Verena J Schuenemann

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6507785/publications.pdf

Version: 2024-02-01

39 papers 3,531 citations

257450 24 h-index 302126 39 g-index

43 all docs

43 docs citations

43 times ranked

4612 citing authors

#	Article	IF	CITATIONS
1	Evolutionary Processes in the Emergence and Recent Spread of the Syphilis Agent, <i>Treponema pallidum </i> Nolecular Biology and Evolution, 2022, 39, .	8.9	16
2	Non-destructive extraction of DNA from preserved tissues in medical collections. BioTechniques, 2022, 72, 60-64.	1.8	4
3	Archival influenza virus genomes from Europe reveal genomic variability during the 1918 pandemic. Nature Communications, 2022, 13, 2314.	12.8	25
4	Ancient mitochondrial and modern whole genomes unravel massive genetic diversity loss during near extinction of Alpine ibex. Molecular Ecology, 2022, 31, 3548-3565.	3.9	9
5	A refined proposal for the origin of dogs: the case study of GnirshÃ \P hle, a Magdalenian cave site. Scientific Reports, 2021, 11, 5137.	3.3	15
6	Mycobacterium leprae diversity and population dynamics in medieval Europe from novel ancient genomes. BMC Biology, 2021, 19, 220.	3.8	14
7	One Health Approaches to Trace Mycobacterium leprae's Zoonotic Potential Through Time. Frontiers in Microbiology, 2021, 12, 762263.	3.5	5
8	Leprosy in wild chimpanzees. Nature, 2021, 598, 652-656.	27.8	30
9	Ancient DNA suggests modern wolves trace their origin to a Late Pleistocene expansion from Beringia. Molecular Ecology, 2020, 29, 1596-1610.	3.9	70
10	New ancient Eastern European <i>Yersinia pestis</i> genomes illuminate the dispersal of plague in Europe. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190569.	4.0	20
11	Insights into health and disease from ancient biomolecules. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190568.	4.0	4
12	Ancient Bacterial Genomes Reveal a High Diversity of Treponema pallidum Strains in Early Modern Europe. Current Biology, 2020, 30, 3788-3803.e10.	3.9	47
13	Variola virus genome sequenced from an eighteenth-century museum specimen supports the recent origin of smallpox. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190572.	4.0	24
14	Host Diversity and Origin of Zoonoses: The Ancient and the New. Animals, 2020, 10, 1672.	2.3	33
15	2000-year-old pathogen genomes reconstructed from metagenomic analysis of Egyptian mummified individuals. BMC Biology, 2020, 18, 108.	3.8	29
16	Comparison of target enrichment strategies for ancient pathogen DNA. BioTechniques, 2020, 69, 455-459.	1.8	17
17	Ancient genomes reveal social and genetic structure of Late Neolithic Switzerland. Nature Communications, 2020, 11, 1915.	12.8	50
18	Geographically structured genomic diversity of non-human primate-infecting Treponema pallidum subsp. pertenue. Microbial Genomics, 2020, 6, .	2.0	2

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19	Large-scale mitogenomic analysis of the phylogeography of the Late Pleistocene cave bear. Scientific Reports, 2019, 9, 10700.	3.3	57
20	Human mitochondrial DNA lineages in Iron-Age Fennoscandia suggest incipient admixture and eastern introduction of farming-related maternal ancestry. Scientific Reports, 2019, 9, 16883.	3.3	14
21	Ratio of mitochondrial to nuclear DNA affects contamination estimates in ancient DNA analysis. Scientific Reports, 2018, 8, 14075.	3.3	48
22	Nonhuman primates across sub-Saharan Africa are infected with the yaws bacterium <i>Treponema pallidum</i> subsp. <i>pertenue</i> Emerging Microbes and Infections, 2018, 7, 1-4.	6.5	41
23	Historic Treponema pallidum genomes from Colonial Mexico retrieved from archaeological remains. PLoS Neglected Tropical Diseases, 2018, 12, e0006447.	3.0	58
24	Ancient genomes reveal a high diversity of Mycobacterium leprae in medieval Europe. PLoS Pathogens, 2018, 14, e1006997.	4.7	98
25	Origin of modern syphilis and emergence of a pandemic Treponema pallidum cluster. Nature Microbiology, 2017, 2, 16245.	13.3	138
26	Ancient Egyptian mummy genomes suggest an increase of Sub-Saharan African ancestry in post-Roman periods. Nature Communications, 2017, 8, 15694.	12.8	131
27	Extraction of ultrashort DNA molecules from herbarium specimens. BioTechniques, 2017, 62, 76-79.	1.8	53
28	Eighteenth century Yersinia pestis genomes reveal the long-term persistence of an historical plague focus. ELife, 2016, 5, e12994.	6.0	139
29	Effect of X-ray irradiation on ancient DNA in sub-fossil bones – Guidelines for safe X-ray imaging. Scientific Reports, 2016, 6, 32969.	3.3	74
30	Mitochondrial Genomes of Giant Deers Suggest their Late Survival in Central Europe. Scientific Reports, 2015, 5, 10853.	3.3	28
31	Insight into the evolution and origin of leprosy bacilli from the genome sequence of <i>Mycobacterium lepromatosis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 4459-4464.	7.1	134
32	Parallel detection of ancient pathogens via array-based DNA capture. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20130375.	4.0	38
33	Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. Nature, 2014, 514, 494-497.	27.8	506
34	Mycobacterium leprae genomes from a British medieval leprosy hospital: towards understanding an ancient epidemic. BMC Genomics, 2014, 15, 270.	2.8	60
35	Genome-Wide Comparison of Medieval and Modern <i>Mycobacterium leprae</i> . Science, 2013, 341, 179-183.	12.6	313
36	The rise and fall of the Phytophthora infestans lineage that triggered the Irish potato famine. ELife, 2013, 2, e00731.	6.0	339

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37	A draft genome of Yersinia pestis from victims of the Black Death. Nature, 2011, 478, 506-510.	27.8	619
38	Targeted enrichment of ancient pathogens yielding the pPCP1 plasmid of <i>Yersinia pestis</i> from victims of the Black Death. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E746-52.	7.1	211
39	The Southernmost Pre-Columbian Dogs in the Americas: Phenotype, Chronology, Diet and Genetics. Environmental Archaeology, 0, , 1-32.	1.2	8