

# Martin Farrall

## List of Publications by Year in descending order

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Version: 2024-02-01

73  
papers

24,460  
citations

53660

45  
h-index

85405

71  
g-index

76  
all docs

76  
docs citations

76  
times ranked

32608  
citing authors

#	ARTICLE	IF	CITATIONS
1	Robust estimates of heritable coronary disease risk in individuals with type 2 diabetes. <i>Genetic Epidemiology</i> , 2022, 46, 51-62.	0.6	5
2	Data-driven modelling of mutational hotspots and in silico predictors in hypertrophic cardiomyopathy. <i>Journal of Medical Genetics</i> , 2021, 58, 556-564.	1.5	2
3	Heritability and family-based GWAS analyses of the N-acyl ethanolamine and ceramide plasma lipidome. <i>Human Molecular Genetics</i> , 2021, 30, 500-513.	1.4	13
4	Common genetic variants and modifiable risk factors underpin hypertrophic cardiomyopathy susceptibility and expressivity. <i>Nature Genetics</i> , 2021, 53, 135-142.	9.4	165
5	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.	1.8	2
6	Heritability of haemodynamics in the ascending aorta. <i>Scientific Reports</i> , 2020, 10, 14356.	1.6	5
7	Reevaluation of the South Asian MYBPC3 <sup>rs25bp</sup> Intronic Deletion in Hypertrophic Cardiomyopathy. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002783.	1.6	31
8	Marked variation in heritability estimates of left ventricular mass depending on modality of measurement. <i>Scientific Reports</i> , 2019, 9, 13556.	1.6	3
9	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019, 188, 1033-1054.	1.6	85
10	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.	1.4	31
11	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.	9.4	112
12	Manhattan++: displaying genome-wide association summary statistics with multiple annotation layers. <i>BMC Bioinformatics</i> , 2019, 20, 610.	1.2	6
13	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.	1.1	44
14	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.	2.6	123
15	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. <i>Nature Genetics</i> , 2018, 50, 42-53.	9.4	426
16	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.	1.1	20
17	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	9.4	924
18	Plasma cytokines and risk of coronary heart disease in the PROCARDIS study. <i>Open Heart</i> , 2018, 5, e000807.	0.9	24

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19	Lack of genetic support for shared aetiology of Coronary Artery Disease and Late-onset Alzheimer's disease. <i>Scientific Reports</i> , 2018, 8, 7102.	1.6	9
20	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.	1.1	94
21	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , 2017, 49, 403-415.	9.4	492
22	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.	3.8	148
23	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.	1.2	214
24	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.	1.6	21
25	Association analyses based on false discovery rate implicate new loci for coronary artery disease. <i>Nature Genetics</i> , 2017, 49, 1385-1391.	9.4	571
26	Reassessment of Mendelian gene pathogenicity using 7,855 cardiomyopathy cases and 60,706 reference samples. <i>Genetics in Medicine</i> , 2017, 19, 192-203.	1.1	585
27	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.	3.9	78
28	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. <i>BioData Mining</i> , 2017, 10, 25.	2.2	7
29	Identifying systematic heterogeneity patterns in genetic association meta-analysis studies. <i>PLoS Genetics</i> , 2017, 13, e1006755.	1.5	20
30	Phenotypic Characterization of Genetically Lowered Human Lipoprotein(a) Levels. <i>Journal of the American College of Cardiology</i> , 2016, 68, 2761-2772.	1.2	186
31	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, 2578-2589.	1.2	723
32	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, 13357.	5.8	74
33	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.	9.4	362
34	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. <i>Scientific Reports</i> , 2016, 6, 35278.	1.6	25
35	Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. <i>International Journal of Epidemiology</i> , 2016, 45, 1927-1937.	0.9	94
36	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.	1.5	331

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37	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	13.7	1,328
38	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
39	Mendelian randomization of blood lipids for coronary heart disease. <i>European Heart Journal</i> , 2015, 36, 539-550.	1.0	567
40	A comprehensive 1000 Genomes-based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , 2015, 47, 1121-1130.	9.4	2,054
41	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. <i>Nature</i> , 2015, 518, 102-106.	13.7	581
42	Cardiovascular Twist to the Rapidly Evolving Apolipoprotein L1 Story. <i>Circulation Research</i> , 2014, 114, 746-747.	2.0	6
43	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. <i>PLoS Genetics</i> , 2014, 10, e1004494.	1.5	351
44	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, 349-360.	2.6	158
45	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, 223-232.	2.6	287
46	A Common <i>LPA</i> Null Allele Associates With Lower Lipoprotein(a) Levels and Coronary Artery Disease Risk. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2014, 34, 2095-2099.	1.1	45
47	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.	2.6	109
48	Global Genetic Architecture of an Erythroid Quantitative Trait Locus, <i>HMIP-2</i> . <i>Annals of Human Genetics</i> , 2014, 78, 434-451.	0.3	24
49	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	9.4	1,818
50	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. <i>BMJ</i> , 2014, 349, g4164-g4164.	3.0	528
51	Meta-analysis of gene-level tests for rare variant association. <i>Nature Genetics</i> , 2014, 46, 200-204.	9.4	178
52	Novel childhood asthma genes interact with in utero and early-life tobacco smoke exposure. <i>Journal of Allergy and Clinical Immunology</i> , 2014, 133, 885-888.	1.5	47
53	Abstract 534: A Common Null Allele of LPA is Associated With Lp(a) Levels and Coronary Artery Disease Risk. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2014, 34, .	1.1	0
54	Secretory Phospholipase A2-IIA and Cardiovascular Disease. <i>Journal of the American College of Cardiology</i> , 2013, 62, 1966-1976.	1.2	115

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55	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. <i>Nature</i> , 2010, 464, 713-720.	13.7	737
56	A Large-Scale, Consortium-Based Genomewide Association Study of Asthma. <i>New England Journal of Medicine</i> , 2010, 363, 1211-1221.	13.9	1,762
57	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, 806-814.	1.4	472
58	Genetic susceptibility to coronary artery disease: from promise to progress. <i>Nature Reviews Genetics</i> , 2006, 7, 163-173.	7.7	176
59	Genome-Wide Mapping of Susceptibility to Coronary Artery Disease Identifies a Novel Replicated Locus on Chromosome 17. <i>PLoS Genetics</i> , 2006, 2, e72.	1.5	69
60	Interpreting gene-association studies. <i>Human Molecular Genetics</i> , 2005, 14, 2489-2489.	1.4	0
61	Gearing up for genome-wide gene-association studies. <i>Human Molecular Genetics</i> , 2005, 14, R157-R162.	1.4	43
62	Genotype at the $\alpha^{174G/C}$ Polymorphism of the Interleukin-6 Gene Is Associated With Common Carotid Artery Intimal-Medial Thickness. <i>Stroke</i> , 2005, 36, 2215-2219.	1.0	40
63	Quantitative genetic variation: a post-modern view. <i>Human Molecular Genetics</i> , 2004, 13, 1R-7.	1.4	73
64	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.	0.7	35
65	Fine-mapping of an ancestral recombination breakpoint in DCP1. <i>Nature Genetics</i> , 1999, 23, 270-271.	9.4	42
66	Absence of linkage of the epithelial sodium channel to hypertension in black Caribbeans. <i>American Journal of Hypertension</i> , 1998, 11, 942-945.	1.0	16
67	Measured Haplotype Analysis of the Angiotensin-I Converting Enzyme Gene. <i>Human Molecular Genetics</i> , 1998, 7, 1745-1751.	1.4	197
68	Affected sibpair linkage tests for multiple linked susceptibility genes. , 1997, 14, 103-115.		45
69	A genome-wide search for human type 1 diabetes susceptibility genes. <i>Nature</i> , 1994, 371, 130-136.	13.7	1,326
70	Mapping of mutation causing Friedreich's ataxia to human chromosome 9. <i>Nature</i> , 1988, 334, 248-250.	13.7	343
71	Linkage of an X-chromosome cleft palate gene. <i>Nature</i> , 1987, 326, 91-92.	13.7	115
72	A candidate for the cystic fibrosis locus isolated by selection for methylation-free islands. <i>Nature</i> , 1987, 326, 840-845.	13.7	364

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73	Localization of cystic fibrosis locus to human chromosome 7cenâ€“q22. Nature, 1985, 318, 384-385.	13.7	494