

A genomic history of Aboriginal Australia

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Archaic admixture in human history. <i>Current Opinion in Genetics and Development</i> , 2016, 41, 93-97.	1.5	26
2	A map of human wanderlust. <i>Nature</i> , 2016, 538, 179-180.	13.7	25
3	Off the beaten track. <i>Nature Reviews Genetics</i> , 2016, 17, 657-657.	7.7	0
4	Tracing the peopling of the world through genomics. <i>Nature</i> , 2017, 541, 302-310.	13.7	562
5	A working model of the deep relationships of diverse modern human genetic lineages outside of Africa. <i>Molecular Biology and Evolution</i> , 2017, 34, msw293.	3.5	55
6	Aboriginal mitogenomes reveal 50,000 years of regionalism in Australia. <i>Nature</i> , 2017, 544, 180-184.	13.7	195
7	Population genomics reveals that an anthropophilic population of <i>Aedes aegypti</i> mosquitoes in West Africa recently gave rise to American and Asian populations of this major disease vector. <i>BMC Biology</i> , 2017, 15, 16.	1.7	96
8	Inferring Human Demographic Histories of Non-African Populations from Patterns of Allele Sharing. <i>American Journal of Human Genetics</i> , 2017, 100, 766-772.	2.6	23
9	Mitochondrial DNA diversity of present-day Aboriginal Australians and implications for human evolution in Oceania. <i>Journal of Human Genetics</i> , 2017, 62, 343-353.	1.1	24
10	A composite window into human history. <i>Science</i> , 2017, 356, 1118-1120.	6.0	42
11	The timetable of evolution. <i>Science Advances</i> , 2017, 3, e1603076.	4.7	186
12	Data-sharing for indigenous peoples. <i>Nature</i> , 2017, 546, 474-474.	13.7	19
13	Experiences with integrative Indigenous and Western knowledge in water research and management: a systematic realist review of literature from Canada, Australia, New Zealand, and the United States. <i>Environmental Reviews</i> , 2017, 25, 323-333.	2.1	20
14	A genetic chronology for the Indian Subcontinent points to heavily sex-biased dispersals. <i>BMC Evolutionary Biology</i> , 2017, 17, 88.	3.2	59
15	Living in an adaptive world: Genomic dissection of the genus <i>Homo</i> and its immune response. <i>Journal of Experimental Medicine</i> , 2017, 214, 877-894.	4.2	34
16	Aboriginal Australian mitochondrial genome variation “an increased understanding of population antiquity and diversity. <i>Scientific Reports</i> , 2017, 7, 43041.	1.6	39
17	Genomic data detect corresponding signatures of population size change on an ecological time scale in two salamander species. <i>Molecular Ecology</i> , 2017, 26, 1060-1074.	2.0	39
18	Dental phenotypic shape variation supports a multiple dispersal model for anatomically modern humans in Southeast Asia. <i>Journal of Human Evolution</i> , 2017, 112, 41-56.	1.3	18

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19	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , 2017, 358, 659-662.	6.0	263
20	Loci associated with skin pigmentation identified in African populations. <i>Science</i> , 2017, 358, .	6.0	260
21	A Neolithic expansion, but strong genetic structure, in the independent history of New Guinea. <i>Science</i> , 2017, 357, 1160-1163.	6.0	45
22	Testing support for the northern and southern dispersal routes out of Africa: an analysis of Levantine and southern Arabian populations. <i>American Journal of Physical Anthropology</i> , 2017, 164, 736-749.	2.1	19
23	Inferring Demographic History Using Genomic Data. <i>Population Genomics</i> , 2017, , 511-537.	0.2	16
24	Early signs of human presence in Australia. <i>Nature</i> , 2017, 547, 285-286.	13.7	3
25	Chemistry and physics happily wed. <i>Nature</i> , 2017, 547, 287-288.	13.7	1
26	Human occupation of northern Australia by 65,000 years ago. <i>Nature</i> , 2017, 547, 306-310.	13.7	691
27	Discerning the Origins of the Negritos, First Sundaland People: Deep Divergence and Archaic Admixture. <i>Genome Biology and Evolution</i> , 2017, 9, 2013-2022.	1.1	54
28	Range Expansion Compromises Adaptive Evolution in an Outcrossing Plant. <i>Current Biology</i> , 2017, 27, 2544-2551.e4.	1.8	75
29	Evolution of Complex Traits in Human Populations. , 2017, , 165-186.		0
30	Data sharing: do scientists know best?. <i>Nature</i> , 2017, 548, 281-281.	13.7	2
31	On the origin of modern humans: Asian perspectives. <i>Science</i> , 2017, 358, .	6.0	264
32	Trapped by history: democracy, human rights and justice for indigenous people in Australia. <i>Australian Journal of Human Rights</i> , 2017, 23, 220-241.	0.6	5
33	Early Modern Humans from Tam P'Å Ling, Laos. <i>Current Anthropology</i> , 2017, 58, S527-S538.	0.8	32
34	Genome-Wide Analysis of Colonization History and Concomitant Selection in <i>Arabidopsis lyrata</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, 2665-2677.	3.5	31
35	Carriers of mitochondrial DNA macrohaplogroup R colonized Eurasia and Australasia from a southeast Asia core area. <i>BMC Evolutionary Biology</i> , 2017, 17, 115.	3.2	19
36	Risks for Mental Illness in Indigenous Australian Children: A Descriptive Study Demonstrating High Levels of Vulnerability. <i>Milbank Quarterly</i> , 2017, 95, 319-357.	2.1	22

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37	Conservation Genetics of the Cheetah: Lessons Learned and New Opportunities. <i>Journal of Heredity</i> , 2017, 108, 671-677.	1.0	28
38	Introgressive replacement of natives by invading <i>Arion</i> pest slugs. <i>Scientific Reports</i> , 2017, 7, 14908.	1.6	31
39	Human Colonization of Asia in the Late Pleistocene. <i>Current Anthropology</i> , 2017, 58, S373-S382.	0.8	66
40	Comparison of Single Genome and Allele Frequency Data Reveals Discordant Demographic Histories. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3605-3620.	0.8	70
41	A Genomic View of the Pleistocene Population History of Asia. <i>Current Anthropology</i> , 2017, 58, S397-S405.	0.8	12
42	Madjedbebe and genomic histories of Aboriginal Australia. <i>Australian Archaeology</i> , 2017, 83, 174-177.	0.3	11
43	The Multiple Histories of Western Asia: Perspectives from Ancient and Modern Genomes. <i>Human Biology</i> , 2017, 89, 107.	0.4	6
44	<i>Winhangaâ€duriâ€nya</i> (to reflect). <i>Medical Journal of Australia</i> , 2017, 207, 472-473.	0.8	2
46	Long-term balancing selection contributes to adaptation in <i>Arabidopsis</i> and its relatives. <i>Genome Biology</i> , 2017, 18, 217.	3.8	43
47	Massively parallel sequencing of 165 ancestry informative SNPs in two Chinese Tibetan-Burmese minority ethnicities. <i>Forensic Science International: Genetics</i> , 2018, 34, 141-147.	1.6	44
48	Reply to comments on Clarkson etÂal. (2017) â€Human occupation of northern Australia by 65,000 years agoâ€™. <i>Australian Archaeology</i> , 2018, 84, 84-89.	0.3	16
49	Subdecadal phytolith and charcoal records from Lake Malawi, East Africa imply minimal effects on human evolution from the â ¹ /474Âka Toba supereruption. <i>Journal of Human Evolution</i> , 2018, 116, 75-94.	1.3	41
50	Genomic structure of the native inhabitants of Peninsular Malaysia and North Borneo suggests complex human population history in Southeast Asia. <i>Human Genetics</i> , 2018, 137, 161-173.	1.8	20
51	The success of failed <i>Homo sapiens</i> dispersals out of Africa and into Asia. <i>Nature Ecology and Evolution</i> , 2018, 2, 212-219.	3.4	39
52	150,000-year palaeoclimate record from northern Ethiopia supports early, multiple dispersals of modern humans from Africa. <i>Scientific Reports</i> , 2018, 8, 1077.	1.6	41
53	Sea-level change and demography during the last glacial termination and early Holocene across the Australian continent. <i>Quaternary Science Reviews</i> , 2018, 182, 144-154.	1.4	74
54	The Gateway from Near into Remote Oceania: New Insights from Genome-Wide Data. <i>Molecular Biology and Evolution</i> , 2018, 35, 871-886.	3.5	38
55	Ancient Genomics of Modern Humans: The First Decade. <i>Annual Review of Genomics and Human Genetics</i> , 2018, 19, 381-404.	2.5	161

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56	The arms race between man and Mycobacterium tuberculosis: Time to regroup. <i>Infection, Genetics and Evolution</i> , 2018, 66, 361-375.	1.0	17
57	The origin and expansion of PamañNyungan languages across Australia. <i>Nature Ecology and Evolution</i> , 2018, 2, 741-749.	3.4	54
58	Moving past the ãNeolithic problemã™: The development and interaction of subsistence systems across northern Sahul. <i>Quaternary International</i> , 2018, 489, 46-62.	0.7	13
59	Impact of Model Violations on the Inference of Species Boundaries Under the Multispecies Coalescent. <i>Systematic Biology</i> , 2018, 67, 269-284.	2.7	76
60	An early colonisation pathway into northwest Australia 70-60,000 years ago. <i>Quaternary Science Reviews</i> , 2018, 180, 229-239.	1.4	61
61	Archeological Issues in the Middle and Upper Paleolithic of the Levant and Its Neighboring Regions. , 2018, , 1-8.		0
62	Dating Antarctic ice sheet collapse: Proposing a molecular genetic approach. <i>Quaternary Science Reviews</i> , 2018, 179, 153-157.	1.4	11
63	Early human dispersals within the Americas. <i>Science</i> , 2018, 362, .	6.0	230
64	Reply to ãNo evidence for unknown archaic ancestry in South Asiaã™. <i>Nature Genetics</i> , 2018, 50, 1637-1639.	9.4	4
66	Principles of Archaeogenetics and the Current Trends of Ancient Genome Studies. <i>Korean Journal of Physical Anthropology</i> , 2018, 31, 105.	0.2	0
67	Ancient nuclear genomes enable repatriation of Indigenous human remains. <i>Science Advances</i> , 2018, 4, eaau5064.	4.7	41
68	AE3 and AE4: On the Road Again. , 2018, , 105-170.		0
69	The genetic makings of South Asia. <i>Current Opinion in Genetics and Development</i> , 2018, 53, 128-133.	1.5	11
70	Anti-Darwin comments in India outrage scientists. <i>Nature</i> , 2018, 554, 16-17.	13.7	1
72	Human evolutionary history of Eastern Africa. <i>Current Opinion in Genetics and Development</i> , 2018, 53, 134-139.	1.5	8
73	Population genomic analysis reveals that homoploid hybrid speciation can be a lengthy process. <i>Molecular Ecology</i> , 2018, 27, 4875-4887.	2.0	45
74	ãTelling our story... Creating our own historyã™: caregiversã™ reasons for participating in an Australian longitudinal study of Indigenous children. <i>International Journal for Equity in Health</i> , 2018, 17, 143.	1.5	3
75	Human Population Genomics. <i>Computational Biology</i> , 2018, , 467-496.	0.1	0

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76	Outstanding questions in the study of archaic hominin admixture. PLoS Genetics, 2018, 14, e1007349.	1.5	50
77	Human Genetic Variation and HIV/AIDS in Papua New Guinea: Time to Connect the Dots. Current HIV/AIDS Reports, 2018, 15, 431-440.	1.1	2
78	Detecting archaic introgression using an unadmixed outgroup. PLoS Genetics, 2018, 14, e1007641.	1.5	78
79	Physical sedimentary controls on subtropical coastal and shelf sedimentary systems: Initial application in conceptual models and computer visualizations to support archaeology. Geoarchaeology - an International Journal, 2018, 33, 661-679.	0.7	12
80	Who were the Nataruk people? Mandibular morphology among late Pleistocene and early Holocene fisher-forager populations of West Turkana (Kenya). Journal of Human Evolution, 2018, 121, 235-253.	1.3	6
81	Palaeogeography and voyage modeling indicates early human colonization of Australia was likely from Timor-Roti. Quaternary Science Reviews, 2018, 191, 431-439.	1.4	52
82	Leaving Africa. , 2018, , 75-103.		1
83	Boneâ€™s Intrinsic Traits: Why Animals Eat Animals. , 2018, , 89-102.		0
84	Evolutionary history and adaptation of a human pygmy population of Flores Island, Indonesia. Science, 2018, 361, 511-516.	6.0	56
85	When did <i>Homo sapiens</i> first reach Southeast Asia and Sahul?. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 8482-8490.	3.3	186
86	Global Scale Dissemination of ST93: A Divergent Staphylococcus aureus Epidemic Lineage That Has Recently Emerged From Remote Northern Australia. Frontiers in Microbiology, 2018, 9, 1453.	1.5	29
87	Inference of population history using coalescent HMMs: review and outlook. Current Opinion in Genetics and Development, 2018, 53, 70-76.	1.5	51
88	Walking backwards into the future: the need for a holistic evolutionary approach in Pacific health research. Annals of Human Biology, 2018, 45, 175-187.	0.4	2
89	National supercomputing in Denmark. , 2018, , .		2
90	Big genetic data and its big data protection challenges. Computer Law and Security Review, 2018, 34, 1000-1018.	1.3	20
91	The evolutionary history and human settlement of Australia and the Pacific. Current Opinion in Genetics and Development, 2018, 53, 53-59.	1.5	11
92	Fine-tuning of Approximate Bayesian Computation for human population genomics. Current Opinion in Genetics and Development, 2018, 53, 60-69.	1.5	6
93	Migration and Climate in World History. , 2018, , 413-444.		7

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94	Israeli fossils are the oldest modern humans ever found outside of Africa. <i>Nature</i> , 2018, 554, 15-16.	13.7	3
95	The demographic and adaptive history of central African hunter-gatherers and farmers. <i>Current Opinion in Genetics and Development</i> , 2018, 53, 90-97.	1.5	17
96	DNA recovery from wild chimpanzee tools. <i>PLoS ONE</i> , 2018, 13, e0189657.	1.1	2
97	Something old, something borrowed: admixture and adaptation in human evolution. <i>Current Opinion in Genetics and Development</i> , 2018, 53, 1-8.	1.5	79
98	The Exodus Out of Africa. , 2018, , 105-132.		0
99	The Occupation of Southeast Asia, Indonesia, and Australia. , 2018, , 257-309.		0
100	Direct Evidence of an Increasing Mutational Load in Humans. <i>Molecular Biology and Evolution</i> , 2019, 36, 2823-2829.	3.5	12
101	Inference of complex population histories using whole-genome sequences from multiple populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17115-17120.	3.3	52
103	Mixed Methods and Cross Disciplinary Research. <i>Contemporary Systems Thinking</i> , 2019, , .	0.3	21
104	Genetics, adaptation to environmental changes and archaic admixture in the pathogenesis of diabetes mellitus in Indigenous Australians. <i>Reviews in Endocrine and Metabolic Disorders</i> , 2019, 20, 321-332.	2.6	2
105	Strategies to improve control of sexually transmissible infections in remote Australian Aboriginal communities: a stepped-wedge, cluster-randomised trial. <i>The Lancet Global Health</i> , 2019, 7, e1553-e1563.	2.9	11
106	Adaptive archaic introgression of copy number variants and the discovery of previously unknown human genes. <i>Science</i> , 2019, 366, .	6.0	65
107	Health Challenges of the Pacific Region: Insights From History, Geography, Social Determinants, Genetics, and the Microbiome. <i>Frontiers in Immunology</i> , 2019, 10, 2184.	2.2	31
108	The global diversity of <i>Haemonchus contortus</i> is shaped by human intervention and climate. <i>Nature Communications</i> , 2019, 10, 4811.	5.8	63
109	Influence of the tree prior and sampling scale on Bayesian phylogenetic estimates of the origin times of language families. <i>Journal of Language Evolution</i> , 2019, 4, 108-123.	2.2	12
110	Deciphering African late middle Pleistocene hominin diversity and the origin of our species. <i>Nature Communications</i> , 2019, 10, 3406.	5.8	52
111	Indigenous groups look to ancient DNA to bring their ancestors home. <i>Nature</i> , 2019, 568, 294-297.	13.7	5
112	Age estimates for hominin fossils and the onset of the Upper Palaeolithic at Denisova Cave. <i>Nature</i> , 2019, 565, 640-644.	13.7	137

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113	The Idea of Human Rights. , 2019, , 41-85.		0
115	Minimum founding populations for the first peopling of Sahul. <i>Nature Ecology and Evolution</i> , 2019, 3, 1057-1063.	3.4	34
116	The first hominin fleet. <i>Nature Ecology and Evolution</i> , 2019, 3, 999-1000.	3.4	10
117	The population history of northeastern Siberia since the Pleistocene. <i>Nature</i> , 2019, 570, 182-188.	13.7	259
118	Developing an ecological framework of factors associated with substance use and related harms among Aboriginal and Torres Strait Islander people: protocol for a systematic review. <i>BMJ Open</i> , 2019, 9, e024418.	0.8	5
119	Upper Paleolithic cultural diversity in the Iranian Zagros Mountains and the expansion of modern humans into Eurasia. <i>Journal of Human Evolution</i> , 2019, 132, 101-118.	1.3	17
120	Human Migration and the Spread of the Nematode Parasite <i>Wuchereria bancrofti</i> . <i>Molecular Biology and Evolution</i> , 2019, 36, 1931-1941.	3.5	29
121	Analyses of Neanderthal introgression suggest that Levantine and southern Arabian populations have a shared population history. <i>American Journal of Physical Anthropology</i> , 2019, 169, 227-239.	2.1	11
122	A case for not adjusting birthweight customized standards for ethnicity: observations from a unique Australian cohort. <i>American Journal of Obstetrics and Gynecology</i> , 2019, 220, 277.e1-277.e10.	0.7	5
124	Human Disease Variation in the Light of Population Genomics. <i>Cell</i> , 2019, 177, 115-131.	13.5	75
125	Analysis of the South Australian Aboriginal population using the Global AIMS Nano ancestry test. <i>Forensic Science International: Genetics</i> , 2019, 41, 34-41.	1.6	2
126	Tracing Ancient Human Migrations into Sahul Using Hepatitis B Virus Genomes. <i>Molecular Biology and Evolution</i> , 2019, 36, 942-954.	3.5	26
127	A strontium isoscape of north-east Australia for human provenance and repatriation. <i>Geoarchaeology - an International Journal</i> , 2019, 34, 231-251.	0.7	28
128	Multiple Deeply Divergent Denisovan Ancestries in Papuans. <i>Cell</i> , 2019, 177, 1010-1021.e32.	13.5	181
129	Genome-Wide Characterization of Arabian Peninsula Populations: Shedding Light on the History of a Fundamental Bridge between Continents. <i>Molecular Biology and Evolution</i> , 2019, 36, 575-586.	3.5	45
130	Can the gap in Aboriginal outcomes be explained by DOHaD. <i>Journal of Developmental Origins of Health and Disease</i> , 2019, 10, 5-16.	0.7	12
131	Aboriginal employment opportunities in a low-carbon economy. <i>International Journal of Society Systems Science</i> , 2019, 11, 257.	0.1	0
132	A Population Genetic Perspective on Korean Prehistory. <i>Korean Studies</i> , 2019, , .	0.2	0

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133	Single haplotype admixture models using large scale HLA genotype frequencies to reproduce human admixture. <i>Immunogenetics</i> , 2019, 71, 589-604.	1.2	2
134	Archaeogenetics and human evolution: the ontogeny of a biological discipline. <i>World Archaeology</i> , 2019, 51, 546-559.	0.5	17
135	Giving it a burl: towards the integration of genetics, isotope chemistry, and osteoarchaeology in Cape York, Tropical North Queensland, Australia. <i>World Archaeology</i> , 2019, 51, 602-619.	0.5	20
136	Denisovan, modern human and mouse TNFAIP3 alleles tune A20 phosphorylation and immunity. <i>Nature Immunology</i> , 2019, 20, 1299-1310.	7.0	53
137	Identification of African-Specific Admixture between Modern and Archaic Humans. <i>American Journal of Human Genetics</i> , 2019, 105, 1254-1261.	2.6	16
138	Approximate Bayesian computation with deep learning supports a third archaic introgression in Asia and Oceania. <i>Nature Communications</i> , 2019, 10, 246.	5.8	97
139	Comprehensive blood group antigen profile predictions for Western Desert Indigenous Australians from whole exome sequence data. <i>Transfusion</i> , 2019, 59, 768-778.	0.8	18
140	The Archaeology of Pleistocene Coastal Environments and Human Dispersals in the Red Sea: Insights from the Farasan Islands. , 2019, , 583-604.		6
141	Conservation genomic analysis reveals ancient introgression and declining levels of genetic diversity in Madagascar's hibernating dwarf lemurs. <i>Heredity</i> , 2020, 124, 236-251.	1.2	16
142	Archaic hominin introgression into modern human genomes. <i>American Journal of Physical Anthropology</i> , 2020, 171, 60-73.	2.1	33
143	Distinguishing among complex evolutionary models using unphased whole-genome data through random forest approximate Bayesian computation. <i>Molecular Ecology Resources</i> , 2020, 21, 2614-2628.	2.2	4
144	Perspectives of my lived experiences for addressing suicides among aboriginal communities in the North Queensland tropics. <i>AlterNative</i> , 2020, 16, 211-219.	0.7	1
145	The Impact of Ancient Genome Studies in Archaeology. <i>Annual Review of Anthropology</i> , 2020, 49, 277-298.	0.4	13
146	Reference exome data for Australian Aboriginal populations to support health-based research. <i>Scientific Data</i> , 2020, 7, 129.	2.4	0
147	Stairway Plot 2: demographic history inference with folded SNP frequency spectra. <i>Genome Biology</i> , 2020, 21, 280.	3.8	125
148	Pama's Nyungan grandparent systems change with grandchildren, but not cross-cousin terms or social norms. <i>Evolutionary Human Sciences</i> , 2020, 2, .	0.9	3
149	Insights Into Aboriginal Australian Mortuary Practices: Perspectives From Ancient DNA. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	4
150	Methods for detecting introgressed archaic sequences. <i>Current Opinion in Genetics and Development</i> , 2020, 62, 85-90.	1.5	6

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151	Fostering Responsible Research on Ancient DNA. <i>American Journal of Human Genetics</i> , 2020, 107, 183-195.	2.6	57
152	Current Trends in Ancient DNA Study. , 2020, , 1-16.		0
153	Contrasting signatures of genomic divergence during sympatric speciation. <i>Nature</i> , 2020, 588, 106-111.	13.7	115
154	A different paradigm for the colonisation of Sahul. <i>Archaeology in Oceania</i> , 2020, 55, 182-191.	0.3	1
155	The reversal of human phylogeny: Homo left Africa as erectus, came back as sapiens sapiens. <i>Hereditas</i> , 2020, 157, 51.	0.5	3
156	A Revised Model of Anatomically Modern Human Expansions Out of Africa through a Machine Learning Approximate Bayesian Computation Approach. <i>Genes</i> , 2020, 11, 1510.	1.0	4
157	Ancient Hybridization with an Unknown Population Facilitated High-Altitude Adaptation of Canids. <i>Molecular Biology and Evolution</i> , 2020, 37, 2616-2629.	3.5	46
158	A high-coverage Neandertal genome from Chagyrskaya Cave. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 15132-15136.	3.3	176
159	Papuan mitochondrial genomes and the settlement of Sahul. <i>Journal of Human Genetics</i> , 2020, 65, 875-887.	1.1	24
160	A Population Genetic Perspective on Korean Prehistory. <i>Korean Studies</i> , 2020, 44, 27-53.	0.2	0
161	Tracking human population structure through time from whole genome sequences. <i>PLoS Genetics</i> , 2020, 16, e1008552.	1.5	71
162	The Early Peopling of the Philippines based on mtDNA. <i>Scientific Reports</i> , 2020, 10, 4901.	1.6	15
163	Insights into human genetic variation and population history from 929 diverse genomes. <i>Science</i> , 2020, 367, .	6.0	534
164	Heterogeneity in Auction Price Distributions for Australian Indigenous Artists. <i>Economic Record</i> , 2020, 96, 177-186.	0.2	2
165	Voices behind the Statistics: A Systematic Literature Review of the Lived Experience of Rheumatic Heart Disease. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 1347.	1.2	25
166	Hunter-gatherer multilevel sociality accelerates cumulative cultural evolution. <i>Science Advances</i> , 2020, 6, eaax5913.	4.7	66
167	Does a change in immigration affect the unemployment rate in host countries? Evidence from Australia. <i>Journal of Applied Economics</i> , 2020, 23, 21-43.	0.6	8
168	Identifying and Interpreting Apparent Neanderthal Ancestry in African Individuals. <i>Cell</i> , 2020, 180, 677-687.e16.	13.5	159

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169	Genomic landscape of the signals of positive natural selection in populations of Northern Eurasia: A view from Northern Russia. <i>PLoS ONE</i> , 2020, 15, e0228778.	1.1	6
170	Evolutionary history of modern Samoans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9458-9465.	3.3	14
171	Population Genomics Reveals Incipient Speciation, Introgression, and Adaptation in the African Mona Monkey (<i>Cercopithecus mona</i>). <i>Molecular Biology and Evolution</i> , 2021, 38, 876-890.	3.5	15
172	Application of the ecocultural range expansion model to modern human dispersals in Asia. <i>Quaternary International</i> , 2021, 596, 171-184.	0.7	5
173	Origins of modern human ancestry. <i>Nature</i> , 2021, 590, 229-237.	13.7	166
174	Paternal gene pool of Malays in Southeast Asia and its applications for the early expansion of Austronesians. <i>American Journal of Human Biology</i> , 2021, 33, e23486.	0.8	3
175	Sedimentary unknowns constrain the current use of frequency analysis of radiocarbon data sets in forming regional models of demographic change. <i>Geoarchaeology - an International Journal</i> , 2021, 36, 546-570.	0.7	8
176	The deep population history in Africa. <i>Human Molecular Genetics</i> , 2021, 30, R2-R10.	1.4	15
177	Inferring Human Demographic History from Genetic Data. , 2021, , 187-204.		0
178	Recent Evolutionary History of Tigers Highlights Contrasting Roles of Genetic Drift and Selection. <i>Molecular Biology and Evolution</i> , 2021, 38, 2366-2379.	3.5	35
179	How old are the oldest <i>Homo sapiens</i> in Far East Asia?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	7
180	Genomic Signatures for Species-Specific Adaptation in Lake Victoria Cichlids Derived from Large-Scale Standing Genetic Variation. <i>Molecular Biology and Evolution</i> , 2021, 38, 3111-3125.	3.5	9
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