Ripan S Malhi

List of Publications by Year in descending order

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94269 6,019 87 37 citations h-index papers

73 g-index 94 94 94 5564 docs citations times ranked citing authors all docs

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#	Article	IF	CITATIONS
1	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. Nature, 2014, 506, 225-229.	13.7	500
2	Beringian Standstill and Spread of Native American Founders. PLoS ONE, 2007, 2, e829.	1.1	499
3	Genomic evidence for the Pleistocene and recent population history of Native Americans. Science, 2015, 349, aab3884.	6.0	449
4	Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. Nature, 2018, 553, 203-207.	13.7	304
5	The population history of northeastern Siberia since the Pleistocene. Nature, 2019, 570, 182-188.	13.7	259
6	The ancestry and affiliations of Kennewick Man. Nature, 2015, 523, 455-458.	13.7	241
7	Early human dispersals within the Americas. Science, 2018, 362, .	6.0	230
8	Genetic analysis of early holocene skeletal remains from Alaska and its implications for the settlement of the Americas. American Journal of Physical Anthropology, 2007, 132, 605-621.	2.1	221
9	Late Pleistocene Human Skeleton and mtDNA Link Paleoamericans and Modern Native Americans. Science, 2014, 344, 750-754.	6.0	147
10	Rights, interests and expectations: Indigenous perspectives on unrestricted access to genomic data. Nature Reviews Genetics, 2020, 21, 377-384.	7.7	141
11	The evolutionary history of dogs in the Americas. Science, 2018, 361, 81-85.	6.0	140
12	Ancient human parallel lineages within North America contributed to a coastal expansion. Science, 2018, 360, 1024-1027.	6.0	138
13	A time transect of exomes from a Native American population before and after European contact. Nature Communications, 2016, 7, 13175.	5.8	134
14	Central Place Models of Acorn and Mussel Processing. Journal of Archaeological Science, 1997, 24, 887-899.	1.2	130
15	Reconciling migration models to the Americas with the variation of North American native mitogenomes. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14308-14313.	3.3	122
16	Current evidence allows multiple models for the peopling of the Americas. Science Advances, 2018, 4, eaat5473.	4.7	114
17	Dog domestication and the dual dispersal of people and dogs into the Americas. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	112
18	Advancing the ethics of paleogenomics. Science, 2018, 360, 384-385.	6.0	110

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19	Distribution of mtDNA haplogroup X among Native North Americans. American Journal of Physical Anthropology, 1999, 110, 271-284.	2.1	106
20	Ancient individuals from the North American Northwest Coast reveal 10,000 years of regional genetic continuity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 4093-4098.	3.3	100
21	Comparative and population mitogenomic analyses of Madagascar's extinct, giant â€~subfossil' lemurs. Journal of Human Evolution, 2015, 79, 45-54.	1.3	86
22	The Structure of Diversity within New World Mitochondrial DNA Haplogroups: Implications for the Prehistory of North America. American Journal of Human Genetics, 2002, 70, 905-919.	2.6	85
23	Evaluating the Farming/Language Dispersal Hypothesis with genetic variation exhibited by populations in the Southwest and Mesoamerica. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6759-6764.	3.3	85
24	Native American mtDNA prehistory in the American Southwest. American Journal of Physical Anthropology, 2003, 120, 108-124.	2.1	83
25	Mitochondrial DNA studies of Native Americans: Conceptions and misconceptions of the population prehistory of the Americas. Evolutionary Anthropology, 2003, 12, 7-18.	1.7	82
26	Patterns of Admixture and Population Structure in Native Populations of Northwest North America. PLoS Genetics, 2014, 10, e1004530.	1.5	81
27	Haplotypic Background of a Private Allele at High Frequency in the Americas. Molecular Biology and Evolution, 2009, 26, 995-1016.	3.5	74
28	Ancient DNA suggests modern wolves trace their origin to a Late Pleistocene expansion from Beringia. Molecular Ecology, 2020, 29, 1596-1610.	2.0	70
29	Race and diversity in U.S. Biological Anthropology: A decade of AAPA initiatives. American Journal of Physical Anthropology, 2018, 165, 158-180.	2.1	63
30	Distribution of Mitochondrial DNA Lineages among Native American Tribes of Northeastern North America. Human Biology, 2001, 73, 17-55.	0.4	61
31	Mitochondrial haplogroup M discovered in prehistoric North Americans. Journal of Archaeological Science, 2007, 34, 642-648.	1.2	60
32	Ancient DNA Analysis of Mid-Holocene Individuals from the Northwest Coast of North America Reveals Different Evolutionary Paths for Mitogenomes. PLoS ONE, 2013, 8, e66948.	1.1	56
33	DNA analysis of ancient dogs of the Americas: Identifying possible founding haplotypes and reconstructing population histories. Journal of Human Evolution, 2015, 79, 105-118.	1.3	47
34	Implications of the distribution of Albumin Naskapi and Albumin Mexico for new world prehistory. American Journal of Physical Anthropology, 2000, 111, 557-572.	2.1	45
35	Brief communication: Haplogroup X confirmed in prehistoric North America. American Journal of Physical Anthropology, 2002, 119, 84-86.	2.1	42
36	Arrival routes of first Americans uncertain. Science, 2018, 359, 1224-1225.	6.0	42

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37	Multiple Asian pig origins revealed through genomic analyses. Molecular Phylogenetics and Evolution, 2010, 54, 680-686.	1.2	41
38	MamuSNP: A Resource for Rhesus Macaque (Macaca mulatta) Genomics. PLoS ONE, 2007, 2, e438.	1.1	40
39	A comparison of proteomic, genomic, and osteological methods of archaeological sex estimation. Scientific Reports, 2020, 10, 11897.	1.6	40
40	The effect of SNP discovery method and sample size on estimation of population genetic data for Chinese and Indian rhesus macaques (Macaca mulatta). Primates, 2011, 52, 129-138.	0.7	37
41	Mitochondrial DNA and Prehistoric Settlements: Native Migrations on the Western Edge of North America. Human Biology, 2004, 76, 55-75.	0.4	36
42	Influence of fruit and invertebrate consumption on the gut microbiota of wild whiteâ€faced capuchins (<i>Cebus capucinus</i>). American Journal of Physical Anthropology, 2018, 165, 576-588.	2.1	36
43	Brief communication: Mitochondrial haplotype C4c confirmed as a founding genome in the Americas. American Journal of Physical Anthropology, 2010, 141, 494-497.	2.1	35
44	Patterns of Genetic Coding Variation in a Native American Population before and after European Contact. American Journal of Human Genetics, 2018, 102, 806-815.	2.6	33
45	trnL outperforms rbcL as a DNA metabarcoding marker when compared with the observed plant component of the diet of wild white-faced capuchins (Cebus capucinus, Primates). PLoS ONE, 2018, 13, e0199556.	1.1	32
46	Low Mitochondrial DNA Diversity in an Ancient Population from China: Insight into Social Organization at the Fujia Site. Human Biology, 2015, 87, 71.	0.4	30
47	Integrating feeding behavior, ecological data, and DNA barcoding to identify developmental differences in invertebrate foraging strategies in wild whiteâ€faced capuchins (⟨i⟩Cebus capucinus⟨ i⟩). American Journal of Physical Anthropology, 2017, 162, 241-254.	2.1	25
48	Chaco Canyon Dig Unearths Ethical Concerns. Human Biology, 2017, 89, 177.	0.4	25
49	Patterns of mtDNA Diversity in Northwestern North America. Human Biology, 2004, 76, 33-54.	0.4	21
50	Diversification of porcine MHC class II genes: evidence for selective advantage. Immunogenetics, 2009, 61, 119-129.	1.2	21
51	Engaging Native Americans in Genomics Research. American Anthropologist, 2015, 117, 743-744.	0.7	20
52	Isotopic and genetic analyses of a mass grave in central <scp>C</scp> alifornia: Implications for precontact hunterâ€gatherer warfare. American Journal of Physical Anthropology, 2016, 159, 116-125.	2.1	16
53	Tracing the phylogeographic history of Southeast Asian long-tailed macaques through mitogenomes of museum specimens. Molecular Phylogenetics and Evolution, 2017, 116, 227-238.	1.2	16
54	Ancient DNA analysis of a nineteenth century tobacco pipe from a Maryland slave quarter. Journal of Archaeological Science, 2019, 105, 11-18.	1.2	15

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55	Mitochondrial DNA evidence of an early Holocene population expansion of threespine sticklebacks from Scotland. Molecular Phylogenetics and Evolution, 2006, 40, 148-154.	1.2	14
56	Genotyping single nucleotide polymorphisms (SNPs) across species in Old World Monkeys. American Journal of Primatology, 2011, 73, 1031-1040.	0.8	14
57	Complete Mitochondrial Genome Sequencing of a Burial from a Romano–Christian Cemetery in the Dakhleh Oasis, Egypt: Preliminary Indications. Genes, 2017, 8, 262.	1.0	14
58	Accurate Sex Identification of Ancient Elephant and Other Animal Remains Using Low-Coverage DNA Shotgun Sequencing Data. G3: Genes, Genomes, Genetics, 2020, 10, 1427-1432.	0.8	14
59	Social convergence of gut microbiomes in vampire bats. Biology Letters, 2021, 17, 20210389.	1.0	14
60	Integrative analysis of DNA, macroscopic remains and stable isotopes of dog coprolites to reconstruct community diet. Scientific Reports, 2021, 11, 3113.	1.6	12
61	Evolutionary and phylogenetic insights from a nuclear genome sequence of the extinct, giant, "subfossil―koala lemur <i>Megaladapis edwardsi</i> . Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	12
62	A South American Prehistoric Mitogenome: Context, Continuity, and the Origin of Haplogroup C1d. PLoS ONE, 2015, 10, e0141808.	1.1	12
63	Implications of the Genographic Project for Molecular Anthropologists. International Journal of Cultural Property, 2009, 16, 193-194.	0.2	11
64	Population genetics of wild <i>Macaca fascicularis</i> with lowâ€coverage shotgun sequencing of museum specimens. American Journal of Physical Anthropology, 2020, 173, 21-33.	2.1	11
65	Police Endorse Color-Blind Racial Beliefs More Than Laypersons. Race and Social Problems, 2016, 8, 160-170.	1.2	10
66	Assessing the comparability of different DNA extraction and amplification methods in gut microbial community profiling. Access Microbiology, 2019, 1, e000060.	0.2	10
67	Ancient and modern genomics of the Ohlone Indigenous population of California. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2111533119.	3.3	10
68	Opinion: Demystifying Native American genetic opposition to research. Evolutionary Anthropology, 2006, 15, 88-92.	1.7	9
69	Species identification and mitochondrial genomes of ancient fish bones from the Riverine Kachemak tradition of the Kenai Peninsula, Alaska. Mitochondrial DNA Part B: Resources, 2018, 3, 409-411.	0.2	9
70	Genetic Structure and Diversity Among Historic and Modern Populations of the Sumatran Rhinoceros (Dicerorhinus sumatrensis). Journal of Heredity, 2018, 109, 553-565.	1.0	8
71	How Subjectivity Strengthens Research: Developing an Integrative Approach to Investigating Human Diet in the Pacific Northwest Coast. American Anthropologist, 2019, 121, 476-478.	0.7	8
72	Sourcing Elephant Ivory from a Sixteenth-Century Portuguese Shipwreck. Current Biology, 2021, 31, 621-628.e4.	1.8	7

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73	The evolutionary history of <i>SLC6A4</i> and the role of plasticity in <i>macaca</i> American Journal of Physical Anthropology, 2014, 153, 605-616.	2.1	5
74	Distribution of mtDNA haplogroup X among Native North Americans., 1999, 110, 271.		5
75	Case Study on Ancestry Estimation in an Alaskan Native Family: Identity and Safeguards against Reductionism. Human Biology, 2015, 87, 338.	0.4	5
76	Anthropological Genetics. American Anthropologist, 2015, 117, 736-737.	0.7	4
77	Response to Comment on "Late Pleistocene human skeleton and mtDNA link Paleoamericans and modern Native Americans― Science, 2015, 347, 835-835.	6.0	4
78	Patterns of genetic variation and the role of selection in HTR1A and HTR1B in macaques (Macaca). BMC Genetics, 2014, 15, 116.	2.7	2
79	Genetic Structure of First Nation Communities in the Pacific Northwest. Human Biology, 2016, 88, 251.	0.4	2
80	Community-Oriented Research and the Future of Anthropological Genetics., 2019,, 37-44.		2
81	Uses and limitations of genetic data relating to Athapaskan migrations: A reply to Seymour. American Journal of Physical Anthropology, 2009, 140, 203-204.	2.1	1
82	Developing SNPs and STR DNA markers for snub-nosed monkeys (Rhinopithecus roxellana) using next-generation sequencing technology. Conservation Genetics Resources, 2012, 4, 451-453.	0.4	1
83	Loxodonta Localizer: A Software Tool for Inferring the Provenance of African Elephants and Their Ivory Using Mitochondrial DNA. Journal of Heredity, 2019, 110, 761-768.	1.0	1
84	Population Structure Analyses Provide Insight into the Source Populations Underlying Rural Isolated Communities in Illinois. Human Biology, 2019, 91, 31.	0.4	1
85	Contributions to Anti-Racist Science: Introduction to Race, Racism, and the Genetic Structure of Human Populations Special Issue. Human Biology, 2020, 92, 133.	0.4	1
86	Early Americans: Misstated results. Science, 2014, 345, 390-390.	6.0	0
87	Introduction: Providing a Venue for Influential Research in Anthropological Genomics. Human Biology, 2014, 86, 5.	0.4	0