

Julien Y Dutheil

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

4,391
citations

186265

28
h-index

175258

52
g-index

90
all docs

90
docs citations

90
times ranked

5553
citing authors

#	ARTICLE	IF	CITATIONS
1	The Structural Determinants of Intra-Protein Compensatory Substitutions. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	3
2	Plant pathogens provide clues to the potential origin of bat white-nose syndrome <i><i>Pseudogymnoascus destructans</i></i> . <i>Virulence</i> , 2022, 13, 1020-1031.	4.4	6
3	Population Genomics of the Maize Pathogen <i><i>Ustilago maydis</i></i> : Demographic History and Role of Virulence Clusters in Adaptation. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	11
4	Variation of the adaptive substitution rate between species and within genomes. <i>Evolutionary Ecology</i> , 2020, 34, 315-338.	1.2	30
5	The insertion of a mitochondrial selfish element into the nuclear genome and its consequences. <i>Ecology and Evolution</i> , 2020, 10, 11117-11132.	1.9	4
6	On Variant Discovery in Genomes of Fungal Plant Pathogens. <i>Frontiers in Microbiology</i> , 2020, 11, 626.	3.5	16
7	A Population Genomics Lexicon. <i>Methods in Molecular Biology</i> , 2020, 2090, 3-17.	0.9	3
8	Processing and Analyzing Multiple Genomes Alignments with MafFilter. <i>Methods in Molecular Biology</i> , 2020, 2090, 21-48.	0.9	3
9	Ancestral Population Genomics. <i>Methods in Molecular Biology</i> , 2019, 1910, 555-589.	0.9	2
10	Inference of recombination maps from a single pair of genomes and its application to ancient samples. <i>PLoS Genetics</i> , 2019, 15, e1008449.	3.5	34
11	The Impact of Protein Architecture on Adaptive Evolution. <i>Molecular Biology and Evolution</i> , 2019, 36, 2013-2028.	8.9	42
12	The genomic determinants of adaptive evolution in a fungal pathogen. <i>Evolution Letters</i> , 2019, 3, 299-312.	3.3	61
13	Title is missing!. , 2019, 15, e1008449.		0
14	Title is missing!. , 2019, 15, e1008449.		0
15	Title is missing!. , 2019, 15, e1008449.		0
16	Title is missing!. , 2019, 15, e1008449.		0
17	Fine-Scale Recombination Maps of Fungal Plant Pathogens Reveal Dynamic Recombination Landscapes and Intragenic Hotspots. <i>Genetics</i> , 2018, 208, 1209-1229.	2.9	61
18	Positively Selected Effector Genes and Their Contribution to Virulence in the Smut Fungus <i>Sporisorium reilianum</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 629-645.	2.5	48

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19	The Evolution of Gene-Specific Transcriptional Noise Is Driven by Selection at the Pathway Level. <i>Genetics</i> , 2018, 208, 173-189.	2.9	41
20	Hidden Markov Models in Population Genomics. <i>Methods in Molecular Biology</i> , 2017, 1552, 149-164.	0.9	6
21	The WOPR Protein Ros1 Is a Master Regulator of Sporogenesis and Late Effector Gene Expression in the Maize Pathogen <i>Ustilago maydis</i> . <i>PLoS Pathogens</i> , 2016, 12, e1005697.	4.7	65
22	hotspot: software to support sperm-typing for investigating recombination hotspots. <i>Bioinformatics</i> , 2016, 32, 2554-2555.	4.1	1
23	A Tale of Genome Compartmentalization: The Evolution of Virulence Clusters in Smut Fungi. <i>Genome Biology and Evolution</i> , 2016, 8, 681-704.	2.5	125
24	Extreme selective sweeps independently targeted the X chromosomes of the great apes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6413-6418.	7.1	75
25	Optimization of sequence alignments according to the number of sequences vs. number of sites trade-off. <i>BMC Bioinformatics</i> , 2015, 16, 190.	2.6	6
26	Strong Selective Sweeps on the X Chromosome in the Human-Chimpanzee Ancestor Explain Its Low Divergence. <i>PLoS Genetics</i> , 2015, 11, e1005451.	3.5	56
27	MafFilter: a highly flexible and extensible multiple genome alignment files processor. <i>BMC Genomics</i> , 2014, 15, 53.	2.8	68
28	Mitochondrial scpDNA as a tool for reconstructing past life history traits in mammals. <i>Journal of Evolutionary Biology</i> , 2014, 27, 899-910.	1.7	17
29	A fine-scale recombination map of the human-chimpanzee ancestor reveals faster change in humans than in chimpanzees and a strong impact of GC-biased gene conversion. <i>Genome Research</i> , 2014, 24, 467-474.	5.5	37
30	Bio++: Efficient Extensible Libraries and Tools for Computational Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2013, 30, 1745-1750.	8.9	163
31	A New Isolation with Migration Model along Complete Genomes Infers Very Different Divergence Processes among Closely Related Great Ape Species. <i>PLoS Genetics</i> , 2012, 8, e1003125.	3.5	102
32	Detecting coevolving positions in a molecule: why and how to account for phylogeny. <i>Briefings in Bioinformatics</i> , 2012, 13, 228-243.	6.5	41
33	Efficient Selection of Branch-Specific Models of Sequence Evolution. <i>Molecular Biology and Evolution</i> , 2012, 29, 1861-1874.	8.9	56
34	Fusion of two divergent fungal individuals led to the recent emergence of a unique widespread pathogen species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 10954-10959.	7.1	171
35	Accelerated evolution and coevolution drove the evolutionary history of AGPase sub-units during angiosperm radiation. <i>Annals of Botany</i> , 2012, 109, 693-708.	2.9	9
36	Ancestral Population Genomics. <i>Methods in Molecular Biology</i> , 2012, 856, 293-313.	0.9	15

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37	Comparing Fungal Genomes: Insight into Functional and Evolutionary Processes. <i>Methods in Molecular Biology</i> , 2012, 835, 531-548.	0.9	7
38	Fast and Robust Characterization of Time-Heterogeneous Sequence Evolutionary Processes Using Substitution Mapping. <i>PLoS ONE</i> , 2012, 7, e33852.	2.5	47
39	The bonobo genome compared with the chimpanzee and human genomes. <i>Nature</i> , 2012, 486, 527-531.	27.8	445
40	Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , 2012, 483, 169-175.	27.8	663
41	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	27.8	541
42	The making of a new pathogen: Insights from comparative population genomics of the domesticated wheat pathogen <i>Mycosphaerella graminicola</i> and its wild sister species. <i>Genome Research</i> , 2011, 21, 2157-2166.	5.5	191
43	Incomplete lineage sorting patterns among human, chimpanzee, and orangutan suggest recent orangutan speciation and widespread selection. <i>Genome Research</i> , 2011, 21, 349-356.	5.5	192
44	IMPACT: Integrated Multiprogram Platform for Analyses in ConTest. <i>Journal of Heredity</i> , 2011, 102, 366-369.	2.4	2
45	Estimating Divergence Time and Ancestral Effective Population Size of Bornean and Sumatran Orangutan Subspecies Using a Coalescent Hidden Markov Model. <i>PLoS Genetics</i> , 2011, 7, e1001319.	3.5	79
46	Base Pairing Constraints Drive Structural Epistasis in Ribosomal RNA Sequences. <i>Molecular Biology and Evolution</i> , 2010, 27, 1868-1876.	8.9	32
47	Ancestral Population Genomics: The Coalescent Hidden Markov Model Approach. <i>Genetics</i> , 2009, 183, 259-274.	2.9	96
48	Detecting Site-Specific Biochemical Constraints Through Substitution Mapping. <i>Journal of Molecular Evolution</i> , 2008, 67, 257-265.	1.8	11
49	Non-homogeneous models of sequence evolution in the Bio++ suite of libraries and programs. <i>BMC Evolutionary Biology</i> , 2008, 8, 255.	3.2	122
50	Evolutionary Modeling of Rate Shifts Reveals Specificity Determinants in HIV-1 Subtypes. <i>PLoS Computational Biology</i> , 2008, 4, e1000214.	3.2	30
51	Coevolution within and between Genes. , 2007, 3, 1-12.		6
52	Detecting groups of co-evolving positions in a molecule: a clustering approach. <i>BMC Evolutionary Biology</i> , 2007, 7, 242.	3.2	46
53	Bio++: a set of C++ libraries for sequence analysis, phylogenetics, molecular evolution and population genetics. <i>BMC Bioinformatics</i> , 2006, 7, 188.	2.6	101
54	Recombination Difference between Sexes: A Role for Haploid Selection. <i>PLoS Biology</i> , 2005, 3, e63.	5.6	238

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55	A Model-Based Approach for Detecting Coevolving Positions in a Molecule. <i>Molecular Biology and Evolution</i> , 2005, 22, 1919-1928.	8.9	131