Martin Farrall

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/9366552/publications.pdf

Version: 2024-02-01

73 papers	24,460 citations	53794 45 h-index	85541 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. Genetic Epidemiology, 2022, 46, 51-62.	1.3	5
2	Data-driven modelling of mutational hotspots and in silico predictors in hypertrophic cardiomyopathy. Journal of Medical Genetics, 2021, 58, 556-564.	3.2	2
3	Heritability and family-based GWAS analyses of the N-acyl ethanolamine and ceramide plasma lipidome. Human Molecular Genetics, 2021, 30, 500-513.	2.9	13
4	Common genetic variants and modifiable risk factors underpin hypertrophic cardiomyopathy susceptibility and expressivity. Nature Genetics, 2021, 53, 135-142.	21.4	165
5	Identifying small-effect genetic associations overlooked by the conventional fixed-effect model in a large-scale meta-analysis of coronary artery disease. Bioinformatics, 2020, 36, 552-557.	4.1	2
6	Heritability of haemodynamics in the ascending aorta. Scientific Reports, 2020, 10, 14356.	3.3	5
7	Reevaluation of the South Asian MYBPC3 ^{Î”25bp} Intronic Deletion in Hypertrophic Cardiomyopathy. Circulation Genomic and Precision Medicine, 2020, 13, e002783.	3.6	31
8	Marked variation in heritability estimates of left ventricular mass depending on modality of measurement. Scientific Reports, 2019, 9, 13556.	3.3	3
9	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
10	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
11	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
12	Manhattan++: displaying genome-wide association summary statistics with multiple annotation layers. BMC Bioinformatics, 2019, 20, 610.	2.6	6
13	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.	2.4	44
14	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.	6.2	123
15	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	21.4	426
16	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.	2.4	20
17	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
18	Plasma cytokines and risk of coronary heart disease in the PROCARDIS study. Open Heart, 2018, 5, e000807.	2.3	24

#	Article	IF	Citations
19	Lack of genetic support for shared aetiology of Coronary Artery Disease and Late-onset Alzheimerâ€™s disease. Scientific Reports, 2018, 8, 7102.	3.3	9
20	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
21	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	21.4	492
22	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.	7.4	148
23	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	2.8	214
24	A mouse-to-man candidate gene study identifies association of chronic otitis media with the loci TGIF1 and FBXO11. Scientific Reports, 2017, 7, 12496.	3.3	21
25	Association analyses based on false discovery rate implicate new loci for coronary artery disease. Nature Genetics, 2017, 49, 1385-1391.	21.4	571
26	Reassessment of Mendelian gene pathogenicity using 7,855 cardiomyopathy cases and 60,706 reference samples. Genetics in Medicine, 2017, 19, 192-203.	2.4	585
27	Vitamin D levels and susceptibility to asthma, elevated immunoglobulin E levels, and atopic dermatitis: A Mendelian randomization study. PLoS Medicine, 2017, 14, e1002294.	8.4	78
28	Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. BioData Mining, 2017, 10, 25.	4.0	7
29	Identifying systematic heterogeneity patterns in genetic association meta-analysis studies. PLoS Genetics, 2017, 13, e1006755.	3.5	20
30	Phenotypic Characterization of GeneticallyÂLowered Human Lipoprotein(a) Levels. Journal of the American College of Cardiology, 2016, 68, 2761-2772.	2.8	186
31	Diagnostic Yield and Clinical Utility of Sequencing Familial Hypercholesterolemia Genes in Patients With Severe Hypercholesterolemia. Journal of the American College of Cardiology, 2016, 67, 2578-2589.	2.8	723
32	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
33	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
34	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. Scientific Reports, 2016, 6, 35278.	3.3	25
35	Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. International Journal of Epidemiology, 2016, 45, 1927-1937.	1.9	94
36	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	3.5	331

#	Article	IF	Citations
37	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
38	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
39	Mendelian randomization of blood lipids for coronary heart disease. European Heart Journal, 2015, 36, 539-550.	2.2	567
40	A comprehensive 1000 Genomesâ€“based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	21.4	2,054
41	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106.	27.8	581
42	Cardiovascular Twist to the Rapidly Evolving Apolipoprotein L1 Story. Circulation Research, 2014, 114, 746-747.	4.5	6
43	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494.	3.5	351
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, 349-360.	6.2	158
45	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, 223-232.	6.2	287
46	A Common LPA Null Allele Associates With Lower Lipoprotein(a) Levels and Coronary Artery Disease Risk. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 2095-2099.	2.4	45
47	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.	6.2	109
48	Global Genetic Architecture of an Erythroid Quantitative Trait Locus,HMIP-2. Annals of Human Genetics, 2014, 78, 434-451.	0.8	24
49	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
50	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	6.0	528
51	Meta-analysis of gene-level tests for rare variant association. Nature Genetics, 2014, 46, 200-204.	21.4	178
52	Novel childhood asthma genes interact with in utero and early-life tobacco smoke exposure. Journal of Allergy and Clinical Immunology, 2014, 133, 885-888.	2.9	47
53	Abstract 534: A Common Null Allele of LPA is Associated With Lp(a) Levels and Coronary Artery Disease Risk. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, .	2.4	0
54	Secretory Phospholipase A2-IIA and Cardiovascular Disease. Journal of the American College of Cardiology, 2013, 62, 1966-1976.	2.8	115

#	Article	IF	Citations
55	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. Nature, 2010, 464, 713-720.	27.8	737
56	A Large-Scale, Consortium-Based Genomewide Association Study of Asthma. New England Journal of Medicine, 2010, 363, 1211-1221.	27.0	1,762
57	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, 806-814.	2.9	472
58	Genetic susceptibility to coronary artery disease: from promise to progress. Nature Reviews Genetics, 2006, 7, 163-173.	16.3	176
59	Genome-Wide Mapping of Susceptibility to Coronary Artery Disease Identifies a Novel Replicated Locus on Chromosome 17. PLoS Genetics, 2006, 2, e72.	3.5	69
60	Interpreting gene-association studies. Human Molecular Genetics, 2005, 14, 2489-2489.	2.9	0
61	Gearing up for genome-wide gene-association studies. Human Molecular Genetics, 2005, 14, R157-R162.	2.9	43
62	Genotype at the â˜'174G/C Polymorphism of the Interleukin-6 Gene Is Associated With Common Carotid Artery Intimal-Medial Thickness. Stroke, 2005, 36, 2215-2219.	2.0	40
63	Quantitative genetic variation: a post-modern view. Human Molecular Genetics, 2004, 13, 1R-7.	2.9	73
64	A candidate gene study of F cell levels in sibling pairs using a joint linkage and association analysis. GeneScreen, 2000, 1, 9-14.	0.6	35
65	Fine-mapping of an ancestral recombination breakpoint in DCP1. Nature Genetics, 1999, 23, 270-271.	21.4	42
66	Absence of linkage of the epithelial sodium channel to hypertension in black Caribbeans. American Journal of Hypertension, 1998, 11, 942-945.	2.0	16
67	Measured Haplotype Analysis of the Angiotensin-I Converting Enzyme Gene. Human Molecular Genetics, 1998, 7, 1745-1751.	2.9	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. Nature, 1994, 371, 130-136.	27.8	1,326
70	Mapping of mutation causing Friedreich's ataxia to human chromosome 9. Nature, 1988, 334, 248-250.	27.8	343
71	Linkage of an X-chromosome cleft palate gene. Nature, 1987, 326, 91-92.	27.8	115
72	A candidate for the cystic fibrosis locus isolated by selection for methylation-free islands. Nature, 1987, 326, 840-845.	27.8	364

#	Article	IF	Citations
73	Localization of cystic fibrosis locus to human chromosome 7cenâ€“q22. Nature, 1985, 318, 384-385.	27.8	494