

Toomas Kivisild

List of Publications by Year in descending order

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Version: 2024-02-01

175
papers

22,885
citations

10351

72
h-index

9839

141
g-index

197
all docs

197
docs citations

197
times ranked

14805
citing authors

#	ARTICLE	IF	CITATIONS
1	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. <i>Nature</i> , 2016, 538, 201-206.	13.7	1,216
2	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , 2014, 513, 409-413.	13.7	1,179
3	Tracing European Founder Lineages in the Near Eastern mtDNA Pool. <i>American Journal of Human Genetics</i> , 2000, 67, 1251-1276.	2.6	837
4	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , 2014, 505, 87-91.	13.7	821
5	Ancient human genome sequence of an extinct Palaeo-Eskimo. <i>Nature</i> , 2010, 463, 757-762.	13.7	750
6	An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. <i>Science</i> , 2011, 334, 94-98.	6.0	675
7	Y-Chromosomal Diversity in Europe Is Clinal and Influenced Primarily by Geography, Rather than by Language. <i>American Journal of Human Genetics</i> , 2000, 67, 1526-1543.	2.6	519
8	Beringian Standstill and Spread of Native American Founders. <i>PLoS ONE</i> , 2007, 2, e829.	1.1	499
9	Phylogeographic Differentiation of Mitochondrial DNA in Han Chinese. <i>American Journal of Human Genetics</i> , 2002, 70, 635-651.	2.6	491
10	Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015, 349, aab3884.	6.0	449
11	A "Copernican" Reassessment of the Human Mitochondrial DNA Tree from its Root. <i>American Journal of Human Genetics</i> , 2012, 90, 675-684.	2.6	416
12	The Molecular Dissection of mtDNA Haplogroup H Confirms That the Franco-Cantabrian Glacial Refuge Was a Major Source for the European Gene Pool. <i>American Journal of Human Genetics</i> , 2004, 75, 910-918.	2.6	397
13	The Role of Selection in the Evolution of Human Mitochondrial Genomes. <i>Genetics</i> , 2006, 172, 373-387.	1.2	395
14	The Genetic Heritage of the Earliest Settlers Persists Both in Indian Tribal and Caste Populations. <i>American Journal of Human Genetics</i> , 2003, 72, 313-332.	2.6	368
15	The Emerging Limbs and Twigs of the East Asian mtDNA Tree. <i>Molecular Biology and Evolution</i> , 2002, 19, 1737-1751.	3.5	360
16	Genomic analyses inform on migration events during the peopling of Eurasia. <i>Nature</i> , 2016, 538, 238-242.	13.7	360
17	Genetic Evidence on the Origins of Indian Caste Populations. <i>Genome Research</i> , 2001, 11, 994-1004.	2.4	359
18	Use of Y Chromosome and Mitochondrial DNA Population Structure in Tracing Human Migrations. <i>Annual Review of Genetics</i> , 2007, 41, 539-564.	3.2	358

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19	The Effective Mutation Rate at Y Chromosome Short Tandem Repeats, with Application to Human Population-Divergence Time. <i>American Journal of Human Genetics</i> , 2004, 74, 50-61.	2.6	353
20	A recent bottleneck of Y chromosome diversity coincides with a global change in culture. <i>Genome Research</i> , 2015, 25, 459-466.	2.4	348
21	Excavating Y-chromosome haplotype strata in Anatolia. <i>Human Genetics</i> , 2004, 114, 127-148.	1.8	318
22	Most of the extant mtDNA boundaries in south and southwest Asia were likely shaped during the initial settlement of Eurasia by anatomically modern humans. <i>BMC Genetics</i> , 2004, 5, 26.	2.7	305
23	Global diversity, population stratification, and selection of human copy-number variation. <i>Science</i> , 2015, 349, aab3761.	6.0	293
24	Reconstructing the Origin of Andaman Islanders. <i>Science</i> , 2005, 308, 996-996.	6.0	291
25	Tracing European founder lineages in the Near Eastern mtDNA pool. <i>American Journal of Human Genetics</i> , 2000, 67, 1251-76.	2.6	288
26	Deep common ancestry of Indian and western-Eurasian mitochondrial DNA lineages. <i>Current Biology</i> , 1999, 9, 1331-1334.	1.8	270
27	A Signal, from Human mtDNA, of Postglacial Recolonization in Europe. <i>American Journal of Human Genetics</i> , 2001, 69, 844-852.	2.6	267
28	The genetic prehistory of the New World Arctic. <i>Science</i> , 2014, 345, 1255832.	6.0	264
29	Genomic insights into the peopling of the Southwest Pacific. <i>Nature</i> , 2016, 538, 510-513.	13.7	262
30	Phylogeography of Y-Chromosome Haplogroup I Reveals Distinct Domains of Prehistoric Gene Flow in Europe. <i>American Journal of Human Genetics</i> , 2004, 75, 128-137.	2.6	256
31	Ethiopian Mitochondrial DNA Heritage: Tracking Gene Flow Across and Around the Gate of Tears. <i>American Journal of Human Genetics</i> , 2004, 75, 752-770.	2.6	234
32	A major Y-chromosome haplogroup R1b Holocene era founder effect in Central and Western Europe. <i>European Journal of Human Genetics</i> , 2011, 19, 95-101.	1.4	224
33	Revealing the prehistoric settlement of Australia by Y chromosome and mtDNA analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 8726-8730.	3.3	204
34	The Western and Eastern Roots of the Saami—the Story of Genetic “Outliers” Told by Mitochondrial DNA and Y Chromosomes. <i>American Journal of Human Genetics</i> , 2004, 74, 661-682.	2.6	202
35	Paleo-Eskimo mtDNA Genome Reveals Matrilineal Discontinuity in Greenland. <i>Science</i> , 2008, 320, 1787-1789.	6.0	184
36	Traces of Archaic Mitochondrial Lineages Persist in Austronesian-Speaking Formosan Populations. <i>PLoS Biology</i> , 2005, 3, e247.	2.6	178

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37	Ethiopian Genetic Diversity Reveals Linguistic Stratification and Complex Influences on the Ethiopian Gene Pool. <i>American Journal of Human Genetics</i> , 2012, 91, 83-96.	2.6	177
38	Genetic Signatures Reveal High-Altitude Adaptation in a Set of Ethiopian Populations. <i>Molecular Biology and Evolution</i> , 2013, 30, 1877-1888.	3.5	173
39	Disuniting Uniformity: A Pied Cladistic Canvas of mtDNA Haplogroup H in Eurasia. <i>Molecular Biology and Evolution</i> , 2004, 21, 2012-2021.	3.5	170
40	The Caucasus as an Asymmetric Semipermeable Barrier to Ancient Human Migrations. <i>Molecular Biology and Evolution</i> , 2012, 29, 359-365.	3.5	161
41	Separating the post-Glacial coancestry of European and Asian Y chromosomes within haplogroup R1a. <i>European Journal of Human Genetics</i> , 2010, 18, 479-484.	1.4	153
42	Tracing the Route of Modern Humans out of Africa by Using 225 Human Genome Sequences from Ethiopians and Egyptians. <i>American Journal of Human Genetics</i> , 2015, 96, 986-991.	2.6	152
43	Shared and Unique Components of Human Population Structure and Genome-Wide Signals of Positive Selection in South Asia. <i>American Journal of Human Genetics</i> , 2011, 89, 731-744.	2.6	149
44	The Genetic Legacy of the Expansion of Turkic-Speaking Nomads across Eurasia. <i>PLoS Genetics</i> , 2015, 11, e1005068.	1.5	149
45	Origin and Diffusion of mtDNA Haplogroup X. <i>American Journal of Human Genetics</i> , 2003, 73, 1178-1190.	2.6	148
46	Origin and Expansion of Haplogroup H, the Dominant Human Mitochondrial DNA Lineage in West Eurasia: The Near Eastern and Caucasian Perspective. <i>Molecular Biology and Evolution</i> , 2007, 24, 436-448.	3.5	148
47	A counter-clockwise northern route of the Y-chromosome haplogroup N from Southeast Asia towards Europe. <i>European Journal of Human Genetics</i> , 2007, 15, 204-211.	1.4	142
48	The Matrilineal Ancestry of Ashkenazi Jewry: Portrait of a Recent Founder Event. <i>American Journal of Human Genetics</i> , 2006, 78, 487-497.	2.6	140
49	Ancient human parallel lineages within North America contributed to a coastal expansion. <i>Science</i> , 2018, 360, 1024-1027.	6.0	138
50	A prehistory of Indian Y chromosomes: Evaluating demic diffusion scenarios. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 843-848.	3.3	135
51	Population Genetic Structure in Indian Austroasiatic Speakers: The Role of Landscape Barriers and Sex-Specific Admixture. <i>Molecular Biology and Evolution</i> , 2011, 28, 1013-1024.	3.5	135
52	Genome-Wide Analysis of Cold Adaptation in Indigenous Siberian Populations. <i>PLoS ONE</i> , 2014, 9, e98076.	1.1	128
53	Two Sources of the Russian Patrilineal Heritage in Their Eurasian Context. <i>American Journal of Human Genetics</i> , 2008, 82, 236-250.	2.6	122
54	The phylogenetic and geographic structure of Y-chromosome haplogroup R1a. <i>European Journal of Human Genetics</i> , 2015, 23, 124-131.	1.4	122

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55	Philippine Mitochondrial DNA Diversity: A Populated Viaduct between Taiwan and Indonesia?. <i>Molecular Biology and Evolution</i> , 2010, 27, 21-31.	3.5	121
56	Population increase and environmental deterioration correspond with microlithic innovations in South Asia ca. 35,000 years ago. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12261-12266.	3.3	119
57	A Selective Sweep on a Deleterious Mutation in CPT1A in Arctic Populations. <i>American Journal of Human Genetics</i> , 2014, 95, 584-589.	2.6	119
58	Phylogeography of the second plague pandemic revealed through analysis of historical <i>Yersinia pestis</i> genomes. <i>Nature Communications</i> , 2019, 10, 4470.	5.8	113
59	Extensive Farming in Estonia Started through a Sex-Biased Migration from the Steppe. <i>Current Biology</i> , 2017, 27, 2185-2193.e6.	1.8	111
60	What evidence is there for the existence of individual genes with antagonistic pleiotropic effects?. <i>Mechanisms of Ageing and Development</i> , 2005, 126, 421-429.	2.2	109
61	Identification of Native American Founder mtDNAs Through the Analysis of Complete mtDNA Sequences: Some Caveats. <i>Annals of Human Genetics</i> , 2003, 67, 512-524.	0.3	103
62	Continuity and Admixture in the Last Five Millennia of Levantine History from Ancient Canaanite and Present-Day Lebanese Genome Sequences. <i>American Journal of Human Genetics</i> , 2017, 101, 274-282.	2.6	102
63	Counting the Founders: The Matrilineal Genetic Ancestry of the Jewish Diaspora. <i>PLoS ONE</i> , 2008, 3, e2062.	1.1	101
64	Ancient <i>Yersinia pestis</i> genomes from across Western Europe reveal early diversification during the First Pandemic (541â€“750). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12363-12372.	3.3	100
65	Human Y Chromosome Haplogroup N: A Non-trivial Time-Resolved Phylogeography that Cuts across Language Families. <i>American Journal of Human Genetics</i> , 2016, 99, 163-173.	2.6	98
66	Maternal ancestry and population history from whole mitochondrial genomes. <i>Investigative Genetics</i> , 2015, 6, 3.	3.3	94
67	Y Chromosome Sequences Reveal a Short Beringian Standstill, Rapid Expansion, and early Population structure of Native American Founders. <i>Current Biology</i> , 2019, 29, 149-157.e3.	1.8	94
68	The Light Skin Allele of SLC24A5 in South Asians and Europeans Shares Identity by Descent. <i>PLoS Genetics</i> , 2013, 9, e1003912.	1.5	93
69	Genetic Heritage of the Balto-Slavic Speaking Populations: A Synthesis of Autosomal, Mitochondrial and Y-Chromosomal Data. <i>PLoS ONE</i> , 2015, 10, e0135820.	1.1	91
70	The Genomic Impact of European Colonization of the Americas. <i>Current Biology</i> , 2019, 29, 3974-3986.e4.	1.8	89
71	Questioning Evidence for Recombination in Human Mitochondrial DNA. <i>Science</i> , 2000, 288, 1931a-1931.	6.0	88
72	Validation of microarray-based resequencing of 93 worldwide mitochondrial genomes. <i>Human Mutation</i> , 2009, 30, 115-122.	1.1	83

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73	The Arrival of Siberian Ancestry Connecting the Eastern Baltic to Uralic Speakers further East. <i>Current Biology</i> , 2019, 29, 1701-1711.e16.	1.8	80
74	Peopling of South Asia: investigating the casteâ€“tribe continuum in India. <i>BioEssays</i> , 2007, 29, 91-100.	1.2	79
75	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
76	Distinguishing the co-ancestries of haplogroup G Y-chromosomes in the populations of Europe and the Caucasus. <i>European Journal of Human Genetics</i> , 2012, 20, 1275-1282.	1.4	74
77	The study of human Y chromosome variation through ancient DNA. <i>Human Genetics</i> , 2017, 136, 529-546.	1.8	72
78	The emergence of Y-chromosome haplogroup J1e among Arabic-speaking populations. <i>European Journal of Human Genetics</i> , 2010, 18, 348-353.	1.4	71
79	Herders of Indian and European Cattle Share Their Predominant Allele for Lactase Persistence. <i>Molecular Biology and Evolution</i> , 2012, 29, 249-260.	3.5	67
80	Selective sweep on human amylase genes postdates the split with Neanderthals. <i>Scientific Reports</i> , 2016, 6, 37198.	1.6	67
81	Genes reveal traces of common recent demographic history for most of the Uralic-speaking populations. <i>Genome Biology</i> , 2018, 19, 139.	3.8	67
82	Y chromosomal heritage of Croatian population and its island isolates. <i>European Journal of Human Genetics</i> , 2003, 11, 535-542.	1.4	66
83	Reconstruction of patrilineages and matrilineages of Samaritans and other Israeli populations from Y-Chromosome and mitochondrial DNA sequence Variation. <i>Human Mutation</i> , 2004, 24, 248-260.	1.1	66
84	Mitochondrial DNA coding region sequences support the phylogenetic distinction of two Indian wolf species. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2007, 45, 163-172.	0.6	66
85	Evolution of the Pygmy Phenotype: Evidence of Positive Selection from Genome-wide Scans in African, Asian, and Melanesian Pygmies. <i>Human Biology</i> , 2013, 85, 251-284.	0.4	66
86	MtDNA Profile of West Africa Guineans: Towards a Better Understanding of the Senegambia Region. <i>Annals of Human Genetics</i> , 2004, 68, 340-352.	0.3	65
87	Malagasy Genetic Ancestry Comes from an Historical Malay Trading Post in Southeast Borneo. <i>Molecular Biology and Evolution</i> , 2016, 33, 2396-2400.	3.5	62
88	Different population histories of the Mundari- and Mon-Khmer-speaking Austro-Asiatic tribes inferred from the mtDNA 9-bp deletion/insertion polymorphism in Indian populations. <i>Human Genetics</i> , 2005, 116, 507-517.	1.8	60
89	Evaluating genotype imputation pipeline for ultra-low coverage ancient genomes. <i>Scientific Reports</i> , 2020, 10, 18542.	1.6	60
90	Y-chromosome Lineages from Portugal, Madeira and Açores Record Elements of Sephardim and Berber Ancestry. <i>Annals of Human Genetics</i> , 2005, 69, 443-454.	0.3	56

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91	An mtDNA perspective of French genetic variation. <i>Annals of Human Biology</i> , 2007, 34, 68-79.	0.4	55
92	The Andean Adaptive Toolkit to Counteract High Altitude Maladaptation: Genome-Wide and Phenotypic Analysis of the Collas. <i>PLoS ONE</i> , 2014, 9, e93314.	1.1	55
93	Population structure of modern-day Italians reveals patterns of ancient and archaic ancestries in Southern Europe. <i>Science Advances</i> , 2019, 5, eaaw3492.	4.7	53
94	Multi-layered population structure in Island Southeast Asians. <i>European Journal of Human Genetics</i> , 2016, 24, 1605-1611.	1.4	50
95	Persistent Immune Responses Induced by a Human Immunodeficiency Virus DNA Vaccine Delivered in Association with Electroporation in the Skin of Nonhuman Primates. <i>Human Gene Therapy</i> , 2009, 20, 1291-1307.	1.4	48
96	Divorcing the Late Upper Palaeolithic demographic histories of mtDNA haplogroups M1 and U6 in Africa. <i>BMC Evolutionary Biology</i> , 2012, 12, 234.	3.2	48
97	Validity of visceral adiposity estimates from DXA against MRI in Kuwaiti men and women. <i>Nutrition and Diabetes</i> , 2017, 7, e238-e238.	1.5	48
98	Genetic evidence on modern human dispersals in South Asia: Y chromosome and mitochondrial DNA perspectives: The world through the eyes of two haploid genomes. , 2007, , 229-244.		47
99	Genetic Evidence on the Origins of Indian Caste Populations. <i>Genome Research</i> , 2001, 11, 994-1004.	2.4	47
100	Phylogeography of mtDNA haplogroup R7 in the Indian peninsula. <i>BMC Evolutionary Biology</i> , 2008, 8, 227.	3.2	45
101	Shifts in the Genetic Landscape of the Western Eurasian Steppe Associated with the Beginning and End of the Scythian Dominance. <i>Current Biology</i> , 2019, 29, 2430-2441.e10.	1.8	44
102	Maternal Footprints of Southeast Asians in North India. <i>Human Heredity</i> , 2008, 66, 1-9.	0.4	43
103	High penetrance of sequencing errors and interpretative shortcomings in mtDNA sequence analysis of LHON patients. <i>Biochemical and Biophysical Research Communications</i> , 2007, 352, 283-291.	1.0	42
104	Identification of Polynesian mtDNA haplogroups in remains of Botocudo Amerindians from Brazil. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6465-6469.	3.3	42
105	To Trust or Not to Trust an Idiosyncratic Mitochondrial Data Set. <i>American Journal of Human Genetics</i> , 2003, 72, 1341-1346.	2.6	41
106	The Genetic Ancestry of Modern Indus Valley Populations from Northwest India. <i>American Journal of Human Genetics</i> , 2018, 103, 918-929.	2.6	38
107	Ancient genomes reveal structural shifts after the arrival of Steppe-related ancestry in the Italian Peninsula. <i>Current Biology</i> , 2021, 31, 2576-2591.e12.	1.8	38
108	A Transient Pulse of Genetic Admixture from the Crusaders in the Near East Identified from Ancient Genome Sequences. <i>American Journal of Human Genetics</i> , 2019, 104, 977-984.	2.6	35

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109	Evaluating macroscopic sex estimation methods using genetically sexed archaeological material: The medieval skeletal collection from St John's Divinity School, Cambridge. <i>American Journal of Physical Anthropology</i> , 2019, 168, 340-351.	2.1	35
110	Genetic Diversity among Ancient Nordic Populations. <i>PLoS ONE</i> , 2010, 5, e11898.	1.1	34
111	Y-chromosome lineages in Cabo Verde Islands witness the diverse geographic origin of its first male settlers. <i>Human Genetics</i> , 2003, 113, 467-472.	1.8	33
112	Mitochondrial portraits of the Madeira and Açores archipelagos witness different genetic pools of its settlers. <i>Human Genetics</i> , 2003, 114, 77-86.	1.8	32
113	Median network analysis of defectively sequenced entire mitochondrial genomes from early and contemporary disease studies. <i>Journal of Human Genetics</i> , 2009, 54, 174-181.	1.1	32
114	Positive selection of AS3MT to arsenic water in Andean populations. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2015, 780, 97-102.	0.4	32
115	Genetic ancestry changes in Stone to Bronze Age transition in the East European plain. <i>Science Advances</i> , 2021, 7, .	4.7	32
116	Phylogenetic applications of whole Y-chromosome sequences and the Near Eastern origin of Ashkenazi Levites. <i>Nature Communications</i> , 2013, 4, 2928.	5.8	31
117	Traces of sub-Saharan and Middle Eastern lineages in Indian Muslim populations. <i>European Journal of Human Genetics</i> , 2010, 18, 354-363.	1.4	30
118	The genetic legacy of continental scale admixture in Indian Austroasiatic speakers. <i>Scientific Reports</i> , 2019, 9, 3818.	1.6	30
119	Rare mtDNA haplogroups and genetic differences in rich and poor Danish Iron Age villages. <i>American Journal of Physical Anthropology</i> , 2008, 135, 206-215.	2.1	29
120	Evaluation of the 124-plex SNP typing microarray for forensic testing. <i>Forensic Science International: Genetics</i> , 2009, 4, 43-48.	1.6	29
121	The Phylogeography of Y-Chromosome Haplogroup H1a1a-M82 Reveals the Likely Indian Origin of the European Romani Populations. <i>PLoS ONE</i> , 2012, 7, e48477.	1.1	29
122	Evidence of Early-Stage Selection on EPAS1 and GPR126 Genes in Andean High Altitude Populations. <i>Scientific Reports</i> , 2017, 7, 13042.	1.6	29
123	“Like sugar in milk” reconstructing the genetic history of the Parsi population. <i>Genome Biology</i> , 2017, 18, 110.	3.8	29
124	The Influence of Natural Barriers in Shaping the Genetic Structure of Maharashtra Populations. <i>PLoS ONE</i> , 2010, 5, e15283.	1.1	29
125	East Anglian early Neolithic monument burial linked to contemporary Megaliths. <i>Annals of Human Biology</i> , 2019, 46, 145-149.	0.4	28
126	Genetic diversity and evidence for population admixture in Batak Negritos from Palawan. <i>American Journal of Physical Anthropology</i> , 2011, 146, 62-72.	2.1	27

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127	Mitochondrial genes and schizophrenia. <i>Schizophrenia Research</i> , 2005, 72, 267-269.	1.1	26
128	The evidence of mtDNA haplogroup F in a European population and its ethnohistoric implications. <i>European Journal of Human Genetics</i> , 2001, 9, 717-723.	1.4	25
129	The population history of the Croatian linguistic minority of Molise (southern Italy): a maternal view. <i>European Journal of Human Genetics</i> , 2005, 13, 902-912.	1.4	25
130	Origin and spread of human mitochondrial DNA haplogroup U7. <i>Scientific Reports</i> , 2017, 7, 46044.	1.6	25
131	Explaining the Imperfection of the Molecular Clock of Hominid Mitochondria. <i>PLoS ONE</i> , 2009, 4, e8260.	1.1	25
132	Quality Assessment of DNA Sequence Data: Autopsy of A Mis-Sequenced mtDNA Population Sample. <i>Annals of Human Genetics</i> , 2008, 70, 314-326.	0.3	24
133	Language Shift by Indigenous Population: A Model Genetic Study in South Asia. <i>International Journal of Human Genetics</i> , 2008, 8, 41-50.	0.1	24
134	Evidence of Authentic DNA from Danish Viking Age Skeletons Untouched by Humans for 1,000 Years. <i>PLoS ONE</i> , 2008, 3, e2214.	1.1	24
135	Global Patterns of Diversity and Selection in Human Tyrosinase Gene. <i>PLoS ONE</i> , 2013, 8, e74307.	1.1	21
136	Ancestry-Specific Analyses Reveal Differential Demographic Histories and Opposite Selective Pressures in Modern South Asian Populations. <i>Molecular Biology and Evolution</i> , 2019, 36, 1628-1642.	3.5	20
137	Response to Comment on "Reconstructing the Origin of Andaman Islanders". <i>Science</i> , 2006, 311, 470b-470b.	6.0	18
138	A general linear model-based approach for inferring selection to climate. <i>BMC Genetics</i> , 2013, 14, 87.	2.7	18
139	Genetic and phenotypic differentiation of an Andean intermediate altitude population. <i>Physiological Reports</i> , 2015, 3, e12376.	0.7	18
140	Refining the Use of Linkage Disequilibrium as a Robust Signature of Selective Sweeps. <i>Genetics</i> , 2016, 203, 1807-1825.	1.2	18
141	Different population histories of the Mundari- and Mon-Khmer-speaking Austro-Asiatic tribes inferred from the mtDNA 9-bp deletion/insertion polymorphism in Indian populations. <i>Human Genetics</i> , 2006, 119, 223-224.	1.8	17
142	Unravelling the distinct strains of Tharu ancestry. <i>European Journal of Human Genetics</i> , 2014, 22, 1404-1412.	1.4	17
143	Early Alpine occupation backdates westward human migration in Late Glacial Europe. <i>Current Biology</i> , 2021, 31, 2484-2493.e7.	1.8	17
144	West Asian sources of the Eurasian component in Ethiopians: a reassessment. <i>Scientific Reports</i> , 2019, 9, 18811.	1.6	14

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145	Reply to Cordaux and Stoneking. <i>American Journal of Human Genetics</i> , 2003, 72, 1590-1593.	2.6	13
146	The Pioneer Settlement of Modern Humans in Asia. , 2006, , 181-199.		13
147	An invasive <i>Haemophilus influenzae</i> serotype b infection in an Anglo-Saxon plague victim. <i>Genome Biology</i> , 2022, 23, 22.	3.8	13
148	Questioning evidence for recombination in human mitochondrial DNA. <i>Science</i> , 2000, 288, 1931.	6.0	13
149	The Trans-Caucasus and the Expansion of the Caucasoid-Specific Human Mitochondrial DNA. , 1999, , 121-133.		12
150	Decreased Rate of Evolution in Y Chromosome STR Loci of Increased Size of the Repeat Unit. <i>PLoS ONE</i> , 2009, 4, e7276.	1.1	12
151	Evolution of the Pygmy Phenotype: Evidence of Positive Selection from Genome-wide Scans in African, Asian, and Melanesian Pygmies. <i>Human Biology</i> , 2013, 85, 251.	0.4	12
152	Patterns of genetic connectedness between modern and medieval Estonian genomes reveal the origins of a major ancestry component of the Finnish population. <i>American Journal of Human Genetics</i> , 2021, 108, 1792-1806.	2.6	11
153	High Prevalence of The CCR5 Δ 32 HIV-Resistance Mutation among Estonian HIV Type 1-Infected Individuals. <i>AIDS Research and Human Retroviruses</i> , 2007, 23, 193-197.	0.5	9
154	The Genetic Origin of Daunians and the Pan-Mediterranean Southern Italian Iron Age Context. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	9
155	Reply to Silva et al.. <i>American Journal of Human Genetics</i> , 2003, 72, 1348-1349.	2.6	7
156	The World mtDNA Phylogeny. , 2006, , 149-179.		7
157	A Model for the Dispersal of Modern Humans out of Africa. , 2006, , 225-265.		6
158	The unresolved location of A-tzi's mtDNA within haplogroup K. <i>American Journal of Physical Anthropology</i> , 2007, 132, 590-591.	2.1	6
159	Continental-scale genomic analysis suggests shared post-admixture adaptation in the Americas. <i>Human Molecular Genetics</i> , 2021, 30, 2123-2134.	1.4	6
160	Lab-Specific Mutation Processes. , 2006, , 117-146.		5
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