

# Rasmus Nielsen

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

328  
papers

65,078  
citations

122  
h-index

254  
g-index

362  
ext. papers

78,292  
ext. citations

14.8  
avg, IF

7.88  
L-index

#	Paper	IF	Citations
328	Inferring person-to-person networks of Plasmodium falciparum transmission: are analyses of routine surveillance data up to the task?. <i>Malaria Journal</i> , <b>2022</b> , 21, 58	3.6	0
327	Covariance of pairwise differences on a multi-species coalescent tree and implications for .. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2022</b> , 377, 20200415	5.8	2
326	The Tibetan-Yi region is both a corridor and a barrier for human gene flow.. <i>Cell Reports</i> , <b>2022</b> , 39, 110720.6	10.6	0
325	Whole-genome sequence analysis unveils different origins of European and Asiatic mouflon and domestication-related genes in sheep. <i>Communications Biology</i> , <b>2021</b> , 4, 1307	6.7	2
324	Detecting selection in multiple populations by modelling ancestral admixture components. <i>Molecular Biology and Evolution</i> , <b>2021</b> ,	8.3	6
323	AncestralClust: Clustering of Divergent Nucleotide Sequences by Ancestral Sequence Reconstruction using Phylogenetic Trees. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	1
322	Synonymous mutations and the molecular evolution of SARS-CoV-2 origins. <i>Virus Evolution</i> , <b>2021</b> , 7, veaa098	3.7	34
321	Convergent evolution of increased urine-concentrating ability in desert mammals. <i>Mammal Review</i> , <b>2021</b> , 51, 482-491	5	1
320	Investigate the origins of COVID-19. <i>Science</i> , <b>2021</b> , 372, 694	33.3	39
319	The history and evolution of the Denisovan- haplotype in Tibetans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	12
318	Assessing Uncertainty in the Rooting of the SARS-CoV-2 Phylogeny. <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 1537-1543	8.3	19
317	Disentangling selection on genetically correlated polygenic traits via whole-genome genealogies. <i>American Journal of Human Genetics</i> , <b>2021</b> , 108, 219-239	11	19
316	The genomics of mimicry: Gene expression throughout development provides insights into convergent and divergent phenotypes in a Māorian mimicry system. <i>Molecular Ecology</i> , <b>2021</b> , 30, 4039-4061	5.7	3
315	Life in Deserts: The Genetic Basis of Mammalian Desert Adaptation. <i>Trends in Ecology and Evolution</i> , <b>2021</b> , 36, 637-650	10.9	4
314	Human-Mediated Admixture and Selection Shape the Diversity on the Modern Swine ( <i>Sus scrofa</i> ) Y Chromosomes. <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 5051-5065	8.3	1
313	The distribution of waiting distances in ancestral recombination graphs. <i>Theoretical Population Biology</i> , <b>2021</b> , 141, 34-43	1.2	0
312	Inferring Adaptive Introgression Using Hidden Markov Models. <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 2152-2165	8.3	6

311	Ancient Hybridization with an Unknown Population Facilitated High-Altitude Adaptation of Canids. <i>Molecular Biology and Evolution</i> , <b>2020</b> , 37, 2616-2629	8.3	16
310	VolcanoFinder: Genomic scans for adaptive introgression. <i>PLoS Genetics</i> , <b>2020</b> , 16, e1008867	6	20
309	Massive haplotypes underlie ecotypic differentiation in sunflowers. <i>Nature</i> , <b>2020</b> , 584, 602-607	50.4	81
308	Phenotypic Convergence Is Not Mirrored at the Protein Level in a Lizard Adaptive Radiation. <i>Molecular Biology and Evolution</i> , <b>2020</b> , 37, 1604-1614	8.3	3
307	On the Distribution of Tract Lengths During Adaptive Introgression. <i>G3: Genes, Genomes, Genetics</i> , <b>2020</b> , 10, 3663-3673	3.2	12
306	A Bayesian Framework for Inferring the Influence of Sequence Context on Point Mutations. <i>Molecular Biology and Evolution</i> , <b>2020</b> , 37, 893-903	8.3	4
305	No statistical evidence for an effect of CCR5- $\beta$ 2 on lifespan in the UK Biobank cohort. <i>Nature Medicine</i> , <b>2020</b> , 26, 178-180	50.5	10
304	Pronounced somatic bottleneck in mitochondrial DNA of human hair. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2020</b> , 375, 20190175	5.8	13
303	The genetic architecture of sporadic and multiple consecutive miscarriage. <i>Nature Communications</i> , <b>2020</b> , 11, 5980	17.4	11
302	Population genomics of the Viking world. <i>Nature</i> , <b>2020</b> , 585, 390-396	50.4	35
301	Inferring the ancestry of parents and grandparents from genetic data. <i>PLoS Computational Biology</i> , <b>2020</b> , 16, e1008065	5	2
300	Divergence, gene flow, and the origin of leapfrog geographic distributions: The history of colour pattern variation in <i>Phyllobates</i> poison-dart frogs. <i>Molecular Ecology</i> , <b>2020</b> , 29, 3702-3719	5.7	1
299	A likelihood method for estimating present-day human contamination in ancient male samples using low-depth X-chromosome data. <i>Bioinformatics</i> , <b>2020</b> , 36, 828-841	7.2	7
298	VolcanoFinder: Genomic scans for adaptive introgression <b>2020</b> , 16, e1008867		
297	VolcanoFinder: Genomic scans for adaptive introgression <b>2020</b> , 16, e1008867		
296	VolcanoFinder: Genomic scans for adaptive introgression <b>2020</b> , 16, e1008867		
295	VolcanoFinder: Genomic scans for adaptive introgression <b>2020</b> , 16, e1008867		
294	Natural selection on the <i>Arabidopsis thaliana</i> genome in present and future climates. <i>Nature</i> , <b>2019</b> , 573, 126-129	50.4	63

293	An approximate full-likelihood method for inferring selection and allele frequency trajectories from DNA sequence data. <i>PLoS Genetics</i> , <b>2019</b> , 15, e1008384	6	25
292	Joint Estimation of Pedigrees and Effective Population Size Using Markov Chain Monte Carlo. <i>Genetics</i> , <b>2019</b> , 212, 855-868	4	3
291	CCR5- $\Delta$ 32 is deleterious in the homozygous state in humans. <i>Nature Medicine</i> , <b>2019</b> , 25, 909-910	50.5	46
290	The population history of northeastern Siberia since the Pleistocene. <i>Nature</i> , <b>2019</b> , 570, 182-188	50.4	137
289	Temporal genomic contrasts reveal rapid evolutionary responses in an alpine mammal during recent climate change. <i>PLoS Genetics</i> , <b>2019</b> , 15, e1008119	6	33
288	Human Disease Variation in the Light of Population Genomics. <i>Cell</i> , <b>2019</b> , 177, 115-131	56.2	34
287	Detecting Natural Selection <b>2019</b> , 397-40		5
286	Retraction Note: CCR5- $\Delta$ 32 is deleterious in the homozygous state in humans. <i>Nature Medicine</i> , <b>2019</b> , 25, 1796	50.5	3
285	Parallel adaptation of rabbit populations to myxoma virus. <i>Science</i> , <b>2019</b> , 363, 1319-1326	33.3	66
284	Bottleneck and selection in the germline and maternal age influence transmission of mitochondrial DNA in human pedigrees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 25172-25178	11.5	32
283	Passage Adaptation Correlates With the Reduced Efficacy of the Influenza Vaccine. <i>Clinical Infectious Diseases</i> , <b>2019</b> , 69, 1198-1204	11.6	10
282	Genetic rescue and the maintenance of native ancestry. <i>Conservation Genetics</i> , <b>2019</b> , 20, 59-64	2.6	19
281	Emergence and Spread of Basal Lineages of <i>Yersinia pestis</i> during the Neolithic Decline. <i>Cell</i> , <b>2019</b> , 176, 295-305.e10	56.2	93
280	Origins and genetic legacies of the Caribbean Taino. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, 2341-2346	11.5	45
279	Physiological and Genetic Adaptations to Diving in Sea Nomads. <i>Cell</i> , <b>2018</b> , 173, 569-580.e15	56.2	82
278	Population genomics of finless porpoises reveal an incipient cetacean species adapted to freshwater. <i>Nature Communications</i> , <b>2018</b> , 9, 1276	17.4	37
277	A Population Phylogenetic View of Mitochondrial Heteroplasmy. <i>Genetics</i> , <b>2018</b> , 208, 1261-1274	4	23
276	Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. <i>Nature</i> , <b>2018</b> , 553, 203-207	50.4	178

275	Molecular Footprints of Aquatic Adaptation Including Bone Mass Changes in Cetaceans. <i>Genome Biology and Evolution</i> , <b>2018</b> , 10, 967-975	3.9	17
274	Human adaptation to extreme environmental conditions. <i>Current Opinion in Genetics and Development</i> , <b>2018</b> , 53, 77-82	4.9	32
273	On the number of siblings and p-th cousins in a large population sample. <i>Journal of Mathematical Biology</i> , <b>2018</b> , 77, 1279-1298	2	5
272	137 ancient human genomes from across the Eurasian steppes. <i>Nature</i> , <b>2018</b> , 557, 369-374	50.4	197
271	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. <i>Science</i> , <b>2018</b> , 360,	33.3	162
270	Genomic Takeover by Transposable Elements in the Strawberry Poison Frog. <i>Molecular Biology and Evolution</i> , <b>2018</b> , 35, 2913-2927	8.3	27
269	Novel Form of Alternative Splicing of NFKB1. Its Role in Polycythemia and Adaptation to High Altitude in Andean Aymara. <i>Blood</i> , <b>2018</b> , 132, 2316-2316	2.2	0
268	Early human dispersals within the Americas. <i>Science</i> , <b>2018</b> , 362,	33.3	118
267	Estimating the Timing of Multiple Admixture Pulses During Local Ancestry Inference. <i>Genetics</i> , <b>2018</b> , 210, 1089-1107	4	19
266	Genomic Analyses from Non-invasive Prenatal Testing Reveal Genetic Associations, Patterns of Viral Infections, and Chinese Population History. <i>Cell</i> , <b>2018</b> , 175, 347-359.e14	56.2	123
265	The Genetic Basis of Adaptation following Plastic Changes in Coloration in a Novel Environment. <i>Current Biology</i> , <b>2018</b> , 28, 2970-2977.e7	6.3	45
264	Pervasive introgression facilitated domestication and adaptation in the Bos species complex. <i>Nature Ecology and Evolution</i> , <b>2018</b> , 2, 1139-1145	12.3	90
263	Tracing the peopling of the world through genomics. <i>Nature</i> , <b>2017</b> , 541, 302-310	50.4	338
262	Selection in Europeans on Fatty Acid Desaturases Associated with Dietary Changes. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 1307-1318	8.3	50
261	Fast admixture analysis and population tree estimation for SNP and NGS data. <i>Bioinformatics</i> , <b>2017</b> , 33, 2148-2155	7.2	29
260	The Evolutionary Pathway to Virulence of an RNA Virus. <i>Cell</i> , <b>2017</b> , 169, 35-46.e19	56.2	77
259	Asian wild rice is a hybrid swarm with extensive gene flow and feralization from domesticated rice. <i>Genome Research</i> , <b>2017</b> , 27, 1029-1038	9.7	60
258	Natural Selection on Genes Related to Cardiovascular Health in High-Altitude Adapted Andeans. <i>American Journal of Human Genetics</i> , <b>2017</b> , 101, 752-767	11	53

257	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , <b>2017</b> , 358, 659-662	33.3	160
256	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> , <b>2017</b> , 13, e1006529	6	71
255	Composite likelihood method for inferring local pedigrees. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006963	6	15
254	Q&A: Where did the Neanderthals go?. <i>BMC Biology</i> , <b>2017</b> , 15, 73	7.3	2
253	Genome-wide signatures of complex introgression and adaptive evolution in the big cats. <i>Science Advances</i> , <b>2017</b> , 3, e1700299	14.3	67
252	Archaic Adaptive Introgression in TBX15/WARS2. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 509-524	8.3	63
251	A genomic history of Aboriginal Australia. <i>Nature</i> , <b>2016</b> , 538, 207-214	50.4	268
250	Genomic analyses inform on migration events during the peopling of Eurasia. <i>Nature</i> , <b>2016</b> , 538, 238-242	50.4	234
249	Detecting recent selective sweeps while controlling for mutation rate and background selection. <i>Molecular Ecology</i> , <b>2016</b> , 25, 142-56	5.7	91
248	SweepFinder2: increased sensitivity, robustness and flexibility. <i>Bioinformatics</i> , <b>2016</b> , 32, 1895-7	7.2	122
247	REPdenovo: Inferring De Novo Repeat Motifs from Short Sequence Reads. <i>PLoS ONE</i> , <b>2016</b> , 11, e0150719	9.7	30
246	Evolution of GOUNDRY, a cryptic subgroup of <i>Anopheles gambiae</i> s.l., and its impact on susceptibility to Plasmodium infection. <i>Molecular Ecology</i> , <b>2016</b> , 25, 1494-510	5.7	11
245	Fumio Tajima and the Origin of Modern Population Genetics. <i>Genetics</i> , <b>2016</b> , 204, 389-390	4	
244	The Genetic Cost of Neanderthal Introgression. <i>Genetics</i> , <b>2016</b> , 203, 881-91	4	201
243	Estimating IBD tracts from low coverage NGS data. <i>Bioinformatics</i> , <b>2016</b> , 32, 2096-102	7.2	23
242	The Power of Inbreeding: NGS-Based GWAS of Rice Reveals Convergent Evolution during Rice Domestication. <i>Molecular Plant</i> , <b>2016</b> , 9, 975-85	14.4	66
241	Postglacial viability and colonization in North America's ice-free corridor. <i>Nature</i> , <b>2016</b> , 537, 45-49	50.4	213
240	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> , <b>2015</b> , 52, 12-21	0.6	18

239	POPULATION GENETICS. Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , <b>2015</b> , 349, aab3884	33.3	317
238	Phylogenetic ANOVA: The Expression Variance and Evolution Model for Quantitative Trait Evolution. <i>Systematic Biology</i> , <b>2015</b> , 64, 695-708	8.4	47
237	The ancestry and affiliations of Kennewick Man. <i>Nature</i> , <b>2015</b> , 523, 455-458	50.4	157
236	Fitting the Balding-Nichols model to forensic databases. <i>Forensic Science International: Genetics</i> , <b>2015</b> , 19, 86-91	4.3	1
235	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> , <b>2015</b> , 282, 20141950	4.4	7
234	A genome-wide scan for signatures of directional selection in domesticated pigs. <i>BMC Genomics</i> , <b>2015</b> , 16, 130	4.5	47
233	Evidence for archaic adaptive introgression in humans. <i>Nature Reviews Genetics</i> , <b>2015</b> , 16, 359-71	30.1	328
232	A recent bottleneck of Y chromosome diversity coincides with a global change in culture. <i>Genome Research</i> , <b>2015</b> , 25, 459-66	9.7	235
231	Early divergent strains of <i>Yersinia pestis</i> in Eurasia 5,000 years ago. <i>Cell</i> , <b>2015</b> , 163, 571-82	56.2	294
230	Greenlandic Inuit show genetic signatures of diet and climate adaptation. <i>Science</i> , <b>2015</b> , 349, 1343-7	33.3	298
229	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> , <b>2015</b> , 52, 1-4	0.6	
228	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> , <b>2015</b> , 112, E6889-97	11.5	89
227	The origin and evolution of maize in the Southwestern United States. <i>Nature Plants</i> , <b>2015</b> , 1, 14003	11.5	99
226	Reticulate Speciation and Barriers to Introgression in the <i>Anopheles gambiae</i> Species Complex. <i>Genome Biology and Evolution</i> , <b>2015</b> , 7, 3116-31	3.9	26
225	De novo assembly of a haplotype-resolved human genome. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 617-22	44.5	57
224	Population genomics of Bronze Age Eurasia. <i>Nature</i> , <b>2015</b> , 522, 167-72	50.4	827
223	Uncovering the genetic history of the present-day Greenlandic population. <i>American Journal of Human Genetics</i> , <b>2015</b> , 96, 54-69	11	61
222	Convergent evolution of the genomes of marine mammals. <i>Nature Genetics</i> , <b>2015</b> , 47, 272-5	36.3	263

221	Adaptation and possible ancient interspecies introgression in pigs identified by whole-genome sequencing. <i>Nature Genetics</i> , <b>2015</b> , 47, 217-25	36.3	188
220	Association Mapping for Compound Heterozygous Traits Using Phenotypic Distance and Integer Programming. <i>Lecture Notes in Computer Science</i> , <b>2015</b> , 136-147	0.9	1
219	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , <b>2014</b> , 506, 225-9	50.4	357
218	On detecting incomplete soft or hard selective sweeps using haplotype structure. <i>Molecular Biology and Evolution</i> , <b>2014</b> , 31, 1275-91	8.3	214
217	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> , <b>2014</b> , 94, 479	11	78
216	Population genomics reveal recent speciation and rapid evolutionary adaptation in polar bears. <i>Cell</i> , <b>2014</b> , 157, 785-94	56.2	242
215	ngsTools: methods for population genetics analyses from next-generation sequencing data. <i>Bioinformatics</i> , <b>2014</b> , 30, 1486-7	7.2	154
214	Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. <i>Nature</i> , <b>2014</b> , 507, 225-8	50.4	235
213	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , <b>2014</b> , 505, 87-91	50.4	581
212	Paleogenomics. Genomic structure in Europeans dating back at least 36,200 years. <i>Science</i> , <b>2014</b> , 346, 1113-8	33.3	232
211	The lengths of admixture tracts. <i>Genetics</i> , <b>2014</b> , 197, 953-67	4	83
210	Genome-wide ancestry patterns in Rapanui suggest pre-European admixture with Native Americans. <i>Current Biology</i> , <b>2014</b> , 24, 2518-25	6.3	39
209	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , <b>2014</b> , 24, R1035-7	6.3	62
208	A Selective Sweep on a Deleterious Mutation in CPT1A in Arctic Populations. <i>American Journal of Human Genetics</i> , <b>2014</b> , 95, 584-589	11	86
207	Costs and benefits of mutational robustness in RNA viruses. <i>Cell Reports</i> , <b>2014</b> , 8, 1026-36	10.6	38
206	Error-prone polymerase activity causes multinucleotide mutations in humans. <i>Genome Research</i> , <b>2014</b> , 24, 1445-54	9.7	51
205	Altitude adaptation in Tibetans caused by introgression of Denisovan-like DNA. <i>Nature</i> , <b>2014</b> , 512, 194-7	50.4	605
204	The genetic prehistory of the New World Arctic. <i>Science</i> , <b>2014</b> , 345, 1255832	33.3	204



203	A common Greenlandic TBC1D4 variant confers muscle insulin resistance and type 2 diabetes. <i>Nature</i> , <b>2014</b> , 512, 190-3	50.4	258
202	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> , <b>2014</b> , 111, 15474-9 <sup>11.5</sup>	11.5	140
201	Natural selection reduced diversity on human y chromosomes. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004064	6	69
200	Classic selective sweeps revealed by massive sequencing in cattle. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004148	6	158
199	Selection on a variant associated with improved viral clearance drives local, adaptive pseudogenization of interferon lambda 4 (IFNL4). <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004681	6	66
198	A model-based approach for identifying signatures of ancient balancing selection in genetic data. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004561	6	118
197	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> , <b>2014</b> , 111, E5661-9	11.5	197
196	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> , <b>2014</b> , 111, 18655-60	11.5	133
195	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> , <b>2014</b> , 22, 1040-5	5.3	23
194	ANGSD: Analysis of Next Generation Sequencing Data. <i>BMC Bioinformatics</i> , <b>2014</b> , 15, 356	3.6	1087
193	Modeling gene expression evolution with an extended Ornstein-Uhlenbeck process accounting for within-species variation. <i>Molecular Biology and Evolution</i> , <b>2014</b> , 31, 201-11	8.3	68
192	bammds: a tool for assessing the ancestry of low-depth whole-genome data using multidimensional scaling (MDS). <i>Bioinformatics</i> , <b>2014</b> , 30, 2962-4	7.2	31
191	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> , <b>2013</b> , 93, 1072-86	11	109
190	Molecular footprints of domestication and improvement in soybean revealed by whole genome re-sequencing. <i>BMC Genomics</i> , <b>2013</b> , 14, 579	4.5	155
189	Unlocking the vault: next-generation museum population genomics. <i>Molecular Ecology</i> , <b>2013</b> , 22, 6018-33.7	33.7	250
188	Bacterial natural transformation by highly fragmented and damaged DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 19860-5	11.5	111
187	Detecting adaptive trait loci in nonmodel systems: divergence or admixture mapping?. <i>Molecular Ecology</i> , <b>2013</b> , 22, 6131-48	5.7	20
186	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , <b>2013</b> , 499, 74-8	50.4	563

185	Quantifying population genetic differentiation from next-generation sequencing data. <i>Genetics</i> , <b>2013</b> , 195, 979-92	4	141
184	Genetic signatures reveal high-altitude adaptation in a set of ethiopian populations. <i>Molecular Biology and Evolution</i> , <b>2013</b> , 30, 1877-88	8.3	137
183	Inferring demographic history from a spectrum of shared haplotype lengths. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003521	172	
182	Genetic architecture of vitamin B12 and folate levels uncovered applying deeply sequenced large datasets. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003530	6	72
181	Estimating inbreeding coefficients from NGS data: Impact on genotype calling and allele frequency estimation. <i>Genome Research</i> , <b>2013</b> , 23, 1852-61	9.7	59
180	A scan for human-specific relaxation of negative selection reveals unexpected polymorphism in proteasome genes. <i>Molecular Biology and Evolution</i> , <b>2013</b> , 30, 1808-15	8.3	16
179	Calculation of Tajima's D and other neutrality test statistics from low depth next-generation sequencing data. <i>BMC Bioinformatics</i> , <b>2013</b> , 14, 289	3.6	140
178	Estimating population divergence time and phylogeny from single-nucleotide polymorphisms data with outgroup ascertainment bias. <i>Molecular Ecology</i> , <b>2012</b> , 21, 974-86	5.7	10
177	Looking for Darwin in genomic sequences--validity and success of statistical methods. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 2889-93	8.3	26
176	A metagenome-wide association study of gut microbiota in type 2 diabetes. <i>Nature</i> , <b>2012</b> , 490, 55-60	50.4	3779
175	Evidence for positive selection on a number of MicroRNA regulatory interactions during recent human evolution. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002578	6	52
174	Distinguishing between selective sweeps from standing variation and from a de novo mutation. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1003011	6	134
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