

# Yun Zhu

## List of Publications by Year in descending order

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Version: 2024-02-01

35  
papers

1,359  
citations

394421

19  
h-index

345221

36  
g-index

36  
all docs

36  
docs citations

36  
times ranked

2970  
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene and pathway-based second-wave analysis of genome-wide association studies. <i>European Journal of Human Genetics</i> , 2010, 18, 111-117.	2.8	228
2	Short Leukocyte Telomere Length Predicts Risk of Diabetes in American Indians: the Strong Heart Family Study. <i>Diabetes</i> , 2014, 63, 354-362.	0.6	133
3	Genome-wide gene and pathway analysis. <i>European Journal of Human Genetics</i> , 2010, 18, 1045-1053.	2.8	99
4	A genome-wide profiling of brain DNA hydroxymethylation in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2017, 13, 674-688.	0.8	83
5	Brain and blood metabolome for Alzheimer's dementia: findings from a targeted metabolomics analysis. <i>Neurobiology of Aging</i> , 2020, 86, 123-133.	3.1	83
6	Childhood Trauma, DNA Methylation of Stress-Related Genes, and Depression: Findings From Two Monozygotic Twin Studies. <i>Psychosomatic Medicine</i> , 2018, 80, 599-608.	2.0	74
7	A Novel Statistic for Genome-Wide Interaction Analysis. <i>PLoS Genetics</i> , 2010, 6, e1001131.	3.5	64
8	Urinary triclosan concentrations are inversely associated with body mass index and waist circumference in the US general population: Experience in NHANES 2003-2010. <i>International Journal of Hygiene and Environmental Health</i> , 2015, 218, 401-406.	4.3	60
9	Genome-wide profiling of DNA methylome and transcriptome in peripheral blood monocytes for major depression: A Monozygotic Discordant Twin Study. <i>Translational Psychiatry</i> , 2019, 9, 215.	4.8	49
10	Family-Based Association Studies for Next-Generation Sequencing. <i>American Journal of Human Genetics</i> , 2012, 90, 1028-1045.	6.2	48
11	Quantitative trait locus analysis for next-generation sequencing with the functional linear models. <i>Journal of Medical Genetics</i> , 2012, 49, 513-524.	3.2	38
12	Shared Causal Paths underlying Alzheimer's dementia and Type 2 Diabetes. <i>Scientific Reports</i> , 2020, 10, 4107.	3.3	37
13	Effects of shear stresses and antioxidant concentrations on the production of reactive oxygen species in lung cancer cells. <i>Biomicrofluidics</i> , 2013, 7, 064108.	2.4	31
14	A Gene-Family Analysis of 61 Genetic Variants in the Nicotinic Acetylcholine Receptor Genes for Insulin Resistance and Type 2 Diabetes in American Indians. <i>Diabetes</i> , 2012, 61, 1888-1894.	0.6	27
15	DNA methylation variability in Alzheimer's disease. <i>Neurobiology of Aging</i> , 2019, 76, 35-44.	3.1	25
16	Genome-wide gene-gene interaction analysis for next-generation sequencing. <i>European Journal of Human Genetics</i> , 2016, 24, 421-428.	2.8	23
17	Urinary metals and leukocyte telomere length in American Indian communities: The Strong Heart and the Strong Heart Family Study. <i>Environmental Pollution</i> , 2019, 246, 311-318.	7.5	23
18	Metabolic profiles of biological aging in American Indians: The strong heart family study. <i>Aging</i> , 2014, 6, 176-186.	3.1	22

#	ARTICLE	IF	CITATIONS
19	Smoothed functional principal component analysis for testing association of the entire allelic spectrum of genetic variation. <i>European Journal of Human Genetics</i> , 2013, 21, 217-224.	2.8	21
20	DNA Methylation of Five Core Circadian Genes Jointly Contributes to Glucose Metabolism: A Gene-Set Analysis in Monozygotic Twins. <i>Frontiers in Genetics</i> , 2019, 10, 329.	2.3	20
21	Implication of next-generation sequencing on association studies. <i>BMC Genomics</i> , 2011, 12, 322.	2.8	19
22	Telomere length and cancer mortality in American Indians: the Strong Heart Study. <i>GeroScience</i> , 2019, 41, 351-361.	4.6	18
23	QTL mapping of leukocyte telomere length in American Indians: The Strong Heart Family Study. <i>Aging</i> , 2013, 5, 704-716.	3.1	17
24	Metabolic Profiles of Obesity in American Indians: The Strong Heart Family Study. <i>PLoS ONE</i> , 2016, 11, e0159548.	2.5	16
25	Perinatal Exposure to Western Diet Programs Autonomic Dysfunction in the Male Offspring. <i>Cellular and Molecular Neurobiology</i> , 2018, 38, 233-242.	3.3	15
26	Impact of biological aging on arterial aging in American Indians: findings from the Strong Heart Family Study. <i>Aging</i> , 2016, 8, 1583-1592.	3.1	13
27	A quadratically regularized functional canonical correlation analysis for identifying the global structure of pleiotropy with NGS data. <i>PLoS Computational Biology</i> , 2017, 13, e1005788.	3.2	12
28	Weighted pedigree-based statistics for testing the association of rare variants. <i>BMC Genomics</i> , 2012, 13, 667.	2.8	11
29	Joint Associations of 61 Genetic Variants in the Nicotinic Acetylcholine Receptor Genes with Subclinical Atherosclerosis in American Indians. <i>Circulation: Cardiovascular Genetics</i> , 2013, 6, 89-96.	5.1	11
30	Joint Association of Nicotinic Acetylcholine Receptor Variants with Abdominal Obesity in American Indians: The Strong Heart Family Study. <i>PLoS ONE</i> , 2014, 9, e102220.	2.5	10
31	Genetic variants in nicotinic acetylcholine receptor genes jointly contribute to kidney function in American Indians. <i>Journal of Hypertension</i> , 2014, 32, 1042-1049.	0.5	7
32	Pathway analysis with next-generation sequencing data. <i>European Journal of Human Genetics</i> , 2015, 23, 507-515.	2.8	7
33	Depressive symptoms are associated with leukocyte telomere length in American Indians: findings from the Strong Heart Family Study. <i>Aging</i> , 2016, 8, 2961-2970.	3.1	6
34	Methylation biomarkers of polybrominated diphenyl ethers (PBDEs) and association with breast cancer risk at the time of menopause. <i>Environment International</i> , 2021, 156, 106772.	10.0	5
35	A Novel Genome-Information Content-Based Statistic for Genome-Wide Association Analysis Designed for Next-Generation Sequencing Data. <i>Journal of Computational Biology</i> , 2012, 19, 731-744.	1.6	3