Alan R Rogers

List of Publications by Year
in descending order

63 papers	**5,786** citations	126907 **33** h-index	118850 **62** g-index
74 all docs	**74** docs citations	**74** times ranked	**5027** citing authors

#	Article	IF	Citations
1	Estimating bonobo (*Pan* *paniscus*) and chimpanzee (*Pan* *troglodytes*) evolutionary history from nucleotide site patterns. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2200858119.	7.1	5
2	Sexual dimorphism in skeletal shape in voles (Arvicolinae): disparate selection on male bodies and female heads. Journal of Mammalogy, 2020, 101, 951-957.	1.3	1
3	Neanderthal-Denisovan ancestors interbred with a distantly related hominin. Science Advances, 2020, 6, eaay5483.	10.3	43
4	Legofit: estimating population history from genetic data. BMC Bioinformatics, 2019, 20, 526.	2.6	12
5	Early history of Neanderthals and Denisovans. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 9859-9863.	7.1	66
6	Reply to Mafessoni and Prüfer: Inferences with and without singleton site patterns. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E10258-E10260.	7.1	9
7	Evolutionary history of Tibetans inferred from whole-genome sequencing. PLoS Genetics, 2017, 13, e1006675.	3.5	89
8	The heritability of gestational age in a two-million member cohort: implications for spontaneous preterm birth. Human Genetics, 2015, 134, 803-808.	3.8	42
9	Bias in estimators of archaic admixture. Theoretical Population Biology, 2015, 100, 63-78.	1.1	25
10	How Population Growth Affects Linkage Disequilibrium. Genetics, 2014, 197, 1329-1341.	2.9	46
11	A Late Holocene Population Bottleneck in California Tule Elk (Cervus elaphus nannodes): Provisional Support from Ancient DNA. Journal of Archaeological Method and Theory, 2013, 20, 495-524.	3.0	15
12	Genetic relatedness to sisters' children has been underestimated. Proceedings of the Royal Society B: Biological Sciences, 2013, 280, 20121937.	2.6	10
13	Mobile elements reveal small population size in the ancient ancestors of *Homo sapiens*. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2147-2152.	7.1	44
14	Linkage Disequilibrium Between Loci With Unknown Phase. Genetics, 2009, 182, 839-844.	2.9	73
15	Estimating the age of retrotransposon subfamilies using maximum likelihood. Genomics, 2009, 94, 78-82.	2.9	11
16	Ancestral Alleles and Population Origins: Inferences Depend on Mutation Rate. Molecular Biology and Evolution, 2007, 24, 990-997.	8.9	8
17	Genomics refutes an exclusively African origin of humans. Journal of Human Evolution, 2005, 49, 1-18.	2.6	111
18	Modeling the Amplification Dynamics of Human Alu Retrotransposons. PLoS Computational Biology, 2005, 1, e44.	3.2	12

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19	Genetic Analysis of Lice Supports Direct Contact between Modern and Archaic Humans. PLoS Biology, 2004, 2, e340.	5.6	223
20	When is technology worth the trouble?. Journal of Archaeological Science, 2003, 30, 1315-1329.	2.4	137
21	Genetic Variation Among World Populations: Inferences From 100 *Alu* Insertion Polymorphisms. Genome Research, 2003, 13, 1607-1618.	5.5	191
22	Sequence variations in the public human genome data reflect a bottlenecked population history. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 376-381.	7.1	113
23	Economics and the evolution of life histories. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 9114-9115.	7.1	10
24	The Matrix Coalescent and an Application to Human Single-Nucleotide Polymorphisms. Genetics, 2002, 161, 1641-1650.	2.9	50
25	Selective Transport of Animal Parts by Ancient Hunters: A New Statistical Method and an Application to the Emeryville Shellmound Fauna. Journal of Archaeological Science, 2001, 28, 763-773.	2.4	26
26	Order emerging from chaos in human evolutionary genetics. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 779-780.	7.1	38
27	Analysis of Bone Counts by Maximum Likelihood. Journal of Archaeological Science, 2000, 27, 111-125.	2.4	37
28	On the Value of Soft Bones in Faunal Analysis. Journal of Archaeological Science, 2000, 27, 635-639.	2.4	11
29	On Equifinality in Faunal Analysis. American Antiquity, 2000, 65, 709-723.	1.1	37
30	Genetic Perspectives on Human Origins and Differentiation. Annual Review of Genomics and Human Genetics, 2000, 1, 361-385.	6.2	326
31	Using mitochondrial and nuclear DNA markers to reconstruct human evolution. BioEssays, 1998, 20, 126-136.	2.5	157
32	Population Structure and Modern Human Origins. The IMA Volumes in Mathematics and Its Applications, 1997, , 55-79.	0.5	34
33	Evolution and Human Choice Over Time. Novartis Foundation Symposium, 1997, 208, 231-252.	1.1	3
34	Mitochondrial mismatch analysis is insensitive to the mutational process. Molecular Biology and Evolution, 1996, 13, 895-902.	8.9	124
35	Genetic admixture in the Late Pleistocene. , 1996, 100, 1-5.		22
36	Estimating sexual dimorphism by method-of-moments. American Journal of Physical Anthropology, 1996, 100, 191-206.	2.1	39

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37	Ascertainment bias in estimates of average heterozygosity. American Journal of Human Genetics, 1996, 58, 1033-41.	6.2	58
38	GENETIC EVIDENCE FOR A PLEISTOCENE POPULATION EXPLOSION. Evolution; International Journal of Organic Evolution, 1995, 49, 608-615.	2.3	916
39	The male's dilemma: Increased offspring production is more paternity to steal. Evolutionary Ecology, 1995, 9, 662-677.	1.2	89
40	Genetic Evidence for a Pleistocene Population Explosion. Evolution; International Journal of Organic Evolution, 1995, 49, 608.	2.3	471
41	How Much Can Fossils Tell Us about Regional Continuity?. Current Anthropology, 1995, 36, 674-676.	1.6	11
42	Why menopause?. Evolutionary Ecology, 1993, 7, 406-420.	1.2	130
43	The Genetic Structure of Ancient Human Populations. Current Anthropology, 1993, 34, 483-496.	1.6	562
44	QUANTITATIVE GENETICS OF SEXUAL DIMORPHISM IN HUMAN BODY SIZE. Evolution; International Journal of Organic Evolution, 1992, 46, 226-234.	2.3	51
45	Conserving resources for children. Human Nature, 1991, 2, 73-82.	1.6	69
46	Group Selection by Selective Emigration: The Effects of Migration and Kin Structure. American Naturalist, 1990, 135, 398-413.	2.1	132
47	Evolutionary economics of human reproduction. Ethology and Sociobiology, 1990, 11, 479-495.	1.5	105
48	Fitness in stratified societies. Ethology and Sociobiology, 1990, 11, 497-509.	1.5	17
49	Resource partitioning and the stability of population dynamics: A reply to Åomnicki and Sedziwy. Journal of Theoretical Biology, 1989, 138, 545-549.	1.7	2
50	Three components of genetic drift in subdivided populations. American Journal of Physical Anthropology, 1988, 77, 435-449.	2.1	14
51	Statistical analysis of the migration component of genetic drift. American Journal of Physical Anthropology, 1988, 77, 451-457.	2.1	7
52	Does Biology Constrain Culture. American Anthropologist, 1988, 90, 819-831.	1.4	613
53	A Model of Kin-Structured Migration. Evolution; International Journal of Organic Evolution, 1987, 41, 417.	2.3	8
54	Human sociobiology. American Journal of Physical Anthropology, 1987, 30, 127-150.	2.1	23

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55	On Wright's mechanism for intergroup selection. Journal of Theoretical Biology, 1987, 127, 51-61.	1.7	57
56	Population Differences in Quantitative Characters as Opposed to Gene Frequencies. American Naturalist, 1986, 127, 729-730.	2.1	45
57	Correlations between relatives in small populations. American Journal of Physical Anthropology, 1986, 71, 377-380.	2.1	4
58	Population dynamics under exploitation competition. Journal of Theoretical Biology, 1986, 119, 363-368.	1.7	16
59	The Sociobiology of Sex and Sexes Today [and Comments and Reply]. Current Anthropology, 1984, 25, 193-212.	1.6	1
60	Assortative mating and the segregation variance. Theoretical Population Biology, 1983, 23, 110-113.	1.1	6
61	POPULATION STRUCTURE AND QUANTITATIVE CHARACTERS. Genetics, 1983, 105, 985-1002.	2.9	117
62	Data collection and information loss in the study of spatial pattern. World Archaeology, 1982, 14, 249-258.	1.1	4
63	An efficient algorithm for estimating population history from genetic data. , 0, 2, .		4