

David Reich

List of Publications by Year in descending order

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Version: 2024-02-01

154
papers

55,299
citations

8181

76
h-index

6654

156
g-index

187
all docs

187
docs citations

187
times ranked

44614
citing authors

#	ARTICLE	IF	CITATIONS
1	Principal components analysis corrects for stratification in genome-wide association studies. <i>Nature Genetics</i> , 2006, 38, 904-909.	21.4	8,889
2	Population Structure and Eigenanalysis. <i>PLoS Genetics</i> , 2006, 2, e190.	3.5	4,163
3	A Draft Sequence of the Neandertal Genome. <i>Science</i> , 2010, 328, 710-722.	12.6	3,588
4	Ancient Admixture in Human History. <i>Genetics</i> , 2012, 192, 1065-1093.	2.9	2,012
5	The complete genome sequence of a Neanderthal from the Altai Mountains. <i>Nature</i> , 2014, 505, 43-49.	27.8	1,830
6	A High-Coverage Genome Sequence from an Archaic Denisovan Individual. <i>Science</i> , 2012, 338, 222-226.	12.6	1,695
7	Genetic history of an archaic hominin group from Denisova Cave in Siberia. <i>Nature</i> , 2010, 468, 1053-1060.	27.8	1,537
8	Reconstructing Indian population history. <i>Nature</i> , 2009, 461, 489-494.	27.8	1,442
9	Massive migration from the steppe was a source for Indo-European languages in Europe. <i>Nature</i> , 2015, 522, 207-211.	27.8	1,435
10	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. <i>Nature</i> , 2016, 538, 201-206.	27.8	1,216
11	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , 2014, 513, 409-413.	27.8	1,179
12	Genome-wide patterns of selection in 230 ancient Eurasians. <i>Nature</i> , 2015, 528, 499-503.	27.8	1,160
13	Testing for Ancient Admixture between Closely Related Populations. <i>Molecular Biology and Evolution</i> , 2011, 28, 2239-2252.	8.9	1,078
14	Cost-effective, high-throughput DNA sequencing libraries for multiplexed target capture. <i>Genome Research</i> , 2012, 22, 939-946.	5.5	976
15	The genomic landscape of Neanderthal ancestry in present-day humans. <i>Nature</i> , 2014, 507, 354-357.	27.8	877
16	Genome sequence of a 45,000-year-old modern human from western Siberia. <i>Nature</i> , 2014, 514, 445-449.	27.8	856
17	Genomic insights into the origin of farming in the ancient Near East. <i>Nature</i> , 2016, 536, 419-424.	27.8	733
18	The genetic history of Ice Age Europe. <i>Nature</i> , 2016, 534, 200-205.	27.8	729

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19	Reconstructing Native American population history. <i>Nature</i> , 2012, 488, 370-374.	27.8	699
20	An early modern human from Romania with a recent Neanderthal ancestor. <i>Nature</i> , 2015, 524, 216-219.	27.8	633
21	A Revised Timescale for Human Evolution Based on Ancient Mitochondrial Genomes. <i>Current Biology</i> , 2013, 23, 553-559.	3.9	540
22	Insights into human genetic variation and population history from 929 diverse genomes. <i>Science</i> , 2020, 367, .	12.6	534
23	Denisova Admixture and the First Modern Human Dispersals into Southeast Asia and Oceania. <i>American Journal of Human Genetics</i> , 2011, 89, 516-528.	6.2	525
24	The Genetic Ancestry of African Americans, Latinos, and European Americans across the United States. <i>American Journal of Human Genetics</i> , 2015, 96, 37-53.	6.2	516
25	The Beaker phenomenon and the genomic transformation of northwest Europe. <i>Nature</i> , 2018, 555, 190-196.	27.8	503
26	A high-coverage Neandertal genome from Vindija Cave in Croatia. <i>Science</i> , 2017, 358, 655-658.	12.6	501
27	The genomic history of southeastern Europe. <i>Nature</i> , 2018, 555, 197-203.	27.8	479
28	Inferring Admixture Histories of Human Populations Using Linkage Disequilibrium. <i>Genetics</i> , 2013, 193, 1233-1254.	2.9	445
29	Methods for High-Density Admixture Mapping of Disease Genes. <i>American Journal of Human Genetics</i> , 2004, 74, 979-1000.	6.2	437
30	The formation of human populations in South and Central Asia. <i>Science</i> , 2019, 365, .	12.6	383
31	Partial uracilâ€“DNAâ€“glycosylase treatment for screening of ancient DNA. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130624.	4.0	381
32	The Combined Landscape of Denisovan and Neanderthal Ancestry in Present-Day Humans. <i>Current Biology</i> , 2016, 26, 1241-1247.	3.9	377
33	Genetic evidence for two founding populations of the Americas. <i>Nature</i> , 2015, 525, 104-108.	27.8	348
34	The genomic history of the Iberian Peninsula over the past 8000 years. <i>Science</i> , 2019, 363, 1230-1234.	12.6	340
35	Reduced Neutrophil Count in People of African Descent Is Due To a Regulatory Variant in the Duffy Antigen Receptor for Chemokines Gene. <i>PLoS Genetics</i> , 2009, 5, e1000360.	3.5	335
36	Gibbon genome and the fast karyotype evolution of small apes. <i>Nature</i> , 2014, 513, 195-201.	27.8	320

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37	The landscape of recombination in African Americans. <i>Nature</i> , 2011, 476, 170-175.	27.8	319
38	Reconstructing Prehistoric African Population Structure. <i>Cell</i> , 2017, 171, 59-71.e21.	28.9	308
39	Ancient mitochondrial DNA provides high-resolution time scale of the peopling of the Americas. <i>Science Advances</i> , 2016, 2, e1501385.	10.3	306
40	Parallel palaeogenomic transects reveal complex genetic history of early European farmers. <i>Nature</i> , 2017, 551, 368-372.	27.8	306
41	Ancient DNA Reveals Key Stages in the Formation of Central European Mitochondrial Genetic Diversity. <i>Science</i> , 2013, 342, 257-261.	12.6	293
42	Global diversity, population stratification, and selection of human copy-number variation. <i>Science</i> , 2015, 349, aab3761.	12.6	293
43	Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies. <i>ELife</i> , 2019, 8, .	6.0	276
44	The genetic prehistory of southern Africa. <i>Nature Communications</i> , 2012, 3, 1143.	12.8	271
45	Complete Genomes Reveal Signatures of Demographic and Genetic Declines in the Woolly Mammoth. <i>Current Biology</i> , 2015, 25, 1395-1400.	3.9	263
46	Genomic insights into the peopling of the Southwest Pacific. <i>Nature</i> , 2016, 538, 510-513.	27.8	262
47	Reconstructing the Deep Population History of Central and South America. <i>Cell</i> , 2018, 175, 1185-1197.e22.	28.9	259
48	Ancient genomes document multiple waves of migration in Southeast Asian prehistory. <i>Science</i> , 2018, 361, 92-95.	12.6	250
49	Measurement of the human allele frequency spectrum demonstrates greater genetic drift in East Asians than in Europeans. <i>Nature Genetics</i> , 2007, 39, 1251-1255.	21.4	249
50	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.	7.1	246
51	A whole-genome admixture scan finds a candidate locus for multiple sclerosis susceptibility. <i>Nature Genetics</i> , 2005, 37, 1113-1118.	21.4	243
52	Genetic Evidence for Recent Population Mixture in India. <i>American Journal of Human Genetics</i> , 2013, 93, 422-438.	6.2	234
53	Toward a new history and geography of human genes informed by ancient DNA. <i>Trends in Genetics</i> , 2014, 30, 377-389.	6.7	227
54	The History of African Gene Flow into Southern Europeans, Levantines, and Jews. <i>PLoS Genetics</i> , 2011, 7, e1001373.	3.5	224

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55	Genomic insights into the formation of human populations in East Asia. <i>Nature</i> , 2021, 591, 413-419.	27.8	216
56	Ancient DNA indicates human population shifts and admixture in northern and southern China. <i>Science</i> , 2020, 369, 282-288.	12.6	214
57	Archaeogenomic evidence reveals prehistoric matrilineal dynasty. <i>Nature Communications</i> , 2017, 8, 14115.	12.8	210
58	Genetic origins of the Minoans and Mycenaeans. <i>Nature</i> , 2017, 548, 214-218.	27.8	203
59	Reconstructing the genetic history of late Neanderthals. <i>Nature</i> , 2018, 555, 652-656.	27.8	197
60	No evidence that selection has been less effective at removing deleterious mutations in Europeans than in Africans. <i>Nature Genetics</i> , 2015, 47, 126-131.	21.4	182
61	Admixture Mapping of an Allele Affecting Interleukin 6 Soluble Receptor and Interleukin 6 Levels. <i>American Journal of Human Genetics</i> , 2007, 80, 716-726.	6.2	160
62	Reconstructing Austronesian population history in Island Southeast Asia. <i>Nature Communications</i> , 2014, 5, 4689.	12.8	158
63	Ancient genomes indicate population replacement in Early Neolithic Britain. <i>Nature Ecology and Evolution</i> , 2019, 3, 765-771.	7.8	156
64	The genetic prehistory of the Baltic Sea region. <i>Nature Communications</i> , 2018, 9, 442.	12.8	151
65	A comprehensive genomic history of extinct and living elephants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2566-E2574.	7.1	142
66	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.	7.1	141
67	The contribution of rare variation to prostate cancer heritability. <i>Nature Genetics</i> , 2016, 48, 30-35.	21.4	139
68	The genetic history of admixture across inner Eurasia. <i>Nature Ecology and Evolution</i> , 2019, 3, 966-976.	7.8	135
69	The promise of discovering population-specific disease-associated genes in South Asia. <i>Nature Genetics</i> , 2017, 49, 1403-1407.	21.4	129
70	Efficient Moment-Based Inference of Admixture Parameters and Sources of Gene Flow. <i>Molecular Biology and Evolution</i> , 2013, 30, 1788-1802.	8.9	121
71	Palaeo-Eskimo genetic ancestry and the peopling of Chukotka and North America. <i>Nature</i> , 2019, 570, 236-240.	27.8	118
72	Current evidence allows multiple models for the peopling of the Americas. <i>Science Advances</i> , 2018, 4, eaat5473.	10.3	114

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73	Ancient human genome-wide data from a 3000-year interval in the Caucasus corresponds with eco-geographic regions. <i>Nature Communications</i> , 2019, 10, 590.	12.8	113
74	A genomic view of the peopling of the Americas. <i>Current Opinion in Genetics and Development</i> , 2016, 41, 27-35.	3.3	103
75	Ancestry and demography and descendants of Iron Age nomads of the Eurasian Steppe. <i>Nature Communications</i> , 2017, 8, 14615.	12.8	96
76	Ancient DNA reveals a multistep spread of the first herders into sub-Saharan Africa. <i>Science</i> , 2019, 365, .	12.6	96
77	Genetic history from the Middle Neolithic to present on the Mediterranean island of Sardinia. <i>Nature Communications</i> , 2020, 11, 939.	12.8	96
78	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.	7.8	95
79	Non-crossover gene conversions show strong GC bias and unexpected clustering in humans. <i>ELife</i> , 2015, 4, .	6.0	95
80	Population Turnover in Remote Oceania Shortly after Initial Settlement. <i>Current Biology</i> , 2018, 28, 1157-1165.e7.	3.9	91
81	Differences in the rare variant spectrum among human populations. <i>PLoS Genetics</i> , 2017, 13, e1006581.	3.5	88
82	Natural hybridization reveals incompatible alleles that cause melanoma in swordtail fish. <i>Science</i> , 2020, 368, 731-736.	12.6	86
83	Ancient West African foragers in the context of African population history. <i>Nature</i> , 2020, 577, 665-670.	27.8	86
84	Large-scale migration into Britain during the Middle to Late Bronze Age. <i>Nature</i> , 2022, 601, 588-594.	27.8	86
85	African evolutionary history inferred from whole genome sequence data of 44 indigenous African populations. <i>Genome Biology</i> , 2019, 20, 82.	8.8	84
86	Assessing the performance of qpAdm: a statistical tool for studying population admixture. <i>Genetics</i> , 2021, 217, .	2.9	84
87	Will admixture mapping work to find disease genes?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2005, 360, 1605-1607.	4.0	78
88	Dominance of Deleterious Alleles Controls the Response to a Population Bottleneck. <i>PLoS Genetics</i> , 2015, 11, e1005436.	3.5	78
89	Interpreting short tandem repeat variations in humans using mutational constraint. <i>Nature Genetics</i> , 2017, 49, 1495-1501.	21.4	78
90	Extreme selective sweeps independently targeted the X chromosomes of the great apes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6413-6418.	7.1	75

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91	Ancient DNA from Chalcolithic Israel reveals the role of population mixture in cultural transformation. <i>Nature Communications</i> , 2018, 9, 3336.	12.8	71
92	Leveraging population admixture to characterize the heritability of complex traits. <i>Nature Genetics</i> , 2014, 46, 1356-1362.	21.4	69
93	Genome-wide Scan of 29,141 African Americans Finds No Evidence of Directional Selection since Admixture. <i>American Journal of Human Genetics</i> , 2014, 95, 437-444.	6.2	69
94	Reconciling material cultures in archaeology with genetic data: The nomenclature of clusters emerging from archaeogenomic analysis. <i>Scientific Reports</i> , 2018, 8, 13003.	3.3	69
95	A Paleogenomic Reconstruction of the Deep Population History of the Andes. <i>Cell</i> , 2020, 181, 1131-1145.e21.	28.9	69
96	Differential DNA methylation of vocal and facial anatomy genes in modern humans. <i>Nature Communications</i> , 2020, 11, 1189.	12.8	69
97	A genetic history of the pre-contact Caribbean. <i>Nature</i> , 2021, 590, 103-110.	27.8	67
98	A high-resolution picture of kinship practices in an Early Neolithic tomb. <i>Nature</i> , 2022, 601, 584-587.	27.8	65
99	An Ancient Harappan Genome Lacks Ancestry from Steppe Pastoralists or Iranian Farmers. <i>Cell</i> , 2019, 179, 729-735.e10.	28.9	62
100	A unified genealogy of modern and ancient genomes. <i>Science</i> , 2022, 375, eabi8264.	12.6	59
101	A working model of the deep relationships of diverse modern human genetic lineages outside of Africa. <i>Molecular Biology and Evolution</i> , 2017, 34, msw293.	8.9	55
102	The Promise of Paleogenomics Beyond Our Own Species. <i>Trends in Genetics</i> , 2019, 35, 319-329.	6.7	55
103	The Genomic History of the Bronze Age Southern Levant. <i>Cell</i> , 2020, 181, 1146-1157.e11.	28.9	51
104	Ancient DNA and deep population structure in sub-Saharan African foragers. <i>Nature</i> , 2022, 603, 290-296.	27.8	51
105	Palaeogenomes of Eurasian straight-tusked elephants challenge the current view of elephant evolution. <i>ELife</i> , 2017, 6, .	6.0	50
106	Calibrating the Human Mutation Rate via Ancestral Recombination Density in Diploid Genomes. <i>PLoS Genetics</i> , 2015, 11, e1005550.	3.5	49
107	Ethics of DNA research on human remains: five globally applicable guidelines. <i>Nature</i> , 2021, 599, 41-46.	27.8	49
108	Dairying enabled Early Bronze Age Yamnaya steppe expansions. <i>Nature</i> , 2021, 598, 629-633.	27.8	47

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109	Dynamic changes in genomic and social structures in third millennium BCE central Europe. <i>Science Advances</i> , 2021, 7, .	10.3	46
110	Arrival routes of first Americans uncertain. <i>Science</i> , 2018, 359, 1224-1225.	12.6	42
111	A Re-Appraisal of the Early Andean Human Remains from Lauricocha in Peru. <i>PLoS ONE</i> , 2015, 10, e0127141.	2.5	41
112	A multi-stage genome-wide association study of uterine fibroids in African Americans. <i>Human Genetics</i> , 2017, 136, 1363-1373.	3.8	39
113	Biological Sexing of a 4000-Year-Old Egyptian Mummy Head to Assess the Potential of Nuclear DNA Recovery from the Most Damaged and Limited Forensic Specimens. <i>Genes</i> , 2018, 9, 135.	2.4	39
114	Genomic transformation and social organization during the Copper Age–Bronze Age transition in southern Iberia. <i>Science Advances</i> , 2021, 7, eabi7038.	10.3	39
115	Human auditory ossicles as an alternative optimal source of ancient DNA. <i>Genome Research</i> , 2020, 30, 427-436.	5.5	37
116	Interactions between earliest Linearbandkeramik farmers and central European hunter gatherers at the dawn of European Neolithization. <i>Scientific Reports</i> , 2019, 9, 19544.	3.3	35
117	Kinship and social organization in Copper Age Europe. A cross-disciplinary analysis of archaeology, DNA, isotopes, and anthropology from two Bell Beaker cemeteries. <i>PLoS ONE</i> , 2020, 15, e0241278.	2.5	35
118	A minimally destructive protocol for DNA extraction from ancient teeth. <i>Genome Research</i> , 2021, 31, 472-483.	5.5	31
119	Stone Age <i>Yersinia pestis</i> genomes shed light on the early evolution, diversity, and ecology of plague. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2116722119.	7.1	31
120	ContamLD: estimation of ancient nuclear DNA contamination using breakdown of linkage disequilibrium. <i>Genome Biology</i> , 2020, 21, 199.	8.8	29
121	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 379-384.	7.1	28
122	Ancient genomes in South Patagonia reveal population movements associated with technological shifts and geography. <i>Nature Communications</i> , 2020, 11, 3868.	12.8	28
123	Three Phases of Ancient Migration Shaped the Ancestry of Human Populations in Vanuatu. <i>Current Biology</i> , 2020, 30, 4846-4856.e6.	3.9	27
124	Whole-exome sequencing of over 4100 men of African ancestry and prostate cancer risk. <i>Human Molecular Genetics</i> , 2016, 25, 371-381.	2.9	26
125	Ancient genomes reveal origin and rapid trans-Eurasian migration of 7th century Avar elites. <i>Cell</i> , 2022, 185, 1402-1413.e21.	28.9	26
126	Ancient DNA reveals monozygotic newborn twins from the Upper Palaeolithic. <i>Communications Biology</i> , 2020, 3, 650.	4.4	25

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127	Genome diversity in the Neolithic Globular Amphorae culture and the spread of Indo-European languages. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20171540.	2.6	24
128	A Late Bronze Age II clay coffin from Tel Shaddud in the Central Jezreel Valley, Israel: context and historical implications. <i>Levant</i> , 2017, 49, 105-135.	0.9	21
129	South-to-north migration preceded the advent of intensive farming in the Maya region. <i>Nature Communications</i> , 2022, 13, 1530.	12.8	21
130	An integrative skeletal and paleogenomic analysis of stature variation suggests relatively reduced health for early European farmers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2106743119.	7.1	21
131	Ancient DNA from the skeletons of Roopkund Lake reveals Mediterranean migrants in India. <i>Nature Communications</i> , 2019, 10, 3670.	12.8	19
132	Mitochondrial DNA analysis of eneolithic trypillians from Ukraine reveals neolithic farming genetic roots. <i>PLoS ONE</i> , 2017, 12, e0172952.	2.5	19
133	Indian genetic heritage in Southeast Asian populations. <i>PLoS Genetics</i> , 2022, 18, e1010036.	3.5	19
134	Failure to replicate a genetic signal for sex bias in the steppe migration into central Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3873-E3874.	7.1	18
135	Discussion: Are the Origins of Indo-European Languages Explained by the Migration of the Yamnaya Culture to the West?. <i>European Journal of Archaeology</i> , 2018, 21, 3-17.	0.5	17
136	No statistical evidence for an effect of CCR5- $\Delta 32$ on lifespan in the UK Biobank cohort. <i>Nature Medicine</i> , 2020, 26, 178-180.	30.7	16
137	The return of the Beaker folk? Rethinking migration and population change in British prehistory. <i>Antiquity</i> , 2021, 95, 1464-1477.	1.0	14
138	Social stratification without genetic differentiation at the site of Kulubnarti in Christian Period Nubia. <i>Nature Communications</i> , 2021, 12, 7283.	12.8	13
139	Ancient DNA reveals five streams of migration into Micronesia and matrilocality in early Pacific seafarers. <i>Science</i> , 2022, 377, 72-79.	12.6	13
140	Genome-wide analysis of nearly all the victims of a 6200 year old massacre. <i>PLoS ONE</i> , 2021, 16, e0247332.	2.5	11
141	Ancient mitochondrial genomes from the Argentinian Pampas inform the early peopling of the Southern Cone of South America. <i>iScience</i> , 2021, 24, 102553.	4.1	11
142	African Ancestry Analysis and Admixture Genetic Mapping for Proliferative Diabetic Retinopathy in African Americans. , 2015, 56, 3999.		10
143	Two genetic variants explain the association of European ancestry with multiple sclerosis risk in African-Americans. <i>Scientific Reports</i> , 2020, 10, 16902.	3.3	10
144	Increased rate of close-kin unions in the central Andes in the half millennium before European contact. <i>Current Biology</i> , 2020, 30, R980-R981.	3.9	9

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145	Genetic landscape of Gullah African Americans. <i>American Journal of Physical Anthropology</i> , 2021, 175, 905-919.	2.1	9
146	No evidence for unknown archaic ancestry in South Asia. <i>Nature Genetics</i> , 2018, 50, 632-633.	21.4	7
147	An ancient DNA Pacific journey: a case study of collaboration between archaeologists and geneticists. <i>World Archaeology</i> , 2019, 51, 620-639.	1.1	7
148	Combining ancient DNA and radiocarbon dating data to increase chronological accuracy. <i>Journal of Archaeological Science</i> , 2021, 133, 105452.	2.4	7
149	The Kalash Genetic Isolate? The Evidence for Recent Admixture. <i>American Journal of Human Genetics</i> , 2016, 98, 396-397.	6.2	6
150	Direct dating of human skeletal material from Ganj Dareh, Early Neolithic of the Iranian Zagros. <i>Journal of Archaeological Science: Reports</i> , 2017, 12, 165-172.	0.5	4
151	Mitochondrial genome diversity on the Central Siberian Plateau with particular reference to the prehistory of northernmost Eurasia. <i>PLoS ONE</i> , 2021, 16, e0244228.	2.5	4
152	Revisiting ancient DNA insights into the human history of the Pacific Islands. <i>Archaeology in Oceania</i> , 2019, 54, 53-56.	0.7	3
153	Ancestry and demography and descendants of Iron Age nomads of the Eurasian Steppe. , 0, .		1
154	A High-Density Admixture Scan in 1,670 African Americans with Hypertension. <i>PLoS Genetics</i> , 2005, preprint, e196.	3.5	0