

The Simons Genome Diversity Project: 300 genomes from

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Archaic adaptive introgression in <i>TBX15/WARS2</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, msw283.	3.5	101
2	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016, 538, 207-214.	13.7	439
3	A map of human wanderlust. <i>Nature</i> , 2016, 538, 179-180.	13.7	25
4	Off the beaten track. <i>Nature Reviews Genetics</i> , 2016, 17, 657-657.	7.7	0
5	Tracing the peopling of the world through genomics. <i>Nature</i> , 2017, 541, 302-310.	13.7	562
6	Population and clinical genetics of human transposable elements in the (post) genomic era. <i>Mobile Genetic Elements</i> , 2017, 7, 1-20.	1.8	22
7	Fuyan human of 120±80 kya cannot challenge the Out-of-Africa theory for modern human dispersal. <i>Science Bulletin</i> , 2017, 62, 316-318.	4.3	0
8	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.	3.5	55
9	Insertions and Deletions Target Lineage-Defining Genes in Human Cancers. <i>Cell</i> , 2017, 168, 460-472.e14.	13.5	106
10	Why only us: Recent questions and answers. <i>Journal of Neurolinguistics</i> , 2017, 43, 166-177.	0.5	65
11	Population structure and infectious disease risk in southern Africa. <i>Molecular Genetics and Genomics</i> , 2017, 292, 499-509.	1.0	21
12	A genomic view of short tandem repeats. <i>Current Opinion in Genetics and Development</i> , 2017, 44, 9-16.	1.5	123
13	Diversity in non-repetitive human sequences not found in the reference genome. <i>Nature Genetics</i> , 2017, 49, 588-593.	9.4	70
14	The study of human Y chromosome variation through ancient DNA. <i>Human Genetics</i> , 2017, 136, 529-546.	1.8	72
15	Genome-wide profiling of heritable and de novo STR variations. <i>Nature Methods</i> , 2017, 14, 590-592.	9.0	240
17	Inferring Human Demographic Histories of Non-African Populations from Patterns of Allele Sharing. <i>American Journal of Human Genetics</i> , 2017, 100, 766-772.	2.6	23
18	African genomes illuminate the early history and transition to selfing in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 5213-5218.	3.3	142
19	Language without narrow syntax. <i>Linguistic Review</i> , 2017, 34, .	0.2	2

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20	The timetable of evolution. <i>Science Advances</i> , 2017, 3, e1603076.	4.7	186
21	Paleogenomic Evidence for Multi-generational Mixing between Neolithic Farmers and Mesolithic Hunter-Gatherers in the Lower Danube Basin. <i>Current Biology</i> , 2017, 27, 1801-1810.e10.	1.8	110
22	The Omo-Kibish I pelvis. <i>Journal of Human Evolution</i> , 2017, 108, 199-219.	1.3	23
23	Population genetics: The deep roots of non-Africans. <i>Nature Ecology and Evolution</i> , 2017, 1, .	3.4	0
24	Soft sweeps and beyond: understanding the patterns and probabilities of selection footprints under rapid adaptation. <i>Methods in Ecology and Evolution</i> , 2017, 8, 700-716.	2.2	235
25	The Authors Reply. <i>Kidney International</i> , 2017, 91, 989-990.	2.6	0
26	A genetic chronology for the Indian Subcontinent points to heavily sex-biased dispersals. <i>BMC Evolutionary Biology</i> , 2017, 17, 88.	3.2	59
27	Living in an adaptive world: Genomic dissection of the genus <i>Homo</i> and its immune response. <i>Journal of Experimental Medicine</i> , 2017, 214, 877-894.	4.2	34
28	Absence of APOL1 risk alleles in a remote living Australian Aboriginal group with high rates of CKD, hypertension, diabetes, and cardiovascular disease. <i>Kidney International</i> , 2017, 91, 990.	2.6	5
29	Dental phenotypic shape variation supports a multiple dispersal model for anatomically modern humans in Southeast Asia. <i>Journal of Human Evolution</i> , 2017, 112, 41-56.	1.3	18
30	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , 2017, 358, 659-662.	6.0	263
31	A high-coverage Neandertal genome from Vindija Cave in Croatia. <i>Science</i> , 2017, 358, 655-658.	6.0	501
32	The Contribution of Neanderthals to Phenotypic Variation in Modern Humans. <i>American Journal of Human Genetics</i> , 2017, 101, 578-589.	2.6	140
33	Southern African ancient genomes estimate modern human divergence to 350,000 to 260,000 years ago. <i>Science</i> , 2017, 358, 652-655.	6.0	351
34	Reconstructing Prehistoric African Population Structure. <i>Cell</i> , 2017, 171, 59-71.e21.	13.5	308
35	Genetic Ancestry of Rapanui before and after European Contact. <i>Current Biology</i> , 2017, 27, 3209-3215.e6.	1.8	25
36	40,000-Year-Old Individual from Asia Provides Insight into Early Population Structure in Eurasia. <i>Current Biology</i> , 2017, 27, 3202-3208.e9.	1.8	191
37	Loci associated with skin pigmentation identified in African populations. <i>Science</i> , 2017, 358, .	6.0	260

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38	Demographic history and biologically relevant genetic variation of Native Mexicans inferred from whole-genome sequencing. <i>Nature Communications</i> , 2017, 8, 1005.	5.8	44
39	Population Stratification in Genetic Association Studies. <i>Current Protocols in Human Genetics</i> , 2017, 95, 1.22.1-1.22.23.	3.5	108
40	Variation and Functional Impact of Neanderthal Ancestry in Western Asia. <i>Genome Biology and Evolution</i> , 2017, 9, 3516-3524.	1.1	14
41	Genetic and linguistic histories in Central Asia inferred using approximate Bayesian computations. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170706.	1.2	11
42	Interpreting short tandem repeat variations in humans using mutational constraint. <i>Nature Genetics</i> , 2017, 49, 1495-1501.	9.4	78
43	A Neolithic expansion, but strong genetic structure, in the independent history of New Guinea. <i>Science</i> , 2017, 357, 1160-1163.	6.0	45
44	Testing support for the northern and southern dispersal routes out of Africa: an analysis of Levantine and southern Arabian populations. <i>American Journal of Physical Anthropology</i> , 2017, 164, 736-749.	2.1	19
45	Population resequencing of European mitochondrial genomes highlights sex-bias in Bronze Age demographic expansions. <i>Scientific Reports</i> , 2017, 7, 12086.	1.6	23
46	Human occupation of northern Australia by 65,000 years ago. <i>Nature</i> , 2017, 547, 306-310.	13.7	691
47	Genetic adaptation to historical pathogen burdens. <i>Infection, Genetics and Evolution</i> , 2017, 54, 299-307.	1.0	7
48	The promise of discovering population-specific disease-associated genes in South Asia. <i>Nature Genetics</i> , 2017, 49, 1403-1407.	9.4	129
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50	AIDS in chimpanzees: the role of MHC genes. <i>Immunogenetics</i> , 2017, 69, 499-509.	1.2	10
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54	Precise dating of the Middle-to-Upper Paleolithic transition in Murcia (Spain) supports late Neanderthal persistence in Iberia. <i>Heliyon</i> , 2017, 3, e00435.	1.4	117
55	Archaic Hominin Populations in Asia before the Arrival of Modern Humans. <i>Current Anthropology</i> , 2017, 58, S418-S433.	0.8	45

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56	Distinctiveness of the Roma population within <i>CYP2B6</i> worldwide variation. <i>Pharmacogenomics</i> , 2017, 18, 1575-1587.	0.6	6
57	Parallel palaeogenomic transects reveal complex genetic history of early European farmers. <i>Nature</i> , 2017, 551, 368-372.	13.7	306
58	The Nature and Evolution of Genomic Diversity in the <i>Mycobacterium tuberculosis</i> Complex. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1019, 1-26.	0.8	52
59	A phylogenetic view of the Out of Asia/Eurasia and Out of Africa hypotheses in the light of recent molecular and palaeontological finds. <i>Gene</i> , 2017, 627, 473-476.	1.0	5
60	Evolution of local mutation rate and its determinants. <i>Molecular Biology and Evolution</i> , 2017, 34, msx060.	3.5	27
61	Differentiated demographic histories and local adaptations between Sherpas and Tibetans. <i>Genome Biology</i> , 2017, 18, 115.	3.8	67
62	Conservation Genetics of the Cheetah: Lessons Learned and New Opportunities. <i>Journal of Heredity</i> , 2017, 108, 671-677.	1.0	28
63	Human Colonization of Asia in the Late Pleistocene. <i>Current Anthropology</i> , 2017, 58, S373-S382.	0.8	66
64	Comparison of Single Genome and Allele Frequency Data Reveals Discordant Demographic Histories. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3605-3620.	0.8	70
65	A Genomic View of the Pleistocene Population History of Asia. <i>Current Anthropology</i> , 2017, 58, S397-S405.	0.8	12
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69	Rapid evolution of the human mutation spectrum. <i>ELife</i> , 2017, 6, .	2.8	144
70	Rearrangement moves on rooted phylogenetic networks. <i>PLoS Computational Biology</i> , 2017, 13, e1005611.	1.5	15
71	Using the Neandertal genome to study the evolution of small insertions and deletions in modern humans. <i>BMC Evolutionary Biology</i> , 2017, 17, 179.	3.2	14
72	Between Lake Baikal and the Baltic Sea: genomic history of the gateway to Europe. <i>BMC Genetics</i> , 2017, 18, 110.	2.7	34
73	Mitochondrial-DNA Phylogenetic Information and the Reconstruction of Human Population History: The South American Case. <i>Human Biology</i> , 2017, 89, 229.	0.4	4
74	Ancient DNA comes of age, but still has some teenage problems. <i>South African Journal of Science</i> , 2017, 113, 2.	0.3	6

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75	The Beaker phenomenon and the genomic transformation of northwest Europe. <i>Nature</i> , 2018, 555, 190-196.	13.7	503
76	The genomic history of southeastern Europe. <i>Nature</i> , 2018, 555, 197-203.	13.7	479
77	Origins and genetic legacies of the Caribbean Taino. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2341-2346.	3.3	64
78	A racial classification for medical genetics. <i>Philosophical Studies</i> , 2018, 175, 1013-1037.	0.5	11
79	MSeq-CNV: accurate detection of Copy Number Variation from Sequencing of Multiple samples. <i>Scientific Reports</i> , 2018, 8, 4009.	1.6	18
80	Language continuity despite population replacement in Remote Oceania. <i>Nature Ecology and Evolution</i> , 2018, 2, 731-740.	3.4	91
81	Genetic relatedness of indigenous ethnic groups in northern Borneo to neighboring populations from Southeast Asia, as inferred from genome-wide SNP data. <i>Annals of Human Genetics</i> , 2018, 82, 216-226.	0.3	13
82	The genetic assimilation in language borrowing inferred from Jing People. <i>American Journal of Physical Anthropology</i> , 2018, 166, 638-648.	2.1	15
83	Reply to comments on Clarkson et al. (2017) "Human occupation of northern Australia by 65,000 years ago". <i>Australian Archaeology</i> , 2018, 84, 84-89.	0.3	16
84	PGC.Population: a database for understanding the genomic diversity and genetic ancestry of human populations. <i>Nucleic Acids Research</i> , 2018, 46, D984-D993.	6.5	12
85	Model-based detection and analysis of introgressed Neanderthal ancestry in modern humans. <i>Molecular Ecology</i> , 2018, 27, 3873-3888.	2.0	67
86	Homo sapiens in Arabia by 85,000 years ago. <i>Nature Ecology and Evolution</i> , 2018, 2, 800-809.	3.4	143
87	Insights into Modern Human Prehistory Using Ancient Genomes. <i>Trends in Genetics</i> , 2018, 34, 184-196.	2.9	50
88	Tandem repeats mediating genetic plasticity in health and disease. <i>Nature Reviews Genetics</i> , 2018, 19, 286-298.	7.7	300
89	Subdecadal phytolith and charcoal records from Lake Malawi, East Africa imply minimal effects on human evolution from the ~1474 ka Toba supereruption. <i>Journal of Human Evolution</i> , 2018, 116, 75-94.	1.3	41
90	Contrasting maternal and paternal genetic variation of hunter-gatherer groups in Thailand. <i>Scientific Reports</i> , 2018, 8, 1536.	1.6	23
91	Genomic structure of the native inhabitants of Peninsular Malaysia and North Borneo suggests complex human population history in Southeast Asia. <i>Human Genetics</i> , 2018, 137, 161-173.	1.8	20
92	Inferring genetic origins and phenotypic traits of George Bähr, the architect of the Dresden Frauenkirche. <i>Scientific Reports</i> , 2018, 8, 2115.	1.6	11

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93	SRGAP2 and the gradual evolution of the modern human language faculty. <i>Journal of Language Evolution</i> , 2018, 3, 67-78.	0.4	9
94	The success of failed <i>Homo sapiens</i> dispersals out of Africa and into Asia. <i>Nature Ecology and Evolution</i> , 2018, 2, 212-219.	3.4	39
95	Mosdepth: quick coverage calculation for genomes and exomes. <i>Bioinformatics</i> , 2018, 34, 867-868.	1.8	638
96	150,000-year palaeoclimate record from northern Ethiopia supports early, multiple dispersals of modern humans from Africa. <i>Scientific Reports</i> , 2018, 8, 1077.	1.6	41
97	Whole sequence analysis indicates a recent southern origin of Mongolian Y-chromosome C2c1a1a1-M407. <i>Molecular Genetics and Genomics</i> , 2018, 293, 657-663.	1.0	16
98	glactools: a command-line toolset for the management of genotype likelihoods and allele counts. <i>Bioinformatics</i> , 2018, 34, 1398-1400.	1.8	13
99	Tales of Human Migration, Admixture, and Selection in Africa. <i>Annual Review of Genomics and Human Genetics</i> , 2018, 19, 405-428.	2.5	78
100	Ancient Genomics of Modern Humans: The First Decade. <i>Annual Review of Genomics and Human Genetics</i> , 2018, 19, 381-404.	2.5	161
101	No evidence for unknown archaic ancestry in South Asia. <i>Nature Genetics</i> , 2018, 50, 632-633.	9.4	7
102	Whole-Genome-Sequence-Based Haplotypes Reveal Single Origin of the Sickle Allele during the Holocene Wet Phase. <i>American Journal of Human Genetics</i> , 2018, 102, 547-556.	2.6	77
103	Analysis of Human Sequence Data Reveals Two Pulses of Archaic Denisovan Admixture. <i>Cell</i> , 2018, 173, 53-61.e9.	13.5	271
104	The uncertainty of population relationship and divergence time inferred by the multiple sequentially Markovian coalescent model. <i>Journal of Human Genetics</i> , 2018, 63, 775-777.	1.1	3
105	Genetic Ancestry of Hadza and Sandawe Peoples Reveals Ancient Population Structure in Africa. <i>Genome Biology and Evolution</i> , 2018, 10, 875-882.	1.1	6
106	Pleistocene North African genomes link Near Eastern and sub-Saharan African human populations. <i>Science</i> , 2018, 360, 548-552.	6.0	142
107	Inference on admixture fractions in a mechanistic model of recurrent admixture. <i>Theoretical Population Biology</i> , 2018, 122, 149-157.	0.5	9
108	Reconstructing the genetic history of late Neanderthals. <i>Nature</i> , 2018, 555, 652-656.	13.7	197
109	Different Selected Mechanisms Attenuated the Inhibitory Interaction of KIR2DL1 with C2+ HLA-C in Two Indigenous Human Populations in Southern Africa. <i>Journal of Immunology</i> , 2018, 200, 2640-2655.	0.4	32
110	The arms race between man and <i>Mycobacterium tuberculosis</i> : Time to regroup. <i>Infection, Genetics and Evolution</i> , 2018, 66, 361-375.	1.0	17

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111	The demographic history and mutational load of African hunter-gatherers and farmers. <i>Nature Ecology and Evolution</i> , 2018, 2, 721-730.	3.4	38
112	Population genomic analysis of elongated skulls reveals extensive female-biased immigration in Early Medieval Bavaria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3494-3499.	3.3	73
113	<i>findGSE</i> : estimating genome size variation within human and <i>Arabidopsis</i> using <i>k</i> -mer frequencies. <i>Bioinformatics</i> , 2018, 34, 550-557.	1.8	167
114	An early colonisation pathway into northwest Australia 70-60,000 years ago. <i>Quaternary Science Reviews</i> , 2018, 180, 229-239.	1.4	61
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116	A missense point mutation in COL10A1 identified with whole-genome deep sequencing in a 7-generation Pakistan dwarf family. <i>Heredity</i> , 2018, 120, 83-89.	1.2	6
119	The genetic prehistory of the Andean highlands 7000 years BP through European contact. <i>Science Advances</i> , 2018, 4, eaau4921.	4.7	115
120	Early human dispersals within the Americas. <i>Science</i> , 2018, 362, .	6.0	230
121	Clarifying distinct models of modern human origins in Africa. <i>Current Opinion in Genetics and Development</i> , 2018, 53, 148-156.	1.5	51
122	Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe. <i>Nature Communications</i> , 2018, 9, 5018.	5.8	86
123	Reply to "No evidence for unknown archaic ancestry in South Asia". <i>Nature Genetics</i> , 2018, 50, 1637-1639.	9.4	4
125	Whole-genome sequencing of 175 Mongolians uncovers population-specific genetic architecture and gene flow throughout North and East Asia. <i>Nature Genetics</i> , 2018, 50, 1696-1704.	9.4	38
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127	Immune diversity sheds light on missing variation in worldwide genetic diversity panels. <i>PLoS ONE</i> , 2018, 13, e0206512.	1.1	75
128	Reconstructing the Deep Population History of Central and South America. <i>Cell</i> , 2018, 175, 1185-1197.e22.	13.5	259
129	Principles of Archaeogenetics and the Current Trends of Ancient Genome Studies. <i>Korean Journal of Physical Anthropology</i> , 2018, 31, 105.	0.2	0
130	Origin and age of the causative mutations in KLC2, IMPA1, MED25 and WNT7A unravelled through Brazilian admixed populations. <i>Scientific Reports</i> , 2018, 8, 16552.	1.6	6
131	Variation in proviral content among human genomes mediated by LTR recombination. <i>Mobile DNA</i> , 2018, 9, 36.	1.3	71

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132	Latin Americans show wide-spread Converso ancestry and imprint of local Native ancestry on physical appearance. <i>Nature Communications</i> , 2018, 9, 5388.	5.8	123
133	The evolutionary history of Southern Africa. <i>Current Opinion in Genetics and Development</i> , 2018, 53, 157-164.	1.5	10
134	<i>FADS1</i> and the Timing of Human Adaptation to Agriculture. <i>Molecular Biology and Evolution</i> , 2018, 35, 2957-2970.	3.5	113
135	Turning Vice into Virtue: Using Batch-Effects to Detect Errors in Large Genomic Data Sets. <i>Genome Biology and Evolution</i> , 2018, 10, 2697-2708.	1.1	7
136	The genetic makings of South Asia. <i>Current Opinion in Genetics and Development</i> , 2018, 53, 128-133.	1.5	11
137	Anti-Darwin comments in India outrage scientists. <i>Nature</i> , 2018, 554, 16-17.	13.7	1
138	Cultural Innovations Influence Patterns of Genetic Diversity in Northwestern Amazonia. <i>Molecular Biology and Evolution</i> , 2018, 35, 2719-2735.	3.5	17
139	Characterization of Duck (<i>Anas platyrhynchos</i>) Short Tandem Repeat Variation by Population-Scale Genome Resequencing. <i>Frontiers in Genetics</i> , 2018, 9, 520.	1.1	3
140	A polymorphic residue that attenuates the antiviral potential of interferon lambda 4 in hominid lineages. <i>PLoS Pathogens</i> , 2018, 14, e1007307.	2.1	25
141	Demographic and Genetic Portraits of the Ulchi Population. <i>Russian Journal of Genetics</i> , 2018, 54, 1245-1253.	0.2	2
142	Outstanding questions in the study of archaic hominin admixture. <i>PLoS Genetics</i> , 2018, 14, e1007349.	1.5	50
143	Genomic history of the Sardinian population. <i>Nature Genetics</i> , 2018, 50, 1426-1434.	9.4	71
144	SAGE: a comprehensive resource of genetic variants integrating South Asian whole genomes and exomes. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, 1-10.	1.4	20
145	Positive and balancing selection on <i>SLC18A1</i> gene associated with psychiatric disorders and human-unique personality traits. <i>Evolution Letters</i> , 2018, 2, 499-510.	1.6	16
146	Detecting archaic introgression using an unadmixed outgroup. <i>PLoS Genetics</i> , 2018, 14, e1007641.	1.5	78
147	Understanding 6th-century barbarian social organization and migration through paleogenomics. <i>Nature Communications</i> , 2018, 9, 3547.	5.8	111
148	Evolutionary and Medical Consequences of Archaic Introgression into Modern Human Genomes. <i>Genes</i> , 2018, 9, 358.	1.0	28
149	Detecting past and ongoing natural selection among ethnically Tibetan women at high altitude in Nepal. <i>PLoS Genetics</i> , 2018, 14, e1007650.	1.5	43

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151	The Year In Genetic Anthropology: New Lands, New Technologies, New Questions. <i>American Anthropologist</i> , 2018, 120, 266-277.	0.7	5
152	Who were the Nataruk people? Mandibular morphology among late Pleistocene and early Holocene fisher-forager populations of West Turkana (Kenya). <i>Journal of Human Evolution</i> , 2018, 121, 235-253.	1.3	6
153	Dynamic Copy Number Evolution of X- and Y-Linked Ampliconic Genes in Human Populations. <i>Genetics</i> , 2018, 209, 907-920.	1.2	32
154	Ancient genomes document multiple waves of migration in Southeast Asian prehistory. <i>Science</i> , 2018, 361, 92-95.	6.0	250
155	Human-Specific NOTCH2NL Genes Affect Notch Signaling and Cortical Neurogenesis. <i>Cell</i> , 2018, 173, 1356-1369.e22.	13.5	366
156	Ancient human parallel lineages within North America contributed to a coastal expansion. <i>Science</i> , 2018, 360, 1024-1027.	6.0	138
157	The prehistoric peopling of Southeast Asia. <i>Science</i> , 2018, 361, 88-92.	6.0	291
158	Leaving Africa. , 2018, , 75-103.		1
159	Bone's Intrinsic Traits: Why Animals Eat Animals. , 2018, , 89-102.		0
160	snpAD: an ancient DNA genotype caller. <i>Bioinformatics</i> , 2018, 34, 4165-4171.	1.8	52
161	Four-Generation Pedigree of Monozygotic Female Twins Reveals Genetic Factors in Twinning Process by Whole-Genome Sequencing. <i>Twin Research and Human Genetics</i> , 2018, 21, 361-368.	0.3	32
162	Exploring Cuba's population structure and demographic history using genome-wide data. <i>Scientific Reports</i> , 2018, 8, 11422.	1.6	31
163	Evolutionary history and adaptation of a human pygmy population of Flores Island, Indonesia. <i>Science</i> , 2018, 361, 511-516.	6.0	56
164	When did <i>Homo sapiens</i> first reach Southeast Asia and Sahul?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 8482-8490.	3.3	186
165	Predicting the clinical impact of human mutation with deep neural networks. <i>Nature Genetics</i> , 2018, 50, 1161-1170.	9.4	288
166	Inference of population history using coalescent HMMs: review and outlook. <i>Current Opinion in Genetics and Development</i> , 2018, 53, 70-76.	1.5	51
167	De novo human genome assemblies reveal spectrum of alternative haplotypes in diverse populations. <i>Nature Communications</i> , 2018, 9, 3040.	5.8	81

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168	A Census of Tandemly Repeated Polymorphic Loci in Genic Regions Through the Comparative Integration of Human Genome Assemblies. <i>Frontiers in Genetics</i> , 2018, 9, 155.	1.1	9
169	Paternal origin of Paleo-Indians in Siberia: insights from Y-chromosome sequences. <i>European Journal of Human Genetics</i> , 2018, 26, 1687-1696.	1.4	21
170	Did Our Species Evolve in Subdivided Populations across Africa, and Why Does It Matter?. <i>Trends in Ecology and Evolution</i> , 2018, 33, 582-594.	4.2	315
171	Human local adaptation of the TRPM8 cold receptor along a latitudinal cline. <i>PLoS Genetics</i> , 2018, 14, e1007298.	1.5	75
172	A finely resolved phylogeny of Y chromosome Hg J illuminates the processes of Phoenician and Greek colonizations in the Mediterranean. <i>Scientific Reports</i> , 2018, 8, 7465.	1.6	9
173	African genetic diversity provides novel insights into evolutionary history and local adaptations. <i>Human Molecular Genetics</i> , 2018, 27, R209-R218.	1.4	38
174	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. <i>Science</i> , 2018, 360, .	6.0	262
175	In-solution Y-chromosome capture-enrichment on ancient DNA libraries. <i>BMC Genomics</i> , 2018, 19, 608.	1.2	20
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