

# Bin Chen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1849005/publications.pdf>

Version: 2024-02-01

20  
papers

1,035  
citations

623188

14  
h-index

713013

21  
g-index

25  
all docs

25  
docs citations

25  
times ranked

1840  
citing authors

#	ARTICLE	IF	CITATIONS
1	Reversal of cancer gene expression correlates with drug efficacy and reveals therapeutic targets. Nature Communications, 2017, 8, 16022.	5.8	151
2	Leveraging big data to transform target selection and drug discovery. Clinical Pharmacology and Therapeutics, 2016, 99, 285-297.	2.3	147
3	Comprehensive transcriptomic analysis of cell lines as models of primary tumors across 22 tumor types. Nature Communications, 2019, 10, 3574.	5.8	111
4	Harnessing big omics data and AI for drug discovery in hepatocellular carcinoma. Nature Reviews Gastroenterology and Hepatology, 2020, 17, 238-251.	8.2	90
5	Computational Discovery of Niclosamide Ethanolamine, a Repurposed Drug Candidate That Reduces Growth of Hepatocellular Carcinoma Cells In Vitro and in Mice by Inhibiting Cell Division Cycle 37 Signaling. Gastroenterology, 2017, 152, 2022-2036.	0.6	81
6	Evaluating cell lines as models for metastatic breast cancer through integrative analysis of genomic data. Nature Communications, 2019, 10, 2138.	5.8	58
7	Experimental and real-world evidence supporting the computational repurposing of bumetanide for APOE4-related Alzheimer's disease. Nature Aging, 2021, 1, 932-947.	5.3	58
8	Relating hepatocellular carcinoma tumor samples and cell lines using gene expression data in translational research. BMC Medical Genomics, 2015, 8, S5.	0.7	56
9	Combined inhibition of atypical PKC and histone deacetylase 1 is cooperative in basal cell carcinoma treatment. JCI Insight, 2017, 2, .	2.3	49
10	Relating Chemical Structure to Cellular Response: An Integrative Analysis of Gene Expression, Bioactivity, and Structural Data Across 11,000 Compounds. CPT: Pharmacometrics and Systems Pharmacology, 2015, 4, 576-584.	1.3	47
11	Selecting precise reference normal tissue samples for cancer research using a deep learning approach. BMC Medical Genomics, 2019, 12, 21.	0.7	37
12	In silico and in vitro drug screening identifies new therapeutic approaches for Ewing sarcoma. Oncotarget, 2017, 8, 4079-4095.	0.8	34
13	Leveraging Big Data to Transform Drug Discovery. Methods in Molecular Biology, 2019, 1939, 91-118.	0.4	27
14	OCTAD: an open workspace for virtually screening therapeutics targeting precise cancer patient groups using gene expression features. Nature Protocols, 2021, 16, 728-753.	5.5	24
15	Gene expression signatures identify paediatric patients with multiple organ dysfunction who require advanced life support in the intensive care unit. EBioMedicine, 2020, 62, 103122.	2.7	17
16	Published anti-SARS-CoV-2 in vitro hits share common mechanisms of action that synergize with antivirals. Briefings in Bioinformatics, 2021, 22, .	3.2	8
17	Integrating Clinical Phenotype and Gene Expression Data to Prioritize Novel Drug Uses. CPT: Pharmacometrics and Systems Pharmacology, 2016, 5, 599-607.	1.3	7
18	Ibrutinib Blocks YAP1 Activation and Reverses BRAF Inhibitor Resistance in Melanoma Cells. Molecular Pharmacology, 2022, 101, 1-12.	1.0	5

#	ARTICLE	IF	CITATIONS
19	Semantic Breakthrough in Drug Discovery. Synthesis Lectures on the Semantic Web: Theory and Technology, 2014, 4, 1-142.	5.0	4
20	A systematic assessment of linking gene expression with genetic variants for prioritizing candidate targets. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 383-94.	0.7	2