Guillaume Blanc

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Diversity of Giant Viruses Infecting Vermamoeba vermiformis. Frontiers in Microbiology, 2022, 13, .	1.5	1
2	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, .	3.3	37
3	The Kaumoebavirus LCC10 Genome Reveals a Unique Gene Strand Bias among "Extended Asfarviridae― Viruses, 2021, 13, 148.	1.5	7
4	Pacmanvirus S19, the Second Pacmanvirus Isolated from Sewage Waters in Oran, Algeria. Microbiology Resource Announcements, 2021, 10, e0069321.	0.3	4
5	A High Rate Algal Pond Hosting a Dynamic Community of RNA Viruses. Viruses, 2021, 13, 2163.	1.5	6
6	Long-read only assembly of Drechmeria coniospora genomes reveals widespread chromosome plasticity and illustrates the limitations of current nanopore methods. GigaScience, 2020, 9, .	3.3	11
7	Comparative Genomics Unveils Regionalized Evolution of the Faustovirus Genomes. Viruses, 2020, 12, 577.	1.5	7
8	The lichen symbiosis re-viewed through the genomes of Cladonia grayi and its algal partner Asterochloris glomerata. BMC Genomics, 2019, 20, 605.	1.2	98
9	The <i>Physcomitrella patens</i> chromosomeâ€scale assembly reveals moss genome structure and evolution. Plant Journal, 2018, 93, 515-533.	2.8	406
10	Exploring the microbiome of the "star―freshwater diatom <i>Asterionella formosa</i> in a laboratory context. Environmental Microbiology, 2018, 20, 3601-3615.	1.8	6
11	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, .	1.5	59
12	Complete mitochondrial genome sequence of the freshwater diatom Asterionella formosa. Mitochondrial DNA Part B: Resources, 2017, 2, 97-98.	0.2	13
13	A Climpse of Nucleo-Cytoplasmic Large DNA Virus Biodiversity through the Eukaryotic Genomics Window. Viruses, 2017, 9, 17.	1.5	72
14	Study of Gene Trafficking between <i>Acanthamoeba</i> and Giant Viruses Suggests an Undiscovered Family of Amoeba-Infecting Viruses. Genome Biology and Evolution, 2016, 8, 3351-3363.	1.1	59
15	Giant viruses at the core of microscopic wars with global impacts. Current Opinion in Virology, 2016, 17, 130-137.	2.6	5
16	Lipidomic and transcriptomic analyses of <i>Chlamydomonas reinhardtii</i> under heat stress unveil a direct route for the conversion of membrane lipids into storage lipids. Plant, Cell and Environment, 2016, 39, 834-847.	2.8	124
17	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.	3.3	89
18	Global Analysis of Chlorella variabilis NC64A mRNA Profiles during the Early Phase of Paramecium bursaria Chlorella Virus-1 Infection. PLoS ONE, 2014, 9, e90988.	1.1	16

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19	Characterization of a UDP-N-acetylglucosamine biosynthetic pathway encoded by the giant DNA virus Mimivirus. Glycobiology, 2014, 24, 51-61.	1.3	24
20	Plant genomes enclose footprints of past infections by giant virus relatives. Nature Communications, 2014, 5, 4268.	5.8	92
21	Deep RNA Sequencing Reveals Hidden Features and Dynamics of Early Gene Transcription in Paramecium bursaria Chlorella Virus 1. PLoS ONE, 2014, 9, e90989.	1.1	65
22	Towards defining the chloroviruses: a genomic journey through a genus of large DNA viruses. BMC Genomics, 2013, 14, 158.	1.2	79
23	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.	1.1	10
24	Potassium Ion Channels: Could They Have Evolved from Viruses?. Plant Physiology, 2013, 162, 1215-1224.	2.3	19
25	Paramecium bursaria Chlorella Virus 1 Proteome Reveals Novel Architectural and Regulatory Features of a Giant Virus. Journal of Virology, 2012, 86, 8821-8834.	1.5	64
26	The genome of the polar eukaryotic microalga Coccomyxa subellipsoidea reveals traits of cold adaptation. Genome Biology, 2012, 13, R39.	13.9	289
27	BLAST-EXPLORER helps you building datasets for phylogenetic analysis. BMC Evolutionary Biology, 2010, 10, 8.	3.2	633
28	Gene Expression in Proliferating Cells of the Dinoflagellate Alexandrium catenella (Dinophyceae). Applied and Environmental Microbiology, 2010, 76, 4521-4529.	1.4	71
29	The <i>Chlorella variabilis</i> NC64A Genome Reveals Adaptation to Photosymbiosis, Coevolution with Viruses, and Cryptic Sex Â. Plant Cell, 2010, 22, 2943-2955.	3.1	441
30	Insights into the Musa genome: Syntenic relationships to rice and between Musa species. BMC Genomics, 2008, 9, 58.	1.2	105
31	Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Research, 2008, 36, W465-W469.	6.5	4,135
32	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.	1.5	146
33	Lateral gene transfer between obligate intracellular bacteria: Evidence from the <i>Rickettsia massiliae</i> genome. Genome Research, 2007, 17, 1657-1664.	2.4	123
34	Reductive Genome Evolution from the Mother of Rickettsia. PLoS Genetics, 2007, 3, e14.	1.5	167
35	History, protohistory and prehistory of the Arabidopsis thaliana chromosome complement. Trends in Plant Science, 2006, 11, 267-273.	4.3	47
36	Sca1, a previously undescribed paralog from autotransporter protein-encoding genes in Rickettsia species. BMC Microbiology, 2006, 6, 12.	1.3	46

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37	Impact of the Excision of an Ancient Repeat Insertion on Rickettsia conorii Guanylate Kinase Activity. Molecular Biology and Evolution, 2006, 23, 2112-2122.	3.5	14
38	Computational Analyses of Ancient Polyploidy. Current Bioinformatics, 2006, 1, 131-146.	0.7	5
39	Genome Sequence of Rickettsia bellii Illuminates the Role of Amoebae in Gene Exchanges between Intracellular Pathogens. PLoS Genetics, 2006, 2, e76.	1.5	286
40	Rickettsia felis, from Culture to Genome Sequencing. Annals of the New York Academy of Sciences, 2005, 1063, 26-34.	1.8	24
41	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.	1.8	19
42	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.	1.8	19
43	The Genome Sequence of Rickettsia felis Identifies the First Putative Conjugative Plasmid in an Obligate Intracellular Parasite. PLoS Biology, 2005, 3, e248.	2.6	242
44	Molecular Evolution of Rickettsia Surface Antigens: Evidence of Positive Selection. Molecular Biology and Evolution, 2005, 22, 2073-2083.	3.5	119
45	Widespread Paleopolyploidy in Model Plant Species Inferred from Age Distributions of Duplicate Genes[W]. Plant Cell, 2004, 16, 1667-1678.	3.1	1,106
46	Functional Divergence of Duplicated Genes Formed by Polyploidy during Arabidopsis Evolution[W]. Plant Cell, 2004, 16, 1679-1691.	3.1	996
47	Structural divergence of chromosomal segments that arose from successive duplication events in the Arabidopsis genome. Nucleic Acids Research, 2003, 31, 1339-1350.	6.5	41
48	A Recent Polyploidy Superimposed on Older Large-Scale Duplications in the Arabidopsis Genome. Genome Research, 2003, 13, 137-144.	2.4	638
49	The Organization of Cytoplasmic Ribosomal Protein Genes in the Arabidopsis Genome. Plant Physiology, 2001, 127, 398-415.	2.3	272
50	Extensive Duplication and Reshuffling in the Arabidopsis Genome. Plant Cell, 2000, 12, 1093-1101.	3.1	512