Frank Dudbridge

List of Publications by Year
in descending order

164 papers	27,551 citations	20797 60 h-index	7152 153 g-index
185 all docs	185 docs citations	185 times ranked	34430 citing authors

#	Article	IF	Citations
1	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067
2	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. Nature Genetics, 2013, 45, 1150-1159.	9.4	1,395
3	Power and Predictive Accuracy of Polygenic Risk Scores. PLoS Genetics, 2013, 9, e1003348.	1.5	1,238
4	Haplotype tagging for the identification of common disease genes. Nature Genetics, 2001, 29, 233-237.	9.4	1,118
5	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
6	Pedigree disequilibrium tests for multilocus haplotypes. Genetic Epidemiology, 2003, 25, 115-121.	0.6	1,094
7	Common variants on chromosome 6p22.1 are associated with schizophrenia. Nature, 2009, 460, 753-757.	13.7	1,063
8	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
9	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
10	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
11	Guidelines for performing Mendelian randomization investigations. Wellcome Open Research, 2019, 4, 186.	0.9	661
12	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	13.5	623
13	Estimation of significance thresholds for genomewide association scans. Genetic Epidemiology, 2008, 32, 227-234.	0.6	618
14	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
15	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
16	Likelihood-Based Association Analysis for Nuclear Families and Unrelated Subjects with Missing Genotype Data. Human Heredity, 2008, 66, 87-98.	0.4	570
17	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
18	Mendelian randomization of blood lipids for coronary heart disease. European Heart Journal, 2015, 36, 539-550.	1.0	567

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19	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
20	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
21	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	3.0	528
22	Guidelines for performing Mendelian randomization investigations. Wellcome Open Research, 2019, 4, 186.	0.9	511
23	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
24	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
25	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
26	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
27	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
28	Using genetic data to strengthen causal inference in observational research. Nature Reviews Genetics, 2018, 19, 566-580.	7.7	298
29	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
30	Unbiased analysis of potential targets of breast cancer susceptibility loci by Capture Hi-C. Genome Research, 2014, 24, 1854-1868.	2.4	219
31	A HaemAtlas: characterizing gene expression in differentiated human blood cells. Blood, 2009, 113, e1-e9.	0.6	215
32	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
33	Variants in the fetal genome near FLT1 are associated with risk of preeclampsia. Nature Genetics, 2017, 49, 1255-1260.	9.4	205
34	What role for genetics in the prediction of multiple sclerosis?. Annals of Neurology, 2010, 67, 3-10.	2.8	196
35	Polygenic Epidemiology. Genetic Epidemiology, 2016, 40, 268-272.	0.6	160
36	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

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37	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
38	Estimation of a significance threshold for epigenomeâ€wide association studies. Genetic Epidemiology, 2018, 42, 20-33.	0.6	133
39	A functional genomics approach reveals novel quantitative trait loci associated with platelet signaling pathways. Blood, 2009, 114, 1405-1416.	0.6	131
40	Epigenome-based cancer risk prediction: rationale, opportunities and challenges. Nature Reviews Clinical Oncology, 2018, 15, 292-309.	12.5	129
41	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
42	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
43	Replication analysis identifies TYK2 as a multiple sclerosis susceptibility factor. European Journal of Human Genetics, 2009, 17, 1309-1313.	1.4	115
44	Rank truncated product ofP-values, with application to genomewide association scans. Genetic Epidemiology, 2003, 25, 360-366.	0.6	113
45	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
46	Unbiased Application of the Transmission/Disequilibrium Test to Multilocus Haplotypes. American Journal of Human Genetics, 2000, 66, 2009-2012.	2.6	109
47	Genetic predisposition to hypertension is associated with preeclampsia in European and Central Asian women. Nature Communications, 2020, 11, 5976.	5.8	102
48	Maximizing association statistics over genetic models. Genetic Epidemiology, 2008, 32, 246-254.	0.6	101
49	Capture Hi-C identifies putative target genes at 33 breast cancer risk loci. Nature Communications, 2018, 9, 1028.	5.8	98
50	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
51	Polygenic risk scores in cardiovascular risk prediction: A cohort study and modelling analyses. PLoS Medicine, 2021, 18, e1003498.	3.9	95
52	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
53	Sixty-Five Common Genetic Variants and Prediction of Type 2 Diabetes. Diabetes, 2015, 64, 1830-1840.	0.3	91
54	Transcription profiling in human platelets reveals LRRFIP1 as a novel protein regulating platelet function. Blood, 2010, 116, 4646-4656.	0.6	90

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55	Adjustment for index event bias in genome-wide association studies of subsequent events. Nature Communications, 2019, 10, 1561.	5.8	87
56	Robust methods in Mendelian randomization via penalization of heterogeneous causal estimates. PLoS ONE, 2019, 14, e0222362.	1.1	80
57	Gene-Environment Dependence Creates Spurious Gene-Environment Interaction. American Journal of Human Genetics, 2014, 95, 301-307.	2.6	79
58	Whole-genome sequence-based analysis of thyroid function. Nature Communications, 2015, 6, 5681.	5.8	75
59	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
60	Functional genomics in zebrafish permits rapid characterization of novel platelet membrane proteins. Blood, 2009, 113, 4754-4762.	0.6	69
61	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
62	Clonal architecture in mesothelioma is prognostic and shapes the tumour microenvironment. Nature Communications, 2021, 12, 1751.	5.8	66
63	Fractal block coding of images. Electronics Letters, 1992, 28, 1053-1055.	0.5	65
64	Multiâ€“Polygenic Score Approach to Identifying Individual Vulnerabilities Associated With the Risk of Exposure to Bullying. JAMA Psychiatry, 2019, 76, 730.	6.0	65
65	Genetic association studies in pre-eclampsia: systematic meta-analyses and field synopsis. International Journal of Epidemiology, 2012, 41, 1764-1775.	0.9	62
66	Genome-Wide Association Study of Multiplex Schizophrenia Pedigrees. American Journal of Psychiatry, 2012, 169, 963-973.	4.0	61
67	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
68	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
69	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
70	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
71	Unbiased estimation of odds ratios: combining genomewide association scans with replication studies. Genetic Epidemiology, 2009, 33, 406-418.	0.6	56
72	Are Genetic Risk Factors for Psychosis Also Associated with Dimension-Specific Psychotic Experiences in Adolescence?. PLoS ONE, 2014, 9, e94398.	1.1	56

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73	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. Nature Communications, 2018, 9, 711.	5.8	54
74	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
75	Evaluation of Nyholtâ€™s Procedure for Multiple Testing Correction. Human Heredity, 2005, 60, 19-25.	0.4	45
76	Linkage and association mapping of the LRP5 locus on chromosomeÂ11q13 in typeÂ1 diabetes. Human Genetics, 2003, 113, 99-105.	1.8	44
77	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
78	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
79	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
80	Comparison of Methods for Competitive Tests of Pathway Analysis. PLoS ONE, 2012, 7, e41018.	1.1	40
81	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
82	Typhoid Fever and Genetic Polymorphisms at the Natural Resistanceâ€“Associated Macrophage Protein 1. Journal of Infectious Diseases, 2001, 183, 1156-1160.	1.9	39
83	Detecting multiple associations in genome-wide studies. Human Genomics, 2006, 2, 310.	1.4	39
84	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
85	Identification of a Role for the ARHGEF3 Gene in Postmenopausal Osteoporosis. American Journal of Human Genetics, 2008, 82, 1262-1269.	2.6	38
86	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
87	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
88	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
89	Characterisation of genetic regulatory effects for osteoporosis risk variants in human osteoclasts. Genome Biology, 2020, 21, 80.	3.8	36
90	Rendering algorithms for deterministic fractals. IEEE Computer Graphics and Applications, 1995, 15, 32-41.	1.0	33

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91	Polygenic Mendelian Randomization. Cold Spring Harbor Perspectives in Medicine, 2021, 11, a039586.	2.9	33
92	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
93	Predictive accuracy of combined genetic and environmental risk scores. Genetic Epidemiology, 2018, 42, 4-19.	0.6	32
94	A flexible and parallelizable approach to genomeâ€wide polygenic risk scores. Genetic Epidemiology, 2019, 43, 730-741.	0.6	32
95	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
96	Association of Common Genetic Variants with Lipid Traits in the Indian Population. PLoS ONE, 2014, 9, e101688.	1.1	31
97	Genetic sensitivity analysis: Adjusting for genetic confounding in epidemiological associations. PLoS Genetics, 2021, 17, e1009590.	1.5	30
98	A robust method for collider bias correction in conditional genome-wide association studies. Nature Communications, 2022, 13, 619.	5.8	29
99	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
100	Impact of Selection Bias on Estimation of Subsequent Event Risk. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	28
101	Marginal role for 53 common genetic variants in cardiovascular disease prediction. Heart, 2016, 102, 1640-1647.	1.2	27
102	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
103	A Note on Permutation Tests in Multistage Association Scans. American Journal of Human Genetics, 2006, 78, 1094-1095.	2.6	26
104	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
105	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
106	A genome-wide association study of asthma symptoms in Latin American children. BMC Genetics, 2015, 16, 141.	2.7	24
107	A survey of current software for linkage analysis. Human Genomics, 2003, 1, 63.	1.4	23
108	Pelican: pedigree editor for linkage computer analysis. Bioinformatics, 2004, 20, 2327-2328.	1.8	23

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109	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
110	Polygenic risk scores for coronary artery disease and subsequent event risk amongst established cases. Human Molecular Genetics, 2020, 29, 1388-1395.	1.4	23
111	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
112	Further genetic evidence suggesting a role for the RhoGTPase-RhoGEF pathway in osteoporosis. Bone, 2009, 45, 387-391.	1.4	22
113	Exploration of a Polygenic Risk Score for Alcohol Consumption: A Longitudinal Analysis from the ALSPAC Cohort. PLoS ONE, 2016, 11, e0167360.	1.1	22
114	Interaction of Cigarette Smoking and Polygenic Risk Score on Reduced Lung Function. JAMA Network Open, 2021, 4, e2139525.	2.8	22
115	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
116	Are your covariates under control? How normalization can re-introduce covariate effects. European Journal of Human Genetics, 2018, 26, 1194-1201.	1.4	21
117	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
118	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
119	Genetic Prediction of Quantitative Lipid Traits: Comparing Shrinkage Models to Gene Scores. Genetic Epidemiology, 2014, 38, 72-83.	0.6	19
120	Genetic overlap and causal associations between smoking behaviours and mental health. Scientific Reports, 2021, 11, 14871.	1.6	19
121	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
122	Subsequent Event Risk in Individuals With Established Coronary Heart Disease. Circulation Genomic and Precision Medicine, 2019, 12, e002470.	1.6	17
123	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
124	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
125	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
126	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

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127	Genetic overlap between psychotic experiences in the community across age and with psychiatric disorders. Translational Psychiatry, 2020, 10, 86.	2.4	15
128	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
129	Accuracy of Gene Scores when Pruning Markers by Linkage Disequilibrium. Human Heredity, 2015, 80, 178-186.	0.4	14
130	Mendelian Randomisation study of the influence of eGFR on coronary heart disease. Scientific Reports, 2016, 6, 28514.	1.6	14
131	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
132	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
133	Candidate gene-environment interactions in breast cancer. BMC Medicine, 2014, 12, 195.	2.3	12
134	Utilising Familyâ€Based Designs for Detecting Rare Variant Disease Associations. Annals of Human Genetics, 2014, 78, 129-140.	0.3	12
135	Association between Protective and Deleterious HLA Alleles with Multiple Sclerosis in Central East Sardinia. PLoS ONE, 2009, 4, e6526.	1.1	12
136	A Flexible Model for Association Analysis in Sibships with Missing Genotype Data. Annals of Human Genetics, 2011, 75, 428-438.	0.3	11
137	Two novel pathway analysis methods based on a hierarchical model. Bioinformatics, 2014, 30, 690-697.	1.8	11
138	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
139	Association of Factor V Leiden With Subsequent Atherothrombotic Events. Circulation, 2020, 142, 546-555.	1.6	11
140	Identifying high-confidence capture Hi-C interactions using CHiCANE. Nature Protocols, 2021, 16, 2257-2285.	5.5	11
141	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
142	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
143	Criteria for evaluating risk prediction of multiple outcomes. Statistical Methods in Medical Research, 2020, 29, 3492-3510.	0.7	8
144	Causal relationships between lipid and glycemic levels in an Indian population: A bidirectional Mendelian randomization approach. PLoS ONE, 2020, 15, e0228269.	1.1	8

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145	Comparison of multimarker logistic regression models, with application to a genomewide scan of schizophrenia. BMC Genetics, 2010, 11, 80.	2.7	7
146	Commentary: Tobacco consumption and body weight: Mendelian randomization across a range of exposure. International Journal of Epidemiology, 2016, 45, e1-e3.	0.9	7
147	Applying Mendelian randomization to appraise causality in relationships between nutrition and cancer. Cancer Causes and Control, 2022, 33, 631-652.	0.8	7
148	Adjusting for collider bias in genetic association studies using instrumental variable methods. Genetic Epidemiology, 2022, 46, 303-316.	0.6	7
149	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
150	Re. Epidemiology, 2016, 27, e12.	1.2	6
151	Mendelian randomisation of eosinophils and other cell types in relation to lung function and disease. Thorax, 2023, 78, 496-503.	2.7	6
152	How many cases of disease in a pedigree imply familial disease?. Annals of Human Genetics, 2018, 82, 109-113.	0.3	5
153	Genome-wide analysis of thyroid function in Australian adolescents highlights SERPINA7 and NCOA3. European Journal of Endocrinology, 2021, 185, 743-753.	1.9	5
154	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
155	Editorial: Fractal Image Encoding and Analysis. Fractals, 1997, 05, 1-2.	1.8	0
156	Linkage Analysis of Genetic Analysis Workshop 12 Simulated Data Based on Affected Individuals Only. Genetic Epidemiology, 2001, 21, S510-5.	0.6	0
157	Interpreting Association Signals. , 2011, , 261-276.		0
158	Impact of past obstetric history and cervical excision on preterm birth rate. Acta Obstetricia Et Gynecologica Scandinavica, 2021, 100, 1995-2002.	1.3	0
159	Family-Based Association Studies. Methods in Molecular Biology, 2011, 713, 119-127.	0.4	0
160	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
161	Title is missing!. , 2020, 15, e0228269.		0
162	Title is missing!. , 2020, 15, e0228269.		0

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163	Title is missing!. , 2020, 15, e0228269.		0
164	Title is missing!. , 2020, 15, e0228269.		0