

# Toomas Kivisild

## List of Publications by Year in descending order

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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 Genetic Origin of Daunians and the Pan-Mediterranean Southern Italian Iron Age Context. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	9
2	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
3	Response to Wyckelsma etÂal.: Loss of Î±-actinin-3 during human evolution provides superior cold resilience and muscle heat generation. <i>American Journal of Human Genetics</i> , 2022, 109, 967-972.	2.6	4
4	Dissecting the paternal founders of Mundari (Austroasiatic) speakers associated with the language dispersal in South Asia. <i>European Journal of Human Genetics</i> , 2021, 29, 528-532.	1.4	2
5	Genetic ancestry changes in Stone to Bronze Age transition in the East European plain. <i>Science Advances</i> , 2021, 7, .	4.7	32
6	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
7	Early Alpine occupation backdates westward human migration in Late Glacial Europe. <i>Current Biology</i> , 2021, 31, 2484-2493.e7.	1.8	17
8	Continental-scale genomic analysis suggests shared post-admixture adaptation in the Americas. <i>Human Molecular Genetics</i> , 2021, 30, 2123-2134.	1.4	6
9	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
10	Evaluating genotype imputation pipeline for ultra-low coverage ancient genomes. <i>Scientific Reports</i> , 2020, 10, 18542.	1.6	60
11	<i>Anthropological Genetics.</i> , 2020, , 430-444.		0
12	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
13	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
14	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
15	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
16	East Anglian early Neolithic monument burial linked to contemporary Megaliths. <i>Annals of Human Biology</i> , 2019, 46, 145-149.	0.4	28
17	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
18	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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19	Genetic Variation and the Colonization of Eurasia. , 2019, , 151-164.		0
20	The genetic legacy of continental scale admixture in Indian Austroasiatic speakers. Scientific Reports, 2019, 9, 3818.	1.6	30
21	Ancestry-Specific Analyses Reveal Differential Demographic Histories and Opposite Selective Pressures in Modern South Asian Populations. Molecular Biology and Evolution, 2019, 36, 1628-1642.	3.5	20
22	West Asian sources of the Eurasian component in Ethiopians: a reassessment. Scientific Reports, 2019, 9, 18811.	1.6	14
23	Evaluating macroscopic sex estimation methods using genetically sexed archaeological material: The medieval skeletal collection from St John's Divinity School, Cambridge. American Journal of Physical Anthropology, 2019, 168, 340-351.	2.1	35
24	Y Chromosome Sequences Reveal a Short Beringian Standstill, Rapid Expansion, and early Population structure of Native American Founders. Current Biology, 2019, 29, 149-157.e3.	1.8	94
25	The Genomic Impact of European Colonization of the Americas. Current Biology, 2019, 29, 3974-3986.e4.	1.8	89
26	Response to Glem. American Journal of Human Genetics, 2018, 102, 331.	2.6	1
27	The Genetic Ancestry of Modern Indus Valley Populations from Northwest India. American Journal of Human Genetics, 2018, 103, 918-929.	2.6	38
28	Genes reveal traces of common recent demographic history for most of the Uralic-speaking populations. Genome Biology, 2018, 19, 139.	3.8	67
29	Ancient human parallel lineages within North America contributed to a coastal expansion. Science, 2018, 360, 1024-1027.	6.0	138
30	Anthropological Genetics. , 2018, , 1-14.		0
31	Validity of visceral adiposity estimates from DXA against MRI in Kuwaiti men and women. Nutrition and Diabetes, 2017, 7, e238-e238.	1.5	48
32	The study of human Y chromosome variation through ancient DNA. Human Genetics, 2017, 136, 529-546.	1.8	72
33	Origin and spread of human mitochondrial DNA haplogroup U7. Scientific Reports, 2017, 7, 46044.	1.6	25
34	Evidence of Early-Stage Selection on EPAS1 and GPR126 Genes in Andean High Altitude Populations. Scientific Reports, 2017, 7, 13042.	1.6	29
35	Extensive Farming in Estonia Started through a Sex-Biased Migration from the Steppe. Current Biology, 2017, 27, 2185-2193.e6.	1.8	111
36	Continuity and Admixture in the Last Five Millennia of Levantine History from Ancient Canaanite and Present-Day Lebanese Genome Sequences. American Journal of Human Genetics, 2017, 101, 274-282.	2.6	102

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37	“Like sugar in milk” reconstructing the genetic history of the Parsi population. <i>Genome Biology</i> , 2017, 18, 110.	3.8	29
38	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
39	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
40	Genomic insights into the peopling of the Southwest Pacific. <i>Nature</i> , 2016, 538, 510-513.	13.7	262
41	Refining the Use of Linkage Disequilibrium as a Robust Signature of Selective Sweeps. <i>Genetics</i> , 2016, 203, 1807-1825.	1.2	18
42	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. <i>Nature</i> , 2016, 538, 201-206.	13.7	1,216
43	Genomic analyses inform on migration events during the peopling of Eurasia. <i>Nature</i> , 2016, 538, 238-242.	13.7	360
44	Selective sweep on human amylase genes postdates the split with Neanderthals. <i>Scientific Reports</i> , 2016, 6, 37198.	1.6	67
45	Multi-layered population structure in Island Southeast Asians. <i>European Journal of Human Genetics</i> , 2016, 24, 1605-1611.	1.4	50
46	Genetic and phenotypic differentiation of an Andean intermediate altitude population. <i>Physiological Reports</i> , 2015, 3, e12376.	0.7	18
47	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
48	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
49	The Genetic Legacy of the Expansion of Turkic-Speaking Nomads across Eurasia. <i>PLoS Genetics</i> , 2015, 11, e1005068.	1.5	149
50	Global diversity, population stratification, and selection of human copy-number variation. <i>Science</i> , 2015, 349, aab3761.	6.0	293
51	Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015, 349, aab3884.	6.0	449
52	Maternal ancestry and population history from whole mitochondrial genomes. <i>Investigative Genetics</i> , 2015, 6, 3.	3.3	94
53	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
54	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

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55	The phylogenetic and geographic structure of Y-chromosome haplogroup R1a. <i>European Journal of Human Genetics</i> , 2015, 23, 124-131.	1.4	122
56	Genome-Wide Analysis of Cold Adaptation in Indigenous Siberian Populations. <i>PLoS ONE</i> , 2014, 9, e98076.	1.1	128
57	Unravelling the distinct strains of Tharu ancestry. <i>European Journal of Human Genetics</i> , 2014, 22, 1404-1412.	1.4	17
58	Genome-wide evidence of Austronesian-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
59	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , 2014, 505, 87-91.	13.7	821
60	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
61	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , 2014, 513, 409-413.	13.7	1,179
62	The genetic prehistory of the New World Arctic. <i>Science</i> , 2014, 345, 1255832.	6.0	264
63	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
64	Variation at Diabetes- and Obesity-Associated Loci May Mirror Neutral Patterns of Human Population Diversity and Diabetes Prevalence in India. <i>Annals of Human Genetics</i> , 2013, 77, 392-408.	0.3	3
65	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
66	A general linear model-based approach for inferring selection to climate. <i>BMC Genetics</i> , 2013, 14, 87.	2.7	18
67	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
68	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
69	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
70	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
71	Brief communication: Effect of nomadic subsistence practices on lactase persistence associated genetic variation in Kuwait. <i>American Journal of Physical Anthropology</i> , 2013, 152, 140-144.	2.1	1
72	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

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73	Global Patterns of Diversity and Selection in Human Tyrosinase Gene. PLoS ONE, 2013, 8, e74307.	1.1	21
74	Herders of Indian and European Cattle Share Their Predominant Allele for Lactase Persistence. Molecular Biology and Evolution, 2012, 29, 249-260.	3.5	67
75	Divorcing the Late Upper Palaeolithic demographic histories of mtDNA haplogroups M1 and U6 in Africa. BMC Evolutionary Biology, 2012, 12, 234.	3.2	48
76	The Caucasus as an Asymmetric Semipermeable Barrier to Ancient Human Migrations. Molecular Biology and Evolution, 2012, 29, 1891-1891.	3.5	2
77	The Phylogeography of Y-Chromosome Haplogroup H1a1a-M82 Reveals the Likely Indian Origin of the European Romani Populations. PLoS ONE, 2012, 7, e48477.	1.1	29
78	Distinguishing the co-ancestries of haplogroup G Y-chromosomes in the populations of Europe and the Caucasus. European Journal of Human Genetics, 2012, 20, 1275-1282.	1.4	74
79	The Caucasus as an Asymmetric Semipermeable Barrier to Ancient Human Migrations. Molecular Biology and Evolution, 2012, 29, 359-365.	3.5	161
80	A "Copernican" Reassessment of the Human Mitochondrial DNA Tree from its Root. American Journal of Human Genetics, 2012, 90, 675-684.	2.6	416
81	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
82	Shared and Unique Components of Human Population Structure and Genome-Wide Signals of Positive Selection in South Asia. American Journal of Human Genetics, 2012, 90, 378-379.	2.6	1
83	A "Copernican" Reassessment of the Human Mitochondrial DNA Tree from Its Root. American Journal of Human Genetics, 2012, 90, 936.	2.6	5
84	A major Y-chromosome haplogroup R1b Holocene era founder effect in Central and Western Europe. European Journal of Human Genetics, 2011, 19, 95-101.	1.4	224
85	An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. Science, 2011, 334, 94-98.	6.0	675
86	Shared and Unique Components of Human Population Structure and Genome-Wide Signals of Positive Selection in South Asia. American Journal of Human Genetics, 2011, 89, 731-744.	2.6	149
87	Genetic diversity and evidence for population admixture in Batak Negritos from Palawan. American Journal of Physical Anthropology, 2011, 146, 62-72.	2.1	27
88	Population Genetic Structure in Indian Austroasiatic Speakers: The Role of Landscape Barriers and Sex-Specific Admixture. Molecular Biology and Evolution, 2011, 28, 1013-1024.	3.5	135
89	The emergence of Y-chromosome haplogroup J1e among Arabic-speaking populations. European Journal of Human Genetics, 2010, 18, 348-353.	1.4	71
90	Traces of sub-Saharan and Middle Eastern lineages in Indian Muslim populations. European Journal of Human Genetics, 2010, 18, 354-363.	1.4	30

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91	Ancient human genome sequence of an extinct Palaeo-Eskimo. <i>Nature</i> , 2010, 463, 757-762.	13.7	750
92	Genetic Diversity among Ancient Nordic Populations. <i>PLoS ONE</i> , 2010, 5, e11898.	1.1	34
93	Philippine Mitochondrial DNA Diversity: A Populated Viaduct between Taiwan and Indonesia?. <i>Molecular Biology and Evolution</i> , 2010, 27, 1736-1737.	3.5	0
94	Philippine Mitochondrial DNA Diversity: A Populated Viaduct between Taiwan and Indonesia?. <i>Molecular Biology and Evolution</i> , 2010, 27, 21-31.	3.5	121
95	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
96	The genetic structure of south Asian populations as revealed by 650 000 SNPs. <i>Genome Biology</i> , 2010, 11, 08.	13.9	0
97	The Influence of Natural Barriers in Shaping the Genetic Structure of Maharashtra Populations. <i>PLoS ONE</i> , 2010, 5, e15283.	1.1	29
98	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
99	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
100	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
101	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
102	Validation of microarray-based resequencing of 93 worldwide mitochondrial genomes. <i>Human Mutation</i> , 2009, 30, 115-122.	1.1	83
103	P17-11. HIV DNA vaccine delivery in association with electroporation in the skin of nonhuman primates. <i>Retrovirology</i> , 2009, 6, .	0.9	0
104	Evaluation of the 124-plex SNP typing microarray for forensic testing. <i>Forensic Science International: Genetics</i> , 2009, 4, 43-48.	1.6	29
105	Explaining the Imperfection of the Molecular Clock of Hominid Mitochondria. <i>PLoS ONE</i> , 2009, 4, e8260.	1.1	25
106	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
107	Paleo-Eskimo mtDNA Genome Reveals Matrilineal Discontinuity in Greenland. <i>Science</i> , 2008, 320, 1787-1789.	6.0	184
108	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

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109	Phylogeography of mtDNA haplogroup R7 in the Indian peninsula. <i>BMC Evolutionary Biology</i> , 2008, 8, 227.	3.2	45
110	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
111	Maternal Footprints of Southeast Asians in North India. <i>Human Heredity</i> , 2008, 66, 1-9.	0.4	43
112	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
113	Counting the Founders: The Matrilineal Genetic Ancestry of the Jewish Diaspora. <i>PLoS ONE</i> , 2008, 3, e2062.	1.1	101
114	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
115	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
116	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
117	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
118	High Prevalence of The CCR5 $\Delta$ 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
119	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
120	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
121	An mtDNA perspective of French genetic variation. <i>Annals of Human Biology</i> , 2007, 34, 68-79.	0.4	55
122	Peopling of South Asia: investigating the caste $\leftrightarrow$ tribe continuum in India. <i>BioEssays</i> , 2007, 29, 91-100.	1.2	79
123	Reply to Winters. <i>BioEssays</i> , 2007, 29, 499-499.	1.2	2
124	The unresolved location of $\Delta$ -tzi's mtDNA within haplogroup K. <i>American Journal of Physical Anthropology</i> , 2007, 132, 590-591.	2.1	6
125	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
126	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



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127	Beringian Standstill and Spread of Native American Founders. PLoS ONE, 2007, 2, e829.	1.1	499
128	A Model for the Dispersal of Modern Humans out of Africa. , 2006, , 225-265.		6
129	The World mtDNA Phylogeny. , 2006, , 149-179.		7
130	The Matrilineal Ancestry of Ashkenazi Jewry: Portrait of a Recent Founder Event. American Journal of Human Genetics, 2006, 78, 487-497.	2.6	140
131	A prehistory of Indian Y chromosomes: Evaluating demic diffusion scenarios. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 843-848.	3.3	135
132	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. Human Genetics, 2006, 119, 223-224.	1.8	17
133	Response to Comment on "Reconstructing the Origin of Andaman Islanders". Science, 2006, 311, 470b-470b.	6.0	18
134	Lab-Specific Mutation Processes. , 2006, , 117-146.		5
135	The Pioneer Settlement of Modern Humans in Asia. , 2006, , 181-199.		13
136	The Role of Selection in the Evolution of Human Mitochondrial Genomes. Genetics, 2006, 172, 373-387.	1.2	395
137	Y-chromosome Lineages from Portugal, Madeira and Açores Record Elements of Sephardim and Berber Ancestry. Annals of Human Genetics, 2005, 69, 443-454.	0.3	56
138	The population history of the Croatian linguistic minority of Molise (southern Italy): a maternal view. European Journal of Human Genetics, 2005, 13, 902-912.	1.4	25
139	What evidence is there for the existence of individual genes with antagonistic pleiotropic effects?. Mechanisms of Ageing and Development, 2005, 126, 421-429.	2.2	109
140	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. Human Genetics, 2005, 116, 507-517.	1.8	60
141	Traces of Archaic Mitochondrial Lineages Persist in Austronesian-Speaking Formosan Populations. PLoS Biology, 2005, 3, e247.	2.6	178
142	Reconstructing the Origin of Andaman Islanders. Science, 2005, 308, 996-996.	6.0	291
143	Mitochondrial genes and schizophrenia. Schizophrenia Research, 2005, 72, 267-269.	1.1	26
144	Disuniting Uniformity: A Pied Cladistic Canvas of mtDNA Haplogroup H in Eurasia. Molecular Biology and Evolution, 2004, 21, 2012-2021.	3.5	170

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145	Excavating Y-chromosome haplotype strata in Anatolia. <i>Human Genetics</i> , 2004, 114, 127-148.	1.8	318
146	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
147	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
148	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
149	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
150	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
151	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
152	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
153	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
154	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
155	Mitochondrial portraits of the Madeira and Azores archipelagos witness different genetic pools of its settlers. <i>Human Genetics</i> , 2003, 114, 77-86.	1.8	32
156	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
157	Y chromosomal heritage of Croatian population and its island isolates. <i>European Journal of Human Genetics</i> , 2003, 11, 535-542.	1.4	66
158	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
159	Reply to Silva et al.. <i>American Journal of Human Genetics</i> , 2003, 72, 1348-1349.	2.6	7
160	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
161	Reply to Cordaux and Stoneking. <i>American Journal of Human Genetics</i> , 2003, 72, 1590-1593.	2.6	13
162	Origin and Diffusion of mtDNA Haplogroup X. <i>American Journal of Human Genetics</i> , 2003, 73, 1178-1190.	2.6	148

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163	The Emerging Limbs and Twigs of the East Asian mtDNA Tree. <i>Molecular Biology and Evolution</i> , 2002, 19, 1737-1751.	3.5	360
164	Phylogeographic Differentiation of Mitochondrial DNA in Han Chinese. <i>American Journal of Human Genetics</i> , 2002, 70, 635-651.	2.6	491
165	A Signal, from Human mtDNA, of Postglacial Recolonization in Europe. <i>American Journal of Human Genetics</i> , 2001, 69, 844-852.	2.6	267
166	Genetic Evidence on the Origins of Indian Caste Populations. <i>Genome Research</i> , 2001, 11, 994-1004.	2.4	359
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