

Aristeidis G Telonis

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7935270/publications.pdf>

Version: 2024-02-01

26
papers

1,958
citations

361413

20
h-index

610901

24
g-index

28
all docs

28
docs citations

28
times ranked

2758
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of 13 cell types reveals evidence for the expression of numerous novel primate- and tissue-specific microRNAs. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1106-15.	7.1	376
2	Knowledge about the presence or absence of miRNA isoforms (isomiRs) can successfully discriminate amongst 32 TCGA cancer types. Nucleic Acids Research, 2017, 45, 2973-2985.	14.5	158
3	MINTbase v2.0: a comprehensive database for tRNA-derived fragments that includes nuclear and mitochondrial fragments from all The Cancer Genome Atlas projects. Nucleic Acids Research, 2018, 46, D152-D159.	14.5	155
4	Dissecting tRNA-derived fragment complexities using personalized transcriptomes reveals novel fragment classes and unexpected dependencies. Oncotarget, 2015, 6, 24797-24822.	1.8	146
5	Beyond the one-locus-one-miRNA paradigm: microRNA isoforms enable deeper insights into breast cancer heterogeneity. Nucleic Acids Research, 2015, 43, 9158-9175.	14.5	134
6	MINTmap: fast and exhaustive profiling of nuclear and mitochondrial tRNA fragments from short RNA-seq data. Scientific Reports, 2017, 7, 41184.	3.3	123
7	N-BLR, a primate-specific non-coding transcript leads to colorectal cancer invasion and migration. Genome Biology, 2017, 18, 98.	8.8	97
8	Race Disparities in the Contribution of miRNA Isoforms and tRNA-Derived Fragments to Triple-Negative Breast Cancer. Cancer Research, 2018, 78, 1140-1154.	0.9	90
9	MINTbase: a framework for the interactive exploration of mitochondrial and nuclear tRNA fragments. Bioinformatics, 2016, 32, 2481-2489.	4.1	89
10	YAMAT-seq: an efficient method for high-throughput sequencing of mature transfer RNAs. Nucleic Acids Research, 2017, 45, gkx005.	14.5	84
11	tRNA Fragments Show Intertwining with mRNAs of Specific Repeat Content and Have Links to Disparities. Cancer Research, 2019, 79, 3034-3049.	0.9	72
12	Profiles of miRNA Isoforms and tRNA Fragments in Prostate Cancer. Scientific Reports, 2018, 8, 5314.	3.3	57
13	GPRC5A is a potential oncogene in pancreatic ductal adenocarcinoma cells that is upregulated by gemcitabine with help from HuR. Cell Death and Disease, 2016, 7, e2294-e2294.	6.3	50
14	Targeting the mRNA-binding protein HuR impairs malignant characteristics of pancreatic ductal adenocarcinoma cells. Oncotarget, 2015, 6, 27312-27331.	1.8	47
15	Lactate Efflux From Intervertebral Disc Cells Is Required for Maintenance of Spine Health. Journal of Bone and Mineral Research, 2020, 35, 550-570.	2.8	46
16	Assessment of isomiR Discrimination Using Commercial qPCR Methods. Non-coding RNA, 2017, 3, 18.	2.6	40
17	Consequential considerations when mapping tRNA fragments. BMC Bioinformatics, 2016, 17, 123.	2.6	38
18	Mitochondrial tRNA-lookalikes in nuclear chromosomes: Could they be functional?. RNA Biology, 2015, 12, 375-380.	3.1	37

#	ARTICLE	IF	CITATIONS
19	Nuclear and mitochondrial tRNA-lookalikes in the human genome. <i>Frontiers in Genetics</i> , 2014, 5, 344.	2.3	36
20	Unification of miRNA and isomiR research: the mirGFF3 format and the mirtop API. <i>Bioinformatics</i> , 2020, 36, 698-703.	4.1	33
21	Accurate Profiling and Quantification of tRNA Fragments from RNA-Seq Data: A Vade Mecum for MINTmap. <i>Methods in Molecular Biology</i> , 2018, 1680, 237-255.	0.9	21
22	IsoMiRmap: fast, deterministic and exhaustive mining of isomiRs from short RNA-seq datasets. <i>Bioinformatics</i> , 2021, 37, 1828-1838.	4.1	11
23	Refugee "crisis"™ and social services in Greece: social workers'™ profile and working conditions. <i>European Journal of Social Work</i> , 2020, 23, 1005-1018.	0.9	9
24	The transcriptional trajectories of pluripotency and differentiation comprise genes with antithetical architecture and repetitive-element content. <i>BMC Biology</i> , 2021, 19, 60.	3.8	5
25	Development of a Fast and Reproducible Assay for the Clinical Implementation of Epigenetic Biomarkers to Predict Decitabine Response in Patients with Chronic Myelomonocytic Leukemia. <i>Blood</i> , 2021, 138, 1515-1515.	1.4	0
26	Intronic Architecture Links DNA Methylation to Gene Expression and Helps Drive Subtype-Specific Transcriptional Landscapes in <i>DNMT3A</i> - and <i>IDH1/2</i> -Mutant Acute Myeloid Leukemias (AML). <i>Blood</i> , 2021, 138, 3290-3290.	1.4	0