

# Zongli Xu

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

67

papers

3,624

citations

28

h-index

60

g-index

68

ext. papers

4,448

ext. citations

6.8

avg, IF

5.46

L-index

#	Paper	IF	Citations
67	Differential Gene Expression in Bladder Tumors from Workers Occupationally Exposed to Arylamines. <i>BioMed Research International</i> , <b>2021</b> , 2021, 2624433	3	0
66	Associations of Body Composition and Physical Activity Level With Multiple Measures of Epigenetic Age Acceleration. <i>American Journal of Epidemiology</i> , <b>2021</b> , 190, 984-993	3.8	9
65	Wavelet Screening identifies regions highly enriched for differentially methylated loci for orofacial clefts. <i>NAR Genomics and Bioinformatics</i> , <b>2021</b> , 3, lqab035	3.7	
64	Alcohol Consumption and Methylation-Based Measures of Biological Age. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , <b>2021</b> , 76, 2107-2111	6.4	4
63	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , <b>2021</b> , 22, 194	18.3	14
62	Reliability of DNA methylation measures using Illumina methylation BeadChip. <i>Epigenetics</i> , <b>2021</b> , 16, 495-502	5.7	4
61	ipDMR: identification of differentially methylated regions with interval P-values. <i>Bioinformatics</i> , <b>2021</b> , 37, 711-713	7.2	5
60	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> , <b>2021</b> , 186, 173-182	3.5	6
59	Blood DNA methylation profiles improve breast cancer prediction. <i>Molecular Oncology</i> , <b>2021</b> ,	7.9	3
58	The ENmix DNA methylation analysis pipeline for Illumina BeadChip and comparisons with seven other preprocessing pipelines. <i>Clinical Epigenetics</i> , <b>2021</b> , 13, 216	7.7	2
57	Prediagnostic Immune Cell Profiles and Breast Cancer. <i>JAMA Network Open</i> , <b>2020</b> , 3, e1919536	10.4	14
56	Long-term ambient fine particulate matter and DNA methylation in inflammation pathways: results from the Sister Study. <i>Epigenetics</i> , <b>2020</b> , 15, 524-535	5.7	10
55	Gene-methylation interactions: discovering region-wise DNA methylation levels that modify SNP-associated disease risk. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 109	7.7	5
54	Blood DNA Methylation and Breast Cancer: A Prospective Case-Cohort Analysis in the Sister Study. <i>Journal of the National Cancer Institute</i> , <b>2020</b> , 112, 87-94	9.7	41
53	Association of Neighborhood Deprivation With Epigenetic Aging Using 4 Clock Metrics. <i>JAMA Network Open</i> , <b>2020</b> , 3, e2024329	10.4	17
52	Shift work, DNA methylation and epigenetic age. <i>International Journal of Epidemiology</i> , <b>2019</b> , 48, 1536-1544	7.8	21
51	A comparison of DNA methylation in newborn blood samples from infants with and without orofacial clefts. <i>Clinical Epigenetics</i> , <b>2019</b> , 11, 40	7.7	10

50	Hormone therapy use and breast tissue DNA methylation: analysis of epigenome wide data from the normal breast study. <i>Epigenetics</i> , <b>2019</b> , 14, 146-157	5.7	4
49	Persistent epigenetic changes in adult daughters of older mothers. <i>Epigenetics</i> , <b>2019</b> , 14, 467-476	5.7	6
48	Alcohol and DNA Methylation: An Epigenome-Wide Association Study in Blood and Normal Breast Tissue. <i>American Journal of Epidemiology</i> , <b>2019</b> , 188, 1055-1065	3.8	25
47	Methylation-Based Biological Age and Breast Cancer Risk. <i>Journal of the National Cancer Institute</i> , <b>2019</b> , 111, 1051-1058	9.7	67
46	Air pollution, particulate matter composition and methylation-based biologic age. <i>Environment International</i> , <b>2019</b> , 132, 105071	12.9	33
45	Reproduction, DNA methylation and biological age. <i>Human Reproduction</i> , <b>2019</b> , 34, 1965-1973	5.7	15
44	Epigenetic mortality predictors and incidence of breast cancer. <i>Aging</i> , <b>2019</b> , 11, 11975-11987	5.6	14
43	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. <i>International Journal of Epidemiology</i> , <b>2018</b> , 47, 22-23u	7.8	62
42	Vitamin D, DNA methylation, and breast cancer. <i>Breast Cancer Research</i> , <b>2018</b> , 20, 70	8.3	34
41	Soy Formula and Epigenetic Modifications: Analysis of Vaginal Epithelial Cells from Infant Girls in the IFED Study. <i>Environmental Health Perspectives</i> , <b>2017</b> , 125, 447-452	8.4	28
40	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> , <b>2017</b> , 26, 4067-4085	5.6	151
39	RELIC: a novel dye-bias correction method for Illumina Methylation BeadChip. <i>BMC Genomics</i> , <b>2017</b> , 18, 4	4.5	53
38	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> , <b>2017</b> , 54, 8021-8032	6.2	12
37	oxBS-MLE: an efficient method to estimate 5-methylcytosine and 5-hydroxymethylcytosine in paired bisulfite and oxidative bisulfite treated DNA. <i>Bioinformatics</i> , <b>2016</b> , 32, 3667-3669	7.2	13
36	RCP: a novel probe design bias correction method for Illumina Methylation BeadChip. <i>Bioinformatics</i> , <b>2016</b> , 32, 2659-63	7.2	64
35	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> , <b>2016</b> , 25, 1203-14	5.6	20
34	ENmix: a novel background correction method for Illumina HumanMethylation450 BeadChip. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, e20	20.1	157
33	Maternal Age at Delivery Is Associated with an Epigenetic Signature in Both Newborns and Adults. <i>PLoS ONE</i> , <b>2016</b> , 11, e0156361	3.7	37

32	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. <i>American Journal of Human Genetics</i> , <b>2016</b> , 98, 680-96	11	489
31	Genome-wide Meta-analysis on the Sense of Smell Among US Older Adults. <i>Medicine (United States)</i> , <b>2015</b> , 94, e1892	1.8	10
30	In utero exposure to diethylstilbestrol and blood DNA methylation in women ages 40-59 years from the sister study. <i>PLoS ONE</i> , <b>2015</b> , 10, e0118757	3.7	12
29	Body mass index associated with genome-wide methylation in breast tissue. <i>Breast Cancer Research and Treatment</i> , <b>2015</b> , 151, 453-63	4.4	21
28	Potential sex differences in nonmotor symptoms in early drug-naive Parkinson disease. <i>Neurology</i> , <b>2015</b> , 84, 2107-15	6.5	69
27	Non-Steroidal Anti-Inflammatory Drug Use and Genomic DNA Methylation in Blood. <i>PLoS ONE</i> , <b>2015</b> , 10, e0138920	3.7	7
26	Genome-wide age-related DNA methylation changes in blood and other tissues relate to histone modification, expression and cancer. <i>Carcinogenesis</i> , <b>2014</b> , 35, 356-64	4.6	86
25	CpG sites associated with cigarette smoking: analysis of epigenome-wide data from the Sister Study. <i>Environmental Health Perspectives</i> , <b>2014</b> , 122, 673-8	8.4	79
24	Identification of DNA methylation changes in newborns related to maternal smoking during pregnancy. <i>Environmental Health Perspectives</i> , <b>2014</b> , 122, 1147-53	8.4	153
23	Global DNA methylation and one-carbon metabolism gene polymorphisms and the risk of breast cancer in the Sister Study. <i>Carcinogenesis</i> , <b>2014</b> , 35, 333-8	4.6	44
22	Admixture mapping of prostate cancer in African Americans participating in the North Carolina-Louisiana Prostate Cancer Project (PCaP). <i>Prostate</i> , <b>2014</b> , 74, 1-9	4.2	20
21	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> , <b>2013</b> , 73, 11-22	4.2	57
20	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> , <b>2013</b> , 15, R42	8.3	81
19	Neonatal bilirubin levels and childhood asthma in the US Collaborative Perinatal Project, 1959-1965. <i>American Journal of Epidemiology</i> , <b>2013</b> , 178, 1691-7	3.8	24
18	Epigenome-wide association study of breast cancer using prospectively collected sister study samples. <i>Journal of the National Cancer Institute</i> , <b>2013</b> , 105, 694-700	9.7	103
17	Recreational and household physical activity at different time points and DNA global methylation. <i>European Journal of Cancer</i> , <b>2013</b> , 49, 2199-206	7.5	59
16	No association between DNA repair gene XRCC1 and amyotrophic lateral sclerosis. <i>Neurobiology of Aging</i> , <b>2012</b> , 33, 1015.e25-6	5.6	5
15	Genetic ancestry, self-reported race and ethnicity in African Americans and European Americans in the PCaP cohort. <i>PLoS ONE</i> , <b>2012</b> , 7, e30950	3.7	25

14	Association between genetic variants in DNA and histone methylation and telomere length. <i>PLoS ONE</i> , <b>2012</b> , 7, e40504	3.7	23
13	Inhibition of fried meat-induced colorectal DNA damage and altered systemic genotoxicity in humans by crucifera, chlorophyllin, and yogurt. <i>PLoS ONE</i> , <b>2011</b> , 6, e18707	3.7	38
12	Genome-wide analysis of loss of heterozygosity and copy number amplification in uterine leiomyomas using the 100K single nucleotide polymorphism array. <i>Experimental and Molecular Pathology</i> , <b>2011</b> , 91, 434-9	4.4	4
11	GWAS SNP Replication among African American and European American men in the North Carolina-Louisiana prostate cancer project (PCaP). <i>Prostate</i> , <b>2011</b> , 71, 881-91	4.2	26
10	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. <i>Nature Genetics</i> , <b>2010</b> , 42, 978-84	36.3	408
9	SNPinfo: integrating GWAS and candidate gene information into functional SNP selection for genetic association studies. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, W600-5	20.1	537
8	Assessing Candidate Gene nsSNPs for Phenotypic Differences in Double-Strand Break Repair Using Radiation-Induced gammaH2A.X Foci. <i>Journal of Cancer Epidemiology</i> , <b>2008</b> , 2008, 387423	2.8	2
7	Sinomenine, a natural dextrorotatory morphinan analog, is anti-inflammatory and neuroprotective through inhibition of microglial NADPH oxidase. <i>Journal of Neuroinflammation</i> , <b>2007</b> , 4, 23	10.1	108
6	Tag SNP selection for candidate gene association studies using HapMap and gene resequencing data. <i>European Journal of Human Genetics</i> , <b>2007</b> , 15, 1063-70	5.3	35
5	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> , <b>2007</b> , 616, 60-9	3.3	55
4	TAGster: efficient selection of LD tag SNPs in single or multiple populations. <i>Bioinformatics</i> , <b>2007</b> , 23, 3254-5	7.2	30
3	Assessing the significance of quantitative trait loci in replicable mapping populations. <i>Genetics</i> , <b>2006</b> , 174, 1063-8	4	10
2	Improving quantitative trait loci mapping resolution in experimental crosses by the use of genotypically selected samples. <i>Genetics</i> , <b>2005</b> , 170, 401-8	4	43
1	Gene-methylation interactions: Discovering region-wise DNA methylation levels that modify SNP-associated disease risk		1