

Sonika Tyagi

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

1,217
citations

567281

15
h-index

501196

28
g-index

36
all docs

36
docs citations

36
times ranked

2585
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptomic analysis reveals myometrial topologically associated domains linked to onset of human term labor. <i>Molecular Human Reproduction</i> , 2022, , .	2.8	3
2	A multi-modal data harmonisation approach for discovery of COVID-19 drug targets. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	13
3	A Survey of Current Resources to Study lncRNA-Protein Interactions. <i>Non-coding RNA</i> , 2021, 7, 33.	2.6	7
4	Towards a comprehensive pipeline to identify and functionally annotate long noncoding RNA (lncRNA). <i>Computers in Biology and Medicine</i> , 2020, 127, 104028.	7.0	16
5	Integrative computational epigenomics to build data-driven gene regulation hypotheses. <i>GigaScience</i> , 2020, 9, .	6.4	13
6	CEP3 levels affect starvation-related growth responses of the primary root. <i>Journal of Experimental Botany</i> , 2019, 70, 4763-4774.	4.8	32
7	Navigating the non-coding genome in heart development and Congenital Heart Disease. <i>Differentiation</i> , 2019, 107, 11-23.	1.9	17
8	Computational prediction of microRNAs in marine bacteria of the genus <i>Thalassospira</i> . <i>PLoS ONE</i> , 2019, 14, e0212996.	2.5	12
9	Establishing a distributed national research infrastructure providing bioinformatics support to life science researchers in Australia. <i>Briefings in Bioinformatics</i> , 2019, 20, 384-389.	6.5	11
10	BOSC 2019, the 20th annual Bioinformatics Open Source Conference. <i>F1000Research</i> , 2019, 8, 2132.	1.6	3
11	Insights into the neurochemical signature of the Innervation of Beige Fat. <i>Molecular Metabolism</i> , 2018, 11, 47-58.	6.5	15
12	The molecular characterisation of mitochondrial DNA deficient oocytes using a pig model. <i>Human Reproduction</i> , 2018, 33, 942-953.	0.9	19
13	The Intercellular Tight Junction and Spontaneous Coronary Artery Dissection. <i>Journal of the American College of Cardiology</i> , 2018, 72, 1752-1753.	2.8	19
14	Four simple recommendations to encourage best practices in research software. <i>F1000Research</i> , 2017, 6, 876.	1.6	88
15	Best practice data life cycle approaches for the life sciences. <i>F1000Research</i> , 2017, 6, 1618.	1.6	21
16	Best practice data life cycle approaches for the life sciences. <i>F1000Research</i> , 2017, 6, 1618.	1.6	23
17	Towards an open, collaborative, reusable framework for sharing hands-on bioinformatics training workshops. <i>Briefings in Bioinformatics</i> , 2016, 18, bbw013.	6.5	4
18	Characterisation of mouse epididymosomes reveals a complex profile of microRNAs and a potential mechanism for modification of the sperm epigenome. <i>Scientific Reports</i> , 2016, 6, 31794.	3.3	181

#	ARTICLE	IF	CITATIONS
19	Next Generation Sequencing Analysis Reveals Segmental Patterns of microRNA Expression in Mouse Epididymal Epithelial Cells. PLoS ONE, 2015, 10, e0135605.	2.5	42
20	Assessment of microRNA expression in mouse epididymal epithelial cells and spermatozoa by next generation sequencing. Genomics Data, 2015, 6, 208-211.	1.3	21
21	The MicroRNA Signature of Mouse Spermatozoa Is Substantially Modified During Epididymal Maturation1. Biology of Reproduction, 2015, 93, 91.	2.7	156
22	Next-generation sequencing: a challenge to meet the increasing demand for training workshops in Australia. Briefings in Bioinformatics, 2013, 14, 563-574.	6.5	17
23	Frequent somatic mutations in MAP3K5 and MAP3K9 in metastatic melanoma identified by exome sequencing. Nature Genetics, 2012, 44, 165-169.	21.4	170
24	Whole Genome Expression Array Profiling Highlights Differences in Mucosal Defense Genes in Barrett's Esophagus and Esophageal Adenocarcinoma. PLoS ONE, 2011, 6, e22513.	2.5	36
25	Gene expression alterations in formalin-fixed, paraffin-embedded Barrett esophagus and esophageal adenocarcinoma tissues.. Cancer Biology and Therapy, 2010, 10, 172-179.	3.4	22
26	Characterization of the Melanoma miRNAome by Deep Sequencing. PLoS ONE, 2010, 5, e9685.	2.5	181
27	webFOG: A web tool to map genomic features onto genes. Biochemical and Biophysical Research Communications, 2010, 401, 447-450.	2.1	0
28	CID-miRNA: A web server for prediction of novel miRNA precursors in human genome. Biochemical and Biophysical Research Communications, 2008, 372, 831-834.	2.1	52
29	Differential use of multiple replication origins in the ribosomal DNA episome of the protozoan parasite Entamoeba histolytica. Nucleic Acids Research, 2003, 31, 2035-2044.	14.5	9
30	multiomics: A user-friendly multi-omics data harmonisation R pipeline. F1000Research, 0, 10, 538.	1.6	2
31	Advancing the international data science workforce through shared training and education. F1000Research, 0, 8, 251.	1.6	0