Dimitrios M Vitsios

List of Publications by Year
in descending order

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	Rare variant contribution to human disease in 281,104 UK Biobank exomes. Nature, 2021, 597, 527-532.	27.8	224
2	mRNA 3′ uridylation and poly(A) tail length sculpt the mammalian maternal transcriptome. Nature, 2017, 548, 347-351.	27.8	142
3	Chimira: analysis of small RNA sequencing data and microRNA modifications. Bioinformatics, 2015, 31, 3365-3367.	4.1	118
4	Mirnovo: genome-free prediction of microRNAs from small RNA sequencing data and single-cells using decision forests. Nucleic Acids Research, 2017, 45, e177-e177.	14.5	54
5	A programmed wave of uridylation-primed mRNA degradation is essential for meiotic progression and mammalian spermatogenesis. Cell Research, 2019, 29, 221-232.	12.0	48
6	Large-scale analysis of microRNA expression, epi-transcriptomic features and biogenesis. Nucleic Acids Research, 2017, 45, 1079-1090.	14.5	44
7	Spontaneous Coronary Artery Dissection. Circulation Genomic and Precision Medicine, 2020, 13, e003030.	3.6	43
8	Exome-Based Rare-Variant Analyses in CKD. Journal of the American Society of Nephrology: JASN, 2019, 30, 1109-1122.	6.1	40
9	Prioritizing non-coding regions based on human genomic constraint and sequence context with deep learning. Nature Communications, 2021, 12, 1504.	12.8	40
10	Identification of a missense variant in SPDL1 associated with idiopathic pulmonary fibrosis. Communications Biology, 2021, 4, 392.	4.4	28
11	Re-annotation of 191 developmental and epileptic encephalopathy-associated genes unmasks de novo variants in SCN1A. Npj Genomic Medicine, 2019, 4, 31.	3.8	27
12	Mantis-ml: Disease-Agnostic Gene Prioritization from High-Throughput Genomic Screens by Stochastic Semi-supervised Learning. American Journal of Human Genetics, 2020, 106, 659-678.	6.2	24
13	A MILI-independent piRNA biogenesis pathway empowers partial germline reprogramming. Nature Structural and Molecular Biology, 2017, 24, 604-606.	8.2	18
14	In situ functional dissection of RNA cis-regulatory elements by multiplex CRISPR-Cas9 genome engineering. Nature Communications, 2017, 8, 2109.	12.8	11
15	RNA-sequencing analysis of umbilical cord plasma microRNAs from healthy newborns. PLoS ONE, 2018, 13, e0207952.	2.5	8
16	Real-time urban traffic information extraction from GPS tracking of a bus fleet. , 2013, , .		6
17	BioPAXViz: a cytoscape application for the visual exploration of metabolic pathway evolution. Bioinformatics, 2017, 33, 1418-1420.	4.1	5
18	Gene-SCOUT: identifying genes with similar continuous trait fingerprints from phenome-wide association analyses. Nucleic Acids Research, 2022, 50, 4289-4301.	14.5	3

#	Article	IF	Citations
19	Inference of Pathway Decomposition Across Multiple Species Through Gene Clustering. International Journal on Artificial Intelligence Tools, 2015, 24, 1540003.	1.0	0