

Simon Dellicour

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

105
papers

2,915
citations

30
h-index

51
g-index

127
ext. papers

4,833
ext. citations

9.4
avg, IF

5.3
L-index

#	Paper	IF	Citations
105	Genome-wide diversity of Zika virus: Exploring spatio-temporal dynamics to guide a new nomenclature proposal.. <i>Virus Evolution</i> , 2022 , 8, veac029	3.7	0
104	Phycova - a tool for exploring covariates of pathogen spread.. <i>Virus Evolution</i> , 2022 , 8, veac015	3.7	0
103	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. 2021 ,		3
102	Considerable escape of SARS-CoV-2 Omicron to antibody neutralization.. <i>Nature</i> , 2021 ,	50.4	230
101	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> , 2021 ,	8.3	3
100	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	21	0
99	Leveraging of SARS-CoV-2 PCR Cycle Thresholds Values to Forecast COVID-19 Trends. <i>Frontiers in Medicine</i> , 2021 , 8, 743988	4.9	3
98	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	11.6	8
97	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	56.2	55
96	Dispersal dynamics of SARS-CoV-2 lineages during the first epidemic wave in New York City. <i>PLoS Pathogens</i> , 2021 , 17, e1009571	7.6	5
95	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	4.8	4
94	Untangling introductions and persistence in COVID-19 resurgence in Europe. <i>Nature</i> , 2021 , 595, 713-717	50.4	37
93	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	5.7	3
92	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	3.5	2
91	The evolution of ant worker polymorphism correlates with multiple social traits. <i>Behavioral Ecology and Sociobiology</i> , 2021 , 75, 1	2.5	3
90	Variant Analysis of SARS-CoV-2 Genomes from Belgian Military Personnel Engaged in Overseas Missions and Operations. <i>Viruses</i> , 2021 , 13,	6.2	3
89	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021 , 373, 889-895	53.3	41

88	Massive parallelization boosts big Bayesian multidimensional scaling. <i>Journal of Computational and Graphical Statistics</i> , 2021 , 30, 11-24	1.4	7
87	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	8.3	36
86	Global effects of extreme temperatures on wild bumblebees. <i>Conservation Biology</i> , 2021 , 35, 1507-1518	6	15
85	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	18.9	16
84	Host relatedness and landscape connectivity shape pathogen spread in the puma, a large secretive carnivore. <i>Communications Biology</i> , 2021 , 4, 12	6.7	6
83	SARS-CoV-2 European resurgence foretold: interplay of introductions and persistence by leveraging genomic and mobility data 2021 ,		6
82	Early introductions and community transmission of SARS-CoV-2 variant B.1.1.7 in the United States 2021 ,		9
81	Relax, Keep Walking - A Practical Guide to Continuous Phylogeographic Inference with BEAST. <i>Molecular Biology and Evolution</i> , 2021 , 38, 3486-3493	8.3	4
80	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	4	5
79	Genomic sequencing of SARS-CoV-2 in Rwanda reveals the importance of incoming travelers on lineage diversity. <i>Nature Communications</i> , 2021 , 12, 5705	17.4	2
78	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	4.9	2
77	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. 2021 ,		2
76	Wildlife conservation strategies should incorporate both taxon identity and geographical context - further evidence with bumblebees. <i>Diversity and Distributions</i> , 2020 , 26, 1741-1751	5	8
75	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	11.5	46
74	Genomic Epidemiology, Evolution, and Transmission Dynamics of Porcine Deltacoronavirus. <i>Molecular Biology and Evolution</i> , 2020 , 37, 2641-2654	8.3	36
73	nosoi: A stochastic agent-based transmission chain simulation framework in r. <i>Methods in Ecology and Evolution</i> , 2020 , 11, 1002-1007	7.7	6
72	In Search of Covariates of HIV-1 Subtype B Spread in the United States-A Cautionary Tale of Large-Scale Bayesian Phylogeography. <i>Viruses</i> , 2020 , 12,	6.2	6
71	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020 , 30, 2275-2283.e7	10.6	24

70	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	4.4	6
69	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	5.8	19
68	The impact of anthropogenic and environmental factors on human rabies cases in China. <i>Transboundary and Emerging Diseases</i> , 2020 , 67, 2544-2553	4.2	1
67	HIV persists throughout deep tissues with repopulation from multiple anatomical sources. <i>Journal of Clinical Investigation</i> , 2020 , 130, 1699-1712	15.9	60
66	Symptom evolution following the emergence of maize streak virus. <i>ELife</i> , 2020 , 9,	8.9	9
65	Incorporating heterogeneous sampling probabilities in continuous phylogeographic inference - Application to H5N1 spread in the Mekong region. <i>Bioinformatics</i> , 2020 , 36, 2098-2104	7.2	4
64	Epidemiological hypothesis testing using a phylogeographic and phylodynamic framework. <i>Nature Communications</i> , 2020 , 11, 5620	17.4	7
63	Genomic Surveillance of Yellow Fever Virus Epizootic in S8 Paulo, Brazil, 2016 - 2018. <i>PLoS Pathogens</i> , 2020 , 16, e1008699	7.6	18
62	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020 , 369, 1255-1260	33.3	277
61	Comparative Circulation Dynamics of the Five Main HIV Types in China. <i>Journal of Virology</i> , 2020 , 94,	6.6	13
60	HIV Rebound Is Predominantly Fueled by Genetically Identical Viral Expansions from Diverse Reservoirs. <i>Cell Host and Microbe</i> , 2019 , 26, 347-358.e7	23.4	62
59	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	3.6	4
58	Mass migration to Europe: an opportunity for elimination of hepatitis B virus?. <i>The Lancet Gastroenterology and Hepatology</i> , 2019 , 4, 315-323	18.8	12
57	Comparing patterns and scales of plant virus phylogeography: in Madagascar and in continental Africa. <i>Virus Evolution</i> , 2019 , 5, vez023	3.7	10
56	Phylogeography of Lassa Virus in Nigeria. <i>Journal of Virology</i> , 2019 , 93,	6.6	30
55	A32 Genomic surveillance of Zika virus transmission in the Amazonas State, Brazil. <i>Virus Evolution</i> , 2019 , 5,	3.7	78
54	Using phylogeographic approaches to analyse the dispersal history, velocity and direction of viral lineages - Application to rabies virus spread in Iran. <i>Molecular Ecology</i> , 2019 , 28, 4335-4350	5.7	17
53	Identifying the patterns and drivers of enzootic dynamics using reservoir sampling. <i>Virus Evolution</i> , 2019 , 5, vez009	3.7	10

52	Distinct rates and patterns of spread of the major HIV-1 subtypes in Central and East Africa. <i>PLoS Pathogens</i> , 2019 , 15, e1007976	7.6	25
51	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	3.1	36
50	Divergent geographic patterns of genetic diversity among wild bees: Conservation implications. <i>Diversity and Distributions</i> , 2018 , 24, 1860-1868	5	2
49	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018 , 361, 894-899	33.3	184
48	On the importance of negative controls in viral landscape phylogeography. <i>Virus Evolution</i> , 2018 , 4, vey037	3.7	18
47	Phylogenetic assessment of intervention strategies for the West African Ebola virus outbreak. <i>Nature Communications</i> , 2018 , 9, 2222	17.4	39
46	Transmission dynamics of re-emerging rabies in domestic dogs of rural China. <i>PLoS Pathogens</i> , 2018 , 14, e1007392	7.6	18
45	Recent advances in computational phylodynamics. <i>Current Opinion in Virology</i> , 2018 , 31, 24-32	7.5	29
44	Molecular archaeoparasitology identifies cultural changes in the Medieval Hanseatic trading centre of Lübeck. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018 , 285,	4.4	13
43	The hitchhiker's guide to single-locus species delimitation. <i>Molecular Ecology Resources</i> , 2018 , 18, 1234-1246	12.46	68
42	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	4.1	24
41	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017 , 544, 309-315	50.4	238
40	Glacial survival of trophically linked boreal species in northern Europe. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017 , 284,	4.4	10
39	Conservation genetics of European bees: new insights from the continental scale. <i>Conservation Genetics</i> , 2017 , 18, 585-596	2.6	9
38	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	8.3	39
37	Cross-border spread, lineage displacement and evolutionary rate estimation of rabies virus in Yunnan Province, China. <i>Virology Journal</i> , 2017 , 14, 102	6.1	12
36	Host Genetic Variation Does Not Determine Spatio-Temporal Patterns of European Bat 1 Lyssavirus. <i>Genome Biology and Evolution</i> , 2017 , 9, 3202-3213	3.9	14
35	Distribution and predictors of wing shape and size variability in three sister species of solitary bees. <i>PLoS ONE</i> , 2017 , 12, e0173109	3.7	12

34	Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases. <i>Virus Evolution</i> , 2016 , 2, vew016	3.7	89
33	Spatio-temporal analysis of Nova virus, a divergent hantavirus circulating in the European mole in Belgium. <i>Molecular Ecology</i> , 2016 , 25, 5994-6008	5.7	19
32	Explaining the geographic spread of emerging epidemics: a framework for comparing viral phylogenies and environmental landscape data. <i>BMC Bioinformatics</i> , 2016 , 17, 82	3.6	62
31	SERAPHIM: studying environmental rasters and phylogenetically informed movements. <i>Bioinformatics</i> , 2016 , 32, 3204-3206	7.2	73
30	Delimiting Species-Poor Data Sets using Single Molecular Markers: A Study of Barcode Gaps, Haplowebs and GMYC. <i>Systematic Biology</i> , 2015 , 64, 900-8	8.4	65
29	Impact of past climatic changes and resource availability on the population demography of three food-specialist bees. <i>Molecular Ecology</i> , 2015 , 24, 1074-90	5.7	16
28	Methods for species delimitation in bumblebees (Hymenoptera, Apidae, Bombus): towards an integrative approach. <i>Zoologica Scripta</i> , 2015 , 44, 281-297	2.5	39
27	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	1.9	15
26	An integrative taxonomic approach to assess the status of Corsican bumblebees: implications for conservation. <i>Animal Conservation</i> , 2015 , 18, 236-248	3.2	32
25	spads 1.0: a toolbox to perform spatial analyses on DNA sequence data sets. <i>Molecular Ecology Resources</i> , 2014 , 14, 647-51	8.4	77
24	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, 2371-85	3.8	17
23	Comparing phylogeographic hypotheses by simulating DNA sequences under a spatially explicit model of coalescence. <i>Molecular Biology and Evolution</i> , 2014 , 31, 3359-72	8.3	11
22	Inferring the mode of colonization of the rapid range expansion of a solitary bee from multilocus DNA sequence variation. <i>Journal of Evolutionary Biology</i> , 2014 , 27, 116-32	2.3	14
21	Molecular phylogeny, biogeography, and host plant shifts in the bee genus <i>Melitta</i> (Hymenoptera: Anthophila). <i>Molecular Phylogenetics and Evolution</i> , 2014 , 70, 412-9	4.1	24
20	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	46
19	GCALIGNER 1.0: an alignment program to compute a multiple sample comparison data matrix from large eco-chemical datasets obtained by GC. <i>Journal of Separation Science</i> , 2013 , 36, 3206-9	3.4	24
18	Patterns of genetic and reproductive traits differentiation in Mainland vs. Corsican populations of bumblebees. <i>PLoS ONE</i> , 2013 , 8, e65642	3.7	55
17	Molecular and chemical characters to evaluate species status of two cuckoo bumblebees: <i>Bombus barbutellus</i> and <i>Bombus maxillosus</i> (Hymenoptera, Apidae, Bombini). <i>Systematic Entomology</i> , 2011 , 36, 453-469	3.4	31

16	Population structure and genetic diversity of red deer (<i>Cervus elaphus</i>) in forest fragments in north-western France. <i>Conservation Genetics</i> , 2011 , 12, 1287-1297	2.6	18
15	Considerable escape of SARS-CoV-2 Omicron to antibody neutralization. <i>Nature</i> ,	50.4	34
14	Considerable escape of SARS-CoV-2 variant Omicron to antibody neutralization		37
13	Biologie, observations et collectes de trois espèces surs du genre <i>Melitta</i> Kirby, 1802 (Hymenoptera, Melittidae). <i>Osmia</i> ,4, 29-34		1
12	A phylodynamic workflow to rapidly gain insights into the dispersal history and dynamics of SARS-CoV-2 lineages		16
11	Evolution and epidemic spread of SARS-CoV-2 in Brazil		6
10	A world apart: levels and factors of excess mortality due to COVID-19 in care homes. The case of Wallonia - Belgium		7
9	Tracing foot-and-mouth disease virus phylogeographical patterns and transmission dynamics		2
8	Genomic Surveillance of Yellow Fever Virus Epizootic in So Paulo, Brazil, 2016 -2018		4
7	Virus genomes reveal the factors that spread and sustained the West African Ebola epidemic		2
6	Phylodynamic assessment of intervention strategies for the West African Ebola virus outbreak		1
5	<i>Bombus gerstaeckeri</i> Morawitz, 1881 (Hymenoptera, Apidae) : observations sur la biologie d'un bourdon localiset oligolectique. <i>Osmia</i> ,5, 12-14		
4	Oligolectisme de <i>Bombus brodmannicus delmasi</i> Tkalc1973 (Hymenoptera, Apidae) : observations et analyses. <i>Osmia</i> ,5, 8-11		1
3	Genomic Sequencing of SARS-CoV-2 in Rwanda: evolution and regional dynamics		6
2	KoT: an automatic implementation of the K/method for species delimitation		2
1	Phylogenetic analyses of SARS-CoV-2 B.1.1.7 lineage suggest a single origin followed by multiple exportation events versus convergent evolution		2