

# 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	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	13.7	2,860
2	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
3	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
4	GREENC: a Wiki-based database of plant lncRNAs. <i>Nucleic Acids Research</i> , 2016, 44, D1161-D1166.	6.5	196
5	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
6	PRGdb: a bioinformatics platform for plant resistance gene analysis. <i>Nucleic Acids Research</i> , 2010, 38, D814-D821.	6.5	149
7	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
8	PRGdb 3.0: a comprehensive platform for prediction and analysis of plant disease resistance genes. <i>Nucleic Acids Research</i> , 2018, 46, D1197-D1201.	6.5	135
9	Transcriptomic response of durum wheat to nitrogen starvation. <i>Scientific Reports</i> , 2017, 7, 1176.	1.6	134
10	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
11	Three-Dimensional Genomic Structure and Cohesin Occupancy Correlate with Transcriptional Activity during Spermatogenesis. <i>Cell Reports</i> , 2019, 28, 352-367.e9.	2.9	112
12	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
13	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
14	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
15	Can the enteric nervous system be an alternative entrance door in SARS-CoV2 neuroinvasion?. <i>Brain, Behavior, and Immunity</i> , 2020, 87, 93-94.	2.0	84
16	An improved assembly and annotation of the melon ( <i>Cucumis melo</i> L.) reference genome. <i>Scientific Reports</i> , 2018, 8, 8088.	1.6	81
17	The potential of cannabidiol in the COVID-19 pandemic. <i>British Journal of Pharmacology</i> , 2020, 177, 4967-4970.	2.7	81
18	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

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19	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. <i>DNA Research</i> , 2018, 25, 149-160.	1.5	68
20	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
21	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
22	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> . <i>Algal Research</i> , 2018, 35, 125-141.	2.4	55
23	Flowering and trichome development share hormonal and transcription factor regulation. <i>Journal of Experimental Botany</i> , 2016, 67, 1209-1219.	2.4	53
24	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
25	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
26	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
27	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
28	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
29	GreeNC 2.0: a comprehensive database of plant long non-coding RNAs. <i>Nucleic Acids Research</i> , 2022, 50, D1442-D1447.	6.5	33
30	Maize RNA PolIV affects the expression of genes with nearby TE insertions and has a genome-wide repressive impact on transcription. <i>BMC Plant Biology</i> , 2017, 17, 161.	1.6	32
31	Genome-wide identification and analysis of candidate genes for disease resistance in tomato. <i>Molecular Breeding</i> , 2014, 33, 227-233.	1.0	30
32	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
33	LOXL2-mediated H3K4 oxidation reduces chromatin accessibility in triple-negative breast cancer cells. <i>Oncogene</i> , 2020, 39, 79-121.	2.6	28
34	Broad phenotypic spectrum and genotype-phenotype correlations in GMPPB-related dystroglycanopathies: an Italian cross-sectional study. <i>Orphanet Journal of Rare Diseases</i> , 2018, 13, 170.	1.2	26
35	Assessment of genomic changes in a CRISPR/Cas9 <i>Phaeodactylum tricorutum</i> mutant through whole genome resequencing. <i>PeerJ</i> , 2018, 6, e5507.	0.9	26
36	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

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37	The hypothesis that <i>Helicobacter pylori</i> predisposes to Alzheimer's disease is biologically plausible. <i>Scientific Reports</i> , 2017, 7, 7817.	1.6	24
38	Sequencing, <i>De Novo</i> Assembly, and Annotation of the Complete Genome of a New <i>Thraustochytrid</i> Species, Strain CCAP_4062/3. <i>Genome Announcements</i> , 2018, 6, .	0.8	17
39	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
40	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
41	The pulmonary mycobiome—A study of subjects with and without chronic obstructive pulmonary disease. <i>PLoS ONE</i> , 2021, 16, e0248967.	1.1	16
42	Rapid genome resequencing of an atoxigenic strain of <i>Aspergillus carbonarius</i> . <i>Scientific Reports</i> , 2015, 5, 9086.	1.6	15
43	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
44	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
45	Genomic diversity in ochratoxigenic and non ochratoxigenic strains of <i>Aspergillus carbonarius</i> . <i>Scientific Reports</i> , 2018, 8, 5439.	1.6	12
46	A de novo transcriptome assembly approach elucidates the dynamics of ovarian maturation in the swordfish ( <i>Xiphias gladius</i> ). <i>Scientific Reports</i> , 2019, 9, 7375.	1.6	12
47	Phytotherapies in COVID19 : Why palmitoylethanolamide?. <i>Phytotherapy Research</i> , 2021, 35, 2514-2522.	2.8	12
48	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
49	Next-Generation Probiotics for Inflammatory Bowel Disease. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5466.	1.8	10
50	Careful with That Axe, Gene, Genome Perturbation after a PEG-Mediated Protoplast Transformation in <i>Fusarium verticillioides</i> . <i>Toxins</i> , 2017, 9, 183.	1.5	9
51	Exploiting the great potential of Sequence Capture data by a new tool, SUPER-CAP. <i>DNA Research</i> , 2016, 24, dsw050.	1.5	8
52	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
53	Distribution, Characteristics, and Regulatory Potential of Long Noncoding RNAs in Brown-Rot Fungi. <i>International Journal of Genomics</i> , 2019, 2019, 1-12.	0.8	8
54	A Walkthrough to the Use of GreenC: The Plant lncRNA Database. <i>Methods in Molecular Biology</i> , 2019, 1933, 397-414.	0.4	7

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55	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
56	A semi-automated protocol for NGS metabarcoding and fungal analysis in forensic. <i>Forensic Science International</i> , 2020, 306, 110052.	1.3	5
57	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
58	External ear canal mycobiome of some rabbit breeds. <i>Medical Mycology</i> , 2021, 59, 683-693.	0.3	3
59	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
60	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
61	A study of the airway mycobiome in COPD patients and controls. , 2019, , .		1
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