David Balding

List of Publications by Year in descending order

238 papers	28,664 citations	12303 69 h-index	6113 159 g-index
324 all docs	324 docs citations	324 times ranked	40132 citing authors

#	Article	IF	Citations
1	Animal research: Reporting in vivo experiments: The ARRIVE guidelines. British Journal of Pharmacology, 2010, 160, 1577-1579.	2.7	3,150
2	A genome-wide association study identifies novel risk loci for type 2 diabetes. Nature, 2007, 445, 881-885.	13.7	2,651
3	Approximate Bayesian Computation in Population Genetics. Genetics, 2002, 162, 2025-2035.	1.2	2,220
4	A tutorial on statistical methods for population association studies. Nature Reviews Genetics, 2006, 7, 781-791.	7.7	1,120
5	Epigenome-wide association studies for common human diseases. Nature Reviews Genetics, 2011, 12, 529-541.	7.7	1,110
6	Identifying adaptive genetic divergence among populations from genome scans. Molecular Ecology, 2004, 13, 969-980.	2.0	906
7	Inferring Coalescence Times From DNA Sequence Data. Genetics, 1997, 145, 505-518.	1.2	678
8	Improved Heritability Estimation from Genome-wide SNPs. American Journal of Human Genetics, 2012, 91, 1011-1021.	2.6	656
9	Inferring population history withDIY ABC: a user-friendly approach to approximate Bayesian computation. Bioinformatics, 2008, 24, 2713-2719.	1.8	616
10	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
11	Assessment of cumulative evidence on genetic associations: interim guidelines. International Journal of Epidemiology, 2008, 37, 120-132.	0.9	506
12	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
13	Common genetic variation near MC4R is associated with waist circumference and insulin resistance. Nature Genetics, 2008, 40, 716-718.	9.4	456
14	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
15	Reevaluation of SNP heritability in complex human traits. Nature Genetics, 2017, 49, 986-992.	9.4	427
16	Bayesian statistical methods for genetic association studies. Nature Reviews Genetics, 2009, 10, 681-690.	7.7	400
17	Population Structure and Cryptic Relatedness in Genetic Association Studies. Statistical Science, 2009, 24, .	1.6	372
18	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

#	Article	IF	Citations
19	Genome-wide mega-analysis identifies 16 loci and highlights diverse biological mechanisms in the common epilepsies. Nature Communications, 2018, 9, 5269.	5.8	331
20	Simultaneous Analysis of All SNPs in Genome-Wide and Re-Sequencing Association Studies. PLoS Genetics, 2008, 4, e1000130.	1.5	298
21	Chromosome-wide distribution of haplotype blocks and the role of recombination hot spots. Nature Genetics, 2003, 33, 382-387.	9.4	268
22	Genetic determinants of common epilepsies: a meta-analysis of genome-wide association studies. Lancet Neurology, The, 2014, 13, 893-903.	4.9	264
23	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
24	MultiBLUP: improved SNP-based prediction for complex traits. Genome Research, 2014, 24, 1550-1557.	2.4	258
25	Genealogical Inference From Microsatellite Data. Genetics, 1998, 150, 499-510.	1.2	250
26	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
27	Animal Research: Reporting In Vivo Experiments: The ARRIVE Guidelines. Journal of Gene Medicine, 2010, 12, 561-563.	1.4	230
28	Relatedness in the post-genomic era: is it still useful?. Nature Reviews Genetics, 2015, 16, 33-44.	7.7	228
29	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
30	A mathematical model of tumour-induced capillary growth. Journal of Theoretical Biology, 1985, 114, 53-73.	0.8	206
31	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
32	Patterns of Human Diversity, within and among Continents, Inferred from Biallelic DNA Polymorphisms. Genome Research, 2002, 12, 602-612.	2.4	188
33	Genomeâ€wide significance for dense SNP and resequencing data. Genetic Epidemiology, 2008, 32, 179-185.	0.6	187
34	SumHer better estimates the SNP heritability of complex traits from summary statistics. Nature Genetics, 2019, 51, 277-284.	9.4	181
35	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
36	The genomic and phenotypic diversity of Schizosaccharomyces pombe. Nature Genetics, 2015, 47, 235-241.	9.4	174

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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	Interpreting low template DNA profiles. Forensic Science International: Genetics, 2009, 4, 1-10.	1.6	167
39	Identification of the remains of King Richard III. Nature Communications, 2014, 5, 5631.	5.8	163
40	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
41	AIPMutation in Pituitary Adenomas in the 18th Century and Today. New England Journal of Medicine, 2011, 364, 43-50.	13.9	151
42	Optimizing genomic medicine in epilepsy through a gene-customized approach to missense variant interpretation. Genome Research, 2017, 27, 1715-1729.	2.4	150
43	In defence of model-based inference in phylogeography. Molecular Ecology, 2010, 19, 436-446.	2.0	141
44	Likelihood-based inference for genetic correlation coefficients. Theoretical Population Biology, 2003, 63, 221-230.	0.5	137
45	Pathway Analysis of GWAS Provides New Insights into Genetic Susceptibility to 3 Inflammatory Diseases. PLoS ONE, 2009, 4, e8068.	1.1	131
46	A GWAS in Latin Americans highlights the convergent evolution of lighter skin pigmentation in Eurasia. Nature Communications, 2019, 10, 358.	5.8	130
47	Efficient pooling designs for library screening. Genomics, 1995, 26, 21-30.	1.3	128
48	Evaluating and improving heritability models using summary statistics. Nature Genetics, 2020, 52, 458-462.	9.4	128
49	Fine-Scale Mapping of Disease Loci via Shattered Coalescent Modeling of Genealogies. American Journal of Human Genetics, 2002, 70, 686-707.	2.6	123
50	Population Structure and Inbreeding From Pedigree Analysis of Purebred Dogs. Genetics, 2008, 179, 593-601.	1.2	123
51	Latin Americans show wide-spread Converso ancestry and imprint of local Native ancestry on physical appearance. Nature Communications, 2018, 9, 5388.	5.8	123
52	A Genome-Wide Association Study of the Metabolic Syndrome in Indian Asian Men. PLoS ONE, 2010, 5, e11961.	1.1	116
53	Using Genetic Distance to Infer the Accuracy of Genomic Prediction. PLoS Genetics, 2016, 12, e1006288.	1.5	112
54	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

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55	On Optimal Selection of Summary Statistics for Approximate Bayesian Computation. Statistical Applications in Genetics and Molecular Biology, 2010, 9, Article34.	0.2	102
56	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
57	Sequence-Level Population Simulations Over Large Genomic Regions. Genetics, 2007, 177, 1725-1731.	1.2	99
58	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
59	Bayesian Fine-Scale Mapping of Disease Loci, by Hidden Markov Models. American Journal of Human Genetics, 2000, 67, 155-169.	2.6	95
60	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
61	Logistic regression protects against population structure in genetic association studies. Genome Research, 2005, 16, 290-296.	2.4	94
62	Models of Sequence Evolution for DNA Sequences Containing Gaps. Molecular Biology and Evolution, 2001, 18, 481-490.	3.5	92
63	Inference in Forensic Identification. Journal of the Royal Statistical Society Series A: Statistics in Society, 1995, 158, 21.	0.6	88
64	Measuring departures from Hardyâ€“Weinberg: a Markov chain Monte Carlo method for estimating the inbreeding coefficient. Heredity, 1998, 80, 769-777.	1.2	88
65	Gametic phase estimation over large genomic regions using an adaptive window approach. Human Genomics, 2003, 1, 7.	1.4	88
66	Describing the genetic architecture of epilepsy through heritability analysis. Brain, 2014, 137, 2680-2689.	3.7	87
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	Confounding between recombination and selection, and the Ped/Pop method for detecting selection. Genome Research, 2008, 18, 1304-1313.	2.4	81
69	A genome-wide association study identifies multiple loci for variation in human ear morphology. Nature Communications, 2015, 6, 7500.	5.8	80
70	PopABC: a program to infer historical demographic parameters. Bioinformatics, 2009, 25, 2747-2749.	1.8	77
71	Animal Research: Reporting In Vivo Experiments: The ARRIVE guidelines. Journal of Physiology, 2010, 588, 2519-2521.	1.3	75
72	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

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73	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
74	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
75	A Genome-Wide Association Study of Neuroticism in a Population-Based Sample. PLoS ONE, 2010, 5, e11504.	1.1	71
76	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
77	Genetic association of the major histocompatibility complex with rheumatoid arthritis implicates two nonâ€DRB1 loci. Arthritis and Rheumatism, 2009, 60, 53-62.	6.7	68
78	Effects of population structure on DNA fingerprint analysis in forensic science. Heredity, 1991, 66, 297-302.	1.2	67
79	Multiple Quantitative Trait Analysis Using Bayesian Networks. Genetics, 2014, 198, 129-137.	1.2	67
80	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
81	Evaluating DNA Profile Evidence When the Suspect Is Identified Through a Database Search. Journal of Forensic Sciences, 1996, 41, 603-607.	0.9	66
82	Statistical Evaluation of Forensic DNA Profile Evidence. Annual Review of Statistics and Its Application, 2014, 1, 361-384.	4.1	65
83	A Comparative Survey of Non-Adaptive Pooling Designs. , 1996, , 133-154.		64
84	Significant genetic correlations among Caucasians at forensic DNA loci. Heredity, 1997, 78, 583-589.	1.2	63
85	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
86	Fregene: Simulation of realistic sequence-level data in populations and ascertained samples. BMC Bioinformatics, 2008, 9, 364.	1.2	57
87	Fine mapping of disease genes via haplotype clustering. Genetic Epidemiology, 2006, 30, 170-179.	0.6	49
88	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
89	Estimating Products in Forensic Identification Using DNA Profiles. Journal of the American Statistical Association, 1995, 90, 839-844.	1.8	46
90	Population genetics of STR loci in Caucasians. International Journal of Legal Medicine, 1996, 108, 300-305.	1.2	46

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91	Estimating the Age of the Common Ancestor of Men from the ZFY Intron. Science, 1996, 272, 1356-1362.	6.0	45
92	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
93	Estimating the Age of the Common Ancestor of Men from the ZFY Intron. Science, 1996, 272, 1357-1359.	6.0	44
94	cnvHap: an integrative population and haplotypeâ€“based multiplatform model of SNPs and CNVs. Nature Methods, 2010, 7, 541-546.	9.0	44
95	Optimal Pooling Designs with Error Detection. Journal of Combinatorial Theory - Series A, 1996, 74, 131-140.	0.5	43
96	Differential coexpression analysis of obesity-associated networks in human subcutaneous adipose tissue. International Journal of Obesity, 2012, 36, 137-147.	1.6	42
97	Variation in estimated recombination rates across human populations. Human Genetics, 2007, 122, 301-310.	1.8	40
98	How convincing is a matching Y-chromosome profile?. PLoS Genetics, 2017, 13, e1007028.	1.5	38
99	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
100	Worldwide FST Estimates Relative to Five Continental-Scale Populations. Annals of Human Genetics, 2014, 78, 468-477.	0.3	35
101	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
102	Coalescent Theory. , 2008, , 843-877.		33
103	Analysis of Population Subdivision. , 2008, , 980-1020.		33
104	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
105	Detecting gene conversion: primate visual pigment genes. Proceedings of the Royal Society B: Biological Sciences, 1992, 249, 275-280.	1.2	32
106	The DN A Database Search Controversy. Biometrics, 2002, 58, 241-244.	0.8	32
107	Functional constraint and small insertions and deletions in the ENCODE regions of the human genome. Genome Biology, 2007, 8, R180.	13.9	32
108	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

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109	Inferring combined CNV/SNP haplotypes from genotype data. Bioinformatics, 2010, 26, 1437-1445.	1.8	31
110	Animal Research: Reporting In Vivo Experiments: The ARRIVE guidelines. Experimental Physiology, 2010, 95, 842-844.	0.9	30
111	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
112	How convincing is DNA evidence?. Nature, 1994, 368, 285-286.	13.7	27
113	The Design of Pooling Experiments for Screening a Clone Map. Fungal Genetics and Biology, 1997, 21, 302-307.	0.9	27
114	Evaluation of low-template DNA profiles using peak heights. Statistical Applications in Genetics and Molecular Biology, 2016, 15, 431-445.	0.2	27
115	Risk factors and heart disease mortality: A regional perspective. Medical Journal of Australia, 1986, 144, 20-22.	0.8	26
116	Diffusion-controlled reactions in one dimension: Exact solutions and deterministic approximations. Physical Review A, 1989, 40, 4585-4592.	1.0	26
117	Verifying likelihoods for low template DNA profiles using multiple replicates. Forensic Science International: Genetics, 2014, 13, 82-89.	1.6	25
118	A comment on the PCAST report: Skip the â€œmatchâ€/â€œnon-matchâ€•stage. Forensic Science International, 2017, 272, e7-e9.	1.3	25
119	Increased Population Risk ofAIP-Related Acromegaly and Gigantism in Ireland. Human Mutation, 2017, 38, 78-85.	1.1	25
120	Decision-making in familial database searching: KI alone or not alone?. Forensic Science International: Genetics, 2013, 7, 52-54.	1.6	24
121	Inference of haplotypic phase and missing genotypes in polyploid organisms and variable copy number genomic regions. BMC Bioinformatics, 2008, 9, 513.	1.2	23
122	A comparison of software for the evaluation of complex DNA profiles. Forensic Science International: Genetics, 2019, 40, 114-119.	1.6	23
123	Measuring Gametic Disequilibrium From Multilocus Data. Genetics, 2001, 157, 413-423.	1.2	23
124	Disease association tests by inferring ancestral haplotypes using a hidden markov model. Bioinformatics, 2008, 24, 972-978.	1.8	22
125	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
126	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

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127	Bayesian models for syndrome- and gene-specific probabilities of novel variant pathogenicity. Genome Medicine, 2015, 7, 5.	3.6	22
128	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
129	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
130	Implications for DNA identification arising from an analysis of Australian forensic databases. Forensic Science International, 2002, 129, 90-98.	1.3	21
131	Using Penalised Logistic Regression to Fine Map HLA Variants for Rheumatoid Arthritis. Annals of Human Genetics, 2011, 75, 655-664.	0.3	20
132	How many individuals share a mitochondrial genome?. PLoS Genetics, 2018, 14, e1007774.	1.5	20
133	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
134	Discrimination of half-siblings when maternal genotypes are known. Forensic Science International, 2006, 159, 141-147.	1.3	18
135	Response to Lee etÂal.: SNP-Based Heritability Analysis with Dense Data. American Journal of Human Genetics, 2013, 93, 1155-1157.	2.6	17
136	Improving the efficiency of genomic selection. Statistical Applications in Genetics and Molecular Biology, 2013, 12, 517-27.	0.2	17
137	The association between polymorphisms in RLIP76 and drug response in epilepsy. Pharmacogenomics, 2007, 8, 1715-1722.	0.6	16
138	Y-profile evidence: Close paternal relatives and mixtures. Forensic Science International: Genetics, 2019, 38, 48-53.	1.6	16
139	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
140	Disentangling Signatures of Selection Before and After European Colonization in Latin Americans. Molecular Biology and Evolution, 2022, 39, .	3.5	16
141	Family-based association analysis with ordered categorical phenotypes, covariates and interactions. Genetic Epidemiology, 2007, 31, 1-8.	0.6	15
142	Time for DNA Disclosure. Science, 2009, 326, 1631-1632.	6.0	15
143	Integrated analysis of genome-wide genetic and epigenetic association data for identification of disease mechanisms. Epigenetics, 2013, 8, 1236-1244.	1.3	15
144	Significant genetic correlations among Caucasians at forensic DNA loci. Heredity, 1997, 78, 583-589.	1.2	15

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145	Linkage Disequilibrium, Recombination and Selection. , 2008, , 909-944.		14
146	[DNA Fingerprinting: A Review of the Controversy]: Comment: Some Causes for Concern about DNA Profiles. Statistical Science, 1994, 9, .	1.6	14
147	Dysregulation of Complement System and CD4+ T Cell Activation Pathways Implicated in Allergic Response. PLoS ONE, 2013, 8, e74821.	1.1	14
148	SNPâ€based heritability and selection analyses: Improved models and new results. BioEssays, 2022, 44, e2100170.	1.2	14
149	Statistical Techniques in Metabolic Profiling. , 2008, , 347-373.		13
150	Adaptive Molecular Evolution. , 2008, , 375-406.		13
151	Multiple single nucleotide polymorphism analysis using penalized regression in nonlinear mixed-effect pharmacokinetic models. Pharmacogenetics and Genomics, 2013, 23, 167-174.	0.7	13
152	Estimating Products in Forensic Identification Using DNA Profiles. , 0, .		13
153	Clustering of Protein Domains in the Human Genome. Journal of Molecular Biology, 2004, 340, 991-1004.	2.0	12
154	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
155	Interpreting DNA Evidence: Can Probability Theory Help?. , 2000, , 51-70.		12
156	Bayesian inference of ancestral recombination graphs. PLoS Computational Biology, 2022, 18, e1009960.	1.5	12
157	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
158	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
159	Limit theorems for sequences of random trees. Test, 2009, 18, 302-315.	0.7	11
160	Assessing the Forensic Value of DNA Evidence from Y Chromosomes and Mitogenomes. Genes, 2021, 12, 1209.	1.0	11
161	Including diverse and admixed populations in genetic epidemiology research. Genetic Epidemiology, 2022, 46, 347-371.	0.6	11
162	Diffusion-reaction in one dimension. Journal of Applied Probability, 1988, 25, 733-743.	0.4	10

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163	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
164	Using common genetic variants to find drugs for common epilepsies. Brain Communications, 2021, 3, fcab287.	1.5	9
165	Evolutionary Quantitative Genetics. , 2008, , 533-586.		8
166	Summary statistic analyses can mistake confounding bias for heritability. Genetic Epidemiology, 2019, 43, 930-940.	0.6	8
167	Diffusion-reaction in one dimension. Journal of Applied Probability, 1988, 25, 733-743.	0.4	7
168	MAC5: Bayesian inference of phylogenetic trees from DNA sequences incorporating gaps. Bioinformatics, 2001, 17, 479-480.	1.8	7
169	Paternity index calculations when some individuals share common ancestry. Forensic Science International, 2005, 151, 101-103.	1.3	7
170	A Likelihood Ratio Approach to Family-based Association Studies with Covariates. Annals of Human Genetics, 2006, 70, 131-139.	0.3	7
171	Design and analysis of chromosome physical mapping experiments. Philosophical Transactions of the Royal Society B: Biological Sciences, 1994, 344, 329-335.	1.8	6
172	Quantitative Trait Loci in Inbred Lines. , 2008, , 587-622.		6
173	Mathematical Models in Population Genetics. , 2008, , 753-780.		6
174	Linkage Analysis. , 2008, , 1141-1167.		6
175	Whole Genome Association. , 2008, , 1238-1263.		6
176	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
177	Prediction of eye, hair and skin colour in Latin Americans. Forensic Science International: Genetics, 2021, 53, 102517.	1.6	6
178	Conservation Genetics. , 2008, , 1021-1066.		5
179	Epidemiology and Genetic Epidemiology. , 2008, , 1109-1140.		5
180	Evaluating DNA evidence in a genetically complex population. Forensic Science International: Genetics, 2018, 36, 141-147.	1.6	5

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181	How can courts take into account the uncertainty in a likelihood ratio?. Forensic Science International: Genetics, 2020, 48, 102361.	1.6	5
182	Shared genetic basis between genetic generalized epilepsy and background electroencephalographic oscillations. Epilepsia, 2021, 62, 1518-1527.	2.6	5
183	Genome-wide association, prediction and heritability in bacteria with application to Streptococcus pneumoniae. NAR Genomics and Bioinformatics, 2022, 4, lqac011.	1.5	5
184	Editorial. Human Genomics, 2005, 2, 79-80.	1.4	4
185	Inference Under the Coalescent. , 2008, , 878-908.		4
186	Population Association. , 2008, , 1216-1237.		4
187	Forensics. , 2008, , 1368-1392.		4
188	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
189	A general framework for moment-based analysis of genetic data. Journal of Mathematical Biology, 2019, 78, 1727-1769.	0.8	4
190	Chromosome Maps. , 2008, , 1-39.		3
191	Marker-Assisted Selection and Introgression. , 2008, , 718-751.		3
192	Inference in complex systems. Interface Focus, 2011, 1, 805-806.	1.5	3
193	Admixture provides new insights into recombination. Nature Genetics, 2011, 43, 819-820.	9.4	3
194	Integrating dynamic mixed-effect modelling and penalized regression to explore genetic association with pharmacokinetics. Pharmacogenetics and Genomics, 2015, 25, 231-238.	0.7	3
195	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
196	Risk factors and heart disease mortality. A regional perspective. Medical Journal of Australia, 1986, 144, 20-2.	0.8	3
197	Inferences from Mixed Models in Quantitative Genetics. , 2008, , 678-717.		2
198	Inference, Simulation and Enumeration of Genealogies. , 2008, , 781-807.		2

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199	Population Admixture and Stratification in Genetic Epidemiology. , 2008, , 1190-1215.		2
200	Bayesian Methods for Microarray Data. , 2008, , 267-295.		2
201	Genetic and isotopic analysis and the UK Border Agency. Significance, 2010, 7, 58-61.	0.3	2
202	A Simulation Approach for Change-Points on Phylogenetic Trees. Journal of Computational Biology, 2015, 22, 10-24.	0.8	2
203	Fine-scale mapping of disease loci. GeneScreen, 2000, 1, 101-102.	0.7	1
204	A question of identity. Significance, 2005, 2, 20-23.	0.3	1
205	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
206	Probabilistic Models for the Study of Protein Evolution. , 2008, , 439-459.		1
207	Family-Based Association. , 2008, , 1264-1285.		1
208	Comparative Genomics. , 2008, , 160-199.		1
209	Statistical Inference for Microarray Studies. , 2008, , 231-266.		1
210	Inferring Causal Associations between Genes and Disease via the Mapping of Expression Quantitative Trait Loci. , 2008, , 296-326.		1
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