

Paul S De Vries

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

5,501
citations

201575

27
h-index

133188

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. <i>Human Molecular Genetics</i> , 2022, 31, 1171-1182.	1.4	4
2	Whole genome sequence analysis of platelet traits in the NHLBI Trans-Omics for Precision Medicine (TOPMed) initiative. <i>Human Molecular Genetics</i> , 2022, 31, 347-361.	1.4	9
3	Rare coding variants in 35 genes associate with circulating lipid levels—A multi-ancestry analysis of 170,000 exomes. <i>American Journal of Human Genetics</i> , 2022, 109, 81-96.	2.6	24
4	American Heart Association's Life's Simple 7: Lifestyle Recommendations, Polygenic Risk, and Lifetime Risk of Coronary Heart Disease. <i>Circulation</i> , 2022, 145, 808-818.	1.6	63
5	Rare coding variants in RCN3 are associated with blood pressure. <i>BMC Genomics</i> , 2022, 23, 148.	1.2	2
6	Elucidating mechanisms of genetic cross-disease associations at the PROCRA vascular disease locus. <i>Nature Communications</i> , 2022, 13, 1222.	5.8	5
7	Multi-phenotype analyses of hemostatic traits with cardiovascular events reveal novel genetic associations. <i>Journal of Thrombosis and Haemostasis</i> , 2022, 20, 1331-1349.	1.9	12
8	Gene-lifestyle interactions in the genomics of human complex traits. <i>European Journal of Human Genetics</i> , 2022, 30, 730-739.	1.4	11
9	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. <i>Hypertension</i> , 2022, 79, 1656-1667.	1.3	12
10	Multi-ancestry genome-wide gene-sleep interactions identify novel loci for blood pressure. <i>Molecular Psychiatry</i> , 2021, 26, 6293-6304.	4.1	13
11	A System for Phenotype Harmonization in the National Heart, Lung, and Blood Institute Trans-Omics for Precision Medicine (TOPMed) Program. <i>American Journal of Epidemiology</i> , 2021, 190, 1977-1992.	1.6	29
12	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2021, 108, 874-893.	2.6	28
13	FGL1 as a modulator of plasma D-dimer levels: Exome-wide marker analysis of plasma tPA, PAI-1, and D-dimer. <i>Journal of Thrombosis and Haemostasis</i> , 2021, 19, 2019-2028.	1.9	1
14	Genetic susceptibility, obesity and lifetime risk of type 2 diabetes: The ARIC study and Rotterdam Study. <i>Diabetic Medicine</i> , 2021, 38, e14639.	1.2	9
15	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2021, 108, 1836-1851.	2.6	14
16	Lifestyle Risk Score: handling missingness of individual lifestyle components in meta-analysis of gene-by-lifestyle interactions. <i>European Journal of Human Genetics</i> , 2021, 29, 839-850.	1.4	0
17	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	13.7	353
18	A Mendelian randomization of HbA_{1c} and total fibrinogen levels in relation to venous thromboembolism and ischemic stroke. <i>Blood</i> , 2020, 136, 3062-3069.	0.6	25

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19	Mendelian Randomization Analysis of Hemostatic Factors and Their Contribution to Peripheral Artery Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2020, 41, 380-386.	1.1	14
20	Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002772.	1.6	11
21	Deriving stratified effects from joint models investigating gene-environment interactions. <i>BMC Bioinformatics</i> , 2020, 21, 251.	1.2	2
22	Identifying blood pressure loci whose effects are modulated by multiple lifestyle exposures. <i>Genetic Epidemiology</i> , 2020, 44, 629-641.	0.6	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. <i>PLoS ONE</i> , 2020, 15, e0230035.	1.1	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. <i>Molecular Psychiatry</i> , 2019, 24, 1920-1932.	4.1	44
25	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. <i>Blood</i> , 2019, 134, 1645-1657.	0.6	162
26	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. <i>Nature Communications</i> , 2019, 10, 5121.	5.8	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. <i>American Journal of Human Genetics</i> , 2019, 105, 706-718.	2.6	44
28	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
29	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376.	5.8	64
30	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019, 570, 71-76.	13.7	248
31	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. <i>PLoS ONE</i> , 2019, 14, e0216222.	1.1	17
32	Serum metabolic signatures of coronary and carotid atherosclerosis and subsequent cardiovascular disease. <i>European Heart Journal</i> , 2019, 40, 2883-2896.	1.0	107
33	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
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. <i>PLoS Genetics</i> , 2019, 15, e1008500.	1.5	203
35	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. <i>Circulation</i> , 2019, 139, 620-635.	1.6	102
36	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. <i>Journal of the American College of Cardiology</i> , 2019, 73, 58-66.	1.2	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. <i>American Journal of Human Genetics</i> , 2019, 104, 260-274.	2.6	103
38	Functionally oriented analysis of cardiometabolic traits in a trans-ethnic sample. <i>Human Molecular Genetics</i> , 2019, 28, 1212-1224.	1.4	12
39	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. <i>Blood</i> , 2019, 133, 967-977.	0.6	34
40	Von Willebrand factor and ADAMTS13 activity in relation to risk of dementia: a population-based study. <i>Scientific Reports</i> , 2018, 8, 5474.	1.6	20
41	A systematic analysis highlights multiple long non-coding RNAs associated with cardiometabolic disorders. <i>Journal of Human Genetics</i> , 2018, 63, 431-446.	1.1	17
42	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , 2018, 103, 691-706.	2.6	326
43	Reply to "Misestimation of heritability and prediction accuracy of male-pattern baldness". <i>Nature Communications</i> , 2018, 9, 2538.	5.8	0
44	DNA methylation age is associated with an altered hemostatic profile in a multiethnic meta-analysis. <i>Blood</i> , 2018, 132, 1842-1850.	0.6	16
45	CD163+ macrophages promote angiogenesis and vascular permeability accompanied by inflammation in atherosclerosis. <i>Journal of Clinical Investigation</i> , 2018, 128, 1106-1124.	3.9	209
46	GWAS for male-pattern baldness identifies 71 susceptibility loci explaining 38% of the risk. <i>Nature Communications</i> , 2017, 8, 1584.	5.8	61
47	Whole-genome sequencing study of serum peptide levels: the Atherosclerosis Risk in Communities study. <i>Human Molecular Genetics</i> , 2017, 26, 3442-3450.	1.4	25
48	ADAMTS13 activity as a novel risk factor for incident type 2 diabetes mellitus: a population-based cohort study. <i>Diabetologia</i> , 2017, 60, 280-286.	2.9	23
49	Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study. <i>PLoS ONE</i> , 2017, 12, e0167742.	1.1	29
50	Whole genome sequence analysis of serum amino acid levels. <i>Genome Biology</i> , 2016, 17, 237.	3.8	17
51	von Willebrand Factor, ADAMTS13 Activity, and Decline in Kidney Function: A Population-Based Cohort Study. <i>American Journal of Kidney Diseases</i> , 2016, 68, 726-732.	2.1	12
52	Workflow for Integrated Processing of Multicohort Untargeted ¹ H NMR Metabolomics Data in Large-Scale Metabolic Epidemiology. <i>Journal of Proteome Research</i> , 2016, 15, 4188-4194.	1.8	37
53	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. <i>Human Molecular Genetics</i> , 2016, 25, 358-370.	1.4	73
54	Incremental predictive value of 152 single nucleotide polymorphisms in the 10-year risk prediction of incident coronary heart disease: the Rotterdam Study. <i>International Journal of Epidemiology</i> , 2015, 44, 682-688.	0.9	44

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55	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. <i>Blood</i> , 2015, 126, e19-e29.	0.6	55
56	Adiposity as a cause of cardiovascular disease: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2015, 44, 578-586.	0.9	123
57	Genetic variants in the ADAMTS13 and SUPT3H genes are associated with ADAMTS13 activity. <i>Blood</i> , 2015, 125, 3949-3955.	0.6	24
58	Association of Rare Loss-Of-Function Alleles in <i>HAL</i> , Serum Histidine. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 351-355.	5.1	41
59	A comprehensive 1000 Genomesâ€‘based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , 2015, 47, 1121-1130.	9.4	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. <i>Human Mutation</i> , 2014, 35, 1524-1531.	1.1	45