Wenjie Shu

List of Publications by Year
in descending order

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	Single‐cell RNA‐Seq reveals a highly coordinated transcriptional program in mouse germ cells during primordial follicle formation. Aging Cell, 2021, 20, e13424.	6.7	15
2	Cytosine and adenine deaminase base-editors induce broad and nonspecific changes in gene expression and splicing. Communications Biology, 2021, 4, 882.	4.4	5
3	Integrative proteome analysis implicates aberrant RNA splicing in impaired developmental potential of aged mouse oocytes. Aging Cell, 2021, 20, e13482.	6.7	12
4	METTL3-mediated m^{6}A is required for murine oocyte maturation and maternal-to-zygotic transition. Cell Cycle, 2020, 19, 391-404.	2.6	69
5	Characterization of Metabolic Patterns in Mouse Oocytes during Meiotic Maturation. Molecular Cell, 2020, 80, 525-540.e9.	9.7	74
6	High-resolution annotation of the mouse preimplantation embryo transcriptome using long-read sequencing. Nature Communications, 2020, 11, 2653.	12.8	17
7	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
8	Differential roles of Stella in the modulation of DNA methylation during oocyte and zygotic development. Cell Discovery, 2019, 5, 9.	6.7	19
9	LIVE: a manually curated encyclopedia of experimentally validated interactions of lncRNAs. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	8
10	Deep Learning and Its Applications in Biomedicine. Genomics, Proteomics and Bioinformatics, 2018, 16, 17-32.	6.9	420
11	Accurate identification of RNA editing sites from primitive sequence with deep neural networks. Scientific Reports, 2018, 8, 6005.	3.3	16
12	Embryonic defects induced by maternal obesity in mice derive from Stella insufficiency in oocytes. Nature Genetics, 2018, 50, 432-442.	21.4	112
13	Lnc2Catlas: an atlas of long noncoding RNAs associated with risk of cancers. Scientific Reports, 2018, 8, 1909.	3.3	26
14	The landscape of the A-to-I RNA editome from 462 human genomes. Scientific Reports, 2018, 8, 12069.	3.3	15
15	BiRen: predicting enhancers with a deep-learning-based model using the DNA sequence alone. Bioinformatics, 2017, 33, 1930-1936.	4.1	121
16	Functional annotation of structural ncRNAs within enhancer RNAs in the human genome: implications for human disease. Scientific Reports, 2017, 7, 15518.	3.3	26
17	Genome-wide identification and characterisation of HOT regions in the human genome. BMC Genomics, 2016, 17, 733.	2.8	11
18	PEDLA: predicting enhancers with a deep learning-based algorithmic framework. Scientific Reports, 2016, 6, 28517.	3.3	88

#	Article	IF	Citations
19	*DeÂnovo* identification of replication-timing domains in the human genome by deep learning. Bioinformatics, 2016, 32, 641-649.	4.1	48
20	iFORM: Incorporating Find Occurrence of Regulatory Motifs. PLoS ONE, 2016, 11, e0168607.	2.5	2
21	Functional annotation of HOT regions in the human genome: implications for human disease and cancer. Scientific Reports, 2015, 5, 11633.	3.3	24
22	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
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	UNSCENTED TRANSFORM AND ITS APPLICATION IN ATC TRACKING. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2005, 38, 1137-1142.	0.4	0
25	Computing configuration space obstacles using polynomial transforms. , 2004, , .		2
26	Neural dual particle filter and its application in speech enhancement. , 0, , .		2