Zhiyuan Chen

List of Publications by Year
in descending order

16	1,146	567144 15	940416 16
papers	citations	h-index	g-index

18	18	18	1312
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Role of Mammalian DNA Methyltransferases in Development. Annual Review of Biochemistry, 2020, 89, 135-158.	5.0	182
2	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
3	Large offspring syndrome. Epigenetics, 2013, 8, 591-601.	1.3	125
4	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
5	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
6	Allelic H3K27me3 to allelic DNA methylation switch maintains noncanonical imprinting in extraembryonic cells. Science Advances, 2019, 5, eaay7246.	4.7	83
7	Distinct dynamics and functions of H2AK119ub1 and H3K27me3 in mouse preimplantation embryos. Nature Genetics, 2021, 53, 551-563.	9.4	83
8	Global assessment of imprinted gene expression in the bovine conceptus by next generation sequencing. Epigenetics, 2016, 11, 501-516.	1.3	65
9	Maternal H3K27me3-dependent autosomal and X chromosome imprinting. Nature Reviews Genetics, 2020, 21, 555-571.	7.7	53
10	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
11	Maternal-biased H3K27me3 correlates with paternal-specific gene expression in the human morula. Genes and Development, 2019, 33, 382-387.	2.7	47
12	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
13	Global misregulation of genes largely uncoupled to DNA methylome epimutations characterizes a congenital overgrowth syndrome. Scientific Reports, 2017, 7, 12667.	1.6	30
14	The chromatin remodeler Snf2h is essential for oocyte meiotic cell cycle progression. Genes and Development, 2020, 34, 166-178.	2.7	21
15	DPPA2 and DPPA4 are dispensable for mouse zygotic genome activation and pre-implantation development. Development (Cambridge), 2021, 148, .	1.2	17
16	Cell typeâ€“specific mechanism of Setd1a heterozygosity in schizophrenia pathogenesis. Science Advances, 2022, 8, eabm1077.	4.7	16