

# Shijie C Zheng

## List of Publications by Citations

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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.

21  
papers

736  
citations

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h-index

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ext. papers

1,129  
ext. citations

13.1  
avg, IF

4.5  
L-index

#	Paper	IF	Citations
21	A comparison of reference-based algorithms for correcting cell-type heterogeneity in Epigenome-Wide Association Studies. <i>BMC Bioinformatics</i> , <b>2017</b> , 18, 105	3.6	147
20	Correlation of an epigenetic mitotic clock with cancer risk. <i>Genome Biology</i> , <b>2016</b> , 17, 205	18.3	116
19	Cell-type deconvolution in epigenome-wide association studies: a review and recommendations. <i>Epigenomics</i> , <b>2017</b> , 9, 757-768	4.4	87
18	Epigenetic drift, epigenetic clocks and cancer risk. <i>Epigenomics</i> , <b>2016</b> , 8, 705-19	4.4	81
17	Identification of differentially methylated cell types in epigenome-wide association studies. <i>Nature Methods</i> , <b>2018</b> , 15, 1059-1066	21.6	75
16	A novel cell-type deconvolution algorithm reveals substantial contamination by immune cells in saliva, buccal and cervix. <i>Epigenomics</i> , <b>2018</b> , 10, 925-940	4.4	66
15	Correcting for cell-type heterogeneity in epigenome-wide association studies: revisiting previous analyses. <i>Nature Methods</i> , <b>2017</b> , 14, 216-217	21.6	47
14	Cell and tissue type independent age-associated DNA methylation changes are not rare but common. <i>Aging</i> , <b>2018</b> , 10, 3541-3557	5.6	28
13	The multi-omic landscape of transcription factor inactivation in cancer. <i>Genome Medicine</i> , <b>2016</b> , 8, 89	14.4	20
12	A cell-type deconvolution meta-analysis of whole blood EWAS reveals lineage-specific smoking-associated DNA methylation changes. <i>Nature Communications</i> , <b>2020</b> , 11, 4779	17.4	14
11	A metagenomic approach to dissect the genetic composition of enterotypes in Han Chinese and two Muslim groups. <i>Systematic and Applied Microbiology</i> , <b>2018</b> , 41, 1-12	4.2	13
10	EpiDISH web server: Epigenetic Dissection of Intra-Sample-Heterogeneity with online GUI. <i>Bioinformatics</i> , <b>2019</b> ,	7.2	10
9	ebGSEA: an improved Gene Set Enrichment Analysis method for Epigenome-Wide-Association Studies. <i>Bioinformatics</i> , <b>2019</b> , 35, 3514-3516	7.2	8
8	DNA Methylation Signatures in Vaginal Fluid Samples for Detection of Cervical and Endometrial Cancer. <i>International Journal of Gynecological Cancer</i> , <b>2016</b> ,	3.5	7
7	Universal prediction of cell-cycle position using transfer learning.. <i>Genome Biology</i> , <b>2022</b> , 23, 41	18.3	3
6	recount3: summaries and queries for large-scale RNA-seq expression and splicing. <i>Genome Biology</i> , <b>2021</b> , 22, 323	18.3	3
5	Calling differential DNA methylation at cell-type resolution: an objective status-quo		3

- 4 Limb development genes underlie variation in human fingerprint patterns.. *Cell*, **2022**, 185, 95-112.e18 56.2 2
- 3 Identification of differentially methylated cell-types in Epigenome-Wide Association Studies 2
- 2 ebayGSEA: An improved Gene Set Enrichment Analysis method for Epigenome-Wide-Association Studies 1
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