

# Yi-An Chen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9544480/publications.pdf>

Version: 2024-02-01

25  
papers

607  
citations

777949

13  
h-index

889612

19  
g-index

26  
all docs

26  
docs citations

26  
times ranked

1097  
citing authors

#	ARTICLE	IF	CITATIONS
1	Dietary Vitamin B1 Intake Influences Gut Microbial Community and the Consequent Production of Short-Chain Fatty Acids. <i>Nutrients</i> , 2022, 14, 2078.	1.7	14
2	Comprehensive analysis of gut microbiota of a healthy population and covariates affecting microbial variation in two large Japanese cohorts. <i>BMC Microbiology</i> , 2021, 21, 151.	1.3	30
3	MANTA, an integrative database and analysis platform that relates microbiome and phenotypic data. <i>PLoS ONE</i> , 2020, 15, e0243609.	1.1	6
4	MANTA, an integrative database and analysis platform that relates microbiome and phenotypic data. , 2020, 15, e0243609.		0
5	MANTA, an integrative database and analysis platform that relates microbiome and phenotypic data. , 2020, 15, e0243609.		0
6	MANTA, an integrative database and analysis platform that relates microbiome and phenotypic data. , 2020, 15, e0243609.		0
7	MANTA, an integrative database and analysis platform that relates microbiome and phenotypic data. , 2020, 15, e0243609.		0
8	MANTA, an integrative database and analysis platform that relates microbiome and phenotypic data. , 2020, 15, e0243609.		0
9	MANTA, an integrative database and analysis platform that relates microbiome and phenotypic data. , 2020, 15, e0243609.		0
10	Impact of quality trimming on the efficiency of reads joining and diversity analysis of Illumina paired-end reads in the context of QIIME1 and QIIME2 microbiome analysis frameworks. <i>BMC Bioinformatics</i> , 2019, 20, 581.	1.2	52
11	The TargetMine Data Warehouse: Enhancement and Updates. <i>Frontiers in Genetics</i> , 2019, 10, 934.	1.1	21
12	Assessing drug target suitability using TargetMine. <i>F1000Research</i> , 2019, 8, 233.	0.8	8
13	Assessing drug target suitability using TargetMine. <i>F1000Research</i> , 2019, 8, 233.	0.8	2
14	An integrative data analysis platform for gene set analysis and knowledge discovery in a data warehouse framework. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw009.	1.4	34
15	BIG3 Inhibits the Estrogen-Dependent Nuclear Translocation of PHB2 via Multiple Karyopherin-Alpha Proteins in Breast Cancer Cells. <i>PLoS ONE</i> , 2015, 10, e0127707.	1.1	19
16	Implementation of linked data in the life sciences at BioHackathon 2011. <i>Journal of Biomedical Semantics</i> , 2015, 6, 3.	0.9	15
17	Integrated Pathway Clusters with Coherent Biological Themes for Target Prioritisation. <i>PLoS ONE</i> , 2014, 9, e99030.	1.1	38
18	BioHackathon series in 2011 and 2012: penetration of ontology and linked data in life science domains. <i>Journal of Biomedical Semantics</i> , 2014, 5, 5.	0.9	47

#	ARTICLE	IF	CITATIONS
19	Brefeldin A-inhibited guanine nucleotide-exchange protein 3 (BIG3) is predicted to interact with its partner through an ARM-type $\alpha$ -helical structure. <i>BMC Research Notes</i> , 2014, 7, 435.	0.6	9
20	Understanding the Biological Context of NS5A-Host Interactions in HCV Infection: A Network-Based Approach. <i>Journal of Proteome Research</i> , 2013, 12, 2537-2551.	1.8	33
21	Inhibitory Roles of Signal Transducer and Activator of Transcription 3 in Antitumor Immunity during Carcinogen-Induced Lung Tumorigenesis. <i>Cancer Research</i> , 2012, 72, 2990-2999.	0.4	48
22	Proteomic Analysis of Hepatitis C Virus (HCV) Core Protein Transfection and Host Regulator PA28 <sup>3</sup> Knockout in HCV Pathogenesis: A Network-Based Study. <i>Journal of Proteome Research</i> , 2012, 11, 3664-3679.	1.8	13
23	TargetMine, an Integrated Data Warehouse for Candidate Gene Prioritisation and Target Discovery. <i>PLoS ONE</i> , 2011, 6, e17844.	1.1	115
24	Differential functional genomic effects of anti-inflammatory phytochemicals on immune signaling. <i>BMC Genomics</i> , 2010, 11, 513.	1.2	29
25	An optimized procedure greatly improves EST vector contamination removal. <i>BMC Genomics</i> , 2007, 8, 416.	1.2	74