

Sebastien Calvignac-Spencer

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9495567/publications.pdf>

Version: 2024-02-01

98
papers

4,655
citations

94433

37
h-index

118850

62
g-index

116
all docs

116
docs citations

116
times ranked

6887
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.	6.9	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.	3.4	214
3	Connecting Earth observation to high-throughput biodiversity data. <i>Nature Ecology and Evolution</i> , 2017, 1, 176.	7.8	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.	3.9	144
5	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021, 374, 423-431.	12.6	144
6	A taxonomy update for the family Polyomaviridae. <i>Archives of Virology</i> , 2016, 161, 1739-1750.	2.1	134
7	Identification of a Novel Human Polyomavirus in Organs of the Gastrointestinal Tract. <i>PLoS ONE</i> , 2013, 8, e58021.	2.5	131
8	Resurgence of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks. <i>Nature</i> , 2021, 597, 539-543.	27.8	113
9	Biology, evolution, and medical importance of polyomaviruses: An update. <i>Infection, Genetics and Evolution</i> , 2017, 54, 18-38.	2.3	112
10	Assessing the Evidence Supporting Fruit Bats as the Primary Reservoirs for Ebola Viruses. <i>EcoHealth</i> , 2016, 13, 18-25.	2.0	109
11	ICTV Virus Taxonomy Profile: Polyomaviridae. <i>Journal of General Virology</i> , 2017, 98, 1159-1160.	2.9	107
12	Wild great apes as sentinels and sources of infectious disease. <i>Clinical Microbiology and Infection</i> , 2012, 18, 521-527.	6.0	103
13	Measles virus and rinderpest virus divergence dated to the sixth century BCE. <i>Science</i> , 2020, 368, 1367-1370.	12.6	102
14	Novel <i>Mycobacterium tuberculosis</i> Complex Isolate from a Wild Chimpanzee. <i>Emerging Infectious Diseases</i> , 2013, 19, 969-976.	4.3	100
15	Persistent anthrax as a major driver of wildlife mortality in a tropical rainforest. <i>Nature</i> , 2017, 548, 82-86.	27.8	95
16	Combined analysis of fourteen nuclear genes refines the Ursidae phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 2008, 47, 73-83.	2.7	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.	3.9	91
18	iDNA 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.	2.0	89

#	ARTICLE	IF	CITATIONS
19	Monkeypox virus emergence in wild chimpanzees reveals distinct clinical outcomes and viral diversity. <i>Nature Microbiology</i> , 2020, 5, 955-965.	13.3	86
20	One Hundred Twenty Years of Koala Retrovirus Evolution Determined from Museum Skins. <i>Molecular Biology and Evolution</i> , 2013, 30, 299-304.	8.9	85
21	Preventing the pollution of mitochondrial datasets with nuclear mitochondrial paralogs (numts). <i>Mitochondrion</i> , 2011, 11, 246-254.	3.4	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.	3.0	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.	2.6	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.	4.1	74
25	Risk of human-wildlife transmission of SARS-CoV-2. <i>Mammal Review</i> , 2021, 51, 272-292.	4.8	69
26	An invertebrate stomach's view on vertebrate ecology. <i>BioEssays</i> , 2013, 35, 1004-1013.	2.5	66
27	Evidence for continuing cross-species transmission of SIVsmm to humans. <i>Aids</i> , 2013, 27, 2488-2491.	2.2	66
28	Human coronavirus OC43 outbreak in wild chimpanzees, Côte d'Ivoire, 2016. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-4.	6.5	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.	3.4	54
30	Multiple Cross-Species Transmission Events of Human Adenoviruses (HAdV) during Hominine Evolution. <i>Molecular Biology and Evolution</i> , 2015, 32, 2072-2084.	8.9	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.	12.8	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.	7.1	50
33	Ancient Recombination Events between Human Herpes Simplex Viruses. <i>Molecular Biology and Evolution</i> , 2017, 34, 1713-1721.	8.9	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.	3.4	46
35	Targeted detection of mammalian species using carrion fly-derived <i>scp</i> -DNA. <i>Molecular Ecology Resources</i> , 2015, 15, 285-294.	4.8	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.	6.5	41

#	ARTICLE	IF	CITATIONS
37	DNA from extinct giant lemurs links archaeolemurids to extant indriids. <i>BMC Evolutionary Biology</i> , 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. <i>EcoHealth</i> , 2016, 13, 499-510.	2.0	39
39	Origin of Human T-Lymphotropic Virus Type 1 in Rural Côte d'Ivoire. <i>Emerging Infectious Diseases</i> , 2012, 18, 830-833.	4.3	35
40	Novel Polyomaviruses of Nonhuman Primates: Genetic and Serological Predictors for the Existence of Multiple Unknown Polyomaviruses within the Human Population. <i>PLoS Pathogens</i> , 2013, 9, e1003429.	4.7	35
41	Aquatic biodiversity assessment for the lazy. <i>Molecular Ecology</i> , 2016, 25, 846-848.	3.9	34
42	Fly-derived DNA and camera traps are complementary tools for assessing mammalian biodiversity. <i>Environmental DNA</i> , 2020, 2, 63-76.	5.8	33
43	Lassa Virus in Multimammate Rats, Côte d'Ivoire, 2013. <i>Emerging Infectious Diseases</i> , 2015, 21, 1481-1483.	4.3	31
44	Factors influencing bacterial microbiome composition in a wild non-human primate community in Taï National Park, Côte d'Ivoire. <i>ISME Journal</i> , 2018, 12, 2559-2574.	9.8	31
45	Bushmeat Hunting and Zoonotic Transmission of Simian T-Lymphotropic Virus 1 in Tropical West and Central Africa. <i>Journal of Virology</i> , 2017, 91, .	3.4	30
46	Leprosy in wild chimpanzees. <i>Nature</i> , 2021, 598, 652-656.	27.8	30
47	Malaria parasite detection increases during pregnancy in wild chimpanzees. <i>Malaria Journal</i> , 2014, 13, 413.	2.3	27
48	Integrating phylogeography, physiology and habitat modelling to explore species range determinants. <i>Journal of Biogeography</i> , 2014, 41, 687-699.	3.0	27
49	Tropical rainforest flies carrying pathogens form stable associations with social nonhuman primates. <i>Molecular Ecology</i> , 2019, 28, 4242-4258.	3.9	27
50	Tools for opening new chapters in the book of <i>Treponema pallidum</i> evolutionary history. <i>Clinical Microbiology and Infection</i> , 2016, 22, 916-921.	6.0	26
51	Evidence for Human <i>Streptococcus pneumoniae</i> in wild and captive chimpanzees: A potential threat to wild populations. <i>Scientific Reports</i> , 2017, 7, 14581.	3.3	26
52	Cytomegalovirus distribution and evolution in hominines. <i>Virus Evolution</i> , 2019, 5, vez015.	4.9	26
53	Clock Rooting Further Demonstrates that Guinea 2014 EBOV is a Member of the Zaïre Lineage. <i>PLOS Currents</i> , 2014, 6, .	1.4	26
54	Age-related effects on malaria parasite infection in wild chimpanzees. <i>Biology Letters</i> , 2013, 9, 20121160.	2.3	25

#	ARTICLE	IF	CITATIONS
55	Archival influenza virus genomes from Europe reveal genomic variability during the 1918 pandemic. <i>Nature Communications</i> , 2022, 13, 2314.	12.8	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.	2.4	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.	3.4	23
58	Novel Polyomaviruses in Mammals from Multiple Orders and Reassessment of Polyomavirus Evolution and Taxonomy. <i>Viruses</i> , 2019, 11, 930.	3.3	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.	4.0	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.	3.4	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.	3.4	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.	8.9	20
63	Novel polyomaviruses in shrews (Soricidae) with close similarity to human polyomavirus 12. <i>Journal of General Virology</i> , 2017, 98, 3060-3067.	2.9	20
64	Antibody escape and global spread of SARS-CoV-2 lineage A.27. <i>Nature Communications</i> , 2022, 13, 1152.	12.8	20
65	Assessing the feasibility of fly based surveillance of wildlife infectious diseases. <i>Scientific Reports</i> , 2016, 6, 37952.	3.3	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.	4.3	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.	1.5	18
68	Metabarcoding of eukaryotic parasite communities describes diverse parasite assemblages spanning the primate phylogeny. <i>Molecular Ecology Resources</i> , 2020, 20, 204-215.	4.8	18
69	Comparison of target enrichment strategies for ancient pathogen DNA. <i>BioTechniques</i> , 2020, 69, 455-459.	1.8	17
70	Adenovirus in Rural Côte D'Ivoire: High Diversity and Cross-Species Detection. <i>EcoHealth</i> , 2015, 12, 441-452.	2.0	16
71	Human Respiratory Syncytial Virus and Streptococcus pneumoniae Infection in Wild Bonobos. <i>EcoHealth</i> , 2018, 15, 462-466.	2.0	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, .	7.1	16

#	ARTICLE	IF	CITATIONS
73	Cytomegaloviruses in a Community of Wild Nonhuman Primates in Taï National Park, Côte d'Ivoire. <i>Viruses</i> , 2018, 10, 11.	3.3	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.	8.9	13
75	E box motifs as mediators of proviral latency of human retroviruses. <i>Retrovirology</i> , 2009, 6, 81.	2.0	11
76	Search for polyoma-, herpes-, and bornaviruses in squirrels of the family Sciuridae. <i>Virology Journal</i> , 2020, 17, 42.	3.4	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.	4.3	11
78	Blow flies as urban wildlife sensors. <i>Molecular Ecology Resources</i> , 2018, 18, 502-510.	4.8	10
79	Seasonal and inter-annual variation of malaria parasite detection in wild chimpanzees. <i>Malaria Journal</i> , 2018, 17, 38.	2.3	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.	1.7	9
81	A great ape perspective on the origins and evolution of human viruses. <i>Advances in Virus Research</i> , 2021, 110, 1-26.	2.1	9
82	Rise and Fall of SARS-CoV-2 Lineage A.27 in Germany. <i>Viruses</i> , 2021, 13, 1491.	3.3	9
83	Zoonotic origin of the human malaria parasite <i>Plasmodium malariae</i> from African apes. <i>Nature Communications</i> , 2022, 13, 1868.	12.8	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, .	4.1	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.	2.3	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.	1.0	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.	3.3	5
89	Detection of Retroviral Super-Infection from Non-Invasive Samples. <i>PLoS ONE</i> , 2012, 7, e36570.	2.5	4
90	Detection of possible spillover of a novel hantavirus in a Natal mastomys from Guinea. <i>Virus Genes</i> , 2020, 56, 95-98.	1.6	4

#	ARTICLE	IF	CITATIONS
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, .	7.0	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.	2.1	3
93	Molecular archeology of human viruses. <i>Advances in Virus Research</i> , 2021, 111, 31-61.	2.1	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.	3.4	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, .	2.0	2
96	The cost of living in larger primate groups includes higher fly densities. <i>EcoHealth</i> , 0, , .	2.0	2
97	The One Past Health workshop: connecting ancient DNA and zoonosis research. <i>BioEssays</i> , 2017, 39, 1700075.	2.5	1
98	The chimpanzees of the Taï Forest as models for hominine microorganism ecology and evolution. , 2019, , 366-384.		0