

# Julia Tzu-Ya Weng

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7241664/publications.pdf>

Version: 2024-02-01

14  
papers

281  
citations

1040056

9  
h-index

1199594

12  
g-index

14  
all docs

14  
docs citations

14  
times ranked

685  
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene expression profiling identifies candidate biomarkers for active and latent tuberculosis. BMC Bioinformatics, 2016, 17, 3.	2.6	50
2	SOHSite: incorporating evolutionary information and physicochemical properties to identify protein S-sulfonylation sites. BMC Genomics, 2016, 17, 9.	2.8	45
3	Integrative epigenetic profiling analysis identifies DNA methylation changes associated with chronic alcohol consumption. Computers in Biology and Medicine, 2015, 64, 299-306.	7.0	30
4	Investigation and identification of functional post-translational modification sites associated with drug binding and protein-protein interactions. BMC Systems Biology, 2017, 11, 132.	3.0	28
5	Systematic Expression Profiling Analysis Identifies Specific MicroRNA-Gene Interactions that May Differentiate between Active and Latent Tuberculosis Infection. BioMed Research International, 2014, 2014, 1-9.	1.9	26
6	UbiNet: an online resource for exploring the functional associations and regulatory networks of protein ubiquitylation. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw054.	3.0	25
7	Metagenome and Metatranscriptome Profiling of Moderate and Severe COPD Sputum in Taiwanese Han Males. PLoS ONE, 2016, 11, e0159066.	2.5	23
8	Gene Expression Profiling of Biological Pathway Alterations by Radiation Exposure. BioMed Research International, 2014, 2014, 1-9.	1.9	18
9	A novel algorithm for mining closed temporal patterns from interval-based data. Knowledge and Information Systems, 2016, 46, 151-183.	3.2	16
10	Incremental mining of temporal patterns in interval-based database. Knowledge and Information Systems, 2016, 46, 423-448.	3.2	9
11	A new scheme to discover functional associations and regulatory networks of E3 ubiquitin ligases. BMC Systems Biology, 2016, 10, 3.	3.0	6
12	Novel Bioinformatics Approaches for Analysis of High-Throughput Biological Data. BioMed Research International, 2014, 2014, 1-3.	1.9	5
13	Epigenetic profiling of DNA methylation changes associated with chronic alcohol consumption: A 12-year follow-up study. , 2013, , .		0
14	Time-course gene expression profiling of high glucose-induced endothelial cell apoptosis. , 2014, , .		0