

Dimitrios M Vitsios

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

920
citations

687363

13
h-index

888059

17
g-index

26
all docs

26
docs citations

26
times ranked

1793
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene-SCOUT: identifying genes with similar continuous trait fingerprints from phenome-wide association analyses. <i>Nucleic Acids Research</i> , 2022, 50, 4289-4301.	14.5	3
2	Prioritizing non-coding regions based on human genomic constraint and sequence context with deep learning. <i>Nature Communications</i> , 2021, 12, 1504.	12.8	40
3	Identification of a missense variant in SPDL1 associated with idiopathic pulmonary fibrosis. <i>Communications Biology</i> , 2021, 4, 392.	4.4	28
4	Rare variant contribution to human disease in 281,104 UK Biobank exomes. <i>Nature</i> , 2021, 597, 527-532.	27.8	224
5	Mantis-ml: Disease-Agnostic Gene Prioritization from High-Throughput Genomic Screens by Stochastic Semi-supervised Learning. <i>American Journal of Human Genetics</i> , 2020, 106, 659-678.	6.2	24
6	Spontaneous Coronary Artery Dissection. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e003030.	3.6	43
7	Exome-Based Rare-Variant Analyses in CKD. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 1109-1122.	6.1	40
8	Re-annotation of 191 developmental and epileptic encephalopathy-associated genes unmasks de novo variants in SCN1A. <i>Npj Genomic Medicine</i> , 2019, 4, 31.	3.8	27
9	A programmed wave of uridylation-primed mRNA degradation is essential for meiotic progression and mammalian spermatogenesis. <i>Cell Research</i> , 2019, 29, 221-232.	12.0	48
10	RNA-sequencing analysis of umbilical cord plasma microRNAs from healthy newborns. <i>PLoS ONE</i> , 2018, 13, e0207952.	2.5	8
11	Large-scale analysis of microRNA expression, epi-transcriptomic features and biogenesis. <i>Nucleic Acids Research</i> , 2017, 45, 1079-1090.	14.5	44
12	A MILI-independent piRNA biogenesis pathway empowers partial germline reprogramming. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 604-606.	8.2	18
13	BioPAXViz: a cytoscape application for the visual exploration of metabolic pathway evolution. <i>Bioinformatics</i> , 2017, 33, 1418-1420.	4.1	5
14	Mirnova: genome-free prediction of microRNAs from small RNA sequencing data and single-cells using decision forests. <i>Nucleic Acids Research</i> , 2017, 45, e177-e177.	14.5	54
15	mRNA 3' uridylation and poly(A) tail length sculpt the mammalian maternal transcriptome. <i>Nature</i> , 2017, 548, 347-351.	27.8	142
16	In situ functional dissection of RNA cis-regulatory elements by multiplex CRISPR-Cas9 genome engineering. <i>Nature Communications</i> , 2017, 8, 2109.	12.8	11
17	Inference of Pathway Decomposition Across Multiple Species Through Gene Clustering. <i>International Journal on Artificial Intelligence Tools</i> , 2015, 24, 1540003.	1.0	0
18	Chimira: analysis of small RNA sequencing data and microRNA modifications. <i>Bioinformatics</i> , 2015, 31, 3365-3367.	4.1	118

#	ARTICLE	IF	CITATIONS
19	Real-time urban traffic information extraction from GPS tracking of a bus fleet. , 2013, , .		6