

# Chen-Ching Lin

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10884333/publications.pdf>

Version: 2024-02-01

19  
papers

740  
citations

623734

14  
h-index

794594

19  
g-index

20  
all docs

20  
docs citations

20  
times ranked

1259  
citing authors

#	ARTICLE	IF	CITATIONS
1	Reduced lipolysis in lipoma phenocopies lipid accumulation in obesity. <i>International Journal of Obesity</i> , 2021, 45, 565-576.	3.4	14
2	Dendritic Cells Regulate GPR34 through Mitogenic Signals and Undergo Apoptosis in Its Absence. <i>Journal of Immunology</i> , 2016, 196, 2504-2513.	0.8	20
3	Co-expression analysis identifies long noncoding RNA <i>SNHG1</i> as a novel predictor for event-free survival in neuroblastoma. <i>Oncotarget</i> , 2016, 7, 58022-58037.	1.8	59
4	Regulation rewiring analysis reveals mutual regulation between STAT1 and miR-155-5p in tumor immunosurveillance in seven major cancers. <i>Scientific Reports</i> , 2015, 5, 12063.	3.3	19
5	Concordant dysregulation of miR-5p and miR-3p arms of the same precursor microRNA may be a mechanism in inducing cell proliferation and tumorigenesis: a lung cancer study. <i>Rna</i> , 2015, 21, 1055-1065.	3.5	36
6	A cross-cancer differential co-expression network reveals microRNA-regulated oncogenic functional modules. <i>Molecular BioSystems</i> , 2015, 11, 3244-3252.	2.9	9
7	A Gene Gravity Model for the Evolution of Cancer Genomes: A Study of 3,000 Cancer Genomes across 9 Cancer Types. <i>PLoS Computational Biology</i> , 2015, 11, e1004497.	3.2	65
8	Functional consequences of somatic mutations in cancer using protein pocket-based prioritization approach. <i>Genome Medicine</i> , 2014, 6, 81.	8.2	31
9	Mirin: identifying microRNA regulatory modules in protein-protein interaction networks. <i>Bioinformatics</i> , 2014, 30, 2527-2528.	4.1	6
10	Studying Tumorigenesis through Network Evolution and Somatic Mutational Perturbations in the Cancer Interactome. <i>Molecular Biology and Evolution</i> , 2014, 31, 2156-2169.	8.9	79
11	Functional Evolution of Cardiac MicroRNAs in Heart Development and Functions. <i>Molecular Biology and Evolution</i> , 2014, 31, 2722-2734.	8.9	21
12	A Tri-Component Conservation Strategy Reveals Highly Confident MicroRNA-mRNA Interactions and Evolution of MicroRNA Regulatory Networks. <i>PLoS ONE</i> , 2014, 9, e103142.	2.5	3
13	MicroRNA-Regulated Protein-Protein Interaction Networks and Their Functions in Breast Cancer. <i>International Journal of Molecular Sciences</i> , 2013, 14, 11560-11606.	4.1	56
14	Link Clustering Reveals Structural Characteristics and Biological Contexts in Signed Molecular Networks. <i>PLoS ONE</i> , 2013, 8, e67089.	2.5	7
15	Crosstalk between transcription factors and microRNAs in human protein interaction network. <i>BMC Systems Biology</i> , 2012, 6, 18.	3.0	53
16	Integrative network analysis reveals active microRNAs and their functions in gastric cancer. <i>BMC Systems Biology</i> , 2011, 5, 99.	3.0	78
17	Dynamic functional modules in co-expressed protein interaction networks of dilated cardiomyopathy. <i>BMC Systems Biology</i> , 2010, 4, 138.	3.0	45
18	Essential Core of Protein-Protein Interaction Network in <i>Escherichia coli</i> . <i>Journal of Proteome Research</i> , 2009, 8, 1925-1931.	3.7	30

#	ARTICLE	IF	CITATIONS
19	Predicting essential genes based on network and sequence analysis. <i>Molecular BioSystems</i> , 2009, 5, 1672.	2.9	109