

Kenjiro Shirane

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

2,295
citations

623734

14
h-index

839539

18
g-index

19
all docs

19
docs citations

19
times ranked

3123
citing authors

#	ARTICLE	IF	CITATIONS
1	Derivation of Human Trophoblast Stem Cells. <i>Cell Stem Cell</i> , 2018, 22, 50-63.e6.	11.1	570
2	Mouse Oocyte Methylomes at Base Resolution Reveal Genome-Wide Accumulation of Non-CpG Methylation and Role of DNA Methyltransferases. <i>PLoS Genetics</i> , 2013, 9, e1003439.	3.5	263
3	<i>Setdb1</i> is required for germline development and silencing of H3K9me3-marked endogenous retroviruses in primordial germ cells. <i>Genes and Development</i> , 2014, 28, 2041-2055.	5.9	228
4	Generation of human oogonia from induced pluripotent stem cells in vitro. <i>Science</i> , 2018, 362, 356-360.	12.6	221
5	De novo DNA methylation drives 5hmC accumulation in mouse zygotes. <i>Nature Cell Biology</i> , 2016, 18, 225-233.	10.3	205
6	In Vitro Derivation and Propagation of Spermatogonial Stem Cell Activity from Mouse Pluripotent Stem Cells. <i>Cell Reports</i> , 2016, 17, 2789-2804.	6.4	136
7	DNA methylation and gene expression dynamics during spermatogonial stem cell differentiation in the early postnatal mouse testis. <i>BMC Genomics</i> , 2015, 16, 624.	2.8	112
8	Global Landscape and Regulatory Principles of DNA Methylation Reprogramming for Germ Cell Specification by Mouse Pluripotent Stem Cells. <i>Developmental Cell</i> , 2016, 39, 87-103.	7.0	106
9	Allele-Specific Methylome and Transcriptome Analysis Reveals Widespread Imprinting in the Human Placenta. <i>American Journal of Human Genetics</i> , 2016, 99, 1045-1058.	6.2	103
10	NSD1-deposited H3K36me2 directs de novo methylation in the mouse male germline and counteracts Polycomb-associated silencing. <i>Nature Genetics</i> , 2020, 52, 1088-1098.	21.4	96
11	In vitro expansion of mouse primordial germ cell-like cells recapitulates an epigenetic blank slate. <i>EMBO Journal</i> , 2017, 36, 1888-1907.	7.8	92
12	LTR retrotransposons transcribed in oocytes drive species-specific and heritable changes in DNA methylation. <i>Nature Communications</i> , 2018, 9, 3331.	12.8	65
13	Software updates in the Illumina HiSeq platform affect whole-genome bisulfite sequencing. <i>BMC Genomics</i> , 2017, 18, 31.	2.8	29
14	Repression of germline genes by PRC1.6 and SETDB1 in the early embryo precedes DNA methylation-mediated silencing. <i>Nature Communications</i> , 2021, 12, 7020.	12.8	26
15	The DNMT3A PWWP domain is essential for the normal DNA methylation landscape in mouse somatic cells and oocytes. <i>PLoS Genetics</i> , 2021, 17, e1009570.	3.5	17
16	Paternal MTHFR deficiency leads to hypomethylation of young retrotransposons and reproductive decline across two successive generations. <i>Development (Cambridge)</i> , 2021, 148, .	2.5	15
17	Dual role of <i>Ovol2</i> on the germ cell lineage segregation during gastrulation in mouse embryogenesis. <i>Development (Cambridge)</i> , 2022, 149, .	2.5	6
18	The dynamic chromatin landscape and mechanisms of DNA methylation during mouse germ cell development. <i>Genes and Genetic Systems</i> , 2022, , .	0.7	4