Yawei Li

List of Publications by Year
in descending order

12 papers	479 citations	1478280 6 h-index	1281743 11 g-index
14 all docs	14 docs citations	14 times ranked	844 citing authors

#	ARTICLE	IF	CITATIONS
1	Extremely high genetic diversity in a single tumor points to prevalence of non-Darwinian cell evolution. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6496-505.	3.3	313
2	Statistical and machine learning methods for spatially resolved transcriptomics data analysis. Genome Biology, 2022, 23, 83.	3.8	66
3	*Mycobacterium tuberculosis* clinical isolates carry mutational signatures of host immune environments. Science Advances, 2020, 6, eaba4901.	4.7	33
4	Spatiotemporal localization of proteins in mycobacteria. Cell Reports, 2021, 37, 110154.	2.9	16
5	Genetic Load and Potential Mutational Meltdown in Cancer Cell Populations. Molecular Biology and Evolution, 2019, 36, 541-552.	3.5	14
6	Performance‐weighted‐voting model: An ensemble machine learning method for cancer type classification using whole‐exome sequencing mutation. Quantitative Biology, 2020, 8, 347-358.	0.3	14
7	Optimizing the evaluation of gene-targeted panels for tumor mutational burden estimation. Scientific Reports, 2021, 11, 21072.	1.6	9
8	Evolution under Spatially Heterogeneous Selection in Solid Tumors. Molecular Biology and Evolution, 2022, 39, .	3.5	5
9	RNA-Seq Analyses Reveal Roles of the HVCN1 Proton Channel in Cardiac pH Homeostasis. Frontiers in Cell and Developmental Biology, 2022, 10, 860502.	1.8	4
10	Genomic sequencing identifies a few mutations driving the independent origin of primary liver tumors in a chronic hepatitis murine model. PLoS ONE, 2017, 12, e0187551.	1.1	1
11	Using an Unsupervised Clustering Model to Detect the Early Spread of SARS-CoV-2 Worldwide. Genes, 2022, 13, 648.	1.0	1
12	Unsupervised clustering analysis of SARS-Cov-2 population structure reveals six major subtypes at early stage across the world. , 2021, , .		0