Christy L Avery

List of Publications by Year
in descending order

84 papers	3,103 citations	331670 21 h-index	189892 50 g-index
90 all docs	90 docs citations	90 times ranked	7220 citing authors

#	Article	IF	Citations
1	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	27.8	679
2	Genetic Diversity and Association Studies in US Hispanic/Latino Populations: Applications in the Hispanic Community Health Study/Study of Latinos. American Journal of Human Genetics, 2016, 98, 165-184.	6.2	266
3	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. Nature Communications, 2014, 5, 5068.	12.8	216
4	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
5	American Heart Association's Life's Simple 7: Avoiding Heart Failure and Preserving Cardiac Structure and Function. American Journal of Medicine, 2015, 128, 970-976.e2.	1.5	153
6	Reducing the Blood Pressure–Related Burden of Cardiovascular Disease: Impact of Achievable Improvements in Blood Pressure Prevention and Control. Journal of the American Heart Association, 2015, 4, e002276.	3.7	148
7	Estimating Error in Using Ambient PM2.5 Concentrations as Proxies for Personal Exposures: A Review. Epidemiology, 2010, 21, 215-223.	2.7	102
8	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	12.8	95
9	A Phenomics-Based Strategy Identifies Loci on APOC1, BRAP, and PLCG1 Associated with Metabolic Syndrome Phenotype Domains. PLoS Genetics, 2011, 7, e1002322.	3.5	92
10	The Population Burden of Heart Failure Attributable to Modifiable Risk Factors. Journal of the American College of Cardiology, 2012, 60, 1640-1646.	2.8	91
11	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
12	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
13	Variation in Population Attributable Fraction of Dementia Associated With Potentially Modifiable Risk Factors by Race and Ethnicity in the US. JAMA Network Open, 2022, 5, e2219672.	5.9	49
14	Estimating Error in Using Residential Outdoor PM$_{2.5}$ Concentrations as Proxies for Personal Exposures: A Meta-analysis. Environmental Health Perspectives, 2010, 118, 673-678.	6.0	48
15	A powerful statistical framework for generalization testing in GWAS, with application to the HCHS/SOL. Genetic Epidemiology, 2017, 41, 251-258.	1.3	41
16	Outcomes of Patients With Anemia and Acute Decompensated Heart Failure With Preserved Versus Reduced Ejection Fraction (from the ARIC Study Community Surveillance). American Journal of Cardiology, 2014, 114, 1850-1854.	1.6	40
17	Longitudinal Patterns of Change in Systolic Blood Pressure and Incidence of Cardiovascular Disease. Hypertension, 2016, 67, 1150-1156.	2.7	37
18	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

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19	Heterogeneity in Blood Pressure Transitions Over the Life Course. JAMA Cardiology, 2017, 2, 653.	6.1	31
20	Meta-analysis of genome-wide association studies of HDL cholesterol response to statins. Journal of Medical Genetics, 2016, 53, 835-845.	3.2	28
21	Analyses of biomarker traits in diverse UK biobank participants identify associations missed by European-centric analysis strategies. Journal of Human Genetics, 2022, 67, 87-93.	2.3	27
22	Midlife Alcohol Consumption and the Risk of Stroke in the Atherosclerosis Risk in Communities Study. Stroke, 2015, 46, 3124-3130.	2.0	24
23	US acculturation and poor sleep among an intergenerational cohort of adult Latinos in Sacramento, California. Sleep, 2019, 42, .	1.1	24
24	Waist Circumference Change is Associated with Blood Pressure Change Independent of BMI Change. Obesity, 2020, 28, 146-153.	3.0	24
25	GWAS of the electrocardiographic QT interval in Hispanics/Latinos generalizes previously identified loci and identifies population-specific signals. Scientific Reports, 2017, 7, 17075.	3.3	23
26	Cardiovascular Genetic Risk Testing for Targeting Statin Therapy in the Primary Prevention of Atherosclerotic Cardiovascular Disease. Circulation: Cardiovascular Quality and Outcomes, 2018, 11, e004171.	2.2	22
27	Circulating Short-Chain Fatty Acids Are Positively Associated with Adiposity Measures in Chinese Adults. Nutrients, 2020, 12, 2127.	4.1	21
28	Rapid detection of identity-by-descent tracts for mega-scale datasets. Nature Communications, 2021, 12, 3546.	12.8	20
29	Linkage Analysis of Diabetes Status Among Hypertensive Families: The Hypertension Genetic Epidemiology Network Study. Diabetes, 2004, 53, 3307-3312.	0.6	19
30	Fine mapping of QT interval regions in global populations refines previously identified QT interval loci and identifies signals unique to African and Hispanic descent populations. Heart Rhythm, 2017, 14, 572-580.	0.7	19
31	Evaluating markers of epithelial-mesenchymal transition to identify cancer patients at risk for metastatic disease. Clinical and Experimental Metastasis, 2016, 33, 53-62.	3.3	18
32	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. Heart Rhythm, 2017, 14, 1675-1684.	0.7	18
33	Gut Microbiota and Host Plasma Metabolites in Association with Blood Pressure in Chinese Adults. Hypertension, 2021, 77, 706-717.	2.7	18
34	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
35	Discovery, fine-mapping, and conditional analyses of genetic variants associated with C-reactive protein in multiethnic populations using the Metabochip in the Population Architecture using Genomics and Epidemiology (PAGE) study. Human Molecular Genetics, 2018, 27, 2940-2953.	2.9	16
36	Longitudinal Associations of US Acculturation With Cognitive Performance, Cognitive Impairment, and Dementia. American Journal of Epidemiology, 2020, 189, 1292-1305.	3.4	16

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37	A phenome-wide association study (PheWAS) in the Population Architecture using Genomics and Epidemiology (PAGE) study reveals potential pleiotropy in African Americans. PLoS ONE, 2019, 14, e0226771.	2.5	15
38	Multi-ethnic GWAS and fine-mapping of glycaemic traits identify novel loci in the PAGE Study. Diabetologia, 2022, 65, 477-489.	6.3	15
39	Long-term association between self-reported signs and symptoms and heart failure hospitalizations: the Atherosclerosis Risk In Communities (ARIC) Study. European Journal of Heart Failure, 2010, 12, 232-238.	7.1	14
40	Impact of long-term measures of glucose and blood pressure on the retinal microvasculature. Atherosclerosis, 2012, 225, 412-417.	0.8	14
41	Fine-Mapping and Initial Characterization of QT Interval Loci in African Americans. PLoS Genetics, 2012, 8, e1002870.	3.5	13
42	Sparse meta-analysis with high-dimensional data. Biostatistics, 2016, 17, 205-220.	1.5	13
43	Genome-wide association study of PR interval in Hispanics/Latinos identifies novel locus at *ID2*. Heart, 2018, 104, 904-911.	2.9	12
44	Transcriptome-Wide Association Study of Blood Cell Traits in African Ancestry and Hispanic/Latino Populations. Genes, 2021, 12, 1049.	2.4	11
45	Changes in nonnutritive sweetener intake in a cohort of preschoolers after the implementation of Chile's Law of Food Labelling and Advertising. Pediatric Obesity, 2022, 17, e12895.	2.8	11
46	Accuracy of haplotype estimation in a region of low linkage disequilibrium. BMC Genetics, 2005, 6, S80.	2.7	10
47	Disparities in Early Transitions to Obesity in Contemporary Multi-Ethnic U.S. Populations. PLoS ONE, 2016, 11, e0158025.	2.5	10
48	Obesity Duration, Severity, and Distribution Trajectories and Cardiovascular Disease Risk in the Atherosclerosis Risk in Communities Study. Journal of the American Heart Association, 2021, 10, e019946.	3.7	10
49	A genome-wide interaction analysis of tricyclic/tetracyclic antidepressants and RR and QT intervals: a pharmacogenomics study from the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium. Journal of Medical Genetics, 2017, 54, 313-323.	3.2	9
50	Associations of sodium and potassium consumption with the gut microbiota and host metabolites in a population-based study in Chinese adults. American Journal of Clinical Nutrition, 2020, 112, 1599-1612.	4.7	9
51	Genome-wide association of trajectories of systolic blood pressure change. BMC Proceedings, 2016, 10, 321-327.	1.6	8
52	GWAS of QRS duration identifies new loci specific to Hispanic/Latino populations. PLoS ONE, 2019, 14, e0217796.	2.5	8
53	Evidence of heterogeneity in statin-associated type 2 diabetes mellitus risk: A meta-analysis of randomized controlled trials and observational studies. Diabetes Research and Clinical Practice, 2019, 151, 96-105.	2.8	8
54	Genome-wide Association Study of Susceptibility to Particulate Matter–Associated QT Prolongation. Environmental Health Perspectives, 2017, 125, 067002.	6.0	7

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55	Genetic association studies and the effect of misclassification and selection bias in putative confounders. BMC Proceedings, 2009, 3, S48.	1.6	6
56	Primary prevention of chronic kidney disease through population‐based strategies for blood pressure control: The ARIC study. Journal of Clinical Hypertension, 2018, 20, 1018-1026.	2.0	6
57	Comparison of 20-Year Obesity-Associated Cancer Mortality Trends With Heart Disease Mortality Trends in the US. JAMA Network Open, 2021, 4, e218356.	5.9	6
58	Multi-ethnic genome-wide association analyses of white blood cell and platelet traits in the Population Architecture using Genomics and Epidemiology (PAGE) study. BMC Genomics, 2021, 22, 432.	2.8	6
59	Associations Between Echocardiographic Arterial Compliance and Incident Cardiovascular Disease in Blacks: The ARIC Study. American Journal of Hypertension, 2015, 28, 81-88.	2.0	5
60	Predicted gene expression in ancestrally diverse populations leads to discovery of susceptibility loci for lifestyle and cardiometabolic traits. American Journal of Human Genetics, 2022, 109, 669-679.	6.2	5
61	Strengthening Causal Inference in Exposomics Research: Application of Genetic Data and Methods. Environmental Health Perspectives, 2022, 130, 55001.	6.0	5
62	Targeting physical activity interventions for adults: When should intervention occur?. Preventive Medicine, 2017, 97, 13-18.	3.4	4
63	Genome-wide association study and meta-analysis identify loci associated with ventricular and supraventricular ectopy. Scientific Reports, 2018, 8, 5675.	3.3	4
64	A Family Based Study of Carbon Monoxide and Nitric Oxide Signalling Genes and Preeclampsia. Paediatric and Perinatal Epidemiology, 2018, 32, 1-12.	1.7	4
65	Diagnostic accuracy and prediction increment of markers of epithelial-mesenchymal transition to assess cancer cell detachment from primary tumors. BMC Cancer, 2018, 18, 82.	2.6	4
66	Multi-Ethnic Genome-Wide Association Study of Decomposed Cardioelectric Phenotypes Illustrates Strategies to Identify and Characterize Evidence of Shared Genetic Effects for Complex Traits. Circulation Genomic and Precision Medicine, 2020, 13, e002680.	3.6	4
67	Population-based genetic effects for developmental stuttering. Human Genetics and Genomics Advances, 2022, 3, 100073.	1.7	4
68	Comparison of 2 models for gene–environment interactions: an example of simulated gene–medication interactions on systolic blood pressure in family-based data. BMC Proceedings, 2016, 10, 371-377.	1.6	3
69	Projections of incident atherosclerotic cardiovascular disease and incident type 2 diabetes across evolving statin treatment guidelines and recommendations: A modelling study. PLoS Medicine, 2020, 17, e1003280.	8.4	3
70	Trends in US Cancer and Heart Disease Mortality, 1999–2018. Circulation, 2021, 143, 287-288.	1.6	3
71	Leisure-time physical activity volume, intensity, and duration from mid- to late-life in U.S. subpopulations by race and sex. The Atherosclerosis Risk In Communities (ARIC) Study. Aging, 2020, 12, 4592-4602.	3.1	2
72	Transitions from Ideal to Intermediate Cholesterol Levels may vary by Cholesterol Metric. Scientific Reports, 2018, 8, 2782.	3.3	1

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73	Comparison of adaptive multiple phenotype association tests using summary statistics in genome-wide association studies. Human Molecular Genetics, 2021, 30, 1371-1383.	2.9	1
74	GWAS of Variant-by-Thiazide Interaction on Lipids Identifies a Novel Low-Density Lipoprotein Cholesterol Locus. Circulation Research, 0, , .	4.5	1
75	Abstract P113: The Probability of Maintaining Ideal Levels of Glucose in US Populations: The Hispanic Community Health Study/Study of Latinos (HCHS/SOL) and the National Health and Nutrition Examination Survey (NHANES). Circulation, 2014, 129, .	1.6	0
76	Abstract P261: Genome-wide Association Study of Susceptibility to Particulate Matter-associated Reduced Heart Rate Variability. Circulation, 2016, 133, .	1.6	0
77	Abstract 053: Genome-wide Tcea3 -SNP Interaction Study Identifies Novel QT Interval Loci. Circulation, 2018, 137, .	1.6	0
78	Do Genetic Variants Modify the Effect of Smoking on Risk of Preeclampsia in Pregnancy?. American Journal of Perinatology, 2024, 41, 044-052.	1.4	0
79	Title is missing!. , 2020, 17, e1003280.		0
80	Title is missing!. , 2020, 17, e1003280.		0
81	Title is missing!. , 2020, 17, e1003280.		0
82	Title is missing!. , 2020, 17, e1003280.		0
83	Title is missing!. , 2020, 17, e1003280.		0
84	Abstract P291: Projected Heterogeneity in the Long-term Effects of Obesity Interventions Across the Life Course. Circulation, 2016, 133, .	1.6	0