Walter Sanseverino

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	GreeNC 2.0: a comprehensive database of plant long non-coding RNAs. Nucleic Acids Research, 2022, 50, D1442-D1447.	14.5	33
2	PRGdb 4.0: an updated database dedicated to genes involved in plant disease resistance process. Nucleic Acids Research, 2022, 50, D1483-D1490.	14.5	30
3	A longitudinal study of the pulmonary mycobiome in subjects with and without chronic obstructive pulmonary disease. PLoS ONE, 2022, 17, e0267195.	2.5	3
4	Next-Generation Probiotics for Inflammatory Bowel Disease. International Journal of Molecular Sciences, 2022, 23, 5466.	4.1	10
5	Engineered Lactobacillus paracasei Producing Palmitoylethanolamide (PEA) Prevents Colitis in Mice. International Journal of Molecular Sciences, 2021, 22, 2945.	4.1	16
6	The pulmonary mycobiome—A study of subjects with and without chronic obstructive pulmonary disease. PLoS ONE, 2021, 16, e0248967.	2.5	16
7	A Palmitoylethanolamide Producing Lactobacillus paracasei Improves Clostridium difficile Toxin A-Induced Colitis. Frontiers in Pharmacology, 2021, 12, 639728.	3.5	6
8	The impact of chromosomal fusions on 3D genome folding and recombination in the germ line. Nature Communications, 2021, 12, 2981.	12.8	34
9	An anchored chromosomeâ€scale genome assembly of spinach improves annotation and reveals extensive gene rearrangements in euasterids. Plant Genome, 2021, 14, e20101.	2.8	13
10	Phytotherapics in COVID19 : Why palmitoylethanolamide?. Phytotherapy Research, 2021, 35, 2514-2522.	5.8	12
11	External ear canal mycobiome of some rabbit breeds. Medical Mycology, 2021, 59, 683-693.	0.7	3
12	LOXL2-mediated H3K4 oxidation reduces chromatin accessibility in triple-negative breast cancer cells. Oncogene, 2020, 39, 79-121.	5.9	28
13	A semi-automated protocol for NGS metabarcoding and fungal analysis in forensic. Forensic Science International, 2020, 306, 110052.	2.2	5
14	Complex migration history is revealed by genetic diversity of tomato samples collected in Italy during the eighteenth and nineteenth centuries. Horticulture Research, 2020, 7, 100.	6.3	4
15	Daily intake of probiotic strain Bacillus subtilis DE111 supports a healthy microbiome in children attending day-care. Beneficial Microbes, 2020, 11, 611-620.	2.4	17
16	Fruit Development in Ficus carica L.: Morphological and Genetic Approaches to Fig Buds for an Evolution From Monoecy Toward Dioecy. Frontiers in Plant Science, 2020, 11, 1208.	3.6	15
17	The potential of cannabidiol in the COVIDâ€19 pandemic. British Journal of Pharmacology, 2020, 177, 4967-4970.	5.4	81
18	Comprehensive characterization of HBV in tumor and non-tumor liver tissues from patients with HBV related-HCC. Digestive and Liver Disease, 2020, 52, e3-e4.	0.9	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.	4.1	84
20	Three-Dimensional Genomic Structure and Cohesin Occupancy Correlate with Transcriptional Activity during Spermatogenesis. Cell Reports, 2019, 28, 352-367.e9.	6.4	112
21	A de novo transcriptome assembly approach elucidates the dynamics of ovarian maturation in the swordfish (Xiphias gladius). Scientific Reports, 2019, 9, 7375.	3.3	12
22	Distribution, Characteristics, and Regulatory Potential of Long Noncoding RNAs in Brown-Rot Fungi. International Journal of Genomics, 2019, 2019, 1-12.	1.6	8
23	A Walkthrough to the Use of GreeNC: The Plant IncRNA Database. Methods in Molecular Biology, 2019, 1933, 397-414.	0.9	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 Aspergillus carbonarius. Scientific Reports, 2018, 8, 5439.	3.3	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.	3.4	68
27	PRGdb 3.0: a comprehensive platform for prediction and analysis of plant disease resistance genes. Nucleic Acids Research, 2018, 46, D1197-D1201.	14.5	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.	2.7	26
30	Proposal of a new thraustochytrid genus Hondaea gen. nov. and comparison of its lipid dynamics with the closely related pseudo-cryptic genus Aurantiochytrium. Algal Research, 2018, 35, 125-141.	4.6	55
31	An improved assembly and annotation of the melon (Cucumis melo L.) reference genome. Scientific Reports, 2018, 8, 8088.	3.3	81
32	Assessment of genomic changes in a CRISPR/Cas9 <i>Phaeodactylum tricornutum</i> mutant through whole genome resequencing. PeerJ, 2018, 6, e5507.	2.0	26
33	Transcriptomic response of durum wheat to nitrogen starvation. Scientific Reports, 2017, 7, 1176.	3.3	134
34	The hypothesis that Helicobacter pylori predisposes to Alzheimer's disease is biologically plausible. Scientific Reports, 2017, 7, 7817.	3.3	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.	3.6	32
36	Careful with That Axe, Gene, Genome Perturbation after a PEG-Mediated Protoplast Transformation in Fusarium verticillioides. Toxins, 2017, 9, 183.	3.4	9

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37	Stress-induced and epigenetic-mediated maize transcriptome regulation study by means of transcriptome reannotation and differential expression analysis. Scientific Reports, 2016, 6, 30446.	3.3	57
38	Exploiting the great potential of Sequence Capture data by a new tool, SUPER-CAP. DNA Research, 2016, 24, dsw050.	3.4	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. Genome Biology, 2016, 17, 32.	8.8	166
40	A high-quality carrot genome assembly provides new insights into carotenoid accumulation and asterid genome evolution. Nature Genetics, 2016, 48, 657-666.	21.4	432
41	Pentatricopeptide repeat 336 as the candidate gene for paternal sorting of mitochondria (Psm) in cucumber. Theoretical and Applied Genetics, 2016, 129, 1951-1959.	3.6	8
42	Spermatozoa from infertile patients exhibit differences of DNA methylation associated with spermatogenesis-related processes: an array-based analysis. Reproductive BioMedicine Online, 2016, 33, 709-719.	2.4	40
43	Effects of Mecp2 loss of function in embryonic cortical neurons: a bioinformatics strategy to sort out non-neuronal cells variability from transcriptome profiling. BMC Bioinformatics, 2016, 17, 14.	2.6	10
44	GREENC: a Wiki-based database of plant lncRNAs. Nucleic Acids Research, 2016, 44, D1161-D1166.	14.5	196
45	Flowering and trichome development share hormonal and transcription factor regulation. Journal of Experimental Botany, 2016, 67, 1209-1219.	4.8	53
46	Rapid genome resequencing of an atoxigenic strain of Aspergillus carbonarius. Scientific Reports, 2015, 5, 9086.	3.3	15
47	Menadione-Induced Oxidative Stress Re-Shapes the Oxylipin Profile of Aspergillus flavus and Its Lifestyle. Toxins, 2015, 7, 4315-4329.	3.4	34
48	Use of targeted SNP selection for an improved anchoring of the melon (Cucumis melo L.) scaffold genome assembly. BMC Genomics, 2015, 16, 4.	2.8	67
49	Transposon Insertions, Structural Variations, and SNPs Contribute to the Evolution of the Melon Genome. Molecular Biology and Evolution, 2015, 32, 2760-2774.	8.9	80
50	The <i>Solanum commersonii</i> Genome Sequence Provides Insights into Adaptation to Stress Conditions and Genome Evolution of Wild Potato Relatives. Plant Cell, 2015, 27, 954-968.	6.6	149
51	Genome-wide identification and analysis of candidate genes for disease resistance in tomato. Molecular Breeding, 2014, 33, 227-233.	2.1	30
52	Nextâ€generation sequencing, <scp>FISH</scp> mapping and syntenyâ€based modeling reveal mechanisms of decreasing dysploidy in <i><scp>C</scp>ucumis</i> . Plant Journal, 2014, 77, 16-30.	5.7	90
53	Genome-wide analysis of histone modifiers in tomato: gaining an insight into their developmental roles. BMC Genomics, 2013, 14, 57.	2.8	125
54	Overview of tomato (<i>Solanum lycopersicum</i>) candidate pathogen recognition genes reveals important <i>Solanum</i> R locus dynamics. New Phytologist, 2013, 197, 223-237.	7.3	90

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55	PRGdb 2.0: towards a community-based database model for the analysis of R-genes in plants. Nucleic Acids Research, 2012, 41, D1167-D1171.	14.5	100
56	In silico approach to predict candidate R proteins and to define their domain architecture. BMC Research Notes, 2012, 5, 678.	1.4	41
57	The tomato genome sequence provides insights into fleshy fruit evolution. Nature, 2012, 485, 635-641.	27.8	2,860
58	The genome of melon (<i>Cucumis melo</i> L.). Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11872-11877.	7.1	654
59	Genetic and genomic approaches for R-gene mediated disease resistance in tomato: retrospects and prospects. Plant Cell Reports, 2012, 31, 973-985.	5.6	50
60	Evolution of Parallel Spindles Like genes in plants and highlight of unique domain architecture#. BMC Evolutionary Biology, 2011, 11, 78.	3.2	25
61	PRGdb: a bioinformatics platform for plant resistance gene analysis. Nucleic Acids Research, 2010, 38, D814-D821.	14.5	149
62	Study of the variation of the Malassezia load in the interdigital fold of dogs with pododermatitis. Veterinary Research Communications, 0, , .	1.6	0