Guillaume Blanc

List of Publications by Year
in descending order

51 papers	11,907 citations	147801 31 h-index	182427 51 g-index
51 all docs	51 docs citations	51 times ranked	16427 citing authors

#	Article	IF	Citations
1	Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Research, 2008, 36, W465-W469.	14.5	4,135
2	Widespread Paleopolyploidy in Model Plant Species Inferred from Age Distributions of Duplicate Genes[W]. Plant Cell, 2004, 16, 1667-1678.	6.6	1,106
3	Functional Divergence of Duplicated Genes Formed by Polyploidy during Arabidopsis Evolution[W]. Plant Cell, 2004, 16, 1679-1691.	6.6	996
4	A Recent Polyploidy Superimposed on Older Large-Scale Duplications in the Arabidopsis Genome. Genome Research, 2003, 13, 137-144.	5.5	638
5	BLAST-EXPLORER helps you building datasets for phylogenetic analysis. BMC Evolutionary Biology, 2010, 10, 8.	3.2	633
6	Extensive Duplication and Reshuffling in the Arabidopsis Genome. Plant Cell, 2000, 12, 1093-1101.	6.6	512
7	The Chlorella variabilis NC64A Genome Reveals Adaptation to Photosymbiosis, Coevolution with Viruses, and Cryptic Sex Â. Plant Cell, 2010, 22, 2943-2955.	6.6	441
8	The Physcomitrella patens chromosomeâ€scale assembly reveals moss genome structure and evolution. Plant Journal, 2018, 93, 515-533.	5.7	406
9	The genome of the polar eukaryotic microalga Coccomyxa subellipsoidea reveals traits of cold adaptation. Genome Biology, 2012, 13, R39.	9.6	289
10	Genome Sequence of Rickettsia bellii Illuminates the Role of Amoebae in Gene Exchanges between Intracellular Pathogens. PLoS Genetics, 2006, 2, e76.	3.5	286
11	The Organization of Cytoplasmic Ribosomal Protein Genes in the Arabidopsis Genome. Plant Physiology, 2001, 127, 398-415.	4.8	272
12	The Genome Sequence of Rickettsia felis Identifies the First Putative Conjugative Plasmid in an Obligate Intracellular Parasite. PLoS Biology, 2005, 3, e248.	5.6	242
13	Reductive Genome Evolution from the Mother of Rickettsia. PLoS Genetics, 2007, 3, e14.	3.5	167
14	The Genome of Borrelia recurrentis, the Agent of Deadly Louse-Borne Relapsing Fever, Is a Degraded Subset of Tick-Borne Borrelia duttonii. PLoS Genetics, 2008, 4, e1000185.	3.5	146
15	Lipidomic and transcriptomic analyses of Chlamydomonas reinhardtii under heat stress unveil a direct route for the conversion of membrane lipids into storage lipids. Plant, Cell and Environment, 2016, 39, 834-847.	5.7	124
16	Lateral gene transfer between obligate intracellular bacteria: Evidence from the Rickettsia massiliae genome. Genome Research, 2007, 17, 1657-1664.	5.5	123
17	Molecular Evolution of Rickettsia Surface Antigens: Evidence of Positive Selection. Molecular Biology and Evolution, 2005, 22, 2073-2083.	8.9	119
18	Insights into the Musa genome: Syntenic relationships to rice and between Musa species. BMC Genomics, 2008, 9, 58.	2.8	105

#	Article	IF	Citations
19	The lichen symbiosis re-viewed through the genomes of Cladonia grayi and its algal partner Asterochloris glomerata. BMC Genomics, 2019, 20, 605.	2.8	98
20	Plant genomes enclose footprints of past infections by giant virus relatives. Nature Communications, 2014, 5, 4268.	12.8	92
21	Provirophages in the Bigelowiella genome bear testimony to past encounters with giant viruses. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5318-26.	7.1	89
22	Towards defining the chloroviruses: a genomic journey through a genus of large DNA viruses. BMC Genomics, 2013, 14, 158.	2.8	79
23	A Glimpse of Nucleo-Cytoplasmic Large DNA Virus Biodiversity through the Eukaryotic Genomics Window. Viruses, 2017, 9, 17.	3.3	72
24	Gene Expression in Proliferating Cells of the Dinoflagellate Alexandrium catenella (Dinophyceae). Applied and Environmental Microbiology, 2010, 76, 4521-4529.	3.1	71
25	Deep RNA Sequencing Reveals Hidden Features and Dynamics of Early Gene Transcription in Paramecium bursaria Chlorella Virus 1. PLoS ONE, 2014, 9, e90989.	2.5	65
26	Paramecium bursaria Chlorella Virus 1 Proteome Reveals Novel Architectural and Regulatory Features of a Giant Virus. Journal of Virology, 2012, 86, 8821-8834.	3.4	64
27	Study of Gene Trafficking betweenAcanthamoebaand Giant Viruses Suggests an Undiscovered Family of Amoeba-Infecting Viruses. Genome Biology and Evolution, 2016, 8, 3351-3363.	2.5	59
28	Comparative Genomics of Chrysochromulina Ericina Virus and Other Microalga-Infecting Large DNA Viruses Highlights Their Intricate Evolutionary Relationship with the Established Mimiviridae Family. Journal of Virology, 2017, 91, .	3.4	59
29	History, protohistory and prehistory of the Arabidopsis thaliana chromosome complement. Trends in Plant Science, 2006, 11, 267-273.	8.8	47
30	Sca1, a previously undescribed paralog from autotransporter protein-encoding genes in Rickettsia species. BMC Microbiology, 2006, 6, 12.	3.3	46
31	Structural divergence of chromosomal segments that arose from successive duplication events in the Arabidopsis genome. Nucleic Acids Research, 2003, 31, 1339-1350.	14.5	41
32	The Organization of Cytoplasmic Ribosomal Protein Genes in the Arabidopsis Genome. Plant Physiology, 2001, 127, 398-415.	4.8	38
33	Phylogenomic fingerprinting of tempo and functions of horizontal gene transfer within ochrophytes. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	37
34	Rickettsia felis, from Culture to Genome Sequencing. Annals of the New York Academy of Sciences, 2005, 1063, 26-34.	3.8	24
35	Characterization of a UDP-N-acetylglucosamine biosynthetic pathway encoded by the giant DNA virus Mimivirus. Glycobiology, 2014, 24, 51-61.	2.5	24
36	Phylogenic Analysis of Rickettsial Patatin-like Protein with Conserved Phospholipase A2 Active Sites. Annals of the New York Academy of Sciences, 2005, 1063, 83-86.	3.8	19

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37	Phylogenetic Study of Rickettsia Species Using Sequences of the Autotransporter Protein-Encoding Gene sca2. Annals of the New York Academy of Sciences, 2005, 1063, 94-99.	3.8	19
38	Potassium Ion Channels: Could They Have Evolved from Viruses?. Plant Physiology, 2013, 162, 1215-1224.	4.8	19
39	Global Analysis of Chlorella variabilis NC64A mRNA Profiles during the Early Phase of Paramecium bursaria Chlorella Virus-1 Infection. PLoS ONE, 2014, 9, e90988.	2.5	16
40	Impact of the Excision of an Ancient Repeat Insertion on Rickettsia conorii Guanylate Kinase Activity. Molecular Biology and Evolution, 2006, 23, 2112-2122.	8.9	14
41	Complete mitochondrial genome sequence of the freshwater diatom Asterionella formosa. Mitochondrial DNA Part B: Resources, 2017, 2, 97-98.	0.4	13
42	Long-read only assembly of Drechmeria coniospora genomes reveals widespread chromosome plasticity and illustrates the limitations of current nanopore methods. GigaScience, 2020, 9, .	6.4	11
43	Evaluation of higher plant virus resistance genes in the green alga, Chlorella variabilis NC64A, during the early phase of infection with Paramecium bursaria chlorella virus-1. Virology, 2013, 442, 101-113.	2.4	10
44	Comparative Genomics Unveils Regionalized Evolution of the Faustovirus Genomes. Viruses, 2020, 12, 577.	3.3	7
45	The Kaumoebavirus LCC10 Genome Reveals a Unique Gene Strand Bias among â€œExtended Asfarviridaeâ€• Viruses, 2021, 13, 148.	3.3	7
46	Exploring the microbiome of the â€œstarâ€•freshwater diatom Asterionella formosa in a laboratory context. Environmental Microbiology, 2018, 20, 3601-3615.	3.8	6
47	A High Rate Algal Pond Hosting a Dynamic Community of RNA Viruses. Viruses, 2021, 13, 2163.	3.3	6
48	Computational Analyses of Ancient Polyploidy. Current Bioinformatics, 2006, 1, 131-146.	1.5	5
49	Giant viruses at the core of microscopic wars with global impacts. Current Opinion in Virology, 2016, 17, 130-137.	5.4	5
50	Pacmanvirus S19, the Second Pacmanvirus Isolated from Sewage Waters in Oran, Algeria. Microbiology Resource Announcements, 2021, 10, e0069321.	0.6	4
51	Diversity of Giant Viruses Infecting Vermamoeba vermiformis. Frontiers in Microbiology, 2022, 13, .	3.5	1