

# Wei Liu

## List of Publications by Year in descending order

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Version: 2024-02-01

30  
papers

537  
citations

759055

12  
h-index

677027

22  
g-index

32  
all docs

32  
docs citations

32  
times ranked

969  
citing authors

#	ARTICLE	IF	CITATIONS
1	Reference Module-Based Analysis of Ovarian Cancer Transcriptome Identifies Important Modules and Potential Drugs. <i>Biochemical Genetics</i> , 2022, 60, 433-451.	0.8	6
2	TissueSpace: a web tool for rank-based transcriptome representation and its applications in molecular medicine. <i>Genes and Genomics</i> , 2022, , .	0.5	0
3	Identification of Immune-Related Prognostic Biomarkers Based on the Tumor Microenvironment in 20 Malignant Tumor Types With Poor Prognosis. <i>Frontiers in Oncology</i> , 2020, 10, 1008.	1.3	11
4	SemanticGO: a tool for gene functional similarity analysis in <i>Arabidopsis thaliana</i> and rice. <i>Plant Science</i> , 2020, 297, 110527.	1.7	3
5	Large-scale analysis of zebrafish ( <i>Danio rerio</i> ) transcriptomes identifies functional modules associated with phenotypes. <i>Marine Genomics</i> , 2020, 53, 100770.	0.4	2
6	Drug vector representation: a tool for drug similarity analysis. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1055-1062.	1.0	3
7	CoFly: A gene coexpression database for the fruit fly <i>Drosophila melanogaster</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2020, 105, e21693.	0.6	2
8	Differential Expression Proteins Contribute to Race-Specific Resistant Ability in Rice ( <i>Oryza sativa</i> L.). <i>Plants</i> , 2019, 8, 29.	1.6	3
9	Gene co-expression network analysis identifies trait-related modules in <i>Arabidopsis thaliana</i> . <i>Planta</i> , 2019, 249, 1487-1501.	1.6	44
10	Hydrothermal synthesis of carbon dots codoped with nitrogen and phosphorus as a turn-on fluorescent probe for cadmium(II). <i>Mikrochimica Acta</i> , 2019, 186, 147.	2.5	62
11	Chromosome-based gene co-expression analysis reveals regions associated with cancers: chromosome 1 as an example. <i>Molecular Biology Reports</i> , 2019, 46, 1551-1553.	1.0	1
12	Rice Stress-Resistant SNP Database. <i>Rice</i> , 2019, 12, 97.	1.7	9
13	Prediction of protein-protein interactions between fungus ( <i>Magnaporthe grisea</i> ) and rice ( <i>Oryza</i> ) Tj ETQq1 1 0.784314 rgBT /Overl 3.2 21	0.784314	21
14	Transcriptome-derived stromal and immune scores infer clinical outcomes of patients with cancer. <i>Oncology Letters</i> , 2018, 15, 4351-4357.	0.8	54
15	Rapid and visual readout of vitamin B1 based on the electrostatic interaction induced aggregation of gold nanoparticles. <i>RSC Advances</i> , 2018, 8, 35850-35854.	1.7	7
16	Construction and Analysis of Gene Co-Expression Networks in <i>Escherichia coli</i> . <i>Cells</i> , 2018, 7, 19.	1.8	39
17	Role of COL6A3 in colorectal cancer. <i>Oncology Reports</i> , 2018, 39, 2527-2536.	1.2	37
18	Revisiting Connectivity Map from a gene co-expression network analysis. <i>Experimental and Therapeutic Medicine</i> , 2018, 16, 493-500.	0.8	10

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19	Functional Annotation of <i>Caenorhabditis elegans</i> Genes by Analysis of Gene Co-Expression Networks. <i>Biomolecules</i> , 2018, 8, 70.	1.8	4
20	Prediction and identification of the effectors of heterotrimeric G proteins in rice ( <i>Oryza</i> ). <i>Journal of Proteomics</i> , 2016, 10, 150-162.	3.2	8
21	From <i>Saccharomyces cerevisiae</i> to human: The important gene co-expression modules. <i>Biomedical Reports</i> , 2017, 7, 153-158.	0.9	29
22	Impact of SNPs on Protein Phosphorylation Status in Rice ( <i>Oryza sativa</i> L.). <i>International Journal of Molecular Sciences</i> , 2016, 17, 1738.	1.8	4
23	Sal668 Proteomic Analysis of Nonalcoholic Fatty Liver Disease: Attenuation of Coactosin-like Protein-1 Protects Liver from Steatosis and Injury. <i>Gastroenterology</i> , 2016, 150, S1090.	0.6	1
24	Transcriptional networks implicated in human nonalcoholic fatty liver disease. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1793-1804.	1.0	16
25	Gene co-expression analysis identifies common modules related to prognosis and drug resistance in cancer cell lines. <i>International Journal of Cancer</i> , 2014, 135, 2795-2803.	2.3	24
26	Co-expression network analysis identifies transcriptional modules in the mouse liver. <i>Molecular Genetics and Genomics</i> , 2014, 289, 847-853.	1.0	17
27	Network-based analysis reveals the difference between inflammatory and fibrogenic livers of children with biliary atresia. <i>Journal of Pediatric Surgery</i> , 2014, 49, 500.	0.8	0
28	Connectivity-based risk score for hepatocellular carcinoma prognosis. <i>Hepatology</i> , 2013, 58, 1191-1192.	3.6	2
29	Network-based discovery of gene signature for vascular invasion prediction in HCC. <i>Journal of Hepatology</i> , 2012, 56, 1423.	1.8	1
30	Sample preparation method for isolation of single-cell types from mouse liver for proteomic studies. <i>Proteomics</i> , 2011, 11, 3556-3564.	1.3	86