

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	esATAC: an easy-to-use systematic pipeline for ATAC-seq data analysis. <i>Bioinformatics</i> , 2018, 34, 2664-2665.	4.1	50
2	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
3	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
4	HCSGD: An integrated database of human cellular senescence genes. <i>Journal of Genetics and Genomics</i> , 2017, 44, 227-234.	3.9	15
5	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
6	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
7	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