John C Whittaker

List of Publications by Year
in descending order

165 papers	15,884 citations	22153 59 h-index	18130 120 g-index
171 all docs	171 docs citations	171 times ranked	26200 citing authors

#	Article	IF	Citations
1	Polymorphisms in Natural Killer Cell Receptor Protein 2D (NKG2D) as a Risk Factor for Cholangiocarcinoma. Journal of Clinical and Experimental Hepatology, 2019, 9, 171-175.	0.9	9
2	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. Nature Genetics, 2019, 51, 481-493.	21.4	350
3	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. Nature Communications, 2018, 9, 711.	12.8	54
4	Mendelian Randomisation study of the influence of eGFR on coronary heart disease. Scientific Reports, 2016, 6, 28514.	3.3	14
5	Selecting instruments for Mendelian randomization in the wake of genome-wide association studies. International Journal of Epidemiology, 2016, 45, 1600-1616.	1.9	232
6	Plasma urate concentration and risk of coronary heart disease: a Mendelian randomisation analysis. Lancet Diabetes and Endocrinology,the, 2016, 4, 327-336.	11.4	122
7	Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. International Journal of Epidemiology, 2016, 45, 1927-1937.	1.9	94
8	Replication and Characterization of Association between ABO SNPs and Red Blood Cell Traits by Meta-Analysis in Europeans. PLoS ONE, 2016, 11, e0156914.	2.5	22
9	IL8 polymorphisms and overall survival in pazopanib- or sunitinib-treated patients with renal cell carcinoma. British Journal of Cancer, 2015, 112, 1190-1198.	6.4	35
10	The support of human genetic evidence for approved drug indications. Nature Genetics, 2015, 47, 856-860.	21.4	1,112
11	The role and interaction of imprinted genes in human fetal growth. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140074.	4.0	113
12	Sixty-Five Common Genetic Variants and Prediction of Type 2 Diabetes. Diabetes, 2015, 64, 1830-1840.	0.6	91
13	Refinement of Variant Selection for the LDL Cholesterol Genetic Risk Score in the Diagnosis of the Polygenic Form of Clinical Familial Hypercholesterolemia and Replication in Samples from 6 Countries. Clinical Chemistry, 2015, 61, 231-238.	3.2	166
14	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. Lancet, The, 2015, 385, 351-361.	13.7	562
15	Testing for non-linear causal effects using a binary genotype in a Mendelian randomization study: application to alcohol and cardiovascular traits. International Journal of Epidemiology, 2014, 43, 1781-1790.	1.9	57
16	Genetic Prediction of Quantitative Lipid Traits: Comparing Shrinkage Models to Gene Scores. Genetic Epidemiology, 2014, 38, 72-83.	1.3	19
17	A Comprehensive Analysis of Common Genetic Variation Around Six Candidate Loci for Intrahepatic Cholestasis of Pregnancy. American Journal of Gastroenterology, 2014, 109, 76-84.	0.4	103
18	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	6.0	528

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19	Association of vitamin D status with arterial blood pressure and hypertension risk: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2014, 2, 719-729.	11.4	319
20	The Benefits of Using Genetic Information to Design Prevention Trials. American Journal of Human Genetics, 2013, 92, 547-557.	6.2	16
21	Association Between the Chromosome 9p21 Locus and Angiographic Coronary Artery Disease Burden. Journal of the American College of Cardiology, 2013, 61, 957-970.	2.8	58
22	Use of low-density lipoprotein cholesterol gene score to distinguish patients with polygenic and monogenic familial hypercholesterolaemia: a case-control study. Lancet, The, 2013, 381, 1293-1301.	13.7	485
23	Causal Relationship between Obesity and Vitamin D Status: Bi-Directional Mendelian Randomization Analysis of Multiple Cohorts. PLoS Medicine, 2013, 10, e1001383.	8.4	753
24	Influence of common genetic variation on blood lipid levels, cardiovascular risk, and coronary events in two British prospective cohort studies. European Heart Journal, 2013, 34, 972-981.	2.2	33
25	Apolipoprotein E genotype, cardiovascular biomarkers and risk of stroke: Systematic review and meta-analysis of 14 015 stroke cases and pooled analysis of primary biomarker data from up to 60 883 individuals. International Journal of Epidemiology, 2013, 42, 475-492.	1.9	145
26	Causal Relevance of Blood Lipid Fractions in the Development of Carotid Atherosclerosis. Circulation: Cardiovascular Genetics, 2013, 6, 63-72.	5.1	36
27	Genetic association analysis of vitamin D pathway with obesity traits. International Journal of Obesity, 2013, 37, 1399-1406.	3.4	42
28	Gene-Centric Analysis Identifies Variants Associated With Interleukin-6 Levels and Shared Pathways With Other Inflammation Markers. Circulation: Cardiovascular Genetics, 2013, 6, 163-170.	5.1	44
29	The impact of targeting all elderly persons in England and Wales for yearly influenza vaccination: excess mortality due to pneumonia or influenza and time trend study. BMJ Open, 2013, 3, e002743.	1.9	9
30	Gene-centric association signals for haemostasis and thrombosis traits identified with the HumanCVD BeadChip. Thrombosis and Haemostasis, 2013, 110, 995-1003.	3.4	8
31	Population Genomics of Cardiometabolic Traits: Design of the University College London-London School of Hygiene and Tropical Medicine-Edinburgh-Bristol (UCLEB) Consortium. PLoS ONE, 2013, 8, e71345.	2.5	39
32	Genome-wide association study in multiple human prion diseases suggests genetic risk factors additional to PRNP. Human Molecular Genetics, 2012, 21, 1897-1906.	2.9	73
33	Sequencing of Lp-PLA2-encoding PLA2G7 gene in 2000 Europeans reveals several rare loss-of-function mutations. Pharmacogenomics Journal, 2012, 12, 425-431.	2.0	24
34	Complement factor H genetic variant and age-related macular degeneration: effect size, modifiers and relationship to disease subtype. International Journal of Epidemiology, 2012, 41, 250-262.	1.9	79
35	Comparative analysis of genome-wide association studies signals for lipids, diabetes, and coronary heart disease: Cardiovascular Biomarker Genetics Collaboration. European Heart Journal, 2012, 33, 393-407.	2.2	93
36	Integration of Genetics into a Systems Model of Electrocardiographic Traits Using HumanCVD BeadChip. Circulation: Cardiovascular Genetics, 2012, 5, 630-638.	5.1	12

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37	The interleukin-6 receptor as a target for prevention of coronary heart disease: a mendelian randomisation analysis. Lancet, The, 2012, 379, 1214-1224.	13.7	886
38	A Multi-SNP Locus-Association Method Reveals a Substantial Fraction of the Missing Heritability. American Journal of Human Genetics, 2012, 91, 863-871.	6.2	47
39	Potential Impact of Adding Genetic Markers to Clinical Parameters in Predicting Prostate Biopsy Outcomes in Men Following an Initial Negative Biopsy: Findings from the REDUCE Trial. European Urology, 2012, 62, 953-961.	1.9	85
40	Deep Resequencing Unveils Genetic Architecture of ADIPOQ and Identifies a Novel Low-Frequency Variant Strongly Associated With Adiponectin Variation. Diabetes, 2012, 61, 1297-1301.	0.6	29
41	How informative is a negative finding in a small pharmacogenetic study?. Pharmacogenomics Journal, 2012, 12, 93-95.	2.0	7
42	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838.	6.2	227
43	Predictive Models of Choroidal Neovascularization and Geographic Atrophy Incidence Applied to Clinical Trial Design. American Journal of Ophthalmology, 2012, 154, 568-578.e12.	3.3	11
44	An Abundance of Rare Functional Variants in 202 Drug Target Genes Sequenced in 14,002 People. Science, 2012, 337, 100-104.	12.6	626
45	Deep sequencing of theLRRK2gene in 14,002 individuals reveals evidence of purifying selection and independent origin of the p.Arg1628Pro mutation in Europe. Human Mutation, 2012, 33, 1087-1098.	2.5	24
46	Maternal Inheritance of a Promoter Variant in the Imprinted PHLDA2 Gene Significantly Increases Birth Weight. American Journal of Human Genetics, 2012, 90, 715-719.	6.2	40
47	A Comparison of <scp>B</scp>ayesian and Frequentist Approaches to Incorporating External Information for the Prediction of Prostate Cancer Risk. Genetic Epidemiology, 2012, 36, 71-83.	1.3	15
48	Evaluation of Genetic Markers as Instruments for Mendelian Randomization Studies on Vitamin D. PLoS ONE, 2012, 7, e37465.	2.5	81
49	Comparison of Statistical Tests for Association between Rare Variants and Binary Traits. PLoS ONE, 2012, 7, e42530.	2.5	11
50	Application of the Lasso to Expression Quantitative Trait Loci Mapping. Statistical Applications in Genetics and Molecular Biology, 2011, 10, .	0.6	1
51	Meta analysis of candidate gene variants outside the LPA locus with Lp(a) plasma levels in 14,500 participants of six White European cohorts. Atherosclerosis, 2011, 217, 447-451.	0.8	20
52	Effect modification by population dietary folate on the association between MTHFR genotype, homocysteine, and stroke risk: a meta-analysis of genetic studies and randomised trials. Lancet, The, 2011, 378, 584-594.	13.7	273
53	Carriage of the V279F Null Allele within the Gene Encoding Lp-PLA2 Is Protective from Coronary Artery Disease in South Korean Males. PLoS ONE, 2011, 6, e18208.	2.5	43
54	Performance of Genotype Imputation for Rare Variants Identified in Exons and Flanking Regions of Genes. PLoS ONE, 2011, 6, e24945.	2.5	49

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55	Maternal and Fetal Characteristics Associated With Meconium-Stained Amniotic Fluid. Obstetrics and Gynecology, 2011, 117, 828-835.	2.4	73
56	Genetic Variants Associated with von Willebrand Factor Levels in Healthy Men and Women Identified Using the HumanCVD BeadChip. Annals of Human Genetics, 2011, 75, 456-467.	0.8	28
57	Blood Pressure Loci Identified with a Gene-Centric Array. American Journal of Human Genetics, 2011, 89, 688-700.	6.2	159
58	Variants of ADRA2A are associated with fasting glucose, blood pressure, body mass index and type 2 diabetes risk: meta-analysis of four prospective studies. Diabetologia, 2011, 54, 1710-1719.	6.3	34
59	Comparison of methods and sampling designs to test for association between rare variants and quantitative traits. Genetic Epidemiology, 2011, 35, 226-235.	1.3	11
60	Bayesian semiparametric meta-analysis for genetic association studies. Genetic Epidemiology, 2011, 35, 333-340.	1.3	5
61	Novel method to estimate the phenotypic variation explained by genome-wide association studies reveals large fraction of the missing heritability. Genetic Epidemiology, 2011, 35, 341-349.	1.3	23
62	Association between C reactive protein and coronary heart disease: mendelian randomisation analysis based on individual participant data. BMJ: British Medical Journal, 2011, 342, d548-d548.	2.3	530
63	High-Dose Vitamin D Supplements Are Not Associated with Linear Growth in a Large Finnish Cohort1â€“3. Journal of Nutrition, 2011, 141, 843-848.	2.9	17
64	Genetic Factors in the Pathogenesis of Cholangiocarcinoma. Digestive Diseases, 2011, 29, 93-97.	1.9	29
65	Pazopanib Efficacy in Renal Cell Carcinoma: Evidence for Predictive Genetic Markers in Angiogenesis-Related and Exposure-Related Genes. Journal of Clinical Oncology, 2011, 29, 2557-2564.	1.6	152
66	HLA-DQA1*02:01 Is a Major Risk Factor for Lapatinib-Induced Hepatotoxicity in Women With Advanced Breast Cancer. Journal of Clinical Oncology, 2011, 29, 667-673.	1.6	261
67	Four Genetic Loci Influencing Electrocardiographic Indices of Left Ventricular Hypertrophy. Circulation: Cardiovascular Genetics, 2011, 4, 626-635.	5.1	28
68	Maternal Hb during pregnancy and offspring's educational achievement: a prospective cohort study over 30 years. British Journal of Nutrition, 2010, 104, 1363-1368.	2.3	17
69	A variance components factor model for genetic association studies: A Bayesian analysis. Genetic Epidemiology, 2010, 34, 529-536.	1.3	0
70	Bayesian methods for metaâ€analysis of causal relationships estimated using genetic instrumental variables. Statistics in Medicine, 2010, 29, 1298-1311.	1.6	22
71	Evidence for both copy number and allelic (NA1/NA2) risk at the FCGR3B locus in systemic lupus erythematosus. European Journal of Human Genetics, 2010, 18, 1027-1031.	2.8	51
72	Ancestry as a Determinant of Mean Population C-Reactive Protein Values. Circulation: Cardiovascular Genetics, 2010, 3, 436-444.	5.1	67

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73	Genome-Wide Association Study of Major Recurrent Depression in the U.K. Population. American Journal of Psychiatry, 2010, 167, 949-957.	7.2	221
74	An Ecological Correlation Study of Late Age-Related Macular Degeneration and the Complement Factor H Y402H Polymorphism. , 2010, 51, 2393.		24
75	Epigenetic signatures of Silver-Russell syndrome. Journal of Medical Genetics, 2010, 47, 150-154.	3.2	22
76	Genetic variation in complement factor H and risk of coronary heart disease: Eight new studies and a meta-analysis of around 48,000 individuals. Atherosclerosis, 2010, 213, 184-190.	0.8	27
77	Causal Relationship of Susceptibility Genes to Ischemic Stroke: Comparison to Ischemic Heart Disease and Biochemical Determinants. PLoS ONE, 2010, 5, e9136.	2.5	70
78	Ischaemic Stroke Subtypes and Their Genetic Basis: A Comprehensive Meta-Analysis of Small and Large Vessel Stroke. European Neurology, 2009, 61, 76-86.	1.4	38
79	Evidence for an Interaction Between Familial Liability and Prenatal Exposure to Infection in the Causation of Schizophrenia. American Journal of Psychiatry, 2009, 166, 1025-1030.	7.2	189
80	Genetic Determinants of Height Growth Assessed Longitudinally from Infancy to Adulthood in the Northern Finland Birth Cohort 1966. PLoS Genetics, 2009, 5, e1000409.	3.5	131
81	Genetic risk factors for variant Creutzfeldtâ€“Jakob disease: a genome-wide association study. Lancet Neurology, The, 2009, 8, 57-66.	10.2	131
82	Evaluation of folate metabolism gene polymorphisms as risk factors for open and closed neural tube defects. American Journal of Medical Genetics, Part A, 2009, 149A, 1585-1589.	1.2	23
83	Age of onset and death in inherited prion disease are heritable. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2009, 150B, 496-501.	1.7	11
84	The clonal evolution of metastases from primary serous epithelial ovarian cancers. International Journal of Cancer, 2009, 124, 1579-1586.	5.1	68
85	Review of factors that influence the abundance of ions produced in a tandem mass spectrometer and statistical methods for discovering these factors. Mass Spectrometry Reviews, 2009, 28, 177-187.	5.4	42
86	Generic reversible jump MCMC using graphical models. Statistics and Computing, 2009, 19, 395-408.	1.5	76
87	The heritability and genetics of complement C3 expression in UK SLE families. Genes and Immunity, 2009, 10, 525-530.	4.1	15
88	The effect of exclusion of cases with unrecorded best estimate of gestational age on the estimates of preterm birth rate. BJOG: an International Journal of Obstetrics and Gynaecology, 2009, 116, 1218-1224.	2.3	0
89	Searching for Genotype-Phenotype Structure: Using Hierarchical Log-Linear Models in Crohn Disease. American Journal of Human Genetics, 2009, 84, 178-187.	6.2	7
90	Multilocus Bayesian Meta-Analysis of Gene-Disease Associations. American Journal of Human Genetics, 2009, 84, 567-580.	6.2	28

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91	Gene-centric Association Signals for Lipids and Apolipoproteins Identified via the HumanCVD BeadChip. American Journal of Human Genetics, 2009, 85, 628-642.	6.2	183
92	A Novel Protective Prion Protein Variant that Colocalizes with Kuru Exposure. New England Journal of Medicine, 2009, 361, 2056-2065.	27.0	157
93	Collaborative pooled analysis of data on C-reactive protein gene variants and coronary disease: judging causality by Mendelian randomisation. European Journal of Epidemiology, 2008, 23, 531-540.	5.7	51
94	Fine-mapping the genetic basis of CRP regulation in African Americans: a Bayesian approach. Human Genetics, 2008, 123, 633-642.	3.8	9
95	Genomeâ€wide significance for dense SNP and resequencing data. Genetic Epidemiology, 2008, 32, 179-185.	1.3	187
96	Analysis of multiple SNPs in a candidate gene or region. Genetic Epidemiology, 2008, 32, 560-566.	1.3	92
97	Familial clustering of nonâ€nuclear autoantibodies and C3 and C4 complement components in systemic lupus erythematosus. Arthritis and Rheumatism, 2008, 58, 1116-1124.	6.7	16
98	Marker-Assisted Selection and Introgression. , 2008, , 718-751.		3
99	Polymorphism at the TNF superfamily gene TNFSF4 confers susceptibility to systemic lupus erythematosus. Nature Genetics, 2008, 40, 83-89.	21.4	193
100	Quantification of the Genetic Component of Basal Câ€Reactive Protein Expression in SLE Nuclear Families. Annals of Human Genetics, 2008, 72, 611-620.	0.8	9
101	Fregene: Simulation of realistic sequence-level data in populations and ascertained samples. BMC Bioinformatics, 2008, 9, 364.	2.6	57
102	Bayesian Meta-Analysis of Genetic Association Studies with Different Sets of Markers. American Journal of Human Genetics, 2008, 82, 859-872.	6.2	54
103	Predicting Clinical Outcome in Patients Diagnosed with Synchronous Ovarian and Endometrial Cancer. Clinical Cancer Research, 2008, 14, 5840-5848.	7.0	41
104	Simultaneous Analysis of All SNPs in Genome-Wide and Re-Sequencing Association Studies. PLoS Genetics, 2008, 4, e1000130.	3.5	298
105	Timing of Planned Cesarean Delivery by Racial Group. Obstetrics and Gynecology, 2008, 111, 659-666.	2.4	32
106	The Genetics of Primary Haemorrhagic Stroke, Subarachnoid Haemorrhage and Ruptured Intracranial Aneurysms in Adults. PLoS ONE, 2008, 3, e3691.	2.5	56
107	Sequence-Level Population Simulations Over Large Genomic Regions. Genetics, 2007, 177, 1725-1731.	2.9	99
108	Racial variation in the association between gestational age and perinatal mortality: prospective study. BMJ: British Medical Journal, 2007, 334, 833.	2.3	73

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109	Genetics of Ischaemic Stroke among Persons of Non-European Descent: A Meta-Analysis of Eight Genes Involving â^¼ 32,500 Individuals. PLoS Medicine, 2007, 4, e131.	8.4	96
110	Reed Elsevier and the arms trade revisited. Lancet, The, 2007, 369, 987.	13.7	1
111	Using Statistical Models To Identify Factors That Have a Role in Defining the Abundance of Ions Produced by Tandem MS. Analytical Chemistry, 2007, 79, 5601-5607.	6.5	22
112	Functional Variants of the Central Bile Acid Sensor FXR Identified in Intrahepatic Cholestasis of Pregnancy. Gastroenterology, 2007, 133, 507-516.	1.3	215
113	Familyâ€based association analysis with ordered categorical phenotypes, covariates and interactions. Genetic Epidemiology, 2007, 31, 1-8.	1.3	15
114	The use of Meta-Analysis Risk Estimates for Candidate Genes in Combination to Predict Coronary Heart Disease Risk. Annals of Human Genetics, 2007, 71, 611-619.	0.8	41
115	Elevated placental expression of the imprinted PHLDA2 gene is associated with low birth weight. Journal of Molecular Medicine, 2007, 85, 379-387.	3.9	126
116	Bayesian Graphical Models for Genomewide Association Studies. American Journal of Human Genetics, 2006, 79, 100-112.	6.2	63
117	A Likelihood Ratio Approach to Family-based Association Studies with Covariates. Annals of Human Genetics, 2006, 70, 131-139.	0.8	7
118	Association analysis of the chromosome 4p-located G protein-coupled receptor 78 (GPR78) gene in bipolar affective disorder and schizophrenia. Molecular Psychiatry, 2006, 11, 384-394.	7.9	24
119	Fine mapping of disease genes via haplotype clustering. Genetic Epidemiology, 2006, 30, 170-179.	1.3	49
120	A Bayesian toolkit for genetic association studies. Genetic Epidemiology, 2006, 30, 231-247.	1.3	84
121	Evidence for unique association signals in SLE at the CD28â€“CTLA4â€“ICOS locus in a family-based study. Human Molecular Genetics, 2006, 15, 3195-3205.	2.9	56
122	Inconsistent Association Between the STK15 F31I Genetic Polymorphism and Breast Cancer Risk. Journal of the National Cancer Institute, 2006, 98, 1014-1018.	6.3	48
123	Ethanol Intake and Risk of Lung Cancer in the European Prospective Investigation into Cancer and Nutrition (EPIC). American Journal of Epidemiology, 2006, 164, 1103-1114.	3.4	28
124	Limits to Causal Inference based on Mendelian Randomization: A Comparison with Randomized Controlled Trials. American Journal of Epidemiology, 2006, 163, 397-403.	3.4	181
125	SNP Selection for Association Studies: Maximizing Power across SNP Choice and Study Size. Annals of Human Genetics, 2005, 69, 733-746.	0.8	9
126	A hierarchical Bayesian model for predicting the functional consequences of amino-acid polymorphisms. Journal of the Royal Statistical Society Series C: Applied Statistics, 2005, 54, 191-206.	1.0	16

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127	Integrated transcriptional profiling and linkage analysis for identification of genes underlying disease. Nature Genetics, 2005, 37, 243-253.	21.4	476
128	No association between E- and L-selectin genes and SLE: soluble L-selectin levels do correlate with genotype and a subset in SLE. Genes and Immunity, 2005, 6, 422-429.	4.1	15
129	Bayesian modelling of multivariate quantitative traits using seemingly unrelated regressions. Genetic Epidemiology, 2005, 28, 313-325.	1.3	23
130	On the Structural Differences Between Markers and Genomic AC Microsatellites. Journal of Molecular Evolution, 2005, 60, 688-693.	1.8	6
131	Statistical design and analysis of pharmacogenetic trials. Statistics in Medicine, 2005, 24, 1495-1508.	1.6	31
132	Are reported preterm birth rates reliable? An analysis of interhospital differences in the calculation of the weeks of gestation at delivery and preterm birth rate. BJOG: an International Journal of Obstetrics and Gynaecology, 2004, 111, 160-163.	2.3	21
133	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.	6.2	66
134	SNP Subset Selection for Genetic Association Studies. Annals of Human Genetics, 2003, 67, 543-556.	0.8	30
135	Variance components linkage analysis for adjusted systolic blood pressure in the Framingham Heart Study. BMC Genetics, 2003, 4, S4.	2.7	2
136	Estimation and Testing of Parent-of-Origin Effects for Quantitative Traits. American Journal of Human Genetics, 2003, 72, 1035-1039.	6.2	20
137	Polymorphism at the C-reactive protein locus influences gene expression and predisposes to systemic lupus erythematosus. Human Molecular Genetics, 2003, 13, 137-147.	2.9	250
138	A Bayesian approach to disease gene location using allelic association. Biostatistics, 2003, 4, 399-409.	1.5	5
139	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.	7.1	28
140	The Structure of Interrupted Human AC Microsatellites. Molecular Biology and Evolution, 2003, 20, 453-459.	8.9	32
141	Likelihood-Based Estimation of Microsatellite Mutation Rates. Genetics, 2003, 164, 781-787.	2.9	145
142	Generalized estimating equations: A hybrid approach for mean parameters in multivariate regression models. Statistical Modelling, 2002, 2, 163-181.	1.1	7
143	Fine-Scale Mapping of Disease Loci via Shattered Coalescent Modeling of Genealogies. American Journal of Human Genetics, 2002, 70, 686-707.	6.2	123
144	A Maximum-Likelihood Approach to Fitting Equilibrium Models of Microsatellite Evolution. Molecular Biology and Evolution, 2001, 18, 413-417.	8.9	30

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145	Controlling misdiagnosis errors in preimplantation genetic diagnosis: a comprehensive model encompassing extrinsic and intrinsic sources of error. Human Reproduction, 2001, 16, 43-50.	0.9	81
146	Mapping Quantitative Trait Loci Using Generalized Estimating Equations. Genetics, 2001, 159, 1325-1337.	2.9	45
147	On Prediction of Genetic Values in Marker-Assisted Selection. Genetics, 2001, 159, 1375-1381.	2.9	27
148	Family-based tests of association and/or linkage. Annals of Human Genetics, 2001, 65, 407-19.	0.8	6
149	Marker-assisted selection using ridge regression. Genetical Research, 2000, 75, 249-252.	0.9	310
150	Title is missing!. Molecular Breeding, 2000, 6, 11-24.	2.1	4
151	Bayesian Fine-Scale Mapping of Disease Loci, by Hidden Markov Models. American Journal of Human Genetics, 2000, 67, 155-169.	6.2	95
152	The Problems of Using the Transmission/Disequilibrium Test to Infer Tight Linkage. American Journal of Human Genetics, 2000, 67, 523-526.	6.2	17
153	Fine scale association mapping of disease loci using simplex families. Annals of Human Genetics, 2000, 64, 223-37.	0.8	0
154	Finite-Sample Properties of Family-Based Association Tests. American Journal of Human Genetics, 1999, 64, 910-915.	6.2	6
155	Power Comparisons of the Transmission/Disequilibrium Test and Sibâ€“Transmission/Disequilibrium-Test Statistics. American Journal of Human Genetics, 1999, 65, 578-580.	6.2	31
156	Generalization of the extended transmission disequilibrium test to two unlinked disease loci. Genetic Epidemiology, 1999, 17, S661-6.	1.3	4
157	Using information from both parents when testing for association between marker and disease loci. , 1998, 15, 193-200.		4
158	The Effect of Family Structure on Linkage Tests Using Allelic Association. American Journal of Human Genetics, 1998, 63, 889-897.	6.2	31
159	Optimal weighting of information in marker-assisted selection. Genetical Research, 1997, 69, 137-144.	0.9	26
160	A likelihood ratio test for detecting patterns of disease-marker association. Annals of Human Genetics, 1997, 61, 335-350.	0.8	29
161	Using marker-maps in marker-assisted selection. Genetical Research, 1995, 66, 255-265.	0.9	60
162	The Finite Horizon War of Attrition. Games and Economic Behavior, 1995, 11, 193-236.	0.8	16

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163	A Resource Allocation Problem. Journal of Theoretical Biology, 1994, 167, 397-405.	1.7	7
164	Multiple Trial Two Strategy Conflicts. Journal of Theoretical Biology, 1994, 169, 113-124.	1.7	2
165	A two-trial two-strategy conflict. Journal of Theoretical Biology, 1991, 149, 281-286.	1.7	7