

Rasmus Nielsen

List of Publications by Year in descending order

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Version: 2024-02-01

311
papers

86,733
citations

630

127
h-index

498

275
g-index

362
all docs

362
docs citations

362
times ranked

76975
citing authors

#	ARTICLE	IF	CITATIONS
1	Detecting Selection in Multiple Populations by Modeling Ancestral Admixture Components. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	24
2	AncestralClust: clustering of divergent nucleotide sequences by ancestral sequence reconstruction using phylogenetic trees. <i>Bioinformatics</i> , 2022, 38, 663-670.	1.8	3
3	SCONCE: a method for profiling copy number alterations in cancer evolution using single-cell whole genome sequencing. <i>Bioinformatics</i> , 2022, 38, 1801-1808.	1.8	11
4	Inferring person-to-person networks of <i>Plasmodium falciparum</i> transmission: are analyses of routine surveillance data up to the task?. <i>Malaria Journal</i> , 2022, 21, 58.	0.8	1
5	Evaluation of methods for estimating coalescence times using ancestral recombination graphs. <i>Genetics</i> , 2022, 221, .	1.2	22
6	Covariance of pairwise differences on a multi-species coalescent tree and implications for F_{ST} . <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, 20200415.	1.8	2
7	The Tibetan-Yi region is both a corridor and a barrier for human gene flow. <i>Cell Reports</i> , 2022, 39, 110720.	2.9	8
8	distAngsd: Fast and Accurate Inference of Genetic Distances for Next-Generation Sequencing Data. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	1
9	Population Genomics of Variegated Toad-Headed Lizard <i>Phrynocephalus versicolor</i> and Its Adaptation to the Colorful Sand of the Gobi Desert. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	3
10	Estimating the timing of multiple admixture events using 3-locus linkage disequilibrium. <i>PLoS Genetics</i> , 2022, 18, e1010281.	1.5	3
11	Assessing Uncertainty in the Rooting of the SARS-CoV-2 Phylogeny. <i>Molecular Biology and Evolution</i> , 2021, 38, 1537-1543.	3.5	37
12	Disentangling selection on genetically correlated polygenic traits via whole-genome genealogies. <i>American Journal of Human Genetics</i> , 2021, 108, 219-239.	2.6	48
13	Convergent evolution of increased urine-concentrating ability in desert mammals. <i>Mammal Review</i> , 2021, 51, 482-491.	2.2	7
14	Investigate the origins of COVID-19. <i>Science</i> , 2021, 372, 694-694.	6.0	92
15	The history and evolution of the Denisovan-EPAS1 haplotype in Tibetans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	48
16	The genomics of mimicry: Gene expression throughout development provides insights into convergent and divergent phenotypes in a Müllerian mimicry system. <i>Molecular Ecology</i> , 2021, 30, 4039-4061.	2.0	20
17	Life in Deserts: The Genetic Basis of Mammalian Desert Adaptation. <i>Trends in Ecology and Evolution</i> , 2021, 36, 637-650.	4.2	35
18	Human-Mediated Admixture and Selection Shape the Diversity on the Modern Swine (<i>Sus scrofa</i>) Y Chromosomes. <i>Molecular Biology and Evolution</i> , 2021, 38, 5051-5065.	3.5	9

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19	The distribution of waiting distances in ancestral recombination graphs. <i>Theoretical Population Biology</i> , 2021, 141, 34-43.	0.5	15
20	Inferring Adaptive Introgression Using Hidden Markov Models. <i>Molecular Biology and Evolution</i> , 2021, 38, 2152-2165.	3.5	21
21	Synonymous mutations and the molecular evolution of SARS-CoV-2 Origins. <i>Virus Evolution</i> , 2021, 7, veaa098.	2.2	52
22	Whole-genome sequence analysis unveils different origins of European and Asiatic mouflon and domestication-related genes in sheep. <i>Communications Biology</i> , 2021, 4, 1307.	2.0	38
23	A likelihood method for estimating present-day human contamination in ancient male samples using low-depth X-chromosome data. <i>Bioinformatics</i> , 2020, 36, 828-841.	1.8	14
24	A Bayesian Framework for Inferring the Influence of Sequence Context on Point Mutations. <i>Molecular Biology and Evolution</i> , 2020, 37, 893-903.	3.5	7
25	No statistical evidence for an effect of CCR5-Δ32 on lifespan in the UK Biobank cohort. <i>Nature Medicine</i> , 2020, 26, 178-180.	15.2	16
26	Pronounced somatic bottleneck in mitochondrial DNA of human hair. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190175.	1.8	29
27	The genetic architecture of sporadic and multiple consecutive miscarriage. <i>Nature Communications</i> , 2020, 11, 5980.	5.8	52
28	Population genomics of the Viking world. <i>Nature</i> , 2020, 585, 390-396.	13.7	143
29	Inferring the ancestry of parents and grandparents from genetic data. <i>PLoS Computational Biology</i> , 2020, 16, e1008065.	1.5	9
30	Divergence, gene flow, and the origin of leapfrog geographic distributions: The history of colour pattern variation in <i>Phylllobates</i> poison-dart frogs. <i>Molecular Ecology</i> , 2020, 29, 3702-3719.	2.0	14
31	Ancient Hybridization with an Unknown Population Facilitated High-Altitude Adaptation of Canids. <i>Molecular Biology and Evolution</i> , 2020, 37, 2616-2629.	3.5	46
32	VolcanoFinder: Genomic scans for adaptive introgression. <i>PLoS Genetics</i> , 2020, 16, e1008867.	1.5	62
33	Massive haplotypes underlie ecotypic differentiation in sunflowers. <i>Nature</i> , 2020, 584, 602-607.	13.7	263
34	Phenotypic Convergence Is Not Mirrored at the Protein Level in a Lizard Adaptive Radiation. <i>Molecular Biology and Evolution</i> , 2020, 37, 1604-1614.	3.5	19
35	On the Distribution of Tract Lengths During Adaptive Introgression. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3663-3673.	0.8	23
36	VolcanoFinder: Genomic scans for adaptive introgression. , 2020, 16, e1008867.		0

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37	VolcanoFinder: Genomic scans for adaptive introgression. , 2020, 16, e1008867.		0
38	VolcanoFinder: Genomic scans for adaptive introgression. , 2020, 16, e1008867.		0
39	VolcanoFinder: Genomic scans for adaptive introgression. , 2020, 16, e1008867.		0
40	Natural selection on the Arabidopsis thaliana genome in present and future climates. Nature, 2019, 573, 126-129.	13.7	148
41	An approximate full-likelihood method for inferring selection and allele frequency trajectories from DNA sequence data. PLoS Genetics, 2019, 15, e1008384.	1.5	100
42	Joint Estimation of Pedigrees and Effective Population Size Using Markov Chain Monte Carlo. Genetics, 2019, 212, 855-868.	1.2	5
43	CCR5- $\Delta 32$ is deleterious in the homozygous state in humans. Nature Medicine, 2019, 25, 909-910.	15.2	61
44	The population history of northeastern Siberia since the Pleistocene. Nature, 2019, 570, 182-188.	13.7	259
45	Temporal genomic contrasts reveal rapid evolutionary responses in an alpine mammal during recent climate change. PLoS Genetics, 2019, 15, e1008119.	1.5	70
46	Human Disease Variation in the Light of Population Genomics. Cell, 2019, 177, 115-131.	13.5	75
47	Parallel adaptation of rabbit populations to myxoma virus. Science, 2019, 363, 1319-1326.	6.0	124
48	Bottleneck and selection in the germline and maternal age influence transmission of mitochondrial DNA in human pedigrees. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25172-25178.	3.3	71
49	Passage Adaptation Correlates With the Reduced Efficacy of the Influenza Vaccine. Clinical Infectious Diseases, 2019, 69, 1198-1204.	2.9	18
50	Genetic rescue and the maintenance of native ancestry. Conservation Genetics, 2019, 20, 59-64.	0.8	37
51	Emergence and Spread of Basal Lineages of Yersinia Pestis during the Neolithic Decline. Cell, 2019, 176, 295-305.e10.	13.5	168
52	Origins and genetic legacies of the Caribbean Taino. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 2341-2346.	3.3	64
53	Physiological and Genetic Adaptations to Diving in Sea Nomads. Cell, 2018, 173, 569-580.e15.	13.5	129
54	Population genomics of finless porpoises reveal an incipient cetacean species adapted to freshwater. Nature Communications, 2018, 9, 1276.	5.8	80

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55	A Population Phylogenetic View of Mitochondrial Heteroplasmy. <i>Genetics</i> , 2018, 208, 1261-1274.	1.2	41
56	Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. <i>Nature</i> , 2018, 553, 203-207.	13.7	304
57	Molecular Footprints of Aquatic Adaptation Including Bone Mass Changes in Cetaceans. <i>Genome Biology and Evolution</i> , 2018, 10, 967-975.	1.1	23
58	Early human dispersals within the Americas. <i>Science</i> , 2018, 362, .	6.0	230
59	Estimating the Timing of Multiple Admixture Pulses During Local Ancestry Inference. <i>Genetics</i> , 2018, 210, 1089-1107.	1.2	37
60	Genomic Analyses from Non-invasive Prenatal Testing Reveal Genetic Associations, Patterns of Viral Infections, and Chinese Population History. <i>Cell</i> , 2018, 175, 347-359.e14.	13.5	213
61	The Genetic Basis of Adaptation following Plastic Changes in Coloration in a Novel Environment. <i>Current Biology</i> , 2018, 28, 2970-2977.e7.	1.8	83
62	Pervasive introgression facilitated domestication and adaptation in the <i>Bos</i> species complex. <i>Nature Ecology and Evolution</i> , 2018, 2, 1139-1145.	3.4	157
63	Human adaptation to extreme environmental conditions. <i>Current Opinion in Genetics and Development</i> , 2018, 53, 77-82.	1.5	43
64	On the number of siblings and p-th cousins in a large population sample. <i>Journal of Mathematical Biology</i> , 2018, 77, 1279-1298.	0.8	9
65	137 ancient human genomes from across the Eurasian steppes. <i>Nature</i> , 2018, 557, 369-374.	13.7	325
66	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. <i>Science</i> , 2018, 360, .	6.0	262
67	Novel Form of Alternative Splicing of NFKB1. Its Role in Polycythemia and Adaptation to High Altitude in Andean Aymara. <i>Blood</i> , 2018, 132, 2316-2316.	0.6	2
68	Archaic adaptive introgression in <i>TBX15/WARS2</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, msw283.	3.5	101
69	Tracing the peopling of the world through genomics. <i>Nature</i> , 2017, 541, 302-310.	13.7	562
70	Selection in Europeans on Fatty Acid Desaturases Associated with Dietary Changes. <i>Molecular Biology and Evolution</i> , 2017, 34, 1307-1318.	3.5	90
71	Fast admixture analysis and population tree estimation for SNP and NGS data. <i>Bioinformatics</i> , 2017, 33, 2148-2155.	1.8	40
72	The Evolutionary Pathway to Virulence of an RNA Virus. <i>Cell</i> , 2017, 169, 35-46.e19.	13.5	113

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73	Asian wild rice is a hybrid swarm with extensive gene flow and feralization from domesticated rice. <i>Genome Research</i> , 2017, 27, 1029-1038.	2.4	100
74	Natural Selection on Genes Related to Cardiovascular Health in High-Altitude Adapted Andeans. <i>American Journal of Human Genetics</i> , 2017, 101, 752-767.	2.6	99
75	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , 2017, 358, 659-662.	6.0	263
76	Genome-wide signatures of complex introgression and adaptive evolution in the big cats. <i>Science Advances</i> , 2017, 3, e1700299.	4.7	142
77	A Hidden Markov Model Approach for Simultaneously Estimating Local Ancestry and Admixture Time Using Next Generation Sequence Data in Samples of Arbitrary Ploidy. <i>PLoS Genetics</i> , 2017, 13, e1006529.	1.5	117
78	Composite likelihood method for inferring local pedigrees. <i>PLoS Genetics</i> , 2017, 13, e1006963.	1.5	21
79	Q&A: Where did the Neanderthals go?. <i>BMC Biology</i> , 2017, 15, 73.	1.7	3
80	REPdenovo: Inferring De Novo Repeat Motifs from Short Sequence Reads. <i>PLoS ONE</i> , 2016, 11, e0150719.	1.1	45
81	Evolution of <i>GOUNDRY</i> , a cryptic subgroup of <i>Anopheles gambiae</i> , and its impact on susceptibility to <i>Plasmodium</i> infection. <i>Molecular Ecology</i> , 2016, 25, 1494-1510.	2.0	18
82	Fumio Tajima and the Origin of Modern Population Genetics. <i>Genetics</i> , 2016, 204, 389-390.	1.2	0
83	The Genetic Cost of Neanderthal Introgression. <i>Genetics</i> , 2016, 203, 881-891.	1.2	342
84	Estimating IBD tracts from low coverage NGS data. <i>Bioinformatics</i> , 2016, 32, 2096-2102.	1.8	36
85	The Power of Inbreeding: NGS-Based GWAS of Rice Reveals Convergent Evolution during Rice Domestication. <i>Molecular Plant</i> , 2016, 9, 975-985.	3.9	102
86	Postglacial viability and colonization in North America's ice-free corridor. <i>Nature</i> , 2016, 537, 45-49.	13.7	363
87	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016, 538, 207-214.	13.7	439
88	Genomic analyses inform on migration events during the peopling of Eurasia. <i>Nature</i> , 2016, 538, 238-242.	13.7	360
89	Detecting recent selective sweeps while controlling for mutation rate and background selection. <i>Molecular Ecology</i> , 2016, 25, 142-156.	2.0	157
90	SweepFinder2: increased sensitivity, robustness and flexibility. <i>Bioinformatics</i> , 2016, 32, 1895-1897.	1.8	238

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91	The origin and evolution of maize in the Southwestern United States. <i>Nature Plants</i> , 2015, 1, 14003.	4.7	138
92	Reticulate Speciation and Barriers to Introgression in the <i>Anopheles gambiae</i> Species Complex. <i>Genome Biology and Evolution</i> , 2015, 7, 3116-3131.	1.1	32
93	De novo assembly of a haplotype-resolved human genome. <i>Nature Biotechnology</i> , 2015, 33, 617-622.	9.4	73
94	Population genomics of Bronze Age Eurasia. <i>Nature</i> , 2015, 522, 167-172.	13.7	1,166
95	Uncovering the Genetic History of the Present-Day Greenlandic Population. <i>American Journal of Human Genetics</i> , 2015, 96, 54-69.	2.6	85
96	Convergent evolution of the genomes of marine mammals. <i>Nature Genetics</i> , 2015, 47, 272-275.	9.4	392
97	Adaptation and possible ancient interspecies introgression in pigs identified by whole-genome sequencing. <i>Nature Genetics</i> , 2015, 47, 217-225.	9.4	288
98	The mind, the lab, and the field: Three kinds of populations in scientific practice. <i>Studies in History and Philosophy of Science Part C: Studies in History and Philosophy of Biological and Biomedical Sciences</i> , 2015, 52, 12-21.	0.8	20
99	Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015, 349, aab3884.	6.0	449
100	Phylogenetic ANOVA: The Expression Variance and Evolution Model for Quantitative Trait Evolution. <i>Systematic Biology</i> , 2015, 64, 695-708.	2.7	92
101	The ancestry and affiliations of Kennewick Man. <i>Nature</i> , 2015, 523, 455-458.	13.7	241
102	Fitting the Balding-Nichols model to forensic databases. <i>Forensic Science International: Genetics</i> , 2015, 19, 86-91.	1.6	2
103	Number of genes controlling a quantitative trait in a hybrid zone of the aposematic frog <i>Ranitomeya imitator</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20141950.	1.2	10
104	A genome-wide scan for signatures of directional selection in domesticated pigs. <i>BMC Genomics</i> , 2015, 16, 130.	1.2	67
105	Evidence for archaic adaptive introgression in humans. <i>Nature Reviews Genetics</i> , 2015, 16, 359-371.	7.7	471
106	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
107	Early Divergent Strains of <i>Yersinia pestis</i> in Eurasia 5,000 Years Ago. <i>Cell</i> , 2015, 163, 571-582.	13.5	425
108	Greenlandic Inuit show genetic signatures of diet and climate adaptation. <i>Science</i> , 2015, 349, 1343-1347.	6.0	397

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109	Introduction: Genomics and philosophy of race. <i>Studies in History and Philosophy of Science Part C: Studies in History and Philosophy of Biological and Biomedical Sciences</i> , 2015, 52, 1-4.	0.8	0
110	Tracking the origins of Yakutian horses and the genetic basis for their fast adaptation to subarctic environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E6889-97.	3.3	139
111	Genomic takeover by transposable elements in the Strawberry poison frog. <i>Molecular Biology and Evolution</i> , 2014, 35, 2913-2927.	3.5	45
112	Maternal age effect and severe germ-line bottleneck in the inheritance of human mitochondrial DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15474-15479.	3.3	201
113	Natural Selection Reduced Diversity on Human Y Chromosomes. <i>PLoS Genetics</i> , 2014, 10, e1004064.	1.5	91
114	Classic Selective Sweeps Revealed by Massive Sequencing in Cattle. <i>PLoS Genetics</i> , 2014, 10, e1004148.	1.5	254
115	Selection on a Variant Associated with Improved Viral Clearance Drives Local, Adaptive Pseudogenization of Interferon Lambda 4 (IFNL4). <i>PLoS Genetics</i> , 2014, 10, e1004681.	1.5	87
116	A Model-Based Approach for Identifying Signatures of Ancient Balancing Selection in Genetic Data. <i>PLoS Genetics</i> , 2014, 10, e1004561.	1.5	159
117	Prehistoric genomes reveal the genetic foundation and cost of horse domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5661-9.	3.3	260
118	Speciation with gene flow in equids despite extensive chromosomal plasticity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18655-18660.	3.3	183
119	Variation and association to diabetes in 2000 full mtDNA sequences mined from an exome study in a Danish population. <i>European Journal of Human Genetics</i> , 2014, 22, 1040-1045.	1.4	26
120	ANGSD: Analysis of Next Generation Sequencing Data. <i>BMC Bioinformatics</i> , 2014, 15, 356.	1.2	1,935
121	Modeling Gene Expression Evolution with an Extended Ornstein-Uhlenbeck Process Accounting for Within-Species Variation. <i>Molecular Biology and Evolution</i> , 2014, 31, 201-211.	3.5	110
122	<i>bammds</i> : a tool for assessing the ancestry of low-depth whole-genome data using multidimensional scaling (MDS). <i>Bioinformatics</i> , 2014, 30, 2962-2964.	1.8	40
123	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , 2014, 506, 225-229.	13.7	500
124	On Detecting Incomplete Soft or Hard Selective Sweeps Using Haplotype Structure. <i>Molecular Biology and Evolution</i> , 2014, 31, 1275-1291.	3.5	335
125	Population Genomics Reveal Recent Speciation and Rapid Evolutionary Adaptation in Polar Bears. <i>Cell</i> , 2014, 157, 785-794.	13.5	363
126	<i>ngsTools</i> : methods for population genetics analyses from next-generation sequencing data. <i>Bioinformatics</i> , 2014, 30, 1486-1487.	1.8	227

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127	Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. <i>Nature</i> , 2014, 507, 225-228.	13.7	328
128	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , 2014, 505, 87-91.	13.7	821
129	Genomic structure in Europeans dating back at least 36,200 years. <i>Science</i> , 2014, 346, 1113-1118.	6.0	287
130	The Lengths of Admixture Tracts. <i>Genetics</i> , 2014, 197, 953-967.	1.2	121
131	Genome-wide Ancestry Patterns in Rapanui Suggest Pre-European Admixture with Native Americans. <i>Current Biology</i> , 2014, 24, 2518-2525.	1.8	50
132	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , 2014, 24, R1035-R1037.	1.8	73
133	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
134	Costs and Benefits of Mutational Robustness in RNA Viruses. <i>Cell Reports</i> , 2014, 8, 1026-1036.	2.9	49
135	Error-prone polymerase activity causes multinucleotide mutations in humans. <i>Genome Research</i> , 2014, 24, 1445-1454.	2.4	92
136	Altitude adaptation in Tibetans caused by introgression of Denisovan-like DNA. <i>Nature</i> , 2014, 512, 194-197.	13.7	904
137	The genetic prehistory of the New World Arctic. <i>Science</i> , 2014, 345, 1255832.	6.0	264
138	A common Greenlandic TBC1D4 variant confers muscle insulin resistance and type 2 diabetes. <i>Nature</i> , 2014, 512, 190-193.	13.7	338
139	Whole-Exome Sequencing of 2,000 Danish Individuals and the Role of Rare Coding Variants in Type 2 Diabetes. <i>American Journal of Human Genetics</i> , 2013, 93, 1072-1086.	2.6	124
140	Molecular footprints of domestication and improvement in soybean revealed by whole genome re-sequencing. <i>BMC Genomics</i> , 2013, 14, 579.	1.2	186
141	Unlocking the vault: next-generation museum population genomics. <i>Molecular Ecology</i> , 2013, 22, 6018-6032.	2.0	329
142	Bacterial natural transformation by highly fragmented and damaged DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19860-19865.	3.3	170
143	Detecting adaptive trait loci in nonmodel systems: divergence or admixture mapping?. <i>Molecular Ecology</i> , 2013, 22, 6131-6148.	2.0	28
144	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013, 499, 74-78.	13.7	717

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145	Quantifying Population Genetic Differentiation from Next-Generation Sequencing Data. <i>Genetics</i> , 2013, 195, 979-992.	1.2	187
146	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
147	Inferring Demographic History from a Spectrum of Shared Haplotype Lengths. <i>PLoS Genetics</i> , 2013, 9, e1003521.	1.5	228
148	Genetic Architecture of Vitamin B12 and Folate Levels Uncovered Applying Deeply Sequenced Large Datasets. <i>PLoS Genetics</i> , 2013, 9, e1003530.	1.5	112
149	Estimating inbreeding coefficients from NGS data: Impact on genotype calling and allele frequency estimation. <i>Genome Research</i> , 2013, 23, 1852-1861.	2.4	89
150	A Scan for Human-Specific Relaxation of Negative Selection Reveals Unexpected Polymorphism in Proteasome Genes. <i>Molecular Biology and Evolution</i> , 2013, 30, 1808-1815.	3.5	23
151	Calculation of Tajima's D and other neutrality test statistics from low depth next-generation sequencing data. <i>BMC Bioinformatics</i> , 2013, 14, 289.	1.2	211
152	Evidence for Positive Selection on a Number of MicroRNA Regulatory Interactions during Recent Human Evolution. <i>PLoS Genetics</i> , 2012, 8, e1002578.	1.5	63
153	Distinguishing between Selective Sweeps from Standing Variation and from a De Novo Mutation. <i>PLoS Genetics</i> , 2012, 8, e1003011.	1.5	201
154	Looking for Darwin in Genomic Sequences—Validity and Success of Statistical Methods. <i>Molecular Biology and Evolution</i> , 2012, 29, 2889-2893.	3.5	28
155	A metagenome-wide association study of gut microbiota in type 2 diabetes. <i>Nature</i> , 2012, 490, 55-60.	13.7	5,345
156	Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. <i>Nature Biotechnology</i> , 2012, 30, 105-111.	9.4	818
157	Estimating population divergence time and phylogeny from single-nucleotide polymorphisms data with outgroup ascertainment bias. <i>Molecular Ecology</i> , 2012, 21, 974-986.	2.0	13
158	SNP Calling, Genotype Calling, and Sample Allele Frequency Estimation from New-Generation Sequencing Data. <i>PLoS ONE</i> , 2012, 7, e37558.	1.1	336
159	Genome sequencing and comparison of two nonhuman primate animal models, the cynomolgus and Chinese rhesus macaques. <i>Nature Biotechnology</i> , 2011, 29, 1019-1023.	9.4	284
160	Species-specific responses of Late Quaternary megafauna to climate and humans. <i>Nature</i> , 2011, 479, 359-364.	13.7	586
161	Genotype and SNP calling from next-generation sequencing data. <i>Nature Reviews Genetics</i> , 2011, 12, 443-451.	7.7	1,238
162	The evolution of gene expression levels in mammalian organs. <i>Nature</i> , 2011, 478, 343-348.	13.7	1,080

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163	An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. <i>Science</i> , 2011, 334, 94-98.	6.0	675
164	Q&A: Who is <i>H. sapiens</i> really, and how do we know?. <i>BMC Biology</i> , 2011, 9, 20.	1.7	6
165	Estimation of allele frequency and association mapping using next-generation sequencing data. <i>BMC Bioinformatics</i> , 2011, 12, 231.	1.2	170
166	A method for detecting IBD regions simultaneously in multiple individuals with applications to disease genetics. <i>Genome Research</i> , 2011, 21, 1168-1180.	2.4	42
167	Signatures of Environmental Genetic Adaptation Pinpoint Pathogens as the Main Selective Pressure through Human Evolution. <i>PLoS Genetics</i> , 2011, 7, e1002355.	1.5	464
168	Natural Selection Affects Multiple Aspects of Genetic Variation at Putatively Neutral Sites across the Human Genome. <i>PLoS Genetics</i> , 2011, 7, e1002326.	1.5	146
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