

# Laurent Excoffier

## 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.

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	The impact of purifying and background selection on the inference of population history: problems and prospects <b>2021</b> ,		3
205	Demographic inference. <i>Current Biology</i> , <b>2021</b> , 31, R276-R279	6.3	6
204	Genomic insights into population history and biological adaptation in Oceania. <i>Nature</i> , <b>2021</b> , 592, 583-589	30.4	26
203	Long-term evolution and short-term adaptation of microbiota strains and sub-strains in mice. <i>Cell Host and Microbe</i> , <b>2021</b> , 29, 650-663.e9	23.4	11
202	Reply to "Re-evaluating the evidence for facilitation of stickleback speciation by admixture in the Lake Constance basin". <i>Nature Communications</i> , <b>2021</b> , 12, 2807	17.4	
201	fastsimcoal2: demographic inference under complex evolutionary scenarios. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	14
200	Recent Evolutionary History of Tigers Highlights Contrasting Roles of Genetic Drift and Selection. <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 2366-2379	8.3	11
199	The Impact of Purifying and Background Selection on the Inference of Population History: Problems and Prospects. <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 2986-3003	8.3	9
198	Runs of homozygosity in killer whale genomes provide a global record of demographic histories. <i>Molecular Ecology</i> , <b>2021</b> , 30, 6162-6177	5.7	6
197	Simulations of Human Dispersal and Genetic Diversity. <i>Evolutionary Studies</i> , <b>2021</b> , 231-256	2.5	
196	Polygenic Patterns of Adaptive Introgression in Modern Humans Are Mainly Shaped by Response to Pathogens. <i>Molecular Biology and Evolution</i> , <b>2020</b> , 37, 1420-1433	8.3	20
195	Dissection of the mutation accumulation process during bacterial range expansions. <i>BMC Genomics</i> , <b>2020</b> , 21, 253	4.5	1
194	Gene flow as a simple cause for an excess of high-frequency-derived alleles. <i>Evolutionary Applications</i> , <b>2020</b> , 13, 2254-2263	4.8	4
193	Transition from Background Selection to Associative Overdominance Promotes Diversity in Regions of Low Recombination. <i>Current Biology</i> , <b>2020</b> , 30, 101-107.e3	6.3	19
192	The ecological and genomic basis of explosive adaptive radiation. <i>Nature</i> , <b>2020</b> , 586, 75-79	50.4	54
191	Admixture between old lineages facilitated contemporary ecological speciation in Lake Constance stickleback. <i>Nature Communications</i> , <b>2019</b> , 10, 4240	17.4	18
190	Killer whale genomes reveal a complex history of recurrent admixture and vicariance. <i>Molecular Ecology</i> , <b>2019</b> , 28, 3427-3444	5.7	25

189	The population history of northeastern Siberia since the Pleistocene. <i>Nature</i> , <b>2019</b> , 570, 182-188	50.4	137
188	SPLATCHE3: simulation of serial genetic data under spatially explicit evolutionary scenarios including long-distance dispersal. <i>Bioinformatics</i> , <b>2019</b> , 35, 4480-4483	7.2	22
187	Ancient admixture from an extinct ape lineage into bonobos. <i>Nature Ecology and Evolution</i> , <b>2019</b> , 3, 957-965	26.5	28
186	Mutational and Selective Processes Involved in Evolution during Bacterial Range Expansions. <i>Molecular Biology and Evolution</i> , <b>2019</b> , 36, 2313-2327	8.3	4
185	The Evolutionary History of Nebraska Deer Mice: Local Adaptation in the Face of Strong Gene Flow. <i>Molecular Biology and Evolution</i> , <b>2018</b> , 35, 792-806	8.3	43
184	Genomics of Parallel Ecological Speciation in Lake Victoria Cichlids. <i>Molecular Biology and Evolution</i> , <b>2018</b> , 35, 1489-1506	8.3	60
183	Background selection and biased gene conversion affect more than 95% of the human genome and bias demographic inferences. <i>ELife</i> , <b>2018</b> , 7,	8.9	59
182	Slightly deleterious genomic variants and transcriptome perturbations in Down syndrome embryonic selection. <i>Genome Research</i> , <b>2018</b> , 28, 1-10	9.7	27
181	Relaxed Selection During a Recent Human Expansion. <i>Genetics</i> , <b>2018</b> , 208, 763-777	4	28
180	Mutation load dynamics during environmentally-driven range shifts. <i>PLoS Genetics</i> , <b>2018</b> , 14, e1007450	6	19
179	Ancient hybridization fuels rapid cichlid fish adaptive radiations. <i>Nature Communications</i> , <b>2017</b> , 8, 14363	17.4	317
178	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , <b>2017</b> , 358, 659-662	33.3	160
177	Detecting gene subnetworks under selection in biological pathways. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, e149	20.1	35
176	Accumulation of Deleterious Mutations During Bacterial Range Expansions. <i>Genetics</i> , <b>2017</b> , 207, 669-684	4	47
175	Detection of Pathways Affected by Positive Selection in Primate Lineages Ancestral to Humans. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 1391-1402	8.3	33
174	Genomic landscape of early ecological speciation initiated by selection on nuptial colour. <i>Molecular Ecology</i> , <b>2017</b> , 26, 7-24	5.7	19
173	Long-distance dispersal suppresses introgression of local alleles during range expansions. <i>Heredity</i> , <b>2017</b> , 118, 135-142	3.6	13
172	Demographic modelling with whole-genome data reveals parallel origin of similar Pundamilia cichlid species after hybridization. <i>Molecular Ecology</i> , <b>2017</b> , 26, 123-141	5.7	75

171	A genomic history of Aboriginal Australia. <i>Nature</i> , <b>2016</b> , 538, 207-214	50.4	268
170	EXPANSION LOAD <b>2016</b> , 218-231		
169	Genome-culture coevolution promotes rapid divergence of killer whale ecotypes. <i>Nature Communications</i> , <b>2016</b> , 7, 11693	17.4	161
168	Chimpanzee genomic diversity reveals ancient admixture with bonobos. <i>Science</i> , <b>2016</b> , 354, 477-481	33.3	139
167	Long-Distance Dispersal Shaped Patterns of Human Genetic Diversity in Eurasia. <i>Molecular Biology and Evolution</i> , <b>2016</b> , 33, 946-58	8.3	28
166	The SIB Swiss Institute of Bioinformatics Presources: focus on curated databases. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D27-37	20.1	41
165	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> , <b>2016</b> , 113, E440-9	11.5	149
164	Genomics of Rapid Incipient Speciation in Sympatric Threespine Stickleback. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1005887	6	146
163	Genetic surfing in human populations: from genes to genomes. <i>Current Opinion in Genetics and Development</i> , <b>2016</b> , 41, 53-61	4.9	26
162	Expansion load and the evolutionary dynamics of a species range. <i>American Naturalist</i> , <b>2015</b> , 185, E81-93	3.7	88
161	Expansion load: recessive mutations and the role of standing genetic variation. <i>Molecular Ecology</i> , <b>2015</b> , 24, 2084-94	5.7	100
160	Inference of Evolutionary Forces Acting on Human Biological Pathways. <i>Genome Biology and Evolution</i> , <b>2015</b> , 7, 1546-58	3.9	12
159	Detection of convergent genome-wide signals of adaptation to tropical forests in humans. <i>PLoS ONE</i> , <b>2015</b> , 10, e0121557	3.7	28
158	Genetic consequences of habitat fragmentation during a range expansion. <i>Heredity</i> , <b>2014</b> , 112, 291-9	3.6	76
157	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> , <b>2014</b> , 111, E3596-603	11.5	70
156	Impact of range expansions on current human genomic diversity. <i>Current Opinion in Genetics and Development</i> , <b>2014</b> , 29, 22-30	4.9	27
155	Widespread signals of convergent adaptation to high altitude in Asia and America. <i>American Journal of Human Genetics</i> , <b>2014</b> , 95, 394-407	11	96
154	Ignoring heterozygous sites biases phylogenomic estimates of divergence times: implications for the evolutionary history of microtus voles. <i>Molecular Biology and Evolution</i> , <b>2014</b> , 31, 817-31	8.3	52

153	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
152	Continental-scale footprint of balancing and positive selection in a small rodent ( <i>Microtus arvalis</i> ). <i>PLoS ONE</i> , <b>2014</b> , 9, e112332	3.7	12
151	Evidence for polygenic adaptation to pathogens in the human genome. <i>Molecular Biology and Evolution</i> , <b>2013</b> , 30, 1544-58	8.3	132
150	Divergent evolutionary processes associated with colonization of offshore islands. <i>Molecular Ecology</i> , <b>2013</b> , 22, 5205-20	5.7	76
149	Influence of admixture and paleolithic range contractions on current European diversity gradients. <i>Molecular Biology and Evolution</i> , <b>2013</b> , 30, 57-61	8.3	35
148	Robust demographic inference from genomic and SNP data. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003905	6	780
147	On the accumulation of deleterious mutations during range expansions. <i>Molecular Ecology</i> , <b>2013</b> , 22, 5972-82	5.7	178
146	Recent colonization of the Galápagos by the tree <i>Geoffroea spinosa</i> Jacq. (Leguminosae). <i>Molecular Ecology</i> , <b>2012</b> , 21, 2743-60	5.7	7
145	Evolutionary forces shaping genomic islands of population differentiation in humans. <i>BMC Genomics</i> , <b>2012</b> , 13, 107	4.5	40
144	Serial founder effects during range expansion: a spatial analog of genetic drift. <i>Genetics</i> , <b>2012</b> , 191, 171-81	8.1	155
143	Consequences of range contractions and range shifts on molecular diversity. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 207-18	8.3	148
142	Parsimony-based pedigree analysis and individual-based landscape genetics suggest topography to restrict dispersal and connectivity in the endangered capercaillie. <i>Biological Conservation</i> , <b>2012</b> , 152, 241-252	6.2	18
141	European phylogeography of the epiphytic lichen fungus <i>Lobaria pulmonaria</i> and its green algal symbiont. <i>Molecular Ecology</i> , <b>2012</b> , 21, 5827-44	5.7	54
140	Reconstructing Native American population history. <i>Nature</i> , <b>2012</b> , 488, 370-4	50.4	498
139	Genomic data reveal a complex making of humans. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002837	6	33
138	PGDSpider: an automated data conversion tool for connecting population genetics and genomics programs. <i>Bioinformatics</i> , <b>2012</b> , 28, 298-9	7.2	647
137	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> , <b>2012</b> , 22, 846-57	1.9	12
136	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> , <b>2011</b> , 8, 2706-33	4.6	2

135	Enhanced AFLP genome scans detect local adaptation in high-altitude populations of a small rodent ( <i>Microtus arvalis</i> ). <i>Molecular Ecology</i> , <b>2011</b> , 20, 1450-62	5.7	106
134	Deep human genealogies reveal a selective advantage to be on an expanding wave front. <i>Science</i> , <b>2011</b> , 334, 1148-50	33.3	68
133	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> , <b>2011</b> , 108, 15129-34	11.5	112
132	fastsimcoal: a continuous-time coalescent simulator of genomic diversity under arbitrarily complex evolutionary scenarios. <i>Bioinformatics</i> , <b>2011</b> , 27, 1332-4	7.2	286
131	Approximate Bayesian analysis of <i>Drosophila melanogaster</i> polymorphism data reveals a recent colonization of Southeast Asia. <i>Molecular Biology and Evolution</i> , <b>2011</b> , 28, 2041-51	8.3	46
130	Contrasting patterns of nuclear and mtDNA diversity in Native American populations. <i>Annals of Human Genetics</i> , <b>2010</b> , 74, 525-38	2.2	41
129	In defence of model-based inference in phylogeography. <i>Molecular Ecology</i> , <b>2010</b> , 19, 436-446	5.7	127
128	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> , <b>2010</b> , 19, 2152-67	5.7	35
127	Distinguishing between population bottleneck and population subdivision by a Bayesian model choice procedure. <i>Molecular Ecology</i> , <b>2010</b> , 19, 4648-60	5.7	91
126	Estimating population structure from AFLP amplification intensity. <i>Molecular Ecology</i> , <b>2010</b> , 19, 4638-47	5.7	58
125	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> , <b>2010</b> , 19, 187-193	1.4	47
124	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> , <b>2010</b> , 27, 337-45	8.3	72
123	SPLATCHE2: a spatially explicit simulation framework for complex demography, genetic admixture and recombination. <i>Bioinformatics</i> , <b>2010</b> , 26, 2993-4	7.2	96
122	Bayesian inference of the demographic history of chimpanzees. <i>Molecular Biology and Evolution</i> , <b>2010</b> , 27, 1425-35	8.3	94
121	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> , <b>2010</b> , 59, 548-72	8.4	52
120	Arlequin suite ver 3.5: a new series of programs to perform population genetics analyses under Linux and Windows. <i>Molecular Ecology Resources</i> , <b>2010</b> , 10, 564-7	8.4	10640
119	A first step towards inferring levels of long-distance dispersal during past expansions. <i>Molecular Ecology Resources</i> , <b>2010</b> , 10, 902-14	8.4	46
118	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> , <b>2010</b> , 10, 886-901	8.4	50

117	Principal component analysis under population genetic models of range expansion and admixture. <i>Molecular Biology and Evolution</i> , <b>2010</b> , 27, 1257-68	8.3	93
116	ABCtoolbox: a versatile toolkit for approximate Bayesian computations. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 116	3.6	259
115	Efficient approximate Bayesian computation coupled with Markov chain Monte Carlo without likelihood. <i>Genetics</i> , <b>2009</b> , 182, 1207-18	4	214
114	Variation in novel exons (RACEfrags) of the MECP2 gene in Rett syndrome patients and controls. <i>Human Mutation</i> , <b>2009</b> , 30, E866-79	4.7	1
113	Gene flow in admixed populations and implications for the conservation of the Western honeybee, <i>Apis mellifera</i> . <i>Journal of Insect Conservation</i> , <b>2009</b> , 13, 317-328	2.1	46
112	Detecting loci under selection in a hierarchically structured population. <i>Heredity</i> , <b>2009</b> , 103, 285-98	3.6	593
111	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> , <b>2009</b> , 73, 95-108	2.2	127
110	Genetic evidence for complexity in ethnic differentiation and history in East Africa. <i>Annals of Human Genetics</i> , <b>2009</b> , 73, 582-600	2.2	32
109	Gene flow and species delimitation. <i>Trends in Ecology and Evolution</i> , <b>2009</b> , 24, 386-93	10.9	579
108	Genetic Consequences of Range Expansions. <i>Annual Review of Ecology, Evolution, and Systematics</i> , <b>2009</b> , 40, 481-501	13.5	835
107	Inferring past demography using spatially explicit population genetic models. <i>Human Biology</i> , <b>2009</b> , 81, 141-57	1.2	27
106	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> , <b>2008</b> , 17, 757-72	5.7	62
105	Italy as a major Ice Age refuge area for the bat <i>Myotis myotis</i> (Chiroptera: Vespertilionidae) in Europe. <i>Molecular Ecology</i> , <b>2008</b> , 17, 1801-14	5.7	55
104	Population transcriptomics of life-history variation in the genus <i>Salmo</i> . <i>Molecular Ecology</i> , <b>2008</b> , 17, 3095-108	5.7	40
103	Surfing during population expansions promotes genetic revolutions and structuration. <i>Trends in Ecology and Evolution</i> , <b>2008</b> , 23, 347-51	10.9	495
102	Geographic patterns of genome admixture in Latin American Mestizos. <i>PLoS Genetics</i> , <b>2008</b> , 4, e10000376		310
101	Reply to Garrigan and Hammer: Ancient lineages and assimilation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, E4-E4	11.5	1
100	Width of gene expression profile drives alternative splicing. <i>PLoS ONE</i> , <b>2008</b> , 3, e3587	3.7	12



99	Contrasted patterns of mitochondrial and nuclear structure among nursery colonies of the bat <i>Myotis myotis</i> . <i>Journal of Evolutionary Biology</i> , <b>2008</b> , 14, 708-720	2.3	135
98	Analysis of Population Subdivision <b>2008</b> , 980-1020		24
97	The hidden side of invasions: massive introgression by local genes. <i>Evolution; International Journal of Organic Evolution</i> , <b>2008</b> , 62, 1908-20	3.8	562
96	Fine-scale genetic structure and dispersal in the common vole ( <i>Microtus arvalis</i> ). <i>Molecular Ecology</i> , <b>2007</b> , 16, 2463-73	5.7	81
95	Bipolar gene flow in deep-sea benthic foraminifera. <i>Molecular Ecology</i> , <b>2007</b> , 16, 4089-96	5.7	112
94	Genetic analysis of potential postglacial watershed crossings in Central Europe by the bullhead ( <i>Cottus gobio</i> L.). <i>Molecular Ecology</i> , <b>2007</b> , 16, 4572-84	5.7	18
93	High variability and non-neutral evolution of the mammalian avpr1a gene. <i>BMC Evolutionary Biology</i> , <b>2007</b> , 7, 176	3	33
92	Statistical evaluation of alternative models of human evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 17614-9	11.5	409
91	Genetic variation and population structure in native Americans. <i>PLoS Genetics</i> , <b>2007</b> , 3, e185	6	392
90	Arlequin (version 3.0): an integrated software package for population genetics data analysis. <i>Evolutionary Bioinformatics</i> , <b>2007</b> , 1, 47-50	1.9	3325
89	Life history shapes gene expression in salmonids. <i>Current Biology</i> , <b>2006</b> , 16, R281-2	6.3	64
88	Neandertal genetic diversity: a fresh look from old samples. <i>Current Biology</i> , <b>2006</b> , 16, R650-2	6.3	12
87	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> , <b>2006</b> , 273, 3101-9	4.4	131
86	Molecular diversity after a range expansion in heterogeneous environments. <i>Genetics</i> , <b>2006</b> , 174, 2009-20		63
85	Mammalian monogamy is not controlled by a single gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 10956-60	11.5	107
84	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> , <b>2006</b> , 313, 172; author reply 172	33.3	47
83	The fate of mutations surfing on the wave of a range expansion. <i>Molecular Biology and Evolution</i> , <b>2006</b> , 23, 482-90	8.3	446
82	Conserved noncoding sequences are selectively constrained and not mutation cold spots. <i>Nature Genetics</i> , <b>2006</b> , 38, 223-7	36.3	184



81	Computer programs for population genetics data analysis: a survival guide. <i>Nature Reviews Genetics</i> , <b>2006</b> , 7, 745-58	30.1	256
80	The effect of the Neolithic expansion on European molecular diversity. <i>Proceedings of the Royal Society B: Biological Sciences</i> , <b>2005</b> , 272, 679-88	4.4	134
79	Arlequin (version 3.0): An integrated software package for population genetics data analysis. <i>Evolutionary Bioinformatics</i> , <b>2005</b> , 1, 117693430500100	1.9	6278
78	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> , <b>2005</b> , 18, 90-100	2.3	28
77	GENETIC STRUCTURE AND COLONIZATION PROCESSES IN EUROPEAN POPULATIONS OF THE COMMON VOLE, MICROTUS ARVALIS. <i>Evolution; International Journal of Organic Evolution</i> , <b>2005</b> , 59, 2231-2242	3.8	109
76	Bayesian estimation of recent migration rates after a spatial expansion. <i>Genetics</i> , <b>2005</b> , 170, 409-17	4	91
75	Bayesian analysis of an admixture model with mutations and arbitrarily linked markers. <i>Genetics</i> , <b>2005</b> , 169, 1727-38	4	201
74	Recovering the geographic origin of early modern humans by realistic and spatially explicit simulations. <i>Genome Research</i> , <b>2005</b> , 15, 1161-7	9.7	78
73	Molecular analysis reveals tighter social regulation of immigration in patrilocal populations than in matrilineal populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 7476-80	11.5	90
72	GENETIC STRUCTURE AND COLONIZATION PROCESSES IN EUROPEAN POPULATIONS OF THE COMMON VOLE, MICROTUS ARVALIS. <i>Evolution; International Journal of Organic Evolution</i> , <b>2005</b> , 59, 2231	3.8	3
71	Genetic structure and colonization processes in European populations of the common vole, <i>Microtus arvalis</i> . <i>Evolution; International Journal of Organic Evolution</i> , <b>2005</b> , 59, 2231-42	3.8	35
70	SIMCOAL 2.0: a program to simulate genomic diversity over large recombining regions in a subdivided population with a complex history. <i>Bioinformatics</i> , <b>2004</b> , 20, 2485-7	7.2	206
69	Modern humans did not admix with Neanderthals during their range expansion into Europe. <i>PLoS Biology</i> , <b>2004</b> , 2, e421	9.7	208
68	Mitochondrial gene diversity in the common vole <i>Microtus arvalis</i> shaped by historical divergence and local adaptations. <i>Molecular Ecology</i> , <b>2004</b> , 13, 3501-14	5.7	83
67	Low levels of mitochondrial DNA variation among central and southern European <i>Esox lucius</i> populations. <i>Journal of Fish Biology</i> , <b>2004</b> , 64, 1442-1449	1.9	22
66	Patterns of DNA sequence diversity and genetic structure after a range expansion: lessons from the infinite-island model. <i>Molecular Ecology</i> , <b>2004</b> , 13, 853-64	5.7	488
65	splatche: a program to simulate genetic diversity taking into account environmental heterogeneity. <i>Molecular Ecology Notes</i> , <b>2004</b> , 4, 139-142		113
64	Analysis of Population Subdivision <b>2004</b> ,		5

63	Gametic phase estimation over large genomic regions using an adaptive window approach. <i>Human Genomics</i> , <b>2003</b> , 1, 7-19	6.8	82
62	Human diversity: our genes tell where we live. <i>Current Biology</i> , <b>2003</b> , 13, R134-6	6.3	8
61	Reconstructing the demography of prehistoric human populations from molecular data. <i>Evolutionary Anthropology</i> , <b>2003</b> , 11, 166-170	4.7	3
60	Comment on "Genetic structure of human populations". <i>Science</i> , <b>2003</b> , 300, 1877; author reply 1877	33.3	44
59	Intra-deme molecular diversity in spatially expanding populations. <i>Molecular Biology and Evolution</i> , <b>2003</b> , 20, 76-86	8.3	461
58	A simulated annealing approach to define the genetic structure of populations. <i>Molecular Ecology</i> , <b>2002</b> , 11, 2571-81	5.7	1425
57	A human genome diversity cell line panel. <i>Science</i> , <b>2002</b> , 296, 261-2	33.3	742
56	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> , <b>2002</b> , 70, 207-23	11	98
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13	The Genetic Basis of Smoltification: Functional Genomics Tools Facilitate the Search for the Needle in the Haystack		183-195
12	Genomic analysis of fast expanding bacteria reveals new molecular adaptive mechanisms		1
11	Detection of pathways affected by positive selection in primate lineages ancestral to humans		2
10	Genetic surfing in human populations: from genes to genomes		1

9	Relaxed selection during a recent human expansion	3
8	Runs of homozygosity in killer whale genomes provide a global record of demographic histories	4
7	The mixed genetic origin of the first farmers of Europe	1
6	The population history of northeastern Siberia since the Pleistocene	1
5	Recent evolutionary history of tigers highlights contrasting roles of genetic drift and selection	3
4	Reconstruction of nine thousand years of agriculture-based diet and impact on human genetic diversity in Asia	1
3	Transition from background selection to associative overdominance promotes diversity in regions of low recombination	3
2	Accumulation of deleterious mutations during bacterial range expansions	1
1	The evolutionary history of Nebraska deer mice: local adaptation in the face of strong gene flow	1