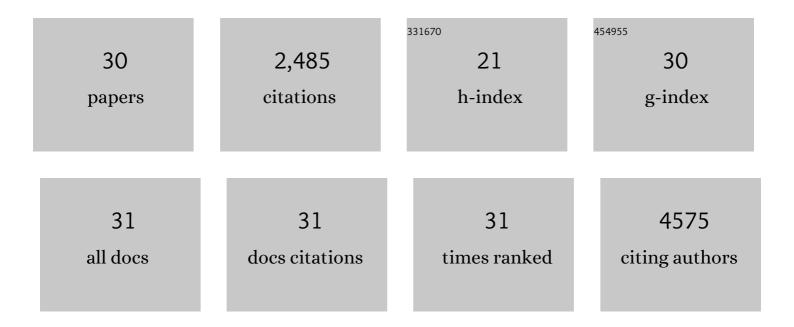
## Andrew Kitchen

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4701986/publications.pdf Version: 2024-02-01



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

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