

Hiroyuki Sasaki

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

6,438
citations

136950

32
h-index

138484

58
g-index

61
all docs

61
docs citations

61
times ranked

7754
citing authors

#	ARTICLE	IF	CITATIONS
1	TFB2M and POLRMT are essential for mammalian mitochondrial DNA replication. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2022, 1869, 119167.	4.1	10
2	A histone H3.3K36M mutation in mice causes an imbalance of histone modifications and defects in chondrocyte differentiation. <i>Epigenetics</i> , 2021, 16, 1123-1134.	2.7	8
3	Reprogramming of the histone H3.3 landscape in the early mouse embryo. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 38-49.	8.2	45
4	Ddhd1 knockout mouse as a model of locomotive and physiological abnormality in familial spastic paraplegia. <i>Bioscience Reports</i> , 2021, 41, .	2.4	2
5	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
6	A convolutional neural network-based regression model to infer the epigenetic crosstalk responsible for CG methylation patterns. <i>BMC Bioinformatics</i> , 2021, 22, 341.	2.6	0
7	Identification of SLC38A7 as a Prognostic Marker and Potential Therapeutic Target of Lung Squamous Cell Carcinoma. <i>Annals of Surgery</i> , 2021, 274, 500-507.	4.2	8
8	Production of functional oocytes requires maternally expressed PIWI genes and piRNAs in golden hamsters. <i>Nature Cell Biology</i> , 2021, 23, 1002-1012.	10.3	30
9	Non-transmissible MV Vector with Segmented RNA Genome Establishes Different Types of iPSCs from Hematopoietic Cells. <i>Molecular Therapy</i> , 2020, 28, 129-141.	8.2	6
10	Characterization of geneticâ€œoriginâ€œdependent monoallelic expression in mouse embryonic stem cells. <i>Genes To Cells</i> , 2020, 25, 54-64.	1.2	1
11	Polycomb Group Proteins Regulate Chromatin Architecture in Mouse Oocytes and Early Embryos. <i>Molecular Cell</i> , 2020, 77, 825-839.e7.	9.7	105
12	Maternal DNMT3A-dependent de novo methylation of the paternal genome inhibits gene expression in the early embryo. <i>Nature Communications</i> , 2020, 11, 5417.	12.8	12
13	CDCA7 and HELLS suppress DNA:RNA hybrid-associated DNA damage at pericentromeric repeats. <i>Scientific Reports</i> , 2020, 10, 17865.	3.3	21
14	Aging of spermatogonial stem cells by Jnk-mediated glycolysis activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 16404-16409.	7.1	39
15	Identification of ZBTB24 protein domains and motifs for heterochromatin localization and transcriptional activation. <i>Genes To Cells</i> , 2019, 24, 746-755.	1.2	3
16	Broad Heterochromatic Domains Open in Gonocyte Development Prior to De Novo DNA Methylation. <i>Developmental Cell</i> , 2019, 51, 21-34.e5.	7.0	26
17	Zfp281 Shapes the Transcriptome of Trophoblast Stem Cells and Is Essential for Placental Development. <i>Cell Reports</i> , 2019, 27, 1742-1754.e6.	6.4	34
18	Histone H3K9 Methyltransferase G9a in Oocytes Is Essential for Preimplantation Development but Dispensable for CG Methylation Protection. <i>Cell Reports</i> , 2019, 27, 282-293.e4.	6.4	62

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19	Identification of Genomic Alterations Acquired During Treatment With EGFR-TKIs in Non-small Cell Lung Cancer. <i>Anticancer Research</i> , 2019, 39, 671-677.	1.1	4
20	Polycomb protein SCML2 facilitates H3K27me3 to establish bivalent domains in the male germline. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4957-4962.	7.1	57
21	Accurate estimation of 5-methylcytosine in mammalian mitochondrial DNA. <i>Scientific Reports</i> , 2018, 8, 5801.	3.3	35
22	DBTSS/DBKERO for integrated analysis of transcriptional regulation. <i>Nucleic Acids Research</i> , 2018, 46, D229-D238.	14.5	48
23	Derivation of Human Trophoblast Stem Cells. <i>Cell Stem Cell</i> , 2018, 22, 50-63.e6.	11.1	570
24	Clinical and Immunological Characterization of ICF Syndrome in Japan. <i>Journal of Clinical Immunology</i> , 2018, 38, 927-937.	3.8	29
25	Generation of human oogonia from induced pluripotent stem cells in vitro. <i>Science</i> , 2018, 362, 356-360.	12.6	221
26	Role of SmcHD1 in establishment of epigenetic states required for the maintenance of the X-inactivated state in mice. <i>Development (Cambridge)</i> , 2018, 145, .	2.5	19
27	CDCA7 and HELLS mutations undermine nonhomologous end joining in centromeric instability syndrome. <i>Journal of Clinical Investigation</i> , 2018, 129, 78-92.	8.2	62
28	Most T790M mutations are present on the same EGFR allele as activating mutations in patients with non-small cell lung cancer. <i>Lung Cancer</i> , 2017, 108, 75-82.	2.0	37
29	Evolution of the sperm methylome of primates is associated with retrotransposon insertions and genome instability. <i>Human Molecular Genetics</i> , 2017, 26, 3508-3519.	2.9	16
30	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
31	Roles of MIWI, MILI and PLD6 in small RNA regulation in mouse growing oocytes. <i>Nucleic Acids Research</i> , 2017, 45, gkx027.	14.5	46
32	Iron-heme-Bach1 axis is involved in erythroblast adaptation to iron deficiency. <i>Haematologica</i> , 2017, 102, 454-465.	3.5	21
33	The 5' region of Xist RNA has the potential to associate with chromatin through the A-repeat. <i>Rna</i> , 2017, 23, 1894-1901.	3.5	8
34	Defects in dosage compensation impact global gene regulation in the mouse trophoblast. <i>Development (Cambridge)</i> , 2017, 144, 2784-2797.	2.5	31
35	Software updates in the Illumina HiSeq platform affect whole-genome bisulfite sequencing. <i>BMC Genomics</i> , 2017, 18, 31.	2.8	29
36	Locus-specific hypomethylation of the mouse IAP retrotransposon is associated with transcription factor-binding sites. <i>Mobile DNA</i> , 2017, 8, 20.	3.6	13

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37	Switching of dominant retrotransposon silencing strategies from posttranscriptional to transcriptional mechanisms during male germ-cell development in mice. <i>PLoS Genetics</i> , 2017, 13, e1006926.	3.5	39
38	Role of UHRF1 in de novo DNA methylation in oocytes and maintenance methylation in preimplantation embryos. <i>PLoS Genetics</i> , 2017, 13, e1007042.	3.5	95
39	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
40	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
41	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
42	De novo DNA methylation drives 5hmC accumulation in mouse zygotes. <i>Nature Cell Biology</i> , 2016, 18, 225-233.	10.3	205
43	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
44	Mutations in CDCA7 and HELLS cause immunodeficiency-centromeric instability-facial anomalies syndrome. <i>Nature Communications</i> , 2015, 6, 7870.	12.8	148
45	Whole-Mount MeFISH: A Novel Technique for Simultaneous Visualization of Specific DNA Methylation and Protein/RNA Expression. <i>PLoS ONE</i> , 2014, 9, e95750.	2.5	15
46	DNMT3L promotes quiescence in postnatal spermatogonial progenitor cells. <i>Development (Cambridge)</i> , 2014, 141, 2402-2413.	2.5	45
47	HSP90 α plays an important role in piRNA biogenesis and retrotransposon repression in mouse. <i>Nucleic Acids Research</i> , 2014, 42, 11903-11911.	14.5	42
48	<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
49	Maternal high-fat diet induces insulin resistance and deterioration of pancreatic β -cell function in adult offspring with sex differences in mice. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2014, 306, E1163-E1175.	3.5	96
50	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
51	Genetic evidence for Dnmt3a-dependent imprinting during oocyte growth obtained by conditional knockout with <i>Zp3-Cre</i> and complete exclusion of Dnmt3b by chimera formation. <i>Genes To Cells</i> , 2010, 15, 169-179.	1.2	97
52	MVH in piRNA processing and gene silencing of retrotransposons. <i>Genes and Development</i> , 2010, 24, 887-892.	5.9	219
53	Epigenetic events in mammalian germ-cell development: reprogramming and beyond. <i>Nature Reviews Genetics</i> , 2008, 9, 129-140.	16.3	752
54	Maternal and zygotic Dnmt1 are necessary and sufficient for the maintenance of DNA methylation imprints during preimplantation development. <i>Genes and Development</i> , 2008, 22, 1607-1616.	5.9	396

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55	Microarray analysis of promoter methylation in lung cancers. <i>Journal of Human Genetics</i> , 2006, 51, 368-374.	2.3	100
56	DNA methylation in epigenetics, development, and imprinting. , 2005, , .		0
57	Essential role for de novo DNA methyltransferase Dnmt3a in paternal and maternal imprinting. <i>Nature</i> , 2004, 429, 900-903.	27.8	1,242
58	Disruption of mesodermal enhancers for <i>Igf2</i> in the minute mutant. <i>Development (Cambridge)</i> , 2002, 129, 1657-1668.	2.5	38
59	The paternal methylation imprint of the mouse <i>H19</i> locus is acquired in the gonocyte stage during foetal testis development. <i>Genes To Cells</i> , 2000, 5, 649-659.	1.2	188
60	Differential chromatin packaging of genomic imprinted regions between expressed and non-expressed alleles. <i>Human Molecular Genetics</i> , 2000, 9, 3029-3035.	2.9	6