David Balding

List of Publications by Year
in descending order

238 papers	28,664 citations	12322 69 h-index	6128 159 g-index
324 all docs	324 docs citations	324 times ranked	40132 citing authors

#	Article	IF	Citations
1	Optimizing sampling design and sequencing strategy for the genomic analysis of quantitative traits in natural populations. Molecular Ecology Resources, 2022, 22, 137-152.	2.2	1
2	Genome-wide association, prediction and heritability in bacteria with application to Streptococcus pneumoniae. NAR Genomics and Bioinformatics, 2022, 4, lqac011.	1.5	5
3	Genomeâ€wide association mapping of Hagberg falling number, protein content, test weight, and grain yield in U.K. wheat. Crop Science, 2022, 62, 965-981.	0.8	10
4	Bayesian inference of ancestral recombination graphs. PLoS Computational Biology, 2022, 18, e1009960.	1.5	12
5	SNPâ€based heritability and selection analyses: Improved models and new results. BioEssays, 2022, 44, e2100170.	1.2	14
6	Disentangling Signatures of Selection Before and After European Colonization in Latin Americans. Molecular Biology and Evolution, 2022, 39, .	3.5	16
7	Including diverse and admixed populations in genetic epidemiology research. Genetic Epidemiology, 2022, 46, 347-371.	0.6	11
8	A GWAS in Latin Americans identifies novel face shape loci, implicating VPS13B and a Denisovan introgressed region in facial variation. Science Advances, 2021, 7, .	4.7	32
9	Shared genetic basis between genetic generalized epilepsy and background electroencephalographic oscillations. Epilepsia, 2021, 62, 1518-1527.	2.6	5
10	Prediction of eye, hair and skin colour in Latin Americans. Forensic Science International: Genetics, 2021, 53, 102517.	1.6	6
11	Assessing the Forensic Value of DNA Evidence from Y Chromosomes and Mitogenomes. Genes, 2021, 12, 1209.	1.0	11
12	Using common genetic variants to find drugs for common epilepsies. Brain Communications, 2021, 3, fcab287.	1.5	9
13	Mixed methods. PLoS Genetics, 2020, 16, e1008950.	1.5	0
14	How can courts take into account the uncertainty in a likelihood ratio?. Forensic Science International: Genetics, 2020, 48, 102361.	1.6	5
15	Evaluating and improving heritability models using summary statistics. Nature Genetics, 2020, 52, 458-462.	9.4	128
16	Summary statistic analyses can mistake confounding bias for heritability. Genetic Epidemiology, 2019, 43, 930-940.	0.6	8
17	A GWAS in Latin Americans highlights the convergent evolution of lighter skin pigmentation in Eurasia. Nature Communications, 2019, 10, 358.	5.8	130
18	A general framework for moment-based analysis of genetic data. Journal of Mathematical Biology, 2019, 78, 1727-1769.	0.8	4

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19	A comparison of software for the evaluation of complex DNA profiles. Forensic Science International: Genetics, 2019, 40, 114-119.	1.6	23
20	Y-profile evidence: Close paternal relatives and mixtures. Forensic Science International: Genetics, 2019, 38, 48-53.	1.6	16
21	SumHer better estimates the SNP heritability of complex traits from summary statistics. Nature Genetics, 2019, 51, 277-284.	9.4	181
22	Bridging trees for posterior inference on ancestral recombination graphs. Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences, 2018, 474, 20180568.	1.0	6
23	The Rise and Fall of BritainsDNA: A Tale of Misleading Claims, Media Manipulation and Threats to Academic Freedom. Genealogy, 2018, 2, 47.	0.4	1
24	Latin Americans show wide-spread Converso ancestry and imprint of local Native ancestry on physical appearance. Nature Communications, 2018, 9, 5388.	5.8	123
25	Genome-wide mega-analysis identifies 16 loci and highlights diverse biological mechanisms in the common epilepsies. Nature Communications, 2018, 9, 5269.	5.8	331
26	How many individuals share a mitochondrial genome?. PLoS Genetics, 2018, 14, e1007774.	1.5	20
27	Evaluating DNA evidence in a genetically complex population. Forensic Science International: Genetics, 2018, 36, 141-147.	1.6	5
28	GWAlpha: genome-wide estimation of additive effects (alpha) based on trait quantile distribution from pool-sequencing experiments. Bioinformatics, 2017, 33, 1246-1247.	1.8	3
29	Reevaluation of SNP heritability in complex human traits. Nature Genetics, 2017, 49, 986-992.	9.4	427
30	Optimizing genomic medicine in epilepsy through a gene-customized approach to missense variant interpretation. Genome Research, 2017, 27, 1715-1729.	2.4	150
31	In-frame seven amino-acid duplication in AIP arose over the last 3000 years, disrupts protein interaction and stability and is associated with gigantism. European Journal of Endocrinology, 2017, 177, 257-266.	1.9	12
32	A comment on the PCAST report: Skip the â€œmatchâ€•â€œnon-matchâ€•stage. Forensic Science International, 2017, 272, e7-e9.	1.3	25
33	Increased Population Risk ofAIP-Related Acromegaly and Gigantism in Ireland. Human Mutation, 2017, 38, 78-85.	1.1	25
34	How convincing is a matching Y-chromosome profile?. PLoS Genetics, 2017, 13, e1007028.	1.5	38
35	A genome-wide association scan in admixed Latin Americans identifies loci influencing facial and scalp hair features. Nature Communications, 2016, 7, 10815.	5.8	159
36	Encoding of low-quality DNA profiles as genotype probability matrices for improved profile comparisons, relatedness evaluation and database searches. Forensic Science International: Genetics, 2016, 25, 227-239.	1.6	4

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37	A genome-wide association scan implicates DCHS2, RUNX2, GLI3, PAX1 and EDAR in human facial variation. Nature Communications, 2016, 7, 11616.	5.8	171
38	Evaluation of low-template DNA profiles using peak heights. Statistical Applications in Genetics and Molecular Biology, 2016, 15, 431-445.	0.2	27
39	Using Genetic Distance to Infer the Accuracy of Genomic Prediction. PLoS Genetics, 2016, 12, e1006288.	1.5	112
40	Evidence for a Common Origin of Blacksmiths and Cultivators in the Ethiopian Ari within the Last 4500 Years: Lessons for Clustering-Based Inference. PLoS Genetics, 2015, 11, e1005397.	1.5	194
41	Integrating dynamic mixed-effect modelling and penalized regression to explore genetic association with pharmacokinetics. Pharmacogenetics and Genomics, 2015, 25, 231-238.	0.7	3
42	The genomic and phenotypic diversity of Schizosaccharomyces pombe. Nature Genetics, 2015, 47, 235-241.	9.4	174
43	Bayesian models for syndrome- and gene-specific probabilities of novel variant pathogenicity. Genome Medicine, 2015, 7, 5.	3.6	22
44	A genome-wide association study identifies multiple loci for variation in human ear morphology. Nature Communications, 2015, 6, 7500.	5.8	80
45	A Simulation Approach for Change-Points on Phylogenetic Trees. Journal of Computational Biology, 2015, 22, 10-24.	0.8	2
46	Relatedness in the post-genomic era: is it still useful?. Nature Reviews Genetics, 2015, 16, 33-44.	7.7	228
47	Multiple Quantitative Trait Analysis Using Bayesian Networks. Genetics, 2014, 198, 129-137.	1.2	67
48	Statistical Evaluation of Forensic DNA Profile Evidence. Annual Review of Statistics and Its Application, 2014, 1, 361-384.	4.1	65
49	Interaction between gas cooking andGSTM1null genotype in bronchial responsiveness: results from the European Community Respiratory Health Survey. Thorax, 2014, 69, 558-564.	2.7	22
50	Admixture in Latin America: Geographic Structure, Phenotypic Diversity and Self-Perception of Ancestry Based on 7,342 Individuals. PLoS Genetics, 2014, 10, e1004572.	1.5	350
51	MultiBLUP: improved SNP-based prediction for complex traits. Genome Research, 2014, 24, 1550-1557.	2.4	258
52	Choice of population database for forensic DNA profile analysis. Science and Justice - Journal of the Forensic Science Society, 2014, 54, 487-493.	1.3	22
53	Identification of the remains of King Richard III. Nature Communications, 2014, 5, 5631.	5.8	163
54	A genome-wide association study and biological pathway analysis of epilepsy prognosis in a prospective cohort of newly treated epilepsy. Human Molecular Genetics, 2014, 23, 247-258.	1.4	33

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55	Storytelling and story testing in domestication. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6159-6164.	3.3	96
56	Describing the genetic architecture of epilepsy through heritability analysis. Brain, 2014, 137, 2680-2689.	3.7	87
57	Worldwide FST Estimates Relative to Five Continental-Scale Populations. Annals of Human Genetics, 2014, 78, 468-477.	0.3	35
58	Verifying likelihoods for low template DNA profiles using multiple replicates. Forensic Science International: Genetics, 2014, 13, 82-89.	1.6	25
59	Genetic determinants of common epilepsies: a meta-analysis of genome-wide association studies. Lancet Neurology, The, 2014, 13, 893-903.	4.9	264
60	Applying association mapping and genomic selection to the dissection of key traits in elite European wheat. Theoretical and Applied Genetics, 2014, 127, 2619-2633.	1.8	100
61	Evaluating forensic DNA profiles using peak heights, allowing for multiple donors, allelic dropout and stutters. Forensic Science International: Genetics, 2013, 7, 555-563.	1.6	73
62	Decision-making in familial database searching: KI alone or not alone?. Forensic Science International: Genetics, 2013, 7, 52-54.	1.6	24
63	Response to Lee etÂal.: SNP-Based Heritability Analysis with Dense Data. American Journal of Human Genetics, 2013, 93, 1155-1157.	2.6	17
64	Improving the efficiency of genomic selection. Statistical Applications in Genetics and Molecular Biology, 2013, 12, 517-27.	0.2	17
65	Integrated analysis of genome-wide genetic and epigenetic association data for identification of disease mechanisms. Epigenetics, 2013, 8, 1236-1244.	1.3	15
66	Genetic screening for Niemann-Pick disease type C in adults with neurological and psychiatric symptoms: findings from the ZOOM study. Human Molecular Genetics, 2013, 22, 4349-4356.	1.4	75
67	Evaluation of mixed-source, low-template DNA profiles in forensic science. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 12241-12246.	3.3	82
68	Multiple single nucleotide polymorphism analysis using penalized regression in nonlinear mixed-effect pharmacokinetic models. Pharmacogenetics and Genomics, 2013, 23, 167-174.	0.7	13
69	Dysregulation of Complement System and CD4+ T Cell Activation Pathways Implicated in Allergic Response. PLoS ONE, 2013, 8, e74821.	1.1	14
70	Genome-wide association study in multiple human prion diseases suggests genetic risk factors additional to PRNP. Human Molecular Genetics, 2012, 21, 1897-1906.	1.4	73
71	Understanding complex traits: from farmers to pharmas. Genome Medicine, 2012, 4, 59.	3.6	1
72	Improved Heritability Estimation from Genome-wide SNPs. American Journal of Human Genetics, 2012, 91, 1011-1021.	2.6	656

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73	Ethiopian Genetic Diversity Reveals Linguistic Stratification and Complex Influences on the Ethiopian Gene Pool. American Journal of Human Genetics, 2012, 91, 83-96.	2.6	177
74	Differential coexpression analysis of obesity-associated networks in human subcutaneous adipose tissue. International Journal of Obesity, 2012, 36, 137-147.	1.6	42
75	Bayesian Networks and Probabilistic Inference in Forensic Science. Law, Probability and Risk, 2011, 10, 355-358.	1.2	1
76	A genome-wide meta-analysis of genetic variants associated with allergic rhinitis and grass sensitization and their interaction with birth order. Journal of Allergy and Clinical Immunology, 2011, 128, 996-1005.	1.5	212
77	Using Penalised Logistic Regression to Fine Map HLA Variants for Rheumatoid Arthritis. Annals of Human Genetics, 2011, 75, 655-664.	0.3	20
78	Epigenome-wide association studies for common human diseases. Nature Reviews Genetics, 2011, 12, 529-541.	7.7	1,110
79	Inference in complex systems. Interface Focus, 2011, 1, 805-806.	1.5	3
80	AIPMutation in Pituitary Adenomas in the 18th Century and Today. New England Journal of Medicine, 2011, 364, 43-50.	13.9	151
81	Admixture provides new insights into recombination. Nature Genetics, 2011, 43, 819-820.	9.4	3
82	Animal Research: Reporting In Vivo Experiments: The ARRIVE Guidelines. Journal of Gene Medicine, 2010, 12, 561-563.	1.4	230
83	Animal research: Reporting in vivo experiments: The ARRIVE guidelines. British Journal of Pharmacology, 2010, 160, 1577-1579.	2.7	3,150
84	Genetic and isotopic analysis and the UK Border Agency. Significance, 2010, 7, 58-61.	0.3	2
85	In defence of model-based inference in phylogeography. Molecular Ecology, 2010, 19, 436-446.	2.0	141
86	Animal Research: Reporting In Vivo Experiments: The ARRIVE guidelines. Experimental Physiology, 2010, 95, 842-844.	0.9	30
87	Animal Research: Reporting In Vivo Experiments: The ARRIVE guidelines. Journal of Physiology, 2010, 588, 2519-2521.	1.3	75
88	cnvHap: an integrative population and haplotypeâ€"based multiplatform model of SNPs and CNVs. Nature Methods, 2010, 7, 541-546.	9.0	44
89	A Genome-Wide Association Study of Neuroticism in a Population-Based Sample. PLoS ONE, 2010, 5, e11504.	1.1	71
90	Inferring combined CNV/SNP haplotypes from genotype data. Bioinformatics, 2010, 26, 1437-1445.	1.8	31

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91	On Optimal Selection of Summary Statistics for Approximate Bayesian Computation. Statistical Applications in Genetics and Molecular Biology, 2010, 9, Article34.	0.2	102
92	Genome-wide association mapping to candidate polymorphism resolution in the unsequenced barley genome. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 21611-21616.	3.3	259
93	A Genome-Wide Association Study of the Metabolic Syndrome in Indian Asian Men. PLoS ONE, 2010, 5, e11961.	1.1	116
94	Pathway Analysis of GWAS Provides New Insights into Genetic Susceptibility to 3 Inflammatory Diseases. PLoS ONE, 2009, 4, e8068.	1.1	131
95	Common Genetic Variation Near Melatonin Receptor MTNR1B Contributes to Raised Plasma Glucose and Increased Risk of Type 2 Diabetes Among Indian Asians and European Caucasians. Diabetes, 2009, 58, 2703-2708.	0.3	95
96	Apolipoprotein E, CI and B Gene Polymorphisms in a Sample of Patients with Coronary Heart Disease in the Kuwaiti Population. Medical Principles and Practice, 2009, 18, 294-299.	1.1	11
97	Time for DNA Disclosure. Science, 2009, 326, 1631-1632.	6.0	15
98	Genetic association of the major histocompatibility complex with rheumatoid arthritis implicates two nonâ€ÐRB1 loci. Arthritis and Rheumatism, 2009, 60, 53-62.	6.7	68
99	Limit theorems for sequences of random trees. Test, 2009, 18, 302-315.	0.7	11
100	Heritability and genetic correlations of insulin resistance and component phenotypes in Asian Indian families using a multivariate analysis. Diabetologia, 2009, 52, 2585-2589.	2.9	34
101	Genome-wide association study for early-onset and morbid adult obesity identifies three new risk loci in European populations. Nature Genetics, 2009, 41, 157-159.	9.4	585
102	Bayesian statistical methods for genetic association studies. Nature Reviews Genetics, 2009, 10, 681-690.	7.7	400
103	Assessing Evidence via Likelihood Ratios. , 2009, , 22-42.		0
104	Crime on An Island. , 2009, , 7-21.		0
105	Some Population Genetics for DNA Evidence. , 2009, , 56-81.		0
106	Other Approaches to Weight of Evidence. , 2009, , 135-144.		0
107	Issues for the Courtroom. , 2009, , 145-156.		0
108	Relatedness. , 2009, , 111-134.		0

#	Article	IF	Citations
109	Typing Technologies. , 2009, , 43-55.		0
110	PopABC: a program to infer historical demographic parameters. Bioinformatics, 2009, 25, 2747-2749.	1.8	77
111	Interpreting low template DNA profiles. Forensic Science International: Genetics, 2009, 4, 1-10.	1.6	167
112	Population Structure and Cryptic Relatedness in Genetic Association Studies. Statistical Science, 2009, 24, .	1.6	372
113	Genomeâ€wide significance for dense SNP and resequencing data. Genetic Epidemiology, 2008, 32, 179-185.	0.6	187
114	Chromosome Maps. , 2008, , 1-39.		3
115	Protein Structure Prediction. , 2008, , 327-346.		0
116	Statistical Techniques in Metabolic Profiling. , 2008, , 347-373.		13
117	Adaptive Molecular Evolution. , 2008, , 375-406.		13
118	Genome Evolution. , 2008, , 407-438.		0
119	Probabilistic Models for the Study of Protein Evolution. , 2008, , 439-459.		1
120	Phylogenetics: Parsimony, Networks, and Distance Methods. , 2008, , 489-532.		0
121	Evolutionary Quantitative Genetics. , 2008, , 533-586.		8
122	Quantitative Trait Loci in Inbred Lines. , 2008, , 587-622.		6
123	Statistical Significance in Biological Sequence Comparison. , 2008, , 40-66.		0
124	Inferences from Mixed Models in Quantitative Genetics. , 2008, , 678-717.		2
125	Marker-Assisted Selection and Introgression. , 2008, , 718-751.		3
126	Mathematical Models in Population Genetics. , 2008, , 753-780.		6

#	Article	IF	Citations
127	Inference, Simulation and Enumeration of Genealogies. , 2008, , 781-807.		2
128	Graphical Models in Genetics. , 2008, , 808-842.		0
129	Coalescent Theory. , 2008, , 843-877.		33
130	Inference Under the Coalescent. , 2008, , 878-908.		4
131	Linkage Disequilibrium, Recombination and Selection. , 2008, , 909-944.		14
132	Analysis of Population Subdivision. , 2008, , 980-1020.		33
133	Bayesian Methods in Biological Sequence Analysis. , 2008, , 67-96.		0
134	Conservation Genetics. , 2008, , 1021-1066.		5
135	Human Genetic Diversity and its History. , 2008, , 1067-1108.		0
136	Epidemiology and Genetic Epidemiology. , 2008, , 1109-1140.		5
137	Linkage Analysis. , 2008, , 1141-1167.		6
138	Non-Parametric Linkage. , 2008, , 1168-1189.		0
139	Population Admixture and Stratification in Genetic Epidemiology. , 2008, , 1190-1215.		2
140	Population Association. , 2008, , 1216-1237.		4
141	Whole Genome Association. , 2008, , 1238-1263.		6
142	Family-Based Association. , 2008, , 1264-1285.		1
143	Cancer Genetics. , 2008, , 1286-1300.		0
144	Ethics Issues in Statistical Genetics. , 2008, , 1323-1345.		0

#	Article	IF	Citations
145	Forensics. , 2008, , 1368-1392.		4
146	Comparative Genomics. , 2008, , 160-199.		1
147	Analysis of Microarray Gene Expression Data. , 2008, , 201-230.		0
148	Statistical Inference for Microarray Studies. , 2008, , 231-266.		1
149	Bayesian Methods for Microarray Data. , 2008, , 267-295.		2
150	Inferring Causal Associations between Genes and Disease via the Mapping of Expression Quantitative Trait Loci. , 2008, , 296-326.		1
151	Reference Author Index. , 2008, , I-LXI.		0
152	Common genetic variation near MC4R is associated with waist circumference and insulin resistance. Nature Genetics, 2008, 40, 716-718.	9.4	456
153	Fregene: Simulation of realistic sequence-level data in populations and ascertained samples. BMC Bioinformatics, 2008, 9, 364.	1.2	57
154	Inference of haplotypic phase and missing genotypes in polyploid organisms and variable copy number genomic regions. BMC Bioinformatics, 2008, 9, 513.	1.2	23
155	Assessment of cumulative evidence on genetic associations: interim guidelines. International Journal of Epidemiology, 2008, 37, 120-132.	0.9	506
156	Inferring population history withDIY ABC: a user-friendly approach to approximate Bayesian computation. Bioinformatics, 2008, 24, 2713-2719.	1.8	616
157	Population Structure and Inbreeding From Pedigree Analysis of Purebred Dogs. Genetics, 2008, 179, 593-601.	1.2	123
158	Disease association tests by inferring ancestral haplotypes using a hidden markov model. Bioinformatics, 2008, 24, 972-978.	1.8	22
159	Confounding between recombination and selection, and the Ped/Pop method for detecting selection. Genome Research, 2008, 18, 1304-1313.	2.4	81
160	Simultaneous Analysis of All SNPs in Genome-Wide and Re-Sequencing Association Studies. PLoS Genetics, 2008, 4, e1000130.	1.5	298
161	Sequence-Level Population Simulations Over Large Genomic Regions. Genetics, 2007, 177, 1725-1731.	1.2	99
162	The association between polymorphisms in RLIP76 and drug response in epilepsy. Pharmacogenomics, 2007, 8, 1715-1722.	0.6	16

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163	Common ABCB1 polymorphisms are not associated with multidrug resistance in epilepsy using a gene-wide tagging approach. Pharmacogenetics and Genomics, 2007, 17, 217-220.	0.7	45
164	Functional constraint and small insertions and deletions in the ENCODE regions of the human genome. Genome Biology, 2007, 8, R180.	13.9	32
165	Family-based association analysis with ordered categorical phenotypes, covariates and interactions. Genetic Epidemiology, 2007, 31, 1-8.	0.6	15
166	Reply: On the value of haplotype-based genotypeâ€“phenotype analysis and on data transformation in pharmacogenetics and -genomics. Nature Reviews Genetics, 2007, 8, 983-983.	7.7	1
167	A genome-wide association study identifies novel risk loci for type 2 diabetes. Nature, 2007, 445, 881-885.	13.7	2,651
168	Variation in estimated recombination rates across human populations. Human Genetics, 2007, 122, 301-310.	1.8	40
169	Exon sequencing and high resolution haplotype analysis of ABC transporter genes implicated in drug resistance. Pharmacogenetics and Genomics, 2006, 16, 439-450.	0.7	62
170	A Likelihood Ratio Approach to Family-based Association Studies with Covariates. Annals of Human Genetics, 2006, 70, 131-139.	0.3	7
171	A tutorial on statistical methods for population association studies. Nature Reviews Genetics, 2006, 7, 781-791.	7.7	1,120
172	Discrimination of half-siblings when maternal genotypes are known. Forensic Science International, 2006, 159, 141-147.	1.3	18
173	Clinical factors and ABCB1 polymorphisms in prediction of antiepileptic drug response: a prospective cohort study. Lancet Neurology, The, 2006, 5, 668-676.	4.9	68
174	Fine mapping of disease genes via haplotype clustering. Genetic Epidemiology, 2006, 30, 170-179.	0.6	49
175	Editorial. Human Genomics, 2005, 2, 79-80.	1.4	4
176	Paternity index calculations when some individuals share common ancestry. Forensic Science International, 2005, 151, 101-103.	1.3	7
177	A question of identity. Significance, 2005, 2, 20-23.	0.3	1
178	Logistic regression protects against population structure in genetic association studies. Genome Research, 2005, 16, 290-296.	2.4	94
179	Identifying adaptive genetic divergence among populations from genome scans. Molecular Ecology, 2004, 13, 969-980.	2.0	906
180	Clustering of Protein Domains in the Human Genome. Journal of Molecular Biology, 2004, 340, 991-1004.	2.0	12

#	Article	IF	Citations
181	Little Loss of Information Due to Unknown Phase for Fine-Scale Linkage-Disequilibrium Mapping with Single-Nucleotideâ€“Polymorphism Genotype Data. American Journal of Human Genetics, 2004, 74, 945-953.	2.6	66
182	Chromosome-wide distribution of haplotype blocks and the role of recombination hot spots. Nature Genetics, 2003, 33, 382-387.	9.4	268
183	Inferences from DNA data: population histories, evolutionary processes and forensic match probabilities. Journal of the Royal Statistical Society Series A: Statistics in Society, 2003, 166, 155-188.	0.6	232
184	Likelihood-based inference for genetic correlation coefficients. Theoretical Population Biology, 2003, 63, 221-230.	0.5	137
185	Multipoint linkage-disequilibrium mapping narrows location interval and identifies mutation heterogeneity. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 13442-13446.	3.3	28
186	Gametic phase estimation over large genomic regions using an adaptive window approach. Human Genomics, 2003, 1, 7.	1.4	88
187	Patterns of Human Diversity, within and among Continents, Inferred from Biallelic DNA Polymorphisms. Genome Research, 2002, 12, 602-612.	2.4	188
188	Fine-Scale Mapping of Disease Loci via Shattered Coalescent Modeling of Genealogies. American Journal of Human Genetics, 2002, 70, 686-707.	2.6	123
189	Implications for DNA identification arising from an analysis of Australian forensic databases. Forensic Science International, 2002, 129, 90-98.	1.3	21
190	The DN A Database Search Controversy. Biometrics, 2002, 58, 241-244.	0.8	32
191	Discussion on the meeting on 'Statistical modelling and analysis of genetic data'. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2002, 64, 737-775.	1.1	11
192	Approximate Bayesian Computation in Population Genetics. Genetics, 2002, 162, 2025-2035.	1.2	2,220
193	Models of Sequence Evolution for DNA Sequences Containing Gaps. Molecular Biology and Evolution, 2001, 18, 481-490.	3.5	92
194	MAC5: Bayesian inference of phylogenetic trees from DNA sequences incorporating gaps. Bioinformatics, 2001, 17, 479-480.	1.8	7
195	Measuring Gametic Disequilibrium From Multilocus Data. Genetics, 2001, 157, 413-423.	1.2	23
196	Analyses of infectious disease data from household outbreaks by Markov chain Monte Carlo methods. Journal of the Royal Statistical Society Series C: Applied Statistics, 2000, 49, 517-542.	0.5	102
197	Fine-scale mapping of disease loci. GeneScreen, 2000, 1, 101-102.	0.7	1
198	Bayesian Fine-Scale Mapping of Disease Loci, by Hidden Markov Models. American Journal of Human Genetics, 2000, 67, 155-169.	2.6	95

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199	Interpreting DNA Evidence: Can Probability Theory Help?. , 2000, , 51-70.		12
200	Interpreting DNA evidence: statistical genetics for forensic scientists. By I. W. EVETT and B. S. WEIR. Sinauer Associates Inc. 1998. ISBN 0 87893 155 4. 278 pages. Price Â£25.95.. Genetical Research, 1999, 73, 85-89.	0.3	0
201	When can a DNA profile be regarded as unique?. Science and Justice - Journal of the Forensic Science Society, 1999, 39, 257-260.	1.3	47
202	Measuring departures from Hardyâ€“Weinberg: a Markov chain Monte Carlo method for estimating the inbreeding coefficient. Heredity, 1998, 80, 769-777.	1.2	88
203	Encyclopedia of Statistical Sciences: Update Volume 1. Biometrics, 1998, 54, 794.	0.8	0
204	Genealogical Inference From Microsatellite Data. Genetics, 1998, 150, 499-510.	1.2	250
205	The Design of Pooling Experiments for Screening a Clone Map. Fungal Genetics and Biology, 1997, 21, 302-307.	0.9	27
206	Significant genetic correlations among Caucasians at forensic DNA loci. Heredity, 1997, 78, 583-589.	1.2	63
207	Significant genetic correlations among Caucasians at forensic DNA loci. Heredity, 1997, 78, 583-589.	1.2	15
208	Inferring Coalescence Times From DNA Sequence Data. Genetics, 1997, 145, 505-518.	1.2	678
209	Estimating the Age of the Common Ancestor of Men from the ZFY Intron. Science, 1996, 272, 1356-1362.	6.0	45
210	Population genetics of STR loci in Caucasians. International Journal of Legal Medicine, 1996, 108, 300-305.	1.2	46
211	Optimal Pooling Designs with Error Detection. Journal of Combinatorial Theory - Series A, 1996, 74, 131-140.	0.5	43
212	A Comparative Survey of Non-Adaptive Pooling Designs. , 1996, , 133-154.		64
213	Estimating the Age of the Common Ancestor of Men from the ZFY Intron. Science, 1996, 272, 1357-1359.	6.0	44
214	Evaluating DNA Profile Evidence When the Suspect Is Identified Through a Database Search. Journal of Forensic Sciences, 1996, 41, 603-607.	0.9	66
215	Inferring identify from DNA profile evidence.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 11741-11745.	3.3	37
216	A method for quantifying differentiation between populations at multi-allelic loci and its implications for investigating identity and paternity. Genetica, 1995, 96, 3-12.	0.5	492

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217	Estimating Products in Forensic Identification Using DNA Profiles. Journal of the American Statistical Association, 1995, 90, 839-844.	1.8	46
218	Inference in Forensic Identification. Journal of the Royal Statistical Society Series A: Statistics in Society, 1995, 158, 21.	0.6	88
219	Efficient pooling designs for library screening. Genomics, 1995, 26, 21-30.	1.3	128
220	A method for quantifying differentiation between populations at multi-allelic loci and its implications for investigating identity and paternity. Contemporary Issues in Genetics and Evolution, 1995, , 3-12.	0.9	16
221	Estimating Products in Forensic Identification Using DNA Profiles. Journal of the American Statistical Association, 1995, 90, 839.	1.8	13
222	DNA profile match probability calculation: how to allow for population stratification, relatedness, database selection and single bands. Forensic Science International, 1994, 64, 125-140.	1.3	445
223	How convincing is DNA evidence?. Nature, 1994, 368, 285-286.	13.7	27
224	Design and analysis of chromosome physical mapping experiments. Philosophical Transactions of the Royal Society B: Biological Sciences, 1994, 344, 329-335.	1.8	6
225	[DNA Fingerprinting: A Review of the Controversy]: Comment: Some Causes for Concern about DNA Profiles. Statistical Science, 1994, 9, .	1.6	14
226	Detecting gene conversion: primate visual pigment genes. Proceedings of the Royal Society B: Biological Sciences, 1992, 249, 275-280.	1.2	32
227	Statistical analysis of DNA fingerprint data for ordered clone physical mapping of human chromosomes. Bulletin of Mathematical Biology, 1991, 53, 853-879.	0.9	21
228	Effects of population structure on DNA fingerprint analysis in forensic science. Heredity, 1991, 66, 297-302.	1.2	67
229	Statistical analysis of DNA fingerprint data for ordered clone physical mapping of human chromosomes. Bulletin of Mathematical Biology, 1991, 53, 853-879.	0.9	19
230	Diffusion-controlled reactions in one dimension: Exact solutions and deterministic approximations. Physical Review A, 1989, 40, 4585-4592.	1.0	26
231	Invasion processes and binary annihilation in one dimension. Physics Letters, Section A: General, Atomic and Solid State Physics, 1988, 126, 481-483.	0.9	21
232	Diffusion-reaction in one dimension. Journal of Applied Probability, 1988, 25, 733-743.	0.4	10
233	Diffusion-reaction in one dimension. Journal of Applied Probability, 1988, 25, 733-743.	0.4	7
234	Risk factors and heart disease mortality: A regional perspective. Medical Journal of Australia, 1986, 144, 20-22.	0.8	26

#	Article	IF	Citations
235	Risk factors and heart disease mortality. A regional perspective. Medical Journal of Australia, 1986, 144, 20-2.	0.8	3
236	A mathematical model of tumour-induced capillary growth. Journal of Theoretical Biology, 1985, 114, 53-73.	0.8	206
237	Reference Author Index. , 0, , I-LXI.		0
238	Statistics in Practice. , 0, , 185-185.		0