

# Wei Zhang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9223219/publications.pdf>

Version: 2024-02-01

7  
papers

131  
citations

1937685

4  
h-index

1872680

6  
g-index

9  
all docs

9  
docs citations

9  
times ranked

232  
citing authors

#	ARTICLE	IF	CITATIONS
1	ARIC: accurate and robust inference of cell type proportions from bulk gene expression or DNA methylation data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	6
2	Evaluating methylation of human ribosomal DNA at each CpG site reveals its utility for cancer detection using cell-free DNA. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	0
3	Genome-wide cell-free DNA methylation analyses improve accuracy of non-invasive diagnostic imaging for early-stage breast cancer. <i>Molecular Cancer</i> , 2021, 20, 36.	19.2	30
4	cfDNApipe: a comprehensive quality control and analysis pipeline for cell-free DNA high-throughput sequencing data. <i>Bioinformatics</i> , 2021, 37, 4251-4252.	4.1	5
5	DISMIR: deep learning-based noninvasive cancer detection by integrating DNA sequence and methylation information of individual cell-free DNA reads. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	24
6	esATAC: an easy-to-use systematic pipeline for ATAC-seq data analysis. <i>Bioinformatics</i> , 2018, 34, 2664-2665.	4.1	50
7	HCSGD: An integrated database of human cellular senescence genes. <i>Journal of Genetics and Genomics</i> , 2017, 44, 227-234.	3.9	15