Shijie C Zheng

List of Publications by Year
in descending order

17 papers	1,461 citations	566801 15 h-index	887659 17 g-index
27 all docs	27 docs citations	27 times ranked	2430 citing authors

#	Article	IF	Citations
1	A comparison of reference-based algorithms for correcting cell-type heterogeneity in Epigenome-Wide Association Studies. BMC Bioinformatics, 2017, 18, 105.	1.2	297
2	Correlation of an epigenetic mitotic clock with cancer risk. Genome Biology, 2016, 17, 205.	3.8	197
3	Identification of differentially methylated cell types in epigenome-wide association studies. Nature Methods, 2018, 15, 1059-1066.	9.0	166
4	Cell-type deconvolution in epigenome-wide association studies: a review and recommendations. Epigenomics, 2017, 9, 757-768.	1.0	131
5	A novel cell-type deconvolution algorithm reveals substantial contamination by immune cells in saliva, buccal and cervix. Epigenomics, 2018, 10, 925-940.	1.0	116
6	recount3: summaries and queries for large-scale RNA-seq expression and splicing. Genome Biology, 2021, 22, 323.	3.8	103
7	Epigenetic drift, epigenetic clocks and cancer risk. Epigenomics, 2016, 8, 705-719.	1.0	101
8	Correcting for cell-type heterogeneity in epigenome-wide association studies: revisiting previous analyses. Nature Methods, 2017, 14, 216-217.	9.0	59
9	Cell and tissue type independent age-associated DNA methylation changes are not rare but common. Aging, 2018, 10, 3541-3557.	1.4	42
10	EpiDISH web server: Epigenetic Dissection of Intra-Sample-Heterogeneity with online GUI. Bioinformatics, 2020, 36, 1950-1951.	1.8	40
11	A cell-type deconvolution meta-analysis of whole blood EWAS reveals lineage-specific smoking-associated DNA methylation changes. Nature Communications, 2020, 11, 4779.	5.8	32
12	Universal prediction of cell-cycle position using transfer learning. Genome Biology, 2022, 23, 41.	3.8	30
13	Limb development genes underlie variation in human fingerprint patterns. Cell, 2022, 185, 95-112.e18.	13.5	30
14	The multi-omic landscape of transcription factor inactivation in cancer. Genome Medicine, 2016, 8, 89.	3.6	26
15	A metagenomic approach to dissect the genetic composition of enterotypes in Han Chinese and two Muslim groups. Systematic and Applied Microbiology, 2018, 41, 1-12.	1.2	24
16	ebGSEA: an improved Gene Set Enrichment Analysis method for Epigenome-Wide-Association Studies. Bioinformatics, 2019, 35, 3514-3516.	1.8	15
17	DNA Methylation Signatures in Vaginal Fluid Samples for Detection of Cervical and Endometrial Cancer. International Journal of Gynecological Cancer, 2016, , 1.	1.2	14