

Simon Dellicour

List of Publications by Year in descending order

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Version: 2024-02-01

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. <i>Nature</i> , 2022, 602, 671-675.	27.8	1,202
2	Hunting alters viral transmission and evolution in a large carnivore. <i>Nature Ecology and Evolution</i> , 2022, 6, 174-182.	7.8	5
3	Phylogeography Reveals Association between Swine Trade and the Spread of Porcine Epidemic Diarrhea Virus in China and across the World. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	35
4	Genome-wide diversity of Zika virus: Exploring spatio-temporal dynamics to guide a new nomenclature proposal. <i>Virus Evolution</i> , 2022, 8, veac029.	4.9	5
5	Phycova " a tool for exploring covariates of pathogen spread. <i>Virus Evolution</i> , 2022, 8, veac015.	4.9	3
6	Accommodating sampling location uncertainty in continuous phylogeography. <i>Virus Evolution</i> , 2022, 8, .	4.9	8
7	Evaluation of Screening Program and Phylogenetic Analysis of SARS-CoV-2 Infections among Hospital Healthcare Workers in Liège, Belgium. <i>Viruses</i> , 2022, 14, 1302.	3.3	2
8	Investigating COVID-19 Vaccine Impact on the Risk of Hospitalisation through the Analysis of National Surveillance Data Collected in Belgium. <i>Viruses</i> , 2022, 14, 1315.	3.3	0
9	Dynamics and Dispersal of Local Human Immunodeficiency Virus Epidemics Within San Diego and Across the San Diego-Tijuana Border. <i>Clinical Infectious Diseases</i> , 2021, 73, e2018-e2025.	5.8	19
10	Massive Parallelization Boosts Big Bayesian Multidimensional Scaling. <i>Journal of Computational and Graphical Statistics</i> , 2021, 30, 11-24.	1.7	15
11	A Phylodynamic Workflow to Rapidly Gain Insights into the Dispersal History and Dynamics of SARS-CoV-2 Lineages. <i>Molecular Biology and Evolution</i> , 2021, 38, 1608-1613.	8.9	79
12	Global effects of extreme temperatures on wild bumblebees. <i>Conservation Biology</i> , 2021, 35, 1507-1518.	4.7	64
13	SARS-CoV-2 genomic characterization and clinical manifestation of the COVID-19 outbreak in Uruguay. <i>Emerging Microbes and Infections</i> , 2021, 10, 51-65.	6.5	33
14	Host relatedness and landscape connectivity shape pathogen spread in the puma, a large secretive carnivore. <i>Communications Biology</i> , 2021, 4, 12.	4.4	20
15	Relax, Keep Walking " A Practical Guide to Continuous Phylogeographic Inference with BEAST. <i>Molecular Biology and Evolution</i> , 2021, 38, 3486-3493.	8.9	31
16	High dispersal capacity of <i>Culicoides obsoletus</i> (Diptera: Ceratopogonidae), vector of bluetongue and Schmallenberg viruses, revealed by landscape genetic analyses. <i>Parasites and Vectors</i> , 2021, 14, 93.	2.5	12
17	Early introductions and transmission of SARS-CoV-2 variant B.1.1.7 in the United States. <i>Cell</i> , 2021, 184, 2595-2604.e13.	28.9	113
18	Dispersal dynamics of SARS-CoV-2 lineages during the first epidemic wave in New York City. <i>PLoS Pathogens</i> , 2021, 17, e1009571.	4.7	24

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19	Mathematical modelling and phylodynamics for the study of dog rabies dynamics and control: A scoping review. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009449.	3.0	15
20	Untangling introductions and persistence in COVID-19 resurgence in Europe. <i>Nature</i> , 2021, 595, 713-717.	27.8	133
21	Phylogeographic analysis of foot-and-mouth disease virus serotype O dispersal and associated drivers in East Africa. <i>Molecular Ecology</i> , 2021, 30, 3815-3825.	3.9	6
22	Investigating the drivers of the spatio-temporal heterogeneity in COVID-19 hospital incidence—Belgium as a study case. <i>International Journal of Health Geographics</i> , 2021, 20, 29.	2.5	7
23	The evolution of ant worker polymorphism correlates with multiple social traits. <i>Behavioral Ecology and Sociobiology</i> , 2021, 75, 1.	1.4	7
24	Variant Analysis of SARS-CoV-2 Genomes from Belgian Military Personnel Engaged in Overseas Missions and Operations. <i>Viruses</i> , 2021, 13, 1359.	3.3	6
25	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021, 373, 889-895.	12.6	142
26	On the Use of Phylogeographic Inference to Infer the Dispersal History of Rabies Virus: A Review Study. <i>Viruses</i> , 2021, 13, 1628.	3.3	9
27	Rivers and landscape ecology of a plant virus, Rice yellow mottle virus along the Niger Valley. <i>Virus Evolution</i> , 2021, 7, .	4.9	9
28	Genomic sequencing of SARS-CoV-2 in Rwanda reveals the importance of incoming travelers on lineage diversity. <i>Nature Communications</i> , 2021, 12, 5705.	12.8	24
29	Estimating Migration of <i>Gonioctena quinquepunctata</i> (Coleoptera: Chrysomelidae) Inside a Mountain Range in a Spatially Explicit Context. <i>Insect Systematics and Diversity</i> , 2021, 5, .	1.7	0
30	Exploiting genomic surveillance to map the spatio-temporal dispersal of SARS-CoV-2 spike mutations in Belgium across 2020. <i>Scientific Reports</i> , 2021, 11, 18580.	3.3	10
31	Leveraging of SARS-CoV-2 PCR Cycle Thresholds Values to Forecast COVID-19 Trends. <i>Frontiers in Medicine</i> , 2021, 8, 743988.	2.6	16
32	Split it up and see: using proxies to highlight divergent inter-population performances in aquaculture standardised conditions. <i>Bmc Ecology and Evolution</i> , 2021, 21, 206.	1.6	3
33	Incorporating heterogeneous sampling probabilities in continuous phylogeographic inference—Application to H5N1 spread in the Mekong region. <i>Bioinformatics</i> , 2020, 36, 2098-2104.	4.1	11
34	Epidemiological hypothesis testing using a phylogeographic and phylodynamic framework. <i>Nature Communications</i> , 2020, 11, 5620.	12.8	35
35	Genomic Surveillance of Yellow Fever Virus Epizootic in São Paulo, Brazil, 2016—2018. <i>PLoS Pathogens</i> , 2020, 16, e1008699.	4.7	39
36	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020, 369, 1255-1260.	12.6	454

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37	Comparative Circulation Dynamics of the Five Main HIV Types in China. <i>Journal of Virology</i> , 2020, 94, .	3.4	26
38	Wildlife conservation strategies should incorporate both taxon identity and geographical context â€• further evidence with bumblebees. <i>Diversity and Distributions</i> , 2020, 26, 1741-1751.	4.1	19
39	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12522-12523.	7.1	68
40	Genomic Epidemiology, Evolution, and Transmission Dynamics of Porcine Deltacoronavirus. <i>Molecular Biology and Evolution</i> , 2020, 37, 2641-2654.	8.9	76
41	nosoi: A stochastic agentâ€•based transmission chain simulation framework in <sc>r</sc>. <i>Methods in Ecology and Evolution</i> , 2020, 11, 1002-1007.	5.2	19
42	In Search of Covariates of HIV-1 Subtype B Spread in the United Statesâ€•A Cautionary Tale of Large-Scale Bayesian Phylogeography. <i>Viruses</i> , 2020, 12, 182.	3.3	15
43	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020, 30, 2275-2283.e7.	6.4	37
44	Getting off on the right foot: Integration of spatial distribution of genetic variability for aquaculture development and regulations, the European perch case. <i>Aquaculture</i> , 2020, 521, 734981.	3.5	11
45	Unravelling the dispersal dynamics and ecological drivers of the African swine fever outbreak in Belgium. <i>Journal of Applied Ecology</i> , 2020, 57, 1619-1629.	4.0	33
46	The impact of anthropogenic and environmental factors on human rabies cases in China. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 2544-2553.	3.0	8
47	HIV persists throughout deep tissues with repopulation from multiple anatomical sources. <i>Journal of Clinical Investigation</i> , 2020, 130, 1699-1712.	8.2	140
48	Symptom evolution following the emergence of maize streak virus. <i>ELife</i> , 2020, 9, .	6.0	13
49	Comparing patterns and scales of plant virus phylogeography: Rice yellow mottle virus in Madagascar and in continental Africa. <i>Virus Evolution</i> , 2019, 5, vez023.	4.9	22
50	Phylogeography of Lassa Virus in Nigeria. <i>Journal of Virology</i> , 2019, 93, .	3.4	49
51	A32â€•f Genomic surveillance of Zika virus transmission in the Amazonas State, Brazil. <i>Virus Evolution</i> , 2019, 5, .	4.9	0
52	Using phylogeographic approaches to analyse the dispersal history, velocity and direction of viral lineagesâ€• Application to rabies virus spread in Iran. <i>Molecular Ecology</i> , 2019, 28, 4335-4350.	3.9	34
53	Identifying the patterns and drivers of Puumala hantavirus enzootic dynamics using reservoir sampling. <i>Virus Evolution</i> , 2019, 5, vez009.	4.9	16
54	HIV Rebound Is Predominantly Fueled by Genetically Identical Viral Expansions from Diverse Reservoirs. <i>Cell Host and Microbe</i> , 2019, 26, 347-358.e7.	11.0	117

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55	Landscape genetic analyses of <i>Cervus elaphus</i> and <i>Sus scrofa</i> : comparative study and analytical developments. <i>Heredity</i> , 2019, 123, 228-241.	2.6	12
56	Mass migration to Europe: an opportunity for elimination of hepatitis B virus?. <i>The Lancet Gastroenterology and Hepatology</i> , 2019, 4, 315-323.	8.1	25
57	Distinct rates and patterns of spread of the major HIV-1 subtypes in Central and East Africa. <i>PLoS Pathogens</i> , 2019, 15, e1007976.	4.7	37
58	Transmission dynamics of re-emerging rabies in domestic dogs of rural China. <i>PLoS Pathogens</i> , 2018, 14, e1007392.	4.7	35
59	Recent advances in computational phylodynamics. <i>Current Opinion in Virology</i> , 2018, 31, 24-32.	5.4	45
60	Molecular archaeoparasitology identifies cultural changes in the Medieval Hanseatic trading centre of L�beck. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20180991.	2.6	21
61	The hitchhiker's guide to single-locus species delimitation. <i>Molecular Ecology Resources</i> , 2018, 18, 1234-1246.	4.8	131
62	Geographical and Historical Patterns in the Emergences of Novel Highly Pathogenic Avian Influenza (HPAI) H5 and H7 Viruses in Poultry. <i>Frontiers in Veterinary Science</i> , 2018, 5, 84.	2.2	72
63	Divergent geographic patterns of genetic diversity among wild bees: Conservation implications. <i>Diversity and Distributions</i> , 2018, 24, 1860-1868.	4.1	4
64	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018, 361, 894-899.	12.6	279
65	On the importance of negative controls in viral landscape phylogeography. <i>Virus Evolution</i> , 2018, 4, vey023.	4.9	29
66	Phylogenetic assessment of intervention strategies for the West African Ebola virus outbreak. <i>Nature Communications</i> , 2018, 9, 2222.	12.8	59
67	Ecological niche modelling and coalescent simulations to explore the recent geographical range history of five widespread bumblebee species in Europe. <i>Journal of Biogeography</i> , 2017, 44, 39-50.	3.0	30
68	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	27.8	346
69	Glacial survival of trophically linked boreal species in northern Europe. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20162799.	2.6	13
70	Conservation genetics of European bees: new insights from the continental scale. <i>Conservation Genetics</i> , 2017, 18, 585-596.	1.5	17
71	Using Viral Gene Sequences to Compare and Explain the Heterogeneous Spatial Dynamics of Virus Epidemics. <i>Molecular Biology and Evolution</i> , 2017, 34, 2563-2571.	8.9	64
72	Cross-border spread, lineage displacement and evolutionary rate estimation of rabies virus in Yunnan Province, China. <i>Virology Journal</i> , 2017, 14, 102.	3.4	24

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73	Host Genetic Variation Does Not Determine Spatio-Temporal Patterns of European Bat 1 Lyssavirus. <i>Genome Biology and Evolution</i> , 2017, 9, 3202-3213.	2.5	19
74	Distribution and predictors of wing shape and size variability in three sister species of solitary bees. <i>PLoS ONE</i> , 2017, 12, e0173109.	2.5	33
75	Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases. <i>Virus Evolution</i> , 2016, 2, vew016.	4.9	105
76	Spatio-temporal analysis of Nova virus, a divergent hantavirus circulating in the European mole in Belgium. <i>Molecular Ecology</i> , 2016, 25, 5994-6008.	3.9	28
77	Explaining the geographic spread of emerging epidemics: a framework for comparing viral phylogenies and environmental landscape data. <i>BMC Bioinformatics</i> , 2016, 17, 82.	2.6	94
78	SERAPHIM: studying environmental rasters and phylogenetically informed movements. <i>Bioinformatics</i> , 2016, 32, 3204-3206.	4.1	124
79	An integrative taxonomic approach to assess the status of <i>Corsican</i> bumblebees: implications for conservation. <i>Animal Conservation</i> , 2015, 18, 236-248.	2.9	42
80	Delimiting Species-Poor Data Sets using Single Molecular Markers: A Study of Barcode Gaps, Haplowebs and GMYC. <i>Systematic Biology</i> , 2015, 64, 900-908.	5.6	91
81	Impact of past climatic changes and resource availability on the population demography of three food-specialist bees. <i>Molecular Ecology</i> , 2015, 24, 1074-1090.	3.9	21
82	Methods for species delimitation in bumblebees (<i>Hymenoptera</i> , <i>Apididae</i>). <i>Trends in Ecology & Evolution</i> , 2015, 30, 100-108.	1.7	51
83	Comparative phylogeography of five bumblebees: impact of range fragmentation, range size and diet specialization. <i>Biological Journal of the Linnean Society</i> , 2015, 116, 926-939.	1.6	20
84	Molecular phylogeny, biogeography, and host plant shifts in the bee genus <i>Melitta</i> (Hymenoptera: <i>Apidae</i>). <i>Trends in Ecology & Evolution</i> , 2014, 29, 100-108.	2.7	34
85	<i>spads</i> 1.0: a toolbox to perform spatial analyses on <i>DNA</i> sequence data sets. <i>Molecular Ecology Resources</i> , 2014, 14, 647-651.	4.8	91
86	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. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, n/a-n/a.	2.3	19
87	Comparing Phylogeographic Hypotheses by Simulating DNA Sequences under a Spatially Explicit Model of Coalescence. <i>Molecular Biology and Evolution</i> , 2014, 31, 3359-3372.	8.9	14
88	Inferring the mode of colonization of the rapid range expansion of a solitary bee from multilocus <i>DNA</i> sequence variation. <i>Journal of Evolutionary Biology</i> , 2014, 27, 116-132.	1.7	15
89	Scent of a break-up: phylogeography and reproductive trait divergences in the red-tailed bumblebee (<i>Bombus lapidarius</i>). <i>BMC Evolutionary Biology</i> , 2013, 13, 263.	3.2	55
90	<i>GALIGNER</i> 1.0: An alignment program to compute a multiple sample comparison data matrix from large <i>ecological</i> datasets obtained by <i>GC</i> . <i>Journal of Separation Science</i> , 2013, 36, 3206-3209.	2.5	25

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91	Patterns of Genetic and Reproductive Traits Differentiation in Mainland vs. Corsican Populations of Bumblebees. PLoS ONE, 2013, 8, e65642.	2.5	72
92	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
93	Population structure and genetic diversity of red deer (<i>Cervus elaphus</i>) in forest fragments in north-western France. Conservation Genetics, 2011, 12, 1287-1297.	1.5	26
94	Biologie, observations et collectes de trois espèces sœurs du genre <i>Melitta</i> Kirby, 1802 (Hymenoptera, Tj ETQq0 0,0 rgBT /Qverlock 10	0.0	2
95	<i>Bombus gerstaeckeri</i> Morawitz, 1881 (Hymenoptera, Apidae) : observations sur la biologie d'un bourdon localisé et oligolectique. Osmia, 0, 5, 12-14.	0.0	0
96	Oligolectisme de <i>Bombus brodmannicus delmasi</i> Tkalc̃, 1973 (Hymenoptera, Apidae) : observations et analyses. Osmia, 0, 5, 8-11.	0.0	2
97	Historical and geographical patterns of new HPAIV emergences and association with spatial factors. Frontiers in Veterinary Science, 0, 6, .	2.2	0
98	Investigating the impact of environmental factors on the African Swine Fever epidemic in Belgium. Frontiers in Veterinary Science, 0, 6, .	2.2	0
99	Considerable escape of SARS-CoV-2 Omicron to antibody neutralization. Nature, 0, , .	27.8	88
100	Transmission networks of SARS-CoV-2 in Coastal Kenya during the first two waves: A retrospective genomic study. ELife, 0, 11, .	6.0	9