Boyang Zhao

List of Publications by Year
in descending order

19 papers	703 citations	759233 12 h-index	839539 18 g-index
21 all docs	21 docs citations	21 times ranked	1476 citing authors

#	Article	IF	Citations
1	Exploiting Temporal Collateral Sensitivity in Tumor Clonal Evolution. Cell, 2016, 165, 234-246.	28.9	111
2	Intratumor heterogeneity alters most effective drugs in designed combinations. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10773-10778.	7.1	94
3	Addressing Genetic Tumor Heterogeneity through Computationally Predictive Combination Therapy. Cancer Discovery, 2014, 4, 166-174.	9.4	92
4	Updates on the web-based VIOLIN vaccine database and analysis system. Nucleic Acids Research, 2014, 42, D1124-D1132.	14.5	66
5	VIOLIN: vaccine investigation and online information network. Nucleic Acids Research, 2007, 36, D923-D928.	14.5	65
6	Acquisition of a single EZH2 D1 domain mutation confers acquired resistance to EZH2-targeted inhibitors. Oncotarget, 2015, 6, 32646-32655.	1.8	65
7	Modeling Tumor Clonal Evolution for Drug Combinations Design. Trends in Cancer, 2016, 2, 144-158.	7.4	43
8	Large-scale phosphoproteomic analysis of membrane proteins in renal proximal and distal tubule. American Journal of Physiology - Cell Physiology, 2011, 300, C755-C770.	4.6	37
9	<scp>CP</scp>hos: A program to calculate and visualize evolutionarily conserved functional phosphorylation sites. Proteomics, 2012, 12, 3299-3303.	2.2	25
10	Multi-scale Predictions of Drug Resistance Epidemiology Identify Design Principles for Rational Drug Design. Cell Reports, 2020, 30, 3951-3963.e4.	6.4	17
11	Evolution of the nonsense-mediated decay pathway is associated with decreased cytolytic immune infiltration. PLoS Computational Biology, 2019, 15, e1007467.	3.2	15
12	Differential selective pressure alters rate of drug resistance acquisition in heterogeneous tumor populations. Scientific Reports, 2016, 6, 36198.	3.3	14
13	Clinical Data Extraction and Normalization of Cyrillic Electronic Health Records Via Deep-Learning Natural Language Processing. JCO Clinical Cancer Informatics, 2019, 3, 1-9.	2.1	14
14	Inherited Disease Genetics Improves the Identification of Cancer-Associated Genes. PLoS Genetics, 2016, 12, e1006081.	3.5	14
15	Large-scale phosphotyrosine proteomic profiling of rat renal collecting duct epithelium reveals predominance of proteins involved in cell polarity determination. American Journal of Physiology - Cell Physiology, 2012, 302, C27-C45.	4.6	11
16	Kinetic Mechanism for the Excision of Hypoxanthine by <i>Escherichia coli</i> AlkA and Evidence for Binding to DNA Ends. Biochemistry, 2011, 50, 4350-4359.	2.5	10
17	Familial Hypercholesterolemia Identification Algorithm in Patients with Acute Cardiovascular Events in A Large Hospital Electronic Database in Bulgaria: A Call for Implementation. Advances in Therapy, 2021, 38, 2323-2338.	2.9	5
18	A pan-CRISPR analysis of mammalian cell specificity identifies ultra-compact sgRNA subsets for genome-scale experiments. Nature Communications, 2022, 13, 625.	12.8	2

#	ARTICLE	IF	CITATIONS
19	Reply to Azuaje: Predicting effective combined therapies for heterogeneous tumors. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4288-E4288.	7.1	0