

Laurent Excoffier

List of Publications by Citations

Source: <https://exaly.com/author-pdf/5988021/laurent-excoffier-publications-by-citations.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

206
papers

56,422
citations

83
h-index

227
g-index

227
ext. papers

63,432
ext. citations

9
avg, IF

8.18
L-index

#	Paper	IF	Citations
206	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, 564-7	8.4	10640
205	Analysis of molecular variance inferred from metric distances among DNA haplotypes: application to human mitochondrial DNA restriction data. <i>Genetics</i> , 1992 , 131, 479-91	4	9836
204	Arlequin (version 3.0): An integrated software package for population genetics data analysis. <i>Evolutionary Bioinformatics</i> , 2005 , 1, 117693430500100	1.9	6278
203	Arlequin (version 3.0): an integrated software package for population genetics data analysis. <i>Evolutionary Bioinformatics</i> , 2007 , 1, 47-50	1.9	3325
202	A simulated annealing approach to define the genetic structure of populations. <i>Molecular Ecology</i> , 2002 , 11, 2571-81	5.7	1425
201	Maximum-likelihood estimation of molecular haplotype frequencies in a diploid population. <i>Molecular Biology and Evolution</i> , 1995 , 12, 921-7	8.3	1330
200	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, 1079-89 ⁴		1146
199	Genetic Consequences of Range Expansions. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2009 , 40, 481-501	13.5	835
198	Robust demographic inference from genomic and SNP data. <i>PLoS Genetics</i> , 2013 , 9, e1003905	6	780
197	A human genome diversity cell line panel. <i>Science</i> , 2002 , 296, 261-2	33.3	742
196	PGDSpider: an automated data conversion tool for connecting population genetics and genomics programs. <i>Bioinformatics</i> , 2012 , 28, 298-9	7.2	647
195	A generic estimation of population subdivision using distances between alleles with special reference for microsatellite loci. <i>Genetics</i> , 1996 , 142, 1061-4	4	633
194	Detecting loci under selection in a hierarchically structured population. <i>Heredity</i> , 2009 , 103, 285-98	3.6	593
193	Gene flow and species delimitation. <i>Trends in Ecology and Evolution</i> , 2009 , 24, 386-93	10.9	579
192	The hidden side of invasions: massive introgression by local genes. <i>Evolution; International Journal of Organic Evolution</i> , 2008 , 62, 1908-20	3.8	562
191	Reconstructing Native American population history. <i>Nature</i> , 2012 , 488, 370-4	50.4	498
190	Surfing during population expansions promotes genetic revolutions and structuration. <i>Trends in Ecology and Evolution</i> , 2008 , 23, 347-51	10.9	495

189	Patterns of DNA sequence diversity and genetic structure after a range expansion: lessons from the infinite-island model. <i>Molecular Ecology</i> , 2004 , 13, 853-64	5.7	488
188	Testing for linkage disequilibrium in genotypic data using the Expectation-Maximization algorithm. <i>Heredity</i> , 1996 , 76 (Pt 4), 377-83	3.6	475
187	Intra-deme molecular diversity in spatially expanding populations. <i>Molecular Biology and Evolution</i> , 2003 , 20, 76-86	8.3	461
186	The fate of mutations surfing on the wave of a range expansion. <i>Molecular Biology and Evolution</i> , 2006 , 23, 482-90	8.3	446
185	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, 17614-9	11.5	409
184	Genetic variation and population structure in native Americans. <i>PLoS Genetics</i> , 2007 , 3, e185	6	392
183	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, 5927-32	11.5	348
182	Using allele frequencies and geographic subdivision to reconstruct gene trees within a species: molecular variance parsimony. <i>Genetics</i> , 1994 , 136, 343-59	4	346
181	The impact of population expansion and mutation rate heterogeneity on DNA sequence polymorphism. <i>Molecular Biology and Evolution</i> , 1996 , 13, 494-504	8.3	341
180	Ancient hybridization fuels rapid cichlid fish adaptive radiations. <i>Nature Communications</i> , 2017 , 8, 14363	17.4	317
179	Geographic patterns of genome admixture in Latin American Mestizos. <i>PLoS Genetics</i> , 2008 , 4, e10000376		310
178	fastsimcoal: a continuous-time coalescent simulator of genomic diversity under arbitrarily complex evolutionary scenarios. <i>Bioinformatics</i> , 2011 , 27, 1332-4	7.2	286
177	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016 , 538, 207-214	50.4	268
176	ABCtoolbox: a versatile toolkit for approximate Bayesian computations. <i>BMC Bioinformatics</i> , 2010 , 11, 116	3.6	259
175	Computer programs for population genetics data analysis: a survival guide. <i>Nature Reviews Genetics</i> , 2006 , 7, 745-58	30.1	256
174	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, 10597-602	11.5	237
173	Efficient approximate Bayesian computation coupled with Markov chain Monte Carlo without likelihood. <i>Genetics</i> , 2009 , 182, 1207-18	4	214
172	Modern humans did not admix with Neanderthals during their range expansion into Europe. <i>PLoS Biology</i> , 2004 , 2, e421	9.7	208

171	SIMCOAL 2.0: a program to simulate genomic diversity over large recombining regions in a subdivided population with a complex history. <i>Bioinformatics</i> , 2004 , 20, 2485-7	7.2	206
170	Bayesian analysis of an admixture model with mutations and arbitrarily linked markers. <i>Genetics</i> , 2005 , 169, 1727-38	4	201
169	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
168	Analysis of mtDNA variation in African populations reveals the most ancient of all human continent-specific haplogroups. <i>American Journal of Human Genetics</i> , 1995 , 57, 133-49	11	195
167	Assessing population genetic structure and variability with RAPD data: Application to <i>Vaccinium macrocarpon</i> (American Cranberry). <i>Journal of Evolutionary Biology</i> , 1996 , 9, 153-171	2.3	190
166	Conserved noncoding sequences are selectively constrained and not mutation cold spots. <i>Nature Genetics</i> , 2006 , 38, 223-7	36.3	184
165	On the accumulation of deleterious mutations during range expansions. <i>Molecular Ecology</i> , 2013 , 22, 5972-82	5.7	178
164	Inferring admixture proportions from molecular data. <i>Molecular Biology and Evolution</i> , 1998 , 15, 1298-318	3	175
163	SIMCOAL: a general coalescent program for the simulation of molecular data in interconnected populations with arbitrary demography. <i>Journal of Heredity</i> , 2000 , 91, 506-9	2.4	167
162	An extensive analysis of Y-chromosomal microsatellite haplotypes in globally dispersed human populations. <i>American Journal of Human Genetics</i> , 2001 , 68, 990-1018	11	167
161	Genome-culture coevolution promotes rapid divergence of killer whale ecotypes. <i>Nature Communications</i> , 2016 , 7, 11693	17.4	161
160	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , 2017 , 358, 659-662	33.3	160
159	Serial founder effects during range expansion: a spatial analog of genetic drift. <i>Genetics</i> , 2012 , 191, 171-81	4	155
158	Distance from sub-Saharan Africa predicts mutational load in diverse human genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E440-9	11.5	149
157	Is the Gibraltar strait a barrier to gene flow for the bat <i>Myotis myotis</i> (Chiroptera: Vespertilionidae)? <i>Molecular Ecology</i> , 2000 , 9, 1761-72	5.7	149
156	Consequences of range contractions and range shifts on molecular diversity. <i>Molecular Biology and Evolution</i> , 2012 , 29, 207-18	8.3	148
155	Genomics of Rapid Incipient Speciation in Sympatric Threespine Stickleback. <i>PLoS Genetics</i> , 2016 , 12, e1005887	6	146
154	Chimpanzee genomic diversity reveals ancient admixture with bonobos. <i>Science</i> , 2016 , 354, 477-481	33.3	139

153	The population history of northeastern Siberia since the Pleistocene. <i>Nature</i> , 2019 , 570, 182-188	50.4	137
152	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	2.3	135
151	The effect of the Neolithic expansion on European molecular diversity. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2005 , 272, 679-88	4.4	134
150	Evidence for polygenic adaptation to pathogens in the human genome. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1544-58	8.3	132
149	Human genetic affinities for Y-chromosome P49a,f/TaqI haplotypes show strong correspondence with linguistics. <i>American Journal of Human Genetics</i> , 1997 , 61, 1015-35	11	131
148	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, 3101-9	4.4	131
147	In defence of model-based inference in phylogeography. <i>Molecular Ecology</i> , 2010 , 19, 436-446	5.7	127
146	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 ^{2.2}	2.2	127
145	Different genetic components in the Ethiopian population, identified by mtDNA and Y-chromosome polymorphisms. <i>American Journal of Human Genetics</i> , 1998 , 62, 420-34	11	125
144	Substitution rate variation among sites in mitochondrial hypervariable region I of humans and chimpanzees. <i>Molecular Biology and Evolution</i> , 1999 , 16, 1357-68	8.3	116
143	splatche: a program to simulate genetic diversity taking into account environmental heterogeneity. <i>Molecular Ecology Notes</i> , 2004 , 4, 139-142		113
142	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, 15129-34	11.5	112
141	Bipolar gene flow in deep-sea benthic foraminifera. <i>Molecular Ecology</i> , 2007 , 16, 4089-96	5.7	112
140	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	3.8	109
139	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, 10956-60	11.5	107
138	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, 1450-62	5.7	106
137	Expansion load: recessive mutations and the role of standing genetic variation. <i>Molecular Ecology</i> , 2015 , 24, 2084-94	5.7	100
136	Molecular analysis of the beta-globin gene cluster in the Niokholo Mandenka population reveals a recent origin of the beta(S) Senegal mutation. <i>American Journal of Human Genetics</i> , 2002 , 70, 207-23	11	98

135	Widespread signals of convergent adaptation to high altitude in Asia and America. <i>American Journal of Human Genetics</i> , 2014 , 95, 394-407	11	96
134	SPLATCHE2: a spatially explicit simulation framework for complex demography, genetic admixture and recombination. <i>Bioinformatics</i> , 2010 , 26, 2993-4	7.2	96
133	Bayesian inference of the demographic history of chimpanzees. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1425-35	8.3	94
132	Principal component analysis under population genetic models of range expansion and admixture. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1257-68	8.3	93
131	Human demographic history: refining the recent African origin model. <i>Current Opinion in Genetics and Development</i> , 2002 , 12, 675-82	4.9	93
130	Evolutionary correlation between control region sequence and restriction polymorphisms in the mitochondrial genome of a large Senegalese Mandinka sample. <i>Molecular Biology and Evolution</i> , 1995 , 12, 334-45	8.3	93
129	Distinguishing between population bottleneck and population subdivision by a Bayesian model choice procedure. <i>Molecular Ecology</i> , 2010 , 19, 4648-60	5.7	91
128	Bayesian estimation of recent migration rates after a spatial expansion. <i>Genetics</i> , 2005 , 170, 409-17	4	91
127	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, 7476-80	11.5	90
126	Expansion load and the evolutionary dynamics of a species range. <i>American Naturalist</i> , 2015 , 185, E81-93	3.7	88
125	Mitochondrial gene diversity in the common vole <i>Microtus arvalis</i> shaped by historical divergence and local adaptations. <i>Molecular Ecology</i> , 2004 , 13, 3501-14	5.7	83
124	Gametic phase estimation over large genomic regions using an adaptive window approach. <i>Human Genomics</i> , 2003 , 1, 7-19	6.8	82
123	Fine-scale genetic structure and dispersal in the common vole (<i>Microtus arvalis</i>). <i>Molecular Ecology</i> , 2007 , 16, 2463-73	5.7	81
122	Incorporating genotypes of relatives into a test of linkage disequilibrium. <i>American Journal of Human Genetics</i> , 1998 , 62, 171-80	11	80
121	Recovering the geographic origin of early modern humans by realistic and spatially explicit simulations. <i>Genome Research</i> , 2005 , 15, 1161-7	9.7	78
120	Genetic consequences of habitat fragmentation during a range expansion. <i>Heredity</i> , 2014 , 112, 291-9	3.6	76
119	Divergent evolutionary processes associated with colonization of offshore islands. <i>Molecular Ecology</i> , 2013 , 22, 5205-20	5.7	76
118	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, 125-39	3.1	76

117	Genetics and history of sub-Saharan Africa. <i>American Journal of Physical Anthropology</i> , 1987 , 30, 151-194	2.5	76
116	Demographic modelling with whole-genome data reveals parallel origin of similar Pundamilia cichlid species after hybridization. <i>Molecular Ecology</i> , 2017 , 26, 123-141	5.7	75
115	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, 337-45	8.3	72
114	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	11.5	70
113	Deep human genealogies reveal a selective advantage to be on an expanding wave front. <i>Science</i> , 2011 , 334, 1148-50	33.3	68
112	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, 81-7	4.4	66
111	Life history shapes gene expression in salmonids. <i>Current Biology</i> , 2006 , 16, R281-2	6.3	64
110	Molecular diversity after a range expansion in heterogeneous environments. <i>Genetics</i> , 2006 , 174, 2009-20		63
109	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, 757-72	5.7	62
108	Origin and differentiation of human mitochondrial DNA. <i>American Journal of Human Genetics</i> , 1989 , 44, 73-85	11	61
107	Genomics of Parallel Ecological Speciation in Lake Victoria Cichlids. <i>Molecular Biology and Evolution</i> , 2018 , 35, 1489-1506	8.3	60
106	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	3.8	60
105	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	3.8	60
104	Background selection and biased gene conversion affect more than 95% of the human genome and bias demographic inferences. <i>ELife</i> , 2018 , 7,	8.9	59
103	Estimating population structure from AFLP amplification intensity. <i>Molecular Ecology</i> , 2010 , 19, 4638-47	5.7	58
102	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	5.3	58
101	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, 1801-14	5.7	55
100	European phylogeography of the epiphytic lichen fungus <i>Lobaria pulmonaria</i> and its green algal symbiont. <i>Molecular Ecology</i> , 2012 , 21, 5827-44	5.7	54

99	The ecological and genomic basis of explosive adaptive radiation. <i>Nature</i> , 2020 , 586, 75-79	50.4	54
98	Ignoring heterozygous sites biases phylogenomic estimates of divergence times: implications for the evolutionary history of microtus voles. <i>Molecular Biology and Evolution</i> , 2014 , 31, 817-31	8.3	52
97	Genomic scans support repetitive continental colonization events during the rapid radiation of voles (Rodentia: Microtus): the utility of AFLPs versus mitochondrial and nuclear sequence markers. <i>Systematic Biology</i> , 2010 , 59, 548-72	8.4	52
96	Mammalian population genetics: why not Y?. <i>Trends in Ecology and Evolution</i> , 2002 , 17, 28-33	10.9	51
95	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	8.4	50
94	Accumulation of Deleterious Mutations During Bacterial Range Expansions. <i>Genetics</i> , 2017 , 207, 669-684	4	47
93	Securing the Conservation of Biodiversity across Administrative Levels and Spatial, Temporal, and Ecological Scales [Research Needs and Approaches of the SCALES Project. <i>Gaia</i> , 2010 , 19, 187-193	1.4	47
92	Comment on "Ongoing adaptive evolution of ASPM, a brain size determinant in <i>Homo sapiens</i> " and "Microcephalin, a gene regulating brain size, continues to evolve adaptively in humans". <i>Science</i> , 2006 , 313, 172; author reply 172	33.3	47
91	A first step towards inferring levels of long-distance dispersal during past expansions. <i>Molecular Ecology Resources</i> , 2010 , 10, 902-14	8.4	46
90	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	2.1	46
89	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, 2041-51	8.3	46
88	Comment on "Genetic structure of human populations". <i>Science</i> , 2003 , 300, 1877; author reply 1877	33.3	44
87	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	8.3	43
86	The SIB Swiss Institute of Bioinformatics Resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016 , 44, D27-37	20.1	41
85	Contrasting patterns of nuclear and mtDNA diversity in Native American populations. <i>Annals of Human Genetics</i> , 2010 , 74, 525-38	2.2	41
84	Evolutionary forces shaping genomic islands of population differentiation in humans. <i>BMC Genomics</i> , 2012 , 13, 107	4.5	40
83	Population transcriptomics of life-history variation in the genus <i>Salmo</i> . <i>Molecular Ecology</i> , 2008 , 17, 3095-108	5.1	40
82	Minisatellite mutational processes reduce F_{st} estimates. <i>Human Genetics</i> , 1999 , 105, 567-76	6.3	38

81	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	1.2	38
80	Influence of admixture and paleolithic range contractions on current European diversity gradients. <i>Molecular Biology and Evolution</i> , 2013 , 30, 57-61	8.3	35
79	Detecting gene subnetworks under selection in biological pathways. <i>Nucleic Acids Research</i> , 2017 , 45, e149	20.1	35
78	Patterns of morphological changes and hybridization between sympatric whitefish morphs (Coregonus spp.) in a Swiss lake: a role for eutrophication?. <i>Molecular Ecology</i> , 2010 , 19, 2152-67	5.7	35
77	Maternal and paternal lineages in Albania and the genetic structure of Indo-European populations. <i>European Journal of Human Genetics</i> , 2000 , 8, 480-6	5.3	35
76	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	3.8	35
75	Detection of Pathways Affected by Positive Selection in Primate Lineages Ancestral to Humans. <i>Molecular Biology and Evolution</i> , 2017 , 34, 1391-1402	8.3	33
74	Genomic data reveal a complex making of humans. <i>PLoS Genetics</i> , 2012 , 8, e1002837	6	33
73	High variability and non-neutral evolution of the mammalian avpr1a gene. <i>BMC Evolutionary Biology</i> , 2007 , 7, 176	3	33
72	Genetic evidence for complexity in ethnic differentiation and history in East Africa. <i>Annals of Human Genetics</i> , 2009 , 73, 582-600	2.2	32
71	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	2.2	29
70	Ancient admixture from an extinct ape lineage into bonobos. <i>Nature Ecology and Evolution</i> , 2019 , 3, 957-965	9.5	28
69	Long-Distance Dispersal Shaped Patterns of Human Genetic Diversity in Eurasia. <i>Molecular Biology and Evolution</i> , 2016 , 33, 946-58	8.3	28
68	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	2.3	28
67	Detection of convergent genome-wide signals of adaptation to tropical forests in humans. <i>PLoS ONE</i> , 2015 , 10, e0121557	3.7	28
66	Relaxed Selection During a Recent Human Expansion. <i>Genetics</i> , 2018 , 208, 763-777	4	28
65	Impact of range expansions on current human genomic diversity. <i>Current Opinion in Genetics and Development</i> , 2014 , 29, 22-30	4.9	27
64	Inferring past demography using spatially explicit population genetic models. <i>Human Biology</i> , 2009 , 81, 141-57	1.2	27

63	HLA-DR polymorphism in a Senegalese Mandenka population: DNA oligotyping and population genetics of DRB1 specificities. <i>American Journal of Human Genetics</i> , 1992 , 51, 592-608	11	27
62	Slightly deleterious genomic variants and transcriptome perturbations in Down syndrome embryonic selection. <i>Genome Research</i> , 2018 , 28, 1-10	9.7	27
61	Genomic insights into population history and biological adaptation in Oceania. <i>Nature</i> , 2021 , 592, 583-589	9.4	26
60	Genetic surfing in human populations: from genes to genomes. <i>Current Opinion in Genetics and Development</i> , 2016 , 41, 53-61	4.9	26
59	Killer whale genomes reveal a complex history of recurrent admixture and vicariance. <i>Molecular Ecology</i> , 2019 , 28, 3427-3444	5.7	25
58	Analysis of Population Subdivision 2008 , 980-1020		24
57	SPLATCHE3: simulation of serial genetic data under spatially explicit evolutionary scenarios including long-distance dispersal. <i>Bioinformatics</i> , 2019 , 35, 4480-4483	7.2	22
56	Low levels of mitochondrial DNA variation among central and southern European <i>Esox lucius</i> populations. <i>Journal of Fish Biology</i> , 2004 , 64, 1442-1449	1.9	22
55	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	8.3	20
54	Genomic landscape of early ecological speciation initiated by selection on nuptial colour. <i>Molecular Ecology</i> , 2017 , 26, 7-24	5.7	19
53	Transition from Background Selection to Associative Overdominance Promotes Diversity in Regions of Low Recombination. <i>Current Biology</i> , 2020 , 30, 101-107.e3	6.3	19
52	Mutation load dynamics during environmentally-driven range shifts. <i>PLoS Genetics</i> , 2018 , 14, e1007450	6	19
51	Admixture between old lineages facilitated contemporary ecological speciation in Lake Constance stickleback. <i>Nature Communications</i> , 2019 , 10, 4240	17.4	18
50	Parsimony-based pedigree analysis and individual-based landscape genetics suggest topography to restrict dispersal and connectivity in the endangered capercaillie. <i>Biological Conservation</i> , 2012 , 152, 241-252	6.2	18
49	Genetic analysis of potential postglacial watershed crossings in Central Europe by the bullhead (<i>Cottus gobio</i> L.). <i>Molecular Ecology</i> , 2007 , 16, 4572-84	5.7	18
48	HLA-DPB1 DNA polymorphism in the Swiss population: linkage disequilibrium with other HLA loci and population genetic affinities. <i>International Journal of Immunogenetics</i> , 1994 , 21, 143-57		16
47	fastsimcoal2: demographic inference under complex evolutionary scenarios. <i>Bioinformatics</i> , 2021 ,	7.2	14
46	Long-distance dispersal suppresses introgression of local alleles during range expansions. <i>Heredity</i> , 2017 , 118, 135-142	3.6	13

45	High diversity of alpha-globin haplotypes in a Senegalese population, including many previously unreported variants. <i>American Journal of Human Genetics</i> , 1995 , 57, 1186-98	11	13
44	Inference of Evolutionary Forces Acting on Human Biological Pathways. <i>Genome Biology and Evolution</i> , 2015 , 7, 1546-58	3.9	12
43	Similarity in recombination rate and linkage disequilibrium at CYP2C and CYP2D cytochrome P450 gene regions among Europeans indicates signs of selection and no advantage of using tagSNPs in population isolates. <i>Pharmacogenetics and Genomics</i> , 2012 , 22, 846-57	1.9	12
42	Width of gene expression profile drives alternative splicing. <i>PLoS ONE</i> , 2008 , 3, e3587	3.7	12
41	Neandertal genetic diversity: a fresh look from old samples. <i>Current Biology</i> , 2006 , 16, R650-2	6.3	12
40	Inferring the impact of linguistic boundaries on population differentiation: application to the Afro-Asiatic-Indo-European case. <i>European Journal of Human Genetics</i> , 2000 , 8, 750-6	5.3	12
39	Minisatellite mutational processes reduce F _{st} estimates. <i>Human Genetics</i> , 1999 , 105, 567-576	6.3	12
38	Continental-scale footprint of balancing and positive selection in a small rodent (<i>Microtus arvalis</i>). <i>PLoS ONE</i> , 2014 , 9, e112332	3.7	12
37	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	23.4	11
36	Recent Evolutionary History of Tigers Highlights Contrasting Roles of Genetic Drift and Selection. <i>Molecular Biology and Evolution</i> , 2021 , 38, 2366-2379	8.3	11
35	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	8.3	9
34	Human diversity: our genes tell where we live. <i>Current Biology</i> , 2003 , 13, R134-6	6.3	8
33	New data for AG haplotype frequencies in Caucasoid populations and selective neutrality of the AG polymorphism. <i>Human Biology</i> , 1994 , 66, 27-48	1.2	8
32	Recent colonization of the Galápagos by the tree <i>Geoffroea spinosa</i> Jacq. (Leguminosae). <i>Molecular Ecology</i> , 2012 , 21, 2743-60	5.7	7
31	Demographic inference. <i>Current Biology</i> , 2021 , 31, R276-R279	6.3	6
30	Runs of homozygosity in killer whale genomes provide a global record of demographic histories. <i>Molecular Ecology</i> , 2021 , 30, 6162-6177	5.7	6
29	Analysis of Population Subdivision 2004 ,		5
28	Mutational and Selective Processes Involved in Evolution during Bacterial Range Expansions. <i>Molecular Biology and Evolution</i> , 2019 , 36, 2313-2327	8.3	4

27	Effect of factors inhibiting HLA-DR antibodies before transplantation on kidney graft survival. <i>Transplantation</i> , 1988 , 46, 581-4	1.8	4
26	Gene flow as a simple cause for an excess of high-frequency-derived alleles. <i>Evolutionary Applications</i> , 2020 , 13, 2254-2263	4.8	4
25	Origine et Évolution de l'ADN mitochondrial humain : le paradigme perdu. <i>Bulletins Et Memoires De La Societe D'Anthropologie De Paris</i> , 1990 , 2, 25-41	0.3	4
24	Runs of homozygosity in killer whale genomes provide a global record of demographic histories		4
23	Reconstructing the demography of prehistoric human populations from molecular data. <i>Evolutionary Anthropology</i> , 2003 , 11, 166-170	4.7	3
22	GENETIC STRUCTURE AND COLONIZATION PROCESSES IN EUROPEAN POPULATIONS OF THE COMMON VOLE, MICROTUS ARVALIS. <i>Evolution; International Journal of Organic Evolution</i> , 2005 , 59, 2231	3.8	3
21	Relaxed selection during a recent human expansion		3
20	The impact of purifying and background selection on the inference of population history: problems and prospects 2021 ,		3
19	Recent evolutionary history of tigers highlights contrasting roles of genetic drift and selection		3
18	Transition from background selection to associative overdominance promotes diversity in regions of low recombination		3
17	Identification of candidate genes and physiological pathways involved in gonad deformation in whitefish (<i>Coregonus</i> spp.) from Lake Thun, Switzerland. <i>International Journal of Environmental Research and Public Health</i> , 2011 , 8, 2706-33	4.6	2
16	Detection of pathways affected by positive selection in primate lineages ancestral to humans		2
15	Dissection of the mutation accumulation process during bacterial range expansions. <i>BMC Genomics</i> , 2020 , 21, 253	4.5	1
14	Variation in novel exons (RACEfrags) of the MECP2 gene in Rett syndrome patients and controls. <i>Human Mutation</i> , 2009 , 30, E866-79	4.7	1
13	Reply to Garrigan and Hammer: Ancient lineages and assimilation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, E4-E4	11.5	1
12	The Genetic Basis of Smoltification: Functional Genomics Tools Facilitate the Search for the Needle in the Haystack 183-195		1
11	Reply to Stoneking. <i>Journal of Molecular Evolution</i> , 1990 , 31, 347-350	3.1	1
10	Genomic analysis of fast expanding bacteria reveals new molecular adaptive mechanisms		1

9	Genetic surfing in human populations: from genes to genomes	1
8	The mixed genetic origin of the first farmers of Europe	1
7	The population history of northeastern Siberia since the Pleistocene	1
6	Reconstruction of nine thousand years of agriculture-based diet and impact on human genetic diversity in Asia	1
5	Accumulation of deleterious mutations during bacterial range expansions	1
4	The evolutionary history of Nebraska deer mice: local adaptation in the face of strong gene flow	1
3	EXPANSION LOAD 2016 , 218-231	
2	Reply to "Re-evaluating the evidence for facilitation of stickleback speciation by admixture in the Lake Constance basin". <i>Nature Communications</i> , 2021 , 12, 2807	17.4
1	Simulations of Human Dispersal and Genetic Diversity. <i>Evolutionary Studies</i> , 2021 , 231-256	2.5