

David Balding

List of Publications by Citations

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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 | Animal research: reporting in vivo experiments: the ARRIVE guidelines. <i>British Journal of Pharmacology</i> , 2010 , 160, 1577-9 | 8.6 | 2654 |
| 277 | A genome-wide association study identifies novel risk loci for type 2 diabetes. <i>Nature</i> , 2007 , 445, 881-5 | 50.4 | 2327 |
| 276 | Approximate Bayesian computation in population genetics. <i>Genetics</i> , 2002 , 162, 2025-35 | 4 | 1784 |
| 275 | A tutorial on statistical methods for population association studies. <i>Nature Reviews Genetics</i> , 2006 , 7, 781-91 | 30.1 | 963 |
| 274 | Epigenome-wide association studies for common human diseases. <i>Nature Reviews Genetics</i> , 2011 , 12, 529-41 | 30.1 | 920 |
| 273 | Identifying adaptive genetic divergence among populations from genome scans. <i>Molecular Ecology</i> , 2004 , 13, 969-80 | 5.7 | 815 |
| 272 | Inferring population history with DIY ABC: a user-friendly approach to approximate Bayesian computation. <i>Bioinformatics</i> , 2008 , 24, 2713-9 | 7.2 | 545 |
| 271 | Inferring coalescence times from DNA sequence data. <i>Genetics</i> , 1997 , 145, 505-18 | 4 | 525 |
| 270 | Genome-wide association study for early-onset and morbid adult obesity identifies three new risk loci in European populations. <i>Nature Genetics</i> , 2009 , 41, 157-9 | 36.3 | 521 |
| 269 | Improved heritability estimation from genome-wide SNPs. <i>American Journal of Human Genetics</i> , 2012 , 91, 1011-21 | 11 | 457 |
| 268 | Assessment of cumulative evidence on genetic associations: interim guidelines. <i>International Journal of Epidemiology</i> , 2008 , 37, 120-32 | 7.8 | 451 |
| 267 | Common genetic variation near MC4R is associated with waist circumference and insulin resistance. <i>Nature Genetics</i> , 2008 , 40, 716-8 | 36.3 | 413 |
| 266 | A method for quantifying differentiation between populations at multi-allelic loci and its implications for investigating identity and paternity. <i>Genetica</i> , 1995 , 96, 3-12 | 1.5 | 371 |
| 265 | DNA profile match probability calculation: how to allow for population stratification, relatedness, database selection and single bands. <i>Forensic Science International</i> , 1994 , 64, 125-40 | 2.6 | 364 |
| 264 | Bayesian statistical methods for genetic association studies. <i>Nature Reviews Genetics</i> , 2009 , 10, 681-90 | 30.1 | 339 |
| 263 | Reevaluation of SNP heritability in complex human traits. <i>Nature Genetics</i> , 2017 , 49, 986-992 | 36.3 | 297 |
| 262 | Population Structure and Cryptic Relatedness in Genetic Association Studies. <i>Statistical Science</i> , 2009 , 24, | 2.4 | 286 |

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| 261 | Admixture in Latin America: geographic structure, phenotypic diversity and self-perception of ancestry based on 7,342 individuals. <i>PLoS Genetics</i> , 2014 , 10, e1004572 | 6 | 261 |
| 260 | Simultaneous analysis of all SNPs in genome-wide and re-sequencing association studies. <i>PLoS Genetics</i> , 2008 , 4, e1000130 | 6 | 245 |
| 259 | Chromosome-wide distribution of haplotype blocks and the role of recombination hot spots. <i>Nature Genetics</i> , 2003 , 33, 382-7 | 36.3 | 243 |
| 258 | Genome-wide association mapping to candidate polymorphism resolution in the unsequenced barley genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 21611-6 | 11.5 | 218 |
| 257 | Genealogical inference from microsatellite data. <i>Genetics</i> , 1998 , 150, 499-510 | 4 | 203 |
| 256 | Genetic determinants of common epilepsies: a meta-analysis of genome-wide association studies. <i>Lancet Neurology</i> , 2014 , 13, 893-903 | 24.1 | 194 |
| 255 | Animal research: reporting in vivo experiments: the ARRIVE guidelines. <i>Journal of Gene Medicine</i> , 2010 , 12, 561-3 | 3.5 | 179 |
| 254 | Inferences from DNA data: population histories, evolutionary processes and forensic match probabilities. <i>Journal of the Royal Statistical Society Series A: Statistics in Society</i> , 2003 , 166, 155-188 | 2.1 | 179 |
| 253 | MultiBLUP: improved SNP-based prediction for complex traits. <i>Genome Research</i> , 2014 , 24, 1550-7 | 9.7 | 175 |
| 252 | A genome-wide meta-analysis of genetic variants associated with allergic rhinitis and grass sensitization and their interaction with birth order. <i>Journal of Allergy and Clinical Immunology</i> , 2011 , 128, 996-1005 | 11.5 | 170 |
| 251 | A mathematical model of tumour-induced capillary growth. <i>Journal of Theoretical Biology</i> , 1985 , 114, 53-73 | 2.3 | 169 |
| 250 | Genome-wide mega-analysis identifies 16 loci and highlights diverse biological mechanisms in the common epilepsies. <i>Nature Communications</i> , 2018 , 9, 5269 | 17.4 | 169 |
| 249 | Genome-wide significance for dense SNP and resequencing data. <i>Genetic Epidemiology</i> , 2008 , 32, 179-85 | 2.6 | 164 |
| 248 | Patterns of human diversity, within and among continents, inferred from biallelic DNA polymorphisms. <i>Genome Research</i> , 2002 , 12, 602-12 | 9.7 | 153 |
| 247 | Relatedness in the post-genomic era: is it still useful?. <i>Nature Reviews Genetics</i> , 2015 , 16, 33-44 | 30.1 | 151 |
| 246 | Interpreting low template DNA profiles. <i>Forensic Science International: Genetics</i> , 2009 , 4, 1-10 | 4.3 | 139 |
| 245 | Ethiopian genetic diversity reveals linguistic stratification and complex influences on the Ethiopian gene pool. <i>American Journal of Human Genetics</i> , 2012 , 91, 83-96 | 11 | 133 |
| 244 | In defence of model-based inference in phylogeography. <i>Molecular Ecology</i> , 2010 , 19, 436-446 | 5.7 | 127 |

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| 243 | Likelihood-based inference for genetic correlation coefficients. <i>Theoretical Population Biology</i> , 2003 , 63, 221-30 | 1.2 | 127 |
| 242 | AIP mutation in pituitary adenomas in the 18th century and today. <i>New England Journal of Medicine</i> , 2011 , 364, 43-50 | 59.2 | 122 |
| 241 | Identification of the remains of King Richard III. <i>Nature Communications</i> , 2014 , 5, 5631 | 17.4 | 118 |
| 240 | Efficient pooling designs for library screening. <i>Genomics</i> , 1995 , 26, 21-30 | 4.3 | 115 |
| 239 | The genomic and phenotypic diversity of <i>Schizosaccharomyces pombe</i> . <i>Nature Genetics</i> , 2015 , 47, 235-41 | 36.3 | 111 |
| 238 | Pathway analysis of GWAS provides new insights into genetic susceptibility to 3 inflammatory diseases. <i>PLoS ONE</i> , 2009 , 4, e8068 | 3.7 | 110 |
| 237 | A genome-wide association scan in admixed Latin Americans identifies loci influencing facial and scalp hair features. <i>Nature Communications</i> , 2016 , 7, 10815 | 17.4 | 108 |
| 236 | Fine-scale mapping of disease loci via shattered coalescent modeling of genealogies. <i>American Journal of Human Genetics</i> , 2002 , 70, 686-707 | 11 | 106 |
| 235 | Evidence for a Common Origin of Blacksmiths and Cultivators in the Ethiopian Ari within the Last 4500 Years: Lessons for Clustering-Based Inference. <i>PLoS Genetics</i> , 2015 , 11, e1005397 | 6 | 104 |
| 234 | A genome-wide association scan implicates DCHS2, RUNX2, GLI3, PAX1 and EDAR in human facial variation. <i>Nature Communications</i> , 2016 , 7, 11616 | 17.4 | 103 |
| 233 | A genome-wide association study of the metabolic syndrome in Indian Asian men. <i>PLoS ONE</i> , 2010 , 5, e11961 | 3.7 | 94 |
| 232 | Population structure and inbreeding from pedigree analysis of purebred dogs. <i>Genetics</i> , 2008 , 179, 593-601 | 6.1 | 93 |
| 231 | Optimizing genomic medicine in epilepsy through a gene-customized approach to missense variant interpretation. <i>Genome Research</i> , 2017 , 27, 1715-1729 | 9.7 | 91 |
| 230 | SumHer better estimates the SNP heritability of complex traits from summary statistics. <i>Nature Genetics</i> , 2019 , 51, 277-284 | 36.3 | 91 |
| 229 | Sequence-level population simulations over large genomic regions. <i>Genetics</i> , 2007 , 177, 1725-31 | 4 | 84 |
| 228 | Logistic regression protects against population structure in genetic association studies. <i>Genome Research</i> , 2006 , 16, 290-6 | 9.7 | 82 |
| 227 | Gametic phase estimation over large genomic regions using an adaptive window approach. <i>Human Genomics</i> , 2003 , 1, 7-19 | 6.8 | 82 |
| 226 | Storytelling and story testing in domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 6159-64 | 11.5 | 80 |

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| 225 | On optimal selection of summary statistics for approximate Bayesian computation. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2010 , 9, Article34 | 1.2 | 80 |
| 224 | 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. <i>Diabetes</i> , 2009 , 58, 2703-8 | 0.9 | 80 |
| 223 | Bayesian fine-scale mapping of disease loci, by hidden Markov models. <i>American Journal of Human Genetics</i> , 2000 , 67, 155-69 | 11 | 77 |
| 222 | Analyses of infectious disease data from household outbreaks by Markov chain Monte Carlo methods. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2000 , 49, 517-542 | 1.5 | 76 |
| 221 | Applying association mapping and genomic selection to the dissection of key traits in elite European wheat. <i>Theoretical and Applied Genetics</i> , 2014 , 127, 2619-33 | 6 | 73 |
| 220 | A GWAS in Latin Americans highlights the convergent evolution of lighter skin pigmentation in Eurasia. <i>Nature Communications</i> , 2019 , 10, 358 | 17.4 | 72 |
| 219 | Measuring departures from Hardy-Weinberg: a Markov chain Monte Carlo method for estimating the inbreeding coefficient. <i>Heredity</i> , 1998 , 80 (Pt 6), 769-77 | 3.6 | 72 |
| 218 | PopABC: a program to infer historical demographic parameters. <i>Bioinformatics</i> , 2009 , 25, 2747-9 | 7.2 | 71 |
| 217 | 2005 , | | 71 |
| 216 | Using Genetic Distance to Infer the Accuracy of Genomic Prediction. <i>PLoS Genetics</i> , 2016 , 12, e1006288 | 6 | 67 |
| 215 | Evaluation of mixed-source, low-template DNA profiles in forensic science. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 12241-6 | 11.5 | 66 |
| 214 | Latin Americans show wide-spread Converso ancestry and imprint of local Native ancestry on physical appearance. <i>Nature Communications</i> , 2018 , 9, 5388 | 17.4 | 65 |
| 213 | Inference in Forensic Identification. <i>Journal of the Royal Statistical Society Series A: Statistics in Society</i> , 1995 , 158, 21 | 2.1 | 64 |
| 212 | Describing the genetic architecture of epilepsy through heritability analysis. <i>Brain</i> , 2014 , 137, 2680-9 | 11.2 | 63 |
| 211 | Evaluating forensic DNA profiles using peak heights, allowing for multiple donors, allelic dropout and stutters. <i>Forensic Science International: Genetics</i> , 2013 , 7, 555-63 | 4.3 | 63 |
| 210 | Clinical factors and ABCB1 polymorphisms in prediction of antiepileptic drug response: a prospective cohort study. <i>Lancet Neurology</i> , 2006 , 5, 668-76 | 24.1 | 63 |
| 209 | Animal research: reporting in vivo experiments: the ARRIVE guidelines. <i>Journal of Physiology</i> , 2010 , 588, 2519-21 | 3.9 | 62 |
| 208 | Little loss of information due to unknown phase for fine-scale linkage-disequilibrium mapping with single-nucleotide-polymorphism genotype data. <i>American Journal of Human Genetics</i> , 2004 , 74, 945-53 | 11 | 62 |

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|-----|---|------|----|
| 207 | Genetic association of the major histocompatibility complex with rheumatoid arthritis implicates two non-DRB1 loci. <i>Arthritis and Rheumatism</i> , 2009 , 60, 53-62 | | 61 |
| 206 | A genome-wide association study of neuroticism in a population-based sample. <i>PLoS ONE</i> , 2010 , 5, e11504 | | 59 |
| 205 | Genetic screening for Niemann-Pick disease type C in adults with neurological and psychiatric symptoms: findings from the ZOOM study. <i>Human Molecular Genetics</i> , 2013 , 22, 4349-56 | 5.6 | 58 |
| 204 | Genome-wide association study in multiple human prion diseases suggests genetic risk factors additional to PRNP. <i>Human Molecular Genetics</i> , 2012 , 21, 1897-906 | 5.6 | 58 |
| 203 | Exon sequencing and high resolution haplotype analysis of ABC transporter genes implicated in drug resistance. <i>Pharmacogenetics and Genomics</i> , 2006 , 16, 439-50 | 1.9 | 58 |
| 202 | Models of sequence evolution for DNA sequences containing gaps. <i>Molecular Biology and Evolution</i> , 2001 , 18, 481-90 | 8.3 | 58 |
| 201 | Effects of population structure on DNA fingerprint analysis in forensic science. <i>Heredity</i> , 1991 , 66 (Pt 2), 297-302 | 3.6 | 56 |
| 200 | Confounding between recombination and selection, and the Ped/Pop method for detecting selection. <i>Genome Research</i> , 2008 , 18, 1304-13 | 9.7 | 52 |
| 199 | Multiple quantitative trait analysis using bayesian networks. <i>Genetics</i> , 2014 , 198, 129-37 | 4 | 49 |
| 198 | Significant genetic correlations among Caucasians at forensic DNA loci. <i>Heredity</i> , 1997 , 78 (Pt 6), 583-9 | 3.6 | 49 |
| 197 | Fregene: simulation of realistic sequence-level data in populations and ascertained samples. <i>BMC Bioinformatics</i> , 2008 , 9, 364 | 3.6 | 49 |
| 196 | Fine mapping of disease genes via haplotype clustering. <i>Genetic Epidemiology</i> , 2006 , 30, 170-9 | 2.6 | 45 |
| 195 | A Comparative Survey of Non-Adaptive Pooling Designs 1996 , 133-154 | | 45 |
| 194 | Evaluating DNA Profile Evidence When the Suspect Is Identified Through a Database Search. <i>Journal of Forensic Sciences</i> , 1996 , 41, 13961J | 1.8 | 44 |
| 193 | A genome-wide association study identifies multiple loci for variation in human ear morphology. <i>Nature Communications</i> , 2015 , 6, 7500 | 17.4 | 42 |
| 192 | Statistical Evaluation of Forensic DNA Profile Evidence. <i>Annual Review of Statistics and Its Application</i> , 2014 , 1, 361-384 | 7.6 | 42 |
| 191 | Common ABCB1 polymorphisms are not associated with multidrug resistance in epilepsy using a gene-wide tagging approach. <i>Pharmacogenetics and Genomics</i> , 2007 , 17, 217-20 | 1.9 | 39 |
| 190 | cnvHap: an integrative population and haplotype-based multiplatform model of SNPs and CNVs. <i>Nature Methods</i> , 2010 , 7, 541-6 | 21.6 | 37 |

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|-----|--|------|----|
| 189 | When can a DNA profile be regarded as unique?. <i>Science and Justice - Journal of the Forensic Science Society</i> , 1999 , 39, 257-60 | 2 | 37 |
| 188 | Estimating Products in Forensic Identification Using DNA Profiles. <i>Journal of the American Statistical Association</i> , 1995 , 90, 839-844 | 2.8 | 36 |
| 187 | Differential coexpression analysis of obesity-associated networks in human subcutaneous adipose tissue. <i>International Journal of Obesity</i> , 2012 , 36, 137-47 | 5.5 | 35 |
| 186 | Estimating the age of the common ancestor of men from the ZFY intron. <i>Science</i> , 1996 , 272, 1357-9; author reply 1361-2 | 33.3 | 35 |
| 185 | Evaluating and improving heritability models using summary statistics. <i>Nature Genetics</i> , 2020 , 52, 458-463 | 36.3 | 34 |
| 184 | Population genetics of STR loci in Caucasians. <i>International Journal of Legal Medicine</i> , 1996 , 108, 300-5 | 3.1 | 33 |
| 183 | Variation in estimated recombination rates across human populations. <i>Human Genetics</i> , 2007 , 122, 301-10 | 10.3 | 31 |
| 182 | Optimal Pooling Designs with Error Detection. <i>Journal of Combinatorial Theory - Series A</i> , 1996 , 74, 131-140 | 140 | 31 |
| 181 | Statistical Approaches in Eukaryotic Gene Prediction 2008 , 97-159 | | 30 |
| 180 | Functional constraint and small insertions and deletions in the ENCODE regions of the human genome. <i>Genome Biology</i> , 2007 , 8, R180 | 18.3 | 30 |
| 179 | Inferring combined CNV/SNP haplotypes from genotype data. <i>Bioinformatics</i> , 2010 , 26, 1437-45 | 7.2 | 29 |
| 178 | A genome-wide association study and biological pathway analysis of epilepsy prognosis in a prospective cohort of newly treated epilepsy. <i>Human Molecular Genetics</i> , 2014 , 23, 247-58 | 5.6 | 28 |
| 177 | Heritability and genetic correlations of insulin resistance and component phenotypes in Asian Indian families using a multivariate analysis. <i>Diabetologia</i> , 2009 , 52, 2585-9 | 10.3 | 28 |
| 176 | How convincing is a matching Y-chromosome profile?. <i>PLoS Genetics</i> , 2017 , 13, e1007028 | 6 | 28 |
| 175 | Worldwide F(ST) estimates relative to five continental-scale populations. <i>Annals of Human Genetics</i> , 2014 , 78, 468-77 | 2.2 | 27 |
| 174 | Inferring identify from DNA profile evidence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995 , 92, 11741-5 | 11.5 | 27 |
| 173 | How convincing is DNA evidence?. <i>Nature</i> , 1994 , 368, 285-6 | 50.4 | 26 |
| 172 | Multipoint linkage-disequilibrium mapping narrows location interval and identifies mutation heterogeneity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 13442-6 | 11.5 | 25 |

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|-----|--|------|----|
| 171 | Detecting gene conversion: primate visual pigment genes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1992 , 249, 275-80 | 4.4 | 25 |
| 170 | Increased Population Risk of AIP-Related Acromegaly and Gigantism in Ireland. <i>Human Mutation</i> , 2017 , 38, 78-85 | 4.7 | 24 |
| 169 | Analysis of Population Subdivision 2008 , 980-1020 | | 24 |
| 168 | The DNA database search controversy. <i>Biometrics</i> , 2002 , 58, 241-4 | 1.8 | 24 |
| 167 | The design of pooling experiments for screening a clone map. <i>Fungal Genetics and Biology</i> , 1997 , 21, 302-7 | 3.9 | 23 |
| 166 | Estimating the age of the common ancestor of men from the ZFY intron. <i>Science</i> , 1996 , 272, 1356-7; author reply 1361-2 | 33.3 | 23 |
| 165 | Diffusion-controlled reactions in one dimension: Exact solutions and deterministic approximations. <i>Physical Review A</i> , 1989 , 40, 4585-4592 | 2.6 | 23 |
| 164 | Risk factors and heart disease mortality: A regional perspective. <i>Medical Journal of Australia</i> , 1986 , 144, 20-22 | 4 | 23 |
| 163 | Inferences from Spatial Population Genetics 2008 , 945-979 | | 22 |
| 162 | Evaluation of low-template DNA profiles using peak heights. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2016 , 15, 431-445 | 1.2 | 21 |
| 161 | Disease association tests by inferring ancestral haplotypes using a hidden markov model. <i>Bioinformatics</i> , 2008 , 24, 972-8 | 7.2 | 21 |
| 160 | Invasion processes and binary annihilation in one dimension. <i>Physics Letters, Section A: General, Atomic and Solid State Physics</i> , 1988 , 126, 481-483 | 2.3 | 20 |
| 159 | Bayesian models for syndrome- and gene-specific probabilities of novel variant pathogenicity. <i>Genome Medicine</i> , 2015 , 7, 5 | 14.4 | 19 |
| 158 | Verifying likelihoods for low template DNA profiles using multiple replicates. <i>Forensic Science International: Genetics</i> , 2014 , 13, 82-9 | 4.3 | 19 |
| 157 | A comment on the PCAST report: Skip the "match"/"non-match" stage. <i>Forensic Science International</i> , 2017 , 272, e7-e9 | 2.6 | 19 |
| 156 | Interaction between gas cooking and GSTM1 null genotype in bronchial responsiveness: results from the European Community Respiratory Health Survey. <i>Thorax</i> , 2014 , 69, 558-64 | 7.3 | 19 |
| 155 | Using penalised logistic regression to fine map HLA variants for rheumatoid arthritis. <i>Annals of Human Genetics</i> , 2011 , 75, 655-64 | 2.2 | 19 |
| 154 | Animal research: reporting in vivo experiments: the ARRIVE guidelines. <i>Experimental Physiology</i> , 2010 , 95, 842-4 | 2.4 | 19 |

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|-----|--|------|----|
| 153 | Statistical analysis of DNA fingerprint data for ordered clone physical mapping of human chromosomes. <i>Bulletin of Mathematical Biology</i> , 1991 , 53, 853-79 | 2.1 | 19 |
| 152 | Choice of population database for forensic DNA profile analysis. <i>Science and Justice - Journal of the Forensic Science Society</i> , 2014 , 54, 487-93 | 2 | 18 |
| 151 | Inference of haplotypic phase and missing genotypes in polyploid organisms and variable copy number genomic regions. <i>BMC Bioinformatics</i> , 2008 , 9, 513 | 3.6 | 18 |
| 150 | A comparison of software for the evaluation of complex DNA profiles. <i>Forensic Science International: Genetics</i> , 2019 , 40, 114-119 | 4.3 | 17 |
| 149 | Decision-making in familial database searching: KI alone or not alone?. <i>Forensic Science International: Genetics</i> , 2013 , 7, 52-4 | 4.3 | 17 |
| 148 | Discrimination of half-siblings when maternal genotypes are known. <i>Forensic Science International</i> , 2006 , 159, 141-7 | 2.6 | 16 |
| 147 | Implications for DNA identification arising from an analysis of Australian forensic databases. <i>Forensic Science International</i> , 2002 , 129, 90-8 | 2.6 | 16 |
| 146 | Response to Lee et al.: SNP-based heritability analysis with dense data. <i>American Journal of Human Genetics</i> , 2013 , 93, 1155-7 | 11 | 15 |
| 145 | Improving the efficiency of genomic selection. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2013 , 12, 517-27 | 1.2 | 15 |
| 144 | The association between polymorphisms in RLIP76 and drug response in epilepsy. <i>Pharmacogenomics</i> , 2007 , 8, 1715-22 | 2.6 | 15 |
| 143 | Measuring gametic disequilibrium from multilocus data. <i>Genetics</i> , 2001 , 157, 413-23 | 4 | 15 |
| 142 | How many individuals share a mitochondrial genome?. <i>PLoS Genetics</i> , 2018 , 14, e1007774 | 6 | 15 |
| 141 | Integrated analysis of genome-wide genetic and epigenetic association data for identification of disease mechanisms. <i>Epigenetics</i> , 2013 , 8, 1236-44 | 5.7 | 14 |
| 140 | Family-based association analysis with ordered categorical phenotypes, covariates and interactions. <i>Genetic Epidemiology</i> , 2007 , 31, 1-8 | 2.6 | 14 |
| 139 | Significant genetic correlations among Caucasians at forensic DNA loci | | 14 |
| 138 | 2015 , | | 13 |
| 137 | Time for DNA disclosure. <i>Science</i> , 2009 , 326, 1631-2 | 33.3 | 13 |
| 136 | Coalescent Theory 2008 , 843-877 | | 12 |

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|-----|---|-----|----|
| 135 | Dysregulation of complement system and CD4+ T cell activation pathways implicated in allergic response. <i>PLoS ONE</i> , 2013 , 8, e74821 | 3.7 | 12 |
| 134 | Multiple single nucleotide polymorphism analysis using penalized regression in nonlinear mixed-effect pharmacokinetic models. <i>Pharmacogenetics and Genomics</i> , 2013 , 23, 167-74 | 1.9 | 12 |
| 133 | In-frame seven amino-acid duplication in arose over the last 3000 years, disrupts protein interaction and stability and is associated with gigantism. <i>European Journal of Endocrinology</i> , 2017 , 177, 257-266 | 6.5 | 11 |
| 132 | Apolipoprotein E, CI and B gene polymorphisms in a sample of patients with coronary heart disease in the Kuwaiti population. <i>Medical Principles and Practice</i> , 2009 , 18, 294-9 | 2.1 | 11 |
| 131 | Estimating Products in Forensic Identification Using DNA Profiles | | 11 |
| 130 | Discussion on the meeting on Statistical modelling and analysis of genetic data \square <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2002 , 64, 737-775 | 3.9 | 10 |
| 129 | A method for quantifying differentiation between populations at multi-allelic loci and its implications for investigating identity and paternity. <i>Contemporary Issues in Genetics and Evolution</i> , 1995 , 3-12 | | 10 |
| 128 | Statistical Techniques in Metabolic Profiling 2008 , 347-373 | | 9 |
| 127 | Clustering of protein domains in the human genome. <i>Journal of Molecular Biology</i> , 2004 , 340, 991-1004 | 6.5 | 9 |
| 126 | Y-profile evidence: Close paternal relatives and mixtures. <i>Forensic Science International: Genetics</i> , 2019 , 38, 48-53 | 4.3 | 9 |
| 125 | Limit theorems for sequences of random trees. <i>Test</i> , 2009 , 18, 302-315 | 1.1 | 8 |
| 124 | [DNA Fingerprinting: A Review of the Controversy]: Comment: Some Causes for Concern about DNA Profiles. <i>Statistical Science</i> , 1994 , 9, | 2.4 | 8 |
| 123 | Statistical Methods for Plant Breeding 2019 , 501-20 | | 8 |
| 122 | Evolutionary Quantitative Genetics 2008 , 533-586 | | 7 |
| 121 | Linkage Disequilibrium, Recombination and Selection 2008 , 909-944 | | 7 |
| 120 | A likelihood ratio approach to family-based association studies with covariates. <i>Annals of Human Genetics</i> , 2006 , 70, 131-9 | 2.2 | 7 |
| 119 | MAC5: Bayesian inference of phylogenetic trees from DNA sequences incorporating gaps. <i>Bioinformatics</i> , 2001 , 17, 479-80 | 7.2 | 7 |
| 118 | Diffusion-reaction in one dimension. <i>Journal of Applied Probability</i> , 1988 , 25, 733-743 | 0.8 | 7 |

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|-----|--|------|---|
| 117 | A GWAS in Latin Americans identifies novel face shape loci, implicating VPS13B and a Denisovan introgressed region in facial variation. <i>Science Advances</i> , 2021 , 7, | 14.3 | 7 |
| 116 | Quantitative Trait Loci in Inbred Lines 2008 , 587-622 | | 6 |
| 115 | Linkage Analysis 2008 , 1141-1167 | | 6 |
| 114 | Diffusion-reaction in one dimension. <i>Journal of Applied Probability</i> , 1988 , 25, 733-743 | 0.8 | 6 |
| 113 | Re-evaluation of SNP heritability in complex human traits | | 6 |
| 112 | Better estimation of SNP heritability from summary statistics provides a new understanding of the genetic architecture of complex traits | | 6 |
| 111 | Interpreting DNA Evidence: Can Probability Theory Help? 2000 , 51-70 | | 6 |
| 110 | Detecting Natural Selection 2019 , 397-40 | | 5 |
| 109 | Introduction to Graphical Modelling 2011 , 235-254 | | 5 |
| 108 | Adaptive Molecular Evolution 2008 , 375-406 | | 5 |
| 107 | Conservation Genetics 2008 , 1021-1066 | | 5 |
| 106 | Whole Genome Association 2008 , 1238-1263 | | 5 |
| 105 | Paternity index calculations when some individuals share common ancestry. <i>Forensic Science International</i> , 2005 , 151, 101-3 | 2.6 | 5 |
| 104 | Statistical analysis of DNA fingerprint data for ordered clone physical mapping of human chromosomes. <i>Bulletin of Mathematical Biology</i> , 1991 , 53, 853-879 | 2.1 | 5 |
| 103 | Coalescent Theory 2019 , 145-30 | | 4 |
| 102 | Summary statistic analyses can mistake confounding bias for heritability. <i>Genetic Epidemiology</i> , 2019 , 43, 930-940 | 2.6 | 4 |
| 101 | Population Association 2008 , 1216-1237 | | 4 |
| 100 | Exposing flaws in S-LDSC; reply to Gazal et al. | | 4 |

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| 99 | Encoding of low-quality DNA profiles as genotype probability matrices for improved profile comparisons, relatedness evaluation and database searches. <i>Forensic Science International: Genetics</i> , 2016 , 25, 227-239 | 4.3 | 4 |
| 98 | Evaluating DNA evidence in a genetically complex population. <i>Forensic Science International: Genetics</i> , 2018 , 36, 141-147 | 4.3 | 4 |
| 97 | Integrating dynamic mixed-effect modelling and penalized regression to explore genetic association with pharmacokinetics. <i>Pharmacogenetics and Genomics</i> , 2015 , 25, 231-8 | 1.9 | 3 |
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