

Sebastian Duchene

List of Publications by Year in descending order

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91
papers

8,589
citations

87888

38
h-index

60623

81
g-index

121
all docs

121
docs citations

121
times ranked

13377
citing authors

#	ARTICLE	IF	CITATIONS
1	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2019, 15, e1006650.	3.2	2,484
2	Neanderthal behaviour, diet, and disease inferred from ancient DNA in dental calculus. <i>Nature</i> , 2017, 544, 357-361.	27.8	398
3	Temporal signal and the phylodynamic threshold of SARS-CoV-2. <i>Virus Evolution</i> , 2020, 6, veaa061.	4.9	317
4	Molecular clock methods for estimating evolutionary rates and timescales. <i>Molecular Ecology</i> , 2014, 23, 5947-5965.	3.9	290
5	Distinct evolutionary dynamics of horizontal gene transfer in drug resistant and virulent clones of <i>Klebsiella pneumoniae</i> . <i>PLoS Genetics</i> , 2019, 15, e1008114.	3.5	228
6	Genome-scale rates of evolutionary change in bacteria. <i>Microbial Genomics</i> , 2016, 2, e000094.	2.0	224
7	Comparative analysis estimates the relative frequencies of co-divergence and cross-species transmission within viral families. <i>PLoS Pathogens</i> , 2017, 13, e1006215.	4.7	224
8	Population genomics of hypervirulent <i>Klebsiella pneumoniae</i> clonal-group 23 reveals early emergence and rapid global dissemination. <i>Nature Communications</i> , 2018, 9, 2703.	12.8	205
9	17th Century Variola Virus Reveals the Recent History of Smallpox. <i>Current Biology</i> , 2016, 26, 3407-3412.	3.9	197
10	The Performance of the Date-Randomization Test in Phylogenetic Analyses of Time-Structured Virus Data. <i>Molecular Biology and Evolution</i> , 2015, 32, 1895-1906.	8.9	172
11	Analyses of evolutionary dynamics in viruses are hindered by a time-dependent bias in rate estimates. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20140732.	2.6	166
12	Tracking the COVID-19 pandemic in Australia using genomics. <i>Nature Communications</i> , 2020, 11, 4376.	12.8	152
13	Large-Scale Phylogenomic Analysis Reveals the Complex Evolutionary History of Rabies Virus in Multiple Carnivore Hosts. <i>PLoS Pathogens</i> , 2016, 12, e1006041.	4.7	147
14	The impact of calibration and clock-model choice on molecular estimates of divergence times. <i>Molecular Phylogenetics and Evolution</i> , 2014, 78, 277-289.	2.7	135
15	Bayesian molecular dating: opening up the black box. <i>Biological Reviews</i> , 2018, 93, 1165-1191.	10.4	128
16	Mitogenome Phylogenetics: The Impact of Using Single Regions and Partitioning Schemes on Topology, Substitution Rate and Divergence Time Estimation. <i>PLoS ONE</i> , 2011, 6, e27138.	2.5	128
17	Atlas of group A streptococcal vaccine candidates compiled using large-scale comparative genomics. <i>Nature Genetics</i> , 2019, 51, 1035-1043.	21.4	120
18	The molecular clock of <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2019, 15, e1008067.	4.7	107

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19	Genomic epidemiology reveals transmission patterns and dynamics of SARS-CoV-2 in Aotearoa New Zealand. <i>Nature Communications</i> , 2020, 11, 6351.	12.8	100
20	The phylogeography and incidence of multi-drug resistant typhoid fever in sub-Saharan Africa. <i>Nature Communications</i> , 2018, 9, 5094.	12.8	98
21	Simulating and detecting autocorrelation of molecular evolutionary rates among lineages. <i>Molecular Ecology Resources</i> , 2015, 15, 688-696.	4.8	87
22	Analysis of Phylogenomic Tree Space Resolves Relationships Among Marsupial Families. <i>Systematic Biology</i> , 2018, 67, 400-412.	5.6	85
23	Marine turtle mitogenome phylogenetics and evolution. <i>Molecular Phylogenetics and Evolution</i> , 2012, 65, 241-250.	2.7	83
24	Bayesian Evaluation of Temporal Signal in Measurably Evolving Populations. <i>Molecular Biology and Evolution</i> , 2020, 37, 3363-3379.	8.9	81
25	Turnip Mosaic Potyvirus Probably First Spread to Eurasian Brassica Crops from Wild Orchids about 1000 Years Ago. <i>PLoS ONE</i> , 2013, 8, e55336.	2.5	81
26	The Emergence of SARS-CoV-2 Variants of Concern Is Driven by Acceleration of the Substitution Rate. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	78
27	Geographic and temporal dynamics of a global radiation and diversification in the killer whale. <i>Molecular Ecology</i> , 2015, 24, 3964-3979.	3.9	74
28	Declining transition/transversion ratios through time reveal limitations to the accuracy of nucleotide substitution models. <i>BMC Evolutionary Biology</i> , 2015, 15, 36.	3.2	73
29	Laboratory and molecular surveillance of paediatric typhoidal <i>Salmonella</i> in Nepal: Antimicrobial resistance and implications for vaccine policy. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006408.	3.0	70
30	Comment on "Phylogenomics resolves the timing and pattern of insect evolution". <i>Science</i> , 2015, 349, 487-487.	12.6	69
31	The paradox of HBV evolution as revealed from a 16th century mummy. <i>PLoS Pathogens</i> , 2018, 14, e1006750.	4.7	66
32	Pan-genome Analysis of Ancient and Modern <i>Salmonella enterica</i> Demonstrates Genomic Stability of the Invasive Para C Lineage for Millennia. <i>Current Biology</i> , 2018, 28, 2420-2428.e10.	3.9	65
33	Time-dependent estimates of molecular evolutionary rates: evidence and causes. <i>Molecular Ecology</i> , 2015, 24, 6007-6012.	3.9	59
34	ClockstaR: choosing the number of relaxed-clock models in molecular phylogenetic analysis. <i>Bioinformatics</i> , 2014, 30, 1017-1019.	4.1	54
35	Understanding dengue virus evolution to support epidemic surveillance and counter-measure development. <i>Infection, Genetics and Evolution</i> , 2018, 62, 279-295.	2.3	53
36	Genomics-informed responses in the elimination of COVID-19 in Victoria, Australia: an observational, genomic epidemiological study. <i>Lancet Public Health</i> , The, 2021, 6, e547-e556.	10.0	53

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37	The Temporal Evolution and Global Spread of Cauliflower mosaic virus, a Plant Pararetrovirus. PLoS ONE, 2014, 9, e85641.	2.5	51
38	Evolution and Global Transmission of a Multidrug-Resistant, Community-Associated Methicillin-Resistant Staphylococcus aureus Lineage from the Indian Subcontinent. MBio, 2019, 10, .	4.1	50
39	Evaluating the Adequacy of Molecular Clock Models Using Posterior Predictive Simulations. Molecular Biology and Evolution, 2015, 32, 2986-2995.	8.9	46
40	PhyloMAAd: efficient assessment of phylogenomic model adequacy. Bioinformatics, 2018, 34, 2300-2301.	4.1	46
41	Linking Branch Lengths across Sets of Loci Provides the Highest Statistical Support for Phylogenetic Inference. Molecular Biology and Evolution, 2020, 37, 1202-1210.	8.9	42
42	Phylogenetic uncertainty can bias the number of evolutionary transitions estimated from ancestral state reconstruction methods. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2015, 324, 517-524.	1.3	39
43	Tree imbalance causes a bias in phylogenetic estimation of evolutionary timescales using heterochronous sequences. Molecular Ecology Resources, 2015, 15, 785-794.	4.8	39
44	Genomic Epidemiology of the First Wave of SARS-CoV-2 in Italy. Viruses, 2020, 12, 1438.	3.3	39
45	Estimating evolutionary rates using time-structured data: a general comparison of phylogenetic methods. Bioinformatics, 2016, 32, 3375-3379.	4.1	38
46	Continental synchronicity of human influenza virus epidemics despite climactic variation. PLoS Pathogens, 2018, 14, e1006780.	4.7	38
47	Can Sequence Phylogenies Safely Infer the Origin of the Global Virome?. MBio, 2019, 10, .	4.1	37
48	Benign Rabbit Caliciviruses Exhibit Evolutionary Dynamics Similar to Those of Their Virulent Relatives. Journal of Virology, 2016, 90, 9317-9329.	3.4	36
49	New Statistical Criteria Detect Phylogenetic Bias Caused by Compositional Heterogeneity. Molecular Biology and Evolution, 2017, 34, 1529-1534.	8.9	35
50	Evolutionary dynamics of multidrug resistant Salmonella enterica serovar 4,[5],12:i:- in Australia. Nature Communications, 2021, 12, 4786.	12.8	35
51	The first wave of the COVID-19 epidemic in Spain was associated with early introductions and fast spread of a dominating genetic variant. Nature Genetics, 2021, 53, 1405-1414.	21.4	35
52	The Recovery, Interpretation and Use of Ancient Pathogen Genomes. Current Biology, 2020, 30, R1215-R1231.	3.9	33
53	The Asian Lineage of Zika Virus: Transmission and Evolution in Asia and the Americas. Virologica Sinica, 2019, 34, 1-8.	3.0	30
54	Multiple introductions of multidrug-resistant typhoid associated with acute infection and asymptomatic carriage, Kenya. ELife, 2021, 10, .	6.0	29

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55	Phylogeography, genetic diversity and population structure of common bottlenose dolphins in the Caribbean inferred from analyses of mitochondrial DNA control region sequences and microsatellite loci: conservation and management implications. <i>Animal Conservation</i> , 2012, 15, 95-112.	2.9	28
56	Using multiple relaxed-clock models to estimate evolutionary timescales from DNA sequence data. <i>Molecular Phylogenetics and Evolution</i> , 2014, 77, 65-70.	2.7	28
57	Substitution Model Adequacy and Assessing the Reliability of Estimates of Virus Evolutionary Rates and Time Scales. <i>Molecular Biology and Evolution</i> , 2016, 33, 255-267.	8.9	28
58	Initial Evidence for Adaptive Selection on the NADH Subunit Two of Freshwater Dolphins by Analyses of Mitochondrial Genomes. <i>PLoS ONE</i> , 2015, 10, e0123543.	2.5	28
59	Tracing Ancient Human Migrations into Sahul Using Hepatitis B Virus Genomes. <i>Molecular Biology and Evolution</i> , 2019, 36, 942-954.	8.9	26
60	Development of Phylodynamic Methods for Bacterial Pathogens. <i>Trends in Microbiology</i> , 2021, 29, 788-797.	7.7	26
61	Phylodynamic Model Adequacy Using Posterior Predictive Simulations. <i>Systematic Biology</i> , 2019, 68, 358-364.	5.6	25
62	Phylogeography and Sex-Biased Dispersal across Riverine Manatee Populations (<i>Trichechus inunguis</i>) Tj ETQq0 0 0 rBT /Overlock 10 Tf	2.5	23
63	A comparison of methods for estimating substitution rates from ancient DNA sequence data. <i>BMC Evolutionary Biology</i> , 2018, 18, 70.	3.2	23
64	Cross-validation to select Bayesian hierarchical models in phylogenetics. <i>BMC Evolutionary Biology</i> , 2016, 16, 115.	3.2	19
65	Characterisation of <i>Treponema pallidum</i> lineages within the contemporary syphilis outbreak in Australia: a genomic epidemiological analysis. <i>Lancet Microbe</i> , The, 2022, 3, e417-e426.	7.3	19
66	Niche-specific genome degradation and convergent evolution shaping <i>Staphylococcus aureus</i> adaptation during severe infections. <i>ELife</i> , 0, 11, .	6.0	18
67	Mammalian genome evolution is governed by multiple pacemakers. <i>Bioinformatics</i> , 2015, 31, 2061-2065.	4.1	17
68	Inferring demographic parameters in bacterial genomic data using Bayesian and hybrid phylogenetic methods. <i>BMC Evolutionary Biology</i> , 2018, 18, 95.	3.2	16
69	Infectious disease phylodynamics with occurrence data. <i>Methods in Ecology and Evolution</i> , 2021, 12, 1498-1507.	5.2	14
70	Evolution, Expression, and Function of Nonneuronal Ligand-Gated Chloride Channels in <i>Drosophila melanogaster</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2003-2012.	1.8	13
71	Estimating the number and assignment of clock models in analyses of multigene datasets. <i>Bioinformatics</i> , 2016, 32, 1281-1285.	4.1	13
72	Differences in Performance among Test Statistics for Assessing Phylogenomic Model Adequacy. <i>Genome Biology and Evolution</i> , 2018, 10, 1375-1388.	2.5	13

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73	Genome Analysis of Coxsackievirus A4 Isolates From Hand, Foot, and Mouth Disease Cases in Shandong, China. <i>Frontiers in Microbiology</i> , 2019, 10, 1001.	3.5	12
74	Exploring the evolution and epidemiology of European CC1-MRSA-IV: tracking a multidrug-resistant community-associated methicillin-resistant <i>Staphylococcus aureus</i> clone. <i>Microbial Genomics</i> , 2021, 7, .	2.0	10
75	Phylogenetic Inference of Bacterial Outbreak Parameters Using Nanopore Sequencing. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	9
76	Evolutionary stasis of viruses?. <i>Nature Reviews Microbiology</i> , 2019, 17, 329-329.	28.6	8
77	Dating the emergence of human pathogens. <i>Science</i> , 2020, 368, 1310-1311.	12.6	8
78	The impact of public health interventions in the Nordic countries during the first year of SARS-CoV-2 transmission and evolution. <i>Eurosurveillance</i> , 2021, 26, .	7.0	8
79	Estimating evolutionary rates in giant viruses using ancient genomes. <i>Virus Evolution</i> , 2018, 4, vey006.	4.9	7
80	The impacts of drift and selection on genomic evolution in insects. <i>PeerJ</i> , 2017, 5, e3241.	2.0	6
81	Genomic epidemiology of <i>Salmonella</i> Typhi in Central Division, Fiji, 2012 to 2016. <i>The Lancet Regional Health - Western Pacific</i> , 2022, 24, 100488.	2.9	6
82	Tightly Constrained Genome Reduction and Relaxation of Purifying Selection during Secondary Plastid Endosymbiosis. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	5
83	SNPPar: identifying convergent evolution and other homoplasies from microbial whole-genome alignments. <i>Microbial Genomics</i> , 2021, 7, .	2.0	5
84	Real-Time and Remote MCMC Trace Inspection with Beastiary. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	5
85	Limited Sustained Local Transmission of HIV-1 CRF01_AE in New South Wales, Australia. <i>Viruses</i> , 2019, 11, 482.	3.3	4
86	Estimating Evolutionary Rates and Timescales from Time-Stamped Data. , 2020, , 157-174.		3
87	The International Virus Bioinformatics Meeting 2022. <i>Viruses</i> , 2022, 14, 973.	3.3	3
88	The Impacts of Low Diversity Sequence Data on Phylogenetic Inference during an Emerging Epidemic. <i>Viruses</i> , 2021, 13, 79.	3.3	2
89	A 16th century <i>Escherichia coli</i> draft genome associated with an opportunistic bile infection. <i>Communications Biology</i> , 2022, 5, .	4.4	2
90	Assessment of Coronavirus Disease 2019 Intervention Strategies in the Nordic Countries Using Genomic Epidemiology. <i>Open Forum Infectious Diseases</i> , 2022, 9, ofab665.	0.9	0

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91	Genomic Characterisation Reveals a Dominant Lineage of SARS-CoV-2 in Papua New Guinea. Virus Evolution, 0, , .	4.9	0