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List of Publications by Year
in descending order

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60 papers	5,501 citations	201674 27 h-index	133252 59 g-index
80 all docs	80 docs citations	80 times ranked	11063 citing authors

#	Article	IF	Citations
1	Associations of carotid intima media thickness with gene expression in whole blood and genetically predicted gene expression across 48 tissues. Human Molecular Genetics, 2022, 31, 1171-1182.	2.9	4
2	Whole genome sequence analysis of platelet traits in the NHLBI Trans-Omics for Precision Medicine (TOPMed) initiative. Human Molecular Genetics, 2022, 31, 347-361.	2.9	9
3	Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	6.2	24
4	American Heart Associationâ€™s Lifeâ€™s Simple 7: Lifestyle Recommendations, Polygenic Risk, and Lifetime Risk of Coronary Heart Disease. Circulation, 2022, 145, 808-818.	1.6	63
5	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	2.8	2
6	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus. Nature Communications, 2022, 13, 1222.	12.8	5
7	Multiâ€phenotype analyses of hemostatic traits with cardiovascular events reveal novel genetic associations. Journal of Thrombosis and Haemostasis, 2022, 20, 1331-1349.	3.8	12
8	Gene-lifestyle interactions in the genomics of human complex traits. European Journal of Human Genetics, 2022, 30, 730-739.	2.8	11
9	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	2.7	12
10	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
11	A System for Phenotype Harmonization in the National Heart, Lung, and Blood Institute Trans-Omics for Precision Medicine (TOPMed) Program. American Journal of Epidemiology, 2021, 190, 1977-1992.	3.4	29
12	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893.	6.2	28
13	FGL1 as a modulator of plasma Dâ€dimer levels: Exomeâ€wide marker analysis of plasma tPA, PAIâ€1, and Dâ€dimer. Journal of Thrombosis and Haemostasis, 2021, 19, 2019-2028.	3.8	1
14	Genetic susceptibility, obesity and lifetime risk of type 2 diabetes: The ARIC study and Rotterdam Study. Diabetic Medicine, 2021, 38, e14639.	2.3	9
15	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 1836-1851.	6.2	14
16	Lifestyle Risk Score: handling missingness of individual lifestyle components in meta-analysis of gene-by-lifestyle interactions. European Journal of Human Genetics, 2021, 29, 839-850.	2.8	0
17	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
18	A Mendelian randomization of Î³â€² and total fibrinogen levels in relation to venous thromboembolism and ischemic stroke. Blood, 2020, 136, 3062-3069.	1.4	25

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19	Mendelian Randomization Analysis of Hemostatic Factors and Their Contribution to Peripheral Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2020, 41, 380-386.	2.4	14
20	Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. Circulation Genomic and Precision Medicine, 2020, 13, e002772.	3.6	11
21	Deriving stratified effects from joint models investigating gene-environment interactions. BMC Bioinformatics, 2020, 21, 251.	2.6	2
22	Identifying blood pressure loci whose effects are modulated by multiple lifestyle exposures. Genetic Epidemiology, 2020, 44, 629-641.	1.3	6
23	Genetic loci associated with prevalent and incident myocardial infarction and coronary heart disease in the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. PLoS ONE, 2020, 15, e0230035.	2.5	5
24	Genome-wide meta-analysis of macronutrient intake of 91,114 European ancestry participants from the cohorts for heart and aging research in genomic epidemiology consortium. Molecular Psychiatry, 2019, 24, 1920-1932.	7.9	44
25	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	1.4	162
26	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	12.8	62
27	Impact of Rare and Common Genetic Variants on Diabetes Diagnosis by Hemoglobin A1c in Multi-Ancestry Cohorts: The Trans-Omics for Precision Medicine Program. American Journal of Human Genetics, 2019, 105, 706-718.	6.2	44
28	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
29	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
30	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	27.8	248
31	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. PLoS ONE, 2019, 14, e0216222.	2.5	17
32	Serum metabolic signatures of coronary and carotid atherosclerosis and subsequent cardiovascular disease. European Heart Journal, 2019, 40, 2883-2896.	2.2	107
33	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
34	Use of >100,000 NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium whole genome sequences improves imputation quality and detection of rare variant associations in admixed African and Hispanic/Latino populations. PLoS Genetics, 2019, 15, e1008500.	3.5	203
35	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. Circulation, 2019, 139, 620-635.	1.6	102
36	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. Journal of the American College of Cardiology, 2019, 73, 58-66.	2.8	147

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37	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. American Journal of Human Genetics, 2019, 104, 260-274.	6.2	103
38	Functionally oriented analysis of cardiometabolic traits in a trans-ethnic sample. Human Molecular Genetics, 2019, 28, 1212-1224.	2.9	12
39	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. Blood, 2019, 133, 967-977.	1.4	34
40	Von Willebrand factor and ADAMTS13 activity in relation to risk of dementia: a population-based study. Scientific Reports, 2018, 8, 5474.	3.3	20
41	A systematic analysis highlights multiple long non-coding RNAs associated with cardiometabolic disorders. Journal of Human Genetics, 2018, 63, 431-446.	2.3	17
42	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	6.2	326
43	Reply to â€˜Misestimation of heritability and prediction accuracy of male-pattern baldnessâ€™. Nature Communications, 2018, 9, 2538.	12.8	0
44	DNA methylation age is associated with an altered hemostatic profile in a multiethnic meta-analysis. Blood, 2018, 132, 1842-1850.	1.4	16
45	CD163+ macrophages promote angiogenesis and vascular permeability accompanied by inflammation in atherosclerosis. Journal of Clinical Investigation, 2018, 128, 1106-1124.	8.2	209
46	GWAS for male-pattern baldness identifies 71 susceptibility loci explaining 38% of the risk. Nature Communications, 2017, 8, 1584.	12.8	61
47	Whole-genome sequencing study of serum peptide levels: the Atherosclerosis Risk in Communities study. Human Molecular Genetics, 2017, 26, 3442-3450.	2.9	25
48	ADAMTS13 activity as a novel risk factor for incident type 2 diabetes mellitus: a population-based cohort study. Diabetologia, 2017, 60, 280-286.	6.3	23
49	Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study. PLoS ONE, 2017, 12, e0167742.	2.5	29
50	Whole genome sequence analysis of serum amino acid levels. Genome Biology, 2016, 17, 237.	8.8	17
51	von Willebrand Factor, ADAMTS13 Activity, and Decline in Kidney Function: A Population-Based Cohort Study. American Journal of Kidney Diseases, 2016, 68, 726-732.	1.9	12
52	Workflow for Integrated Processing of Multicohort Untargeted ¹H NMR Metabolomics Data in Large-Scale Metabolic Epidemiology. Journal of Proteome Research, 2016, 15, 4188-4194.	3.7	37
53	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	2.9	73
54	Incremental predictive value of 152 single nucleotide polymorphisms in the 10-year risk prediction of incident coronary heart disease: the Rotterdam Study. International Journal of Epidemiology, 2015, 44, 682-688.	1.9	44

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55	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. Blood, 2015, 126, e19-e29.	1.4	55
56	Adiposity as a cause of cardiovascular disease: a Mendelian randomization study. International Journal of Epidemiology, 2015, 44, 578-586.	1.9	123
57	Genetic variants in the ADAMTS13 and SUPT3H genes are associated with ADAMTS13 activity. Blood, 2015, 125, 3949-3955.	1.4	24
58	Association of Rare Loss-Of-Function Alleles in HAL , Serum Histidine. Circulation: Cardiovascular Genetics, 2015, 8, 351-355.	5.1	41
59	A comprehensive 1000 Genomesâ€“based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	21.4	2,054
60	A Genetic Variant in the Seed Region of miR-4513 Shows Pleiotropic Effects on Lipid and Glucose Homeostasis, Blood Pressure, and Coronary Artery Disease. Human Mutation, 2014, 35, 1524-1531.	2.5	45