Sujun Li

List of Publications by Year
in descending order

13 papers	363 citations	1170033 9 h-index	1255698 13 g-index
14 all docs	14 docs citations	14 times ranked	557 citing authors

#	ARTICLE	IF	CITATIONS
1	Association between Mutation in SMARCAD1 and Basan Syndrome with Cutaneous Squamous Cell Carcinoma. Disease Markers, 2022, 2022, 1-9.	0.6	1
2	Roles of bacteriophages, plasmids and CRISPR immunity in microbial community dynamics revealed using time-series integrated meta-omics. Nature Microbiology, 2021, 6, 123-135.	5.9	47
3	Using high-abundance proteins as guides for fast and effective peptide/protein identification from human gut metaproteomic data. Microbiome, 2021, 9, 80.	4.9	14
4	Integration of time-series meta-omics data reveals how microbial ecosystems respond to disturbance. Nature Communications, 2020, 11, 5281.	5.8	57
5	Cancer-associated Fibroblasts induce epithelial-mesenchymal transition *via* the Transglutaminase 2-dependent IL-6/IL6R/STAT3 axis in Hepatocellular Carcinoma. International Journal of Biological Sciences, 2020, 16, 2542-2558.	2.6	61
6	A Fast and Memory-Efficient Spectral Library Search Algorithm Using Locality-Sensitive Hashing. Proteomics, 2020, 20, e2000002.	1.3	10
7	Full-Spectrum Prediction of Peptides Tandem Mass Spectra using Deep Neural Network. Analytical Chemistry, 2020, 92, 4275-4283.	3.2	48
8	msCRUSH: Fast Tandem Mass Spectral Clustering Using Locality Sensitive Hashing. Journal of Proteome Research, 2019, 18, 147-158.	1.8	19
9	A Meta-proteogenomic Approach to Peptide Identification Incorporating Assembly Uncertainty and Genomic Variation. Molecular and Cellular Proteomics, 2019, 18, S183-S192.	2.5	17
10	Identification of N-terminal protein processing sites by chemical labeling mass spectrometry. Rapid Communications in Mass Spectrometry, 2019, 33, 1015-1023.	0.7	2
11	Constrained De Novo Sequencing of neo-Epitope Peptides Using Tandem Mass Spectrometry. Lecture Notes in Computer Science, 2018, 10812, 138-153.	1.0	6
12	A Graph-Centric Approach for Metagenome-Guided Peptide and Protein Identification in Metaproteomics. PLoS Computational Biology, 2016, 12, e1005224.	1.5	36
13	On the Accuracy and Limits of Peptide Fragmentation Spectrum Prediction. Analytical Chemistry, 2011, 83, 790-796.	3.2	45