Frank Dudbridge

List of Publications by Year
in descending order

164 papers	27,551 citations	20759 60 h-index	7136 153 g-index
185 all docs	185 docs citations	185 times ranked	34430 citing authors

#	Article	IF	Citations
1	Mendelian randomisation of eosinophils and other cell types in relation to lung function and disease. Thorax, 2023, 78, 496-503.	2.7	6
2	A robust method for collider bias correction in conditional genome-wide association studies. Nature Communications, 2022, 13, 619.	5.8	29
3	The WID-BC-index identifies women with primary poor prognostic breast cancer based on DNA methylation in cervical samples. Nature Communications, 2022, 13, 449.	5.8	21
4	Research Review: How to interpret associations between polygenic scores, environmental risks, and phenotypes. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2022, 63, 1125-1139.	3.1	23
5	Applying Mendelian randomization to appraise causality in relationships between nutrition and cancer. Cancer Causes and Control, 2022, 33, 631-652.	0.8	7
6	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
7	Adjusting for collider bias in genetic association studies using instrumental variable methods. Genetic Epidemiology, 2022, 46, 303-316.	0.6	7
8	Mortality risk comparing walking pace to handgrip strength and a healthy lifestyle: A UK Biobank study. European Journal of Preventive Cardiology, 2021, 28, 704-712.	0.8	25
9	Proportion of Idiopathic Pulmonary Fibrosis Risk Explained by Known Common Genetic Loci in European Populations. American Journal of Respiratory and Critical Care Medicine, 2021, 203, 775-778.	2.5	17
10	Are there causal relationships between attention-deficit/hyperactivity disorder and body mass index? Evidence from multiple genetically informed designs. International Journal of Epidemiology, 2021, 50, 496-509.	0.9	16
11	Epigenome-Wide Association Study of Thyroid Function Traits Identifies Novel Associations of fT3 With KLF9 and DOT1L. Journal of Clinical Endocrinology and Metabolism, 2021, 106, e2191-e2202.	1.8	14
12	Polygenic risk scores in cardiovascular risk prediction: A cohort study and modelling analyses. PLoS Medicine, 2021, 18, e1003498.	3.9	95
13	Clonal architecture in mesothelioma is prognostic and shapes the tumour microenvironment. Nature Communications, 2021, 12, 1751.	5.8	66
14	Identifying high-confidence capture Hi-C interactions using CHiCANE. Nature Protocols, 2021, 16, 2257-2285.	5.5	11
15	Genetic sensitivity analysis: Adjusting for genetic confounding in epidemiological associations. PLoS Genetics, 2021, 17, e1009590.	1.5	30
16	Genetic overlap and causal associations between smoking behaviours and mental health. Scientific Reports, 2021, 11, 14871.	1.6	19
17	Exploiting collider bias to apply two-sample summary data Mendelian randomization methods to one-sample individual level data. PLoS Genetics, 2021, 17, e1009703.	1.5	16
18	Genome-wide analysis of thyroid function in Australian adolescents highlights SERPINA7 and NCOA3. European Journal of Endocrinology, 2021, 185, 743-753.	1.9	5

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19	Robust genetic nurture effects on education: A systematic review and meta-analysis based on 38,654 families across 8 cohorts. American Journal of Human Genetics, 2021, 108, 1780-1791.	2.6	38
20	Polygenic Mendelian Randomization. Cold Spring Harbor Perspectives in Medicine, 2021, 11, a039586.	2.9	33
21	Impact of past obstetric history and cervical excision on preterm birth rate. Acta Obstetricia Et Gynecologica Scandinavica, 2021, 100, 1995-2002.	1.3	0
22	Interaction of Cigarette Smoking and Polygenic Risk Score on Reduced Lung Function. JAMA Network Open, 2021, 4, e2139525.	2.8	22
23	Replication of Newly Identified Genetic Associations Between Abdominal Aortic Aneurysm and SMYD2, LINC00540, PCIF1/MMP9/ZNF335, and ERG. European Journal of Vascular and Endovascular Surgery, 2020, 59, 92-97.	0.8	11
24	Family history of pre-eclampsia and cardiovascular disease as risk factors for pre-eclampsia: the GenPE case-control study. Hypertension in Pregnancy, 2020, 39, 56-63.	0.5	15
25	Association of Factor V Leiden With Subsequent Atherothrombotic Events. Circulation, 2020, 142, 546-555.	1.6	11
26	Chronic obstructive pulmonary disease and related phenotypes: polygenic risk scores in population-based and case-control cohorts. Lancet Respiratory Medicine,the, 2020, 8, 696-708.	5.2	69
27	Genome-wide association study of self-reported walking pace suggests beneficial effects of brisk walking on health and survival. Communications Biology, 2020, 3, 634.	2.0	21
28	Genetic predisposition to hypertension is associated with preeclampsia in European and Central Asian women. Nature Communications, 2020, 11, 5976.	5.8	102
29	Genetic overlap between psychotic experiences in the community across age and with psychiatric disorders. Translational Psychiatry, 2020, 10, 86.	2.4	15
30	Criteria for evaluating risk prediction of multiple outcomes. Statistical Methods in Medical Research, 2020, 29, 3492-3510.	0.7	8
31	Causal relationships between lipid and glycemic levels in an Indian population: A bidirectional Mendelian randomization approach. PLoS ONE, 2020, 15, e0228269.	1.1	8
32	Polygenic risk scores for coronary artery disease and subsequent event risk amongst established cases. Human Molecular Genetics, 2020, 29, 1388-1395.	1.4	23
33	Characterisation of genetic regulatory effects for osteoporosis risk variants in human osteoclasts. Genome Biology, 2020, 21, 80.	3.8	36
34	Title is missing!. , 2020, 15, e0228269.		0
35	Title is missing!. , 2020, 15, e0228269.		0
36	Title is missing!. , 2020, 15, e0228269.		0

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37	Title is missing!. , 2020, 15, e0228269.		0
38	A flexible and parallelizable approach to genomeâ€wide polygenic risk scores. Genetic Epidemiology, 2019, 43, 730-741.	0.6	32
39	Robust methods in Mendelian randomization via penalization of heterogeneous causal estimates. PLoS ONE, 2019, 14, e0222362.	1.1	80
40	Genetic regulatory mechanisms in human osteoclasts suggest a role for the STMP1 and DCSTAMP genes in Pagetâ€™s disease of bone. Scientific Reports, 2019, 9, 1052.	1.6	23
41	Subsequent Event Risk in Individuals With Established Coronary Heart Disease. Circulation Genomic and Precision Medicine, 2019, 12, e002470.	1.6	17
42	Adjustment for index event bias in genome-wide association studies of subsequent events. Nature Communications, 2019, 10, 1561.	5.8	87
43	Multiâ€“Polygenic Score Approach to Identifying Individual Vulnerabilities Associated With the Risk of Exposure to Bullying. JAMA Psychiatry, 2019, 76, 730.	6.0	65
44	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
45	RNA sequencing of identical twins discordant for autism reveals blood-based signatures implicating immune and transcriptional dysregulation. Molecular Autism, 2019, 10, 38.	2.6	14
46	Guidelines for performing Mendelian randomization investigations. Wellcome Open Research, 2019, 4, 186.	0.9	661
47	Guidelines for performing Mendelian randomization investigations. Wellcome Open Research, 2019, 4, 186.	0.9	511
48	Expression Quantitative Trait Locus Study of Bone Mineral Density GWAS Variants in Human Osteoclasts. Journal of Bone and Mineral Research, 2018, 33, 1044-1051.	3.1	43
49	Epigenome-based cancer risk prediction: rationale, opportunities and challenges. Nature Reviews Clinical Oncology, 2018, 15, 292-309.	12.5	129
50	Genomeâ€wide analysis of adolescent psychoticâ€like experiences shows genetic overlap with psychiatric disorders. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2018, 177, 416-425.	1.1	74
51	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. Nature Communications, 2018, 9, 711.	5.8	54
52	Capture Hi-C identifies putative target genes at 33 breast cancer risk loci. Nature Communications, 2018, 9, 1028.	5.8	98
53	Estimation of a significance threshold for epigenomeâ€wide association studies. Genetic Epidemiology, 2018, 42, 20-33.	0.6	133
54	How many cases of disease in a pedigree imply familial disease?. Annals of Human Genetics, 2018, 82, 109-113.	0.3	5

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55	Predictive accuracy of combined genetic and environmental risk scores. Genetic Epidemiology, 2018, 42, 4-19.	0.6	32
56	Association of pre-eclampsia risk with maternal levels of folate, homocysteine and vitamin B12 in Colombia: A case-control study. PLoS ONE, 2018, 13, e0208137.	1.1	27
57	Genomic Risk Prediction of Coronary Artery Disease in 480,000 Adults. Journal of the American College of Cardiology, 2018, 72, 1883-1893.	1.2	557
58	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. American Journal of Human Genetics, 2018, 102, 1185-1194.	2.6	119
59	Are your covariates under control? How normalization can re-introduce covariate effects. European Journal of Human Genetics, 2018, 26, 1194-1201.	1.4	21
60	Using genetic data to strengthen causal inference in observational research. Nature Reviews Genetics, 2018, 19, 566-580.	7.7	298
61	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	13.5	623
62	The Genetic Sphygmomanometer: an argument for routine genome-wide genotyping in the population and a new view on its use to inform clinical practice. Wellcome Open Research, 2018, 3, 138.	0.9	0
63	Causal Associations of Adiposity and Body Fat Distribution With Coronary Heart Disease, Stroke Subtypes, and Type 2 Diabetes Mellitus. Circulation, 2017, 135, 2373-2388.	1.6	304
64	Genome-wide association study meta-analysis for quantitative ultrasound parameters of bone identifies five novel loci for broadband ultrasound attenuation. Human Molecular Genetics, 2017, 26, 2791-2802.	1.4	32
65	Variants in the fetal genome near FLT1 are associated with risk of preeclampsia. Nature Genetics, 2017, 49, 1255-1260.	9.4	205
66	Impact of Selection Bias on Estimation of Subsequent Event Risk. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	28
67	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	9.4	838
68	Exploration of a Polygenic Risk Score for Alcohol Consumption: A Longitudinal Analysis from the ALSPAC Cohort. PLoS ONE, 2016, 11, e0167360.	1.1	22
69	Marginal role for 53 common genetic variants in cardiovascular disease prediction. Heart, 2016, 102, 1640-1647.	1.2	27
70	Mendelian Randomisation study of the influence of eGFR on coronary heart disease. Scientific Reports, 2016, 6, 28514.	1.6	14
71	Combining information on multiple instrumental variables in Mendelian randomization: comparison of allele score and summarized data methods. Statistics in Medicine, 2016, 35, 1880-1906.	0.8	593
72	Polygenic Epidemiology. Genetic Epidemiology, 2016, 40, 268-272.	0.6	160

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73	Re. Epidemiology, 2016, 27, e12.	1.2	6
74	Genome-wide association study using family-based cohorts identifies the WLS and CCDC170/ESR1 loci as associated with bone mineral density. BMC Genomics, 2016, 17, 136.	1.2	44
75	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
76	Commentary: Tobacco consumption and body weight: Mendelian randomization across a range of exposure. International Journal of Epidemiology, 2016, 45, e1-e3.	0.9	7
77	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
78	Cytochrome P450 Allele CYP3A7*1C Associates with Adverse Outcomes in Chronic Lymphocytic Leukemia, Breast, and Lung Cancer. Cancer Research, 2016, 76, 1485-1493.	0.4	28
79	Accuracy of Gene Scores when Pruning Markers by Linkage Disequilibrium. Human Heredity, 2015, 80, 178-186.	0.4	14
80	A genome-wide association study of asthma symptoms in Latin American children. BMC Genetics, 2015, 16, 141.	2.7	24
81	Whole-genome sequence-based analysis of thyroid function. Nature Communications, 2015, 6, 5681.	5.8	75
82	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
83	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
84	Joint Analysis of Psychiatric Disorders Increases Accuracy of Risk Prediction for Schizophrenia, Bipolar Disorder, and Major Depressive Disorder. American Journal of Human Genetics, 2015, 96, 283-294.	2.6	225
85	Re: â€œMultivariable Mendelian Randomization: The Use of Pleiotropic Genetic Variants to Estimate Causal Effectsâ€. American Journal of Epidemiology, 2015, 181, 290-291.	1.6	377
86	A Fast Method that Uses Polygenic Scores to Estimate the Variance Explained by Genome-wide Marker Panels and the Proportion of Variants Affecting a Trait. American Journal of Human Genetics, 2015, 97, 250-259.	2.6	212
87	Mendelian randomization of blood lipids for coronary heart disease. European Heart Journal, 2015, 36, 539-550.	1.0	567
88	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
89	Retrospective analysis of the quality of reports by author-suggested and non-author-suggested reviewers in journals operating on open or single-blind peer review models. BMJ Open, 2015, 5, e008707.	0.8	38
90	Heritability of Individual Psychotic Experiences Captured by Common Genetic Variants in a Community Sample of Adolescents. Behavior Genetics, 2015, 45, 493-502.	1.4	31

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91	New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. International Journal of Epidemiology, 2015, 44, 1706-1721.	0.9	53
92	Sixty-Five Common Genetic Variants and Prediction of Type 2 Diabetes. Diabetes, 2015, 64, 1830-1840.	0.3	91
93	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
94	Candidate gene-environment interactions in breast cancer. BMC Medicine, 2014, 12, 195.	2.3	12
95	Gene-Environment Dependence Creates Spurious Gene-Environment Interaction. American Journal of Human Genetics, 2014, 95, 301-307.	2.6	79
96	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
97	Genetic Prediction of Quantitative Lipid Traits: Comparing Shrinkage Models to Gene Scores. Genetic Epidemiology, 2014, 38, 72-83.	0.6	19
98	Two novel pathway analysis methods based on a hierarchical model. Bioinformatics, 2014, 30, 690-697.	1.8	11
99	Utilising Familyâ€Based Designs for Detecting Rare Variant Disease Associations. Annals of Human Genetics, 2014, 78, 129-140.	0.3	12
100	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	2.6	569
101	Unbiased analysis of potential targets of breast cancer susceptibility loci by Capture Hi-C. Genome Research, 2014, 24, 1854-1868.	2.4	219
102	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	3.0	528
103	Research Review: Polygenic methods and their application to psychiatric traits. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2014, 55, 1068-1087.	3.1	578
104	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. Breast Cancer Research, 2014, 16, R51.	2.2	14
105	Are Genetic Risk Factors for Psychosis Also Associated with Dimension-Specific Psychotic Experiences in Adolescence?. PLoS ONE, 2014, 9, e94398.	1.1	56
106	Association of Common Genetic Variants with Lipid Traits in the Indian Population. PLoS ONE, 2014, 9, e101688.	1.1	31
107	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. Nature Genetics, 2013, 45, 1150-1159.	9.4	1,395
108	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067

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109	Conditional testing of multiple variants associated with bone mineral density in the FLNB gene region suggests that they represent a single association signal. BMC Genetics, 2013, 14, 107.	2.7	8
110	Power and Predictive Accuracy of Polygenic Risk Scores. PLoS Genetics, 2013, 9, e1003348.	1.5	1,238
111	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
112	Candidate genes for obesity-susceptibility show enriched association within a large genome-wide association study for BMI. Human Molecular Genetics, 2012, 21, 4537-4542.	1.4	36
113	Genetic association studies in pre-eclampsia: systematic meta-analyses and field synopsis. International Journal of Epidemiology, 2012, 41, 1764-1775.	0.9	62
114	Estimating Causal Effects of Genetic Risk Variants for Breast Cancer Using Marker Data from Bilateral and Familial Cases. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 262-272.	1.1	6
115	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
116	Genome-Wide Association Study of Clinical Dimensions of Schizophrenia: Polygenic Effect on Disorganized Symptoms. American Journal of Psychiatry, 2012, 169, 1309-1317.	4.0	112
117	9q31.2-rs865686 as a Susceptibility Locus for Estrogen Receptor-Positive Breast Cancer: Evidence from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 1783-1791.	1.1	17
118	Genome-Wide Association Study of Multiplex Schizophrenia Pedigrees. American Journal of Psychiatry, 2012, 169, 963-973.	4.0	61
119	Evaluation of seven common lipid associated loci in a large Indian sib pair study. Lipids in Health and Disease, 2012, 11, 155.	1.2	9
120	Comparison of Methods for Competitive Tests of Pathway Analysis. PLoS ONE, 2012, 7, e41018.	1.1	40
121	A General Framework for Two-Stage Analysis of Genome-wide Association Studies and Its Application to Case-Control Studies. American Journal of Human Genetics, 2012, 90, 760-773.	2.6	25
122	Interpreting Association Signals. , 2011, , 261-276.		0
123	A Flexible Model for Association Analysis in Sibships with Missing Genotype Data. Annals of Human Genetics, 2011, 75, 428-438.	0.3	11
124	Copy Number Variants in Schizophrenia: Confirmation of Five Previous Findings and New Evidence for 3q29 Microdeletions and VIPR2 Duplications. American Journal of Psychiatry, 2011, 168, 302-316.	4.0	398
125	Application of the Optimal Discovery Procedure to Genetic Case-Control Studies: Comparison with p Values and Asymptotic Bayes Factors. Human Heredity, 2011, 71, 37-49.	0.4	1
126	Genetic Variants at Chromosomes 2q35, 5p12, 6q25.1, 10q26.13, and 16q12.1 Influence the Risk of Breast Cancer in Men. PLoS Genetics, 2011, 7, e1002290.	1.5	43

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127	Family-Based Association Studies. Methods in Molecular Biology, 2011, 713, 119-127.	0.4	0
128	Polymorphisms in BDNF (Val66Met) and 5-HTTLPR, morning cortisol and subsequent depression in at-risk adolescents. British Journal of Psychiatry, 2010, 197, 365-371.	1.7	60
129	What role for genetics in the prediction of multiple sclerosis?. Annals of Neurology, 2010, 67, 3-10.	2.8	196
130	Comparison of multimarker logistic regression models, with application to a genomewide scan of schizophrenia. BMC Genetics, 2010, 11, 80.	2.7	7
131	A rare variant of the TYK2 gene is confirmed to be associated with multiple sclerosis. European Journal of Human Genetics, 2010, 18, 502-504.	1.4	60
132	Transcription profiling in human platelets reveals LRRFIP1 as a novel protein regulating platelet function. Blood, 2010, 116, 4646-4656.	0.6	90
133	Unbiased estimation of odds ratios: combining genomewide association scans with replication studies. Genetic Epidemiology, 2009, 33, 406-418.	0.6	56
134	Replication analysis identifies TYK2 as a multiple sclerosis susceptibility factor. European Journal of Human Genetics, 2009, 17, 1309-1313.	1.4	115
135	Common variants on chromosome 6p22.1 are associated with schizophrenia. Nature, 2009, 460, 753-757.	13.7	1,063
136	Common Sequence Variation in FLNB Regulates Bone Structure in Women in the General Population and FLNB mRNA Expression in Osteoblasts In Vitro. Journal of Bone and Mineral Research, 2009, 24, 1989-1997.	3.1	21
137	Further genetic evidence suggesting a role for the RhoGTPase-RhoGEF pathway in osteoporosis. Bone, 2009, 45, 387-391.	1.4	22
138	Functional genomics in zebrafish permits rapid characterization of novel platelet membrane proteins. Blood, 2009, 113, 4754-4762.	0.6	69
139	A HaemAtlas: characterizing gene expression in differentiated human blood cells. Blood, 2009, 113, e1-e9.	0.6	215
140	A functional genomics approach reveals novel quantitative trait loci associated with platelet signaling pathways. Blood, 2009, 114, 1405-1416.	0.6	131
141	Association between Protective and Deleterious HLA Alleles with Multiple Sclerosis in Central East Sardinia. PLoS ONE, 2009, 4, e6526.	1.1	12
142	Estimation of significance thresholds for genomewide association scans. Genetic Epidemiology, 2008, 32, 227-234.	0.6	618
143	Maximizing association statistics over genetic models. Genetic Epidemiology, 2008, 32, 246-254.	0.6	101
144	Identification of a Role for the ARHGEF3 Gene in Postmenopausal Osteoporosis. American Journal of Human Genetics, 2008, 82, 1262-1269.	2.6	38

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145	Likelihood-Based Association Analysis for Nuclear Families and Unrelated Subjects with Missing Genotype Data. Human Heredity, 2008, 66, 87-98.	0.4	570
146	Comparative gene expression profiling of in vitro differentiated megakaryocytes and erythroblasts identifies novel activatory and inhibitory platelet membrane proteins. Blood, 2007, 109, 3260-3269.	0.6	153
147	A Note on Permutation Tests in Multistage Association Scans. American Journal of Human Genetics, 2006, 78, 1094-1095.	2.6	26
148	Detecting multiple associations in genome-wide studies. Human Genomics, 2006, 2, 310.	1.4	39
149	Linkage and potential association of obesity-related phenotypes with two genes on chromosome 12q24 in a female dizygous twin cohort. European Journal of Human Genetics, 2006, 14, 340-348.	1.4	59
150	Evaluation of Nyholtâ€™s Procedure for Multiple Testing Correction. Human Heredity, 2005, 60, 19-25.	0.4	45
151	Pelican: pedigree editor for linkage computer analysis. Bioinformatics, 2004, 20, 2327-2328.	1.8	23
152	Efficient Computation of Significance Levels for Multiple Associations in Large Studies of Correlated Data, Including Genomewide Association Studies. American Journal of Human Genetics, 2004, 75, 424-435.	2.6	154
153	Linkage and association mapping of the LRP5 locus on chromosomeÂ11q13 in typeÂ1 diabetes. Human Genetics, 2003, 113, 99-105.	1.8	44
154	Pedigree disequilibrium tests for multilocus haplotypes. Genetic Epidemiology, 2003, 25, 115-121.	0.6	1,094
155	Rank truncated product ofP-values, with application to genomewide association scans. Genetic Epidemiology, 2003, 25, 360-366.	0.6	113
156	A survey of current software for linkage analysis. Human Genomics, 2003, 1, 63.	1.4	23
157	Genes of the Class II and Class III Major Histocompatibility Complex Are Associated with Typhoid Fever in Vietnam. Journal of Infectious Diseases, 2001, 183, 261-268.	1.9	95
158	Linkage Analysis of Genetic Analysis Workshop 12 Simulated Data Based on Affected Individuals Only. Genetic Epidemiology, 2001, 21, S510-5.	0.6	0
159	Haplotype tagging for the identification of common disease genes. Nature Genetics, 2001, 29, 233-237.	9.4	1,118
160	Typhoid Fever and Genetic Polymorphisms at the Natural Resistanceâ€“Associated Macrophage Protein 1. Journal of Infectious Diseases, 2001, 183, 1156-1160.	1.9	39
161	Unbiased Application of the Transmission/Disequilibrium Test to Multilocus Haplotypes. American Journal of Human Genetics, 2000, 66, 2009-2012.	2.6	109
162	Editorial: Fractal Image Encoding and Analysis. Fractals, 1997, 05, 1-2.	1.8	0

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163	Rendering algorithms for deterministic fractals. IEEE Computer Graphics and Applications, 1995, 15, 32-41.	1.0	33
164	Fractal block coding of images. Electronics Letters, 1992, 28, 1053-1055.	0.5	65