

# Andrew Kitchen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4701986/publications.pdf>

Version: 2024-02-01

30  
papers

2,485  
citations

331670

21  
h-index

454955

30  
g-index

31  
all docs

31  
docs citations

31  
times ranked

4575  
citing authors

#	ARTICLE	IF	CITATIONS
1	Host shifting and host sharing in a genus of specialist flies diversifying alongside their sunflower hosts. <i>Journal of Evolutionary Biology</i> , 2021, 34, 364-379.	1.7	3
2	<i>In trans</i> variant calling reveals enrichment for compound heterozygous variants in genes involved in neuronal development and growth. <i>Genetical Research</i> , 2019, 101, e8.	0.9	3
3	Lineage specific histories of <i>Mycobacterium tuberculosis</i> dispersal in Africa and Eurasia. <i>Molecular Ecology</i> , 2019, 28, 3241-3256.	3.9	86
4	Applications of Bayesian Skyline Plots and Approximate Bayesian Computation for Human Demography. <i>Human Biology</i> , 2019, 91, 279.	0.2	2
5	Global expansion of <i>Mycobacterium tuberculosis</i> lineage 4 shaped by colonial migration and local adaptation. <i>Science Advances</i> , 2018, 4, eaat5869.	10.3	130
6	The evolutionary history of dogs in the Americas. <i>Science</i> , 2018, 361, 81-85.	12.6	140
7	Unlocking pandemic potential: prevalence and spatial patterns of key substitutions in avian influenza H5N1 in Egyptian isolates. <i>BMC Infectious Diseases</i> , 2018, 18, 314.	2.9	8
8	Complete <i>Anopheles funestus</i> mitogenomes reveal an ancient history of mitochondrial lineages and their distribution in southern and central Africa. <i>Scientific Reports</i> , 2018, 8, 9054.	3.3	18
9	How's the Flu Getting Through? Landscape genetics suggests both humans and birds spread H5N1 in Egypt. <i>Infection, Genetics and Evolution</i> , 2017, 49, 293-299.	2.3	15
10	Genetic Discontinuity between the Maritime Archaic and Beothuk Populations in Newfoundland, Canada. <i>Current Biology</i> , 2017, 27, 3149-3156.e11.	3.9	17
11	A molecular portrait of maternal sepsis from Byzantine Troy. <i>ELife</i> , 2017, 6, .	6.0	46
12	<i>Babesia microti</i> from humans and ticks hold a genomic signature of strong population structure in the United States. <i>BMC Genomics</i> , 2016, 17, 888.	2.8	15
13	Bayesian analyses of Yemeni mitochondrial genomes suggest multiple migration events with Africa and Western Eurasia. <i>American Journal of Physical Anthropology</i> , 2016, 159, 382-393.	2.1	19
14	Mitogenomes reveal diversity of the European Lyme borreliosis vector <i>Ixodes ricinus</i> in Italy. <i>Molecular Phylogenetics and Evolution</i> , 2016, 101, 194-202.	2.7	26
15	Armed conflict and population displacement as drivers of the evolution and dispersal of <i>Mycobacterium tuberculosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13881-13886.	7.1	76
16	DNA analysis of ancient dogs of the Americas: Identifying possible founding haplotypes and reconstructing population histories. <i>Journal of Human Evolution</i> , 2015, 79, 105-118.	2.6	47
17	The Role of Selection in Shaping Diversity of Natural <i>M. tuberculosis</i> Populations. <i>PLoS Pathogens</i> , 2013, 9, e1003543.	4.7	138
18	Molecular evolution of the insect-specific flaviviruses. <i>Journal of General Virology</i> , 2012, 93, 223-234.	2.9	141

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19	Shigella sonnei genome sequencing and phylogenetic analysis indicate recent global dissemination from Europe. <i>Nature Genetics</i> , 2012, 44, 1056-1059.	21.4	278
20	Family level phylogenies reveal modes of macroevolution in RNA viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 238-243.	7.1	87
21	Origin of Clothing Lice Indicates Early Clothing Use by Anatomically Modern Humans in Africa. <i>Molecular Biology and Evolution</i> , 2011, 28, 29-32.	8.9	157
22	The Evolutionary Dynamics of Bluetongue Virus. <i>Journal of Molecular Evolution</i> , 2010, 70, 583-592.	1.8	59
23	Yellow Fever Virus Exhibits Slower Evolutionary Dynamics than Dengue Virus. <i>Journal of Virology</i> , 2010, 84, 765-772.	3.4	69
24	Using Time-Structured Data to Estimate Evolutionary Rates of Double-Stranded DNA Viruses. <i>Molecular Biology and Evolution</i> , 2010, 27, 2038-2051.	8.9	279
25	Origin and Phylodynamics of Rabbit Hemorrhagic Disease Virus. <i>Journal of Virology</i> , 2009, 83, 12129-12138.	3.4	76
26	Bayesian phylogenetic analysis of Semitic languages identifies an Early Bronze Age origin of Semitic in the Near East. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2009, 276, 2703-2710.	2.6	162
27	Utility of DNA viruses for studying human host history: Case study of JC virus. <i>Molecular Phylogenetics and Evolution</i> , 2008, 46, 673-682.	2.7	39
28	Updated Three-Stage Model for the Peopling of the Americas. <i>PLoS ONE</i> , 2008, 3, e3199.	2.5	108
29	A Three-Stage Colonization Model for the Peopling of the Americas. <i>PLoS ONE</i> , 2008, 3, e1596.	2.5	180
30	Comment on "Population Size Does Not Influence Mitochondrial Genetic Diversity in Animals". <i>Science</i> , 2006, 314, 1390a-1390a.	12.6	61