

# Sebastian Duchene

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3766362/publications.pdf>

Version: 2024-02-01

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	Tightly Constrained Genome Reduction and Relaxation of Purifying Selection during Secondary Plastid Endosymbiosis. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	5
2	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
3	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
4	Phylodynamic Inference of Bacterial Outbreak Parameters Using Nanopore Sequencing. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	9
5	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
6	Real-Time and Remote MCMC Trace Inspection with Beastiary. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	5
7	The International Virus Bioinformatics Meeting 2022. <i>Viruses</i> , 2022, 14, 973.	3.3	3
8	A 16th century <i>Escherichia coli</i> draft genome associated with an opportunistic bile infection. <i>Communications Biology</i> , 2022, 5, .	4.4	2
9	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
10	The Impacts of Low Diversity Sequence Data on Phylodynamic Inference during an Emerging Epidemic. <i>Viruses</i> , 2021, 13, 79.	3.3	2
11	Infectious disease phylodynamics with occurrence data. <i>Methods in Ecology and Evolution</i> , 2021, 12, 1498-1507.	5.2	14
12	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
13	Evolutionary dynamics of multidrug resistant <i>Salmonella enterica</i> serovar 4,[5],12:i:- in Australia. <i>Nature Communications</i> , 2021, 12, 4786.	12.8	35
14	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
15	The first wave of the COVID-19 epidemic in Spain was associated with early introductions and fast spread of a dominating genetic variant. <i>Nature Genetics</i> , 2021, 53, 1405-1414.	21.4	35
16	Development of Phylodynamic Methods for Bacterial Pathogens. <i>Trends in Microbiology</i> , 2021, 29, 788-797.	7.7	26
17	Multiple introductions of multidrug-resistant typhoid associated with acute infection and asymptomatic carriage, Kenya. <i>ELife</i> , 2021, 10, .	6.0	29
18	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

#	ARTICLE	IF	CITATIONS
19	SNPPar: identifying convergent evolution and other homoplasies from microbial whole-genome alignments. <i>Microbial Genomics</i> , 2021, 7, .	2.0	5
20	Linking Branch Lengths across Sets of Loci Provides the Highest Statistical Support for Phylogenetic Inference. <i>Molecular Biology and Evolution</i> , 2020, 37, 1202-1210.	8.9	42
21	Temporal signal and the phylodynamic threshold of SARS-CoV-2. <i>Virus Evolution</i> , 2020, 6, veaa061.	4.9	317
22	The Recovery, Interpretation and Use of Ancient Pathogen Genomes. <i>Current Biology</i> , 2020, 30, R1215-R1231.	3.9	33
23	Bayesian Evaluation of Temporal Signal in Measurably Evolving Populations. <i>Molecular Biology and Evolution</i> , 2020, 37, 3363-3379.	8.9	81
24	Tracking the COVID-19 pandemic in Australia using genomics. <i>Nature Communications</i> , 2020, 11, 4376.	12.8	152
25	Genomic Epidemiology of the First Wave of SARS-CoV-2 in Italy. <i>Viruses</i> , 2020, 12, 1438.	3.3	39
26	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
27	Dating the emergence of human pathogens. <i>Science</i> , 2020, 368, 1310-1311.	12.6	8
28	Estimating Evolutionary Rates and Timescales from Time-Stamped Data. , 2020, , 157-174.		3
29	Phylodynamic Model Adequacy Using Posterior Predictive Simulations. <i>Systematic Biology</i> , 2019, 68, 358-364.	5.6	25
30	The molecular clock of <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2019, 15, e1008067.	4.7	107
31	The Asian Lineage of Zika Virus: Transmission and Evolution in Asia and the Americas. <i>Virologica Sinica</i> , 2019, 34, 1-8.	3.0	30
32	Atlas of group A streptococcal vaccine candidates compiled using large-scale comparative genomics. <i>Nature Genetics</i> , 2019, 51, 1035-1043.	21.4	120
33	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
34	Limited Sustained Local Transmission of HIV-1 CRF01_AE in New South Wales, Australia. <i>Viruses</i> , 2019, 11, 482.	3.3	4
35	Can Sequence Phylogenies Safely Infer the Origin of the Global Virome?. <i>MBio</i> , 2019, 10, .	4.1	37
36	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

#	ARTICLE	IF	CITATIONS
37	Tracing Ancient Human Migrations into Sahul Using Hepatitis B Virus Genomes. <i>Molecular Biology and Evolution</i> , 2019, 36, 942-954.	8.9	26
38	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. <i>PLoS Computational Biology</i> , 2019, 15, e1006650.	3.2	2,484
39	Evolutionary stasis of viruses?. <i>Nature Reviews Microbiology</i> , 2019, 17, 329-329.	28.6	8
40	Evolution and Global Transmission of a Multidrug-Resistant, Community-Associated Methicillin-Resistant <i>Staphylococcus aureus</i> Lineage from the Indian Subcontinent. <i>MBio</i> , 2019, 10, .	4.1	50
41	Estimating evolutionary rates in giant viruses using ancient genomes. <i>Virus Evolution</i> , 2018, 4, vey006.	4.9	7
42	PhyloMAAd: efficient assessment of phylogenomic model adequacy. <i>Bioinformatics</i> , 2018, 34, 2300-2301.	4.1	46
43	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
44	Analysis of Phylogenomic Tree Space Resolves Relationships Among Marsupial Families. <i>Systematic Biology</i> , 2018, 67, 400-412.	5.6	85
45	Bayesian molecular dating: opening up the black box. <i>Biological Reviews</i> , 2018, 93, 1165-1191.	10.4	128
46	The phylogeography and incidence of multi-drug resistant typhoid fever in sub-Saharan Africa. <i>Nature Communications</i> , 2018, 9, 5094.	12.8	98
47	A comparison of methods for estimating substitution rates from ancient DNA sequence data. <i>BMC Evolutionary Biology</i> , 2018, 18, 70.	3.2	23
48	Differences in Performance among Test Statistics for Assessing Phylogenomic Model Adequacy. <i>Genome Biology and Evolution</i> , 2018, 10, 1375-1388.	2.5	13
49	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
50	Inferring demographic parameters in bacterial genomic data using Bayesian and hybrid phylogenetic methods. <i>BMC Evolutionary Biology</i> , 2018, 18, 95.	3.2	16
51	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
52	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
53	Continental synchronicity of human influenza virus epidemics despite climactic variation. <i>PLoS Pathogens</i> , 2018, 14, e1006780.	4.7	38
54	The paradox of HBV evolution as revealed from a 16th century mummy. <i>PLoS Pathogens</i> , 2018, 14, e1006750.	4.7	66

#	ARTICLE	IF	CITATIONS
55	Neanderthal behaviour, diet, and disease inferred from ancient DNA in dental calculus. <i>Nature</i> , 2017, 544, 357-361.	27.8	398
56	New Statistical Criteria Detect Phylogenetic Bias Caused by Compositional Heterogeneity. <i>Molecular Biology and Evolution</i> , 2017, 34, 1529-1534.	8.9	35
57	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
58	The impacts of drift and selection on genomic evolution in insects. <i>PeerJ</i> , 2017, 5, e3241.	2.0	6
59	Genome-scale rates of evolutionary change in bacteria. <i>Microbial Genomics</i> , 2016, 2, e000094.	2.0	224
60	Cross-validation to select Bayesian hierarchical models in phylogenetics. <i>BMC Evolutionary Biology</i> , 2016, 16, 115.	3.2	19
61	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
62	17th Century Variola Virus Reveals the Recent History of Smallpox. <i>Current Biology</i> , 2016, 26, 3407-3412.	3.9	197
63	Benign Rabbit Caliciviruses Exhibit Evolutionary Dynamics Similar to Those of Their Virulent Relatives. <i>Journal of Virology</i> , 2016, 90, 9317-9329.	3.4	36
64	Estimating evolutionary rates using time-structured data: a general comparison of phylogenetic methods. <i>Bioinformatics</i> , 2016, 32, 3375-3379.	4.1	38
65	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
66	Estimating the number and assignment of clock models in analyses of multigene datasets. <i>Bioinformatics</i> , 2016, 32, 1281-1285.	4.1	13
67	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
68	Phylogenetic uncertainty can bias the number of evolutionary transitions estimated from ancestral state reconstruction methods. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2015, 324, 517-524.	1.3	39
69	Tree imbalance causes a bias in phylogenetic estimation of evolutionary timescales using heterochronous sequences. <i>Molecular Ecology Resources</i> , 2015, 15, 785-794.	4.8	39
70	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
71	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
72	Time-dependent estimates of molecular evolutionary rates: evidence and causes. <i>Molecular Ecology</i> , 2015, 24, 6007-6012.	3.9	59

#	ARTICLE	IF	CITATIONS
73	Evaluating the Adequacy of Molecular Clock Models Using Posterior Predictive Simulations. <i>Molecular Biology and Evolution</i> , 2015, 32, 2986-2995.	8.9	46
74	Mammalian genome evolution is governed by multiple pacemakers. <i>Bioinformatics</i> , 2015, 31, 2061-2065.	4.1	17
75	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
76	Comment on "Phylogenomics resolves the timing and pattern of insect evolution". <i>Science</i> , 2015, 349, 487-487.	12.6	69
77	Simulating and detecting autocorrelation of molecular evolutionary rates among lineages. <i>Molecular Ecology Resources</i> , 2015, 15, 688-696.	4.8	87
78	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
79	The Temporal Evolution and Global Spread of Cauliflower mosaic virus, a Plant Pararetrovirus. <i>PLoS ONE</i> , 2014, 9, e85641.	2.5	51
80	ClockstaR: choosing the number of relaxed-clock models in molecular phylogenetic analysis. <i>Bioinformatics</i> , 2014, 30, 1017-1019.	4.1	54
81	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
82	Molecular clock methods for estimating evolutionary rates and timescales. <i>Molecular Ecology</i> , 2014, 23, 5947-5965.	3.9	290
83	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
84	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
85	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
86	Phylogeography and Sex-Biased Dispersal across Riverine Manatee Populations ( <i>Trichechus inunguis</i> ) in the Neotropics. <i>Molecular Biology and Evolution</i> , 2013, 30, 1017-1019.	2.5	28
87	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
88	Marine turtle mitogenome phylogenetics and evolution. <i>Molecular Phylogenetics and Evolution</i> , 2012, 65, 241-250.	2.7	83
89	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
90	Genomic Characterisation Reveals a Dominant Lineage of SARS-CoV-2 in Papua New Guinea. <i>Virus Evolution</i> , 2020, 6, vnaa010.	4.9	0

#	ARTICLE	IF	CITATIONS
91	Niche-specific genome degradation and convergent evolution shaping <i>Staphylococcus aureus</i> adaptation during severe infections. <i>ELife</i> , 0, 11, .	6.0	18