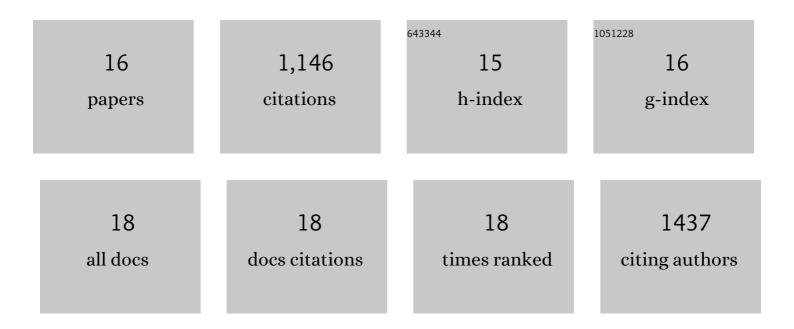
Zhiyuan Chen

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5628935/publications.pdf Version: 2024-02-01



7HIVIIAN CHEN

#	Article	IF	CITATIONS
1	Cell type–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 <i>Eed</i> 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