

# Zongli Xu

## List of Publications by Year in descending order

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Version: 2024-02-01

67  
papers

5,174  
citations

117625

34  
h-index

106344

65  
g-index

68  
all docs

68  
docs citations

68  
times ranked

9634  
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. <i>American Journal of Human Genetics</i> , 2016, 98, 680-696.	6.2	717
2	SNPinfo: integrating GWAS and candidate gene information into functional SNP selection for genetic association studies. <i>Nucleic Acids Research</i> , 2009, 37, W600-W605.	14.5	655
3	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. <i>Nature Genetics</i> , 2010, 42, 978-984.	21.4	493
4	ENmix: a novel background correction method for Illumina HumanMethylation450 BeadChip. <i>Nucleic Acids Research</i> , 2016, 44, e20-e20.	14.5	267
5	Maternal BMI at the start of pregnancy and offspring epigenome-wide DNA methylation: findings from the pregnancy and childhood epigenetics (PACE) consortium. <i>Human Molecular Genetics</i> , 2017, 26, 4067-4085.	2.9	211
6	Identification of DNA Methylation Changes in Newborns Related to Maternal Smoking during Pregnancy. <i>Environmental Health Perspectives</i> , 2014, 122, 1147-1153.	6.0	171
7	Sinomenine, a natural dextrorotatory morphinan analog, is anti-inflammatory and neuroprotective through inhibition of microglial NADPH oxidase. <i>Journal of Neuroinflammation</i> , 2007, 4, 23.	7.2	134
8	Methylation-Based Biological Age and Breast Cancer Risk. <i>Journal of the National Cancer Institute</i> , 2019, 111, 1051-1058.	6.3	124
9	Epigenome-wide Association Study of Breast Cancer Using Prospectively Collected Sister Study Samples. <i>Journal of the National Cancer Institute</i> , 2013, 105, 694-700.	6.3	119
10	RCP: a novel probe design bias correction method for Illumina Methylation BeadChip. <i>Bioinformatics</i> , 2016, 32, 2659-2663.	4.1	107
11	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. <i>International Journal of Epidemiology</i> , 2018, 47, 22-23u.	1.9	105
12	Genome-wide age-related DNA methylation changes in blood and other tissues relate to histone modification, expression and cancer. <i>Carcinogenesis</i> , 2014, 35, 356-364.	2.8	104
13	Serum microRNA expression as an early marker for breast cancer risk in prospectively collected samples from the Sister Study cohort. <i>Breast Cancer Research</i> , 2013, 15, R42.	5.0	96
14	RELIC: a novel dye-bias correction method for Illumina Methylation BeadChip. <i>BMC Genomics</i> , 2017, 18, 4.	2.8	96
15	CpG Sites Associated with Cigarette Smoking: Analysis of Epigenome-Wide Data from the Sister Study. <i>Environmental Health Perspectives</i> , 2014, 122, 673-678.	6.0	91
16	Potential sex differences in nonmotor symptoms in early drug-naive Parkinson disease. <i>Neurology</i> , 2015, 84, 2107-2115.	1.1	90
17	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.	8.8	90
18	Blood DNA Methylation and Breast Cancer: A Prospective Case-Cohort Analysis in the Sister Study. <i>Journal of the National Cancer Institute</i> , 2020, 112, 87-94.	6.3	76

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19	Genetic polymorphism and prostate cancer aggressiveness: A case-only study of 1,536 GWAS and candidate SNPs in African-Americans and European-Americans. <i>Prostate</i> , 2013, 73, 11-22.	2.3	72
20	Recreational and household physical activity at different time points and DNA global methylation. <i>European Journal of Cancer</i> , 2013, 49, 2199-2206.	2.8	71
21	Antimutagenicity of cinnamaldehyde and vanillin in human cells: Global gene expression and possible role of DNA damage and repair. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2007, 616, 60-69.	1.0	70
22	Air pollution, particulate matter composition and methylation-based biologic age. <i>Environment International</i> , 2019, 132, 105071.	10.0	64
23	Maternal Age at Delivery Is Associated with an Epigenetic Signature in Both Newborns and Adults. <i>PLoS ONE</i> , 2016, 11, e0156361.	2.5	62
24	Associations of Body Composition and Physical Activity Level With Multiple Measures of Epigenetic Age Acceleration. <i>American Journal of Epidemiology</i> , 2021, 190, 984-993.	3.4	53
25	Improving Quantitative Trait Loci Mapping Resolution in Experimental Crosses by the Use of Genotypically Selected Samples. <i>Genetics</i> , 2005, 170, 401-408.	2.9	50
26	Association of Neighborhood Deprivation With Epigenetic Aging Using 4 Clock Metrics. <i>JAMA Network Open</i> , 2020, 3, e2024329.	5.9	50
27	Vitamin D, DNA methylation, and breast cancer. <i>Breast Cancer Research</i> , 2018, 20, 70.	5.0	49
28	Global DNA methylation and one-carbon metabolism gene polymorphisms and the risk of breast cancer in the Sister Study. <i>Carcinogenesis</i> , 2014, 35, 333-338.	2.8	48
29	Inhibition of Fried Meat-Induced Colorectal DNA Damage and Altered Systemic Genotoxicity in Humans by Crucifera, Chlorophyllin, and Yogurt. <i>PLoS ONE</i> , 2011, 6, e18707.	2.5	44
30	Alcohol and DNA Methylation: An Epigenome-Wide Association Study in Blood and Normal Breast Tissue. <i>American Journal of Epidemiology</i> , 2019, 188, 1055-1065.	3.4	43
31	Identification of a novel susceptibility locus at 13q34 and refinement of the 20p12.2 region as a multi-signal locus associated with bladder cancer risk in individuals of European ancestry. <i>Human Molecular Genetics</i> , 2016, 25, 1203-1214.	2.9	38
32	Shift work, DNA methylation and epigenetic age. <i>International Journal of Epidemiology</i> , 2019, 48, 1536-1544.	1.9	38
33	Tag SNP selection for candidate gene association studies using HapMap and gene resequencing data. <i>European Journal of Human Genetics</i> , 2007, 15, 1063-1070.	2.8	37
34	TAGster: efficient selection of LD tag SNPs in single or multiple populations. <i>Bioinformatics</i> , 2007, 23, 3254-3255.	4.1	36
35	Soy Formula and Epigenetic Modifications: Analysis of Vaginal Epithelial Cells from Infant Girls in the IFED Study. <i>Environmental Health Perspectives</i> , 2017, 125, 447-452.	6.0	36
36	The ENmix DNA methylation analysis pipeline for Illumina BeadChip and comparisons with seven other preprocessing pipelines. <i>Clinical Epigenetics</i> , 2021, 13, 216.	4.1	35

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37	ipDMR: identification of differentially methylated regions with interval $i$ -values. <i>Bioinformatics</i> , 2021, 37, 711-713.	4.1	31
38	GWAS SNP Replication among African American and European American men in the North Carolina–Louisiana prostate cancer project (PCaP). <i>Prostate</i> , 2011, 71, 881-891.	2.3	30
39	Genetic Ancestry, Self-Reported Race and Ethnicity in African Americans and European Americans in the PCaP Cohort. <i>PLoS ONE</i> , 2012, 7, e30950.	2.5	30
40	Neonatal Bilirubin Levels and Childhood Asthma in the US Collaborative Perinatal Project, 1959–1965. <i>American Journal of Epidemiology</i> , 2013, 178, 1691-1697.	3.4	30
41	Epigenetic mortality predictors and incidence of breast cancer. <i>Aging</i> , 2019, 11, 11975-11987.	3.1	30
42	oxBS-MLE: an efficient method to estimate 5-methylcytosine and 5-hydroxymethylcytosine in paired bisulfite and oxidative bisulfite treated DNA. <i>Bioinformatics</i> , 2016, 32, 3667-3669.	4.1	27
43	Reproduction, DNA methylation and biological age. <i>Human Reproduction</i> , 2019, 34, 1965-1973.	0.9	27
44	Alcohol Consumption and Methylation-Based Measures of Biological Age. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2021, 76, 2107-2111.	3.6	27
45	Body mass index associated with genome-wide methylation in breast tissue. <i>Breast Cancer Research and Treatment</i> , 2015, 151, 453-463.	2.5	25
46	Prediagnostic Immune Cell Profiles and Breast Cancer. <i>JAMA Network Open</i> , 2020, 3, e1919536.	5.9	25
47	Admixture mapping of prostate cancer in African Americans participating in the North Carolina–Louisiana Prostate Cancer Project (PCaP). <i>Prostate</i> , 2014, 74, 1-9.	2.3	24
48	Association between Genetic Variants in DNA and Histone Methylation and Telomere Length. <i>PLoS ONE</i> , 2012, 7, e40504.	2.5	24
49	Long-term ambient fine particulate matter and DNA methylation in inflammation pathways: results from the Sister Study. <i>Epigenetics</i> , 2020, 15, 524-535.	2.7	21
50	Blood DNA methylation profiles improve breast cancer prediction. <i>Molecular Oncology</i> , 2022, 16, 42-53.	4.6	19
51	Reliability of DNA methylation measures using Illumina methylation BeadChip. <i>Epigenetics</i> , 2021, 16, 495-502.	2.7	18
52	Genome-Wide Association Analysis of the Sense of Smell in U.S. Older Adults: Identification of Novel Risk Loci in African-Americans and European-Americans. <i>Molecular Neurobiology</i> , 2017, 54, 8021-8032.	4.0	17
53	A comparison of DNA methylation in newborn blood samples from infants with and without orofacial clefts. <i>Clinical Epigenetics</i> , 2019, 11, 40.	4.1	17
54	Epigenome-wide analysis uncovers a blood-based DNA methylation biomarker of lifetime cannabis use. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2021, 186, 173-182.	1.7	17

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55	In Utero Exposure to Diethylstilbestrol and Blood DNA Methylation in Women Ages 40â€“59 Years from the Sister Study. PLoS ONE, 2015, 10, e0118757.	2.5	16
56	Assessing the Significance of Quantitative Trait Loci in Replicable Mapping Populations. Genetics, 2006, 174, 1063-1068.	2.9	12
57	Genome-wide Meta-analysis on the Sense of Smell Among US Older Adults. Medicine (United States), 2015, 94, e1892.	1.0	12
58	Persistent epigenetic changes in adult daughters of older mothers. Epigenetics, 2019, 14, 467-476.	2.7	10
59	Geneâ€“methylation interactions: discovering region-wise DNA methylation levels that modify SNP-associated disease risk. Clinical Epigenetics, 2020, 12, 109.	4.1	9
60	Non-Steroidal Anti-Inflammatory Drug Use and Genomic DNA Methylation in Blood. PLoS ONE, 2015, 10, e0138920.	2.5	8
61	Hormone therapy use and breast tissue DNA methylation: analysis of epigenome wide data from the normal breast study. Epigenetics, 2019, 14, 146-157.	2.7	7
62	Genome-wide analysis of loss of heterozygosity and copy number amplification in uterine leiomyomas using the 100K single nucleotide polymorphism array. Experimental and Molecular Pathology, 2011, 91, 434-439.	2.1	6
63	No association between DNA repair gene XRCC1 and amyotrophic lateral sclerosis. Neurobiology of Aging, 2012, 33, 1015.e25-1015.e26.	3.1	6
64	Differential Gene Expression in Bladder Tumors from Workers Occupationally Exposed to Arylamines. BioMed Research International, 2021, 2021, 1-7.	1.9	3
65	Assessing Candidate Gene nsSNPs for Phenotypic Differences in Double-Strand Break Repair Using Radiation-Induced <sup>3</sup> H2A.X Foci. Journal of Cancer Epidemiology, 2008, 2008, 1-8.	1.1	2
66	Wavelet Screening identifies regions highly enriched for differentially methylated loci for orofacial clefts. NAR Genomics and Bioinformatics, 2021, 3, lqab035.	3.2	0
67	Shift Work, DNA methylation and Epigenetic Age. ISEE Conference Abstracts, 2021, 2021, .	0.0	0