |
| 27 | PRGdb 3.0: a comprehensive platform for prediction and analysis of plant disease resistance genes. Nucleic Acids Research, 2018, 46, D1197-D1201. | 6.5 | 135 |
| 28 | Sequencing, <i>De Novo</i> Assembly, and Annotation of the Complete Genome of a New Thraustochytrid Species, Strain CCAP_4062/3. Genome Announcements, 2018, 6, . | 0.8 | 17 |
| 29 | Broad phenotypic spectrum and genotype-phenotype correlations in GMPPB-related dystroglycanopathies: an Italian cross-sectional study. Orphanet Journal of Rare Diseases, 2018, 13, 170. | 1.2 | 26 |
| 30 | Proposal of a new thraustochytrid genus <i>Hondaea</i> gen. nov. and comparison of its lipid dynamics with the closely related pseudo-cryptic genus <i>Aurantiochytrium</i> . Algal Research, 2018, 35, 125-141. | 2.4 | 55 |
| 31 | An improved assembly and annotation of the melon (<i>Cucumis melo</i> L.) reference genome. Scientific Reports, 2018, 8, 8088. | 1.6 | 81 |
| 32 | Assessment of genomic changes in a CRISPR/Cas9 <i>Phaeodactylum tricornutum</i> mutant through whole genome resequencing. PeerJ, 2018, 6, e5507. | 0.9 | 26 |
| 33 | Transcriptomic response of durum wheat to nitrogen starvation. Scientific Reports, 2017, 7, 1176. | 1.6 | 134 |
| 34 | The hypothesis that <i>Helicobacter pylori</i> predisposes to Alzheimer's disease is biologically plausible. Scientific Reports, 2017, 7, 7817. | 1.6 | 24 |
| 35 | Maize RNA PolIV affects the expression of genes with nearby TE insertions and has a genome-wide repressive impact on transcription. BMC Plant Biology, 2017, 17, 161. | 1.6 | 32 |
| 36 | Careful with That Axe, Gene, Genome Perturbation after a PEG-Mediated Protoplast Transformation in <i>Fusarium verticillioides</i> . Toxins, 2017, 9, 183. | 1.5 | 9 |

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|----|--|-----|-----------|
| 37 | Stress-induced and epigenetic-mediated maize transcriptome regulation study by means of transcriptome reannotation and differential expression analysis. <i>Scientific Reports</i> , 2016, 6, 30446. | 1.6 | 57 |
| 38 | Exploiting the great potential of Sequence Capture data by a new tool, SUPER-CAP. <i>DNA Research</i> , 2016, 24, dsw050. | 1.5 | 8 |
| 39 | Genome and transcriptome analysis of the Mesoamerican common bean and the role of gene duplications in establishing tissue and temporal specialization of genes. <i>Genome Biology</i> , 2016, 17, 32. | 3.8 | 166 |
| 40 | A high-quality carrot genome assembly provides new insights into carotenoid accumulation and asterid genome evolution. <i>Nature Genetics</i> , 2016, 48, 657-666. | 9.4 | 432 |
| 41 | Pentatricopeptide repeat 336 as the candidate gene for paternal sorting of mitochondria (Psm) in cucumber. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1951-1959. | 1.8 | 8 |
| 42 | Spermatozoa from infertile patients exhibit differences of DNA methylation associated with spermatogenesis-related processes: an array-based analysis. <i>Reproductive BioMedicine Online</i> , 2016, 33, 709-719. | 1.1 | 40 |
| 43 | Effects of <i>Mecp2</i> loss of function in embryonic cortical neurons: a bioinformatics strategy to sort out non-neuronal cells variability from transcriptome profiling. <i>BMC Bioinformatics</i> , 2016, 17, 14. | 1.2 | 10 |
| 44 | GREENC: a Wiki-based database of plant lncRNAs. <i>Nucleic Acids Research</i> , 2016, 44, D1161-D1166. | 6.5 | 196 |
| 45 | Flowering and trichome development share hormonal and transcription factor regulation. <i>Journal of Experimental Botany</i> , 2016, 67, 1209-1219. | 2.4 | 53 |
| 46 | Rapid genome resequencing of an atoxigenic strain of <i>Aspergillus carbonarius</i> . <i>Scientific Reports</i> , 2015, 5, 9086. | 1.6 | 15 |
| 47 | Menadione-Induced Oxidative Stress Re-Shapes the Oxylipin Profile of <i>Aspergillus flavus</i> and Its Lifestyle. <i>Toxins</i> , 2015, 7, 4315-4329. | 1.5 | 34 |
| 48 | Use of targeted SNP selection for an improved anchoring of the melon (<i>Cucumis melo</i> L.) scaffold genome assembly. <i>BMC Genomics</i> , 2015, 16, 4. | 1.2 | 67 |
| 49 | Transposon Insertions, Structural Variations, and SNPs Contribute to the Evolution of the Melon Genome. <i>Molecular Biology and Evolution</i> , 2015, 32, 2760-2774. | 3.5 | 80 |
| 50 | The <i>Solanum commersonii</i> Genome Sequence Provides Insights into Adaptation to Stress Conditions and Genome Evolution of Wild Potato Relatives. <i>Plant Cell</i> , 2015, 27, 954-968. | 3.1 | 149 |
| 51 | Genome-wide identification and analysis of candidate genes for disease resistance in tomato. <i>Molecular Breeding</i> , 2014, 33, 227-233. | 1.0 | 30 |
| 52 | Next-generation sequencing, FISH mapping and synteny-based modeling reveal mechanisms of decreasing dysploidy in <i>Cucumis</i> . <i>Plant Journal</i> , 2014, 77, 16-30. | 2.8 | 90 |
| 53 | Genome-wide analysis of histone modifiers in tomato: gaining an insight into their developmental roles. <i>BMC Genomics</i> , 2013, 14, 57. | 1.2 | 125 |
| 54 | Overview of tomato (<i>Solanum lycopersicum</i>) candidate pathogen recognition genes reveals important <i>Solanum</i> R locus dynamics. <i>New Phytologist</i> , 2013, 197, 223-237. | 3.5 | 90 |

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|----|---|------|-----------|
| 55 | PRGdb 2.0: towards a community-based database model for the analysis of R-genes in plants. <i>Nucleic Acids Research</i> , 2012, 41, D1167-D1171. | 6.5 | 100 |
| 56 | In silico approach to predict candidate R proteins and to define their domain architecture. <i>BMC Research Notes</i> , 2012, 5, 678. | 0.6 | 41 |
| 57 | The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641. | 13.7 | 2,860 |
| 58 | The genome of melon (<i>Cucumis melo</i> L.). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11872-11877. | 3.3 | 654 |
| 59 | Genetic and genomic approaches for R-gene mediated disease resistance in tomato: retrospects and prospects. <i>Plant Cell Reports</i> , 2012, 31, 973-985. | 2.8 | 50 |
| 60 | Evolution of Parallel Spindles Like genes in plants and highlight of unique domain architecture#. <i>BMC Evolutionary Biology</i> , 2011, 11, 78. | 3.2 | 25 |
| 61 | PRGdb: a bioinformatics platform for plant resistance gene analysis. <i>Nucleic Acids Research</i> , 2010, 38, D814-D821. | 6.5 | 149 |
| 62 | Study of the variation of the <i>Malassezia</i> load in the interdigital fold of dogs with pododermatitis. <i>Veterinary Research Communications</i> , 0, , . | 0.6 | 0 |