# Martin Farrall

## List of Publications by Citations



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|---|---|---|---|
| 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 | Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206 | 50.4 | 2687 |
| 71 | A large-scale, consortium-based genomewide association study of asthma. *New England Journal of Medicine*, **2010**, 363, 1211-1221 | 59.2 | 1431 |
| 70 | Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86 | 36.3 | 1339 |
| 69 | A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. *Nature Genetics*, **2015**, 47, 1121-1130 | 36.3 | 1290 |
| 68 | A genome-wide search for human type 1 diabetes susceptibility genes. *Nature*, **1994**, 371, 130-6 | 50.4 | 1175 |
| 67 | New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196 | 50.4 | 920 |
| 66 | Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. *Nature*, **2010**, 464, 713-20 | 50.4 | 639 |
| 65 | Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. *Nature*, **2015**, 518, 102-6 | 50.4 | 463 |
| 64 | Diagnostic Yield and Clinical Utility of Sequencing Familial Hypercholesterolemia Genes in Patients With Severe Hypercholesterolemia. *Journal of the American College of Cardiology*, **2016**, 67, 2578-89 | 15.1 | 458 |
| 63 | Localization of cystic fibrosis locus to human chromosome 7cen-q22. *Nature*, **1985**, 318, 384-5 | 50.4 | 446 |
| 62 | Susceptibility to coronary artery disease and diabetes is encoded by distinct, tightly linked SNPs in the ANRIL locus on chromosome 9p. *Human Molecular Genetics*, **2008**, 17, 806-14 | 5.6 | 420 |
| 61 | Mendelian randomization of blood lipids for coronary heart disease. *European Heart Journal*, **2015**, 36, 539-50 | 9.5 | 417 |
| 60 | Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. *BMJ, The*, **2014**, 349, g4164 | 5.9 | 406 |
| 59 | Reassessment of Mendelian gene pathogenicity using 7,855 cardiomyopathy cases and 60,706 reference samples. *Genetics in Medicine*, **2017**, 19, 192-203 | 8.1 | 386 |
| 58 | Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. *Nature Genetics*, **2018**, 50, 1412-1425 | 36.3 | 386 |
| 57 | Association analyses based on false discovery rate implicate new loci for coronary artery disease. *Nature Genetics*, **2017**, 49, 1385-1391 | 36.3 | 361 |
| 56 | A candidate for the cystic fibrosis locus isolated by selection for methylation-free islands. *Nature*, **1987**, 326, 840-5 | 50.4 | 341 |

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| 55 | Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. *Nature Genetics*, **2017**, 49, 403-415 | 36.3 | 313 |
| 54 | Mapping of mutation causing Friedreich's ataxia to human chromosome 9. *Nature*, **1988**, 334, 248-50 | 50.4 | 297 |
| 53 | The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. *Nature Genetics*, **2016**, 48, 1171-1184 | 36.3 | 251 |
| 52 | Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. *Nature Genetics*, **2018**, 50, 42-53 | 36.3 | 246 |
| 51 | Distribution and medical impact of loss-of-function variants in the Finnish founder population. *PLoS Genetics*, **2014**, 10, e1004494 | 6 | 243 |
| 50 | Association of low-frequency and rare coding-sequence variants with blood lipids and coronary heart disease in 56,000 whites and blacks. *American Journal of Human Genetics*, **2014**, 94, 223-32 | 11 | 233 |
| 49 | The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. *PLoS Genetics*, **2015**, 11, e1005378 | 6 | 220 |
| 48 | Measured haplotype analysis of the angiotensin-I converting enzyme gene. *Human Molecular Genetics*, **1998**, 7, 1745-51 | 5.6 | 177 |
| 47 | Genetic susceptibility to coronary artery disease: from promise to progress. *Nature Reviews Genetics*, **2006**, 7, 163-73 | 30.1 | 150 |
| 46 | Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. *Journal of the American College of Cardiology*, **2017**, 69, 823-836 | 15.1 | 146 |
| 45 | Meta-analysis of gene-level tests for rare variant association. *Nature Genetics*, **2014**, 46, 200-4 | 36.3 | 142 |
| 44 | Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. *American Journal of Human Genetics*, **2014**, 94, 349-60 | 11 | 131 |
| 43 | Phenotypic Characterization of Genetically Lowered Human Lipoprotein(a) Levels. *Journal of the American College of Cardiology*, **2016**, 68, 2761-2772 | 15.1 | 127 |
| 42 | Association of Rare and Common Variation in the Lipoprotein Lipase Gene With Coronary Artery Disease. *JAMA - Journal of the American Medical Association*, **2017**, 317, 937-946 | 27.4 | 109 |
| 41 | Linkage of an X-chromosome cleft palate gene. *Nature*, **1987**, 326, 91-2 | 50.4 | 94 |
| 40 | Secretory phospholipase A(2)-IIA and cardiovascular disease: a mendelian randomization study. *Journal of the American College of Cardiology*, **2013**, 62, 1966-1976 | 15.1 | 91 |
| 39 | Gene-age interactions in blood pressure regulation: a large-scale investigation with the CHARGE, Global BPgen, and ICBP Consortia. *American Journal of Human Genetics*, **2014**, 95, 24-38 | 11 | 80 |
| 38 | Quantitative genetic variation: a post-modern view. *Human Molecular Genetics*, **2004**, 13 Spec No 1, R1-7 | 5.6 | 68 |

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| 37 | Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. *International Journal of Epidemiology*, **2016**, 45, 1927-1937 | 7.8 | 65 |
| 36 | Genome-wide mapping of susceptibility to coronary artery disease identifies a novel replicated locus on chromosome 17. *PLoS Genetics*, **2006**, 2, e72 | 6 | 60 |
| 35 | Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. *Nature Genetics*, **2019**, 51, 636-648 | 36.3 | 59 |
| 34 | A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. *American Journal of Human Genetics*, **2018**, 102, 375-400 | 11 | 59 |
| 33 | Vitamin D levels and susceptibility to asthma, elevated immunoglobulin E levels, and atopic dermatitis: A Mendelian randomization study. *PLoS Medicine*, **2017**, 14, e1002294 | 11.6 | 47 |
| 32 | A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. *Nature Communications*, **2016**, 7, 13357 | 17.4 | 46 |
| 31 | Fine-mapping of an ancestral recombination breakpoint in DCP1. *Nature Genetics*, **1999**, 23, 270-1 | 36.3 | 40 |
| 30 | Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. *American Journal of Epidemiology*, **2019**, 188, 1033-1054 | 3.8 | 39 |
| 29 | Novel childhood asthma genes interact with in utero and early-life tobacco smoke exposure. *Journal of Allergy and Clinical Immunology*, **2014**, 133, 885-8 | 11.5 | 36 |
| 28 | 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. *Stroke*, **2005**, 36, 2215-9 | 6.7 | 36 |
| 27 | Gearing up for genome-wide gene-association studies. *Human Molecular Genetics*, **2005**, 14 Spec No. 2, R157-62 | 5.6 | 36 |
| 26 | Affected sibpair linkage tests for multiple linked susceptibility genes. *Genetic Epidemiology*, **1997**, 14, 103-15 | 2.6 | 34 |
| 25 | A common LPA null allele associates with lower lipoprotein(a) levels and coronary artery disease risk. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2014**, 34, 2095-9 | 9.4 | 33 |
| 24 | Common genetic variants and modifiable risk factors underpin hypertrophic cardiomyopathy susceptibility and expressivity. *Nature Genetics*, **2021**, 53, 135-142 | 36.3 | 33 |
| 23 | Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. *PLoS ONE*, **2018**, 13, e0198166 | 3.7 | 31 |
| 22 | A candidate gene study of F cell levels in sibling pairs using a joint linkage and association analysis. *GeneScreen*, **2000**, 1, 9-14 | | 31 |
| 21 | Analysis of 51 proposed hypertrophic cardiomyopathy genes from genome sequencing data in sarcomere negative cases has negligible diagnostic yield. *Genetics in Medicine*, **2019**, 21, 1576-1584 | 8.1 | 25 |
| 20 | No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. *Scientific Reports*, **2016**, 6, 35278 | 4.9 | 18 |

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| 19 | Global genetic architecture of an erythroid quantitative trait locus, HMIP-2. *Annals of Human Genetics*, **2014**, 78, 434-51 | 2.2 | 18 |
| 18 | Absence of linkage of the epithelial sodium channel to hypertension in black Caribbeans. *American Journal of Hypertension*, **1998**, 11, 942-5 | 2.3 | 16 |
| 17 | Plasma cytokines and risk of coronary heart disease in the PROCARDIS study. *Open Heart*, **2018**, 5, e000807 | 3 | 15 |
| 16 | A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. *Human Molecular Genetics*, **2019**, 28, 2615-2633 | 5.6 | 14 |
| 15 | Reevaluation of the South Asian Intronic Deletion in Hypertrophic Cardiomyopathy. *Circulation Genomic and Precision Medicine*, **2020**, 13, e002783 | 5.2 | 14 |
| 14 | Differential Gene Expression in Macrophages From Human Atherosclerotic Plaques Shows Convergence on Pathways Implicated by Genome-Wide Association Study Risk Variants. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2018**, 38, 2718-2730 | 9.4 | 14 |
| 13 | A mouse-to-man candidate gene study identifies association of chronic otitis media with the loci TGIF1 and FBXO11. *Scientific Reports*, **2017**, 7, 12496 | 4.9 | 12 |
| 12 | Identifying systematic heterogeneity patterns in genetic association meta-analysis studies. *PLoS Genetics*, **2017**, 13, e1006755 | 6 | 12 |
| 11 | Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. *BioData Mining*, **2017**, 10, 25 | 4.3 | 5 |
| 10 | Lack of genetic support for shared aetiology of Coronary Artery Disease and Late-onset Alzheimer's disease. *Scientific Reports*, **2018**, 8, 7102 | 4.9 | 5 |
| 9 | Reassessment of Mendelian gene pathogenicity using 7,855 cardiomyopathy cases and 60,706 reference samples | | 5 |
| 8 | Heritability and family-based GWAS analyses of the N-acyl ethanolamine and ceramide plasma lipidome. *Human Molecular Genetics*, **2021**, 30, 500-513 | 5.6 | 4 |
| 7 | Manhattan++: displaying genome-wide association summary statistics with multiple annotation layers. *BMC Bioinformatics*, **2019**, 20, 610 | 3.6 | 3 |
| 6 | Heritability of haemodynamics in the ascending aorta. *Scientific Reports*, **2020**, 10, 14356 | 4.9 | 2 |
| 5 | Marked variation in heritability estimates of left ventricular mass depending on modality of measurement. *Scientific Reports*, **2019**, 9, 13556 | 4.9 | 1 |
| 4 | Robust estimates of heritable coronary disease risk in individuals with type 2 diabetes. *Genetic Epidemiology*, **2021**, | 2.6 | 1 |
| 3 | Data-driven modelling of mutational hotspots and in silico predictors in hypertrophic cardiomyopathy. *Journal of Medical Genetics*, **2021**, 58, 556-564 | 5.8 | 0 |
| 2 | Identifying small-effect genetic associations overlooked by the conventional fixed-effect model in a large-scale meta-analysis of coronary artery disease. *Bioinformatics*, **2020**, 36, 552-557 | 7.2 | |

1 Interpreting gene-association studies. *Human Molecular Genetics*, **2005**, 14, 2489 5.6