Genomic analyses inform on migration events during the

Nature 538, 238-242

DOI: 10.1038/nature19792

Citation Report

#	Article	IF	CITATIONS
1	Typological bottlenecks: How large-scale regional language typologies help us interpret global prehistory. Linguistic Typology, $2016, 20, \ldots$	0.5	0
2	Refining the Use of Linkage Disequilibrium as a Robust Signature of Selective Sweeps. Genetics, 2016, 203, 1807-1825.	1.2	18
3	A genomic history of Aboriginal Australia. Nature, 2016, 538, 207-214.	13.7	439
4	A map of human wanderlust. Nature, 2016, 538, 179-180.	13.7	25
5	Off the beaten track. Nature Reviews Genetics, 2016, 17, 657-657.	7.7	O
6	Selective sweep on human amylase genes postdates the split with Neanderthals. Scientific Reports, 2016, 6, 37198.	1.6	67
7	It takes a genome to understand a village: Population scale precision medicine. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12344-12346.	3.3	4
8	Tracing the peopling of the world through genomics. Nature, 2017, 541, 302-310.	13.7	562
9	Population and clinical genetics of human transposable elements in the (post) genomic era. Mobile Genetic Elements, 2017, 7, 1-20.	1.8	22
10	Fuyan human of 120–80 kya cannot challenge the Out-of-Africa theory for modern human dispersal. Science Bulletin, 2017, 62, 316-318.	4.3	O
11	A working model of the deep relationships of diverse modern human genetic lineages outside of Africa. Molecular Biology and Evolution, 2017, 34, msw293.	3.5	55
12	Blood is Thicker Than Water. Cross-Cultural Research, 2017, 51, 142-171.	1.6	9
14	Inferring Human Demographic Histories of Non-African Populations from Patterns of Allele Sharing. American Journal of Human Genetics, 2017, 100, 766-772.	2.6	23
15	African genomes illuminate the early history and transition to selfing in <i>Arabidopsis thaliana</i> Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 5213-5218.	3.3	142
16	The timetable of evolution. Science Advances, 2017, 3, e1603076.	4.7	186
17	An earlier revolution: genetic and genomic analyses reveal pre-existing cultural differences leading to Neolithization. Scientific Reports, 2017, 7, 3525.	1.6	6
18	The Omo-Kibish I pelvis. Journal of Human Evolution, 2017, 108, 199-219.	1.3	23
19	A genetic chronology for the Indian Subcontinent points to heavily sex-biased dispersals. BMC Evolutionary Biology, 2017, 17, 88.	3.2	59

#	ARTICLE	IF	CITATIONS
20	Living in an adaptive world: Genomic dissection of the genus Homo and its immune response. Journal of Experimental Medicine, 2017, 214, 877-894.	4.2	34
21	Grammaticalization and language evolution: Focusing the debate. Language Sciences, 2017, 63, 60-68.	0.5	14
22	Dental phenotypic shape variation supports a multiple dispersal model for anatomically modern humans in Southeast Asia. Journal of Human Evolution, 2017, 112, 41-56.	1.3	18
23	Evidence of Early-Stage Selection on EPAS1 and GPR126 Genes in Andean High Altitude Populations. Scientific Reports, 2017, 7, 13042.	1.6	29
24	Loci associated with skin pigmentation identified in African populations. Science, 2017, 358, .	6.0	260
25	Testing support for the northern and southern dispersal routes out of Africa: an analysis of Levantine and southern Arabian populations. American Journal of Physical Anthropology, 2017, 164, 736-749.	2.1	19
26	Human occupation of northern Australia by 65,000 years ago. Nature, 2017, 547, 306-310.	13.7	691
27	Complex Patterns of Admixture across the Indonesian Archipelago. Molecular Biology and Evolution, 2017, 34, 2439-2452.	3.5	65
28	Discerning the Origins of the Negritos, First Sundaland People: Deep Divergence and Archaic Admixture. Genome Biology and Evolution, 2017, 9, 2013-2022.	1.1	54
29	An early modern human presence in Sumatra 73,000–63,000 years ago. Nature, 2017, 548, 322-325.	13.7	200
30	Evolution of Complex Traits in Human Populations. , 2017, , 165-186.		0
31	Inferring patterns of folktale diffusion using genomic data. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 9140-9145.	3.3	37
32	On the origin of modern humans: Asian perspectives. Science, 2017, 358, .	6.0	264
33	Testing Modern Human Out-of-Africa Dispersal Models Using Dental Nonmetric Data. Current Anthropology, 2017, 58, S406-S417.	0.8	17
34	Precise dating of the Middle-to-Upper Paleolithic transition in Murcia (Spain) supports late Neandertal persistence in Iberia. Heliyon, 2017, 3, e00435.	1.4	117
35	Early Modern Humans from Tam PÃ Ling, Laos. Current Anthropology, 2017, 58, S527-S538.	0.8	32
36	Genomic Reconstruction of the History of Native Sheep Reveals the Peopling Patterns of Nomads and the Expansion of Early Pastoralism in East Asia. Molecular Biology and Evolution, 2017, 34, 2380-2395.	3.5	94
37	A phylogenetic view of the Out of Asia/Eurasia and Out of Africa hypotheses in the light of recent molecular and palaeontological finds. Gene, 2017, 627, 473-476.	1.0	5

#	Article	IF	CITATIONS
38	Deeply divergent archaic mitochondrial genome provides lower time boundary for African gene flow into Neanderthals. Nature Communications, 2017, 8, 16046.	5.8	211
39	Conservation Genetics of the Cheetah: Lessons Learned and New Opportunities. Journal of Heredity, 2017, 108, 671-677.	1.0	28
40	Human Colonization of Asia in the Late Pleistocene. Current Anthropology, 2017, 58, S373-S382.	0.8	66
41	Comparison of Single Genome and Allele Frequency Data Reveals Discordant Demographic Histories. G3: Genes, Genomes, Genetics, 2017, 7, 3605-3620.	0.8	70
42	A Genomic View of the Pleistocene Population History of Asia. Current Anthropology, 2017, 58, S397-S405.	0.8	12
43	Madjedbebe and genomic histories of Aboriginal Australia. Australian Archaeology, 2017, 83, 174-177.	0.3	11
44	The Multiple Histories of Western Asia: Perspectives from Ancient and Modern Genomes. Human Biology, 2017, 89, 107.	0.4	6
46	Genetic Diversity, Population Structure and Ancestral Origin of Australian Wheat. Frontiers in Plant Science, 2017, 8, 2115.	1.7	47
47	Between Lake Baikal and the Baltic Sea: genomic history of the gateway to Europe. BMC Genetics, 2017, 18, 110.	2.7	34
49	Origins and genetic legacies of the Caribbean Taino. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 2341-2346.	3.3	64
50	Genetic relatedness of indigenous ethnic groups in northern Borneo to neighboring populations from Southeast Asia, as inferred from genomeâ€wide SNP data. Annals of Human Genetics, 2018, 82, 216-226.	0.3	13
51	Massively parallel sequencing of 165 ancestry informative SNPs in two Chinese Tibetan-Burmese minority ethnicities. Forensic Science International: Genetics, 2018, 34, 141-147.	1.6	44
52	Elucidating recent history by tracing genetic affinity of three 16th century miners from Sweden. Journal of Archaeological Science: Reports, 2018, 19, 651-657.	0.2	0
53	Reply to comments on Clarkson etÂal. (2017) â€~Human occupation of northern Australia by 65,000 years ago'. Australian Archaeology, 2018, 84, 84-89.	0.3	16
54	Homo sapiens in Arabia by 85,000 years ago. Nature Ecology and Evolution, 2018, 2, 800-809.	3.4	143
55	Subdecadal phytolith and charcoal records from Lake Malawi, East Africa imply minimal effects on human evolution from the â^1⁄474Âka Toba supereruption. Journal of Human Evolution, 2018, 116, 75-94.	1.3	41
56	Disentangling Immediate Adaptive Introgression from Selection on Standing Introgressed Variation in Humans. Molecular Biology and Evolution, 2018, 35, 623-630.	3.5	46
57	Genomic structure of the native inhabitants of Peninsular Malaysia and North Borneo suggests complex human population history in Southeast Asia. Human Genetics, 2018, 137, 161-173.	1.8	20

#	ARTICLE	IF	Citations
58	The success of failed Homo sapiens dispersals out of Africa and into Asia. Nature Ecology and Evolution, 2018, 2, 212-219.	3.4	39
59	150,000-year palaeoclimate record from northern Ethiopia supports early, multiple dispersals of modern humans from Africa. Scientific Reports, 2018, 8, 1077.	1.6	41
60	Evaluating methods to visualize patterns of genetic differentiation on a landscape. Molecular Ecology Resources, 2018, 18, 448-460.	2.2	17
61	The black legend on the Spanish presence in the low countries: Verifying shared beliefs on genetic ancestry. American Journal of Physical Anthropology, 2018, 166, 219-227.	2.1	5
62	Ancient Genomics of Modern Humans: The First Decade. Annual Review of Genomics and Human Genetics, 2018, 19, 381-404.	2.5	161
63	Phylodynamics of Merkel-cell polyomavirus and human polyomavirus 6: A long-term history with humans. Molecular Phylogenetics and Evolution, 2018, 126, 210-220.	1.2	12
64	Global efforts toward the cure of childhood acute lymphoblastic leukaemia. The Lancet Child and Adolescent Health, 2018, 2, 440-454.	2.7	83
65	The uncertainty of population relationship and divergence time inferred by the multiple sequentially Markovian coalescent model. Journal of Human Genetics, 2018, 63, 775-777.	1.1	3
66	The arms race between man and Mycobacterium tuberculosis: Time to regroup. Infection, Genetics and Evolution, 2018, 66, 361-375.	1.0	17
67	Archeological Issues in the Middle and Upper Paleolithic of the Levant and Its Neighboring Regions. , $2018, 18.$		0
68	Mitogenomic diversity and differentiation of the Buryats. Journal of Human Genetics, 2018, 63, 71-81.	1.1	10
69	Whole-genome sequencing of 175 Mongolians uncovers population-specific genetic architecture and gene flow throughout North and East Asia. Nature Genetics, 2018, 50, 1696-1704.	9.4	38
70	Immune diversity sheds light on missing variation in worldwide genetic diversity panels. PLoS ONE, 2018, 13, e0206512.	1.1	75
71	The sequencing and interpretation of the genome obtained from a Serbian individual. PLoS ONE, 2018, 13, e0208901.	1.1	3
72	Environmental change during MIS4 and MIS 3 opened corridors in the Horn of Africa for Homo sapiens expansion. Quaternary Science Reviews, 2018, 202, 139-153.	1.4	23
73	The genetic makings of South Asia. Current Opinion in Genetics and Development, 2018, 53, 128-133.	1.5	11
74	Anti-Darwin comments in India outrage scientists. Nature, 2018, 554, 16-17.	13.7	1
75	Human evolutionary history of Eastern Africa. Current Opinion in Genetics and Development, 2018, 53, 134-139.	1.5	8

#	ARTICLE	IF	CITATIONS
76	Human variation in the shape of the birth canal is significant and geographically structured. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20181807.	1.2	62
77	Human Population Genomics. Computational Biology, 2018, , 467-496.	0.1	0
78	The female ancestor's tale: Longâ€term matrilineal continuity in a nonisolated region of Tuscany. American Journal of Physical Anthropology, 2018, 167, 497-506.	2.1	3
79	Positive and balancing selection on <i>SLC18A1</i> gene associated with psychiatric disorders and human-unique personality traits. Evolution Letters, 2018, 2, 499-510.	1.6	16
80	Impact of non-LTR retrotransposons in the differentiation and evolution of anatomically modern humans. Mobile DNA, 2018, 9, 28.	1.3	18
81	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
82	Hominin expansion into Central Asia during the last interglacial. Earth and Planetary Science Letters, 2018, 494, 148-152.	1.8	7
83	Leaving Africa. , 2018, , 75-103.		1
84	Darwinian Positive Selection on the Pleiotropic Effects of KITLG Explain Skin Pigmentation and Winter Temperature Adaptation in Eurasians. Molecular Biology and Evolution, 2018, 35, 2272-2283.	3.5	27
85	Bone's Intrinsic Traits: Why Animals Eat Animals. , 2018, , 89-102.		0
86	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
87	The Evolution of Bilingualism. , 2018, , 19-44.		0
88	Carriers of mitochondrial DNA macrohaplogroup L3 basal lineages migrated back to Africa from Asia around 70,000 years ago. BMC Evolutionary Biology, 2018, 18, 98.	3.2	22
89	A reassessment of the early archaeological record at Leang Burung 2, a Late Pleistocene rock-shelter site on the Indonesian island of Sulawesi. PLoS ONE, 2018, 13, e0193025.	1.1	27
90	R577X Polymorphism of Alpha-Actinin-3 in the Human Populations of Northeastern Asia. Russian Journal of Genetics: Applied Research, 2018, 8, 59-64.	0.4	4
91	Migration and Climate in World History. , 2018, , 413-444.		7
92	Israeli fossils are the oldest modern humans ever found outside of Africa. Nature, 2018, 554, 15-16.	13.7	3
93	Evolutionary history of human <i>Plasmodium vivax</i> revealed by genome-wide analyses of related ape parasites. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8450-E8459.	3.3	50

#	ARTICLE	IF	CITATIONS
94	Human mobility and innovation spreading in ancient times: a stochastic agent-based simulation approach. EPJ Data Science, $2018, 7, .$	1.5	19
95	The Settlement of the Near East. , 2018, , 133-174.		0
96	Inference of complex population histories using whole-genome sequences from multiple populations. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17115-17120.	3.3	52
98	Different in death: Different in life? Diet and mobility correlates of irregular burials in a Roman necropolis from Bologna (Northern Italy, 1st–4th century CE). Journal of Archaeological Science: Reports, 2019, 27, 101926.	0.2	8
99	Late Middle Stone Age Behavior and Environments at Chaminade I (Karonga, Malawi). Journal of Paleolithic Archaeology, 2019, 2, 258-297.	0.7	9
100	MAPlex - A massively parallel sequencing ancestry analysis multiplex for Asia-Pacific populations. Forensic Science International: Genetics, 2019, 42, 213-226.	1.6	63
101	Deciphering African late middle Pleistocene hominin diversity and the origin of our species. Nature Communications, 2019, 10, 3406.	5.8	52
102	Distinct genetic variation and heterogeneity of the Iranian population. PLoS Genetics, 2019, 15, e1008385.	1.5	34
103	European Roma groups show complex West Eurasian admixture footprints and a common South Asian genetic origin. PLoS Genetics, 2019, 15, e1008417.	1.5	28
105	Killer whale genomes reveal a complex history of recurrent admixture and vicariance. Molecular Ecology, 2019, 28, 3427-3444.	2.0	46
106	Population genetics, diversity and forensic characteristics of Tai–Kadai-speaking Bouyei revealed by insertion/deletions markers. Molecular Genetics and Genomics, 2019, 294, 1343-1357.	1.0	32
107	A Rare Deep-Rooting D0 African Y-Chromosomal Haplogroup and Its Implications for the Expansion of Modern Humans Out of Africa. Genetics, 2019, 212, 1421-1428.	1.2	35
108	Upper Paleolithic cultural diversity in the Iranian Zagros Mountains and the expansion of modern humans into Eurasia. Journal of Human Evolution, 2019, 132, 101-118.	1.3	17
109	Structural variation of centromeric endogenous retroviruses in human populations and their impact on cutaneous T-cell lymphoma, Sézary syndrome, and HIV infection. BMC Medical Genomics, 2019, 12, 58.	0.7	5
110	Nomadic pastoralists and sedentary farmers of the Sahel/Savannah Belt of Africa in the light of geometric morphometrics based on facial portraits. American Journal of Physical Anthropology, 2019, 169, 632-645.	2.1	10
111	Genetic components of human pain sensitivity: a protocol for a genome-wide association study of experimental pain in healthy volunteers. BMJ Open, 2019, 9, e025530.	0.8	17
112	Tai-Kadai-speaking Gelao population: Forensic features, genetic diversity and population structure. Forensic Science International: Genetics, 2019, 40, e231-e239.	1.6	27
113	Analyses of Neanderthal introgression suggest that Levantine and southern Arabian populations have a shared population history. American Journal of Physical Anthropology, 2019, 169, 227-239.	2.1	11

#	Article	IF	CITATIONS
115	Human Disease Variation in the Light of Population Genomics. Cell, 2019, 177, 115-131.	13.5	75
116	The genetic legacy of continental scale admixture in Indian Austroasiatic speakers. Scientific Reports, 2019, 9, 3818.	1.6	30
117	Multiple Deeply Divergent Denisovan Ancestries in Papuans. Cell, 2019, 177, 1010-1021.e32.	13.5	181
118	Mosaic dental morphology in a terminal Pleistocene hominin from Dushan Cave in southern China. Scientific Reports, 2019, 9, 2347.	1.6	18
119	A Population Genetic Perspective on Korean Prehistory. Korean Studies, 2019, , .	0.2	0
120	Analysis of five deep-sequenced trio-genomes of the Peninsular Malaysia Orang Asli and North Borneo populations. BMC Genomics, 2019, 20, 842.	1.2	3
122	Right to the city and human mobility transition: The case of São Paulo. Cities, 2019, 87, 60-67.	2.7	15
123	Shades of complexity: New perspectives on the evolution and genetic architecture of human skin. American Journal of Physical Anthropology, 2019, 168, 4-26.	2.1	45
124	Approximate Bayesian computation with deep learning supports a third archaic introgression in Asia and Oceania. Nature Communications, 2019, 10, 246.	5.8	97
125	The Archaeology of Pleistocene Coastal Environments and Human Dispersals in the Red Sea: Insights from the Farasan Islands. , 2019, , 583-604.		6
126	Comment on Asmerom et al.: Hominin expansion into Central Asia during the last interglacial. Earth and Planetary Science Letters, 2019, 506, 563-565.	1.8	3
127	Skhul lithic technology and the dispersal of Homo sapiens into Southwest Asia. Quaternary International, 2019, 515, 30-52.	0.7	32
128	Genome-wide sequence analyses of ethnic populations across Russia. Genomics, 2020, 112, 442-458.	1.3	19
129	Before the massive modern human dispersal into Eurasia: A 55,000-year-old partial cranium from Manot Cave, Israel. Quaternary International, 2020, 551, 29-39.	0.7	11
130	Is population structure in the genetic biobank era irrelevant, a challenge, or an opportunity?. Human Genetics, 2020, 139, 23-41.	1.8	72
131	Forensic inference of biogeographical ancestry from genotype: The Genetic Ancestry Lab. Wiley Interdisciplinary Reviews Forensic Science, 2020, 2, .	1.2	4
132	Ancestry prediction efficiency of the software GenoGeographer using a z-score method and the ancestry informative markers in the Precision ID Ancestry Panel. Forensic Science International: Genetics, 2020, 44, 102154.	1.6	19
133	Late Pleistocene hominin settlement patterns and population dynamics in the Zagros Mountains: Kermanshah region. Archaeological Research in Asia, 2020, 21, 100161.	0.2	17

#	Article	IF	Citations
134	Distinguishing among complex evolutionary models using unphased wholeâ€genome data through random forest approximate Bayesian computation. Molecular Ecology Resources, 2020, 21, 2614-2628.	2.2	4
135	Neutral evolution of human enamel–dentine junction morphology. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 26183-26189.	3.3	11
136	Deep learning for population size history inference: Design, comparison and combination with approximate Bayesian computation. Molecular Ecology Resources, 2021, 21, 2645-2660.	2.2	53
137	Exome Sequencing of Native Populations From the Amazon Reveals Patterns on the Peopling of South America. Frontiers in Genetics, 2020, 11 , 548507 .	1.1	10
138	Global Picture of Genetic Relatedness and the Evolution of Humankind. Biology, 2020, 9, 392.	1.3	2
139	Methods for detecting introgressed archaic sequences. Current Opinion in Genetics and Development, 2020, 62, 85-90.	1.5	6
140	Coronavirus (SARS-CoV-2) and Mortality Rate in India: The Winning Edge. Frontiers in Public Health, 2020, 8, 397.	1.3	11
141	Current Trends in Ancient DNA Study. , 2020, , 1-16.		0
142	Neanderthal introgression reintroduced functional ancestral alleles lost in Eurasian populations. Nature Ecology and Evolution, 2020, 4, 1332-1341.	3.4	33
143	A different paradigm for the colonisation of Sahul. Archaeology in Oceania, 2020, 55, 182-191.	0.3	1
144	Genetic Association of ACE2 rs2285666 Polymorphism With COVID-19 Spatial Distribution in India. Frontiers in Genetics, 2020, 11, 564741.	1.1	71
145	Most frequent South Asian haplotypes of ACE2 share identity by descent with East Eurasian populations. PLoS ONE, 2020, 15, e0238255.	1.1	26
146	Ape Origins of Human Malaria. Annual Review of Microbiology, 2020, 74, 39-63.	2.9	46
147	Optimizing the genetic prediction of the eye and hair color for North Eurasian populations. BMC Genomics, 2020, 21, 527.	1.2	10
148	The reversal of human phylogeny: Homo left Africa as erectus, came back as sapiens sapiens. Hereditas, 2020, 157, 51.	0.5	3
149	A Revised Model of Anatomically Modern Human Expansions Out of Africa through a Machine Learning Approximate Bayesian Computation Approach. Genes, 2020, 11, 1510.	1.0	4
150	More Rule than Exception: Parallel Evidence of Ancient Migrations in Grammars and Genomes of Finno-Ugric Speakers. Genes, 2020, 11, 1491.	1.0	3
151	The Simons Genome Diversity Project: A Global Analysis of Mobile Element Diversity. Genome Biology and Evolution, 2020, 12, 779-794.	1.1	20

#	Article	IF	Citations
152	Genome-wide DNA methylation and gene expression patterns reflect genetic ancestry and environmental differences across the Indonesian archipelago. PLoS Genetics, 2020, 16, e1008749.	1.5	30
153	Revolutionary Fossils, Ancient Biomolecules, and Reflections in Ethics and Decolonization: Paleoanthropology in 2019. American Anthropologist, 2020, 122, 306-320.	0.7	6
154	Papuan mitochondrial genomes and the settlement of Sahul. Journal of Human Genetics, 2020, 65, 875-887.	1.1	24
155	Whole-genome resequencing of wild and domestic sheep identifies genes associated with morphological and agronomic traits. Nature Communications, 2020, 11, 2815.	5.8	142
156	Characterisation of a second gain of function EDAR variant, encoding EDAR380R, in East Asia. European Journal of Human Genetics, 2020, 28, 1694-1702.	1.4	6
157	A Population Genetic Perspective on Korean Prehistory. Korean Studies, 2020, 44, 27-53.	0.2	0
158	Decoding a highly mixed Kazakh genome. Human Genetics, 2020, 139, 557-568.	1.8	4
159	Tracking human population structure through time from whole genome sequences. PLoS Genetics, 2020, 16, e1008552.	1.5	71
160	Insights into human genetic variation and population history from 929 diverse genomes. Science, 2020, 367, .	6.0	534
161	Evolutionary Selection and Constraint on Human Knee Chondrocyte Regulation Impacts Osteoarthritis Risk. Cell, 2020, 181, 362-381.e28.	13.5	64
162	Skin colour and vitamin D: An update. Experimental Dermatology, 2020, 29, 864-875.	1.4	31
163	Human occupation of northern India spans the Toba super-eruption ~74,000 years ago. Nature Communications, 2020, 11, 961.	5.8	49
164	Hunter-gatherer multilevel sociality accelerates cumulative cultural evolution. Science Advances, 2020, 6, eaax5913.	4.7	66
165	From Apes to Cyborgs. , 2020, , .		1
166	A compilation of tri-allelic SNPs from 1000 Genomes and use of the most polymorphic loci for a large-scale human identification panel. Forensic Science International: Genetics, 2020, 46, 102232.	1.6	34
167	Archaeology and contemporary emerging zoonosis: A framework for predicting future Rift Valley fever virus outbreaks. International Journal of Osteoarchaeology, 2020, 30, 345-354.	0.6	10
168	Genomic landscape of the signals of positive natural selection in populations of Northern Eurasia: A view from Northern Russia. PLoS ONE, 2020, 15, e0228778.	1.1	6
169	Adapting Biased Gene Conversion theory to account for intensive GC-content deterioration in the human genome by novel mutations. PLoS ONE, 2020, 15, e0232167.	1.1	3

#	Article	IF	Citations
170	Corded Ware cultural complexity uncovered using genomic and isotopic analysis from south-eastern Poland. Scientific Reports, 2020, 10, 6885.	1.6	29
171	Fineâ€scale genetic structure of Tujia and central Han Chinese revealing massive genetic admixture under language borrowing. Journal of Systematics and Evolution, 2021, 59, 1-20.	1.6	31
172	A Southeast Asian origin for present-day non-African human Y chromosomes. Human Genetics, 2021, 140, 299-307.	1.8	14
173	Us and them: From prejudice to racism. An original analysis of race and racism. American Journal of Physical Anthropology, 2021, 175, 477-485.	2.1	1
174	Origins of modern human ancestry. Nature, 2021, 590, 229-237.	13.7	166
175	Genomic diversity and post-admixture adaptation in the Uyghurs. National Science Review, 2022, 9, nwab124.	4.6	20
176	Genome diversity in Ukraine. GigaScience, 2021, 10, .	3.3	9
177	Oldest cave art found in Sulawesi. Science Advances, 2021, 7, .	4.7	91
178	Dissecting dynamics and differences of selective pressures in the evolution of human pigmentation. Biology Open, 2021, 10, .	0.6	4
180	Stable isotope geochemistry of the modern Shinfa River, northwestern Ethiopian lowlands: a potential model for interpreting ancient environments of the Middle Stone Age. Geological Society Special Publication, 0, , SP507-2020-219.	0.8	2
181	A Chromosome-Painting-Based Pipeline to Infer Local Ancestry under Limited Source Availability. Genome Biology and Evolution, 2021, 13, .	1.1	3
183	The distinct morphological phenotypes of Southeast Asian aborigines are shaped by novel mechanisms for adaptation to tropical rainforests. National Science Review, 2022, 9, nwab072.	4.6	3
184	Stochastic models support rapid peopling of Late Pleistocene Sahul. Nature Communications, 2021, 12, 2440.	5.8	32
185	Population genetic considerations for using biobanks as international resources in the pandemic era and beyond. BMC Genomics, 2021, 22, 351.	1.2	11
186	The evolution of human skin pigmentation involved the interactions of genetic, environmental, and cultural variables. Pigment Cell and Melanoma Research, 2021, 34, 707-729.	1.5	32
187	The analysis of ancestry with small-scale forensic panels of genetic markers. Emerging Topics in Life Sciences, 2021, 5, 443-453.	1.1	4
189	Origin of ethnic groups, linguistic families, and civilizations in China viewed from the Y chromosome. Molecular Genetics and Genomics, 2021, 296, 783-797.	1.0	17
190	Correlated and geographically predictable Neanderthal and Denisovan legacies are difficult to reconcile with a simple model based on inter-breeding. Royal Society Open Science, 2021, 8, 201229.	1.1	3

#	Article	IF	CITATIONS
191	Related in death? A curious case of a foetus hidden in bishop Peder Winstrup's coffin in Lund, Sweden. Journal of Archaeological Science: Reports, 2021, 37, 102939.	0.2	0
192	Malaria in Europe: A Historical Perspective. Frontiers in Medicine, 2021, 8, 691095.	1.2	22
194	Through 40,000Âyears of human presence in Southern Europe: the Italian case study. Human Genetics, 2021, 140, 1417-1431.	1.8	11
195	Papua New Guinean Genomes Reveal the Complex Settlement of North Sahul. Molecular Biology and Evolution, 2021, 38, 5107-5121.	3.5	11
196	Climatic windows for human migration out of Africa in the past 300,000 years. Nature Communications, 2021, 12, 4889.	5.8	39
197	Development and Evaluation of the Ancestry Informative Marker Panel of the VISAGE Basic Tool. Genes, 2021, 12, 1284.	1.0	20
198	Philippine Ayta possess the highest level of Denisovan ancestry in the world. Current Biology, 2021, 31, 4219-4230.e10.	1.8	37
199	Ancestral Spectrum Analysis With Population-Specific Variants. Frontiers in Genetics, 2021, 12, 724638.	1.1	3
200	The genomic history of the Middle East. Cell, 2021, 184, 4612-4625.e14.	13.5	25
201	Human population dynamics and <i>Yersinia pestis</i> in ancient northeast Asia. Science Advances, 2021, 7, .	4.7	32
202	MSMC and MSMC2: The Multiple Sequentially Markovian Coalescent. Methods in Molecular Biology, 2020, 2090, 147-166.	0.4	114
203	Geneticists attempt to heal rifts with Aboriginal communities. Nature, 2016, 537, 457-458.	13.7	1
214	Inferring sex-specific demographic history from SNP data. PLoS Genetics, 2018, 14, e1007191.	1.5	26
215	Late Pleistocene hominin teeth from Laoya Cave, southern China. Anthropological Science, 2017, 125, 129-140.	0.2	5
216	R577X polymorphism of alpha-actinin-3 in human populations of North-Eastern Asia. Ecological Genetics, 2017, 15, 50.	0.1	2
217	BIOLOGICAL ANTHROPOLOGY IN THE INDO-PACIFIC REGION: NEW APPROACHES TO AGE-OLD QUESTIONS. Journal of Indo-Pacific Archaeology, 0, 41, 78.	0.0	6
218	Comparison of sequencing data processing pipelines and application to underrepresented African human populations. BMC Bioinformatics, 2021, 22, 488.	1.2	5
220	Detection of Neanderthal Adaptively Introgressed Genetic Variants That Modulate Reporter Gene Expression in Human Immune Cells. Molecular Biology and Evolution, 2022, 39, .	3.5	24

#	Article	IF	Citations
221	Revisiting the demographic history of Central African populations from a genetic perspective. , 0, , $1-29$.		1
222	Direct introgression of untapped diversity into elite wheat lines. Nature Food, 2021, 2, 819-827.	6.2	18
223	Revisiting the out of Africa event with a deep-learning approach. American Journal of Human Genetics, 2021, 108, 2037-2051.	2.6	6
225	UneÂperspective génétique surÂnotre histoireÂ: migrations humaines etÂadaptation ÃÂl'environnement. 2017, , 33-60.	,	0
227	Polymorphism of the genes encoding for the carnitine acyltransferases in native populations of Siberia. Ecological Genetics, 2017, 15, 13-18.	0.1	1
230	Population Genetics of Latvians in the Context of Admixture between North-Eastern European Ethnic Groups. Proceedings of the Latvian Academy of Sciences, 2018, 72, 131-151.	0.0	3
237	The mosaic of the Evenks gene pool: Transbaikalian and Amur segments. Moscow University Anthropology Bulletin (Vestnik Moskovskogo Universiteta Seria XXIII Antropologia), 2019, , 67-76.	0.0	3
238	The accuracy of predicting eye and hair pigmentation based on genetic markers in Russian populations. Bulletin of Russian State Medical University, 2019, , 23-38.	0.3	2
241	Human Biodiversity and Close Encounters. , 2020, , 11-26.		0
242	Polymorphism of gene GC, encoding vitamin D binding protein, in aboriginal populations of Siberia. Ecological Genetics, 0, , .	0.1	1
245	Refining models of archaic admixture in Eurasia with ArchaicSeeker 2.0. Nature Communications, 2021, 12, 6232.	5.8	19
247	Sometimes hidden but always there: the assumptions underlying genetic inference of demographic histories. Philosophical Transactions of the Royal Society B: Biological Sciences, 2021, 376, 20190719.	1.8	12
250	Current Trends in Ancient DNA Study. , 2021, , 285-300.		0
252	Genetic association of TMPRSS2 rs2070788 polymorphism with COVID-19 case fatality rate among Indian populations. Infection, Genetics and Evolution, 2022, 98, 105206.	1.0	13
253	A genetic history of migration, diversification, and admixture in Asia., 0,, 1-32.		3
254	Contrasting maternal and paternal genetic histories among five ethnic groups from Khyber Pakhtunkhwa, Pakistan. Scientific Reports, 2022, 12, 1027.	1.6	O
255	Vitamin D and Pigmented Skin. Nutrients, 2022, 14, 325.	1.7	4
256	Fine-Scale Genetic Structure in the United Arab Emirates Reflects Endogamous and Consanguineous Culture, Population History, and Geography. Molecular Biology and Evolution, 2022, 39, .	3.5	3

#	Article	IF	CITATIONS
257	Genetic Connections and Convergent Evolution of Tropical Indigenous Peoples in Asia. Molecular Biology and Evolution, 2022, 39, .	3. 5	2
258	Genetics and Material Culture Support Repeated Expansions into Paleolithic Eurasia from a Population Hub Out of Africa. Genome Biology and Evolution, 2022, 14, .	1.1	15
259	UCE sequencing-derived mitogenomes reveal the timing of mitochondrial replacement in Malagasy shrew tenrecs (Afrosoricida, Tenrecidae, Microgale). Mammalian Biology, 0 , 1 .	0.8	0
260	Adaptive Changes in Fatty Acid Desaturation Genes in Indigenous Populations of Northeast Siberia. Russian Journal of Genetics, 2021, 57, 1461-1466.	0.2	1
261	Tracing of Human Migration and Diversity by Forensic DNA Analysis. , 2022, , 1165-1184.		0
262	Climate effects on archaic human habitats and species successions. Nature, 2022, 604, 495-501.	13.7	55
279	A review of the spread and habitat of the genus <i>Homo</i> :. Anthropological Science, 2022, , .	0.2	0
280	Footprints of interaction among Finniѕspeaking, Slavic, and Turkic-speaking populations in modern gene pool and their reflection in pharmacogenetics. Bulletin of Russian State Medical University, 2022, , .	0.3	2
281	Response to Wyckelsma etÂal.: Loss of α-actinin-3 during human evolution provides superior cold resilience and muscle heat generation. American Journal of Human Genetics, 2022, 109, 967-972.	2.6	4
282	Determining the Area of Ancestral Origin for Individuals From North Eurasia Based on 5,229 SNP Markers. Frontiers in Genetics, 2022, 13, .	1.1	3
285	Helicobacter pylori genomes reveal Paleolithic human migration to the east end of Asia. IScience, 2022, 25, 104477.	1.9	3
287	The arrival of Homo sapiens in the Near East and Europe. , 2022, , 321-347.		3
288	Genotype imputation and polygenic score estimation in northwestern Russian population. PLoS ONE, 2022, 17, e0269434.	1.1	3
290	A Late Pleistocene human genome from Southwest China. Current Biology, 2022, 32, 3095-3109.e5.	1.8	6
291	Lineage-specific positive selection on <i>ACE2</i> contributes to the genetic susceptibility of COVID-19. National Science Review, 2022, 9, .	4.6	2
292	Chronology of natural selection in Oceanian genomes. IScience, 2022, 25, 104583.	1.9	3
293	Vitamin D in the Context of Evolution. Nutrients, 2022, 14, 3018.	1.7	21
294	Analysis of Common SNPs across Continents Reveals Major Genomic Differences between Human Populations. Genes, 2022, 13, 1472.	1.0	5

#	Article	IF	CITATIONS
295	Sequence analyses of Malaysian Indigenous communities reveal historical admixture between Hoabinhian hunter-gatherers and Neolithic farmers. Scientific Reports, 2022, 12, .	1.6	1
296	The genetic echo of the Tarim mummies in modern Central Asians. Molecular Biology and Evolution, 0,	3.5	1
297	Identifying signatures of natural selection in Indian populations. PLoS ONE, 2022, 17, e0271767.	1.1	0
298	Eurasiaplex-2: Shifting the focus to SNPs with high population specificity increases the power of forensic ancestry marker sets. Forensic Science International: Genetics, 2022, 61, 102780.	1.6	0
299	The Anglo-Saxon migration and the formation of the early English gene pool. Nature, 2022, 610, 112-119.	13.7	33
300	The history of climate and society: a review of the influence of climate change on the human past. Environmental Research Letters, 2022, 17, 103001.	2.2	13
301	Twenty years of the Human Genome Diversity Project. , 0, , 1-17.		1
302	MPYS Modulates Fatty Acid Metabolism and Immune Tolerance at Homeostasis Independent of Type I IFNs. Journal of Immunology, 2022, 209, 2114-2132.	0.4	4
303	Ethical challenges in genetic research among Philippine Indigenous Peoples: Insights from fieldwork in Zamboanga and the Sulu Archipelago. Frontiers in Genetics, $0,13,\ldots$	1.1	2
304	How to define humanity? A theoretical and empirical perspective. Bulletins Et Memoires De La Societe D'Anthropologie De Paris, 2022, 34, .	0.0	0
305	Impact of cultural and genetic structure on food choices along the Silk Road. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	4
306	Not by demography alone: Neanderthal extinction and null hypotheses in paleoanthropological explanation. Biology and Philosophy, 2022, 37, .	0.7	1
311	Description and Comparative Morphology of the Hofmeyr Skull. Vertebrate Paleobiology and Paleoanthropology, 2022, , 71-118.	0.1	5
312	Distributing Modern Peoples. , 2022, , 625-650.		0
315	The genetic history of Scandinavia from the Roman Iron Age to the present. Cell, 2023, 186, 32-46.e19.	13.5	9
317	The effect of skin color variation on 25(<scp>OH</scp>) <scp>D</scp> concentration in <scp>P</scp> olish children. American Journal of Biological Anthropology, 0, , .	0.6	0
318	Transferability of the PRS estimates for height and BMI obtained from the European ethnic groups to the Western Russian populations. Frontiers in Genetics, $0,14,.$	1.1	3
319	Is there still evolution in the human population?. Biologia Futura, 2022, 73, 359-374.	0.6	1

#	Article	IF	CITATIONS
321	Fossil and genetic evidence for Neanderthal introgression. , 2023, , 423-453.		0
322	Comparative evaluation of the MAPlex, Precision ID Ancestry Panel, and VISAGE Basic Tool for biogeographical ancestry inference. Forensic Science International: Genetics, 2023, 64, 102850.	1.6	1
323	Development and evaluations of the ancestry informative markers of the VISAGE Enhanced Tool for Appearance and Ancestry. Forensic Science International: Genetics, 2023, 64, 102853.	1.6	3
324	Nutrigenomics in the context of evolution. Redox Biology, 2023, 62, 102656.	3.9	3
325	Modern Humans Disperse From Africa. , 2022, , 581-623.		0
326	Were Neanderthals and Homo sapiens â€~good species'?. Quaternary Science Reviews, 2023, 303, 107975.	1.4	4
328	The first out of Africa migrants. , 2023, , 361-395.		0
329	Prevalence of genetically determined trehalase deficiency in populations of Siberia and Russian Far East. International Journal of Circumpolar Health, 2023, 82, .	0.5	1
330	Pathogenic Variants Associated with Rare Monogenic Diseases Established in Ancient Neanderthal and Denisovan Genome-Wide Data. Genes, 2023, 14, 727.	1.0	0
332	Multiple founding paternal lineages inferred from the newly-developed 639-plex Y-SNP panel suggested the complex admixture and migration history of Chinese people. Human Genomics, 2023, 17, .	1.4	5
333	Recent advances in Forensic DNA Phenotyping of appearance, ancestry and age. Forensic Science International: Genetics, 2023, 65, 102870.	1.6	9
341	More than a decade of genetic research on the Denisovans. Nature Reviews Genetics, 0 , , .	7.7	1