David Balding

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.

278 papers	22,850 citations	65 h-index	150 g-index
324 ext. papers	26,256 ext. citations	8.6 avg, IF	7.23 L-index

#	Paper	IF	Citations
278	Genome-wide association, prediction and heritability in bacteria with application to .. *NAR Genomics and Bioinformatics*, **2022**, 4, lqac011	3.7	2
277	Bayesian inference of ancestral recombination graphs.. *PLoS Computational Biology*, **2022**, 18, e1009960	5	1
276	SNP-based heritability and selection analyses: Improved models and new results.. *BioEssays*, **2022**, e2100170	4.1	0
275	Using common genetic variants to find drugs for common epilepsies.. *Brain Communications*, **2021**, 3, fcab287	4.5	0
274	Shared genetic basis between genetic generalized epilepsy and background electroencephalographic oscillations. *Epilepsia*, **2021**, 62, 1518-1527	6.4	1
273	A GWAS in Latin Americans identifies novel face shape loci, implicating VPS13B and a Denisovan introgressed region in facial variation. *Science Advances*, **2021**, 7,	14.3	7
272	Prediction of eye, hair and skin colour in Latin Americans. *Forensic Science International: Genetics*, **2021**, 53, 102517	4.3	3
271	Assessing the Forensic Value of DNA Evidence from Y Chromosomes and Mitogenomes. *Genes*, **2021**, 12,	4.2	3
270	Evaluating and improving heritability models using summary statistics. *Nature Genetics*, **2020**, 52, 458-462	26.3	34
269	How can courts take into account the uncertainty in a likelihood ratio?. *Forensic Science International: Genetics*, **2020**, 48, 102361	4.3	1
268	A GWAS in Latin Americans highlights the convergent evolution of lighter skin pigmentation in Eurasia. *Nature Communications*, **2019**, 10, 358	17.4	72
267	A general framework for moment-based analysis of genetic data. *Journal of Mathematical Biology*, **2019**, 78, 1727-1769	2	2
266	A comparison of software for the evaluation of complex DNA profiles. *Forensic Science International: Genetics*, **2019**, 40, 114-119	4.3	17
265	Variant Interpretation and Genomic Medicine **2019**, 761-786		
264	Detecting Natural Selection **2019**, 397-40		5
263	Genome-Wide Association Studies **2019**, 597-550		2
262	Prediction of Phenotype from DNA Variants **2019**, 799-20		1

261	Mathematical Models in Population Genetics **2019**, 115-20		0
260	Coalescent Theory **2019**, 145-30		4
259	Population Structure, Demography and Recent Admixture **2019**, 247-274		0
258	Summary statistic analyses can mistake confounding bias for heritability. *Genetic Epidemiology*, **2019**, 43, 930-940	2.6	4
257	Bacterial Population Genomics **2019**, 997-1020		3
256	Inferring Causal Relationships between Risk Factors and Outcomes Using Genetic Variation **2019**, 651-20		0
255	Forensic Genetics **2019**, 531-550		
254	Statistical Methods in Metabolomics **2019**, 949-976		1
253	Disease Risk Models **2019**, 815-842		0
252	Improving Genetic Association Analysis through Integration of Functional Annotations of the Human Genome **2019**, 679-30		
251	Y-profile evidence: Close paternal relatives and mixtures. *Forensic Science International: Genetics*, **2019**, 38, 48-53	4.3	9
250	SumHer better estimates the SNP heritability of complex traits from summary statistics. *Nature Genetics*, **2019**, 51, 277-284	36.3	91
249	Conservation Genetics **2019**, 457-40		3
248	Statistical Methods for Plant Breeding **2019**, 501-20		8
247	Bridging trees for posterior inference on ancestral recombination graphs. *Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences*, **2018**, 474, 20180568	2.4	2
246	The Rise and Fall of BritainsDNA: A Tale of Misleading Claims, Media Manipulation and Threats to Academic Freedom. *Genealogy*, **2018**, 2, 47	0.5	0
245	Latin Americans show wide-spread Converso ancestry and imprint of local Native ancestry on physical appearance. *Nature Communications*, **2018**, 9, 5388	17.4	65
244	Genome-wide mega-analysis identifies 16 loci and highlights diverse biological mechanisms in the common epilepsies. *Nature Communications*, **2018**, 9, 5269	17.4	169

243	How many individuals share a mitochondrial genome?. *PLoS Genetics*, **2018**, 14, e1007774	6	15
242	Evaluating DNA evidence in a genetically complex population. *Forensic Science International: Genetics*, **2018**, 36, 141-147	4.3	4
241	Reevaluation of SNP heritability in complex human traits. *Nature Genetics*, **2017**, 49, 986-992	36.3	297
240	Optimizing genomic medicine in epilepsy through a gene-customized approach to missense variant interpretation. *Genome Research*, **2017**, 27, 1715-1729	9.7	91
239	In-frame seven amino-acid duplication in arose over the last 3000 years, disrupts protein interaction and stability and is associated with gigantism. *European Journal of Endocrinology*, **2017**, 177, 257-266	6.5	11
238	A comment on the PCAST report: Skip the "match"/"non-match" stage. *Forensic Science International*, **2017**, 272, e7-e9	2.6	19
237	Increased Population Risk of AIP-Related Acromegaly and Gigantism in Ireland. *Human Mutation*, **2017**, 38, 78-85	4.7	24
236	How convincing is a matching Y-chromosome profile?. *PLoS Genetics*, **2017**, 13, e1007028	6	28
235	GWAlpha: genome-wide estimation of additive effects (alpha) based on trait quantile distribution from pool-sequencing experiments. *Bioinformatics*, **2017**, 33, 1246-1247	7.2	0
234	A genome-wide association scan implicates DCHS2, RUNX2, GLI3, PAX1 and EDAR in human facial variation. *Nature Communications*, **2016**, 7, 11616	17.4	103
233	Evaluation of low-template DNA profiles using peak heights. *Statistical Applications in Genetics and Molecular Biology*, **2016**, 15, 431-445	1.2	21
232	Using Genetic Distance to Infer the Accuracy of Genomic Prediction. *PLoS Genetics*, **2016**, 12, e1006288	6	67
231	A genome-wide association scan in admixed Latin Americans identifies loci influencing facial and scalp hair features. *Nature Communications*, **2016**, 7, 10815	17.4	108
230	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	4.3	4
229	Bayesian models for syndrome- and gene-specific probabilities of novel variant pathogenicity. *Genome Medicine*, **2015**, 7, 5	14.4	19
228	A genome-wide association study identifies multiple loci for variation in human ear morphology. *Nature Communications*, **2015**, 6, 7500	17.4	42
227	A simulation approach for change-points on phylogenetic trees. *Journal of Computational Biology*, **2015**, 22, 10-24	1.7	1
226	Relatedness in the post-genomic era: is it still useful?. *Nature Reviews Genetics*, **2015**, 16, 33-44	30.1	151

225	**2015**,		13
224	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	6	104
223	Integrating dynamic mixed-effect modelling and penalized regression to explore genetic association with pharmacokinetics. *Pharmacogenetics and Genomics*, **2015**, 25, 231-8	1.9	3
222	The genomic and phenotypic diversity of Schizosaccharomyces pombe. *Nature Genetics*, **2015**, 47, 235-41	36.3	111
221	Storytelling and story testing in domestication. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 6159-64	11.5	80
220	Describing the genetic architecture of epilepsy through heritability analysis. *Brain*, **2014**, 137, 2680-9	11.2	63
219	Worldwide F(ST) estimates relative to five continental-scale populations. *Annals of Human Genetics*, **2014**, 78, 468-77	2.2	27
218	Verifying likelihoods for low template DNA profiles using multiple replicates. *Forensic Science International: Genetics*, **2014**, 13, 82-9	4.3	19
217	Genetic determinants of common epilepsies: a meta-analysis of genome-wide association studies. *Lancet Neurology, The*, **2014**, 13, 893-903	24.1	194
216	Applying association mapping and genomic selection to the dissection of key traits in elite European wheat. *Theoretical and Applied Genetics*, **2014**, 127, 2619-33	6	73
215	Multiple quantitative trait analysis using bayesian networks. *Genetics*, **2014**, 198, 129-37	4	49
214	Statistical Evaluation of Forensic DNA Profile Evidence. *Annual Review of Statistics and Its Application*, **2014**, 1, 361-384	7.6	42
213	Interaction between gas cooking and GSTM1 null genotype in bronchial responsiveness: results from the European Community Respiratory Health Survey. *Thorax*, **2014**, 69, 558-64	7.3	19
212	Admixture in Latin America: geographic structure, phenotypic diversity and self-perception of ancestry based on 7,342 individuals. *PLoS Genetics*, **2014**, 10, e1004572	6	261
211	MultiBLUP: improved SNP-based prediction for complex traits. *Genome Research*, **2014**, 24, 1550-7	9.7	175
210	Choice of population database for forensic DNA profile analysis. *Science and Justice - Journal of the Forensic Science Society*, **2014**, 54, 487-93	2	18
209	Identification of the remains of King Richard III. *Nature Communications*, **2014**, 5, 5631	17.4	118
208	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, 247-58	5.6	28

207	Evaluating forensic DNA profiles using peak heights, allowing for multiple donors, allelic dropout and stutters. *Forensic Science International: Genetics*, **2013**, 7, 555-63	4.3	63
206	Decision-making in familial database searching: KI alone or not alone?. *Forensic Science International: Genetics*, **2013**, 7, 52-4	4.3	17
205	Response to Lee et al.: SNP-based heritability analysis with dense data. *American Journal of Human Genetics*, **2013**, 93, 1155-7	11	15
204	Improving the efficiency of genomic selection. *Statistical Applications in Genetics and Molecular Biology*, **2013**, 12, 517-27	1.2	15
203	Integrated analysis of genome-wide genetic and epigenetic association data for identification of disease mechanisms. *Epigenetics*, **2013**, 8, 1236-44	5.7	14
202	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, 4349-56	5.6	58
201	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, 12241-6	11.5	66
200	Dysregulation of complement system and CD4+ T cell activation pathways implicated in allergic response. *PLoS ONE*, **2013**, 8, e74821	3.7	12
199	Multiple single nucleotide polymorphism analysis using penalized regression in nonlinear mixed-effect pharmacokinetic models. *Pharmacogenetics and Genomics*, **2013**, 23, 167-74	1.9	12
198	Understanding complex traits: from farmers to pharmas. *Genome Medicine*, **2012**, 4, 59	14.4	1
197	Improved heritability estimation from genome-wide SNPs. *American Journal of Human Genetics*, **2012**, 91, 1011-21	11	457
196	Ethiopian genetic diversity reveals linguistic stratification and complex influences on the Ethiopian gene pool. *American Journal of Human Genetics*, **2012**, 91, 83-96	11	133
195	Differential coexpression analysis of obesity-associated networks in human subcutaneous adipose tissue. *International Journal of Obesity*, **2012**, 36, 137-47	5.5	35
194	Genome-wide association study in multiple human prion diseases suggests genetic risk factors additional to PRNP. *Human Molecular Genetics*, **2012**, 21, 1897-906	5.6	58
193	Model Identification by Utilizing Likelihood-Based Methods **2011**, 395-416		
192	Statistical Data Analysis in Metabolomics **2011**, 163-180		2
191	Two Challenges of Systems Biology **2011**, 1-14		2
190	Introduction to Statistical Methods for Complex Systems **2011**, 15-38		

189	Bayesian Inference and Computation **2011**, 39-65		2
188	Data Integration: Towards Understanding Biological Complexity **2011**, 66-82		
187	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	11.5	170
186	Protein Interaction Networks and Their Statistical Analysis **2011**, 200-234		3
185	Recovering Genetic Network from Continuous Data with Dynamic Bayesian Networks **2011**, 255-269		
184	Advanced Applications of Bayesian Networks in Systems Biology **2011**, 270-289		1
183	Random Graph Models and Their Application to Protein–Protein Interaction Networks **2011**, 290-308		2
182	Modelling Biological Networks via Tailored Random Graphs **2011**, 309-329		1
181	Nonlinear Dynamics: A Brief Introduction **2011**, 331-338		
180	Qualitative Inference in Dynamical Systems **2011**, 339-358		1
179	Stochastic Dynamical Systems **2011**, 359-375		1
178	Gaussian Process Inference for Differential Equation Models of Transcriptional Regulation **2011**, 376-394		
177	Inference of Signalling Pathway Models **2011**, 417-439		
176	Modelling Transcription Factor Activity **2011**, 440-450		
175	Host–Pathogen Systems Biology **2011**, 451-466		1
174	Bayesian Approaches for Mass Spectrometry-Based Metabolomics **2011**, 467-476		1
173	Control Engineering Approaches to Reverse Engineering Biomolecular Networks **2011**, 83-113		
172	Algebraic Statistics and Methods in Systems Biology **2011**, 114-132		1

171	Transcriptomic Technologies and Statistical Data Analysis **2011**, 133-162		
170	Imaging and Single-Cell Measurement Technologies **2011**, 181-199		
169	Introduction to Graphical Modelling **2011**, 235-254		5
168	Using penalised logistic regression to fine map HLA variants for rheumatoid arthritis. *Annals of Human Genetics*, **2011**, 75, 655-64	2.2	19
167	Epigenome-wide association studies for common human diseases. *Nature Reviews Genetics*, **2011**, 12, 529-41	30.1	920
166	Systems Biology of microRNAs **2011**, 477-493		
165	Bayesian Networks and Probabilistic Inference in Forensic Science. *Law, Probability and Risk*, **2011**, 10, 355-358	0.6	1
164	Inference in complex systems. *Interface Focus*, **2011**, 1, 805-806	3.9	2
163	AIP mutation in pituitary adenomas in the 18th century and today. *New England Journal of Medicine* , **2011**, 364, 43-50	59.2	122
162	Animal research: reporting in vivo experiments: the ARRIVE guidelines. *British Journal of Pharmacology*, **2010**, 160, 1577-9	8.6	2654
161	Genetic and isotopic analysis and the UK Border Agency. *Significance*, **2010**, 7, 58-61	0.5	2
160	In defence of model-based inference in phylogeography. *Molecular Ecology*, **2010**, 19, 436-446	5.7	127
159	Animal research: reporting in vivo experiments: the ARRIVE guidelines. *Experimental Physiology*, **2010**, 95, 842-4	2.4	19
158	Animal research: reporting in vivo experiments: the ARRIVE guidelines. *Journal of Physiology*, **2010**, 588, 2519-21	3.9	62
157	cnvHap: an integrative population and haplotype-based multiplatform model of SNPs and CNVs. *Nature Methods*, **2010**, 7, 541-6	21.6	37
156	A genome-wide association study of neuroticism in a population-based sample. *PLoS ONE*, **2010**, 5, e11504	3.7	59
155	Inferring combined CNV/SNP haplotypes from genotype data. *Bioinformatics*, **2010**, 26, 1437-45	7.2	29
154	On optimal selection of summary statistics for approximate Bayesian computation. *Statistical Applications in Genetics and Molecular Biology*, **2010**, 9, Article34	1.2	80

153	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, 21611-6	11.5	218
152	Animal research: reporting in vivo experiments: the ARRIVE guidelines. *Journal of Gene Medicine*, **2010**, 12, 561-3	3.5	179
151	A genome-wide association study of the metabolic syndrome in Indian Asian men. *PLoS ONE*, **2010**, 5, e11961	3.7	94
150	Pathway analysis of GWAS provides new insights into genetic susceptibility to 3 inflammatory diseases. *PLoS ONE*, **2009**, 4, e8068	3.7	110
149	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, 2703-8	0.9	80
148	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, 294-9	2.1	11
147	Time for DNA disclosure. *Science*, **2009**, 326, 1631-2	33.3	13
146	Genetic association of the major histocompatibility complex with rheumatoid arthritis implicates two non-DRB1 loci. *Arthritis and Rheumatism*, **2009**, 60, 53-62		61
145	Limit theorems for sequences of random trees. *Test*, **2009**, 18, 302-315	1.1	8
144	Heritability and genetic correlations of insulin resistance and component phenotypes in Asian Indian families using a multivariate analysis. *Diabetologia*, **2009**, 52, 2585-9	10.3	28
143	Genome-wide association study for early-onset and morbid adult obesity identifies three new risk loci in European populations. *Nature Genetics*, **2009**, 41, 157-9	36.3	521
142	Bayesian statistical methods for genetic association studies. *Nature Reviews Genetics*, **2009**, 10, 681-90	30.1	339
141	Assessing Evidence via Likelihood Ratios **2009**, 22-42		
140	Crime on An Island **2009**, 7-21		
139	Some Population Genetics for DNA Evidence **2009**, 56-81		
138	Other Approaches to Weight of Evidence **2009**, 135-144		
137	Issues for the Courtroom **2009**, 145-156		
136	Relatedness **2009**, 111-134		

135	Typing Technologies **2009**, 43-55		
134	PopABC: a program to infer historical demographic parameters. *Bioinformatics*, **2009**, 25, 2747-9	7.2	71
133	Interpreting low template DNA profiles. *Forensic Science International: Genetics*, **2009**, 4, 1-10	4.3	139
132	Population Structure and Cryptic Relatedness in Genetic Association Studies. *Statistical Science*, **2009**, 24,	2.4	286
131	Common genetic variation near MC4R is associated with waist circumference and insulin resistance. *Nature Genetics*, **2008**, 40, 716-8	36.3	413
130	Fregene: simulation of realistic sequence-level data in populations and ascertained samples. *BMC Bioinformatics*, **2008**, 9, 364	3.6	49
129	Inference of haplotypic phase and missing genotypes in polyploid organisms and variable copy number genomic regions. *BMC Bioinformatics*, **2008**, 9, 513	3.6	18
128	Assessment of cumulative evidence on genetic associations: interim guidelines. *International Journal of Epidemiology*, **2008**, 37, 120-32	7.8	451
127	Inferring population history with DIY ABC: a user-friendly approach to approximate Bayesian computation. *Bioinformatics*, **2008**, 24, 2713-9	7.2	545
126	Population structure and inbreeding from pedigree analysis of purebred dogs. *Genetics*, **2008**, 179, 593-601	4	93
125	Disease association tests by inferring ancestral haplotypes using a hidden markov model. *Bioinformatics*, **2008**, 24, 972-8	7.2	21
124	Confounding between recombination and selection, and the Ped/Pop method for detecting selection. *Genome Research*, **2008**, 18, 1304-13	9.7	52
123	Simultaneous analysis of all SNPs in genome-wide and re-sequencing association studies. *PLoS Genetics*, **2008**, 4, e1000130	6	245
122	Genome-wide significance for dense SNP and resequencing data. *Genetic Epidemiology*, **2008**, 32, 179-85	2.6	164
121	Chromosome Maps **2008**, 1-39		3
120	Protein Structure Prediction **2008**, 327-346		
119	Statistical Techniques in Metabolic Profiling **2008**, 347-373		9
118	Adaptive Molecular Evolution **2008**, 375-406		5

117	Genome Evolution **2008**, 407-438	
116	Probabilistic Models for the Study of Protein Evolution **2008**, 439-459	0
115	Application of the Likelihood Function in Phylogenetic Analysis **2008**, 460-488	2
114	Phylogenetics: Parsimony, Networks, and Distance Methods **2008**, 489-532	
113	Evolutionary Quantitative Genetics **2008**, 533-586	7
112	Quantitative Trait Loci in Inbred Lines **2008**, 587-622	6
111	Mapping Quantitative Trait Loci in Outbred Pedigrees **2008**, 623-677	2
110	Statistical Significance in Biological Sequence Comparison **2008**, 40-66	
109	Inferences from Mixed Models in Quantitative Genetics **2008**, 678-717	1
108	Marker-Assisted Selection and Introgression **2008**, 718-751	1
107	Mathematical Models in Population Genetics **2008**, 753-780	3
106	Inference, Simulation and Enumeration of Genealogies **2008**, 781-807	1
105	Graphical Models in Genetics **2008**, 808-842	
104	Coalescent Theory **2008**, 843-877	12
103	Inference Under the Coalescent **2008**, 878-908	2
102	Linkage Disequilibrium, Recombination and Selection **2008**, 909-944	7
101	Inferences from Spatial Population Genetics **2008**, 945-979	22
100	Analysis of Population Subdivision **2008**, 980-1020	24

99	Bayesian Methods in Biological Sequence Analysis **2008**, 67-96	
98	Conservation Genetics **2008**, 1021-1066	5
97	Human Genetic Diversity and its History **2008**, 1067-1108	
96	Epidemiology and Genetic Epidemiology **2008**, 1109-1140	2
95	Linkage Analysis **2008**, 1141-1167	6
94	Non-Parametric Linkage **2008**, 1168-1189	
93	Population Admixture and Stratification in Genetic Epidemiology **2008**, 1190-1215	2
92	Population Association **2008**, 1216-1237	4
91	Whole Genome Association **2008**, 1238-1263	5
90	Family-Based Association **2008**, 1264-1285	1
89	Cancer Genetics **2008**, 1286-1300	
88	Statistical Approaches in Eukaryotic Gene Prediction **2008**, 97-159	30
87	Ethics Issues in Statistical Genetics **2008**, 1323-1345	
86	Forensics **2008**, 1368-1392	1
85	Comparative Genomics **2008**, 160-199	1
84	Analysis of Microarray Gene Expression Data **2008**, 201-230	
83	Statistical Inference for Microarray Studies **2008**, 231-266	
82	Bayesian Methods for Microarray Data **2008**, 267-295	1

81	Inferring Causal Associations between Genes and Disease via the Mapping of Expression Quantitative Trait Loci **2008**, 296-326		
80	Family-based association analysis with ordered categorical phenotypes, covariates and interactions. *Genetic Epidemiology*, **2007**, 31, 1-8	2.6	14
79	Reply: On the value of haplotype-based genotype–phenotype analysis and on data transformation in pharmacogenetics and -genomics. *Nature Reviews Genetics*, **2007**, 8, 983-983	30.1	1
78	A genome-wide association study identifies novel risk loci for type 2 diabetes. *Nature*, **2007**, 445, 881-5	50.4	2327
77	Variation in estimated recombination rates across human populations. *Human Genetics*, **2007**, 122, 301-10	4.3	31
76	Sequence-level population simulations over large genomic regions. *Genetics*, **2007**, 177, 1725-31	4	84
75	The association between polymorphisms in RLIP76 and drug response in epilepsy. *Pharmacogenomics*, **2007**, 8, 1715-22	2.6	15
74	Common ABCB1 polymorphisms are not associated with multidrug resistance in epilepsy using a gene-wide tagging approach. *Pharmacogenetics and Genomics*, **2007**, 17, 217-20	1.9	39
73	Functional constraint and small insertions and deletions in the ENCODE regions of the human genome. *Genome Biology*, **2007**, 8, R180	18.3	30
72	Clinical factors and ABCB1 polymorphisms in prediction of antiepileptic drug response: a prospective cohort study. *Lancet Neurology, The*, **2006**, 5, 668-76	24.1	63
71	Fine mapping of disease genes via haplotype clustering. *Genetic Epidemiology*, **2006**, 30, 170-9	2.6	45
70	Logistic regression protects against population structure in genetic association studies. *Genome Research*, **2006**, 16, 290-6	9.7	82
69	Exon sequencing and high resolution haplotype analysis of ABC transporter genes implicated in drug resistance. *Pharmacogenetics and Genomics*, **2006**, 16, 439-50	1.9	58
68	A likelihood ratio approach to family-based association studies with covariates. *Annals of Human Genetics*, **2006**, 70, 131-9	2.2	7
67	A tutorial on statistical methods for population association studies. *Nature Reviews Genetics*, **2006**, 7, 781-91	30.1	963
66	Discrimination of half-siblings when maternal genotypes are known. *Forensic Science International*, **2006**, 159, 141-7	2.6	16
65	Paternity index calculations when some individuals share common ancestry. *Forensic Science International*, **2005**, 151, 101-3	2.6	5
64	A question of identity. *Significance*, **2005**, 2, 20-23	0.5	1

63	**2005**,		71
62	Identifying adaptive genetic divergence among populations from genome scans. *Molecular Ecology*, **2004**, 13, 969-80	5.7	815
61	Clustering of protein domains in the human genome. *Journal of Molecular Biology*, **2004**, 340, 991-1004	6.5	9
60	Little loss of information due to unknown phase for fine-scale linkage-disequilibrium mapping with single-nucleotide-polymorphism genotype data. *American Journal of Human Genetics*, **2004**, 74, 945-53	11	62
59	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, 13442-6	11.5	25
58	Gametic phase estimation over large genomic regions using an adaptive window approach. *Human Genomics*, **2003**, 1, 7-19	6.8	82
57	Chromosome-wide distribution of haplotype blocks and the role of recombination hot spots. *Nature Genetics*, **2003**, 33, 382-7	36.3	243
56	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	2.1	179
55	Likelihood-based inference for genetic correlation coefficients. *Theoretical Population Biology*, **2003**, 63, 221-30	1.2	127
54	Implications for DNA identification arising from an analysis of Australian forensic databases. *Forensic Science International*, **2002**, 129, 90-8	2.6	16
53	The DNA database search controversy. *Biometrics*, **2002**, 58, 241-4	1.8	24
52	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	3.9	10
51	Patterns of human diversity, within and among continents, inferred from biallelic DNA polymorphisms. *Genome Research*, **2002**, 12, 602-12	9.7	153
50	Fine-scale mapping of disease loci via shattered coalescent modeling of genealogies. *American Journal of Human Genetics*, **2002**, 70, 686-707	11	106
49	Approximate Bayesian computation in population genetics. *Genetics*, **2002**, 162, 2025-35	4	1784
48	MAC5: Bayesian inference of phylogenetic trees from DNA sequences incorporating gaps. *Bioinformatics*, **2001**, 17, 479-80	7.2	7
47	Models of sequence evolution for DNA sequences containing gaps. *Molecular Biology and Evolution*, **2001**, 18, 481-90	8.3	58
46	Measuring gametic disequilibrium from multilocus data. *Genetics*, **2001**, 157, 413-23	4	15

45	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	1.5	76
44	Fine-scale mapping of disease loci. *GeneScreen*, **2000**, 1, 101-102		0
43	Bayesian fine-scale mapping of disease loci, by hidden Markov models. *American Journal of Human Genetics*, **2000**, 67, 155-69	11	77
42	Interpreting DNA Evidence: Can Probability Theory Help? **2000**, 51-70		6
41	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 £25.95.. *Genetical Research*, **1999**, 73, 85-89	1.1	
40	When can a DNA profile be regarded as unique?. *Science and Justice - Journal of the Forensic Science Society*, **1999**, 39, 257-60	2	37
39	Measuring departures from Hardy-Weinberg: a Markov chain Monte Carlo method for estimating the inbreeding coefficient. *Heredity*, **1998**, 80 (Pt 6), 769-77	3.6	72
38	Genealogical inference from microsatellite data. *Genetics*, **1998**, 150, 499-510	4	203
37	The design of pooling experiments for screening a clone map. *Fungal Genetics and Biology*, **1997**, 21, 302-7	3.9	23
36	Significant genetic correlations among Caucasians at forensic DNA loci. *Heredity*, **1997**, 78 (Pt 6), 583-9	3.6	49
35	Inferring coalescence times from DNA sequence data. *Genetics*, **1997**, 145, 505-18	4	525
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