

Bin Chen

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

21
papers

569
citations

12
h-index

23
g-index

25
ext. papers

850
ext. citations

8.8
avg, IF

4.23
L-index

#	Paper	IF	Citations
21	Leveraging big data to transform target selection and drug discovery. <i>Clinical Pharmacology and Therapeutics</i> , 2016 , 99, 285-97	6.1	105
20	Reversal of cancer gene expression correlates with drug efficacy and reveals therapeutic targets. <i>Nature Communications</i> , 2017 , 8, 16022	17.4	85
19	Comprehensive transcriptomic analysis of cell lines as models of primary tumors across 22 tumor types. <i>Nature Communications</i> , 2019 , 10, 3574	17.4	58
18	Relating hepatocellular carcinoma tumor samples and cell lines using gene expression data in translational research. <i>BMC Medical Genomics</i> , 2015 , 8 Suppl 2, S5	3.7	44
17	Harnessing big 'omics' data and AI for drug discovery in hepatocellular carcinoma. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2020 , 17, 238-251	24.2	43
16	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. <i>Gastroenterology</i> , 2017 , 152, 2022-2036	13.3	42
15	Relating Chemical Structure to Cellular Response: An Integrative Analysis of Gene Expression, Bioactivity, and Structural Data Across 11,000 Compounds. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2015 , 4, 576-84	4.5	37
14	Combined inhibition of atypical PKC and histone deacetylase 1 is cooperative in basal cell carcinoma treatment. <i>JCI Insight</i> , 2017 , 2,	9.9	32
13	Evaluating cell lines as models for metastatic breast cancer through integrative analysis of genomic data. <i>Nature Communications</i> , 2019 , 10, 2138	17.4	28
12	In silico and in vitro drug screening identifies new therapeutic approaches for Ewing sarcoma. <i>Oncotarget</i> , 2017 , 8, 4079-4095	3.3	26
11	Selecting precise reference normal tissue samples for cancer research using a deep learning approach. <i>BMC Medical Genomics</i> , 2019 , 12, 21	3.7	19
10	Leveraging Big Data to Transform Drug Discovery. <i>Methods in Molecular Biology</i> , 2019 , 1939, 91-118	1.4	12
9	Analysis of Infected Host Gene Expression Reveals Repurposed Drug Candidates and Time-Dependent Host Response Dynamics for COVID-19 2020 ,		10
8	Experimental and real-world evidence supporting the computational repurposing of bumetanide for APOE4-related Alzheimer's disease. <i>Nature Aging</i> , 2021 , 1, 932-947		7
7	OCTAD: an open workspace for virtually screening therapeutics targeting precise cancer patient groups using gene expression features. <i>Nature Protocols</i> , 2021 , 16, 728-753	18.8	5
6	Semantic Breakthrough in Drug Discovery. <i>Synthesis Lectures on the Semantic Web: Theory and Technology</i> , 2014 , 4, 1-142	3.5	4
5	Gene expression signatures identify paediatric patients with multiple organ dysfunction who require advanced life support in the intensive care unit. <i>EBioMedicine</i> , 2020 , 62, 103122	8.8	3

4	Integrating Clinical Phenotype and Gene Expression Data to Prioritize Novel Drug Uses. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2016 , 5, 599-607	4-5	3
3	A systematic assessment of linking gene expression with genetic variants for prioritizing candidate targets. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2015 , 383-94	1-3	2
2	OCTAD: an open workplace for virtually screening therapeutics targeting precise cancer patient groups using gene expression features		2
1	Published anti-SARS-CoV-2 in vitro hits share common mechanisms of action that synergize with antivirals. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13-4	2