

Martin Farrall

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

72
papers

17,570
citations

41
h-index

76
g-index

76
ext. papers

21,895
ext. citations

17.2
avg, IF

5.04
L-index

#	Paper	IF	Citations
72	Robust estimates of heritable coronary disease risk in individuals with type 2 diabetes. <i>Genetic Epidemiology</i> , 2021 ,	2.6	1
71	Data-driven modelling of mutational hotspots and in silico predictors in hypertrophic cardiomyopathy. <i>Journal of Medical Genetics</i> , 2021 , 58, 556-564	5.8	0
70	Heritability and family-based GWAS analyses of the N-acyl ethanolamine and ceramide plasma lipidome. <i>Human Molecular Genetics</i> , 2021 , 30, 500-513	5.6	4
69	Common genetic variants and modifiable risk factors underpin hypertrophic cardiomyopathy susceptibility and expressivity. <i>Nature Genetics</i> , 2021 , 53, 135-142	36.3	33
68	Reevaluation of the South Asian Intronic Deletion in Hypertrophic Cardiomyopathy. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, e002783	5.2	14
67	Identifying small-effect genetic associations overlooked by the conventional fixed-effect model in a large-scale meta-analysis of coronary artery disease. <i>Bioinformatics</i> , 2020 , 36, 552-557	7.2	
66	Heritability of haemodynamics in the ascending aorta. <i>Scientific Reports</i> , 2020 , 10, 14356	4.9	2
65	Marked variation in heritability estimates of left ventricular mass depending on modality of measurement. <i>Scientific Reports</i> , 2019 , 9, 13556	4.9	1
64	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019 , 188, 1033-1054	3.8	39
63	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. <i>Human Molecular Genetics</i> , 2019 , 28, 2615-2633	5.6	14
62	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019 , 51, 636-648	36.3	59
61	Manhattan++: displaying genome-wide association summary statistics with multiple annotation layers. <i>BMC Bioinformatics</i> , 2019 , 20, 610	3.6	3
60	Analysis of 51 proposed hypertrophic cardiomyopathy genes from genome sequencing data in sarcomere negative cases has negligible diagnostic yield. <i>Genetics in Medicine</i> , 2019 , 21, 1576-1584	8.1	25
59	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018 , 102, 375-400	11	59
58	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. <i>Nature Genetics</i> , 2018 , 50, 42-53	36.3	246
57	Lack of genetic support for shared aetiology of Coronary Artery Disease and Late-onset Alzheimer's disease. <i>Scientific Reports</i> , 2018 , 8, 7102	4.9	5
56	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018 , 13, e0198166	3.7	31

55	Differential Gene Expression in Macrophages From Human Atherosclerotic Plaques Shows Convergence on Pathways Implicated by Genome-Wide Association Study Risk Variants. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2018 , 38, 2718-2730	9.4	14
54	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018 , 50, 1412-1425	36.3	386
53	Plasma cytokines and risk of coronary heart disease in the PROCARDIS study. <i>Open Heart</i> , 2018 , 5, e000807	15	
52	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , 2017 , 49, 403-415	36.3	313
51	Association of Rare and Common Variation in the Lipoprotein Lipase Gene With Coronary Artery Disease. <i>JAMA - Journal of the American Medical Association</i> , 2017 , 317, 937-946	27.4	109
50	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2017 , 69, 823-836	15.1	146
49	A mouse-to-man candidate gene study identifies association of chronic otitis media with the loci TGIF1 and FBXO11. <i>Scientific Reports</i> , 2017 , 7, 12496	4.9	12
48	Vitamin D levels and susceptibility to asthma, elevated immunoglobulin E levels, and atopic dermatitis: A Mendelian randomization study. <i>PLoS Medicine</i> , 2017 , 14, e1002294	11.6	47
47	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. <i>BioData Mining</i> , 2017 , 10, 25	4.3	5
46	Association analyses based on false discovery rate implicate new loci for coronary artery disease. <i>Nature Genetics</i> , 2017 , 49, 1385-1391	36.3	361
45	Reassessment of Mendelian gene pathogenicity using 7,855 cardiomyopathy cases and 60,706 reference samples. <i>Genetics in Medicine</i> , 2017 , 19, 192-203	8.1	386
44	Identifying systematic heterogeneity patterns in genetic association meta-analysis studies. <i>PLoS Genetics</i> , 2017 , 13, e1006755	6	12
43	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016 , 7, 13357	17.4	46
42	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016 , 48, 1171-1184	36.3	251
41	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. <i>Scientific Reports</i> , 2016 , 6, 35278	4.9	18
40	Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. <i>International Journal of Epidemiology</i> , 2016 , 45, 1927-1937	7.8	65
39	Phenotypic Characterization of Genetically Lowered Human Lipoprotein(a) Levels. <i>Journal of the American College of Cardiology</i> , 2016 , 68, 2761-2772	15.1	127
38	Diagnostic Yield and Clinical Utility of Sequencing Familial Hypercholesterolemia Genes in Patients With Severe Hypercholesterolemia. <i>Journal of the American College of Cardiology</i> , 2016 , 67, 2578-89	15.1	458

37	Mendelian randomization of blood lipids for coronary heart disease. <i>European Heart Journal</i> , 2015 , 36, 539-50	9.5	417
36	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , 2015 , 47, 1121-1130	36.3	1290
35	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. <i>Nature</i> , 2015 , 518, 102-6	50.4	463
34	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015 , 11, e1005378	6	220
33	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015 , 518, 187-196	50.4	920
32	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015 , 518, 197-206	50.4	2687
31	Association of low-frequency and rare coding-sequence variants with blood lipids and coronary heart disease in 56,000 whites and blacks. <i>American Journal of Human Genetics</i> , 2014 , 94, 223-32	11	233
30	A common LPA null allele associates with lower lipoprotein(a) levels and coronary artery disease risk. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2014 , 34, 2095-9	9.4	33
29	Gene-age interactions in blood pressure regulation: a large-scale investigation with the CHARGE, Global BPgen, and ICBP Consortia. <i>American Journal of Human Genetics</i> , 2014 , 95, 24-38	11	80
28	Global genetic architecture of an erythroid quantitative trait locus, HMIP-2. <i>Annals of Human Genetics</i> , 2014 , 78, 434-51	2.2	18
27	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014 , 46, 1173-86	36.3	1339
26	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. <i>BMJ, The</i> , 2014 , 349, g4164	5.9	406
25	Meta-analysis of gene-level tests for rare variant association. <i>Nature Genetics</i> , 2014 , 46, 200-4	36.3	142
24	Novel childhood asthma genes interact with in utero and early-life tobacco smoke exposure. <i>Journal of Allergy and Clinical Immunology</i> , 2014 , 133, 885-8	11.5	36
23	Distribution and medical impact of loss-of-function variants in the Finnish founder population. <i>PLoS Genetics</i> , 2014 , 10, e1004494	6	243
22	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. <i>American Journal of Human Genetics</i> , 2014 , 94, 349-60	11	131
21	Secretory phospholipase A(2)-IIA and cardiovascular disease: a mendelian randomization study. <i>Journal of the American College of Cardiology</i> , 2013 , 62, 1966-1976	15.1	91
20	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. <i>Nature</i> , 2010 , 464, 713-20	50.4	639

19	A large-scale, consortium-based genomewide association study of asthma. <i>New England Journal of Medicine</i> , 2010 , 363, 1211-1221	59.2	1431
18	Susceptibility to coronary artery disease and diabetes is encoded by distinct, tightly linked SNPs in the ANRIL locus on chromosome 9p. <i>Human Molecular Genetics</i> , 2008 , 17, 806-14	5.6	420
17	Genome-wide mapping of susceptibility to coronary artery disease identifies a novel replicated locus on chromosome 17. <i>PLoS Genetics</i> , 2006 , 2, e72	6	60
16	Genetic susceptibility to coronary artery disease: from promise to progress. <i>Nature Reviews Genetics</i> , 2006 , 7, 163-73	30.1	150
15	Genotype at the -174G/C polymorphism of the interleukin-6 gene is associated with common carotid artery intimal-medial thickness: family study and meta-analysis. <i>Stroke</i> , 2005 , 36, 2215-9	6.7	36
14	Interpreting gene-association studies. <i>Human Molecular Genetics</i> , 2005 , 14, 2489	5.6	
13	Gearing up for genome-wide gene-association studies. <i>Human Molecular Genetics</i> , 2005 , 14 Spec No. 2, R157-62	5.6	36
12	Quantitative genetic variation: a post-modern view. <i>Human Molecular Genetics</i> , 2004 , 13 Spec No 1, R1-7	5.6	68
11	A candidate gene study of F cell levels in sibling pairs using a joint linkage and association analysis. <i>GeneScreen</i> , 2000 , 1, 9-14		31
10	Fine-mapping of an ancestral recombination breakpoint in DCP1. <i>Nature Genetics</i> , 1999 , 23, 270-1	36.3	40
9	Absence of linkage of the epithelial sodium channel to hypertension in black Caribbeans. <i>American Journal of Hypertension</i> , 1998 , 11, 942-5	2.3	16
8	Measured haplotype analysis of the angiotensin-I converting enzyme gene. <i>Human Molecular Genetics</i> , 1998 , 7, 1745-51	5.6	177
7	Affected sibpair linkage tests for multiple linked susceptibility genes. <i>Genetic Epidemiology</i> , 1997 , 14, 103-15	2.6	34
6	A genome-wide search for human type 1 diabetes susceptibility genes. <i>Nature</i> , 1994 , 371, 130-6	50.4	1175
5	Mapping of mutation causing Friedreich's ataxia to human chromosome 9. <i>Nature</i> , 1988 , 334, 248-50	50.4	297
4	Linkage of an X-chromosome cleft palate gene. <i>Nature</i> , 1987 , 326, 91-2	50.4	94
3	A candidate for the cystic fibrosis locus isolated by selection for methylation-free islands. <i>Nature</i> , 1987 , 326, 840-5	50.4	341
2	Localization of cystic fibrosis locus to human chromosome 7cen-q22. <i>Nature</i> , 1985 , 318, 384-5	50.4	446

1 Reassessment of Mendelian gene pathogenicity using 7,855 cardiomyopathy cases and 60,706 reference samples

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