Wenjie Shu

List of Publications by Year
in descending order

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26 papers	1,253 citations	687363 13 h-index	580821 25 g-index
28 all docs	28 docs citations	28 times ranked	1939 citing authors

#	Article	IF	Citations
1	Deep Learning and Its Applications in Biomedicine. Genomics, Proteomics and Bioinformatics, 2018, 16, 17-32.	6.9	420
2	BiRen: predicting enhancers with a deep-learning-based model using the DNA sequence alone. Bioinformatics, 2017, 33, 1930-1936.	4.1	121
3	Embryonic defects induced by maternal obesity in mice derive from Stella insufficiency in oocytes. Nature Genetics, 2018, 50, 432-442.	21.4	112
4	PEDLA: predicting enhancers with a deep learning-based algorithmic framework. Scientific Reports, 2016, 6, 28517.	3.3	88
5	Characterization of Metabolic Patterns in Mouse Oocytes during Meiotic Maturation. Molecular Cell, 2020, 80, 525-540.e9.	9.7	74
6	Oocyte competence is maintained by m6A methyltransferase KIAA1429-mediated RNA metabolism during mouse follicular development. Cell Death and Differentiation, 2020, 27, 2468-2483.	11.2	70
7	METTL3-mediated m⁶A is required for murine oocyte maturation and maternal-to-zygotic transition. Cell Cycle, 2020, 19, 391-404.	2.6	69
8	DeÂnovo identification of replication-timing domains in the human genome by deep learning. Bioinformatics, 2016, 32, 641-649.	4.1	48
9	An integrative analysis of TFBS-clustered regions reveals new transcriptional regulation models on the accessible chromatin landscape. Scientific Reports, 2015, 5, 8465.	3.3	41
10	Functional annotation of structural ncRNAs within enhancer RNAs in the human genome: implications for human disease. Scientific Reports, 2017, 7, 15518.	3.3	26
11	Lnc2Catlas: an atlas of long noncoding RNAs associated with risk of cancers. Scientific Reports, 2018, 8, 1909.	3.3	26
12	Functional annotation of HOT regions in the human genome: implications for human disease and cancer. Scientific Reports, 2015, 5, 11633.	3.3	24
13	Differential roles of Stella in the modulation of DNA methylation during oocyte and zygotic development. Cell Discovery, 2019, 5, 9.	6.7	19
14	High-resolution annotation of the mouse preimplantation embryo transcriptome using long-read sequencing. Nature Communications, 2020, 11, 2653.	12.8	17
15	Accurate identification of RNA editing sites from primitive sequence with deep neural networks. Scientific Reports, 2018, 8, 6005.	3.3	16
16	The landscape of the A-to-I RNA editome from 462 human genomes. Scientific Reports, 2018, 8, 12069.	3.3	15
17	Singleâ€cell RNAâ€Seq reveals a highly coordinated transcriptional program in mouse germ cells during primordial follicle formation. Aging Cell, 2021, 20, e13424.	6.7	15
18	Integrative proteome analysis implicates aberrant RNA splicing in impaired developmental potential of aged mouse oocytes. Aging Cell, 2021, 20, e13482.	6.7	12

#	Article	IF	Citations
19	Genome-wide identification and characterisation of HOT regions in the human genome. BMC Genomics, 2016, 17, 733.	2.8	11
20	LIVE: a manually curated encyclopedia of experimentally validated interactions of lncRNAs. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	8
21	Cytosine and adenine deaminase base-editors induce broad and nonspecific changes in gene expression and splicing. Communications Biology, 2021, 4, 882.	4.4	5
22	Computing configuration space obstacles using polynomial transforms. , 2004, , .		2
23	PERFORMANCE ANALYSIS OF KALMAN-BASED FILTERS AND PARTICLE FILTERS FOR NON-LINEAR/NON-GAUSSIAN BAYESIAN TRACKING. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2005, 38, 1131-1136.	0.4	2
24	Neural dual particle filter and its application in speech enhancement. , 0, , .		2
25	iFORM: Incorporating Find Occurrence of Regulatory Motifs. PLoS ONE, 2016, 11, e0168607.	2.5	2
26	UNSCENTED TRANSFORM AND ITS APPLICATION IN ATC TRACKING. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2005, 38, 1137-1142.	0.4	0