

Vincent Daubin

List of Publications by Year in descending order

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57
papers

6,445
citations

101543

36
h-index

155660

55
g-index

66
all docs

66
docs citations

66
times ranked

6625
citing authors

#	ARTICLE	IF	CITATIONS
1	Global trends of whole-genome duplications revealed by the ciliate <i>Paramecium tetraurelia</i> . <i>Nature</i> , 2006, 444, 171-178.	27.8	744
2	From Gene Trees to Organismal Phylogeny in Prokaryotes: The Case of the $\hat{\Gamma}^3$ -Proteobacteria. <i>PLoS Biology</i> , 2003, 1, e19.	5.6	393
3	Genome characteristics of facultatively symbiotic <i>Frankia</i> sp. strains reflect host range and host plant biogeography. <i>Genome Research</i> , 2006, 17, 7-15.	5.5	352
4	Evolutionary Origins of Genomic Repertoires in Bacteria. <i>PLoS Biology</i> , 2005, 3, e130.	5.6	307
5	A Phylogenomic Approach to Bacterial Phylogeny: Evidence of a Core of Genes Sharing a Common History. <i>Genome Research</i> , 2002, 12, 1080-1090.	5.5	303
6	Phylogenetics and the Cohesion of Bacterial Genomes. <i>Science</i> , 2003, 301, 829-832.	12.6	256
7	Bacterial Genomes as New Gene Homes: The Genealogy of ORFans in <i>E. coli</i> . <i>Genome Research</i> , 2004, 14, 1036-1042.	5.5	248
8	The Inference of Gene Trees with Species Trees. <i>Systematic Biology</i> , 2015, 64, e42-e62.	5.6	226
9	Genome-scale coestimation of species and gene trees. <i>Genome Research</i> , 2013, 23, 323-330.	5.5	223
10	Dealing with incongruence in phylogenomic analyses. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 4023-4029.	4.0	203
11	GC-Content Evolution in Bacterial Genomes: The Biased Gene Conversion Hypothesis Expands. <i>PLoS Genetics</i> , 2015, 11, e1004941.	3.5	200
12	Examining bacterial species under the specter of gene transfer and exchange. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 6595-6599.	7.1	187
13	Efficient Exploration of the Space of Reconciled Gene Trees. <i>Systematic Biology</i> , 2013, 62, 901-912.	5.6	176
14	The source of laterally transferred genes in bacterial genomes. <i>Genome Biology</i> , 2003, 4, R57.	9.6	172
15	Reductive genome evolution at both ends of the bacterial population size spectrum. <i>Nature Reviews Microbiology</i> , 2014, 12, 841-850.	28.6	158
16	Phylogenetic modeling of lateral gene transfer reconstructs the pattern and relative timing of speciations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17513-17518.	7.1	150
17	Phylogeny of the class Actinobacteria revisited in the light of complete genomes. The orders "Frankiales"™ and Micrococcales should be split into coherent entities: proposal of Frankiales ord. nov., Geodermatophilales ord. nov., Acidothermales ord. nov. and Nakamurellales ord. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 3821-3832.	1.7	148
18	The origin of eukaryotes and their relationship with the Archaea: are we at a phylogenomic impasse?. <i>Nature Reviews Microbiology</i> , 2010, 8, 743-752.	28.6	140

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19	Models, algorithms and programs for phylogeny reconciliation. <i>Briefings in Bioinformatics</i> , 2011, 12, 392-400.	6.5	132
20	Databases of homologous gene families for comparative genomics. <i>BMC Bioinformatics</i> , 2009, 10, S3.	2.6	118
21	Genomic Species Are Ecological Species as Revealed by Comparative Genomics in <i>Agrobacterium tumefaciens</i> . <i>Genome Biology and Evolution</i> , 2011, 3, 762-781.	2.5	110
22	Complete genome of the cellulolytic thermophile <i>Acidothermus cellulolyticus</i> 11B provides insights into its ecophysiological and evolutionary adaptations. <i>Genome Research</i> , 2009, 19, 1033-1043.	5.5	109
23	Lateral gene transfer as a support for the tree of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4962-4967.	7.1	108
24	Lateral Gene Transfer from the Dead. <i>Systematic Biology</i> , 2013, 62, 386-397.	5.6	100
25	G+C3 Structuring Along the Genome: A Common Feature in Prokaryotes. <i>Molecular Biology and Evolution</i> , 2003, 20, 471-483.	8.9	79
26	Horizontal Gene Transfer and the History of Life. <i>Cold Spring Harbor Perspectives in Biology</i> , 2016, 8, a018036.	5.5	79
27	Comparative genomics and the evolution of prokaryotes. <i>Trends in Microbiology</i> , 2007, 15, 135-141.	7.7	77
28	Genome-scale phylogenetic analysis finds extensive gene transfer among fungi. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140335.	4.0	77
29	A Bayesian Method for Analyzing Lateral Gene Transfer. <i>Systematic Biology</i> , 2014, 63, 409-420.	5.6	73
30	Genomes as documents of evolutionary history. <i>Trends in Ecology and Evolution</i> , 2010, 25, 224-232.	8.7	63
31	Detecting lateral gene transfers by statistical reconciliation of phylogenetic forests. <i>BMC Bioinformatics</i> , 2010, 11, 324.	2.6	55
32	Start-up entities in the origin of new genes. <i>Current Opinion in Genetics and Development</i> , 2004, 14, 616-619.	3.3	53
33	Gene transfers can date the tree of life. <i>Nature Ecology and Evolution</i> , 2018, 2, 904-909.	7.8	52
34	Single acquisition of protelomerase gave rise to speciation of a large and diverse clade within the <i>Agrobacterium/Rhizobium</i> supercluster characterized by the presence of a linear chromid. <i>Molecular Phylogenetics and Evolution</i> , 2014, 73, 202-207.	2.7	44
35	Response to Comment on "The Origins of Genome Complexity". <i>Science</i> , 2004, 306, 978b-978b.	12.6	41
36	Contrasted evolutionary constraints on secreted and non-secreted proteomes of selected Actinobacteria. <i>BMC Genomics</i> , 2013, 14, 474.	2.8	39

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37	Ecological networks to unravel the routes to horizontal transposon transfers. <i>PLoS Biology</i> , 2017, 15, e2001536.	5.6	39
38	Gene Acquisitions from Bacteria at the Origins of Major Archaeal Clades Are Vastly Overestimated. <i>Molecular Biology and Evolution</i> , 2016, 33, 305-310.	8.9	37
39	Evolution of gene neighborhoods within reconciled phylogenies. <i>Bioinformatics</i> , 2012, 28, i382-i388.	4.1	34
40	DeCoSTAR: Reconstructing the Ancestral Organization of Genes or Genomes Using Reconciled Phylogenies. <i>Genome Biology and Evolution</i> , 2017, 9, 1312-1319.	2.5	32
41	Ancestral Genome Estimation Reveals the History of Ecological Diversification in <i>Agrobacterium</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 3413-3431.	2.5	31
42	Ribosomal proteins: Toward a next generation standard for prokaryotic systematics?. <i>Molecular Phylogenetics and Evolution</i> , 2014, 75, 103-117.	2.7	30
43	Multiple Nuclear Gene Phylogenetic Analysis of the Evolution of Dioecy and Sex Chromosomes in the Genus <i>Silene</i> . <i>PLoS ONE</i> , 2011, 6, e21915.	2.5	29
44	Modeling Gene Family Evolution and Reconciling Phylogenetic Discord. <i>Methods in Molecular Biology</i> , 2012, 856, 29-51.	0.9	29
45	RecPhyloXML: a format for reconciled gene trees. <i>Bioinformatics</i> , 2018, 34, 3646-3652.	4.1	22
46	Quartet Mapping and the Extent of Lateral Transfer in Bacterial Genomes. <i>Molecular Biology and Evolution</i> , 2003, 21, 86-89.	8.9	21
47	Detecting phylogenetic incongruence using BIONJ: an improvement of the ILD test. <i>Molecular Phylogenetics and Evolution</i> , 2004, 33, 687-693.	2.7	21
48	Lateral gene transfer, rearrangement, reconciliation. <i>BMC Bioinformatics</i> , 2013, 14, S4.	2.6	21
49	Treerecs: an integrated phylogenetic tool, from sequences to reconciliations. <i>Bioinformatics</i> , 2020, 36, 4822-4824.	4.1	20
50	Diversity and Evolution of Pigment Types in Marine <i>Synechococcus</i> Cyanobacteria. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	15
51	A bunch of fun-guys: the whole-genome view of yeast evolution. <i>Trends in Genetics</i> , 2005, 21, 1-3.	6.7	13
52	Genome Evolution: Mutation Is the Main Driver of Genome Size in Prokaryotes. <i>Current Biology</i> , 2020, 30, R1083-R1085.	3.9	10
53	Relative Time Constraints Improve Molecular Dating. <i>Systematic Biology</i> , 2022, 71, 797-809.	5.6	9
54	Reconstruction of an ancestral <i>Yersinia pestis</i> genome and comparison with an ancient sequence. <i>BMC Genomics</i> , 2015, 16, S9.	2.8	7

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55	Super-tree Approach for Studying the Phylogeny of Prokaryotes: New Results on Completely Sequenced Genomes. Lecture Notes in Computer Science, 2004, , 700-708.	1.3	0
56	Evolution of the core of genes. , 0, , 123-130.		0
57	Quand les branches de lâ€™arbre du vivant sâ€™entremêlent. Pour la science Fr, 2019, NÂ° 506 - dÃ©cembre, 56-65		0