## Akihiko Sakashita

List of Publications by Year in descending order

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Δειμικό δλελομιτλ

#	Article	IF	CITATIONS
1	Highly rigid H3.1/H3.2–H3K9me3 domains set a barrier for cell fate reprogramming in trophoblast stem cells. Genes and Development, 2022, 36, 84-102.	5.9	10
2	Retrotransposons in the Mammalian Male Germline. Sexual Development, 2022, 16, 404-422.	2.0	3
3	Isolation of Murine Spermatogenic Cells using a Violet-Excited Cell-Permeable DNA Binding Dye. Journal of Visualized Experiments, 2021, , .	0.3	3
4	Meiosis-specific ZFP541 repressor complex promotes developmental progression of meiotic prophase towards completion during mouse spermatogenesis. Nature Communications, 2021, 12, 3184.	12.8	17
5	Comparative analysis of enteroendocrine cells and their hormones between mouse intestinal organoids and native tissues. Bioscience, Biotechnology and Biochemistry, 2020, 84, 936-942.	1.3	10
6	Endogenous retroviruses drive species-specific germline transcriptomes in mammals. Nature Structural and Molecular Biology, 2020, 27, 967-977.	8.2	60
7	Super-enhancer switching drives a burst in gene expression at the mitosis-to-meiosis transition. Nature Structural and Molecular Biology, 2020, 27, 978-988.	8.2	38
8	UHRF1 suppresses retrotransposons and cooperates with PRMT5 and PIWI proteins in male germ cells. Nature Communications, 2019, 10, 4705.	12.8	56
9	Sex-specific histone modifications in mouse fetal and neonatal germ cells. Epigenomics, 2019, 11, 543-561.	2.1	15
10	Attenuated chromatin compartmentalization in meiosis and its maturation in sperm development. Nature Structural and Molecular Biology, 2019, 26, 175-184.	8.2	92
11	XY oocytes of sex-reversed females with a Sry mutation deviate from the normal developmental process beyond the mitotic stageâ€. Biology of Reproduction, 2019, 100, 697-710.	2.7	5
12	Polycomb protein SCML2 facilitates H3K27me3 to establish bivalent domains in the male germline. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4957-4962.	7.1	57
13	Epigenomic and single-cell profiling of human spermatogonial stem cells. Stem Cell Investigation, 2018, 5, 11-11.	3.0	2
14	Chromosome Spread Analyses of Meiotic Sex Chromosome Inactivation. Methods in Molecular Biology, 2018, 1861, 113-129.	0.9	14
15	RNF8 and SCML2 cooperate to regulate ubiquitination and H3K27 acetylation for escape gene activation on the sex chromosomes. PLoS Genetics, 2018, 14, e1007233.	3.5	45
16	LTR retrotransposons transcribed in oocytes drive species-specific and heritable changes in DNA methylation. Nature Communications, 2018, 9, 3331.	12.8	65
17	Polycomb directs timely activation of germline genes in spermatogenesis. Genes and Development, 2017, 31, 1693-1703.	5.9	52
18	DNA Methylation Errors in Cloned Mouse Sperm by Germ Line Barrier Evasion1. Biology of Reproduction, 2016, 94, 128.	2.7	12

#	Article	IF	CITATIONS
19	Repetitive DNA methylome analysis by smallâ€scale and singleâ€cell shotgun bisulfite sequencing. Genes To Cells, 2016, 21, 1209-1222.	1.2	12
20	Sex Specification and Heterogeneity of Primordial Germ Cells in Mice. PLoS ONE, 2015, 10, e0144836.	2.5	17
21	Dynamics of genomic 5â€hydroxymethylcytosine during mouse oocyte growth. Genes To Cells, 2014, 19, 629-636.	1.2	14
22	High-resolution DNA methylome analysis of primordial germ cells identifies gender-specific reprogramming in mice. Genome Research, 2013, 23, 616-627.	5.5	239