

The History of African Gene Flow into Southern Europe

PLoS Genetics

7, e1001373

DOI: [10.1371/journal.pgen.1001373](https://doi.org/10.1371/journal.pgen.1001373)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Perspectives on Human Population Structure at the Cusp of the Sequencing Era. Annual Review of Genomics and Human Genetics, 2011, 12, 245-274.	2.5	69
2	Learning about human population history from ancient and modern genomes. Nature Reviews Genetics, 2011, 12, 603-614.	7.7	172
3	Indian Siddis: African Descendants with Indian Admixture. American Journal of Human Genetics, 2011, 89, 154-161.	2.6	50
4	Genomic Ancestry of North Africans Supports Back-to-Africa Migrations. PLoS Genetics, 2012, 8, e1002397.	1.5	275
5	Inference of Population Splits and Mixtures from Genome-Wide Allele Frequency Data. PLoS Genetics, 2012, 8, e1002967.	1.5	1,997
6	Patterns of Ancestry, Signatures of Natural Selection, and Genetic Association with Stature in Western African Pygmies. PLoS Genetics, 2012, 8, e1002641.	1.5	118
7	The genetic prehistory of southern Africa. Nature Communications, 2012, 3, 1143.	5.8	271
8	Network-Level and Population Genetics Analysis of the Insulin/TOR Signal Transduction Pathway Across Human Populations. Molecular Biology and Evolution, 2012, 29, 1379-1392.	3.5	24
9	The Date of Interbreeding between Neandertals and Modern Humans. PLoS Genetics, 2012, 8, e1002947.	1.5	402
10	The impact of recent events on human genetic diversity. Philosophical Transactions of the Royal Society B: Biological Sciences, 2012, 367, 793-799.	1.8	65
11	Ancient Admixture in Human History. Genetics, 2012, 192, 1065-1093.	1.2	2,012
12	A High-Coverage Genome Sequence from an Archaic Denisovan Individual. Science, 2012, 338, 222-226.	6.0	1,695
13	Re-Examining the Out-of-Africa Theory and the Origin of Europeoids (Caucasoids). Part 2. SNPs, Haplogroups and Haplotypes in the Y Chromosome of Chimpanzee and Humans. Advances in Anthropology, 2012, 02, 198-213.	0.1	5
14	Exploring Population Admixture Dynamics via Empirical and Simulated Genome-wide Distribution of Ancestral Chromosomal Segments. American Journal of Human Genetics, 2012, 91, 849-862.	2.6	36
15	Origins and Genetic Legacy of Neolithic Farmers and Hunter-Gatherers in Europe. Science, 2012, 336, 466-469.	6.0	507
16	Ethiopian Genetic Diversity Reveals Linguistic Stratification and Complex Influences on the Ethiopian Gene Pool. American Journal of Human Genetics, 2012, 91, 83-96.	2.6	177
17	Genetic Evidence for Recent Population Mixture in India. American Journal of Human Genetics, 2013, 93, 422-438.	2.6	234
18	Analyses of genetic ancestry enable key insights for molecular ecology. Molecular Ecology, 2013, 22, 5278-5294.	2.0	31

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19	Genome-wide data substantiate Holocene gene flow from India to Australia. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1803-1808.	3.3	97
20	Higher Levels of Neanderthal Ancestry in East Asians than in Europeans. Genetics, 2013, 194, 199-209.	1.2	219
21	Introducing the Algerian Mitochondrial DNA and Y-Chromosome Profiles into the North African Landscape. PLoS ONE, 2013, 8, e56775.	1.1	53
22	Natural Selection in a Bangladeshi Population from the Cholera-Endemic Ganges River Delta. Science Translational Medicine, 2013, 5, 192ra86.	5.8	77
23	The Geography of Recent Genetic Ancestry across Europe. PLoS Biology, 2013, 11, e1001555.	2.6	316
24	Inferring Admixture Histories of Human Populations Using Linkage Disequilibrium. Genetics, 2013, 193, 1233-1254.	1.2	445
25	Inferring Demographic History from a Spectrum of Shared Haplotype Lengths. PLoS Genetics, 2013, 9, e1003521.	1.5	228
26	Genome-Wide Diversity in the Levant Reveals Recent Structuring by Culture. PLoS Genetics, 2013, 9, e1003316.	1.5	77
27	North Africans traveling north. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11668-11669.	3.3	2
28	Gene flow from North Africa contributes to differential human genetic diversity in southern Europe. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11791-11796.	3.3	174
29	Overview of Policy, Ethical and Social Considerations in Genomic and Personalized Medicine. , 2013, , 392-404.		2
30	Arab gene geography: From population diversities to personalized medical genomics. Global Cardiology Science & Practice, 2014, 2014, 54.	0.3	23
31	Patterns of Admixture and Population Structure in Native Populations of Northwest North America. PLoS Genetics, 2014, 10, e1004530.	1.5	81
32	Population Genomic Analysis of Ancient and Modern Genomes Yields New Insights into the Genetic Ancestry of the Tyrolean Iceman and the Genetic Structure of Europe. PLoS Genetics, 2014, 10, e1004353.	1.5	86
33	Early Back-to-Africa Migration into the Horn of Africa. PLoS Genetics, 2014, 10, e1004393.	1.5	87
34	A Genomic Approach for Distinguishing between Recent and Ancient Admixture as Applied to Cattle. Journal of Heredity, 2014, 105, 445-456.	1.0	15
35	Whole genome sequencing of Turkish genomes reveals functional private alleles and impact of genetic interactions with Europe, Asia and Africa. BMC Genomics, 2014, 15, 963.	1.2	46
36	A genome wide pattern of population structure and admixture in peninsular Malaysia Malays. The HUGO Journal, 2014, 8, 5.	4.1	14

#	ARTICLE	IF	CITATIONS
37	Effect of sampling on the extent and accuracy of the inferred genetic history of recombining genome. <i>Computational Biology and Chemistry</i> , 2014, 50, 68-74.	1.1	0
38	A Genetic Atlas of Human Admixture History. <i>Science</i> , 2014, 343, 747-751.	6.0	691
39	Genome-wide evidence of Austronesianâ€Bantu admixture and cultural reversion in a hunter-gatherer group of Madagascar. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 936-941.	3.3	75
40	The VKORC1 Asp36Tyr variant and VKORC1 haplotype diversity in Ashkenazi and Ethiopian populations. <i>Journal of Applied Genetics</i> , 2014, 55, 163-171.	1.0	5
41	Ancient west Eurasian ancestry in southern and eastern Africa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2632-2637.	3.3	246
42	The Lengths of Admixture Tracts. <i>Genetics</i> , 2014, 197, 953-967.	1.2	121
43	Immunoglobulin genes in Andalusia (Spain). Genetic diversity in the Mediterranean space. <i>Comptes Rendus - Biologies</i> , 2014, 337, 646-656.	0.1	9
44	Genetic ancestry of a Moroccan population as inferred from autosomal STRs. <i>Meta Gene</i> , 2014, 2, 427-438.	0.3	29
45	Toward a new history and geography of human genes informed by ancient DNA. <i>Trends in Genetics</i> , 2014, 30, 377-389.	2.9	227
46	Population-specific common SNPs reflect demographic histories and highlight regions of genomic plasticity with functional relevance. <i>BMC Genomics</i> , 2014, 15, 437.	1.2	40
47	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , 2014, 513, 409-413.	13.7	1,179
48	Mitochondrial DNA and Yâ€chromosome structure at the mediterranean and atlantic faÃ§ades of the iberian peninsula. <i>American Journal of Human Biology</i> , 2014, 26, 130-141.	0.8	9
49	Distribution of ancestral chromosomal segments in admixed genomes and its implications for inferring population history and admixture mapping. <i>European Journal of Human Genetics</i> , 2014, 22, 930-937.	1.4	30
50	Tracing the origin of our species through palaeogenomics. <i>BIO Web of Conferences</i> , 2015, 4, 00005.	0.1	1
51	Genetic Stratigraphy of Key Demographic Events in Arabia. <i>PLoS ONE</i> , 2015, 10, e0118625.	1.1	40
52	Evidence for a Common Origin of Blacksmiths and Cultivators in the Ethiopian Ari within the Last 4500 Years: Lessons for Clustering-Based Inference. <i>PLoS Genetics</i> , 2015, 11, e1005397.	1.5	194
53	Early Holocenic and Historic mtDNA African Signatures in the Iberian Peninsula: The Andalusian Region as a Paradigm. <i>PLoS ONE</i> , 2015, 10, e0139784.	1.1	18
54	Genome-wide insights into the genetic history of human populations. <i>Investigative Genetics</i> , 2015, 6, 6.	3.3	18

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55	Reconstructing Past Admixture Processes from Local Genomic Ancestry Using Wavelet Transformation. <i>Genetics</i> , 2015, 200, 469-481.	1.2	24
56	Complex History of Admixture between Modern Humans and Neandertals. <i>American Journal of Human Genetics</i> , 2015, 96, 448-453.	2.6	140
57	Two Italies? Genes, intelligence and the Italian North-South economic divide. <i>Intelligence</i> , 2015, 49, 44-56.	1.6	19
58	Denisovan Ancestry in East Eurasian and Native American Populations. <i>Molecular Biology and Evolution</i> , 2015, 32, 2665-2674.	3.5	121
59	Genetic evidence for two founding populations of the Americas. <i>Nature</i> , 2015, 525, 104-108.	13.7	348
60	Posterior predictive checks to quantify lack-of-fit in admixture models of latent population structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E3441-50.	3.3	11
61	The fine-scale genetic structure of the British population. <i>Nature</i> , 2015, 519, 309-314.	13.7	416
62	Evidence for archaic adaptive introgression in humans. <i>Nature Reviews Genetics</i> , 2015, 16, 359-371.	7.7	471
63	Bias in estimators of archaic admixture. <i>Theoretical Population Biology</i> , 2015, 100, 63-78.	0.5	25
64	Quantitating and Dating Recent Gene Flow between European and East Asian Populations. <i>Scientific Reports</i> , 2015, 5, 9500.	1.6	25
65	Ancient Ethiopian genome reveals extensive Eurasian admixture in Eastern Africa. <i>Science</i> , 2015, 350, 820-822.	6.0	277
66	Assessment of IrisPlex-based multiplex for eye and skin color prediction with application to a Portuguese population. <i>International Journal of Legal Medicine</i> , 2015, 129, 1191-1200.	1.2	15
67	The Role of Recent Admixture in Forming the Contemporary West Eurasian Genomic Landscape. <i>Current Biology</i> , 2015, 25, 2518-2526.	1.8	68
68	Genotyping of geographically diverse Druze trios reveals substructure and a recent bottleneck. <i>European Journal of Human Genetics</i> , 2015, 23, 1093-1099.	1.4	10
69	The Genetics of Bene Israel from India Reveals Both Substantial Jewish and Indian Ancestry. <i>PLoS ONE</i> , 2016, 11, e0152056.	1.1	17
70	Evolutionary Patterns and Processes: Lessons from Ancient DNA. <i>Systematic Biology</i> , 2017, 66, syw059.	2.7	73
71	Population stratification and its implications: lessons from genome-wide studies. , 0 , 315-340.		1
72	A genetic method for dating ancient genomes provides a direct estimate of human generation interval in the last 45,000 years. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5652-5657.	3.3	141

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73	Genomic insights into the peopling of the Southwest Pacific. <i>Nature</i> , 2016, 538, 510-513.	13.7	262
74	Archaic admixture in human history. <i>Current Opinion in Genetics and Development</i> , 2016, 41, 93-97.	1.5	26
75	TNFA gene variants related to the inflammatory status and its association with cellular aging: From the CORDIOPREV study. <i>Experimental Gerontology</i> , 2016, 83, 56-62.	1.2	11
76	Global diversity in the TAS2R38 bitter taste receptor: revisiting a classic evolutionary PROPosal. <i>Scientific Reports</i> , 2016, 6, 25506.	1.6	69
77	The genetic history of Cochin Jews from India. <i>Human Genetics</i> , 2016, 135, 1127-1143.	1.8	12
78	Genetic affinities of the Jewish populations of India. <i>Scientific Reports</i> , 2016, 6, 19166.	1.6	18
80	Multi-layered population structure in Island Southeast Asians. <i>European Journal of Human Genetics</i> , 2016, 24, 1605-1611.	1.4	50
81	The Italian genome reflects the history of Europe and the Mediterranean basin. <i>European Journal of Human Genetics</i> , 2016, 24, 1056-1062.	1.4	40
82	Model-based analyses of whole-genome data reveal a complex evolutionary history involving archaic introgression in Central African Pygmies. <i>Genome Research</i> , 2016, 26, 291-300.	2.4	87
83	Genetic evidence for an origin of the Armenians from Bronze Age mixing of multiple populations. <i>European Journal of Human Genetics</i> , 2016, 24, 931-936.	1.4	44
84	Atlas of Cryptic Genetic Relatedness Among 1000 Human Genomes. <i>Genome Biology and Evolution</i> , 2016, 8, 777-790.	1.1	8
85	Localizing Ashkenazic Jews to Primeval Villages in the Ancient Iranian Lands of Ashkenaz. <i>Genome Biology and Evolution</i> , 2016, 8, 1132-1149.	1.1	41
86	Implications of human evolution and admixture for mitochondrial replacement therapy. <i>BMC Genomics</i> , 2017, 18, 140.	1.2	44
87	Inference of multiple-wave population admixture by modeling decay of linkage disequilibrium with polynomial functions. <i>Heredity</i> , 2017, 118, 503-510.	1.2	12
88	Micro and macro geographical analysis of Y-chromosome lineages in South Iberia. <i>Forensic Science International: Genetics</i> , 2017, 29, e9-e15.	1.6	5
89	Ancient and recent admixture layers in Sicily and Southern Italy trace multiple migration routes along the Mediterranean. <i>Scientific Reports</i> , 2017, 7, 1984.	1.6	52
90	Disentangling Timing of Admixture, Patterns of Introgression, and Phenotypic Indicators in a Hybridizing Wolf Population. <i>Molecular Biology and Evolution</i> , 2017, 34, 2324-2339.	3.5	62
91	Overview of Policy, Ethical, and Social Considerations in Genomic and Personalized Medicine. , 2017, , 19-43.		1

#	ARTICLE	IF	CITATIONS
92	Genomewide analysis of admixture and adaptation in the Africanized honeybee. <i>Molecular Ecology</i> , 2017, 26, 3603-3617.	2.0	44
93	The Effects of Migration and Assortative Mating on Admixture Linkage Disequilibrium. <i>Genetics</i> , 2017, 205, 375-383.	1.2	31
94	Reconstructing Prehistoric African Population Structure. <i>Cell</i> , 2017, 171, 59-71.e21.	13.5	308
95	Models, methods and tools for ancestry inference and admixture analysis. <i>Quantitative Biology</i> , 2017, 5, 236-250.	0.3	13
96	Genetic structure in the Sherpa and neighboring Nepalese populations. <i>BMC Genomics</i> , 2017, 18, 102.	1.2	21
97	Admixture and Ancestry Inference from Ancient and Modern Samples through Measures of Population Genetic Drift. <i>Human Biology</i> , 2017, 89, 21.	0.4	30
98	The fine-scale genetic structure and evolution of the Japanese population. <i>PLoS ONE</i> , 2017, 12, e0185487.	1.1	27
99	A Hidden Markov Model Approach for Simultaneously Estimating Local Ancestry and Admixture Time Using Next Generation Sequence Data in Samples of Arbitrary Ploidy. <i>PLoS Genetics</i> , 2017, 13, e1006529.	1.5	117
100	Population Turnover in Remote Oceania Shortly after Initial Settlement. <i>Current Biology</i> , 2018, 28, 1157-1165.e7.	1.8	91
101	Inference of multiple-wave admixtures by length distribution of ancestral tracks. <i>Heredity</i> , 2018, 121, 52-63.	1.2	19
102	XPAT: a toolkit to conduct cross-platform association studies with heterogeneous sequencing datasets. <i>Nucleic Acids Research</i> , 2018, 46, e32-e32.	6.5	6
103	Inference on admixture fractions in a mechanistic model of recurrent admixture. <i>Theoretical Population Biology</i> , 2018, 122, 149-157.	0.5	9
104	Dating admixture events is unsolved problem in multi-way admixed populations. <i>Briefings in Bioinformatics</i> , 2020, 21, 144-155.	3.2	15
105	Estimating the Timing of Multiple Admixture Pulses During Local Ancestry Inference. <i>Genetics</i> , 2018, 210, 1089-1107.	1.2	37
106	Statistical methods for detecting admixture. <i>Current Opinion in Genetics and Development</i> , 2018, 53, 121-127.	1.5	9
107	Genomic history of the Sardinian population. <i>Nature Genetics</i> , 2018, 50, 1426-1434.	9.4	71
108	Interspecific Gene Exchange as a Driver of Adaptive Evolution in Fungi. <i>Annual Review of Microbiology</i> , 2018, 72, 377-398.	2.9	40
109	Population genomics of Mesolithic Scandinavia: Investigating early postglacial migration routes and high-latitude adaptation. <i>PLoS Biology</i> , 2018, 16, e2003703.	2.6	174

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110	Genetics and Population Analysis. , 2019, , 363-378.		0
112	Historic migration to South Asia in the last two millennia: A case of Jewish and Parsi populations. Journal of Biosciences, 2019, 44, 1.	0.5	3
113	Deep Learning Approach to Biogeographical Ancestry Inference. Procedia Computer Science, 2019, 159, 552-561.	1.2	5
114	The formation of human populations in South and Central Asia. Science, 2019, 365, .	6.0	383
115	The genetic legacy of the Yaghnobis: A witness of an ancient Eurasian ancestry in the historically reshuffled central Asian gene pool. American Journal of Physical Anthropology, 2019, 168, 717-728.	2.1	6
116	Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula. Nature Communications, 2019, 10, 551.	5.8	63
117	Models of archaic admixture and recent history from two-locus statistics. PLoS Genetics, 2019, 15, e1008204.	1.5	57
118	Dissecting human North African gene-flow into its western coastal surroundings. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20190471.	1.2	13
120	A western route of prehistoric human migration from Africa into the Iberian Peninsula. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20182288.	1.2	47
121	Genome-Wide Characterization of Arabian Peninsula Populations: Shedding Light on the History of a Fundamental Bridge between Continents. Molecular Biology and Evolution, 2019, 36, 575-586.	3.5	45
122	Genomic evidence for shared common ancestry of East African hunting-gathering populations and insights into local adaptation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 4166-4175.	3.3	40
123	Orienting Future Trends in Local Ancestry Deconvolution Models to Optimally Decipher Admixed Individual Genome Variations. , 2019, , .		3
124	The Local South American Chicken Populations Are a Melting-Pot of Genomic Diversity. Frontiers in Genetics, 2019, 10, 1172.	1.1	1
125	Single haplotype admixture models using large scale HLA genotype frequencies to reproduce human admixture. Immunogenetics, 2019, 71, 589-604.	1.2	2
126	Eukaryote hybrid genomes. PLoS Genetics, 2019, 15, e1008404.	1.5	77
127	West Asian sources of the Eurasian component in Ethiopians: a reassessment. Scientific Reports, 2019, 9, 18811.	1.6	14
128	MultiWaver 2.0: modeling discrete and continuous gene flow to reconstruct complex population admixtures. European Journal of Human Genetics, 2019, 27, 133-139.	1.4	23
129	Unbiased Estimation of Linkage Disequilibrium from Unphased Data. Molecular Biology and Evolution, 2020, 37, 923-932.	3.5	26

#	ARTICLE	IF	CITATIONS
130	Human Genomic Diversity Where the Mediterranean Joins the Atlantic. <i>Molecular Biology and Evolution</i> , 2020, 37, 1041-1055.	3.5	11
131	Using Haplotype Information for Conservation Genomics. <i>Trends in Ecology and Evolution</i> , 2020, 35, 245-258.	4.2	69
132	Admixture and natural selection shaped genomes of an Austronesian-speaking population in the Solomon Islands. <i>Scientific Reports</i> , 2020, 10, 6872.	1.6	7
133	Berbers and Arabs: Tracing the genetic diversity and history of Southern Tunisia through genome wide analysis. <i>American Journal of Physical Anthropology</i> , 2020, 173, 697-708.	2.1	5
134	Flexible Mixture Model Approaches That Accommodate Footprint Size Variability for Robust Detection of Balancing Selection. <i>Molecular Biology and Evolution</i> , 2020, 37, 3267-3291.	3.5	23
135	Ancestry deconvolution and partial polygenic score can improve susceptibility predictions in recently admixed individuals. <i>Nature Communications</i> , 2020, 11, 1628.	5.8	66
136	The spread of steppe and Iranian-related ancestry in the islands of the western Mediterranean. <i>Nature Ecology and Evolution</i> , 2020, 4, 334-345.	3.4	95
137	Colonialism and the co- <i>evolution</i> of ethnic and genetic structure in New Mexico. <i>American Journal of Physical Anthropology</i> , 2020, 171, 509-519.	2.1	1
138	Population structure of indigenous inhabitants of Arabia. <i>PLoS Genetics</i> , 2021, 17, e1009210.	1.5	14
139	Rapid adaptation to malaria facilitated by admixture in the human population of Cabo Verde. <i>ELife</i> , 2021, 10, .	2.8	41
140	Inferring Human Demographic History from Genetic Data. , 2021, , 187-204.		0
141	Complex genetic admixture histories reconstructed with Approximate Bayesian Computation. <i>Molecular Ecology Resources</i> , 2021, 21, 1098-1117.	2.2	13
142	A Chromosome-Painting-Based Pipeline to Infer Local Ancestry under Limited Source Availability. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	3
146	Demographic history shapes genomic ancestry in hybrid zones. <i>Ecology and Evolution</i> , 2021, 11, 10290-10302.	0.8	1
147	Human-Mediated Admixture and Selection Shape the Diversity on the Modern Swine (<i>Sus scrofa</i>) Y Chromosomes. <i>Molecular Biology and Evolution</i> , 2021, 38, 5051-5065.	3.5	9
148	An Extended Admixture Pulse Model Reveals the Limitations to Human-Neandertal Introgression Dating. <i>Molecular Biology and Evolution</i> , 2021, 38, 5156-5174.	3.5	9
150	Biomolecular insights into North African-related ancestry, mobility and diet in eleventh-century Al-Andalus. <i>Scientific Reports</i> , 2021, 11, 18121.	1.6	8
151	The genomic history of the Middle East. <i>Cell</i> , 2021, 184, 4612-4625.e14.	13.5	25

#	ARTICLE	IF	CITATIONS
152	Characterisation of body size phenotypes in a middle-aged Maltese population. <i>Journal of Nutritional Science</i> , 2021, 10, e81.	0.7	7
153	Genomic History of Neolithic to Bronze Age Anatolia, Northern Levant, and Southern Caucasus. <i>Cell</i> , 2020, 181, 1158-1175.e28.	13.5	86
164	A Spatial Framework for Understanding Population Structure and Admixture. <i>PLoS Genetics</i> , 2016, 12, e1005703.	1.5	109
165	The time and place of European admixture in Ashkenazi Jewish history. <i>PLoS Genetics</i> , 2017, 13, e1006644.	1.5	25
166	Reconstructing Roma History from Genome-Wide Data. <i>PLoS ONE</i> , 2013, 8, e58633.	1.1	61
167	Native American Admixture in the Quebec Founder Population. <i>PLoS ONE</i> , 2013, 8, e65507.	1.1	13
168	A Genome-Wide Study of Modern-Day Tuscans: Revisiting Herodotus's Theory on the Origin of the Etruscans. <i>PLoS ONE</i> , 2014, 9, e105920.	1.1	23
169	Reconsideration of the "Out of Africa" Concept as Not Having Enough Proof. <i>Advances in Anthropology</i> , 2014, 04, 18-37.	0.1	9
170	Evolutionary genomics of epidemic visceral leishmaniasis in the Indian subcontinent. <i>ELife</i> , 2016, 5, .	2.8	147
171	Selective sorting of ancestral introgression in maize and teosinte along an elevational cline. <i>PLoS Genetics</i> , 2021, 17, e1009810.	1.5	50
183	Comparison of the Frequency of Y-short Tandem Repeats Markers between Sadat and Non-Sadat Populations in Isfahan Province of Iran. <i>Advanced Biomedical Research</i> , 2017, 6, 33.	0.2	1
193	Biogeographical Ancestry Inference from Genotype: A Comparison of Ancestral Informative SNPs and Genome-wide SNPs. , 2020, , .		0
194	Genetic ancestry, admixture, and population structure in rural Dominica. <i>PLoS ONE</i> , 2021, 16, e0258735.	1.1	19
197	An Ethnolinguistic and Genetic Perspective on the Origins of the Dravidian-Speaking Brahui in Pakistan. <i>Man in India</i> , 2017, 97, 267-278.	2.0	3
200	Historic migration to South Asia in the last two millennia: A case of Jewish and Parsi populations. <i>Journal of Biosciences</i> , 2019, 44, .	0.5	1
203	Human genetic admixture through the lens of population genomics. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, 20200410.	1.8	15
206	The spatiotemporal patterns of major human admixture events during the European Holocene. <i>ELife</i> , 0, 11, .	2.8	23
208	Assessing temporal and geographic contacts across the Adriatic Sea through the analysis of genome-wide data from Southern Italy. <i>Genomics</i> , 2022, 114, 110405.	1.3	0

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209	Estimating the timing of multiple admixture events using 3-locus linkage disequilibrium. PLoS Genetics, 2022, 18, e1010281.	1.5	3
210	An efficient method to identify, date, and describe admixture events using haplotype information. Genome Research, 2022, 32, 1553-1564.	2.4	18
211	Signatures of Convergent Evolution and Natural Selection at the Alcohol Dehydrogenase Gene Region are Correlated with Agriculture in Ethnically Diverse Africans. Molecular Biology and Evolution, 2022, 39, .	3.5	5
212	The genetic history of the Southern Arc: A bridge between West Asia and Europe. Science, 2022, 377, .	6.0	31
213	Simultaneous inference of parental admixture proportions and admixture times from unphased local ancestry calls. American Journal of Human Genetics, 2022, 109, 1405-1420.	2.6	5
214	Principal Component Analyses (PCA)-based findings in population genetic studies are highly biased and must be reevaluated. Scientific Reports, 2022, 12, .	1.6	48
215	The genomic analysis of current-day North African populations reveals the existence of trans-Saharan migrations with different origins and dates. Human Genetics, 2023, 142, 305-320.	1.8	5
216	Genome-wide data from medieval German Jews show that the Ashkenazi founder event pre-dated the 14th century. Cell, 2022, 185, 4703-4716.e16.	13.5	12
217	Fossil and genetic evidence for Neanderthal introgression. , 2023, , 423-453.		0
218	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