Zhiyuan Chen

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5628935/publications.pdf

Version: 2024-02-01

16	1,146	643344 15	1051228 16
papers	citations	h-index	g-index

18	18	18	1437
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Cell typeâ€“specific mechanism of Setd1a heterozygosity in schizophrenia pathogenesis. Science Advances, 2022, 8, eabm1077.	4.7	16
2	Distinct dynamics and functions of H2AK119ub1 and H3K27me3 in mouse preimplantation embryos. Nature Genetics, 2021, 53, 551-563.	9.4	83
3	DPPA2 and DPPA4 are dispensable for mouse zygotic genome activation and pre-implantation development. Development (Cambridge), 2021, 148, .	1.2	17
4	The chromatin remodeler Snf2h is essential for oocyte meiotic cell cycle progression. Genes and Development, 2020, 34, 166-178.	2.7	21
5	Role of Mammalian DNA Methyltransferases in Development. Annual Review of Biochemistry, 2020, 89, 135-158.	5.0	182
6	Maternal H3K27me3-dependent autosomal and X chromosome imprinting. Nature Reviews Genetics, 2020, 21, 555-571.	7.7	53
7	Loss of DUX causes minor defects in zygotic genome activation and is compatible with mouse development. Nature Genetics, 2019, 51, 947-951.	9.4	138
8	Maternal-biased H3K27me3 correlates with paternal-specific gene expression in the human morula. Genes and Development, 2019, 33, 382-387.	2.7	47
9	Allelic H3K27me3 to allelic DNA methylation switch maintains noncanonical imprinting in extraembryonic cells. Science Advances, 2019, 5, eaay7246.	4.7	83
10	Maternal Eed knockout causes loss of H3K27me3 imprinting and random X inactivation in the extraembryonic cells. Genes and Development, 2018, 32, 1525-1536.	2.7	93
11	Colony-stimulating factor 2 acts from days 5 to 7 of development to modify programming of the bovine conceptus at day 86 of gestationâ€. Biology of Reproduction, 2017, 96, 743-757.	1.2	30
12	Global misregulation of genes largely uncoupled to DNA methylome epimutations characterizes a congenital overgrowth syndrome. Scientific Reports, 2017, 7, 12667.	1.6	30
13	Global assessment of imprinted gene expression in the bovine conceptus by next generation sequencing. Epigenetics, 2016, 11, 501-516.	1.3	65
14	Characterization of global loss of imprinting in fetal overgrowth syndrome induced by assisted reproduction. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 4618-4623.	3.3	114
15	Large offspring syndrome. Epigenetics, 2013, 8, 591-601.	1.3	125
16	Expression of KCNQ1OT1, CDKN1C, H19, and PLAGL1 and the methylation patterns at the KvDMR1 and H19/IGF2 imprinting control regions is conserved between human and bovine. Journal of Biomedical Science, 2012, 19, 95.	2.6	48