Long chunshen

List of Publications by Year in descending order

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1306789 1281420 11 181 7 11 citations g-index h-index papers 13 13 13 146 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	WGBS combined with RNA-seq analysis revealed that Dnmt1 affects the methylation modification and gene expression changes during mouse oocyte vitrification. Theriogenology, 2022, 177, 11-21.	0.9	11
2	The Cumulative Formation of R-loop Interacts with Histone Modifications to Shape Cell Reprogramming. International Journal of Molecular Sciences, 2022, 23, 1567.	1.8	3
3	Dppa2/4 as a trigger of signaling pathways to promote zygote genome activation by binding to CG-rich region. Briefings in Bioinformatics, 2021, 22, .	3.2	12
4	eHSCPr discriminating the cell identity involved in endothelial to hematopoietic transition. Bioinformatics, 2021, 37, 2157-2164.	1.8	19
5	HelPredictor models single-cell transcriptome to predict human embryo lineage allocation. Briefings in Bioinformatics, 2021, 22, .	3.2	6
6	Nuclear Transfer Arrest Embryos Show Massive Dysregulation of Genes Involved in Transcription Pathways. International Journal of Molecular Sciences, 2021, 22, 8187.	1.8	3
7	Machine Learning of Single-Cell Transcriptome Highly Identifies mRNA Signature by Comparing F-Score Selection with DGE Analysis. Molecular Therapy - Nucleic Acids, 2020, 20, 155-163.	2.3	31
8	Fatty acid metabolism as an indicator for the maternal–to–zygotic transition in porcine IVF embryos revealed by RNA sequencing. Theriogenology, 2020, 151, 128-136.	0.9	7
9	The spatial binding model of the pioneer factor Oct4 with its target genes during cell reprogramming. Computational and Structural Biotechnology Journal, 2019, 17, 1226-1233.	1.9	23
10	EmExplorer: a database for exploring time activation of gene expression in mammalian embryos. Open Biology, 2019, 9, 190054.	1.5	35
11	Transcriptome Comparisons of Multi-Species Identify Differential Genome Activation of Mammals Embryogenesis. IEEE Access, 2019, 7, 7794-7802.	2.6	31