Julien Y Dutheil

List of Publications by Year
in descending order

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	Insights into hominid evolution from the gorilla genome sequence. Nature, 2012, 483, 169-175.	27.8	663
2	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	27.8	541
3	The bonobo genome compared with the chimpanzee and human genomes. Nature, 2012, 486, 527-531.	27.8	445
4	Recombination Difference between Sexes: A Role for Haploid Selection. PLoS Biology, 2005, 3, e63.	5.6	238
5	Incomplete lineage sorting patterns among human, chimpanzee, and orangutan suggest recent orangutan speciation and widespread selection. Genome Research, 2011, 21, 349-356.	5.5	192
6	The making of a new pathogen: Insights from comparative population genomics of the domesticated wheat pathogen *Mycosphaerella graminicola* and its wild sister species. Genome Research, 2011, 21, 2157-2166.	5.5	191
7	Fusion of two divergent fungal individuals led to the recent emergence of a unique widespread pathogen species. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10954-10959.	7.1	171
8	Bio++: Efficient Extensible Libraries and Tools for Computational Molecular Evolution. Molecular Biology and Evolution, 2013, 30, 1745-1750.	8.9	163
9	A Model-Based Approach for Detecting Coevolving Positions in a Molecule. Molecular Biology and Evolution, 2005, 22, 1919-1928.	8.9	131
10	A Tale of Genome Compartmentalization: The Evolution of Virulence Clusters in Smut Fungi. Genome Biology and Evolution, 2016, 8, 681-704.	2.5	125
11	Non-homogeneous models of sequence evolution in the Bio++ suite of libraries and programs. BMC Evolutionary Biology, 2008, 8, 255.	3.2	122
12	A New Isolation with Migration Model along Complete Genomes Infers Very Different Divergence Processes among Closely Related Great Ape Species. PLoS Genetics, 2012, 8, e1003125.	3.5	102
13	Bio++: a set of C++ libraries for sequence analysis, phylogenetics, molecular evolution and population genetics. BMC Bioinformatics, 2006, 7, 188.	2.6	101
14	Ancestral Population Genomics: The Coalescent Hidden Markov Model Approach. Genetics, 2009, 183, 259-274.	2.9	96
15	Estimating Divergence Time and Ancestral Effective Population Size of Bornean and Sumatran Orangutan Subspecies Using a Coalescent Hidden Markov Model. PLoS Genetics, 2011, 7, e1001319.	3.5	79
16	Extreme selective sweeps independently targeted the X chromosomes of the great apes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6413-6418.	7.1	75
17	MafFilter: a highly flexible and extensible multiple genome alignment files processor. BMC Genomics, 2014, 15, 53.	2.8	68
18	The WOPR Protein Ros1 Is a Master Regulator of Sporogenesis and Late Effector Gene Expression in the Maize Pathogen Ustilago maydis. PLoS Pathogens, 2016, 12, e1005697.	4.7	65

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19	Fine-Scale Recombination Maps of Fungal Plant Pathogens Reveal Dynamic Recombination Landscapes and Intragenic Hotspots. Genetics, 2018, 208, 1209-1229.	2.9	61
20	The genomic determinants of adaptive evolution in a fungal pathogen. Evolution Letters, 2019, 3, 299-312.	3.3	61
21	Efficient Selection of Branch-Specific Models of Sequence Evolution. Molecular Biology and Evolution, 2012, 29, 1861-1874.	8.9	56
22	Strong Selective Sweeps on the X Chromosome in the Human-Chimpanzee Ancestor Explain Its Low Divergence. PLoS Genetics, 2015, 11, e1005451.	3.5	56
23	Positively Selected Effector Genes and Their Contribution to Virulence in the Smut Fungus Sporisorium reilianum. Genome Biology and Evolution, 2018, 10, 629-645.	2.5	48
24	Fast and Robust Characterization of Time-Heterogeneous Sequence Evolutionary Processes Using Substitution Mapping. PLoS ONE, 2012, 7, e33852.	2.5	47
25	Detecting groups of co-evolving positions in a molecule: a clustering approach. BMC Evolutionary Biology, 2007, 7, 242.	3.2	46
26	The Impact of Protein Architecture on Adaptive Evolution. Molecular Biology and Evolution, 2019, 36, 2013-2028.	8.9	42
27	Detecting coevolving positions in a molecule: why and how to account for phylogeny. Briefings in Bioinformatics, 2012, 13, 228-243.	6.5	41
28	The Evolution of Gene-Specific Transcriptional Noise Is Driven by Selection at the Pathway Level. Genetics, 2018, 208, 173-189.	2.9	41
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. Genome Research, 2014, 24, 467-474.	5.5	37
30	Inference of recombination maps from a single pair of genomes and its application to ancient samples. PLoS Genetics, 2019, 15, e1008449.	3.5	34
31	Base Pairing Constraints Drive Structural Epistasis in Ribosomal RNA Sequences. Molecular Biology and Evolution, 2010, 27, 1868-1876.	8.9	32
32	Evolutionary Modeling of Rate Shifts Reveals Specificity Determinants in HIV-1 Subtypes. PLoS Computational Biology, 2008, 4, e1000214.	3.2	30
33	Variation of the adaptive substitution rate between species and within genomes. Evolutionary Ecology, 2020, 34, 315-338.	1.2	30
34	Mitochondrial <scp>DNA</scp> as a tool for reconstructing past life‑history traits in mammals. Journal of Evolutionary Biology, 2014, 27, 899-910.	1.7	17
35	On Variant Discovery in Genomes of Fungal Plant Pathogens. Frontiers in Microbiology, 2020, 11, 626.	3.5	16
36	Ancestral Population Genomics. Methods in Molecular Biology, 2012, 856, 293-313.	0.9	15

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37	Detecting Site-Specific Biochemical Constraints Through Substitution Mapping. Journal of Molecular Evolution, 2008, 67, 257-265.	1.8	11
38	Population Genomics of the Maize Pathogen *Ustilago maydis*: Demographic History and Role of Virulence Clusters in Adaptation. Genome Biology and Evolution, 2021, 13, .	2.5	11
39	Accelerated evolution and coevolution drove the evolutionary history of AGPase sub-units during angiosperm radiation. Annals of Botany, 2012, 109, 693-708.	2.9	9
40	Comparing Fungal Genomes: Insight into Functional and Evolutionary Processes. Methods in Molecular Biology, 2012, 835, 531-548.	0.9	7
41	Coevolution within and between Genes. , 2007, 3, 1-12.		6
42	Optimization of sequence alignments according to the number of sequences vs. number of sites trade-off. BMC Bioinformatics, 2015, 16, 190.	2.6	6
43	Hidden Markov Models in Population Genomics. Methods in Molecular Biology, 2017, 1552, 149-164.	0.9	6
44	Plant pathogens provide clues to the potential origin of bat white-nose syndrome *Pseudogymnoascus destructans*. Virulence, 2022, 13, 1020-1031.	4.4	6
45	The insertion of a mitochondrial selfish element into the nuclear genome and its consequences. Ecology and Evolution, 2020, 10, 11117-11132.	1.9	4
46	A Population Genomics Lexicon. Methods in Molecular Biology, 2020, 2090, 3-17.	0.9	3
47	Processing and Analyzing Multiple Genomes Alignments with MafFilter. Methods in Molecular Biology, 2020, 2090, 21-48.	0.9	3
48	The Structural Determinants of Intra-Protein Compensatory Substitutions. Molecular Biology and Evolution, 2022, 39, .	8.9	3
49	IMPACT: Integrated Multiprogram Platform for Analyses in ConTest. Journal of Heredity, 2011, 102, 366-369.	2.4	2
50	Ancestral Population Genomics. Methods in Molecular Biology, 2019, 1910, 555-589.	0.9	2
51	hotspot: software to support sperm-typing for investigating recombination hotspots. Bioinformatics, 2016, 32, 2554-2555.	4.1	1
52	Title is missing!. , 2019, 15, e1008449.		0
53	Title is missing!. , 2019, 15, e1008449.		0
54	Title is missing!. , 2019, 15, e1008449.		0

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55	Title is missing!. , 2019, 15, e1008449.		0