

Rasmus Nielsen

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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	A metagenome-wide association study of gut microbiota in type 2 diabetes. <i>Nature</i> , 2012 , 490, 55-60	50.4	3779
327	A draft sequence of the Neandertal genome. <i>Science</i> , 2010 , 328, 710-722	33.3	2599
326	Bayesian inference of phylogeny and its impact on evolutionary biology. <i>Science</i> , 2001 , 294, 2310-4	33.3	2114
325	Codon-substitution models for heterogeneous selection pressure at amino acid sites. <i>Genetics</i> , 2000 , 155, 431-49	4	1740
324	Bayes empirical bayes inference of amino acid sites under positive selection. <i>Molecular Biology and Evolution</i> , 2005 , 22, 1107-18	8.3	1669
323	Evolution of genes and genomes on the Drosophila phylogeny. <i>Nature</i> , 2007 , 450, 203-18	50.4	1586
322	Evaluation of an improved branch-site likelihood method for detecting positive selection at the molecular level. <i>Molecular Biology and Evolution</i> , 2005 , 22, 2472-9	8.3	1312
321	Estimating synonymous and nonsynonymous substitution rates under realistic evolutionary models. <i>Molecular Biology and Evolution</i> , 2000 , 17, 32-43	8.3	1210
320	Likelihood models for detecting positively selected amino acid sites and applications to the HIV-1 envelope gene. <i>Genetics</i> , 1998 , 148, 929-36	4	1190
319	Multilocus methods for estimating population sizes, migration rates and divergence time, with applications to the divergence of <i>Drosophila pseudoobscura</i> and <i>D. persimilis</i> . <i>Genetics</i> , 2004 , 167, 747-60	4	1137
318	Molecular signatures of natural selection. <i>Annual Review of Genetics</i> , 2005 , 39, 197-218	14.5	1123
317	ANGSD: Analysis of Next Generation Sequencing Data. <i>BMC Bioinformatics</i> , 2014 , 15, 356	3.6	1087
316	Evolutionary and biomedical insights from the rhesus macaque genome. <i>Science</i> , 2007 , 316, 222-34	33.3	1072
315	Distinguishing migration from isolation: a Markov chain Monte Carlo approach. <i>Genetics</i> , 2001 , 158, 885-96	4	1031
314	Sequencing of 50 human exomes reveals adaptation to high altitude. <i>Science</i> , 2010 , 329, 75-8	33.3	1020
313	Codon-substitution models for detecting molecular adaptation at individual sites along specific lineages. <i>Molecular Biology and Evolution</i> , 2002 , 19, 908-17	8.3	993
312	Genotype and SNP calling from next-generation sequencing data. <i>Nature Reviews Genetics</i> , 2011 , 12, 443-51	30.1	959

311	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010 , 463, 311-7	50.4	864
310	Population genomics of Bronze Age Eurasia. <i>Nature</i> , 2015 , 522, 167-72	50.4	827
309	Integration within the Felsenstein equation for improved Markov chain Monte Carlo methods in population genetics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 2785-90	11.5	789
308	The evolution of gene expression levels in mammalian organs. <i>Nature</i> , 2011 , 478, 343-8	50.4	787
307	The diploid genome sequence of an Asian individual. <i>Nature</i> , 2008 , 456, 60-5	50.4	744
306	Statistical tests of selective neutrality in the age of genomics. <i>Heredity</i> , 2001 , 86, 641-7	3.6	707
305	A scan for positively selected genes in the genomes of humans and chimpanzees. <i>PLoS Biology</i> , 2005 , 3, e170	9.7	705
304	Genomic scans for selective sweeps using SNP data. <i>Genome Research</i> , 2005 , 15, 1566-75	9.7	668
303	Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. <i>Nature Biotechnology</i> , 2011 , 30, 105-11	44.5	635
302	Natural selection on protein-coding genes in the human genome. <i>Nature</i> , 2005 , 437, 1153-7	50.4	615
301	Altitude adaptation in Tibetans caused by introgression of Denisovan-like DNA. <i>Nature</i> , 2014 , 512, 194-7	50.4	605
300	Stochastic mapping of morphological characters. <i>Systematic Biology</i> , 2003 , 52, 131-58	8.4	590
299	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , 2014 , 505, 87-91	50.4	581
298	Ancient human genome sequence of an extinct Palaeo-Eskimo. <i>Nature</i> , 2010 , 463, 757-62	50.4	567
297	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013 , 499, 74-8	50.4	563
296	An Aboriginal Australian genome reveals separate human dispersals into Asia. <i>Science</i> , 2011 , 334, 94-8	33.3	528
295	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios. <i>Science</i> , 2003 , 302, 1960-3	33.3	517
294	Species-specific responses of Late Quaternary megafauna to climate and humans. <i>Nature</i> , 2011 , 479, 359-64	50.4	483

293	Assessing the evolutionary impact of amino acid mutations in the human genome. <i>PLoS Genetics</i> , 2008 , 4, e1000083	6	473
292	Synonymous and nonsynonymous rate variation in nuclear genes of mammals. <i>Journal of Molecular Evolution</i> , 1998 , 46, 409-18	3.1	463
291	Accuracy and power of statistical methods for detecting adaptive evolution in protein coding sequences and for identifying positively selected sites. <i>Genetics</i> , 2004 , 168, 1041-51	4	443
290	Effect of recombination on the accuracy of the likelihood method for detecting positive selection at amino acid sites. <i>Genetics</i> , 2003 , 164, 1229-36	4	430
289	Comparative genome sequencing of <i>Drosophila pseudoobscura</i> : chromosomal, gene, and cis-element evolution. <i>Genome Research</i> , 2005 , 15, 1-18	9.7	410
288	Patterns of positive selection in six Mammalian genomes. <i>PLoS Genetics</i> , 2008 , 4, e1000144	6	405
287	The use of coded PCR primers enables high-throughput sequencing of multiple homolog amplification products by 454 parallel sequencing. <i>PLoS ONE</i> , 2007 , 2, e197	3.7	402
286	Pervasive adaptive evolution in mammalian fertilization proteins. <i>Molecular Biology and Evolution</i> , 2003 , 20, 18-20	8.3	382
285	Recent and ongoing selection in the human genome. <i>Nature Reviews Genetics</i> , 2007 , 8, 857-68	30.1	365
284	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , 2014 , 506, 225-9	50.4	357
283	Ascertainment bias in studies of human genome-wide polymorphism. <i>Genome Research</i> , 2005 , 15, 1496-502	50.2	351
282	Signatures of environmental genetic adaptation pinpoint pathogens as the main selective pressure through human evolution. <i>PLoS Genetics</i> , 2011 , 7, e1002355	6	349
281	Localizing recent adaptive evolution in the human genome. <i>PLoS Genetics</i> , 2007 , 3, e90	6	342
280	Tracing the peopling of the world through genomics. <i>Nature</i> , 2017 , 541, 302-310	50.4	338
279	Genome-wide patterns of nucleotide polymorphism in domesticated rice. <i>PLoS Genetics</i> , 2007 , 3, 1745-56		334
278	Evidence for archaic adaptive introgression in humans. <i>Nature Reviews Genetics</i> , 2015 , 16, 359-71	30.1	328
277	Ancient biomolecules from deep ice cores reveal a forested southern Greenland. <i>Science</i> , 2007 , 317, 111-4	33.3	319
276	POPULATION GENETICS. Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015 , 349, aab3884	33.3	317

275	Models of amino acid substitution and applications to mitochondrial protein evolution. <i>Molecular Biology and Evolution</i> , 1998 , 15, 1600-11	8.3	305
274	Proportionally more deleterious genetic variation in European than in African populations. <i>Nature</i> , 2008 , 451, 994-7	50.4	299
273	Greenlandic Inuit show genetic signatures of diet and climate adaptation. <i>Science</i> , 2015 , 349, 1343-7	33.3	298
272	Linkage disequilibrium as a signature of selective sweeps. <i>Genetics</i> , 2004 , 167, 1513-24	4	296
271	Early divergent strains of <i>Yersinia pestis</i> in Eurasia 5,000 years ago. <i>Cell</i> , 2015 , 163, 571-82	56.2	294
270	Mapping mutations on phylogenies. <i>Systematic Biology</i> , 2002 , 51, 729-39	8.4	289
269	Complete resequencing of 40 genomes reveals domestication events and genes in silkworm (<i>Bombyx</i>). <i>Science</i> , 2009 , 326, 433-6	33.3	277
268	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016 , 538, 207-214	50.4	268
267	Resequencing of 200 human exomes identifies an excess of low-frequency non-synonymous coding variants. <i>Nature Genetics</i> , 2010 , 42, 969-72	36.3	264
266	Convergent evolution of the genomes of marine mammals. <i>Nature Genetics</i> , 2015 , 47, 272-5	36.3	263
265	Radiation of extant cetaceans driven by restructuring of the oceans. <i>Systematic Biology</i> , 2009 , 58, 573-85	8.4	263
264	A common Greenlandic TBC1D4 variant confers muscle insulin resistance and type 2 diabetes. <i>Nature</i> , 2014 , 512, 190-3	50.4	258
263	Simultaneous inference of selection and population growth from patterns of variation in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 7882-7	11.5	254
262	The cost of inbreeding in <i>Arabidopsis</i> . <i>Nature</i> , 2002 , 416, 531-4	50.4	251
261	Unlocking the vault: next-generation museum population genomics. <i>Molecular Ecology</i> , 2013 , 22, 6018-33	7	250
260	Estimation of population parameters and recombination rates from single nucleotide polymorphisms. <i>Genetics</i> , 2000 , 154, 931-42	4	243
259	Population genomics reveal recent speciation and rapid evolutionary adaptation in polar bears. <i>Cell</i> , 2014 , 157, 785-94	56.2	242
258	SNP calling, genotype calling, and sample allele frequency estimation from New-Generation Sequencing data. <i>PLoS ONE</i> , 2012 , 7, e37558	3.7	242

257	A recent bottleneck of Y chromosome diversity coincides with a global change in culture. <i>Genome Research</i> , 2015 , 25, 459-66	9.7	235
256	Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. <i>Nature</i> , 2014 , 507, 225-8	50.4	235
255	Genomic analyses inform on migration events during the peopling of Eurasia. <i>Nature</i> , 2016 , 538, 238-242	50.4	234
254	Paleogenomics. Genomic structure in Europeans dating back at least 36,200 years. <i>Science</i> , 2014 , 346, 1113-8	33.3	232
253	Ascertainment biases in SNP chips affect measures of population divergence. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2534-47	8.3	232
252	Mutation-selection models of codon substitution and their use to estimate selective strengths on codon usage. <i>Molecular Biology and Evolution</i> , 2008 , 25, 568-79	8.3	220
251	Genome sequencing and comparison of two nonhuman primate animal models, the cynomolgus and Chinese rhesus macaques. <i>Nature Biotechnology</i> , 2011 , 29, 1019-23	44.5	219
250	Statistical inferences in phylogeography. <i>Molecular Ecology</i> , 2009 , 18, 1034-47	5.7	219
249	On detecting incomplete soft or hard selective sweeps using haplotype structure. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1275-91	8.3	214
248	Postglacial viability and colonization in North America's ice-free corridor. <i>Nature</i> , 2016 , 537, 45-49	50.4	213
247	The genetic prehistory of the New World Arctic. <i>Science</i> , 2014 , 345, 1255-832	33.3	204
246	Ancient bacteria show evidence of DNA repair. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 14401-5	11.5	204
245	The Genetic Cost of Neanderthal Introgression. <i>Genetics</i> , 2016 , 203, 881-91	4	201
244	Targets of balancing selection in the human genome. <i>Molecular Biology and Evolution</i> , 2009 , 26, 2755-64	8.3	199
243	137 ancient human genomes from across the Eurasian steppes. <i>Nature</i> , 2018 , 557, 369-374	50.4	197
242	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	11.5	197
241	Adaptive genic evolution in the <i>Drosophila</i> genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 2271-6	11.5	192
240	Estimating effective paternity number in social insects and the effective number of alleles in a population. <i>Molecular Ecology</i> , 2003 , 12, 3157-64	5.7	189

239	Adaptation and possible ancient interspecies introgression in pigs identified by whole-genome sequencing. <i>Nature Genetics</i> , 2015 , 47, 217-25	36.3	188
238	Taxon sampling and the accuracy of large phylogenies. <i>Systematic Biology</i> , 1998 , 47, 702-10	8.4	184
237	Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. <i>Nature</i> , 2018 , 553, 203-207	50.4	178
236	Balancing selection maintains a form of ERAP2 that undergoes nonsense-mediated decay and affects antigen presentation. <i>PLoS Genetics</i> , 2010 , 6, e1001157	6	175
235	Inferring demographic history from a spectrum of shared haplotype lengths. <i>PLoS Genetics</i> , 2013 , 9, e1003521	16.3	172
234	Ancient DNA reveals late survival of mammoth and horse in interior Alaska. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 22352-7	11.5	170
233	Population genetic inference from genomic sequence variation. <i>Genome Research</i> , 2010 , 20, 291-300	9.7	165
232	The first horse herders and the impact of early Bronze Age steppe expansions into Asia. <i>Science</i> , 2018 , 360,	33.3	162
231	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , 2017 , 358, 659-662	33.3	160
230	Classic selective sweeps revealed by massive sequencing in cattle. <i>PLoS Genetics</i> , 2014 , 10, e1004148	6	158
229	The ancestry and affiliations of Kennewick Man. <i>Nature</i> , 2015 , 523, 455-458	50.4	157
228	Molecular footprints of domestication and improvement in soybean revealed by whole genome re-sequencing. <i>BMC Genomics</i> , 2013 , 14, 579	4.5	155
227	ngsTools: methods for population genetics analyses from next-generation sequencing data. <i>Bioinformatics</i> , 2014 , 30, 1486-7	7.2	154
226	Statistical assignment of DNA sequences using Bayesian phylogenetics. <i>Systematic Biology</i> , 2008 , 57, 750-7	8.4	151
225	Demographic histories and patterns of linkage disequilibrium in Chinese and Indian rhesus macaques. <i>Science</i> , 2007 , 316, 240-3	33.3	146
224	Ancient DNA chronology within sediment deposits: are paleobiological reconstructions possible and is DNA leaching a factor?. <i>Molecular Biology and Evolution</i> , 2007 , 24, 982-9	8.3	145
223	Quantifying population genetic differentiation from next-generation sequencing data. <i>Genetics</i> , 2013 , 195, 979-92	4	141
222	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, 15474-9	11.5	140

221	Calculation of Tajima's D and other neutrality test statistics from low depth next-generation sequencing data. <i>BMC Bioinformatics</i> , 2013 , 14, 289	3.6	140
220	Inference of historical changes in migration rate from the lengths of migrant tracts. <i>Genetics</i> , 2009 , 181, 711-9	4	138
219	The discovery of single-nucleotide polymorphisms--and inferences about human demographic history. <i>American Journal of Human Genetics</i> , 2001 , 69, 1332-47	11	138
218	The population history of northeastern Siberia since the Pleistocene. <i>Nature</i> , 2019 , 570, 182-188	50.4	137
217	Genetic signatures reveal high-altitude adaptation in a set of ethiopian populations. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1877-88	8.3	137
216	Distinguishing between selective sweeps from standing variation and from a de novo mutation. <i>PLoS Genetics</i> , 2012 , 8, e1003011	6	134
215	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, 18655-60	11.5	133
214	Population size changes reshape genomic patterns of diversity. <i>Evolution; International Journal of Organic Evolution</i> , 2007 , 61, 3001-6	3.8	129
213	Genes under positive selection in Escherichia coli. <i>Genome Research</i> , 2007 , 17, 1336-43	9.7	128
212	In defence of model-based inference in phylogeography. <i>Molecular Ecology</i> , 2010 , 19, 436-446	5.7	127
211	Estimation of allele frequency and association mapping using next-generation sequencing data. <i>BMC Bioinformatics</i> , 2011 , 12, 231	3.6	126
210	A Likelihood-Ratio Test of Monophyly. <i>Systematic Biology</i> , 1996 , 45, 546-558	8.4	124
209	Estimating the distribution of selection coefficients from phylogenetic data with applications to mitochondrial and viral DNA. <i>Molecular Biology and Evolution</i> , 2003 , 20, 1231-9	8.3	123
208	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	56.2	123
207	SweepFinder2: increased sensitivity, robustness and flexibility. <i>Bioinformatics</i> , 2016 , 32, 1895-7	7.2	122
206	Darwinian and demographic forces affecting human protein coding genes. <i>Genome Research</i> , 2009 , 19, 838-49	9.7	122
205	A model-based approach for identifying signatures of ancient balancing selection in genetic data. <i>PLoS Genetics</i> , 2014 , 10, e1004561	6	118
204	Early human dispersals within the Americas. <i>Science</i> , 2018 , 362,	33.3	118

203	The population structure of African cultivated rice <i>Oryza glaberrima</i> (Steud.): evidence for elevated levels of linkage disequilibrium caused by admixture with <i>O. sativa</i> and ecological adaptation. <i>Genetics</i> , 2005 , 169, 1639-47	4	117
202	Reconstituting the frequency spectrum of ascertained single-nucleotide polymorphism data. <i>Genetics</i> , 2004 , 168, 2373-82	4	117
201	Correcting for ascertainment biases when analyzing SNP data: applications to the estimation of linkage disequilibrium. <i>Theoretical Population Biology</i> , 2003 , 63, 245-55	1.2	113
200	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, 19860-5	11.5	111
199	Statistical approaches for DNA barcoding. <i>Systematic Biology</i> , 2006 , 55, 162-9	8.4	111
198	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, 1072-86	11	109
197	Natural selection affects multiple aspects of genetic variation at putatively neutral sites across the human genome. <i>PLoS Genetics</i> , 2011 , 7, e1002326	6	107
196	Estimation of 2Nes from temporal allele frequency data. <i>Genetics</i> , 2008 , 179, 497-502	4	107
195	The origin and evolution of maize in the Southwestern United States. <i>Nature Plants</i> , 2015 , 1, 14003	11.5	99
194	Population genetic analysis of ascertained SNP data. <i>Human Genomics</i> , 2004 , 1, 218-24	6.8	95
193	Using nuclear haplotypes with microsatellites to study gene flow between recently separated Cichlid species. <i>Molecular Ecology</i> , 2004 , 13, 909-19	5.7	93
192	Emergence and Spread of Basal Lineages of <i>Yersinia pestis</i> during the Neolithic Decline. <i>Cell</i> , 2019 , 176, 295-305.e10	56.2	93
191	Evolution of the integral membrane desaturase gene family in moths and flies. <i>Genetics</i> , 2002 , 162, 1737-45	4.52	92
190	Detecting recent selective sweeps while controlling for mutation rate and background selection. <i>Molecular Ecology</i> , 2016 , 25, 142-56	5.7	91
189	Statistical approaches to paternity analysis in natural populations and applications to the North Atlantic humpback whale. <i>Genetics</i> , 2001 , 157, 1673-82	4	90
188	Pervasive introgression facilitated domestication and adaptation in the <i>Bos</i> species complex. <i>Nature Ecology and Evolution</i> , 2018 , 2, 1139-1145	12.3	90
187	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	11.5	89
186	Rational design of DNA sequence-based strategies for subtyping <i>Listeria monocytogenes</i> . <i>Journal of Clinical Microbiology</i> , 2002 , 40, 3319-25	9.7	87

185	A Selective Sweep on a Deleterious Mutation in CPT1A in Arctic Populations. <i>American Journal of Human Genetics</i> , 2014 , 95, 584-589	11	86
184	The lengths of admixture tracts. <i>Genetics</i> , 2014 , 197, 953-67	4	83
183	Detecting selection in noncoding regions of nucleotide sequences. <i>Genetics</i> , 2004 , 167, 949-58	4	83
182	Physiological and Genetic Adaptations to Diving in Sea Nomads. <i>Cell</i> , 2018 , 173, 569-580.e15	56.2	82
181	Massive haplotypes underlie ecotypic differentiation in sunflowers. <i>Nature</i> , 2020 , 584, 602-607	50.4	81
180	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> , 2014 , 94, 479	11	78
179	The Evolutionary Pathway to Virulence of an RNA Virus. <i>Cell</i> , 2017 , 169, 35-46.e19	56.2	77
178	Population genetic analysis of shotgun assemblies of genomic sequences from multiple individuals. <i>Genome Research</i> , 2008 , 18, 1020-9	9.7	77
177	A likelihood ratio test for species membership based on DNA sequence data. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2005 , 360, 1969-74	5.8	76
176	Natural selection and the distribution of identity-by-descent in the human genome. <i>Genetics</i> , 2010 , 186, 295-308	4	75
175	An investigation of the statistical power of neutrality tests based on comparative and population genetic data. <i>Molecular Biology and Evolution</i> , 2009 , 26, 273-83	8.3	73
174	Relatedness mapping and tracts of relatedness for genome-wide data in the presence of linkage disequilibrium. <i>Genetic Epidemiology</i> , 2009 , 33, 266-74	2.6	73
173	Microsatellite mutation models: insights from a comparison of humans and chimpanzees. <i>Genetics</i> , 2004 , 168, 383-95	4	73
172	Genetic architecture of vitamin B12 and folate levels uncovered applying deeply sequenced large datasets. <i>PLoS Genetics</i> , 2013 , 9, e1003530	6	72
171	Linkage disequilibrium and inference of ancestral recombination in 538 single-nucleotide polymorphism clusters across the human genome. <i>American Journal of Human Genetics</i> , 2003 , 73, 285-300	11	72
170	A likelihood approach to populations samples of microsatellite alleles. <i>Genetics</i> , 1997 , 146, 711-6	4	72
169	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, e100529	6	71
168	Radiation and speciation of pelagic organisms during periods of global warming: the case of the common minke whale, <i>Balaenoptera acutorostrata</i> . <i>Molecular Ecology</i> , 2007 , 16, 1481-95	5.7	70

167	Natural selection reduced diversity on human y chromosomes. <i>PLoS Genetics</i> , 2014 , 10, e1004064	6	69
166	Design of association studies with pooled or un-pooled next-generation sequencing data. <i>Genetic Epidemiology</i> , 2010 , 34, 479-91	2.6	69
165	Modeling gene expression evolution with an extended Ornstein-Uhlenbeck process accounting for within-species variation. <i>Molecular Biology and Evolution</i> , 2014 , 31, 201-11	8.3	68
164	DISCERNING BETWEEN RECURRENT GENE FLOW AND RECENT DIVERGENCE UNDER A FINITE-SITE MUTATION MODEL APPLIED TO NORTH ATLANTIC AND MEDITERRANEAN SEA FIN WHALE (BALAENOPTERA PHYSALUS) POPULATIONS. <i>Evolution; International Journal of Organic Evolution</i> , 2004 , 58, 670-675	3.8	68
163	Genome-wide signatures of complex introgression and adaptive evolution in the big cats. <i>Science Advances</i> , 2017 , 3, e1700299	14.3	67
162	Detecting site-specific physicochemical selective pressures: applications to the Class I HLA of the human major histocompatibility complex and the SRK of the plant sporophytic self-incompatibility system. <i>Journal of Molecular Evolution</i> , 2005 , 60, 315-26	3.1	67
161	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	6	66
160	The Power of Inbreeding: NGS-Based GWAS of Rice Reveals Convergent Evolution during Rice Domestication. <i>Molecular Plant</i> , 2016 , 9, 975-85	14.4	66
159	Parallel adaptation of rabbit populations to myxoma virus. <i>Science</i> , 2019 , 363, 1319-1326	33.3	66
158	Natural selection on the Arabidopsis thaliana genome in present and future climates. <i>Nature</i> , 2019 , 573, 126-129	50.4	63
157	Archaic Adaptive Introgression in TBX15/WARS2. <i>Molecular Biology and Evolution</i> , 2017 , 34, 509-524	8.3	63
156	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , 2014 , 24, R1035-7	6.3	62
155	Uncovering the genetic history of the present-day Greenlandic population. <i>American Journal of Human Genetics</i> , 2015 , 96, 54-69	11	61
154	Maximum likelihood estimation of ancestral codon usage bias parameters in Drosophila. <i>Molecular Biology and Evolution</i> , 2007 , 24, 228-35	8.3	61
153	Asian wild rice is a hybrid swarm with extensive gene flow and feralization from domesticated rice. <i>Genome Research</i> , 2017 , 27, 1029-1038	9.7	60
152	Estimating inbreeding coefficients from NGS data: Impact on genotype calling and allele frequency estimation. <i>Genome Research</i> , 2013 , 23, 1852-61	9.7	59
151	Adaptionism-30 years after Gould and Lewontin. <i>Evolution; International Journal of Organic Evolution</i> , 2009 , 63, 2487-90	3.8	58
150	De novo assembly of a haplotype-resolved human genome. <i>Nature Biotechnology</i> , 2015 , 33, 617-22	44.5	57

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- 5 Inferring person-to-person networks of Plasmodium falciparum transmission: are analyses of routine surveillance data up to the task?. *Malaria Journal*, **2022**, 21, 58 3.6
- 4 VolcanoFinder: Genomic scans for adaptive introgression **2020**, 16, e1008867
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