Simon Dellicour

List of Publications by Year
in descending order

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100 papers	5,849 citations	147801 31 h-index	106344 65 g-index
127 all docs	127 docs citations	127 times ranked	9563 citing authors

#	Article	IF	Citations
1	Considerable escape of SARS-CoV-2 Omicron to antibody neutralization. Nature, 2022, 602, 671-675.	27.8	1,202
2	Evolution and epidemic spread of SARS-CoV-2 in Brazil. Science, 2020, 369, 1255-1260.	12.6	454
3	Virus genomes reveal factors that spread and sustained the Ebola epidemic. Nature, 2017, 544, 309-315.	27.8	346
4	Genomic and epidemiological monitoring of yellow fever virus transmission potential. Science, 2018, 361, 894-899.	12.6	279
5	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. Science, 2021, 373, 889-895.	12.6	142
6	HIV persists throughout deep tissues with repopulation from multiple anatomical sources. Journal of Clinical Investigation, 2020, 130, 1699-1712.	8.2	140
7	Untangling introductions and persistence in COVID-19 resurgence in Europe. Nature, 2021, 595, 713-717.	27.8	133
8	The hitchhiker's guide to singleâ€•locus species delimitation. Molecular Ecology Resources, 2018, 18, 1234-1246.	4.8	131
9	SERAPHIM: studying environmental rasters and phylogenetically informed movements. Bioinformatics, 2016, 32, 3204-3206.	4.1	124
10	HIV Rebound Is Predominantly Fueled by Genetically Identical Viral Expansions from Diverse Reservoirs. Cell Host and Microbe, 2019, 26, 347-358.e7.	11.0	117
11	Early introductions and transmission of SARS-CoV-2 variant B.1.1.7 in the United States. Cell, 2021, 184, 2595-2604.e13.	28.9	113
12	Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases. Virus Evolution, 2016, 2, vew016.	4.9	105
13	Explaining the geographic spread of emerging epidemics: a framework for comparing viral phylogenies and environmental landscape data. BMC Bioinformatics, 2016, 17, 82.	2.6	94
14	<scp>spads</scp> 1.0: a toolbox to perform spatial analyses on <scp>DNA</scp> sequence data sets. Molecular Ecology Resources, 2014, 14, 647-651.	4.8	91
15	Delimiting Species-Poor Data Sets using Single Molecular Markers: A Study of Barcode Gaps, Haplowebs and GMYC. Systematic Biology, 2015, 64, 900-908.	5.6	91
16	Considerable escape of SARS-CoV-2 Omicron to antibody neutralization. Nature, 0, , .	27.8	88
17	A Phylodynamic Workflow to Rapidly Gain Insights into the Dispersal History and Dynamics of SARS-CoV-2 Lineages. Molecular Biology and Evolution, 2021, 38, 1608-1613.	8.9	79
18	Genomic Epidemiology, Evolution, and Transmission Dynamics of Porcine Deltacoronavirus. Molecular Biology and Evolution, 2020, 37, 2641-2654.	8.9	76

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19	Patterns of Genetic and Reproductive Traits Differentiation in Mainland vs. Corsican Populations of Bumblebees. PLoS ONE, 2013, 8, e65642.	2.5	72
20	Geographical and Historical Patterns in the Emergences of Novel Highly Pathogenic Avian Influenza (HPAI) H5 and H7 Viruses in Poultry. Frontiers in Veterinary Science, 2018, 5, 84.	2.2	72
21	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 12522-12523.	7.1	68
22	Using Viral Gene Sequences to Compare and Explain the Heterogeneous Spatial Dynamics of Virus Epidemics. Molecular Biology and Evolution, 2017, 34, 2563-2571.	8.9	64
23	Global effects of extreme temperatures on wild bumblebees. Conservation Biology, 2021, 35, 1507-1518.	4.7	64
24	Phylodynamic assessment of intervention strategies for the West African Ebola virus outbreak. Nature Communications, 2018, 9, 2222.	12.8	59
25	Scent of a break-up: phylogeography and reproductive trait divergences in the red-tailed bumblebee (Bombus lapidarius). BMC Evolutionary Biology, 2013, 13, 263.	3.2	55
26	Methods for species delimitation in bumblebees (<scp>H</scp>ymenoptera, <scp>A</scp>pidae,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.7	51
27	Phylogeography of Lassa Virus in Nigeria. Journal of Virology, 2019, 93, .	3.4	49
28	Recent advances in computational phylodynamics. Current Opinion in Virology, 2018, 31, 24-32.	5.4	45
29	An integrative taxonomic approach to assess the status of <scp>C</scp>orsican bumblebees: implications for conservation. Animal Conservation, 2015, 18, 236-248.	2.9	42
30	Genomic Surveillance of Yellow Fever Virus Epizootic in SÃ£o Paulo, Brazil, 2016 â€“ 2018. PLoS Pathogens, 2020, 16, e1008699.	4.7	39
31	Distinct rates and patterns of spread of the major HIV-1 subtypes in Central and East Africa. PLoS Pathogens, 2019, 15, e1007976.	4.7	37
32	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. Cell Reports, 2020, 30, 2275-2283.e7.	6.4	37
33	Transmission dynamics of re-emerging rabies in domestic dogs of rural China. PLoS Pathogens, 2018, 14, e1007392.	4.7	35
34	Epidemiological hypothesis testing using a phylogeographic and phylodynamic framework. Nature Communications, 2020, 11, 5620.	12.8	35
35	Phylogeography Reveals Association between Swine Trade and the Spread of Porcine Epidemic Diarrhea Virus in China and across the World. Molecular Biology and Evolution, 2022, 39, .	8.9	35
36	Molecular and chemical characters to evaluate species status of two cuckoo bumblebees: <i>Bombus barbutellus</i> and <i>Bombus maxillosus</i> (Hymenoptera, Apidae, Bombini). Systematic Entomology, 2011, 36, 453-469.	3.9	34

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37	Molecular phylogeny, biogeography, and host plant shifts in the bee genus Melitta (Hymenoptera:) Tj ETQq1 1 0.784314 rgBT /Overlo	2.7	34
38	Using phylogeographic approaches to analyse the dispersal history, velocity and direction of viral lineagesÂâ€”ÂApplication to rabies virus spread in Iran. Molecular Ecology, 2019, 28, 4335-4350.	3.9	34
39	Unravelling the dispersal dynamics and ecological drivers of the African swine fever outbreak in Belgium. Journal of Applied Ecology, 2020, 57, 1619-1629.	4.0	33
40	SARS-CoV-2 genomic characterization and clinical manifestation of the COVID-19 outbreak in Uruguay. Emerging Microbes and Infections, 2021, 10, 51-65.	6.5	33
41	Distribution and predictors of wing shape and size variability in three sister species of solitary bees. PLoS ONE, 2017, 12, e0173109.	2.5	33
42	Relax, Keep Walking â€” A Practical Guide to Continuous Phylogeographic Inference with BEAST. Molecular Biology and Evolution, 2021, 38, 3486-3493.	8.9	31
43	Ecological niche modelling and coalescent simulations to explore the recent geographical range history of five widespread bumblebee species in Europe. Journal of Biogeography, 2017, 44, 39-50.	3.0	30
44	On the importance of negative controls in viral landscape phylogeography. Virus Evolution, 2018, 4, vey023.	4.9	29
45	Spatioâ€temporal analysis of Nova virus, a divergent hantavirus circulating in the European mole in Belgium. Molecular Ecology, 2016, 25, 5994-6008.	3.9	28
46	Population structure and genetic diversity of red deer (Cervus elaphus) in forest fragments in north-western France. Conservation Genetics, 2011, 12, 1287-1297.	1.5	26
47	Comparative Circulation Dynamics of the Five Main HIV Types in China. Journal of Virology, 2020, 94, .	3.4	26
48	<scp>GCALIGNER</scp> 1.0: An alignment program to compute a multiple sample comparison data matrix from large ecoâ€chemical datasets obtained by <scp>GC</scp>. Journal of Separation Science, 2013, 36, 3206-3209.	2.5	25
49	Mass migration to Europe: an opportunity for elimination of hepatitis B virus?. The Lancet Gastroenterology and Hepatology, 2019, 4, 315-323.	8.1	25
50	Cross-border spread, lineage displacement and evolutionary rate estimation of rabies virus in Yunnan Province, China. Virology Journal, 2017, 14, 102.	3.4	24
51	Dispersal dynamics of SARS-CoV-2 lineages during the first epidemic wave in New York City. PLoS Pathogens, 2021, 17, e1009571.	4.7	24
52	Genomic sequencing of SARS-CoV-2 in Rwanda reveals the importance of incoming travelers on lineage diversity. Nature Communications, 2021, 12, 5705.	12.8	24
53	Comparing patterns and scales of plant virus phylogeography: Rice yellow mottle virus in Madagascar and in continental Africa. Virus Evolution, 2019, 5, vez023.	4.9	22
54	Impact of past climatic changes and resource availability on the population demography of three foodâ€specialist bees. Molecular Ecology, 2015, 24, 1074-1090.	3.9	21

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55	Molecular archaeoparasitology identifies cultural changes in the Medieval Hanseatic trading centre of LÃ¼beck. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20180991.	2.6	21
56	Comparative phylogeography of five bumblebees: impact of range fragmentation, range size and diet specialization. Biological Journal of the Linnean Society, 2015, 116, 926-939.	1.6	20
57	Host relatedness and landscape connectivity shape pathogen spread in the puma, a large secretive carnivore. Communications Biology, 2021, 4, 12.	4.4	20
58	INFERRING THE PAST AND PRESENT CONNECTIVITY ACROSS THE RANGE OF A NORTH AMERICAN LEAF BEETLE: COMBINING ECOLOGICAL NICHE MODELING AND A GEOGRAPHICALLY EXPLICIT MODEL OF COALESCENCE. Evolution; International Journal of Organic Evolution, 2014, 68, n/a-n/a.	2.3	19
59	Host Genetic Variation Does Not Determine Spatio-Temporal Patterns of European Bat 1 Lyssavirus. Genome Biology and Evolution, 2017, 9, 3202-3213.	2.5	19
60	Dynamics and Dispersal of Local Human Immunodeficiency Virus Epidemics Within San Diego and Across the San Diegoâ€“Tijuana Border. Clinical Infectious Diseases, 2021, 73, e2018-e2025.	5.8	19
61	Wildlife conservation strategies should incorporate both taxon identity and geographical context â€• further evidence with bumblebees. Diversity and Distributions, 2020, 26, 1741-1751.	4.1	19
62	nosoi: A stochastic agentâ€based transmission chain simulation framework in <scp>r</scp>. Methods in Ecology and Evolution, 2020, 11, 1002-1007.	5.2	19
63	Conservation genetics of European bees: new insights from the continental scale. Conservation Genetics, 2017, 18, 585-596.	1.5	17
64	Identifying the patterns and drivers of Puumala hantavirus enzootic dynamics using reservoir sampling. Virus Evolution, 2019, 5, vez009.	4.9	16
65	Leveraging of SARS-CoV-2 PCR Cycle Thresholds Values to Forecast COVID-19 Trends. Frontiers in Medicine, 2021, 8, 743988.	2.6	16
66	Inferring the mode of colonization of the rapid range expansion of a solitary bee from multilocus <scp>DNA</scp> sequence variation. Journal of Evolutionary Biology, 2014, 27, 116-132.	1.7	15
67	In Search of Covariates of HIV-1 Subtype B Spread in the United Statesâ€”A Cautionary Tale of Large-Scale Bayesian Phylogeography. Viruses, 2020, 12, 182.	3.3	15
68	Massive Parallelization Boosts Big Bayesian Multidimensional Scaling. Journal of Computational and Graphical Statistics, 2021, 30, 11-24.	1.7	15
69	Mathematical modelling and phylodynamics for the study of dog rabies dynamics and control: A scoping review. PLoS Neglected Tropical Diseases, 2021, 15, e0009449.	3.0	15
70	Comparing Phylogeographic Hypotheses by Simulating DNA Sequences under a Spatially Explicit Model of Coalescence. Molecular Biology and Evolution, 2014, 31, 3359-3372.	8.9	14
71	Glacial survival of trophically linked boreal species in northern Europe. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20162799.	2.6	13
72	Symptom evolution following the emergence of maize streak virus. ELife, 2020, 9, .	6.0	13

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73	Landscape genetic analyses of Cervus elaphus and Sus scrofa: comparative study and analytical developments. Heredity, 2019, 123, 228-241.	2.6	12
74	High dispersal capacity of Culicoides obsoletus (Diptera: Ceratopogonidae), vector of bluetongue and Schmallenberg viruses, revealed by landscape genetic analyses. Parasites and Vectors, 2021, 14, 93.	2.5	12
75	Incorporating heterogeneous sampling probabilities in continuous phylogeographic inference â€” Application to H5N1 spread in the Mekong region. Bioinformatics, 2020, 36, 2098-2104.	4.1	11
76	Getting off on the right foot: Integration of spatial distribution of genetic variability for aquaculture development and regulations, the European perch case. Aquaculture, 2020, 521, 734981.	3.5	11
77	Exploiting genomic surveillance to map the spatio-temporal dispersal of SARS-CoV-2 spike mutations in Belgium across 2020. Scientific Reports, 2021, 11, 18580.	3.3	10
78	On the Use of Phylogeographic Inference to Infer the Dispersal History of Rabies Virus: A Review Study. Viruses, 2021, 13, 1628.	3.3	9
79	Rivers and landscape ecology of a plant virus, Rice yellow mottle virus along the Niger Valley. Virus Evolution, 2021, 7, .	4.9	9
80	Transmission networks of SARS-CoV-2 in Coastal Kenya during the first two waves: A retrospective genomic study. ELife, 0, 11, .	6.0	9
81	The impact of anthropogenic and environmental factors on human rabies cases in China. Transboundary and Emerging Diseases, 2020, 67, 2544-2553.	3.0	8
82	Accommodating sampling location uncertainty in continuous phylogeography. Virus Evolution, 2022, 8, .	4.9	8
83	Investigating the drivers of the spatio-temporal heterogeneity in COVID-19 hospital incidenceâ€"Belgium as a study case. International Journal of Health Geographics, 2021, 20, 29.	2.5	7
84	The evolution of ant worker polymorphism correlates with multiple social traits. Behavioral Ecology and Sociobiology, 2021, 75, 1.	1.4	7
85	Phylogeographic analysis of footâ€andâ€mouth disease virus serotype O dispersal and associated drivers in East Africa. Molecular Ecology, 2021, 30, 3815-3825.	3.9	6
86	Variant Analysis of SARS-CoV-2 Genomes from Belgian Military Personnel Engaged in Overseas Missions and Operations. Viruses, 2021, 13, 1359.	3.3	6
87	Hunting alters viral transmission and evolution in a large carnivore. Nature Ecology and Evolution, 2022, 6, 174-182.	7.8	5
88	Genome-wide diversity of Zika virus: Exploring spatio-temporal dynamics to guide a new nomenclature proposal. Virus Evolution, 2022, 8, veac029.	4.9	5
89	Divergent geographic patterns of genetic diversity among wild bees: Conservation implications. Diversity and Distributions, 2018, 24, 1860-1868.	4.1	4
90	Split it up and see: using proxies to highlight divergent inter-populational performances in aquaculture standardised conditions. Bmc Ecology and Evolution, 2021, 21, 206.	1.6	3

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91	Phycova â€” a tool for exploring covariates of pathogen spread. Virus Evolution, 2022, 8, veac015.	4.9	3
92	Biologie, observations et collectes de trois espÃ¨ces sÅ“urs du genre Melitta Kirby, 1802 (Hymenoptera,) Tj ETQq0 0 0 rgBT /Overlock 10	0.0	2
93	Oligolectisme de Bombus brodmannicus delmasi TkalcÅ¯, 1973 (Hymenoptera, Apidae) : observations et analyses. Osmia, 0, 5, 8-11.	0.0	2
94	Evaluation of Screening Program and Phylogenetic Analysis of SARS-CoV-2 Infections among Hospital Healthcare Workers in LiÃ¨ge, Belgium. Viruses, 2022, 14, 1302.	3.3	2
95	A32â€ƒGenomic surveillance of Zika virus transmission in the Amazonas State, Brazil. Virus Evolution, 2019, 5, .	4.9	0
96	Estimating Migration of <i>Gonioctena quinquepunctata</i> (Coleoptera: Chrysomelidae) Inside a Mountain Range in a Spatially Explicit Context. Insect Systematics and Diversity, 2021, 5, .	1.7	0
97	Bombus gerstaeckeri Morawitz, 1881 (Hymenoptera, Apidae) : observations sur la biologie dâ€™un bourdon localisÃ© et oligolectique. Osmia, 0, 5, 12-14.	0.0	0
98	Historical and geographical patterns of new HPAIV emergences and association with spatial factors. Frontiers in Veterinary Science, 0, 6, .	2.2	0
99	Investigating the impact of environmental factors on the African Swine Fever epidemic in Belgium. Frontiers in Veterinary Science, 0, 6, .	2.2	0
100	Investigating COVID-19 Vaccine Impact on the Risk of Hospitalisation through the Analysis of National Surveillance Data Collected in Belgium. Viruses, 2022, 14, 1315.	3.3	0