

Laurent Excoffier

List of Publications by Year in descending order

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195
papers

69,435
citations

4831

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2896

196
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227
all docs

227
docs citations

227
times ranked

51668
citing authors

#	ARTICLE	IF	CITATIONS
1	Arlequin suite ver 3.5: a new series of programs to perform population genetics analyses under Linux and Windows. <i>Molecular Ecology Resources</i> , 2010, 10, 564-567.	2.2	13,484
2	Analysis of molecular variance inferred from metric distances among DNA haplotypes: application to human mitochondrial DNA restriction data.. <i>Genetics</i> , 1992, 131, 479-491.	1.2	11,818
3	Arlequin (version 3.0): An integrated software package for population genetics data analysis. <i>Evolutionary Bioinformatics</i> , 2005, 1, 117693430500100.	0.6	6,908
4	Arlequin (version 3.0): an integrated software package for population genetics data analysis. <i>Evolutionary Bioinformatics</i> , 2007, 1, 47-50.	0.6	3,416
5	A simulated annealing approach to define the genetic structure of populations. <i>Molecular Ecology</i> , 2002, 11, 2571-2581.	2.0	1,670
6	Maximum-likelihood estimation of molecular haplotype frequencies in a diploid population.. <i>Molecular Biology and Evolution</i> , 1995, 12, 921-7.	3.5	1,661
7	Estimation of Past Demographic Parameters From the Distribution of Pairwise Differences When the Mutation Rates Vary Among Sites: Application to Human Mitochondrial DNA. <i>Genetics</i> , 1999, 152, 1079-1089.	1.2	1,297
8	Robust Demographic Inference from Genomic and SNP Data. <i>PLoS Genetics</i> , 2013, 9, e1003905.	1.5	1,185
9	Genetic Consequences of Range Expansions. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2009, 40, 481-501.	3.8	1,072
10	PGDSpider: an automated data conversion tool for connecting population genetics and genomics programs. <i>Bioinformatics</i> , 2012, 28, 298-299.	1.8	1,002
11	A Human Genome Diversity Cell Line Panel. <i>Science</i> , 2002, 296, 261b-262.	6.0	907
12	A Generic Estimation of Population Subdivision Using Distances Between Alleles With Special Reference for Microsatellite Loci. <i>Genetics</i> , 1996, 142, 1061-1064.	1.2	793
13	Detecting loci under selection in a hierarchically structured population. <i>Heredity</i> , 2009, 103, 285-298.	1.2	718
14	Reconstructing Native American population history. <i>Nature</i> , 2012, 488, 370-374.	13.7	699
15	Gene flow and species delimitation. <i>Trends in Ecology and Evolution</i> , 2009, 24, 386-393.	4.2	682
16	THE HIDDEN SIDE OF INVASIONS: MASSIVE INTROGRESSION BY LOCAL GENES. <i>Evolution; International Journal of Organic Evolution</i> , 2008, 62, ???-???	1.1	658
17	Surfing during population expansions promotes genetic revolutions and structuration. <i>Trends in Ecology and Evolution</i> , 2008, 23, 347-351.	4.2	578
18	The Fate of Mutations Surfing on the Wave of a Range Expansion. <i>Molecular Biology and Evolution</i> , 2006, 23, 482-490.	3.5	565

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19	Patterns of DNA sequence diversity and genetic structure after a range expansion: lessons from the infinite-island model. <i>Molecular Ecology</i> , 2004, 13, 853-864.	2.0	550
20	Intra-Deme Molecular Diversity in Spatially Expanding Populations. <i>Molecular Biology and Evolution</i> , 2003, 20, 76-86.	3.5	519
21	Testing for linkage disequilibrium in genotypic data using the Expectation-Maximization algorithm. <i>Heredity</i> , 1996, 76, 377-383.	1.2	517
22	Ancient hybridization fuels rapid cichlid fish adaptive radiations. <i>Nature Communications</i> , 2017, 8, 14363.	5.8	509
23	Statistical evaluation of alternative models of human evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17614-17619.	3.3	497
24	Genetic Variation and Population Structure in Native Americans. <i>PLoS Genetics</i> , 2007, 3, e185.	1.5	454
25	Multiple maternal origins and weak phylogeographic structure in domestic goats. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 5927-5932.	3.3	450
26	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016, 538, 207-214.	13.7	439
27	Using allele frequencies and geographic subdivision to reconstruct gene trees within a species: molecular variance parsimony. <i>Genetics</i> , 1994, 136, 343-359.	1.2	405
28	fastsimcoal: a continuous-time coalescent simulator of genomic diversity under arbitrarily complex evolutionary scenarios. <i>Bioinformatics</i> , 2011, 27, 1332-1334.	1.8	401
29	Geographic Patterns of Genome Admixture in Latin American Mestizos. <i>PLoS Genetics</i> , 2008, 4, e1000037.	1.5	377
30	The impact of population expansion and mutation rate heterogeneity on DNA sequence polymorphism. <i>Molecular Biology and Evolution</i> , 1996, 13, 494-504.	3.5	375
31	Computer programs for population genetics data analysis: a survival guide. <i>Nature Reviews Genetics</i> , 2006, 7, 745-758.	7.7	316
32	ABCtoolbox: a versatile toolkit for approximate Bayesian computations. <i>BMC Bioinformatics</i> , 2010, 11, 116.	1.2	309
33	On the accumulation of deleterious mutations during range expansions. <i>Molecular Ecology</i> , 2013, 22, 5972-5982.	2.0	283
34	Why hunter-gatherer populations do not show signs of Pleistocene demographic expansions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 10597-10602.	3.3	271
35	Efficient Approximate Bayesian Computation Coupled With Markov Chain Monte Carlo Without Likelihood. <i>Genetics</i> , 2009, 182, 1207-1218.	1.2	266
36	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , 2017, 358, 659-662.	6.0	263

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37	Prehistoric genomes reveal the genetic foundation and cost of horse domestication. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5661-9.	3.3	260
38	The population history of northeastern Siberia since the Pleistocene. Nature, 2019, 570, 182-188.	13.7	259
39	Modern Humans Did Not Admix with Neanderthals during Their Range Expansion into Europe. PLoS Biology, 2004, 2, e421.	2.6	242
40	Chimpanzee genomic diversity reveals ancient admixture with bonobos. Science, 2016, 354, 477-481.	6.0	230
41	Serial Founder Effects During Range Expansion: A Spatial Analog of Genetic Drift. Genetics, 2012, 191, 171-181.	1.2	227
42	SIMCOAL 2.0: a program to simulate genomic diversity over large recombining regions in a subdivided population with a complex history. Bioinformatics, 2004, 20, 2485-2487.	1.8	224
43	Distance from sub-Saharan Africa predicts mutational load in diverse human genomes. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E440-9.	3.3	224
44	Bayesian Analysis of an Admixture Model With Mutations and Arbitrarily Linked Markers. Genetics, 2005, 169, 1727-1738.	1.2	223
45	Genome-culture coevolution promotes rapid divergence of killer whale ecotypes. Nature Communications, 2016, 7, 11693.	5.8	222
46	Assessing population genetic structure and variability with RAPD data: Application to Vaccinium macrocarpon (American Cranberry). Journal of Evolutionary Biology, 1996, 9, 153-171.	0.8	217
47	Conserved noncoding sequences are selectively constrained and not mutation cold spots. Nature Genetics, 2006, 38, 223-227.	9.4	214
48	Analysis of mtDNA variation in African populations reveals the most ancient of all human continent-specific haplogroups. American Journal of Human Genetics, 1995, 57, 133-49.	2.6	213
49	Consequences of Range Contractions and Range Shifts on Molecular Diversity. Molecular Biology and Evolution, 2012, 29, 207-218.	3.5	204
50	Inferring admixture proportions from molecular data. Molecular Biology and Evolution, 1998, 15, 1298-1311.	3.5	196
51	Genomics of Rapid Incipient Speciation in Sympatric Threespine Stickleback. PLoS Genetics, 2016, 12, e1005887.	1.5	195
52	An Extensive Analysis of Y-Chromosomal Microsatellite Haplotypes in Globally Dispersed Human Populations. American Journal of Human Genetics, 2001, 68, 990-1018.	2.6	186
53	The effect of the Neolithic expansion on European molecular diversity. Proceedings of the Royal Society B: Biological Sciences, 2005, 272, 679-688.	1.2	185
54	Evidence for Polygenic Adaptation to Pathogens in the Human Genome. Molecular Biology and Evolution, 2013, 30, 1544-1558.	3.5	181

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55	Computer note. SIMCOAL: a general coalescent program for the simulation of molecular data in interconnected populations with arbitrary demography. , 2000, 91, 506-509.		180
56	Contrasted patterns of mitochondrial and nuclear structure among nursery colonies of the bat <i>Myotis myotis</i> . <i>Journal of Evolutionary Biology</i> , 2008, 14, 708-720.	0.8	167
57	Is the Gibraltar Strait a barrier to gene flow for the bat <i>Myotis myotis</i> (Chiroptera: Vespertilionidae)?. <i>Molecular Ecology</i> , 2000, 9, 1761-1772.	2.0	165
58	Human Genetic Affinities for Y-Chromosome P49a,f/TaqI Haplotypes Show Strong Correspondence with Linguistics. <i>American Journal of Human Genetics</i> , 1997, 61, 1015-1035.	2.6	159
59	Substitution rate variation among sites in mitochondrial hypervariable region I of humans and chimpanzees. <i>Molecular Biology and Evolution</i> , 1999, 16, 1357-1368.	3.5	156
60	Recurrent replacement of mtDNA and cryptic hybridization between two sibling bat species <i>Myotis myotis</i> and <i>Myotis blythii</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2006, 273, 3101-3123.	1.2	152
61	Expansion load: recessive mutations and the role of standing genetic variation. <i>Molecular Ecology</i> , 2015, 24, 2084-2094.	2.0	152
62	<i>fastsimcoal2</i> : demographic inference under complex evolutionary scenarios. <i>Bioinformatics</i> , 2021, 37, 4882-4885.	1.8	148
63	Strong reproductive isolation between humans and Neanderthals inferred from observed patterns of introgression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15129-15134.	3.3	146
64	The ecological and genomic basis of explosive adaptive radiation. <i>Nature</i> , 2020, 586, 75-79.	13.7	146
65	In defence of model-based inference in phylogeography. <i>Molecular Ecology</i> , 2010, 19, 436-446.	2.0	141
66	Different Genetic Components in the Ethiopian Population, Identified by mtDNA and Y-Chromosome Polymorphisms. <i>American Journal of Human Genetics</i> , 1998, 62, 420-434.	2.6	140
67	Large Allele Frequency Differences between Human Continental Groups are more Likely to have Occurred by Drift During range Expansions than by Selection. <i>Annals of Human Genetics</i> , 2009, 73, 95-108.	0.3	140
68	Expansion Load and the Evolutionary Dynamics of a Species Range. <i>American Naturalist</i> , 2015, 185, E81-E93.	1.0	137
69	Bipolar gene flow in deep-sea benthic foraminifera. <i>Molecular Ecology</i> , 2007, 16, 4089-4096.	2.0	132
70	Widespread Signals of Convergent Adaptation to High Altitude in Asia and America. <i>American Journal of Human Genetics</i> , 2014, 95, 394-407.	2.6	131
71	splatche: a program to simulate genetic diversity taking into account environmental heterogeneity. <i>Molecular Ecology Notes</i> , 2004, 4, 139-142.	1.7	129
72	Genetic consequences of habitat fragmentation during a range expansion. <i>Heredity</i> , 2014, 112, 291-299.	1.2	128

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73	Enhanced AFLP genome scans detect local adaptation in high-altitude populations of a small rodent (<i>Microtus arvalis</i>). <i>Molecular Ecology</i> , 2011, 20, 1450-1462.	2.0	126
74	Principal Component Analysis under Population Genetic Models of Range Expansion and Admixture. <i>Molecular Biology and Evolution</i> , 2010, 27, 1257-1268.	3.5	125
75	GENETIC STRUCTURE AND COLONIZATION PROCESSES IN EUROPEAN POPULATIONS OF THE COMMON VOLE, <i>MICROTUS ARVALIS</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 2231-2242.	1.1	121
76	Mammalian monogamy is not controlled by a single gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 10956-10960.	3.3	121
77	Background selection and biased gene conversion affect more than 95% of the human genome and bias demographic inferences. <i>ELife</i> , 2018, 7, .	2.8	121
78	Evolutionary correlation between control region sequence and restriction polymorphisms in the mitochondrial genome of a large Senegalese Mandenka sample.. <i>Molecular Biology and Evolution</i> , 1995, 12, 334-45.	3.5	116
79	Molecular Analysis of the β -Globin Gene Cluster in the Niokholo Mandenka Population Reveals a Recent Origin of the β^S Senegal Mutation. <i>American Journal of Human Genetics</i> , 2002, 70, 207-223.	2.6	115
80	SPLATCHE2: a spatially explicit simulation framework for complex demography, genetic admixture and recombination. <i>Bioinformatics</i> , 2010, 26, 2993-2994.	1.8	113
81	Bayesian Estimation of Recent Migration Rates After a Spatial Expansion. <i>Genetics</i> , 2005, 170, 409-417.	1.2	112
82	Bayesian Inference of the Demographic History of Chimpanzees. <i>Molecular Biology and Evolution</i> , 2010, 27, 1425-1435.	3.5	111
83	Distinguishing between population bottleneck and population subdivision by a Bayesian model choice procedure. <i>Molecular Ecology</i> , 2010, 19, 4648-4660.	2.0	110
84	Demographic modelling with whole-genome data reveals parallel origin of similar <i>Pundamilia</i> cichlid species after hybridization. <i>Molecular Ecology</i> , 2017, 26, 123-141.	2.0	106
85	Human demographic history: refining the recent African origin model. <i>Current Opinion in Genetics and Development</i> , 2002, 12, 675-682.	1.5	104
86	Genomics of Parallel Ecological Speciation in Lake Victoria Cichlids. <i>Molecular Biology and Evolution</i> , 2018, 35, 1489-1506.	3.5	103
87	Recovering the geographic origin of early modern humans by realistic and spatially explicit simulations. <i>Genome Research</i> , 2005, 15, 1161-1167.	2.4	100
88	Genomic insights into population history and biological adaptation in Oceania. <i>Nature</i> , 2021, 592, 583-589.	13.7	100
89	Molecular analysis reveals tighter social regulation of immigration in patrilocal populations than in matrilocal populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7476-7480.	3.3	98
90	Evolution of human mitochondrial DNA: Evidence for departure from a pure neutral model of populations at equilibrium. <i>Journal of Molecular Evolution</i> , 1990, 30, 125-139.	0.8	97

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91	A Statistical Evaluation of Models for the Initial Settlement of the American Continent Emphasizes the Importance of Gene Flow with Asia. <i>Molecular Biology and Evolution</i> , 2010, 27, 337-345.	3.5	97
92	Divergent evolutionary processes associated with colonization of offshore islands. <i>Molecular Ecology</i> , 2013, 22, 5205-5220.	2.0	92
93	Genetics and history of sub-Saharan Africa. <i>American Journal of Physical Anthropology</i> , 1987, 30, 151-194.	2.1	91
94	Adaptive, convergent origins of the pygmy phenotype in African rainforest hunter-gatherers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3596-603.	3.3	91
95	Mitochondrial gene diversity in the common vole <i>Microtus arvalis</i> shaped by historical divergence and local adaptations. <i>Molecular Ecology</i> , 2004, 13, 3501-3514.	2.0	90
96	Fine-scale genetic structure and dispersal in the common vole (<i>Microtus arvalis</i>). <i>Molecular Ecology</i> , 2007, 16, 2463-2473.	2.0	90
97	Deep Human Genealogies Reveal a Selective Advantage to Be on an Expanding Wave Front. <i>Science</i> , 2011, 334, 1148-1150.	6.0	89
98	Gametic phase estimation over large genomic regions using an adaptive window approach. <i>Human Genomics</i> , 2003, 1, 7.	1.4	88
99	Incorporating Genotypes of Relatives into a Test of Linkage Disequilibrium. <i>American Journal of Human Genetics</i> , 1998, 62, 171-180.	2.6	86
100	Ignoring Heterozygous Sites Biases Phylogenomic Estimates of Divergence Times: Implications for the Evolutionary History of <i>Microtus</i> Voles. <i>Molecular Biology and Evolution</i> , 2014, 31, 817-831.	3.5	80
101	A simple method of removing the effect of a bottleneck and unequal population sizes on pairwise genetic distances. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2000, 267, 81-87.	1.2	77
102	The Evolutionary History of Nebraska Deer Mice: Local Adaptation in the Face of Strong Gene Flow. <i>Molecular Biology and Evolution</i> , 2018, 35, 792-806.	3.5	76
103	NO EVIDENCE OF BOTTLENECK IN THE POSTGLACIAL RECOLONIZATION OF EUROPE BY THE NOCTULE BAT (<i>NYCTALUS NOCTULA</i>). <i>Evolution; International Journal of Organic Evolution</i> , 1999, 53, 1247-1258.	1.1	75
104	Molecular Diversity After a Range Expansion in Heterogeneous Environments. <i>Genetics</i> , 2006, 174, 2009-2020.	1.2	74
105	Accumulation of Deleterious Mutations During Bacterial Range Expansions. <i>Genetics</i> , 2017, 207, 669-684.	1.2	74
106	Origin and differentiation of human mitochondrial DNA. <i>American Journal of Human Genetics</i> , 1989, 44, 73-85.	2.6	73
107	Colonization history of the Swiss Rhine basin by the bullhead (<i>Cottus gobio</i>): inference under a Bayesian spatially explicit framework. <i>Molecular Ecology</i> , 2008, 17, 757-772.	2.0	71
108	Life history shapes gene expression in salmonids. <i>Current Biology</i> , 2006, 16, R281-R282.	1.8	70

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109	Estimating population structure from AFLP amplification intensity. <i>Molecular Ecology</i> , 2010, 19, 4638-4647.	2.0	66
110	No Evidence of Bottleneck in the Postglacial Recolonization of Europe by the Noctule Bat (<i>Nyctalus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.1	64
111	The SIB Swiss Institute of Bioinformaticsâ€™ resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016, 44, D27-D37.	6.5	64
112	A linkage disequilibrium map of the MHC region based on the analysis of 14 loci haplotypes in 50 French families. <i>European Journal of Human Genetics</i> , 2000, 8, 33-41.	1.4	63
113	European phylogeography of the epiphytic lichen fungus <i>Lobaria pulmonaria</i> and its green algal symbiont. <i>Molecular Ecology</i> , 2012, 21, 5827-5844.	2.0	63
114	Italy as a major Ice Age refuge area for the bat <i>Myotis myotis</i> (Chiroptera: Vespertilionidae) in Europe. <i>Molecular Ecology</i> , 2008, 17, 1801-1814.	2.0	60
115	Recommendations for improving statistical inference in population genomics. <i>PLoS Biology</i> , 2022, 20, e3001669.	2.6	60
116	Genomic Scans Support Repetitive Continental Colonization Events during the Rapid Radiation of Voles (Rodentia: <i>Microtus</i>): the Utility of AFLPs versus Mitochondrial and Nuclear Sequence Markers. <i>Systematic Biology</i> , 2010, 59, 548-572.	2.7	59
117	Ancient admixture from an extinct ape lineage into bonobos. <i>Nature Ecology and Evolution</i> , 2019, 3, 957-965.	3.4	59
118	Long-term evolution and short-term adaptation of microbiota strains and sub-strains in mice. <i>Cell Host and Microbe</i> , 2021, 29, 650-663.e9.	5.1	58
119	Approximate Bayesian Analysis of <i>Drosophila melanogaster</i> Polymorphism Data Reveals a Recent Colonization of Southeast Asia. <i>Molecular Biology and Evolution</i> , 2011, 28, 2041-2051.	3.5	57
120	Gene flow in admixed populations and implications for the conservation of the Western honeybee, <i>Apis mellifera</i> . <i>Journal of Insect Conservation</i> , 2009, 13, 317-328.	0.8	56
121	A first step towards inferring levels of long-distance dispersal during past expansions. <i>Molecular Ecology Resources</i> , 2010, 10, 902-914.	2.2	56
122	The Impact of Purifying and Background Selection on the Inference of Population History: Problems and Prospects. <i>Molecular Biology and Evolution</i> , 2021, 38, 2986-3003.	3.5	56
123	Securing the Conservation of Biodiversity across Administrative Levels and Spatial, Temporal, and Ecological Scales â€” Research Needs and Approaches of the SCALES Project. <i>Gaia</i> , 2010, 19, 187-193.	0.3	54
124	Combining genetic, historical and geographical data to reconstruct the dynamics of bioinvasions: application to the cane toad <i>Bufo marinus</i> . <i>Molecular Ecology Resources</i> , 2010, 10, 886-901.	2.2	54
125	Mammalian population genetics: why not Y?. <i>Trends in Ecology and Evolution</i> , 2002, 17, 28-33.	4.2	53
126	Comment on "Genetic Structure of Human Populations". <i>Science</i> , 2003, 300, 1877b-1877.	6.0	53

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127	Estimation of effective population size and detection of a recent population decline coinciding with habitat fragmentation in a ground beetle. <i>Journal of Evolutionary Biology</i> , 2005, 18, 90-100.	0.8	53
128	Response to Comment on "Ongoing Adaptive Evolution of ASPM, a Brain Size Determinant in Homo sapiens" and "Microcephalin, a Gene Regulating Brain Size, Continues to Evolve Adaptively in Humans". <i>Science</i> , 2006, 313, 172b-172b.	6.0	51
129	Evolutionary forces shaping genomic islands of population differentiation in humans. <i>BMC Genomics</i> , 2012, 13, 107.	1.2	51
130	Relaxed Selection During a Recent Human Expansion. <i>Genetics</i> , 2018, 208, 763-777.	1.2	49
131	Admixture between old lineages facilitated contemporary ecological speciation in Lake Constance stickleback. <i>Nature Communications</i> , 2019, 10, 4240.	5.8	49
132	Influence of Admixture and Paleolithic Range Contractions on Current European Diversity Gradients. <i>Molecular Biology and Evolution</i> , 2013, 30, 57-61.	3.5	48
133	Genetic surfing in human populations: from genes to genomes. <i>Current Opinion in Genetics and Development</i> , 2016, 41, 53-61.	1.5	48
134	Detecting gene subnetworks under selection in biological pathways. <i>Nucleic Acids Research</i> , 2017, 45, e149-e149.	6.5	48
135	Transition from Background Selection to Associative Overdominance Promotes Diversity in Regions of Low Recombination. <i>Current Biology</i> , 2020, 30, 101-107.e3.	1.8	48
136	Detection of Pathways Affected by Positive Selection in Primate Lineages Ancestral to Humans. <i>Molecular Biology and Evolution</i> , 2017, 34, 1391-1402.	3.5	47
137	Killer whale genomes reveal a complex history of recurrent admixture and vicariance. <i>Molecular Ecology</i> , 2019, 28, 3427-3444.	2.0	46
138	Contrasting Patterns of Nuclear and mtDNA Diversity in Native American Populations. <i>Annals of Human Genetics</i> , 2010, 74, 525-538.	0.3	44
139	Genomic Data Reveal a Complex Making of Humans. <i>PLoS Genetics</i> , 2012, 8, e1002837.	1.5	43
140	Minisatellite mutational processes reduce Fst estimates. <i>Human Genetics</i> , 1999, 105, 567-576.	1.8	41
141	Population transcriptomics of life history variation in the genus <i>Salmo</i> . <i>Molecular Ecology</i> , 2008, 17, 3095-3108.	2.0	41
142	SPLATCHE3: simulation of serial genetic data under spatially explicit evolutionary scenarios including long-distance dispersal. <i>Bioinformatics</i> , 2019, 35, 4480-4483.	1.8	41
143	Impact of range expansions on current human genomic diversity. <i>Current Opinion in Genetics and Development</i> , 2014, 29, 22-30.	1.5	40
144	Maternal and paternal lineages in Albania and the genetic structure of Indo-European populations. <i>European Journal of Human Genetics</i> , 2000, 8, 480-486.	1.4	39

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145	Patterns of morphological changes and hybridization between sympatric whitefish morphs (<i>Coregonus</i> spp.) in a Swiss lake: a role for eutrophication?. <i>Molecular Ecology</i> , 2010, 19, 2152-2167.	2.0	39
146	Runs of homozygosity in killer whale genomes provide a global record of demographic histories. <i>Molecular Ecology</i> , 2021, 30, 6162-6177.	2.0	39
147	The genomic origins of the world's first farmers. <i>Cell</i> , 2022, 185, 1842-1859.e18.	13.5	39
148	Polygenic Patterns of Adaptive Introgression in Modern Humans Are Mainly Shaped by Response to Pathogens. <i>Molecular Biology and Evolution</i> , 2020, 37, 1420-1433.	3.5	38
149	Spatial differentiation of RH and GM haplotype frequencies in Sub-Saharan Africa and its relation to linguistic affinities. <i>Human Biology</i> , 1991, 63, 273-307.	0.4	38
150	Genetic structure and colonization processes in European populations of the common vole, <i>Microtus arvalis</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 2231-42.	1.1	38
151	Genetic Evidence for Complexity in Ethnic Differentiation and History in East Africa. <i>Annals of Human Genetics</i> , 2009, 73, 582-600.	0.3	37
152	Long-Distance Dispersal Shaped Patterns of Human Genetic Diversity in Eurasia. <i>Molecular Biology and Evolution</i> , 2016, 33, 946-958.	3.5	36
153	Slightly deleterious genomic variants and transcriptome perturbations in Down syndrome embryonic selection. <i>Genome Research</i> , 2018, 28, 1-10.	2.4	36
154	High variability and non-neutral evolution of the mammalian <i>avpr1a</i> gene. <i>BMC Evolutionary Biology</i> , 2007, 7, 176.	3.2	35
155	Inferring Past Demography Using Spatially Explicit Population Genetic Models. <i>Human Biology</i> , 2009, 81, 141-157.	0.4	35
156	Recent Evolutionary History of Tigers Highlights Contrasting Roles of Genetic Drift and Selection. <i>Molecular Biology and Evolution</i> , 2021, 38, 2366-2379.	3.5	35
157	Analysis of Population Subdivision. , 2008, , 980-1020.		33
158	Demographic inference. <i>Current Biology</i> , 2021, 31, R276-R279.	1.8	32
159	Detection of Convergent Genome-Wide Signals of Adaptation to Tropical Forests in Humans. <i>PLoS ONE</i> , 2015, 10, e0121557.	1.1	32
160	Analysis of Population Subdivision. , 2004, , .		31
161	Nuclear DNA polymorphism in a Mandenka population from Senegal: Comparison with eight other human populations. <i>Annals of Human Genetics</i> , 1995, 59, 43-61.	0.3	29
162	Mutation load dynamics during environmentally-driven range shifts. <i>PLoS Genetics</i> , 2018, 14, e1007450.	1.5	29

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