Erin B Ware

List of Publications by Year
in descending order

49 papers	3,913 citations	430442 18 h-index	197535 49 g-index
63 all docs	63 docs citations	63 times ranked	9600 citing authors

#	Article	IF	Citations
1	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
2	Epigenetic Signatures of Cigarette Smoking. Circulation: Cardiovascular Genetics, 2016, 9, 436-447.	5.1	678
3	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
4	A meta-analysis of genome-wide association studies identifies multiple longevity genes. Nature Communications, 2019, 10, 3669.	5.8	214
5	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
6	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.	2.6	123
7	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.	9.4	112
8	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	3.3	110
9	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.	1.5	98
10	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	1.1	94
11	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. PLoS Genetics, 2017, 13, e1006728.	1.5	88
12	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. Biological Psychiatry, 2017, 82, 322-329.	0.7	84
13	A Statistical Approach for Testing Cross-Phenotype Effects of Rare Variants. American Journal of Human Genetics, 2016, 98, 525-540.	2.6	75
14	Current Applications of Genetic Risk Scores to Cardiovascular Outcomes and Subclinical Phenotypes. Current Epidemiology Reports, 2015, 2, 180-190.	1.1	70
15	Saliva cell type DNA methylation reference panel for epidemiological studies in children. Epigenetics, 2022, 17, 161-177.	1.3	37
16	A multi-ancestry genome-wide study incorporating geneâ€"smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	1.4	31
17	A Statistical Approach for Rare-Variant Association Testing in Affected Sibships. American Journal of Human Genetics, 2015, 96, 543-554.	2.6	21
18	Key influence of sex on urine volume and osmolality. Biology of Sex Differences, 2016, 7, 12.	1.8	19

#	Article	IF	Citations
19	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.	2.6	18
20	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. Nature Communications, 2021, 12, 3987.	5.8	18
21	Rare variants in fox-1 homolog A (RBFOX1) are associated with lower blood pressure. PLoS Genetics, 2017, 13, e1006678.	1.5	18
22	Effect of Demographics on Excretion of Key Urinary Factors Related to Kidney Stone Risk. Urology, 2015, 86, 690-696.	0.5	17
23	Hormone therapy and urine protein excretion: a multiracial cohort study, systematic review, and meta-analysis. Menopause, 2018, 25, 625-634.	0.8	17
24	Considering the APOE locus in Alzheimer's disease polygenic scores in the Health and Retirement Study: a longitudinal panel study. BMC Medical Genomics, 2020, 13, 164.	0.7	17
25	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	4.1	17
26	DNA methylation age is associated with an altered hemostatic profile in a multiethnic meta-analysis. Blood, 2018, 132, 1842-1850.	0.6	16
27	SLC2A9 Genotype Is Associated with SLC2A9 Gene Expression and Urinary Uric Acid Concentration. PLoS ONE, 2015, 10, e0128593.	1.1	16
28	Type 2 Diabetes and Cognitive Status in the Health and Retirement Study: A Mendelian Randomization Approach. Frontiers in Genetics, 2021, 12, 634767.	1.1	15
29	Heritability of dietary traits that contribute to nephrolithiasis in a cohort of adult sibships. Journal of Nephrology, 2016, 29, 45-51.	0.9	13
30	Comparative genome-wide association studies of a depressive symptom phenotype in a repeated measures setting by race/ethnicity in the multi-ethnic study of atherosclerosis. BMC Genetics, 2015, 16, 118.	2.7	12
31	A data-driven prospective study of dementia among older adults in the United States. PLoS ONE, 2020, 15, e0239994.	1.1	12
32	Interaction between Social/Psychosocial Factors and Genetic Variants on Body Mass Index: A Gene-Environment Interaction Analysis in a Longitudinal Setting. International Journal of Environmental Research and Public Health, 2017, 14, 1153.	1.2	11
33	Social regulation of inflammation related gene expression in the multi-ethnic study of atherosclerosis. Psychoneuroendocrinology, 2020, 117, 104654.	1.3	11
34	Expression of socially sensitive genes: The multi-ethnic study of atherosclerosis. PLoS ONE, 2019, 14, e0214061.	1.1	9
35	Prenatal Particulate Matter Exposure Is Associated with Saliva DNA Methylation at Age 15: Applying Cumulative DNA Methylation Scores as an Exposure Biomarker. Toxics, 2021, 9, 262.	1.6	9
36	Applying Novel Methods for Assessing Individual- and Neighborhood-Level Social and Psychosocial Environment Interactions with Genetic Factors in the Prediction of Depressive Symptoms in the Multi-Ethnic Study of Atherosclerosis. Behavior Genetics, 2016, 46, 89-99.	1.4	8

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37	Polymorphisms in Renal Ammonia Metabolism Genes Correlate With 24-Hour Urine pH. Kidney International Reports, 2017, 2, 1111-1121.	0.4	8
38	Cumulative Genetic Risk and APOE Îµ4 Are Independently Associated With Dementia Status in a Multiethnic, Population-Based Cohort. Neurology: Genetics, 2021, 7, e576.	0.9	7
39	Association between Stress Response Genes and Features of Diurnal Cortisol Curves in the Multi-Ethnic Study of Atherosclerosis: A New Multi-Phenotype Approach for Gene-Based Association Tests. PLoS ONE, 2015, 10, e0126637.	1.1	6
40	Genome-wide Association Study of 24-Hour Urinary Excretion of Calcium, Magnesium, and Uric Acid. Mayo Clinic Proceedings Innovations, Quality & Outcomes, 2019, 3, 448-460.	1.2	6
41	Testing crossâ€phenotype effects of rare variants in longitudinal studies of complex traits. Genetic Epidemiology, 2018, 42, 320-332.	0.6	5
42	Combined linkage and association analysis identifies rare and low frequency variants for blood pressure at 1q31. European Journal of Human Genetics, 2019, 27, 269-277.	1.4	5
43	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. Human Genetics and Genomics Advances, 2021, 2, 100013.	1.0	2
44	Type 2 diabetes and dementia in the Health and Retirement Study: A Mendelian randomization approach. Alzheimer's and Dementia, 2020, 16, e041220.	0.4	0
45	Linking gene regions jointly with environment and depression. , 2021, , 69-76.		0
46	A data-driven prospective study of dementia among older adults in the United States. , 2020, 15, e0239994.		0
47	A data-driven prospective study of dementia among older adults in the United States. , 2020, 15, e0239994.		0
48	A data-driven prospective study of dementia among older adults in the United States. , 2020, 15, e0239994.		0
49	A data-driven prospective study of dementia among older adults in the United States. , 2020, 15, e0239994.		0