

# Wei Liu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5027199/publications.pdf>

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11  
papers

834  
citations

1040056

9  
h-index

1281871

11  
g-index

11  
all docs

11  
docs citations

11  
times ranked

1296  
citing authors

#	ARTICLE	IF	CITATIONS
1	Deep proteome profiling promotes whole proteome characterization and drug discovery for esophageal squamous cell carcinoma. <i>Cancer Biology and Medicine</i> , 2022, 19, 1-5.	3.0	2
2	PCLasso: a protein complex-based, group lasso-Cox model for accurate prognosis and risk protein complex discovery. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	11
3	Large-scale and high-resolution mass spectrometry-based proteomics profiling defines molecular subtypes of esophageal cancer for therapeutic targeting. <i>Nature Communications</i> , 2021, 12, 4961.	12.8	63
4	Integration of gene interaction information into a reweighted Lasso-Cox model for accurate survival prediction. <i>Bioinformatics</i> , 2021, 36, 5405-5414.	4.1	17
5	Proteomics identifies new therapeutic targets of early-stage hepatocellular carcinoma. <i>Nature</i> , 2019, 567, 257-261.	27.8	613
6	Integration of gene interaction information into a reweighted random survival forest approach for accurate survival prediction and survival biomarker discovery. <i>Scientific Reports</i> , 2018, 8, 13202.	3.3	14
7	MASAN: a novel staging system for prognosis of patients with oesophageal squamous cell carcinoma. <i>British Journal of Cancer</i> , 2018, 118, 1476-1484.	6.4	13
8	Topologically inferring pathway activity for precise survival outcome prediction: breast cancer as a case. <i>Molecular BioSystems</i> , 2017, 13, 537-548.	2.9	11
9	Topologically inferring pathway activity toward precise cancer classification via integrating genomic and metabolomic data: prostate cancer as a case. <i>Scientific Reports</i> , 2015, 5, 13192.	3.3	25
10	Integration of pathway structure information into a reweighted partial Cox regression approach for survival analysis on high-dimensional gene expression data. <i>Molecular BioSystems</i> , 2015, 11, 1876-1886.	2.9	5
11	Topologically inferring risk-active pathways toward precise cancer classification by directed random walk. <i>Bioinformatics</i> , 2013, 29, 2169-2177.	4.1	60