Ripan S Malhi

List of Publications by Year
in descending order

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87	6,019	94269 37	79541 73
papers	citations	h-index	g-index

94	94	94	5564
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	Sourcing Elephant Ivory from a Sixteenth-Century Portuguese Shipwreck. Current Biology, 2021, 31, 621-628.e4.	1.8	7
3	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
4	Integrative analysis of DNA, macroscopic remains and stable isotopes of dog coprolites to reconstruct community diet. Scientific Reports, 2021, 11, 3113.	1.6	12
5	Evolutionary and phylogenetic insights from a nuclear genome sequence of the extinct, giant, â€œsubfossilâ€koala lemurMegaladapis edwardsi. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	12
6	Social convergence of gut microbiomes in vampire bats. Biology Letters, 2021, 17, 20210389.	1.0	14
7	Ancient DNA suggests modern wolves trace their origin to a Late Pleistocene expansion from Beringia. Molecular Ecology, 2020, 29, 1596-1610.	2.0	70
8	A comparison of proteomic, genomic, and osteological methods of archaeological sex estimation. Scientific Reports, 2020, 10, 11897.	1.6	40
9	Rights, interests and expectations: Indigenous perspectives on unrestricted access to genomic data. Nature Reviews Genetics, 2020, 21, 377-384.	7.7	141
10	Population genetics of wild Macaca fascicularis with lowâ€coverage shotgun sequencing of museum specimens. American Journal of Physical Anthropology, 2020, 173, 21-33.	2.1	11
11	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
12	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
13	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
14	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
15	The population history of northeastern Siberia since the Pleistocene. Nature, 2019, 570, 182-188.	13.7	259
16	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
17	Community-Oriented Research and the Future of Anthropological Genetics. , 2019, , 37-44.		2
18	Assessing the comparability of different DNA extraction and amplification methods in gut microbial community profiling. Access Microbiology, 2019, 1, e000060.	0.2	10

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19	Population Structure Analyses Provide Insight into the Source Populations Underlying Rural Isolated Communities in Illinois. Human Biology, 2019, 91, 31.	0.4	1
20	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
21	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
22	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
23	Influence of fruit and invertebrate consumption on the gut microbiota of wild whiteâ€faced capuchins (Cebus capucinus). American Journal of Physical Anthropology, 2018, 165, 576-588.	2.1	36
24	Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. Nature, 2018, 553, 203-207.	13.7	304
25	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
26	Advancing the ethics of paleogenomics. Science, 2018, 360, 384-385.	6.0	110
27	Arrival routes of first Americans uncertain. Science, 2018, 359, 1224-1225.	6.0	42
28	Early human dispersals within the Americas. Science, 2018, 362, .	6.0	230
29	Ancient human parallel lineages within North America contributed to a coastal expansion. Science, 2018, 360, 1024-1027.	6.0	138
30	The evolutionary history of dogs in the Americas. Science, 2018, 361, 81-85.	6.0	140
31	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
32	Current evidence allows multiple models for the peopling of the Americas. Science Advances, 2018, 4, eaat5473.	4.7	114
33	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
34	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
35	Integrating feeding behavior, ecological data, and DNA barcoding to identify developmental differences in invertebrate foraging strategies in wild whiteâ€faced capuchins (Cebus capucinus). American Journal of Physical Anthropology, 2017, 162, 241-254.	2.1	25
36	Complete Mitochondrial Genome Sequencing of a Burial from a Romanoâ€“Christian Cemetery in the Dakhleh Oasis, Egypt: Preliminary Indications. Genes, 2017, 8, 262.	1.0	14

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37	Chaco Canyon Dig Unearths Ethical Concerns. Human Biology, 2017, 89, 177.	0.4	25
38	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
39	A time transect of exomes from a Native American population before and after European contact. Nature Communications, 2016, 7, 13175.	5.8	134
40	Genetic Structure of First Nation Communities in the Pacific Northwest. Human Biology, 2016, 88, 251.	0.4	2
41	Police Endorse Color-Blind Racial Beliefs More Than Laypersons. Race and Social Problems, 2016, 8, 160-170.	1.2	10
42	Anthropological Genetics. American Anthropologist, 2015, 117, 736-737.	0.7	4
43	Engaging Native Americans in Genomics Research. American Anthropologist, 2015, 117, 743-744.	0.7	20
44	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
45	Comparative and population mitogenomic analyses of Madagascar's extinct, giant â€˜subfossilâ€™ lemurs. Journal of Human Evolution, 2015, 79, 45-54.	1.3	86
46	Response to Comment on â€œLate Pleistocene human skeleton and mtDNA link Paleoamericans and modern Native Americansâ€. Science, 2015, 347, 835-835.	6.0	4
47	Genomic evidence for the Pleistocene and recent population history of Native Americans. Science, 2015, 349, aab3884.	6.0	449
48	The ancestry and affiliations of Kennewick Man. Nature, 2015, 523, 455-458.	13.7	241
49	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
50	Case Study on Ancestry Estimation in an Alaskan Native Family: Identity and Safeguards against Reductionism. Human Biology, 2015, 87, 338.	0.4	5
51	A South American Prehistoric Mitogenome: Context, Continuity, and the Origin of Haplogroup C1d. PLoS ONE, 2015, 10, e0141808.	1.1	12
52	Patterns of genetic variation and the role of selection in HTR1A and HTR1B in macaques (Macaca). BMC Genetics, 2014, 15, 116.	2.7	2
53	Patterns of Admixture and Population Structure in Native Populations of Northwest North America. PLoS Genetics, 2014, 10, e1004530.	1.5	81
54	The evolutionary history of SLC6A4 and the role of plasticity in macaca. American Journal of Physical Anthropology, 2014, 153, 605-616.	2.1	5

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55	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. Nature, 2014, 506, 225-229.	13.7	500
56	Late Pleistocene Human Skeleton and mtDNA Link Paleoamericans and Modern Native Americans. Science, 2014, 344, 750-754.	6.0	147
57	Early Americans: Misstated results. Science, 2014, 345, 390-390.	6.0	0
58	Introduction: Providing a Venue for Influential Research in Anthropological Genomics. Human Biology, 2014, 86, 5.	0.4	0
59	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
60	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
61	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
62	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
63	Genotyping single nucleotide polymorphisms (SNPs) across species in Old World Monkeys. American Journal of Primatology, 2011, 73, 1031-1040.	0.8	14
64	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
65	Multiple Asian pig origins revealed through genomic analyses. Molecular Phylogenetics and Evolution, 2010, 54, 680-686.	1.2	41
66	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
67	Implications of the Genographic Project for Molecular Anthropologists. International Journal of Cultural Property, 2009, 16, 193-194.	0.2	11
68	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
69	Diversification of porcine MHC class II genes: evidence for selective advantage. Immunogenetics, 2009, 61, 119-129.	1.2	21
70	Haplotypic Background of a Private Allele at High Frequency in the Americas. Molecular Biology and Evolution, 2009, 26, 995-1016.	3.5	74
71	Mitochondrial haplogroup M discovered in prehistoric North Americans. Journal of Archaeological Science, 2007, 34, 642-648.	1.2	60
72	MamuSNP: A Resource for Rhesus Macaque (Macaca mulatta) Genomics. PLoS ONE, 2007, 2, e438.	1.1	40

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73	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
74	Beringian Standstill and Spread of Native American Founders. PLoS ONE, 2007, 2, e829.	1.1	499
75	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
76	Opinion: Demystifying Native American genetic opposition to research. Evolutionary Anthropology, 2006, 15, 88-92.	1.7	9
77	Mitochondrial DNA and Prehistoric Settlements: Native Migrations on the Western Edge of North America. Human Biology, 2004, 76, 55-75.	0.4	36
78	Patterns of mtDNA Diversity in Northwestern North America. Human Biology, 2004, 76, 33-54.	0.4	21
79	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
80	Native American mtDNA prehistory in the American Southwest. American Journal of Physical Anthropology, 2003, 120, 108-124.	2.1	83
81	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
82	Brief communication: Haplogroup X confirmed in prehistoric North America. American Journal of Physical Anthropology, 2002, 119, 84-86.	2.1	42
83	Distribution of Mitochondrial DNA Lineages among Native American Tribes of Northeastern North America. Human Biology, 2001, 73, 17-55.	0.4	61
84	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
85	Distribution of mtDNA haplogroup X among Native North Americans. American Journal of Physical Anthropology, 1999, 110, 271-284.	2.1	106
86	Distribution of mtDNA haplogroup X among Native North Americans. , 1999, 110, 271.		5
87	Central Place Models of Acorn and Mussel Processing. Journal of Archaeological Science, 1997, 24, 887-899.	1.2	130