Nishanth Ulhas Nair

List of Publications by Year
in descending order

19 papers	432 citations	933447 10 h-index	888059 17 g-index
25 all docs	25 docs citations	25 times ranked	706 citing authors

#	Article	IF	Citations
1	Synthetic lethality-based prediction of anti-SARS-CoV-2 targets. IScience, 2022, 25, 104311.	4.1	7
2	Synthetic lethality-mediated precision oncology via the tumor transcriptome. Cell, 2021, 184, 2487-2502.e13.	28.9	60
3	Synthetic lethality across normal tissues is strongly associated with cancer risk, onset, and tumor suppressor specificity. Science Advances, 2021, 7, .	10.3	16
4	Synthetic lethal combination targeting BET uncovered intrinsic susceptibility of TNBC to ferroptosis. Science Advances, 2020, 6, .	10.3	85
5	Migration rather than proliferation transcriptomic signatures are strongly associated with breast cancer patient survival. Scientific Reports, 2019, 9, 10989.	3.3	28
6	Genome‐wide prediction of synthetic rescue mediators of resistance to targeted and immunotherapy. Molecular Systems Biology, 2019, 15, e8323.	7.2	25
7	Putative functional genes in idiopathic dilated cardiomyopathy. Scientific Reports, 2018, 8, 66.	3.3	7
8	PYK2 negatively regulates the Hippo pathway in TNBC by stabilizing TAZ protein. Cell Death and Disease, 2018, 9, 985.	6.3	26
9	Prediction and Subtyping of Hypertension from Pan-Tissue Transcriptomic and Genetic Analyses. Genetics, 2017, 207, 1121-1134.	2.9	6
10	A maximum-likelihood approach for building cell-type trees by lifting. BMC Genomics, 2016, 17, 14.	2.8	6
11	Study of cell differentiation by phylogenetic analysis using histone modification data. BMC Bioinformatics, 2014, 15, 269.	2.6	12
12	Probabilistic partitioning methods to find significant patterns in ChIP-Seq data. Bioinformatics, 2014, 30, 2406-2413.	4.1	14
13	Phylogenetic Analysis of Cell Types Using Histone Modifications. Lecture Notes in Computer Science, 2013, , 326-337.	1.3	1
14	Genome-Wide Evaluation of Histone Methylation Changes Associated with Leaf Senescence in Arabidopsis. PLoS ONE, 2012, 7, e33151.	2.5	83
15	ChIPnorm: A Statistical Method for Normalizing and Identifying Differential Regions in Histone Modification ChIP-seq Libraries. PLoS ONE, 2012, 7, e39573.	2.5	32
16	Multi-Pattern Viterbi Algorithm for joint decoding of multiple speech patterns. Signal Processing, 2010, 90, 3278-3283.	3.7	4
17	Joint evaluation of multiple speech patterns for speech recognition and training. Computer Speech and Language, 2010, 24, 307-340.	4.3	10
18	Enhanced flux balance analysis to model metabolic networks. , 2010, , .		0

#	Article	IF	Citations
19	Viterbi Algorithm for multi-pattern joint decoding. , 2009, , .		3