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List of Publications by Year
in descending order

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71 papers	18,664 citations	76326 40 h-index	85541 71 g-index
80 all docs	80 docs citations	80 times ranked	29131 citing authors

#	Article	IF	Citations
1	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	27.8	3,249
2	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
3	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
4	GenABEL: an R library for genome-wide association analysis. Bioinformatics, 2007, 23, 1294-1296.	4.1	1,711
5	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
6	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	21.4	746
7	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. Nature, 2017, 541, 81-86.	27.8	743
8	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
9	Disease variants alter transcription factor levels and methylation of their binding sites. Nature Genetics, 2017, 49, 131-138.	21.4	390
10	Meta-analysis of telomere length in 19â€‰713 subjects reveals high heritability, stronger maternal inheritance and a paternal age effect. European Journal of Human Genetics, 2013, 21, 1163-1168.	2.8	380
11	Identification of context-dependent expression quantitative trait loci in whole blood. Nature Genetics, 2017, 49, 139-145.	21.4	363
12	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	21.4	310
13	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	21.4	308
14	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. Nature Genetics, 2015, 47, 1282-1293.	21.4	294
15	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
16	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
17	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
18	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193

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19	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	12.8	192
20	Meta-analysis of genome-wide association studies from the CHARGE consortium identifies common variants associated with carotid intima media thickness and plaque. Nature Genetics, 2011, 43, 940-947.	21.4	191
21	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. Nature Communications, 2015, 6, 7208.	12.8	178
22	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
23	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
24	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	12.8	153
25	Genome-wide association analysis identifies multiple loci related to resting heart rate. Human Molecular Genetics, 2010, 19, 3885-3894.	2.9	133
26	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	12.8	119
27	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113
28	The â^'514 Câ†'T Hepatic Lipase Promoter Region Polymorphism and Plasma Lipids: A Meta-Analysis. Journal of Clinical Endocrinology and Metabolism, 2004, 89, 3858-3863.	3.6	89
29	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
30	Genomewide metaâ€analysis identifies loci associated with <scp>IGF</scp> â€I and <scp>IGFBP</scp> â€3 levels with impact on ageâ€related traits. Aging Cell, 2016, 15, 811-824.	6.7	83
31	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. PLoS Genetics, 2015, 11, e1005230.	3.5	77
32	A metabolomic profile is associated with the risk of incident coronary heart disease. American Heart Journal, 2014, 168, 45-52.e7.	2.7	74
33	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
34	PNPLA3, TM6SF2, and MBOAT7 Genotypes and Coronary Artery Disease. Gastroenterology, 2017, 152, 912-913.	1.3	72
35	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. Nature Communications, 2018, 9, 2904.	12.8	71
36	A Genome-Wide Association Scan of RR and QT Interval Duration in 3 European Genetically Isolated Populations. Circulation: Cardiovascular Genetics, 2009, 2, 322-328.	5.1	67

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37	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. Nature Communications, 2019, 10, 2581.	12.8	62
38	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
39	Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. Circulation: Cardiovascular Genetics, 2016, 9, 511-520.	5.1	54
40	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. Genome Biology, 2018, 19, 87.	8.8	47
41	Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. Nature Communications, 2015, 6, 6065.	12.8	45
42	Risk Scores of Common Genetic Variants for Lipid Levels Influence Atherosclerosis and Incident Coronary Heart Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, 2233-2239.	2.4	44
43	Fifteen Genetic Loci Associated With the Electrocardiographic P Wave. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	38
44	Dynamic risk assessment to improve quality of care in patients with atrial fibrillation: the 7th AFNET/EHRA Consensus Conference. Europace, 2021, 23, 329-344.	1.7	38
45	Fine-mapping, novel loci identification, and SNP association transferability in a genome-wide association study of QRS duration in African Americans. Human Molecular Genetics, 2016, 25, 4350-4368.	2.9	37
46	Meta-analysis of 49â€…549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant inANGPTL4determining fasting TG levels. Journal of Medical Genetics, 2016, 53, 441-449.	3.2	34
47	Discovery of novel heart rate-associated loci using the Exome Chip. Human Molecular Genetics, 2017, 26, 2346-2363.	2.9	29
48	Genome-wide association meta-analysis of 30,000 samples identifies seven novel loci for quantitative ECG traits. European Journal of Human Genetics, 2019, 27, 952-962.	2.8	29
49	Genome-wide identification of genes regulating DNA methylation using genetic anchors for causal inference. Genome Biology, 2020, 21, 220.	8.8	27
50	Epistatic Effect of Cholesteryl Ester Transfer Protein and Hepatic Lipase on Serum High-Density Lipoprotein Cholesterol Levels. Journal of Clinical Endocrinology and Metabolism, 2007, 92, 2680-2687.	3.6	25
51	Heritabilities, apolipoprotein E, and effects of inbreeding on plasma lipids in a genetically isolated population: The Erasmus Rucphen Family Study. European Journal of Epidemiology, 2007, 22, 99-105.	5.7	25
52	Twenty-eight genetic loci associated with ST-T-wave amplitudes of the electrocardiogram. Human Molecular Genetics, 2016, 25, 2093-2103.	2.9	24
53	Heritability in a SCN5A -mutation founder population with increased female susceptibility to non-nocturnal ventricular tachyarrhythmia and sudden cardiac death. Heart Rhythm, 2017, 14, 1873-1881.	0.7	23
54	DNA methylation signatures of aggression and closely related constructs: A meta-analysis of epigenome-wide studies across the lifespan. Molecular Psychiatry, 2021, 26, 2148-2162.	7.9	21

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55	Heritabilities, proportions of heritabilities explained by GWAS findings, and implications of cross-phenotype effects on PR interval. Human Genetics, 2015, 134, 1211-1219.	3.8	20
56	The cholesteryl ester transfer protein I405V polymorphism is associated with increased high-density lipoprotein levels and decreased risk of myocardial infarction: the Rotterdam Study. European Journal of Cardiovascular Prevention and Rehabilitation, 2007, 14, 419-421.	2.8	19
57	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	3.6	19
58	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2020, 13, 387-395.	3.6	16
59	Metabolomics reveals a link between homocysteine and lipid metabolism and leukocyte telomere length: the ENGAGE consortium. Scientific Reports, 2019, 9, 11623.	3.3	13
60	The Challenges of Genome-Wide Interaction Studies: Lessons to Learn from the Analysis of HDL Blood Levels. PLoS ONE, 2014, 9, e109290.	2.5	13
61	Clinical and electrophysiological predictors of device-detected new-onset atrial fibrillation during 3 years after cardiac surgery. Europace, 2021, 23, 1922-1930.	1.7	12
62	A systematic SNP selection approach to identify mechanisms underlying disease aetiology: linking height to post-menopausal breast and colorectal cancer risk. Scientific Reports, 2017, 7, 41034.	3.3	10
63	Fine mapping the CETP region reveals a common intronic insertion associated to HDL-C. Npj Aging and Mechanisms of Disease, 2015, 1, 15011.	4.5	8
64	A Combined Linkage and Exome Sequencing Analysis for Electrocardiogram Parameters in the Erasmus Rucphen Family Study. Frontiers in Genetics, 2016, 7, 190.	2.3	5
65	Association of the IGF1 gene with fasting insulin levels. European Journal of Human Genetics, 2016, 24, 1337-1343.	2.8	5
66	Genome-wide Association Study of Change in Fasting Glucose over time in 13,807 non-diabetic European Ancestry Individuals. Scientific Reports, 2019, 9, 9439.	3.3	5
67	A combined linkage, microarray and exome analysis suggests MAP3K11 as a candidate gene for left ventricular hypertrophy. BMC Medical Genomics, 2018, 11, 22.	1.5	4
68	Leukocyte gene expression in post-thrombotic syndrome. Thrombosis Research, 2021, 202, 40-42.	1.7	1
69	Considerations for the Assessment of Substrates, Genetics and Risk Factors in Patients with Atrial Fibrillation. Arrhythmia and Electrophysiology Review, 2021, 10, 132-139.	2.4	1
70	Low Density Lipoprotein Exposure of Plasmacytoid Dendritic Cells Blunts Toll-like Receptor 7/9 Signaling via NUR77. Biomedicines, 2022, 10, 1152.	3.2	1
71	New-onset perioperative atrial fibrillation in cardiac surgery patients: transient trouble or persistent problem?â€"Authorsâ€™ reply. Europace, 2021, , .	1.7	0