

# Noah A Rosenberg

## List of Publications by Year in Descending Order

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**Version:** 2024-04-24

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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.

188  
papers

26,690  
citations

49  
h-index

163  
g-index

223  
ext. papers

31,292  
ext. citations

5.7  
avg, IF

7.61  
L-index

#	Paper	IF	Citations
188	Ancient and modern genomics of the Ohlone Indigenous population of California.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2022</b> , 119, e2111533119	11.5	0
187	Celebrating 50 years since Lewontin's apportionment of human diversity.. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2022</b> , 377, 20200405	5.8	0
186	Mathematical constraints on : multiallelic markers in arbitrarily many populations.. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2022</b> , 377, 20200414	5.8	2
185	Enumeration of binary trees compatible with a perfect phylogeny.. <i>Journal of Mathematical Biology</i> , <b>2022</b> , 84, 54	2	
184	A Population-Genetic Perspective on the Similarities and Differences among Worldwide Human Populations. <i>Human Biology</i> , <b>2021</b> , 92, 135-152	1.2	2
183	A compendium of covariances and correlation coefficients of coalescent tree properties. <i>Theoretical Population Biology</i> , <b>2021</b> , 143, 1-13	1.2	0
182	On the Colijn-Plazzotta numbering scheme for unlabeled binary rooted trees. <i>Discrete Applied Mathematics</i> , <b>2021</b> , 291, 88-98	1	
181	Variance and limiting distribution of coalescence times in a diploid model of a consanguineous population. <i>Theoretical Population Biology</i> , <b>2021</b> , 139, 50-65	1.2	2
180	Genetic Adaptation in New York City Rats. <i>Genome Biology and Evolution</i> , <b>2021</b> , 13,	3.9	6
179	Designing gene drives to limit spillover to non-target populations. <i>PLoS Genetics</i> , <b>2021</b> , 17, e1009278	6	4
178	Skin deep: The decoupling of genetic admixture levels from phenotypes that differed between source populations. <i>American Journal of Physical Anthropology</i> , <b>2021</b> , 175, 406-421	2.5	1
177	The effect of consanguinity on coalescence times on the X chromosome. <i>Theoretical Population Biology</i> , <b>2021</b> , 140, 32-43	1.2	0
176	A simple derivation of the mean of the Sackin index of tree balance under the uniform model on rooted binary labeled trees. <i>Mathematical Biosciences</i> , <b>2021</b> , 342, 108688	3.9	0
175	Modelling anti-vaccine sentiment as a cultural pathogen. <i>Evolutionary Human Sciences</i> , <b>2020</b> , 2,	2.2	5
174	Measures of care fragmentation: Mathematical insights from population genetics. <i>Health Services Research</i> , <b>2020</b> , 55, 318-327	3.4	3
173	Human-Genetic Ancestry Inference and False Positives in Forensic Familial Searching. <i>G3: Genes, Genomes, Genetics</i> , <b>2020</b> , 10, 2893-2902	3.2	4
172	Roadblocked monotonic paths and the enumeration of coalescent histories for non-matching caterpillar gene trees and species trees. <i>Advances in Applied Mathematics</i> , <b>2020</b> , 113, 101939-101939	0.8	1

171	Probabilities of Unranked and Ranked Anomaly Zones under Birth-Death Models. <i>Molecular Biology and Evolution</i> , <b>2020</b> , 37, 1480-1494	8.3	3
170	High-resolution inference of genetic relationships among Jewish populations. <i>European Journal of Human Genetics</i> , <b>2020</b> , 28, 804-814	5.3	1
169	On the heterozygosity of an admixed population. <i>Journal of Mathematical Biology</i> , <b>2020</b> , 81, 1217-1250	2	5
168	Assortative mating by population of origin in a mechanistic model of admixture. <i>Theoretical Population Biology</i> , <b>2020</b> , 134, 129-146	1.2	4
167	Distance metrics for ranked evolutionary trees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 28876-28886	11.5	2
166	F and the triangle inequality for biallelic markers. <i>Theoretical Population Biology</i> , <b>2020</b> , 133, 117-129	1.2	0
165	Coalescent Theory of Migration Network Motifs. <i>Molecular Biology and Evolution</i> , <b>2019</b> , 36, 2358-2374	8.3	3
164	The Effect of Consanguinity on Between-Individual Identity-by-Descent Sharing. <i>Genetics</i> , <b>2019</b> , 212, 305-316	4	10
163	Mathematical and Simulation-Based Analysis of the Behavior of Admixed Taxa in the Neighbor-Joining Algorithm. <i>Bulletin of Mathematical Biology</i> , <b>2019</b> , 81, 452-493	2.1	2
162	On the Number of Non-equivalent Ancestral Configurations for Matching Gene Trees and Species Trees. <i>Bulletin of Mathematical Biology</i> , <b>2019</b> , 81, 384-407	2.1	5
161	The probability of reciprocal monophyly of gene lineages in three and four species. <i>Theoretical Population Biology</i> , <b>2019</b> , 129, 133-147	1.2	3
160	Enumeration of compact coalescent histories for matching gene trees and species trees. <i>Journal of Mathematical Biology</i> , <b>2019</b> , 78, 155-188	2	6
159	Use of stochastic patch occupancy models in the California red-legged frog for Bayesian inference regarding past events and future persistence. <i>Conservation Biology</i> , <b>2019</b> , 33, 685-696	6	1
158	The Relationship Between Haplotype-Based and Haplotype Length. <i>Genetics</i> , <b>2019</b> , 213, 281-295	4	2
157	Disease transmission and introgression can explain the long-lasting contact zone of modern humans and Neanderthals. <i>Nature Communications</i> , <b>2019</b> , 10, 5003	17.4	14
156	Network-based hierarchical population structure analysis for large genomic data sets. <i>Genome Research</i> , <b>2019</b> , 29, 2020-2033	9.7	2
155	Mathematical Properties of Linkage Disequilibrium Statistics Defined by Normalization of the Coefficient $D = p_{AB} - p_A p_B$ . <i>Human Heredity</i> , <b>2019</b> , 84, 127-143	1.1	2
154	$D$ , $F_{ST}$ , and $F$ are similarly constrained by allele frequencies: A mathematical, simulation, and empirical study. <i>Molecular Ecology</i> , <b>2019</b> , 28, 1624-1636	5.7	10

153	Interpreting polygenic scores, polygenic adaptation, and human phenotypic differences. <i>Evolution, Medicine and Public Health</i> , <b>2019</b> , 2019, 26-34	3	51
152	Some topics in theoretical population genetics: Editorial commentaries on a selection of Marc Feldman's TPB papers. <i>Theoretical Population Biology</i> , <b>2019</b> , 129, 4-8	1.2	0
151	ENUMERATION OF LONELY PAIRS OF GENE TREES AND SPECIES TREES BY MEANS OF ANTIPODAL CHERRIES. <i>Advances in Applied Mathematics</i> , <b>2019</b> , 102, 1-17	0.8	3
150	Bounding measures of genetic similarity and diversity using majorization. <i>Journal of Mathematical Biology</i> , <b>2018</b> , 77, 711-737	2	1
149	A genome scan for genes underlying adult body size differences between Central African hunter-gatherers and farmers. <i>Human Genetics</i> , <b>2018</b> , 137, 487-509	6.3	14
148	On the joint distribution of tree height and tree length under the coalescent. <i>Theoretical Population Biology</i> , <b>2018</b> , 122, 46-56	1.2	4
147	Statistical Detection of Relatives Typed with Disjoint Forensic and Biomedical Loci. <i>Cell</i> , <b>2018</b> , 175, 848-858	5.2	19
146	Ancient X chromosomes reveal contrasting sex bias in Neolithic and Bronze Age Eurasian migrations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, 2657-2662	11.5	69
145	Mathematical Constraints on : Biallelic Markers in Arbitrarily Many Populations. <i>Genetics</i> , <b>2017</b> , 206, 1581-1600	14	
144	Linkage disequilibrium matches forensic genetic records to disjoint genomic marker sets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, 5671-5676	11.5	27
143	Evaluating allopolyploid origins in strawberries ( <i>Fragaria</i> ) using haplotypes generated from target capture sequencing. <i>BMC Evolutionary Biology</i> , <b>2017</b> , 17, 180	3	47
142	Enumeration of Ancestral Configurations for Matching Gene Trees and Species Trees. <i>Journal of Computational Biology</i> , <b>2017</b> , 24, 831-850	1.7	8
141	Parallel Trajectories of Genetic and Linguistic Admixture in a Genetically Admixed Creole Population. <i>Current Biology</i> , <b>2017</b> , 27, 2529-2535.e3	6.3	8
140	Simulation-Based Evaluation of Hybridization Network Reconstruction Methods in the Presence of Incomplete Lineage Sorting. <i>Evolutionary Bioinformatics</i> , <b>2017</b> , 13, 1176934317691935	1.9	9
139	Reply to Lazaridis and Reich: Robust model-based inference of male-biased admixture during Bronze Age migration from the Pontic-Caspian Steppe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E3875-E3877	11.5	10
138	Consanguinity Rates Predict Long Runs of Homozygosity in Jewish Populations. <i>Human Heredity</i> , <b>2016</b> , 82, 87-102	1.1	13
137	An analytical upper bound on the number of loci required for all splits of a species tree to appear in a set of gene trees. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 417	3.6	1
136	Does Gene Tree Discordance Explain the Mismatch between Macroevolutionary Models and Empirical Patterns of Tree Shape and Branching Times?. <i>Systematic Biology</i> , <b>2016</b> , 65, 628-39	8.4	12

135	Asymptotic Properties of the Number of Matching Coalescent Histories for Caterpillar-Like Families of Species Trees. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2016</b> , 13, 913-925 <sup>3</sup>		10
134	Admixture Models and the Breeding Systems of H. S. Jennings: A GENETICS Connection. <i>Genetics</i> , <b>2016</b> , 202, 9-13	4	5
133	The probability of monophyly of a sample of gene lineages on a species tree. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 8002-9	11.5	12
132	Individual Identifiability Predicts Population Identifiability in Forensic Microsatellite Markers. <i>Current Biology</i> , <b>2016</b> , 26, 935-42	6.3	38
131	Consistency and inconsistency of consensus methods for inferring species trees from gene trees in the presence of ancestral population structure. <i>Theoretical Population Biology</i> , <b>2016</b> , 110, 12-24	1.2	11
130	Clumpak: a program for identifying clustering modes and packaging population structure inferences across K. <i>Molecular Ecology Resources</i> , <b>2015</b> , 15, 1179-91	8.4	1526
129	Enhancing the mathematical properties of new haplotype homozygosity statistics for the detection of selective sweeps. <i>Theoretical Population Biology</i> , <b>2015</b> , 102, 94-101	1.2	20
128	Haplotype Allele Frequency (HAF) Score: Predicting Carriers of Ongoing Selective Sweeps Without Knowledge of the Adaptive Allele. <i>Lecture Notes in Computer Science</i> , <b>2015</b> , 276-280	0.9	1
127	Implications of the apportionment of human genetic diversity for the apportionment of human phenotypic diversity. <i>Studies in History and Philosophy of Science Part C: Studies in History and Philosophy of Biological and Biomedical Sciences</i> , <b>2015</b> , 52, 32-45	0.6	16
126	Genetic Diversity and Societally Important Disparities. <i>Genetics</i> , <b>2015</b> , 201, 1-12	4	17
125	AABC: approximate approximate Bayesian computation for inference in population-genetic models. <i>Theoretical Population Biology</i> , <b>2015</b> , 99, 31-42	1.2	18
124	A General Model of the Relationship between the Apportionment of Human Genetic Diversity and the Apportionment of Human Phenotypic Diversity. <i>Human Biology</i> , <b>2015</b> , 87, 313-337	1.2	12
123	Predicting Carriers of Ongoing Selective Sweeps without Knowledge of the Favored Allele. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005527	6	13
122	Choosing Subsamples for Sequencing Studies by Minimizing the Average Distance to the Closest Leaf. <i>Genetics</i> , <b>2015</b> , 201, 499-511	4	1
121	Beyond 2/3 and 1/3: The Complex Signatures of Sex-Biased Admixture on the X Chromosome. <i>Genetics</i> , <b>2015</b> , 201, 263-79	4	42
120	Coalescent Histories for Lodgepole Species Trees. <i>Journal of Computational Biology</i> , <b>2015</b> , 22, 918-29	1.7	12
119	A comparison of worldwide phonemic and genetic variation in human populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 1265-72	11.5	77
118	Upper bounds on FST in terms of the frequency of the most frequent allele and total homozygosity: the case of a specified number of alleles. <i>Theoretical Population Biology</i> , <b>2014</b> , 97, 20-34	1.2	18

117	Population-genetic influences on genomic estimates of the inbreeding coefficient: a global perspective. <i>Human Heredity</i> , <b>2014</b> , 77, 37-48	1.1	27
116	An empirical evaluation of two-stage species tree inference strategies using a multilocus dataset from North American pines. <i>BMC Evolutionary Biology</i> , <b>2014</b> , 14, 67	3	18
115	Patterns of admixture and population structure in native populations of Northwest North America. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004530	6	49
114	Autosomal admixture levels are informative about sex bias in admixed populations. <i>Genetics</i> , <b>2014</b> , 198, 1209-29	4	19
113	On the Number of Ranked Species Trees Producing Anomalous Ranked Gene Trees. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2014</b> , 11, 1229-38	3	5
112	Theory and applications of a deterministic approximation to the coalescent model. <i>Theoretical Population Biology</i> , <b>2014</b> , 93, 14-29	1.2	11
111	Genotype imputation in a coalescent model with infinitely-many-sites mutation. <i>Theoretical Population Biology</i> , <b>2013</b> , 87, 62-74	1.2	4
110	Runs of homozygosity and parental relatedness. <i>Genetics in Medicine</i> , <b>2013</b> , 15, 753-4	8.1	6
109	Long runs of homozygosity are enriched for deleterious variation. <i>American Journal of Human Genetics</i> , <b>2013</b> , 93, 90-102	11	153
108	Genetics and the history of the Samaritans: Y-chromosomal microsatellites and genetic affinity between Samaritans and Cohanim. <i>Human Biology</i> , <b>2013</b> , 85, 825-58	1.2	2
107	From generation to generation: the genetics of Jewish populations. Introduction. <i>Human Biology</i> , <b>2013</b> , 85, 817-24	1.2	1
106	Mathematical properties of the deep coalescence cost. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2013</b> , 10, 61-72	3	16
105	Coalescent histories for caterpillar-like families. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2013</b> , 10, 1253-62	3	10
104	No evidence from genome-wide data of a Khazar origin for the Ashkenazi Jews. <i>Human Biology</i> , <b>2013</b> , 85, 859-900	1.2	49
103	Population structure in a comprehensive genomic data set on human microsatellite variation. <i>G3: Genes, Genomes, Genetics</i> , <b>2013</b> , 3, 891-907	3.2	73
102	Genotype imputation reference panel selection using maximal phylogenetic diversity. <i>Genetics</i> , <b>2013</b> , 195, 319-30	4	19
101	Discordance of species trees with their most likely gene trees: a unifying principle. <i>Molecular Biology and Evolution</i> , <b>2013</b> , 30, 2709-13	8.3	64
100	Windfalls and pitfalls: Applications of population genetics to the search for disease genes. <i>Evolution, Medicine and Public Health</i> , <b>2013</b> , 2013, 254-72	3	4

99	The relationship between $F_{ST}$ and the frequency of the most frequent allele. <i>Genetics</i> , <b>2013</b> , 193, 515-28	145
98	Geographic sampling scheme as a determinant of the major axis of genetic variation in principal components analysis. <i>Molecular Biology and Evolution</i> , <b>2013</b> , 30, 480-8	8.3 9
97	The behavior of admixed populations in neighbor-joining inference of population trees. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , <b>2013</b> , 273-84	1.3 7
96	HaploScope: a tool for the graphical display of haplotype structure in populations. <i>Genetic Epidemiology</i> , <b>2012</b> , 36, 17-21	2.6 7
95	Refining the relationship between homozygosity and the frequency of the most frequent allele. <i>Journal of Mathematical Biology</i> , <b>2012</b> , 64, 87-108	2 10
94	A maximum-likelihood method to correct for allelic dropout in microsatellite data with no replicate genotypes. <i>Genetics</i> , <b>2012</b> , 192, 651-69	4 40
93	Improvements to a class of distance matrix methods for inferring species trees from gene trees. <i>Journal of Computational Biology</i> , <b>2012</b> , 19, 632-49	1.7 15
92	iGLASS: an improvement to the GLASS method for estimating species trees from gene trees. <i>Journal of Computational Biology</i> , <b>2012</b> , 19, 293-315	1.7 23
91	A characterization of the set of species trees that produce anomalous ranked gene trees. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2012</b> , 9, 1558-68	3 13
90	The probability distribution of ranked gene trees on a species tree. <i>Mathematical Biosciences</i> , <b>2012</b> , 235, 45-55	3.9 23
89	Inferring species trees directly from biallelic genetic markers: bypassing gene trees in a full coalescent analysis. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 1917-32	8.3 553
88	Genomic patterns of homozygosity in worldwide human populations. <i>American Journal of Human Genetics</i> , <b>2012</b> , 91, 275-92	11 281
87	Impact of restricted marital practices on genetic variation in an endogamous Gujarati group. <i>American Journal of Physical Anthropology</i> , <b>2012</b> , 149, 92-103	2.5 14
86	A quantitative comparison of the similarity between genes and geography in worldwide human populations. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002886	6 83
85	A coalescent model for genotype imputation. <i>Genetics</i> , <b>2012</b> , 191, 1239-55	4 18
84	Inference on the strength of balancing selection for epistatically interacting loci. <i>Theoretical Population Biology</i> , <b>2011</b> , 79, 102-13	1.2 7
83	On the size distribution of private microsatellite alleles. <i>Theoretical Population Biology</i> , <b>2011</b> , 80, 100-13	1.2 38
82	Mathematical properties of $F_{ST}$ between admixed populations and their parental source populations. <i>Theoretical Population Biology</i> , <b>2011</b> , 80, 208-16	1.2 14

81	A test of the influence of continental axes of orientation on patterns of human gene flow. <i>American Journal of Physical Anthropology</i> , <b>2011</b> , 146, 515-29	2.5	17
80	Haplotype variation and genotype imputation in African populations. <i>Genetic Epidemiology</i> , <b>2011</b> , 35, 766-80	2.6	31
79	A population-genetic perspective on the similarities and differences among worldwide human populations. <i>Human Biology</i> , <b>2011</b> , 83, 659-84	1.2	57
78	Consistency properties of species tree inference by minimizing deep coalescences. <i>Journal of Computational Biology</i> , <b>2011</b> , 18, 1-15	1.7	66
77	How dormant is Mycobacterium tuberculosis during latency? A study integrating genomics and molecular epidemiology. <i>Infection, Genetics and Evolution</i> , <b>2011</b> , 11, 1164-7	4.5	10
76	Coalescence-time distributions in a serial founder model of human evolutionary history. <i>Genetics</i> , <b>2011</b> , 189, 579-93	4	29
75	A general mechanistic model for admixture histories of hybrid populations. <i>Genetics</i> , <b>2011</b> , 189, 1413-264		54
74	Heterozygosity of the Yellowstone wolves. <i>Molecular Ecology</i> , <b>2010</b> , 19, 3246-9	5.7	6
73	Genome-wide association studies in diverse populations. <i>Nature Reviews Genetics</i> , <b>2010</b> , 11, 356-66	30.1	422
72	Comparing spatial maps of human population-genetic variation using Procrustes analysis. <i>Statistical Applications in Genetics and Molecular Biology</i> , <b>2010</b> , 9, Article 13	1.2	84
71	Unbiased estimation of gene diversity in samples containing related individuals: exact variance and arbitrary ploidy. <i>Genetics</i> , <b>2010</b> , 186, 1367-87	4	5
70	MLH1 founder mutations with moderate penetrance in Spanish Lynch syndrome families. <i>Cancer Research</i> , <b>2010</b> , 70, 7379-91	10.1	28
69	Lack of population diversity in commonly used human embryonic stem-cell lines. <i>New England Journal of Medicine</i> , <b>2010</b> , 362, 183-5	59.2	44
68	Inference of unexpected genetic relatedness among individuals in HapMap Phase III. <i>American Journal of Human Genetics</i> , <b>2010</b> , 87, 457-64	11	89
67	Coalescent histories for discordant gene trees and species trees. <i>Theoretical Population Biology</i> , <b>2010</b> , 77, 145-51	1.2	17
66	Properties of consensus methods for inferring species trees from gene trees. <i>Systematic Biology</i> , <b>2009</b> , 58, 35-54	8.4	116
65	Out of Africa: modern human origins special feature: explaining worldwide patterns of human genetic variation using a coalescent-based serial founder model of migration outward from Africa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 16057-62	11.5	124
64	Sequence determinants of human microsatellite variability. <i>BMC Genomics</i> , <b>2009</b> , 10, 612	4.5	36



63	Replication of genetic associations as pseudoreplication due to shared genealogy. <i>Genetic Epidemiology</i> , <b>2009</b> , 33, 479-87	2.6	6
62	Genomic microsatellites identify shared Jewish ancestry intermediate between Middle Eastern and European populations. <i>BMC Genetics</i> , <b>2009</b> , 10, 80	2.6	41
61	Genotype-imputation accuracy across worldwide human populations. <i>American Journal of Human Genetics</i> , <b>2009</b> , 84, 235-50	11	191
60	The relationship between imputation error and statistical power in genetic association studies in diverse populations. <i>American Journal of Human Genetics</i> , <b>2009</b> , 85, 692-8	11	58
59	Gene tree discordance, phylogenetic inference and the multispecies coalescent. <i>Trends in Ecology and Evolution</i> , <b>2009</b> , 24, 332-40	10.9	1166
58	Haplotypic background of a private allele at high frequency in the Americas. <i>Molecular Biology and Evolution</i> , <b>2009</b> , 26, 995-1016	8.3	48
57	An unbiased estimator of gene diversity in samples containing related individuals. <i>Molecular Biology and Evolution</i> , <b>2009</b> , 26, 501-12	8.3	18
56	Genotype, haplotype and copy-number variation in worldwide human populations. <i>Nature</i> , <b>2008</b> , 451, 998-1003	50.4	662
55	Mathematical properties of the $r^2$ measure of linkage disequilibrium. <i>Theoretical Population Biology</i> , <b>2008</b> , 74, 130-7	1.2	119
54	Population differentiation and migration: coalescence times in a two-sex island model for autosomal and X-linked loci. <i>Theoretical Population Biology</i> , <b>2008</b> , 74, 291-301	1.2	24
53	Discordance of species trees with their most likely gene trees: the case of five taxa. <i>Systematic Biology</i> , <b>2008</b> , 57, 131-40	8.4	87
52	Demographic history of european populations of <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , <b>2008</b> , 4, e10000756		150
51	Nonadaptive explanations for signatures of partial selective sweeps in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , <b>2008</b> , 25, 1025-42	8.3	21
50	ADZE: a rarefaction approach for counting alleles private to combinations of populations. <i>Bioinformatics</i> , <b>2008</b> , 24, 2498-504	7.2	505
49	The relationship between homozygosity and the frequency of the most frequent allele. <i>Genetics</i> , <b>2008</b> , 179, 2027-36	4	16
48	CLUMPP: a cluster matching and permutation program for dealing with label switching and multimodality in analysis of population structure. <i>Bioinformatics</i> , <b>2007</b> , 23, 1801-6	7.2	4312
47	The probability distribution under a population divergence model of the number of genetic founding lineages of a population or species. <i>Theoretical Population Biology</i> , <b>2007</b> , 71, 502-23	1.2	5
46	Statistical tests for taxonomic distinctiveness from observations of monophyly. <i>Evolution; International Journal of Organic Evolution</i> , <b>2007</b> , 61, 317-23	3.8	130

45	Genetic diversity and population structure inferred from the partially duplicated genome of domesticated carp, <i>Cyprinus carpio</i> L. <i>Genetics Selection Evolution</i> , <b>2007</b> , 39, 319-40	4.9	18
44	Estimating the number of ancestral lineages using a maximum-likelihood method based on rejection sampling. <i>Genetics</i> , <b>2007</b> , 176, 1741-57	4	7
43	Genetic variation and population structure in native Americans. <i>PLoS Genetics</i> , <b>2007</b> , 3, e185	6	392
42	On the genealogy of a duplicated microsatellite. <i>Genetics</i> , <b>2007</b> , 177, 2109-22	4	8
41	Counting coalescent histories. <i>Journal of Computational Biology</i> , <b>2007</b> , 14, 360-77	1.7	36
40	Sampling properties of homozygosity-based statistics for linkage disequilibrium. <i>Mathematical Biosciences</i> , <b>2007</b> , 208, 33-47	3.9	5
39	Genetic diversity and population structure inferred from the partially duplicated genome of domesticated carp, <i>Cyprinus carpio</i> L.. <i>Genetics Selection Evolution</i> , <b>2007</b> , 39, 319-340	4.9	1
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7	Variance and limiting distribution of coalescence times in a diploid model of a consanguineous population		1
6	Familial migration of the Neolithic contrasts massive male migration during Bronze Age in Europe inferred from ancient X chromosomes		3
5	Genetic Adaptation in New York City Rats		3
4	Linkage disequilibrium connects genetic records of relatives typed with disjoint genomic marker sets		1
3	Mathematical constraints on FST: multiallelic markers in arbitrarily many populations		1
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1	Extracting hierarchical features of cultural variation using network-based clustering. <i>Evolutionary Human Sciences</i> , 1-35	2.2	0