John C Whittaker

List of Publications by Year
in descending order

165 papers	15,884 citations	22099 59 h-index	18075 120 g-index
171 all docs	171 docs citations	171 times ranked	26200 citing authors

#	Article	IF	Citations
1	The support of human genetic evidence for approved drug indications. Nature Genetics, 2015, 47, 856-860.	9.4	1,112
2	The interleukin-6 receptor as a target for prevention of coronary heart disease: a mendelian randomisation analysis. Lancet, The, 2012, 379, 1214-1224.	6.3	886
3	Causal Relationship between Obesity and Vitamin D Status: Bi-Directional Mendelian Randomization Analysis of Multiple Cohorts. PLoS Medicine, 2013, 10, e1001383.	3.9	753
4	An Abundance of Rare Functional Variants in 202 Drug Target Genes Sequenced in 14,002 People. Science, 2012, 337, 100-104.	6.0	626
5	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. Lancet, The, 2015, 385, 351-361.	6.3	562
6	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.	2.4	530
7	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	3.0	528
8	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.	6.3	485
9	Integrated transcriptional profiling and linkage analysis for identification of genes underlying disease. Nature Genetics, 2005, 37, 243-253.	9.4	476
10	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. Nature Genetics, 2019, 51, 481-493.	9.4	350
11	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.	5.5	319
12	Marker-assisted selection using ridge regression. Genetical Research, 2000, 75, 249-252.	0.3	310
13	Simultaneous Analysis of All SNPs in Genome-Wide and Re-Sequencing Association Studies. PLoS Genetics, 2008, 4, e1000130.	1.5	298
14	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.	6.3	273
15	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.	0.8	261
16	Polymorphism at the C-reactive protein locus influences gene expression and predisposes to systemic lupus erythematosus. Human Molecular Genetics, 2003, 13, 137-147.	1.4	250
17	Selecting instruments for Mendelian randomization in the wake of genome-wide association studies. International Journal of Epidemiology, 2016, 45, 1600-1616.	0.9	232
18	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838.	2.6	227

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19	Genome-Wide Association Study of Major Recurrent Depression in the U.K. Population. American Journal of Psychiatry, 2010, 167, 949-957.	4.0	221
20	Functional Variants of the Central Bile Acid Sensor FXR Identified in Intrahepatic Cholestasis of Pregnancy. Gastroenterology, 2007, 133, 507-516.	0.6	215
21	Polymorphism at the TNF superfamily gene TNFSF4 confers susceptibility to systemic lupus erythematosus. Nature Genetics, 2008, 40, 83-89.	9.4	193
22	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.	4.0	189
23	Genomeâ€wide significance for dense SNP and resequencing data. Genetic Epidemiology, 2008, 32, 179-185.	0.6	187
24	Gene-centric Association Signals for Lipids and Apolipoproteins Identified via the HumanCVD BeadChip. American Journal of Human Genetics, 2009, 85, 628-642.	2.6	183
25	Limits to Causal Inference based on Mendelian Randomization: A Comparison with Randomized Controlled Trials. American Journal of Epidemiology, 2006, 163, 397-403.	1.6	181
26	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.	1.5	166
27	Blood Pressure Loci Identified with a Gene-Centric Array. American Journal of Human Genetics, 2011, 89, 688-700.	2.6	159
28	A Novel Protective Prion Protein Variant that Colocalizes with Kuru Exposure. New England Journal of Medicine, 2009, 361, 2056-2065.	13.9	157
29	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.	0.8	152
30	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.	0.9	145
31	Likelihood-Based Estimation of Microsatellite Mutation Rates. Genetics, 2003, 164, 781-787.	1.2	145
32	Genetic Determinants of Height Growth Assessed Longitudinally from Infancy to Adulthood in the Northern Finland Birth Cohort 1966. PLoS Genetics, 2009, 5, e1000409.	1.5	131
33	Genetic risk factors for variant Creutzfeldtâ€“Jakob disease: a genome-wide association study. Lancet Neurology, The, 2009, 8, 57-66.	4.9	131
34	Elevated placental expression of the imprinted PHLDA2 gene is associated with low birth weight. Journal of Molecular Medicine, 2007, 85, 379-387.	1.7	126
35	Fine-Scale Mapping of Disease Loci via Shattered Coalescent Modeling of Genealogies. American Journal of Human Genetics, 2002, 70, 686-707.	2.6	123
36	Plasma urate concentration and risk of coronary heart disease: a Mendelian randomisation analysis. Lancet Diabetes and Endocrinology,the, 2016, 4, 327-336.	5.5	122

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37	The role and interaction of imprinted genes in human fetal growth. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140074.	1.8	113
38	A Comprehensive Analysis of Common Genetic Variation Around Six Candidate Loci for Intrahepatic Cholestasis of Pregnancy. American Journal of Gastroenterology, 2014, 109, 76-84.	0.2	103
39	Sequence-Level Population Simulations Over Large Genomic Regions. Genetics, 2007, 177, 1725-1731.	1.2	99
40	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.	3.9	96
41	Bayesian Fine-Scale Mapping of Disease Loci, by Hidden Markov Models. American Journal of Human Genetics, 2000, 67, 155-169.	2.6	95
42	Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. International Journal of Epidemiology, 2016, 45, 1927-1937.	0.9	94
43	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.	1.0	93
44	Analysis of multiple SNPs in a candidate gene or region. Genetic Epidemiology, 2008, 32, 560-566.	0.6	92
45	Sixty-Five Common Genetic Variants and Prediction of Type 2 Diabetes. Diabetes, 2015, 64, 1830-1840.	0.3	91
46	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.	0.9	85
47	A Bayesian toolkit for genetic association studies. Genetic Epidemiology, 2006, 30, 231-247.	0.6	84
48	Controlling misdiagnosis errors in preimplantation genetic diagnosis: a comprehensive model encompassing extrinsic and intrinsic sources of error. Human Reproduction, 2001, 16, 43-50.	0.4	81
49	Evaluation of Genetic Markers as Instruments for Mendelian Randomization Studies on Vitamin D. PLoS ONE, 2012, 7, e37465.	1.1	81
50	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.	0.9	79
51	Generic reversible jump MCMC using graphical models. Statistics and Computing, 2009, 19, 395-408.	0.8	76
52	Racial variation in the association between gestational age and perinatal mortality: prospective study. BMJ: British Medical Journal, 2007, 334, 833.	2.4	73
53	Maternal and Fetal Characteristics Associated With Meconium-Stained Amniotic Fluid. Obstetrics and Gynecology, 2011, 117, 828-835.	1.2	73
54	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

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55	Causal Relationship of Susceptibility Genes to Ischemic Stroke: Comparison to Ischemic Heart Disease and Biochemical Determinants. PLoS ONE, 2010, 5, e9136.	1.1	70
56	The clonal evolution of metastases from primary serous epithelial ovarian cancers. International Journal of Cancer, 2009, 124, 1579-1586.	2.3	68
57	Ancestry as a Determinant of Mean Population C-Reactive Protein Values. Circulation: Cardiovascular Genetics, 2010, 3, 436-444.	5.1	67
58	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
59	Bayesian Graphical Models for Genomewide Association Studies. American Journal of Human Genetics, 2006, 79, 100-112.	2.6	63
60	Using marker-maps in marker-assisted selection. Genetical Research, 1995, 66, 255-265.	0.3	60
61	Association Between the Chromosome 9p21 Locus and Angiographic Coronary Artery Disease Burden. Journal of the American College of Cardiology, 2013, 61, 957-970.	1.2	58
62	Fregene: Simulation of realistic sequence-level data in populations and ascertained samples. BMC Bioinformatics, 2008, 9, 364.	1.2	57
63	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.	0.9	57
64	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.	1.4	56
65	The Genetics of Primary Haemorrhagic Stroke, Subarachnoid Haemorrhage and Ruptured Intracranial Aneurysms in Adults. PLoS ONE, 2008, 3, e3691.	1.1	56
66	Bayesian Meta-Analysis of Genetic Association Studies with Different Sets of Markers. American Journal of Human Genetics, 2008, 82, 859-872.	2.6	54
67	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. Nature Communications, 2018, 9, 711.	5.8	54
68	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.	2.5	51
69	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.	1.4	51
70	Fine mapping of disease genes via haplotype clustering. Genetic Epidemiology, 2006, 30, 170-179.	0.6	49
71	Performance of Genotype Imputation for Rare Variants Identified in Exons and Flanking Regions of Genes. PLoS ONE, 2011, 6, e24945.	1.1	49
72	Inconsistent Association Between the STK15 F31I Genetic Polymorphism and Breast Cancer Risk. Journal of the National Cancer Institute, 2006, 98, 1014-1018.	3.0	48

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73	A Multi-SNP Locus-Association Method Reveals a Substantial Fraction of the Missing Heritability. American Journal of Human Genetics, 2012, 91, 863-871.	2.6	47
74	Mapping Quantitative Trait Loci Using Generalized Estimating Equations. Genetics, 2001, 159, 1325-1337.	1.2	45
75	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
76	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.	1.1	43
77	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.	2.8	42
78	Genetic association analysis of vitamin D pathway with obesity traits. International Journal of Obesity, 2013, 37, 1399-1406.	1.6	42
79	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.	0.3	41
80	Predicting Clinical Outcome in Patients Diagnosed with Synchronous Ovarian and Endometrial Cancer. Clinical Cancer Research, 2008, 14, 5840-5848.	3.2	41
81	Maternal Inheritance of a Promoter Variant in the Imprinted PHLDA2 Gene Significantly Increases Birth Weight. American Journal of Human Genetics, 2012, 90, 715-719.	2.6	40
82	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.	1.1	39
83	Ischaemic Stroke Subtypes and Their Genetic Basis: A Comprehensive Meta-Analysis of Small and Large Vessel Stroke. European Neurology, 2009, 61, 76-86.	0.6	38
84	Causal Relevance of Blood Lipid Fractions in the Development of Carotid Atherosclerosis. Circulation: Cardiovascular Genetics, 2013, 6, 63-72.	5.1	36
85	IL8 polymorphisms and overall survival in pazopanib- or sunitinib-treated patients with renal cell carcinoma. British Journal of Cancer, 2015, 112, 1190-1198.	2.9	35
86	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.	2.9	34
87	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.	1.0	33
88	The Structure of Interrupted Human AC Microsatellites. Molecular Biology and Evolution, 2003, 20, 453-459.	3.5	32
89	Timing of Planned Cesarean Delivery by Racial Group. Obstetrics and Gynecology, 2008, 111, 659-666.	1.2	32
90	The Effect of Family Structure on Linkage Tests Using Allelic Association. American Journal of Human Genetics, 1998, 63, 889-897.	2.6	31

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91	Power Comparisons of the Transmission/Disequilibrium Test and Sibâ€“Transmission/Disequilibrium-Test Statistics. American Journal of Human Genetics, 1999, 65, 578-580.	2.6	31
92	Statistical design and analysis of pharmacogenetic trials. Statistics in Medicine, 2005, 24, 1495-1508.	0.8	31
93	A Maximum-Likelihood Approach to Fitting Equilibrium Models of Microsatellite Evolution. Molecular Biology and Evolution, 2001, 18, 413-417.	3.5	30
94	SNP Subset Selection for Genetic Association Studies. Annals of Human Genetics, 2003, 67, 543-556.	0.3	30
95	Genetic Factors in the Pathogenesis of Cholangiocarcinoma. Digestive Diseases, 2011, 29, 93-97.	0.8	29
96	Deep Resequencing Unveils Genetic Architecture of ADIPOQ and Identifies a Novel Low-Frequency Variant Strongly Associated With Adiponectin Variation. Diabetes, 2012, 61, 1297-1301.	0.3	29
97	A likelihood ratio test for detecting patterns of disease-marker association. Annals of Human Genetics, 1997, 61, 335-350.	0.3	29
98	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
99	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.	1.6	28
100	Multilocus Bayesian Meta-Analysis of Gene-Disease Associations. American Journal of Human Genetics, 2009, 84, 567-580.	2.6	28
101	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.	0.3	28
102	Four Genetic Loci Influencing Electrocardiographic Indices of Left Ventricular Hypertrophy. Circulation: Cardiovascular Genetics, 2011, 4, 626-635.	5.1	28
103	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.	0.4	27
104	On Prediction of Genetic Values in Marker-Assisted Selection. Genetics, 2001, 159, 1375-1381.	1.2	27
105	Optimal weighting of information in marker-assisted selection. Genetical Research, 1997, 69, 137-144.	0.3	26
106	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.	4.1	24
107	An Ecological Correlation Study of Late Age-Related Macular Degeneration and the Complement Factor H Y402H Polymorphism. , 2010, 51, 2393.		24
108	Sequencing of Lp-PLA2-encoding PLA2G7 gene in 2000 Europeans reveals several rare loss-of-function mutations. Pharmacogenomics Journal, 2012, 12, 425-431.	0.9	24

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109	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.	1.1	24
110	Bayesian modelling of multivariate quantitative traits using seemingly unrelated regressions. Genetic Epidemiology, 2005, 28, 313-325.	0.6	23
111	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.	0.7	23
112	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.	0.6	23
113	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.	3.2	22
114	Bayesian methods for metaâ€analysis of causal relationships estimated using genetic instrumental variables. Statistics in Medicine, 2010, 29, 1298-1311.	0.8	22
115	Epigenetic signatures of Silver-Russell syndrome. Journal of Medical Genetics, 2010, 47, 150-154.	1.5	22
116	Replication and Characterization of Association between ABO SNPs and Red Blood Cell Traits by Meta-Analysis in Europeans. PLoS ONE, 2016, 11, e0156914.	1.1	22
117	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.	1.1	21
118	Estimation and Testing of Parent-of-Origin Effects for Quantitative Traits. American Journal of Human Genetics, 2003, 72, 1035-1039.	2.6	20
119	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.	0.4	20
120	Genetic Prediction of Quantitative Lipid Traits: Comparing Shrinkage Models to Gene Scores. Genetic Epidemiology, 2014, 38, 72-83.	0.6	19
121	The Problems of Using the Transmission/Disequilibrium Test to Infer Tight Linkage. American Journal of Human Genetics, 2000, 67, 523-526.	2.6	17
122	Maternal Hb during pregnancy and offspring's educational achievement: a prospective cohort study over 30 years. British Journal of Nutrition, 2010, 104, 1363-1368.	1.2	17
123	High-Dose Vitamin D Supplements Are Not Associated with Linear Growth in a Large Finnish Cohort1â€“3. Journal of Nutrition, 2011, 141, 843-848.	1.3	17
124	The Finite Horizon War of Attrition. Games and Economic Behavior, 1995, 11, 193-236.	0.4	16
125	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.	0.5	16
126	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

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127	The Benefits of Using Genetic Information to Design Prevention Trials. American Journal of Human Genetics, 2013, 92, 547-557.	2.6	16
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.	2.2	15
129	Family-based association analysis with ordered categorical phenotypes, covariates and interactions. Genetic Epidemiology, 2007, 31, 1-8.	0.6	15
130	The heritability and genetics of complement C3 expression in UK SLE families. Genes and Immunity, 2009, 10, 525-530.	2.2	15
131	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.	0.6	15
132	Mendelian Randomisation study of the influence of eGFR on coronary heart disease. Scientific Reports, 2016, 6, 28514.	1.6	14
133	Integration of Genetics into a Systems Model of Electrocardiographic Traits Using HumanCVD BeadChip. Circulation: Cardiovascular Genetics, 2012, 5, 630-638.	5.1	12
134	Age of onset and death in inherited prion disease are heritable. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2009, 150B, 496-501.	1.1	11
135	Comparison of methods and sampling designs to test for association between rare variants and quantitative traits. Genetic Epidemiology, 2011, 35, 226-235.	0.6	11
136	Predictive Models of Choroidal Neovascularization and Geographic Atrophy Incidence Applied to Clinical Trial Design. American Journal of Ophthalmology, 2012, 154, 568-578.e12.	1.7	11
137	Comparison of Statistical Tests for Association between Rare Variants and Binary Traits. PLoS ONE, 2012, 7, e42530.	1.1	11
138	SNP Selection for Association Studies: Maximizing Power across SNP Choice and Study Size. Annals of Human Genetics, 2005, 69, 733-746.	0.3	9
139	Fine-mapping the genetic basis of CRP regulation in African Americans: a Bayesian approach. Human Genetics, 2008, 123, 633-642.	1.8	9
140	Quantification of the Genetic Component of Basal Câ€Reactive Protein Expression in SLE Nuclear Families. Annals of Human Genetics, 2008, 72, 611-620.	0.3	9
141	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.	0.8	9
142	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.	0.4	9
143	Gene-centric association signals for haemostasis and thrombosis traits identified with the HumanCVD BeadChip. Thrombosis and Haemostasis, 2013, 110, 995-1003.	1.8	8
144	A two-trial two-strategy conflict. Journal of Theoretical Biology, 1991, 149, 281-286.	0.8	7

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145	A Resource Allocation Problem. Journal of Theoretical Biology, 1994, 167, 397-405.	0.8	7
146	Generalized estimating equations: A hybrid approach for mean parameters in multivariate regression models. Statistical Modelling, 2002, 2, 163-181.	0.5	7
147	A Likelihood Ratio Approach to Family-based Association Studies with Covariates. Annals of Human Genetics, 2006, 70, 131-139.	0.3	7
148	Searching for Genotype-Phenotype Structure: Using Hierarchical Log-Linear Models in Crohn Disease. American Journal of Human Genetics, 2009, 84, 178-187.	2.6	7
149	How informative is a negative finding in a small pharmacogenetic study?. Pharmacogenomics Journal, 2012, 12, 93-95.	0.9	7
150	Finite-Sample Properties of Family-Based Association Tests. American Journal of Human Genetics, 1999, 64, 910-915.	2.6	6
151	On the Structural Differences Between Markers and Genomic AC Microsatellites. Journal of Molecular Evolution, 2005, 60, 688-693.	0.8	6
152	Family-based tests of association and/or linkage. Annals of Human Genetics, 2001, 65, 407-19.	0.3	6
153	A Bayesian approach to disease gene location using allelic association. Biostatistics, 2003, 4, 399-409.	0.9	5
154	Bayesian semiparametric meta-analysis for genetic association studies. Genetic Epidemiology, 2011, 35, 333-340.	0.6	5
155	Using information from both parents when testing for association between marker and disease loci. , 1998, 15, 193-200.		4
156	Generalization of the extended transmission disequilibrium test to two unlinked disease loci. Genetic Epidemiology, 1999, 17, S661-6.	0.6	4
157	Title is missing!. Molecular Breeding, 2000, 6, 11-24.	1.0	4
158	Marker-Assisted Selection and Introgression. , 2008, , 718-751.		3
159	Multiple Trial Two Strategy Conflicts. Journal of Theoretical Biology, 1994, 169, 113-124.	0.8	2
160	Variance components linkage analysis for adjusted systolic blood pressure in the Framingham Heart Study. BMC Genetics, 2003, 4, S4.	2.7	2
161	Reed Elsevier and the arms trade revisited. Lancet, The, 2007, 369, 987.	6.3	1
162	Application of the Lasso to Expression Quantitative Trait Loci Mapping. Statistical Applications in Genetics and Molecular Biology, 2011, 10, .	0.2	1

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163	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.	1.1	0
164	A variance components factor model for genetic association studies: A Bayesian analysis. Genetic Epidemiology, 2010, 34, 529-536.	0.6	0
165	Fine scale association mapping of disease loci using simplex families. Annals of Human Genetics, 2000, 64, 223-37.	0.3	0