Marguerite R Irvin

List of Publications by Year
in descending order

111 papers	7,184 citations	117625 34 h-index	74163 75 g-index
115 all docs	115 docs citations	115 times ranked	13158 citing authors

#	Article	IF	Citations
1	Mendelian randomization in the multivariate general linear model framework. Genetic Epidemiology, 2022, 46, 17-31.	1.3	1
2	Genetic European Ancestry and Incident Diabetes in Black Individuals: Insights From the SPRINT Trial. Circulation Genomic and Precision Medicine, 2022, 15, CIRCGEN121003468.	3.6	3
3	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
4	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
5	<i>APOL1</i> Risk Variants Associated with Serum Albumin in a Population-Based Cohort Study. American Journal of Nephrology, 2022, 53, 182-190.	3.1	0
6	Multi-ethnic GWAS and fine-mapping of glycaemic traits identify novel loci in the PAGE Study. Diabetologia, 2022, 65, 477-489.	6.3	15
7	Association of Polygenic Risk Score With Blood Pressure and Adverse Cardiovascular Outcomes in Individuals With Type II Diabetes: Insights From the ACCORD Trial. Hypertension, 2022, , HYPERTENSIONAHA12218976.	2.7	1
8	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	10.3	36
9	Telomere shortening and the transition to family caregiving in the Reasons for Geographic and Racial Differences in Stroke (REGARDS) study. PLoS ONE, 2022, 17, e0268689.	2.5	0
10	Epigenome-wide association study identifies DNA methylation sites associated with target organ damage in older African Americans. Epigenetics, 2021, 16, 862-875.	2.7	10
11	Neighborhood Walkability as a Predictor of Incident Hypertension in a National Cohort Study. Frontiers in Public Health, 2021, 9, 611895.	2.7	12
12	Whole-Exome Sequencing and hiPSC Cardiomyocyte Models Identify MYRIP, TRAPPC11, and SLC27A6 of Potential Importance to Left Ventricular Hypertrophy in an African Ancestry Population. Frontiers in Genetics, 2021, 12, 588452.	2.3	3
13	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
14	DNA Methylation and Blood Pressure Phenotypes: A Review of the Literature. American Journal of Hypertension, 2021, 34, 267-273.	2.0	9
15	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. Genome Medicine, 2021, 13, 74.	8.2	20
16	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. American Journal of Human Genetics, 2021, 108, 564-582.	6.2	18
17	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	12.8	17
18	Age and sex are associated with the plasma lipidome: findings from the GOLDN study. Lipids in Health and Disease, 2021, 20, 30.	3.0	36

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19	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	8.8	90
20	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. Nature Communications, 2021, 12, 3987.	12.8	18
21	Higher Serum Urate Levels Are Associated With an Increased Risk for Sudden Cardiac Death. Journal of Rheumatology, 2021, 48, 1745-1753.	2.0	3
22	Changes in lipidomic profile by anti-retroviral treatment regimen. Medicine (United States), 2021, 100, e26588.	1.0	1
23	Adverse Cardiovascular Outcomes and Antihypertensive Treatment: A Genomeâ€Wide Interaction Metaâ€Analysis in the International Consortium for Antihypertensive Pharmacogenomics Studies. Clinical Pharmacology and Therapeutics, 2021, 110, 723-732.	4.7	6
24	High triglyceride to HDL cholesterol ratio is associated with increased coronary heart disease among White but not Black adults. American Journal of Preventive Cardiology, 2021, 7, 100198.	3.0	8
25	Lipid Phenotypes and DNA Methylation: a Review of the Literature. Current Atherosclerosis Reports, 2021, 23, 71.	4.8	17
26	Association of Sickle Cell Trait With Incidence of Coronary Heart Disease Among African American Individuals. JAMA Network Open, 2021, 4, e2030435.	5.9	5
27	Genomics of Postprandial Lipidomics in the Genetics of Lipid-Lowering Drugs and Diet Network Study. Nutrients, 2021, 13, 4000.	4.1	2
28	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
29	Genetic Contributors of Incident Stroke in 10,700 African Americans With Hypertension: A Meta-Analysis From the Genetics of Hypertension Associated Treatments and Reasons for Geographic and Racial Differences in Stroke Studies. Frontiers in Genetics, 2021, 12, 781451.	2.3	7
30	APOL1 Nephropathy Risk Alleles and Mortality in African American Adults: A Cohort Study. American Journal of Kidney Diseases, 2020, 75, 54-60.	1.9	7
31	Transitions to family caregiving: enrolling incident caregivers and matched non-caregiving controls from a population-based study. Aging Clinical and Experimental Research, 2020, 32, 1829-1838.	2.9	19
32	Severity of Hypertension Mediates the Association of Hyperuricemia With Stroke in the REGARDS Case Cohort Study. Hypertension, 2020, 75, 246-256.	2.7	37
33	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
34	Carbohydrate and fat intake associated with risk of metabolic diseases through epigenetics of CPT1A. American Journal of Clinical Nutrition, 2020, 112, 1200-1211.	4.7	48
35	Genome-Wide Association Meta-Analysis of Individuals of European Ancestry Identifies Suggestive Loci for Sodium Intake, Potassium Intake, and Their Ratio Measured from 24-Hour or Half-Day Urine Samples. Journal of Nutrition, 2020, 150, 2635-2645.	2.9	4
36	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nature Genetics, 2020, 52, 969-983.	21.4	146

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37	Cardiovascular Health and Transition From Controlled Blood Pressure to Apparent Treatment Resistant Hypertension. Hypertension, 2020, 76, 1953-1961.	2.7	8
38	Genetic-Based Hypertension Subtype Identification Using Informative SNPs. Genes, 2020, 11, 1265.	2.4	5
39	A lipidome-wide association study of the lipoprotein insulin resistance index. Lipids in Health and Disease, 2020, 19, 153.	3.0	6
40	Distracted Driving and Risk of Crash or Near-Crash Involvement Among Older Drivers Using Naturalistic Driving Data With a Case-Crossover Study Design. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2019, 74, 550-555.	3.6	19
41	Genome-wide meta-analysis of SNP-by9-ACEI/ARB and SNP-by-thiazide diuretic and effect on serum potassium in cohorts of European and African ancestry. Pharmacogenomics Journal, 2019, 19, 97-108.	2.0	3
42	Clinical correlates and heritability of cardiac mechanics: The HyperGEN study. International Journal of Cardiology, 2019, 274, 208-213.	1.7	5
43	Genomeâ€wide metaâ€analysis of SNP and antihypertensive medication interactions on left ventricular traits in African Americans. Molecular Genetics & Genomic Medicine, 2019, 7, e00788.	1.2	4
44	Does the Association of Diabetes With Stroke Risk Differ by Age, Race, and Sex? Results From the REasons for Geographic and Racial Differences in Stroke (REGARDS) Study. Diabetes Care, 2019, 42, 1966-1972.	8.6	12
45	Gene Variants at Loci Related to Blood Pressure Account for Variation in Response to Antihypertensive Drugs Between Black and White Individuals. Hypertension, 2019, 74, 614-622.	2.7	14
46	Gain of function in somatic TP53 mutations is associated with immuneâ€rich breast tumors and changes in tumorâ€associated macrophages. Molecular Genetics & Genomic Medicine, 2019, 7, e1001.	1.2	17
47	Genome-Wide Association Study of Apparent Treatment-Resistant Hypertension in the CHARGE Consortium: The CHARGE Pharmacogenetics Working Group. American Journal of Hypertension, 2019, 32, 1146-1153.	2.0	17
48	A PheWAS study of a large observational epidemiological cohort of African Americans from the REGARDS study. BMC Medical Genomics, 2019, 12, 26.	1.5	9
49	Systematic Error Removal Using Random Forest for Normalizing Large-Scale Untargeted Lipidomics Data. Analytical Chemistry, 2019, 91, 3590-3596.	6.5	163
50	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
51	Integrating hypertension phenotype and genotype with hybrid non-negative matrix factorization. Bioinformatics, 2019, 35, 1395-1403.	4.1	12
52	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. American Journal of Human Genetics, 2019, 104, 112-138.	6.2	106
53	Peripheral Blood Cytopenia and Subsequent Risk of Cardiovascular Disease and Mortality. Blood, 2019, 134, 5002-5002.	1.4	0
54	Association of Sickle Cell Trait With Ischemic Stroke Among African Americans. JAMA Neurology, 2018, 75, 802.	9.0	25

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55	The association of nocturnal hypertension and nondipping blood pressure with treatmentâ€resistant hypertension: The Jackson Heart Study. Journal of Clinical Hypertension, 2018, 20, 438-446.	2.0	12
56	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
57	Epigenome-wide association study of metabolic syndrome in African-American adults. Clinical Epigenetics, 2018, 10, 49.	4.1	49
58	West African Ancestry and Nocturnal Blood Pressure in African Americans: The Jackson Heart Study. American Journal of Hypertension, 2018, 31, 706-714.	2.0	4
59	APOL1Nephropathy Risk Variants and Incident Cardiovascular Disease Events in Community-Dwelling Black Adults. Circulation Genomic and Precision Medicine, 2018, 11, e002098.	3.6	26
60	General Cognitive Impairment as a Risk Factor for Motor Vehicle Collision Involvement: A Prospective Population-Based Study. Geriatrics (Switzerland), 2018, 3, 11.	1.7	3
61	Metabolic and inflammatory biomarkers are associated with epigenetic aging acceleration estimates in the GOLDN study. Clinical Epigenetics, 2018, 10, 56.	4.1	68
62	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	21.4	1,124
63	Epigenetic Patterns in Blood Associated With Lipid Traits Predict Incident Coronary Heart Disease Events and Are Enriched for Results From Genome-Wide Association Studies. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	104
64	Sickle Cell Trait and the Risk of ESRD in Blacks. Journal of the American Society of Nephrology: JASN, 2017, 28, 2180-2187.	6.1	79
65	Phenomapping for the Identification of Hypertensive Patients with the Myocardial Substrate for Heart Failure with Preserved Ejection Fraction. Journal of Cardiovascular Translational Research, 2017, 10, 275-284.	2.4	61
66	Genetics of Blood Pressure: New Insights Into a Complex Trait. American Journal of Kidney Diseases, 2017, 69, 723-725.	1.9	3
67	Local Ancestry and Clinical Cardiovascular Events Among African Americans From the Atherosclerosis Risk in Communities Study. Journal of the American Heart Association, 2017, 6, .	3.7	22
68	Genome- and CD4 + T-cell methylome-wide association study of circulating trimethylamine-N-oxide in the Genetics of Lipid Lowering Drugs and Diet Network (GOLDN). Journal of Nutrition & Intermediary Metabolism, 2017, 8, 1-7.	1.7	11
69	Stroke in Indigenous Africans, African Americans, and European Americans. Stroke, 2017, 48, 1169-1175.	2.0	44
70	Advancing stroke genomic research in the age of Trans-Omics big data science: Emerging priorities and opportunities. Journal of the Neurological Sciences, 2017, 382, 18-28.	0.6	15
71	Chronic kidney disease and incident apparent treatmentâ€resistant hypertension among blacks: Data from the Jackson Heart Study. Journal of Clinical Hypertension, 2017, 19, 1117-1124.	2.0	13
72	An epigenome-wide association study of inflammatory response to fenofibrate in the Genetics of Lipid Lowering Drugs and Diet Network. Pharmacogenomics, 2017, 18, 1333-1341.	1.3	16

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73	Association of Estimated SodiumÂIntakeÂWith Adverse Cardiac Structure andÂFunction. Journal of the American College of Cardiology, 2017, 70, 715-724.	2.8	21
74	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	6.2	154
75	Influence of common and rare genetic variation on warfarin dose among Africanâ€“Americans and Europeanâ€“Americans using the exome array. Pharmacogenomics, 2017, 18, 1059-1073.	1.3	12
76	Genome-wide admixture and association study of subclinical atherosclerosis in the Womenâ€™s Interagency HIV Study (WIHS). PLoS ONE, 2017, 12, e0188725.	2.5	11
77	Association of Body Mass Index with DNA Methylation and Gene Expression in Blood Cells and Relations to Cardiometabolic Disease: A Mendelian Randomization Approach. PLoS Medicine, 2017, 14, e1002215.	8.4	246
78	Visual Sensory and Visual-Cognitive Function and Rate of Crash and Near-Crash Involvement Among Older Drivers Using Naturalistic Driving Data. , 2017, 58, 2959.		39
79	Discovery and fine-mapping of adiposity loci using high density imputation of genome-wide association studies in individuals of African ancestry: African Ancestry Anthropometry Genetics Consortium. PLoS Genetics, 2017, 13, e1006719.	3.5	98
80	Behavior related genes, dietary preferences and anthropometric traits. FASEB Journal, 2017, 31, .	0.5	1
81	Whole Exome Analyses to Examine the Impact of Rare Variants on Left Ventricular Traits in African American Participants from the HyperGEN and GENOA Studies. Journal of Hypertension and Management, 2017, 3, .	0.2	0
82	A genome-wide study of lipid response to fenofibrate in Caucasians. Pharmacogenetics and Genomics, 2016, 26, 324-333.	1.5	12
83	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	6.2	60
84	Admixture mapping of serum vitamin D and parathyroid hormone concentrations in the African Americanâ€”Diabetes Heart Study. Bone, 2016, 87, 71-77.	2.9	5
85	Epigenetics of Lipid Phenotypes. Current Cardiovascular Risk Reports, 2016, 10, 1.	2.0	20
86	Association of Central Adiposity With Adverse Cardiac Mechanics. Circulation: Cardiovascular Imaging, 2016, 9, .	2.6	65
87	The effects of omegaâ€3 polyunsaturated fatty acids and genetic variants on methylation levels of the interleukinâ€6 gene promoter. Molecular Nutrition and Food Research, 2016, 60, 410-419.	3.3	41
88	Archeological Echocardiography: Digitization and Speckle Tracking Analysis of Archival Echocardiograms in the Hyper<scp>GEN</scp> Study. Echocardiography, 2016, 33, 386-397.	0.9	24
89	Trans-ethnic Meta-analysis and Functional Annotation Illuminates theÂGenetic Architecture of Fasting Glucose and Insulin. American Journal of Human Genetics, 2016, 99, 56-75.	6.2	55
90	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. Lancet Neurology, The, 2016, 15, 174-184.	10.2	217

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91	Driving with pets and motor vehicle collision involvement among older drivers: A prospective population-based study. Accident Analysis and Prevention, 2016, 88, 169-174.	5.7	3
92	APOL1nephropathy risk variants are associated with altered high-density lipoprotein profiles in African Americans. Nephrology Dialysis Transplantation, 2016, 31, 602-608.	0.7	23
93	Association of DNA Methylation at CPT1A Locus with Metabolic Syndrome in the Genetics of Lipid Lowering Drugs and Diet Network (GOLDN) Study. PLoS ONE, 2016, 11, e0145789.	2.5	54
94	Heritable DNA Methylation in CD4+ Cells among Complex Families Displays Genetic and Non-Genetic Effects. PLoS ONE, 2016, 11, e0165488.	2.5	19
95	Epigenome-wide study identifies novel methylation loci associated with body mass index and waist circumference. Obesity, 2015, 23, 1493-1501.	3.0	152
96	PCSK9 variation and association with blood pressure in African Americans: preliminary findings from the HyperGEN and REGARDS studies. Frontiers in Genetics, 2015, 6, 136.	2.3	25
97	Deep sequencing of RYR3 gene identifies rare and common variants associated with increased carotid intima-media thickness (cIMT) in HIV-infected individuals. Journal of Human Genetics, 2015, 60, 63-67.	2.3	3
98	Apparent Treatment-resistant Hypertension Among Individuals with History of Stroke or Transient Ischemic Attack. American Journal of Medicine, 2015, 128, 707-714.e2.	1.5	23
99	Epigenome-wide association study (EWAS) of BMI, BMI change and waist circumference in African American adults identifies multiple replicated loci. Human Molecular Genetics, 2015, 24, 4464-4479.	2.9	289
100	The effects of angiotensinogen gene polymorphisms on cardiovascular disease outcomes during antihypertensive treatment in the GenHAT study. Frontiers in Pharmacology, 2014, 5, 210.	3.5	14
101	RYR3 gene variants in subclinical atherosclerosis among HIV-infected women in the Women's Interagency HIV Study (WIHS). Atherosclerosis, 2014, 233, 666-672.	0.8	7
102	Apparent treatment-resistant hypertension and risk for stroke, coronary heart disease, and all-cause mortality. Journal of the American Society of Hypertension, 2014, 8, 405-413.	2.3	113
103	Epigenome-Wide Association Study of Fasting Blood Lipids in the Genetics of Lipid-Lowering Drugs and Diet Network Study. Circulation, 2014, 130, 565-572.	1.6	190
104	Healthy Lifestyle Factors and Risk of Cardiovascular Events and Mortality in Treatment-Resistant Hypertension. Hypertension, 2014, 64, 465-471.	2.7	60
105	Genomics of Post-Prandial Lipidomic Phenotypes in the Genetics of Lipid Lowering Drugs and Diet Network (GOLDN) Study. PLoS ONE, 2014, 9, e99509.	2.5	21
106	Genetic and Adverse Health Outcome Associations with Treatment Resistant Hypertension in GenHAT. International Journal of Hypertension, 2013, 2013, 1-10.	1.3	16
107	Prevalence and Correlates of Low Medication Adherence in Apparent Treatmentâ€Resistant Hypertension. Journal of Clinical Hypertension, 2012, 14, 694-700.	2.0	70
108	Rare PPARA variants and extreme response to fenofibrate in the Genetics of Lipid-Lowering Drugs and Diet Network Study. Pharmacogenetics and Genomics, 2012, 22, 367-372.	1.5	11

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109	Genome-Wide Detection of Allele Specific Copy Number Variation Associated with Insulin Resistance in African Americans from the HyperGEN Study. PLoS ONE, 2011, 6, e24052.	2.5	45
110	Pharmacogenetic association of hypertension candidate genes with fasting glucose in the GenHAT Study. Journal of Hypertension, 2010, 28, 2076-2083.	0.5	31
111	Apolipoprotein E Polymorphisms and Postprandial Triglyceridemia Before and After Fenofibrate Treatment in the Genetics of Lipid Lowering and Diet Network (GOLDN) Study. Circulation: Cardiovascular Genetics, 2010, 3, 462-467.	5.1	39