Sebastien Calvignac-Spencer

List of Publications by Year
in descending order

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	Antibody escape and global spread of SARS-CoV-2 lineage A.27. Nature Communications, 2022, 13, 1152.	12.8	20
2	Zoonotic origin of the human malaria parasite Plasmodium malariae from African apes. Nature Communications, 2022, 13, 1868.	12.8	9
3	Nonâ€invasive genomics of respiratory pathogens infecting wild great apes using hybridisation capture. Influenza and Other Respiratory Viruses, 2022, 16, 858-861.	3.4	3
4	Archival influenza virus genomes from Europe reveal genomic variability during the 1918 pandemic. Nature Communications, 2022, 13, 2314.	12.8	25
5	Risk of humanâ€toâ€wildlife transmission of SARSâ€CoVâ€2. Mammal Review, 2021, 51, 272-292.	4.8	69
6	A great ape perspective on the origins and evolution of human viruses. Advances in Virus Research, 2021, 110, 1-26.	2.1	9
7	Discovery of Novel Herpes Simplexviruses in Wild Gorillas, Bonobos, and Chimpanzees Supports Zoonotic Origin of HSV-2. Molecular Biology and Evolution, 2021, 38, 2818-2830.	8.9	13
8	Primate phageomes are structured by superhost phylogeny and environment. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	16
9	Rise and Fall of SARS-CoV-2 Lineage A.27 in Germany. Viruses, 2021, 13, 1491.	3.3	9
10	Resurgence of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks. Nature, 2021, 597, 539-543.	27.8	113
11	Emergence and spread of SARS-CoV-2 lineage B.1.620 with variant of concern-like mutations and deletions. Nature Communications, 2021, 12, 5769.	12.8	51
12	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. Science, 2021, 374, 423-431.	12.6	144
13	Molecular archeology of human viruses. Advances in Virus Research, 2021, 111, 31-61.	2.1	3
14	Leprosy in wild chimpanzees. Nature, 2021, 598, 652-656.	27.8	30
15	Metabarcoding of eukaryotic parasite communities describes diverse parasite assemblages spanning the primate phylogeny. Molecular Ecology Resources, 2020, 20, 204-215.	4.8	18
16	Detection of possible spillover of a novel hantavirus in a Natal mastomys from Guinea. Virus Genes, 2020, 56, 95-98.	1.6	4
17	Flyâ€derived DNA and camera traps are complementary tools for assessing mammalian biodiversity. Environmental DNA, 2020, 2, 63-76.	5.8	33
18	Multiple DNA viruses identified in multimammate mouse (Mastomys natalensis) populations from across regions of sub-Saharan Africa. Archives of Virology, 2020, 165, 2291-2299.	2.1	3

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19	Role of Wildlife in Emergence of Ebola Virus in Kaigbono (Likati), Democratic Republic of the Congo, 2017. Emerging Infectious Diseases, 2020, 26, 2205-2209.	4.3	19
20	Comparison of target enrichment strategies for ancient pathogen DNA. BioTechniques, 2020, 69, 455-459.	1.8	17
21	Leishmania Encodes a Bacterium-like 2,4-Dienoyl-Coenzyme A Reductase That Is Required for Fatty Acid Î²-Oxidation and Intracellular Parasite Survival. MBio, 2020, 11, .	4.1	8
22	Measles virus and rinderpest virus divergence dated to the sixth century BCE. Science, 2020, 368, 1367-1370.	12.6	102
23	Monkeypox virus emergence in wild chimpanzees reveals distinct clinical outcomes and viral diversity. Nature Microbiology, 2020, 5, 955-965.	13.3	86
24	Search for polyoma-, herpes-, and bornaviruses in squirrels of the family Sciuridae. Virology Journal, 2020, 17, 42.	3.4	11
25	Molecular epidemiological typing of Neisseria gonorrhoeae isolates identifies a novel association between genogroup G10557 (G7072) and decreased susceptibility to cefixime, Germany, 2014 to 2017. Eurosurveillance, 2020, 25, .	7.0	4
26	Yaws Disease Caused by Treponema pallidum subspecies pertenue in Wild Chimpanzee, Guinea, 2019. Emerging Infectious Diseases, 2020, 26, 1283-1286.	4.3	11
27	Geographically structured genomic diversity of non-human primate-infecting Treponema pallidum subsp. pertenue. Microbial Genomics, 2020, 6, .	2.0	2
28	Cytomegalovirus distribution and evolution in hominines. Virus Evolution, 2019, 5, vez015.	4.9	26
29	Novel Polyomaviruses in Mammals from Multiple Orders and Reassessment of Polyomavirus Evolution and Taxonomy. Viruses, 2019, 11, 930.	3.3	23
30	Tropical rainforest flies carrying pathogens form stable associations with social nonhuman primates. Molecular Ecology, 2019, 28, 4242-4258.	3.9	27
31	A Novel Orthohepadnavirus Identified in a Dead Maxwellâ€™s Duiker (Philantomba maxwellii) in TaÃ¯ National Park, CÃ´te dâ€™Ivoire. Viruses, 2019, 11, 279.	3.3	5
32	The chimpanzees of the TaÃ¯ Forest as models for hominine microorganism ecology and evolution. , 2019, , 366-384.		0
33	Games academics play and their consequences: how authorship, h-index and journal impact factors are shaping the future of academia. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20192047.	2.6	75
34	Extensive Serological Survey of Multiple African Nonhuman Primate Species Reveals Low Prevalence of Immunoglobulin G Antibodies to 4 Ebola Virus Species. Journal of Infectious Diseases, 2019, 220, 1599-1608.	4.0	23
35	Human Respiratory Syncytial Virus and Streptococcus pneumoniae Infection in Wild Bonobos. EcoHealth, 2018, 15, 462-466.	2.0	16
36	Blow flies as urban wildlife sensors. Molecular Ecology Resources, 2018, 18, 502-510.	4.8	10

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37	Nonhuman primates across sub-Saharan Africa are infected with the yaws bacterium Treponema pallidum subsp. pertenue. Emerging Microbes and Infections, 2018, 7, 1-4.	6.5	41
38	Human coronavirus OC43 outbreak in wild chimpanzees, CÃ´te dÂ'Ivoire, 2016. Emerging Microbes and Infections, 2018, 7, 1-4.	6.5	66
39	Cytomegaloviruses in a Community of Wild Nonhuman Primates in TaÃ¯ National Park, CÃ´te Dâ€™Ivoire. Viruses, 2018, 10, 11.	3.3	13
40	Seasonal and inter-annual variation of malaria parasite detection in wild chimpanzees. Malaria Journal, 2018, 17, 38.	2.3	10
41	Evolutionary history of humanPlasmodium vivaxrevealed by genome-wide analyses of related ape parasites. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8450-E8459.	7.1	50
42	Factors influencing bacterial microbiome composition in a wild non-human primate community in TaÃ¯ National Park, CÃ´te dâ€™Ivoire. ISME Journal, 2018, 12, 2559-2574.	9.8	31
43	Ancient Recombination Events between Human Herpes Simplex Viruses. Molecular Biology and Evolution, 2017, 34, 1713-1721.	8.9	49
44	Biology, evolution, and medical importance of polyomaviruses: An update. Infection, Genetics and Evolution, 2017, 54, 18-38.	2.3	112
45	Connecting Earth observation to high-throughput biodiversity data. Nature Ecology and Evolution, 2017, 1, 176.	7.8	156
46	Bushmeat Hunting and Zoonotic Transmission of Simian T-Lymphotropic Virus 1 in Tropical West and Central Africa. Journal of Virology, 2017, 91, .	3.4	30
47	Persistent anthrax as a major driver of wildlife mortality in a tropical rainforest. Nature, 2017, 548, 82-86.	27.8	95
48	The One Past Health workshop: connecting ancient DNA and zoonosis research. BioEssays, 2017, 39, 1700075.	2.5	1
49	Evidence for Human Streptococcus pneumoniae in wild and captive chimpanzees: A potential threat to wild populations. Scientific Reports, 2017, 7, 14581.	3.3	26
50	ICTV Virus Taxonomy Profile: Polyomaviridae. Journal of General Virology, 2017, 98, 1159-1160.	2.9	107
51	Novel polyomaviruses in shrews (Soricidae) with close similarity to human polyomavirus 12. Journal of General Virology, 2017, 98, 3060-3067.	2.9	20
52	Wild African great apes as natural hosts of malaria parasites: current knowledge and research perspectives. Primate Biology, 2017, 4, 47-59.	1.0	7
53	A taxonomy update for the family Polyomaviridae. Archives of Virology, 2016, 161, 1739-1750.	2.1	134
54	Tools for opening new chapters in the book of Treponema pallidum evolutionary history. Clinical Microbiology and Infection, 2016, 22, 916-921.	6.0	26

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55	Assessing Host-Virus Codivergence for Close Relatives of Merkel Cell Polyomavirus Infecting African Great Apes. Journal of Virology, 2016, 90, 8531-8541.	3.4	21
56	Codetection of Respiratory Syncytial Virus in Habituated Wild Western Lowland Gorillas and Humans During a Respiratory Disease Outbreak. EcoHealth, 2016, 13, 499-510.	2.0	39
57	Assessing the feasibility of fly based surveillance of wildlife infectious diseases. Scientific Reports, 2016, 6, 37952.	3.3	19
58	Assessing the Evidence Supporting Fruit Bats as the Primary Reservoirs for Ebola Viruses. EcoHealth, 2016, 13, 18-25.	2.0	109
59	Aquatic biodiversity assessment for the lazy. Molecular Ecology, 2016, 25, 846-848.	3.9	34
60	Bacillus cereus Biovar Anthracis Causing Anthrax in Sub-Saharan Africaâ€"Chromosomal Monophyly and Broad Geographic Distribution. PLoS Neglected Tropical Diseases, 2016, 10, e0004923.	3.0	77
61	A cautionary note on fecal sampling and molecular epidemiology in predatory wild great apes. American Journal of Primatology, 2015, 77, 833-840.	1.7	9
62	Genome Sequence of a Central Chimpanzee-Associated Polyomavirus Related to BK and JC Polyomaviruses, Pan troglodytes troglodytes Polyomavirus 1. Genome Announcements, 2015, 3, .	0.8	5
63	iDNA from terrestrial haematophagous leeches as a wildlife surveying and monitoring tool â€“ prospects, pitfalls and avenues to be developed. Frontiers in Zoology, 2015, 12, 24.	2.0	89
64	Lassa Virus in Multimammate Rats, CÃ´te dâ€™Ivoire, 2013. Emerging Infectious Diseases, 2015, 21, 1481-1483.	4.3	31
65	Adenovirus in Rural CÃ´te D`Ivoire: High Diversity and Cross-Species Detection. EcoHealth, 2015, 12, 441-452.	2.0	16
66	Investigating the zoonotic origin of the West African Ebola epidemic. EMBO Molecular Medicine, 2015, 7, 17-23.	6.9	347
67	Targeted detection of mammalian species using carrion flyâ€derived <scp>DNA</scp>. Molecular Ecology Resources, 2015, 15, 285-294.	4.8	44
68	Multiple Cross-Species Transmission Events of Human Adenoviruses (HAdV) during Hominine Evolution. Molecular Biology and Evolution, 2015, 32, 2072-2084.	8.9	54
69	Hemoparasites in a wild primate: Infection patterns suggest interaction of Plasmodium and Babesia in a lemur species. International Journal for Parasitology: Parasites and Wildlife, 2015, 4, 385-395.	1.5	18
70	Malaria parasite detection increases during pregnancy in wild chimpanzees. Malaria Journal, 2014, 13, 413.	2.3	27
71	High prevalence and diversity of species D adenoviruses (HAdV-D) in human populations of four Sub-Saharan countries. Virology Journal, 2014, 11, 25.	3.4	22
72	Integrating phylogeography, physiology and habitat modelling to explore species range determinants. Journal of Biogeography, 2014, 41, 687-699.	3.0	27

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73	The ecology of primate retroviruses â€“ An assessment of 12 years of retroviral studies in the TaÃ¯ national park area, CÃ´te d×³Ivoire. Virology, 2014, 460-461, 147-153.	2.4	24
74	Clock Rooting Further Demonstrates that Guinea 2014 EBOV is a Member of the ZaÃ¯re Lineage. PLOS Currents, 2014, 6, .	1.4	26
75	An invertebrate stomach's view on vertebrate ecology. BioEssays, 2013, 35, 1004-1013.	2.5	66
76	Carrion flyâ€derived <scp>DNA</scp> as a tool for comprehensive and costâ€effective assessment of mammalian biodiversity. Molecular Ecology, 2013, 22, 915-924.	3.9	144
77	Mother-Offspring Transmission and Age-Dependent Accumulation of Simian Foamy Virus in Wild Chimpanzees. Journal of Virology, 2013, 87, 5193-5204.	3.4	23
78	Evidence for continuing cross-species transmission of SIVsmm to humans. Aids, 2013, 27, 2488-2491.	2.2	66
79	NovelMycobacterium tuberculosisComplex Isolate from a Wild Chimpanzee. Emerging Infectious Diseases, 2013, 19, 969-976.	4.3	100
80	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.	4.7	35
81	Age-related effects on malaria parasite infection in wild chimpanzees. Biology Letters, 2013, 9, 20121160.	2.3	25
82	One Hundred Twenty Years of Koala Retrovirus Evolution Determined from Museum Skins. Molecular Biology and Evolution, 2013, 30, 299-304.	8.9	85
83	Identification of a Novel Human Polyomavirus in Organs of the Gastrointestinal Tract. PLoS ONE, 2013, 8, e58021.	2.5	131
84	Wild great apes as sentinels and sources of infectious disease. Clinical Microbiology and Infection, 2012, 18, 521-527.	6.0	103
85	Detection of Retroviral Super-Infection from Non-Invasive Samples. PLoS ONE, 2012, 7, e36570.	2.5	4
86	Origin of Human T-Lymphotropic Virus Type 1 in Rural CÃ´te dâ€™Ivoire. Emerging Infectious Diseases, 2012, 18, 830-833.	4.3	35
87	A Novel Human Polyomavirus Closely Related to the African Green Monkey-Derived Lymphotropic Polyomavirus. Journal of Virology, 2011, 85, 4586-4590.	3.4	214
88	Preventing the pollution of mitochondrial datasets with nuclear mitochondrial paralogs (numts). Mitochondrion, 2011, 11, 246-254.	3.4	82
89	African Great Apes Are Naturally Infected with Polyomaviruses Closely Related to Merkel Cell Polyomavirus. Journal of Virology, 2011, 85, 916-924.	3.4	46
90	High Prevalence, Coinfection Rate, and Genetic Diversity of Retroviruses in Wild Red Colobus Monkeys (Piliocolobus badius badius) in Taiˆ National Park, Coˆte d'Ivoire. Journal of Virology, 2010, 84, 7427-7436.	3.4	54

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91	Genetic diversity of endangered brown bear (Ursus arctos) populations at the crossroads of Europe, Asia and Africa. Diversity and Distributions, 2009, 15, 742-750.	4.1	74
92	E box motifs as mediators of proviral latency of human retroviruses. Retrovirology, 2009, 6, 81.	2.0	11
93	Combined analysis of fourteen nuclear genes refines the Ursidae phylogeny. Molecular Phylogenetics and Evolution, 2008, 47, 73-83.	2.7	91
94	Ancient DNA evidence for the loss of a highly divergent brown bear clade during historical times. Molecular Ecology, 2008, 17, 1962-1970.	3.9	91
95	DNA from extinct giant lemurs links archaeolemurids to extant indriids. BMC Evolutionary Biology, 2008, 8, 121.	3.2	40
96	Ancient DNA Identification of Early 20th Century Simian T-Cell Leukemia Virus Type 1. Molecular Biology and Evolution, 2008, 25, 1093-1098.	8.9	20
97	Does the 43â€Šbp sequence from an 800â€Š000 year old Cretan dwarf elephantid really rewrite the textbook on mammoths?. Biology Letters, 2007, 3, 58-60.	2.3	7
98	The cost of living in larger primate groups includes higher fly densities. EcoHealth, 0, , .	2.0	2