Sonika Tyagi

List of Publications by Year
in descending order

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	Characterization of the Melanoma miRNAome by Deep Sequencing. PLoS ONE, 2010, 5, e9685.	2.5	181
2	Characterisation of mouse epididymosomes reveals a complex profile of microRNAs and a potential mechanism for modification of the sperm epigenome. Scientific Reports, 2016, 6, 31794.	3.3	181
3	Frequent somatic mutations in MAP3K5 and MAP3K9 in metastatic melanoma identified by exome sequencing. Nature Genetics, 2012, 44, 165-169.	21.4	170
4	The MicroRNA Signature of Mouse Spermatozoa Is Substantially Modified During Epididymal Maturation1. Biology of Reproduction, 2015, 93, 91.	2.7	156
5	Four simple recommendations to encourage best practices in research software. F1000Research, 2017, 6, 876.	1.6	88
6	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
7	Next Generation Sequencing Analysis Reveals Segmental Patterns of microRNA Expression in Mouse Epididymal Epithelial Cells. PLoS ONE, 2015, 10, e0135605.	2.5	42
8	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
9	CEP3 levels affect starvation-related growth responses of the primary root. Journal of Experimental Botany, 2019, 70, 4763-4774.	4.8	32
10	Best practice data life cycle approaches for the life sciences. F1000Research, 2017, 6, 1618.	1.6	23
11	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
12	Assessment of microRNA expression in mouse epididymal epithelial cells and spermatozoa by next generation sequencing. Genomics Data, 2015, 6, 208-211.	1.3	21
13	Best practice data life cycle approaches for the life sciences. F1000Research, 2017, 6, 1618.	1.6	21
14	The molecular characterisation of mitochondrial DNA deficient oocytes using a pig model. Human Reproduction, 2018, 33, 942-953.	0.9	19
15	The Intercellular TightÂJunction and Spontaneous Coronary Artery Dissection. Journal of the American College of Cardiology, 2018, 72, 1752-1753.	2.8	19
16	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
17	Navigating the non-coding genome in heart development and Congenital Heart Disease. Differentiation, 2019, 107, 11-23.	1.9	17
18	Towards a comprehensive pipeline to identify and functionally annotate long noncoding RNA (lncRNA). Computers in Biology and Medicine, 2020, 127, 104028.	7.0	16

#	Article	IF	Citations
19	Insights into the neurochemical signature of the Innervation of Beige Fat. Molecular Metabolism, 2018, 11, 47-58.	6.5	15
20	Integrative computational epigenomics to build data-driven gene regulation hypotheses. GigaScience, 2020, 9, .	6.4	13
21	A multi-modal data harmonisation approach for discovery of COVID-19 drug targets. Briefings in Bioinformatics, 2021, 22, .	6.5	13
22	Computational prediction of microRNAs in marine bacteria of the genus Thalassospira. PLoS ONE, 2019, 14, e0212996.	2.5	12
23	Establishing a distributed national research infrastructure providing bioinformatics support to life science researchers in Australia. Briefings in Bioinformatics, 2019, 20, 384-389.	6.5	11
24	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
25	A Survey of Current Resources to Study lncRNA-Protein Interactions. Non-coding RNA, 2021, 7, 33.	2.6	7
26	Towards an open, collaborative, reusable framework for sharing hands-on bioinformatics training workshops. Briefings in Bioinformatics, 2016, 18, bbw013.	6.5	4
27	BOSC 2019, the 20th annual Bioinformatics Open Source Conference. F1000Research, 2019, 8, 2132.	1.6	3
28	Transcriptomic analysis reveals myometrial topologically associated domains linked to onset of human term labor. Molecular Human Reproduction, 2022, , .	2.8	3
29	multiomics: A user-friendly multi-omics data harmonisation R pipeline. F1000Research, 0, 10, 538.	1.6	2
30	webFOG: A web tool to map genomic features onto genes. Biochemical and Biophysical Research Communications, 2010, 401, 447-450.	2.1	0
31	Advancing the international data science workforce through shared training and education. F1000Research, 0, 8, 251.	1.6	0