

Nishanth Ulhas Nair

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

432
citations

932766

10
h-index

887659

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. <i>IScience</i> , 2022, 25, 104311.	1.9	7
2	Synthetic lethality-mediated precision oncology via the tumor transcriptome. <i>Cell</i> , 2021, 184, 2487-2502.e13.	13.5	60
3	Synthetic lethality across normal tissues is strongly associated with cancer risk, onset, and tumor suppressor specificity. <i>Science Advances</i> , 2021, 7, .	4.7	16
4	Synthetic lethal combination targeting BET uncovered intrinsic susceptibility of TNBC to ferroptosis. <i>Science Advances</i> , 2020, 6, .	4.7	85
5	Migration rather than proliferation transcriptomic signatures are strongly associated with breast cancer patient survival. <i>Scientific Reports</i> , 2019, 9, 10989.	1.6	28
6	Genome-wide prediction of synthetic rescue mediators of resistance to targeted and immunotherapy. <i>Molecular Systems Biology</i> , 2019, 15, e8323.	3.2	25
7	Putative functional genes in idiopathic dilated cardiomyopathy. <i>Scientific Reports</i> , 2018, 8, 66.	1.6	7
8	PYK2 negatively regulates the Hippo pathway in TNBC by stabilizing TAZ protein. <i>Cell Death and Disease</i> , 2018, 9, 985.	2.7	26
9	Prediction and Subtyping of Hypertension from Pan-Tissue Transcriptomic and Genetic Analyses. <i>Genetics</i> , 2017, 207, 1121-1134.	1.2	6
10	A maximum-likelihood approach for building cell-type trees by lifting. <i>BMC Genomics</i> , 2016, 17, 14.	1.2	6
11	Study of cell differentiation by phylogenetic analysis using histone modification data. <i>BMC Bioinformatics</i> , 2014, 15, 269.	1.2	12
12	Probabilistic partitioning methods to find significant patterns in ChIP-Seq data. <i>Bioinformatics</i> , 2014, 30, 2406-2413.	1.8	14
13	Phylogenetic Analysis of Cell Types Using Histone Modifications. <i>Lecture Notes in Computer Science</i> , 2013, , 326-337.	1.0	1
14	Genome-Wide Evaluation of Histone Methylation Changes Associated with Leaf Senescence in Arabidopsis. <i>PLoS ONE</i> , 2012, 7, e33151.	1.1	83
15	ChIPnorm: A Statistical Method for Normalizing and Identifying Differential Regions in Histone Modification ChIP-seq Libraries. <i>PLoS ONE</i> , 2012, 7, e39573.	1.1	32
16	Multi-Pattern Viterbi Algorithm for joint decoding of multiple speech patterns. <i>Signal Processing</i> , 2010, 90, 3278-3283.	2.1	4
17	Joint evaluation of multiple speech patterns for speech recognition and training. <i>Computer Speech and Language</i> , 2010, 24, 307-340.	2.9	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