

# Yu-Chen Liu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3712291/publications.pdf>

Version: 2024-02-01

10  
papers

522  
citations

1307594

7  
h-index

1372567

10  
g-index

10  
all docs

10  
docs citations

10  
times ranked

1067  
citing authors

#	ARTICLE	IF	CITATIONS
1	CircNet: a database of circular RNAs derived from transcriptome sequencing data. <i>Nucleic Acids Research</i> , 2016, 44, D209-D215.	14.5	304
2	Mechanical stretch induces hair regeneration through the alternative activation of macrophages. <i>Nature Communications</i> , 2019, 10, 1524.	12.8	106
3	Plant miRNAs found in human circulating system provide evidences of cross kingdom RNAi. <i>BMC Genomics</i> , 2017, 18, 112.	2.8	54
4	The novel long noncoding RNA AU021063, induced by IL-6/Arid5a signaling, exacerbates breast cancer invasion and metastasis by stabilizing Trib3 and activating the Mek/Erk pathway. <i>Cancer Letters</i> , 2021, 520, 295-306.	7.2	16
5	Biogenesis mechanisms of circular RNA can be categorized through feature extraction of a machine learning model. <i>Bioinformatics</i> , 2019, 35, 4867-4870.	4.1	10
6	Transcriptome sequencing based annotation and homologous evidence based scaffolding of <i>Anguilla japonica</i> draft genome. <i>BMC Genomics</i> , 2016, 17, 13.	2.8	9
7	Biclustering of transcriptome sequencing data reveals human tissue-specific circular RNAs. <i>BMC Genomics</i> , 2018, 19, 958.	2.8	9
8	Ouroboros resembling competitive endogenous loop (ORCEL) in circular RNAs revealed through transcriptome sequencing dataset analysis. <i>BMC Genomics</i> , 2018, 19, 171.	2.8	6
9	The aquatic animalsâ€™ transcriptome resource for comparative functional analysis. <i>BMC Genomics</i> , 2018, 19, 103.	2.8	5
10	Gene expression profiling of tumor-associated macrophages after exposure to single-dose irradiation. <i>Computational Biology and Chemistry</i> , 2017, 69, 138-146.	2.3	3