

Sebastien Calvignac-Spencer

List of Publications by Year in descending order

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Version: 2024-02-01

98
papers

4,655
citations

108046

37
h-index

134545

62
g-index

116
all docs

116
docs citations

116
times ranked

7505
citing authors

#	ARTICLE	IF	CITATIONS
1	Investigating the zoonotic origin of the West African Ebola epidemic. <i>EMBO Molecular Medicine</i> , 2015, 7, 17-23.	3.3	347
2	A Novel Human Polyomavirus Closely Related to the African Green Monkey-Derived Lymphotropic Polyomavirus. <i>Journal of Virology</i> , 2011, 85, 4586-4590.	1.5	214
3	Connecting Earth observation to high-throughput biodiversity data. <i>Nature Ecology and Evolution</i> , 2017, 1, 176.	3.4	156
4	Carrión fly-derived <i>scp</i> DNA as a tool for comprehensive and cost-effective assessment of mammalian biodiversity. <i>Molecular Ecology</i> , 2013, 22, 915-924.	2.0	144
5	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021, 374, 423-431.	6.0	144
6	A taxonomy update for the family Polyomaviridae. <i>Archives of Virology</i> , 2016, 161, 1739-1750.	0.9	134
7	Identification of a Novel Human Polyomavirus in Organs of the Gastrointestinal Tract. <i>PLoS ONE</i> , 2013, 8, e58021.	1.1	131
8	Resurgence of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks. <i>Nature</i> , 2021, 597, 539-543.	13.7	113
9	Biology, evolution, and medical importance of polyomaviruses: An update. <i>Infection, Genetics and Evolution</i> , 2017, 54, 18-38.	1.0	112
10	Assessing the Evidence Supporting Fruit Bats as the Primary Reservoirs for Ebola Viruses. <i>EcoHealth</i> , 2016, 13, 18-25.	0.9	109
11	ICTV Virus Taxonomy Profile: Polyomaviridae. <i>Journal of General Virology</i> , 2017, 98, 1159-1160.	1.3	107
12	Wild great apes as sentinels and sources of infectious disease. <i>Clinical Microbiology and Infection</i> , 2012, 18, 521-527.	2.8	103
13	Measles virus and rinderpest virus divergence dated to the sixth century BCE. <i>Science</i> , 2020, 368, 1367-1370.	6.0	102
14	Novel <i>Mycobacterium tuberculosis</i> Complex Isolate from a Wild Chimpanzee. <i>Emerging Infectious Diseases</i> , 2013, 19, 969-976.	2.0	100
15	Persistent anthrax as a major driver of wildlife mortality in a tropical rainforest. <i>Nature</i> , 2017, 548, 82-86.	13.7	95
16	Combined analysis of fourteen nuclear genes refines the Ursidae phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 2008, 47, 73-83.	1.2	91
17	Ancient DNA evidence for the loss of a highly divergent brown bear clade during historical times. <i>Molecular Ecology</i> , 2008, 17, 1962-1970.	2.0	91
18	mtDNA from terrestrial haematophagous leeches as a wildlife surveying and monitoring tool – prospects, pitfalls and avenues to be developed. <i>Frontiers in Zoology</i> , 2015, 12, 24.	0.9	89

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19	Monkeypox virus emergence in wild chimpanzees reveals distinct clinical outcomes and viral diversity. <i>Nature Microbiology</i> , 2020, 5, 955-965.	5.9	86
20	One Hundred Twenty Years of Koala Retrovirus Evolution Determined from Museum Skins. <i>Molecular Biology and Evolution</i> , 2013, 30, 299-304.	3.5	85
21	Preventing the pollution of mitochondrial datasets with nuclear mitochondrial paralogs (numts). <i>Mitochondrion</i> , 2011, 11, 246-254.	1.6	82
22	<i>Bacillus cereus</i> Biovar Anthracis Causing Anthrax in Sub-Saharan Africa—Chromosomal Monophyly and Broad Geographic Distribution. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004923.	1.3	77
23	Games academics play and their consequences: how authorship, <i>h</i> -index and journal impact factors are shaping the future of academia. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20192047.	1.2	75
24	Genetic diversity of endangered brown bear (<i>Ursus arctos</i>) populations at the crossroads of Europe, Asia and Africa. <i>Diversity and Distributions</i> , 2009, 15, 742-750.	1.9	74
25	Risk of human-wildlife transmission of SARS-CoV-2. <i>Mammal Review</i> , 2021, 51, 272-292.	2.2	69
26	An invertebrate stomach's view on vertebrate ecology. <i>BioEssays</i> , 2013, 35, 1004-1013.	1.2	66
27	Evidence for continuing cross-species transmission of SIVsmm to humans. <i>Aids</i> , 2013, 27, 2488-2491.	1.0	66
28	Human coronavirus OC43 outbreak in wild chimpanzees, Côte d'Ivoire, 2016. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-4.	3.0	66
29	High Prevalence, Coinfection Rate, and Genetic Diversity of Retroviruses in Wild Red Colobus Monkeys (<i>Ptilocolobus badius badius</i>) in Taï National Park, Côte d'Ivoire. <i>Journal of Virology</i> , 2010, 84, 7427-7436.	1.5	54
30	Multiple Cross-Species Transmission Events of Human Adenoviruses (HAdV) during Hominine Evolution. <i>Molecular Biology and Evolution</i> , 2015, 32, 2072-2084.	3.5	54
31	Emergence and spread of SARS-CoV-2 lineage B.1.620 with variant of concern-like mutations and deletions. <i>Nature Communications</i> , 2021, 12, 5769.	5.8	51
32	Evolutionary history of human <i>Plasmodium vivax</i> revealed by genome-wide analyses of related ape parasites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8450-E8459.	3.3	50
33	Ancient Recombination Events between Human Herpes Simplex Viruses. <i>Molecular Biology and Evolution</i> , 2017, 34, 1713-1721.	3.5	49
34	African Great Apes Are Naturally Infected with Polyomaviruses Closely Related to Merkel Cell Polyomavirus. <i>Journal of Virology</i> , 2011, 85, 916-924.	1.5	46
35	Targeted detection of mammalian species using carrion fly-derived <i>scp</i> -DNA. <i>Molecular Ecology Resources</i> , 2015, 15, 285-294.	2.2	44
36	Nonhuman primates across sub-Saharan Africa are infected with the yaws bacterium <i>Treponema pallidum</i> subsp. <i>pertenue</i> . <i>Emerging Microbes and Infections</i> , 2018, 7, 1-4.	3.0	41

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37	DNA from extinct giant lemurs links archaeolemurids to extant indriids. BMC Evolutionary Biology, 2008, 8, 121.	3.2	40
38	Codetection of Respiratory Syncytial Virus in Habituated Wild Western Lowland Gorillas and Humans During a Respiratory Disease Outbreak. EcoHealth, 2016, 13, 499-510.	0.9	39
39	Origin of Human T-Lymphotropic Virus Type 1 in Rural Côte d'Ivoire. Emerging Infectious Diseases, 2012, 18, 830-833.	2.0	35
40	Novel Polyomaviruses of Nonhuman Primates: Genetic and Serological Predictors for the Existence of Multiple Unknown Polyomaviruses within the Human Population. PLoS Pathogens, 2013, 9, e1003429.	2.1	35
41	Aquatic biodiversity assessment for the lazy. Molecular Ecology, 2016, 25, 846-848.	2.0	34
42	Fly-derived DNA and camera traps are complementary tools for assessing mammalian biodiversity. Environmental DNA, 2020, 2, 63-76.	3.1	33
43	Lassa Virus in Multimammate Rats, Côte d'Ivoire, 2013. Emerging Infectious Diseases, 2015, 21, 1481-1483.	2.0	31
44	Factors influencing bacterial microbiome composition in a wild non-human primate community in Taï National Park, Côte d'Ivoire. ISME Journal, 2018, 12, 2559-2574.	4.4	31
45	Bushmeat Hunting and Zoonotic Transmission of Simian T-Lymphotropic Virus 1 in Tropical West and Central Africa. Journal of Virology, 2017, 91, .	1.5	30
46	Leprosy in wild chimpanzees. Nature, 2021, 598, 652-656.	13.7	30
47	Malaria parasite detection increases during pregnancy in wild chimpanzees. Malaria Journal, 2014, 13, 413.	0.8	27
48	Integrating phylogeography, physiology and habitat modelling to explore species range determinants. Journal of Biogeography, 2014, 41, 687-699.	1.4	27
49	Tropical rainforest flies carrying pathogens form stable associations with social nonhuman primates. Molecular Ecology, 2019, 28, 4242-4258.	2.0	27
50	Tools for opening new chapters in the book of Treponema pallidum evolutionary history. Clinical Microbiology and Infection, 2016, 22, 916-921.	2.8	26
51	Evidence for Human Streptococcus pneumoniae in wild and captive chimpanzees: A potential threat to wild populations. Scientific Reports, 2017, 7, 14581.	1.6	26
52	Cytomegalovirus distribution and evolution in hominines. Virus Evolution, 2019, 5, vez015.	2.2	26
53	Clock Rooting Further Demonstrates that Guinea 2014 EBOV is a Member of the Zaïre Lineage. PLOS Currents, 2014, 6, .	1.4	26
54	Age-related effects on malaria parasite infection in wild chimpanzees. Biology Letters, 2013, 9, 20121160.	1.0	25

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55	Archival influenza virus genomes from Europe reveal genomic variability during the 1918 pandemic. <i>Nature Communications</i> , 2022, 13, 2314.	5.8	25
56	The ecology of primate retroviruses – An assessment of 12 years of retroviral studies in the Taï national park area, Côte d'Ivoire. <i>Virology</i> , 2014, 460-461, 147-153.	1.1	24
57	Mother-Offspring Transmission and Age-Dependent Accumulation of Simian Foamy Virus in Wild Chimpanzees. <i>Journal of Virology</i> , 2013, 87, 5193-5204.	1.5	23
58	Novel Polyomaviruses in Mammals from Multiple Orders and Reassessment of Polyomavirus Evolution and Taxonomy. <i>Viruses</i> , 2019, 11, 930.	1.5	23
59	Extensive Serological Survey of Multiple African Nonhuman Primate Species Reveals Low Prevalence of Immunoglobulin G Antibodies to 4 Ebola Virus Species. <i>Journal of Infectious Diseases</i> , 2019, 220, 1599-1608.	1.9	23
60	High prevalence and diversity of species D adenoviruses (HAdV-D) in human populations of four Sub-Saharan countries. <i>Virology Journal</i> , 2014, 11, 25.	1.4	22
61	Assessing Host-Virus Codivergence for Close Relatives of Merkel Cell Polyomavirus Infecting African Great Apes. <i>Journal of Virology</i> , 2016, 90, 8531-8541.	1.5	21
62	Ancient DNA Identification of Early 20th Century Simian T-Cell Leukemia Virus Type 1. <i>Molecular Biology and Evolution</i> , 2008, 25, 1093-1098.	3.5	20
63	Novel polyomaviruses in shrews (Soricidae) with close similarity to human polyomavirus 12. <i>Journal of General Virology</i> , 2017, 98, 3060-3067.	1.3	20
64	Antibody escape and global spread of SARS-CoV-2 lineage A.27. <i>Nature Communications</i> , 2022, 13, 1152.	5.8	20
65	Assessing the feasibility of fly based surveillance of wildlife infectious diseases. <i>Scientific Reports</i> , 2016, 6, 37952.	1.6	19
66	Role of Wildlife in Emergence of Ebola Virus in Kaigbono (Likati), Democratic Republic of the Congo, 2017. <i>Emerging Infectious Diseases</i> , 2020, 26, 2205-2209.	2.0	19
67	Hemoparasites in a wild primate: Infection patterns suggest interaction of Plasmodium and Babesia in a lemur species. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2015, 4, 385-395.	0.6	18
68	Metabarcoding of eukaryotic parasite communities describes diverse parasite assemblages spanning the primate phylogeny. <i>Molecular Ecology Resources</i> , 2020, 20, 204-215.	2.2	18
69	Comparison of target enrichment strategies for ancient pathogen DNA. <i>BioTechniques</i> , 2020, 69, 455-459.	0.8	17
70	Adenovirus in Rural Côte D'Ivoire: High Diversity and Cross-Species Detection. <i>EcoHealth</i> , 2015, 12, 441-452.	0.9	16
71	Human Respiratory Syncytial Virus and Streptococcus pneumoniae Infection in Wild Bonobos. <i>EcoHealth</i> , 2018, 15, 462-466.	0.9	16
72	Primate phageomes are structured by superhost phylogeny and environment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	16

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73	Cytomegaloviruses in a Community of Wild Nonhuman Primates in Taï National Park, Côte d'Ivoire. <i>Viruses</i> , 2018, 10, 11.	1.5	13
74	Discovery of Novel Herpes Simplexviruses in Wild Gorillas, Bonobos, and Chimpanzees Supports Zoonotic Origin of HSV-2. <i>Molecular Biology and Evolution</i> , 2021, 38, 2818-2830.	3.5	13
75	E box motifs as mediators of proviral latency of human retroviruses. <i>Retrovirology</i> , 2009, 6, 81.	0.9	11
76	Search for polyoma-, herpes-, and bornaviruses in squirrels of the family Sciuridae. <i>Virology Journal</i> , 2020, 17, 42.	1.4	11
77	Yaws Disease Caused by <i>Treponema pallidum</i> subspecies <i>pertenue</i> in Wild Chimpanzee, Guinea, 2019. <i>Emerging Infectious Diseases</i> , 2020, 26, 1283-1286.	2.0	11
78	Blow flies as urban wildlife sensors. <i>Molecular Ecology Resources</i> , 2018, 18, 502-510.	2.2	10
79	Seasonal and inter-annual variation of malaria parasite detection in wild chimpanzees. <i>Malaria Journal</i> , 2018, 17, 38.	0.8	10
80	A cautionary note on fecal sampling and molecular epidemiology in predatory wild great apes. <i>American Journal of Primatology</i> , 2015, 77, 833-840.	0.8	9
81	A great ape perspective on the origins and evolution of human viruses. <i>Advances in Virus Research</i> , 2021, 110, 1-26.	0.9	9
82	Rise and Fall of SARS-CoV-2 Lineage A.27 in Germany. <i>Viruses</i> , 2021, 13, 1491.	1.5	9
83	Zoonotic origin of the human malaria parasite <i>Plasmodium malariae</i> from African apes. <i>Nature Communications</i> , 2022, 13, 1868.	5.8	9
84	<i>Leishmania</i> Encodes a Bacterium-like 2,4-Dienoyl-Coenzyme A Reductase That Is Required for Fatty Acid β -Oxidation and Intracellular Parasite Survival. <i>MBio</i> , 2020, 11, .	1.8	8
85	Does the 43â€šbp sequence from an 800â€š000 year old Cretan dwarf elephantid really rewrite the textbook on mammoths?. <i>Biology Letters</i> , 2007, 3, 58-60.	1.0	7
86	Wild African great apes as natural hosts of malaria parasites: current knowledge and research perspectives. <i>Primate Biology</i> , 2017, 4, 47-59.	0.6	7
87	Genome Sequence of a Central Chimpanzee-Associated Polyomavirus Related to BK and JC Polyomaviruses, Pan troglodytes <i>troglodytes</i> Polyomavirus 1. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
88	A Novel Orthohepadnavirus Identified in a Dead Maxwell's Duiker (<i>Philantomba maxwellii</i>) in Taï National Park, Côte d'Ivoire. <i>Viruses</i> , 2019, 11, 279.	1.5	5
89	Detection of Retroviral Super-Infection from Non-Invasive Samples. <i>PLoS ONE</i> , 2012, 7, e36570.	1.1	4
90	Detection of possible spillover of a novel hantavirus in a Natal mastomys from Guinea. <i>Virus Genes</i> , 2020, 56, 95-98.	0.7	4

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91	Molecular epidemiological typing of <i>Neisseria gonorrhoeae</i> isolates identifies a novel association between genogroup G10557 (G7072) and decreased susceptibility to cefixime, Germany, 2014 to 2017. <i>Eurosurveillance</i> , 2020, 25, .	3.9	4
92	Multiple DNA viruses identified in multimammate mouse (<i>Mastomys natalensis</i>) populations from across regions of sub-Saharan Africa. <i>Archives of Virology</i> , 2020, 165, 2291-2299.	0.9	3
93	Molecular archeology of human viruses. <i>Advances in Virus Research</i> , 2021, 111, 31-61.	0.9	3
94	Non-invasive genomics of respiratory pathogens infecting wild great apes using hybridisation capture. <i>Influenza and Other Respiratory Viruses</i> , 2022, 16, 858-861.	1.5	3
95	Geographically structured genomic diversity of non-human primate-infecting <i>Treponema pallidum</i> subsp. <i>pertenue</i> . <i>Microbial Genomics</i> , 2020, 6, .	1.0	2
96	The cost of living in larger primate groups includes higher fly densities. <i>EcoHealth</i> , 0, , .	0.9	2
97	The One Past Health workshop: connecting ancient DNA and zoonosis research. <i>BioEssays</i> , 2017, 39, 1700075.	1.2	1
98	The chimpanzees of the Taï Forest as models for hominine microorganism ecology and evolution. , 2019, , 366-384.		0