

Hisato Kobayashi

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

3,500
citations

313897

21
h-index

190239

50
g-index

59
all docs

59
docs citations

59
times ranked

4834
citing authors

#	ARTICLE	IF	CITATIONS
1	Conservation and divergence of canonical and non-canonical imprinting in murids. <i>Genome Biology</i> , 2023, 24, .	9.2	9
2	Repeated translocation of a supergene underlying rapid sex chromosome turnover in <i>Takifugu</i> pufferfish. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.6	23
3	Epigenome reprogramming in the male and female germ line. , 2021, , 3-25.		1
4	Paternal age affects offspring via an epigenetic mechanism involving REST/NRSF. <i>EMBO Reports</i> , 2021, 22, e51524.	5.1	42
5	Dynamics of transcription-mediated conversion from euchromatin to facultative heterochromatin at the Xist promoter by Tsix. <i>Cell Reports</i> , 2021, 34, 108912.	6.3	11
6	Canonical and Non-canonical Genomic Imprinting in Rodents. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 713878.	3.8	18
7	Deciphering two rounds of cell lineage segregations during bovine preimplantation development. <i>FASEB Journal</i> , 2021, 35, e21904.	0.5	17
8	Dorso-ventral heterogeneity in tracheal basal stem cells. <i>Biology Open</i> , 2021, 10, .	1.2	4
9	Loop-mediated isothermal amplification (LAMP) and machine learning application for early pregnancy detection using bovine vaginal mucosal membrane. <i>Biochemical and Biophysical Research Communications</i> , 2021, 569, 179-186.	2.2	6
10	Characterization of Frond and Flower Development and Identification of FT and FD Genes From Duckweed <i>Lemna aquinoctialis</i> Nd. <i>Frontiers in Plant Science</i> , 2021, 12, 697206.	3.8	12
11	Maternal DNMT3A-dependent de novo methylation of the paternal genome inhibits gene expression in the early embryo. <i>Nature Communications</i> , 2020, 11, 5417.	13.2	13
12	Germline development in rat revealed by visualization and deletion of <i>Prdm14</i> . <i>Development (Cambridge)</i> , 2020, 147, .	2.6	20
13	Global transcriptome analysis of pig induced pluripotent stem cells derived from six and four reprogramming factors. <i>Scientific Data</i> , 2019, 6, 190034.	5.4	12
14	Distinct cell proliferation, myogenic differentiation, and gene expression in skeletal muscle myoblasts of layer and broiler chickens. <i>Scientific Reports</i> , 2019, 9, 16527.	3.4	37
15	Sex-Specific Histone Modifications in Mouse Fetal and Neonatal Germ Cells. <i>Epigenomics</i> , 2019, 11, 543-561.	2.1	17
16	Signs of biological activities of 28,000-year-old mammoth nuclei in mouse oocytes visualized by live-cell imaging. <i>Scientific Reports</i> , 2019, 9, 4050.	3.4	30
17	Tuning water-use efficiency and drought tolerance in wheat using abscisic acid receptors. <i>Nature Plants</i> , 2019, 5, 153-159.	9.4	226
18	Food-Derived Compounds Apigenin and Luteolin Modulate mRNA Splicing of Introns with Weak Splice Sites. <i>IScience</i> , 2019, 22, 336-352.	4.1	17

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19	Evolution of imprinting via lineage-specific insertion of retroviral promoters. <i>Nature Communications</i> , 2019, 10, 5674.	13.2	45
20	SETDB1 is essential for mouse primordial germ cell fate determination by ensuring BMP signaling. <i>Development (Cambridge)</i> , 2018, 145, .	2.6	18
21	DNMTs and SETDB1 function as co-repressors in MAX-mediated repression of germ cell-related genes in mouse embryonic stem cells. <i>PLoS ONE</i> , 2018, 13, e0205969.	2.5	18
22	Relationship between PIWIL4-Mediated H3K4me2 Demethylation and piRNA-Dependent DNA Methylation. <i>Cell Reports</i> , 2018, 25, 350-356.	6.3	21
23	Repression of Somatic Genes by Selective Recruitment of HDAC3 by BLIMP1 Is Essential for Mouse Primordial Germ Cell Fate Determination. <i>Cell Reports</i> , 2018, 24, 2682-2693.e6.	6.3	14
24	LTR retrotransposons transcribed in oocytes drive species-specific and heritable changes in DNA methylation. <i>Nature Communications</i> , 2018, 9, 3331.	13.2	70
25	Inducible Transposition of a Heat-Activated Retrotransposon in Tissue Culture. <i>Plant and Cell Physiology</i> , 2017, 58, pcw202.	3.2	23
26	Genome-wide methylation profiles in primary intracranial germ cell tumors indicate a primordial germ cell origin for germinomas. <i>Acta Neuropathologica</i> , 2017, 133, 445-462.	7.9	66
27	DNA Methylation Errors in Cloned Mouse Sperm by Germ Line Barrier Evasion1. <i>Biology of Reproduction</i> , 2016, 94, 128.	2.6	12
28	Repetitive DNA methylome analysis by small-scale and single-cell shotgun bisulfite sequencing. <i>Genes To Cells</i> , 2016, 21, 1209-1222.	1.3	14
29	Sex Specification and Heterogeneity of Primordial Germ Cells in Mice. <i>PLoS ONE</i> , 2015, 10, e0144836.	2.5	17
30	Sunflower centromeres consist of a centromere-specific LINE and a chromosome-specific tandem repeat. <i>Frontiers in Plant Science</i> , 2015, 6, 912.	3.8	16
31	DNA methylation and gene expression dynamics during spermatogonial stem cell differentiation in the early postnatal mouse testis. <i>BMC Genomics</i> , 2015, 16, 624.	2.9	117
32	Comprehensive DNA Methylation Analysis of Retrotransposons in Male Germ Cells. <i>Cell Reports</i> , 2015, 12, 1541-1547.	6.3	18
33	Effect of feeding behavior on circadian regulation of endothelin expression in mouse colon. <i>Life Sciences</i> , 2014, 118, 232-237.	4.4	5
34	Dynamics of genomic 5-hydroxymethylcytosine during mouse oocyte growth. <i>Genes To Cells</i> , 2014, 19, 629-636.	1.3	15
35	High-resolution DNA methylome analysis of primordial germ cells identifies gender-specific reprogramming in mice. <i>Genome Research</i> , 2013, 23, 616-627.	5.6	242
36	Epigenetic and transcriptional features of the novel human imprinted lncRNA <i>GPR1AS</i> suggest it is a functional ortholog to mouse <i>Zdbf2linc</i> .	2.9	37

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37	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.	3.4	275
38	Contribution of Intragenic DNA Methylation in Mouse Gametic DNA Methylomes to Establish Oocyte-Specific Heritable Marks. <i>PLoS Genetics</i> , 2012, 8, e1002440.	3.4	466
39	DNA Methylation Analysis of Germ Cells by Using Bisulfite-Based Sequencing Methods. <i>Methods in Molecular Biology</i> , 2012, 825, 223-235.	0.0	9
40	Dynamic stage-specific changes in imprinted differentially methylated regions during early mammalian development and prevalence of non-CpG methylation in oocytes. <i>Development (Cambridge)</i> , 2011, 138, 811-820.	2.6	207
41	DNA methylation errors at imprinted loci after assisted conception originate in the parental sperm. <i>European Journal of Human Genetics</i> , 2009, 17, 1582-1591.	2.9	199
42	Identification of the mouse paternally expressed imprinted gene <i>Zdbf2</i> on chromosome 1 and its imprinted human homolog <i>ZDBF2</i> on chromosome 2. <i>Genomics</i> , 2009, 93, 461-472.	2.9	61
43	Correlation between <i>Shh</i> expression and DNA methylation status of the limb-specific <i>Shh</i> enhancer region during limb regeneration in amphibians. <i>Developmental Biology</i> , 2007, 312, 171-182.	2.1	112
44	Aberrant DNA methylation of imprinted loci in sperm from oligospermic patients. <i>Human Molecular Genetics</i> , 2007, 16, 2542-2551.	3.0	397
45	Effect of feeding on peripheral circadian rhythms and behaviour in mammals. <i>Genes To Cells</i> , 2004, 9, 857-864.	1.3	60
46	Genome-wide Expression Analysis of Mouse Liver Reveals CLOCK-regulated Circadian Output Genes. <i>Journal of Biological Chemistry</i> , 2003, 278, 41519-41527.	3.5	308
47	Sex difference in circadian period of body temperature in <i>Clock</i> mutant mice with <i>Jcl/ICR</i> background. <i>Neuroscience Letters</i> , 2003, 347, 163-166.	2.1	20
48	Differential expressions of <i>mPer1</i> and <i>mPer2</i> mRNAs under a skeleton photoperiod and a complete light-dark cycle. <i>Molecular Brain Research</i> , 2002, 109, 11-17.	2.4	18
49	High-resolution DNA methylome analysis of mouse germ cells. <i>Reproduction Abstracts</i> , 0, , .	0.0	0
50	Food-Derived Compounds Apigenin and Luteolin Modulate mRNA Splicing of Introns with Weak Splice Sites. <i>SSRN Electronic Journal</i> , 0, , .	0.3	0