Hiroyuki Sasaki

List of Publications by Year
in descending order

60	6,438	136950 32	138484 58
papers	citations	h-index	g-index

61	61	61	7754
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Essential role for de novo DNA methyltransferase Dnmt3a in paternal and maternal imprinting. Nature, 2004, 429, 900-903.	27.8	1,242
2	Epigenetic events in mammalian germ-cell development: reprogramming and beyond. Nature Reviews Genetics, 2008, 9, 129-140.	16.3	752
3	Derivation of Human Trophoblast Stem Cells. Cell Stem Cell, 2018, 22, 50-63.e6.	11.1	570
4	Maternal and zygotic Dnmt1 are necessary and sufficient for the maintenance of DNA methylation imprints during preimplantation development. Genes and Development, 2008, 22, 1607-1616.	5.9	396
5	Mouse Oocyte Methylomes at Base Resolution Reveal Genome-Wide Accumulation of Non-CpG Methylation and Role of DNA Methyltransferases. PLoS Genetics, 2013, 9, e1003439.	3.5	263
6	Setdb1 is required for germline development and silencing of H3K9me3-marked endogenous retroviruses in primordial germ cells. Genes and Development, 2014, 28, 2041-2055.	5.9	228
7	Generation of human oogonia from induced pluripotent stem cells in vitro. Science, 2018, 362, 356-360.	12.6	221
8	MVH in piRNA processing and gene silencing of retrotransposons. Genes and Development, 2010, 24, 887-892.	5.9	219
9	De novo DNA methylation drives 5hmC accumulation in mouse zygotes. Nature Cell Biology, 2016, 18, 225-233.	10.3	205
10	The paternal methylation imprint of the mouse H19 locus is acquired in the gonocyte stage during foetal testis development. Genes To Cells, 2000, 5, 649-659.	1.2	188
11	Mutations in CDCA7 and HELLS cause immunodeficiencyâ€“centromeric instabilityâ€“facial anomalies syndrome. Nature Communications, 2015, 6, 7870.	12.8	148
12	InÂVitro Derivation and Propagation of Spermatogonial Stem Cell Activity from Mouse Pluripotent Stem Cells. Cell Reports, 2016, 17, 2789-2804.	6.4	136
13	DNA methylation and gene expression dynamics during spermatogonial stem cell differentiation in the early postnatal mouse testis. BMC Genomics, 2015, 16, 624.	2.8	112
14	Global Landscape and Regulatory Principles of DNA Methylation Reprogramming for Germ Cell Specification by Mouse Pluripotent Stem Cells. Developmental Cell, 2016, 39, 87-103.	7.0	106
15	Polycomb Group Proteins Regulate Chromatin Architecture in Mouse Oocytes and Early Embryos. Molecular Cell, 2020, 77, 825-839.e7.	9.7	105
16	Allele-Specific Methylome and Transcriptome Analysis Reveals Widespread Imprinting in the Human Placenta. American Journal of Human Genetics, 2016, 99, 1045-1058.	6.2	103
17	Microarray analysis of promoter methylation in lung cancers. Journal of Human Genetics, 2006, 51, 368-374.	2.3	100
18	Genetic evidence for Dnmt3aâ€dependent imprinting during oocyte growth obtained by conditional knockout with Zp3â€Cre and complete exclusion of Dnmt3b by chimera formation. Genes To Cells, 2010, 15, 169-179.	1.2	97

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19	Maternal high-fat diet induces insulin resistance and deterioration of pancreatic Î²-cell function in adult offspring with sex differences in mice. American Journal of Physiology - Endocrinology and Metabolism, 2014, 306, E1163-E1175.	3.5	96
20	Role of UHRF1 in de novo DNA methylation in oocytes and maintenance methylation in preimplantation embryos. PLoS Genetics, 2017, 13, e1007042.	3.5	95
21	In vitro expansion of mouse primordial germ cellâ€like cells recapitulates an epigenetic blank slate. EMBO Journal, 2017, 36, 1888-1907.	7.8	92
22	Histone H3K9 Methyltransferase G9a in Oocytes Is Essential for Preimplantation Development but Dispensable for CG Methylation Protection. Cell Reports, 2019, 27, 282-293.e4.	6.4	62
23	CDCA7 and HELLS mutations undermine nonhomologous end joining in centromeric instability syndrome. Journal of Clinical Investigation, 2018, 129, 78-92.	8.2	62
24	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
25	DBTSS/DBKERO for integrated analysis of transcriptional regulation. Nucleic Acids Research, 2018, 46, D229-D238.	14.5	48
26	Roles of MIWI, MILI and PLD6 in small RNA regulation in mouse growing oocytes. Nucleic Acids Research, 2017, 45, gkx027.	14.5	46
27	DNMT3L promotes quiescence in postnatal spermatogonial progenitor cells. Development (Cambridge), 2014, 141, 2402-2413.	2.5	45
28	Reprogramming of the histone H3.3 landscape in the early mouse embryo. Nature Structural and Molecular Biology, 2021, 28, 38-49.	8.2	45
29	HSP90Î± plays an important role in piRNA biogenesis and retrotransposon repression in mouse. Nucleic Acids Research, 2014, 42, 11903-11911.	14.5	42
30	Aging of spermatogonial stem cells by Jnk-mediated glycolysis activation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 16404-16409.	7.1	39
31	Switching of dominant retrotransposon silencing strategies from posttranscriptional to transcriptional mechanisms during male germ-cell development in mice. PLoS Genetics, 2017, 13, e1006926.	3.5	39
32	Disruption of mesodermal enhancers forIgf2in the minute mutant. Development (Cambridge), 2002, 129, 1657-1668.	2.5	38
33	Most T790M mutations are present on the same EGFR allele as activating mutations in patients with nonâ€“small cell lung cancer. Lung Cancer, 2017, 108, 75-82.	2.0	37
34	Accurate estimation of 5-methylcytosine in mammalian mitochondrial DNA. Scientific Reports, 2018, 8, 5801.	3.3	35
35	Zfp281 Shapes the Transcriptome of Trophoblast Stem Cells and Is Essential for Placental Development. Cell Reports, 2019, 27, 1742-1754.e6.	6.4	34
36	Defects in dosage compensation impact global gene regulation in the mouse trophoblast. Development (Cambridge), 2017, 144, 2784-2797.	2.5	31

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37	Production of functional oocytes requires maternally expressed PIWI genes and piRNAs in golden hamsters. Nature Cell Biology, 2021, 23, 1002-1012.	10.3	30
38	Software updates in the Illumina HiSeq platform affect whole-genome bisulfite sequencing. BMC Genomics, 2017, 18, 31.	2.8	29
39	Clinical and Immunological Characterization of ICF Syndrome in Japan. Journal of Clinical Immunology, 2018, 38, 927-937.	3.8	29
40	Broad Heterochromatic Domains Open in Gonocyte Development Prior to De Novo DNA Methylation. Developmental Cell, 2019, 51, 21-34.e5.	7.0	26
41	Iron-heme-Bach1 axis is involved in erythroblast adaptation to iron deficiency. Haematologica, 2017, 102, 454-465.	3.5	21
42	CDCA7 and HELLS suppress DNA:RNA hybrid-associated DNA damage at pericentromeric repeats. Scientific Reports, 2020, 10, 17865.	3.3	21
43	Role of SmcHD1 in establishment of epigenetic states required for the maintenance of the X-inactivated state in mice. Development (Cambridge), 2018, 145, .	2.5	19
44	The DNMT3A PWWP domain is essential for the normal DNA methylation landscape in mouse somatic cells and oocytes. PLoS Genetics, 2021, 17, e1009570.	3.5	17
45	Evolution of the sperm methylome of primates is associated with retrotransposon insertions and genome instability. Human Molecular Genetics, 2017, 26, 3508-3519.	2.9	16
46	Whole-Mount MeFISH: A Novel Technique for Simultaneous Visualization of Specific DNA Methylation and Protein/RNA Expression. PLoS ONE, 2014, 9, e95750.	2.5	15
47	Locus-specific hypomethylation of the mouse IAP retrotransposon is associated with transcription factor-binding sites. Mobile DNA, 2017, 8, 20.	3.6	13
48	Maternal DNMT3A-dependent de novo methylation of the paternal genome inhibits gene expression in the early embryo. Nature Communications, 2020, 11, 5417.	12.8	12
49	TFB2M and POLRMT are essential for mammalian mitochondrial DNA replication. Biochimica Et Biophysica Acta - Molecular Cell Research, 2022, 1869, 119167.	4.1	10
50	The 5â€² region of Xist RNA has the potential to associate with chromatin through the A-repeat. Rna, 2017, 23, 1894-1901.	3.5	8
51	A histone H3.3K36M mutation in mice causes an imbalance of histone modifications and defects in chondrocyte differentiation. Epigenetics, 2021, 16, 1123-1134.	2.7	8
52	Identification of SLC38A7 as a Prognostic Marker and Potential Therapeutic Target of Lung Squamous Cell Carcinoma. Annals of Surgery, 2021, 274, 500-507.	4.2	8
53	Differential chromatin packaging of genomic imprinted regions between expressed and non-expressed alleles. Human Molecular Genetics, 2000, 9, 3029-3035.	2.9	6
54	Non-transmissible MV Vector with Segmented RNA Genome Establishes Different Types of iPSCs from Hematopoietic Cells. Molecular Therapy, 2020, 28, 129-141.	8.2	6

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55	Identification of Genomic Alterations Acquired During Treatment With EGFR-TKIs in Non-small Cell Lung Cancer. Anticancer Research, 2019, 39, 671-677.	1.1	4
56	Identification of ZBTB24 protein domains and motifs for heterochromatin localization and transcriptional activation. Genes To Cells, 2019, 24, 746-755.	1.2	3
57	Ddhd1 knockout mouse as a model of locomotive and physiological abnormality in familial spastic paraplegia. Bioscience Reports, 2021, 41, .	2.4	2
58	Characterization of geneticâ€originâ€dependent monoallelic expression in mouse embryonic stem cells. Genes To Cells, 2020, 25, 54-64.	1.2	1
59	DNA methylation in epigenetics, development, and imprinting. , 2005, , .		0
60	A convolutional neural network-based regression model to infer the epigenetic crosstalk responsible for CG methylation patterns. BMC Bioinformatics, 2021, 22, 341.	2.6	0