Yoichi Shinkai

List of Publications by Year in descending order

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		23567	13771
129	19,906	58	129
papers	citations	h-index	g-index
135	135	135	18346
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Class Switch Recombination and Hypermutation Require Activation-Induced Cytidine Deaminase (AID), a Potential RNA Editing Enzyme. Cell, 2000, 102, 553-563.	28.9	3,089
2	G9a histone methyltransferase plays a dominant role in euchromatic histone H3 lysine 9 methylation and is essential for early embryogenesis. Genes and Development, 2002, 16, 1779-1791.	5.9	1,084
3	Partitioning and Plasticity of Repressive Histone Methylation States in Mammalian Chromatin. Molecular Cell, 2003, 12, 1577-1589.	9.7	1,010
4	Histone Methyltransferases Direct Different Degrees of Methylation to Define Distinct Chromatin Domains. Molecular Cell, 2003, 12, 1591-1598.	9.7	706
5	Histone methyltransferases G9a and GLP form heteromeric complexes and are both crucial for methylation of euchromatin at H3-K9. Genes and Development, 2005, 19, 815-826.	5.9	689
6	Proviral silencing in embryonic stem cells requires the histone methyltransferase ESET. Nature, 2010, 464, 927-931.	27.8	681
7	SET Domain-containing Protein, G9a, Is a Novel Lysine-preferring Mammalian Histone Methyltransferase with Hyperactivity and Specific Selectivity to Lysines 9 and 27 of Histone H3. Journal of Biological Chemistry, 2001, 276, 25309-25317.	3.4	679
8	G9a-mediated irreversible epigenetic inactivation of Oct-3/4 during early embryogenesis. Nature Cell Biology, 2006, 8, 188-194.	10.3	581
9	Large histone H3 lysine 9 dimethylated chromatin blocks distinguish differentiated from embryonic stem cells. Nature Genetics, 2009, 41, 246-250.	21.4	540
10	H3K9 methyltransferase G9a and the related molecule GLP. Genes and Development, 2011, 25, 781-788.	5.9	473
11	DNA Methylation and SETDB1/H3K9me3 Regulate Predominantly Distinct Sets of Genes, Retroelements, and Chimeric Transcripts in mESCs. Cell Stem Cell, 2011, 8, 676-687.	11.1	427
12	PGC7 binds histone H3K9me2 to protect against conversion of 5mC to 5hmC in early embryos. Nature, 2012, 486, 415-419.	27.8	397
13	De novo DNA methylation promoted by G9a prevents reprogramming of embryonically silenced genes. Nature Structural and Molecular Biology, 2008, 15, 1176-1183.	8.2	396
14	Cellular dynamics associated with the genome-wide epigenetic reprogramming in migrating primordial germ cells in mice. Development (Cambridge), 2007, 134, 2627-2638.	2.5	388
15	G9a/GLP complexes independently mediate H3K9 and DNA methylation to silence transcription. EMBO Journal, 2008, 27, 2681-2690.	7.8	342
16	Protein lysine methyltransferase G9a acts on non-histone targets. Nature Chemical Biology, 2008, 4, 344-346.	8.0	309
17	Two distinct pathways of specific killing revealed by perforin mutant cytotoxic T lymphocytes. Immunity, 1994, 1, 357-364.	14.3	294
18	Functional dynamics of H3K9 methylation during meiotic prophase progression. EMBO Journal, 2007, 26, 3346-3359.	7.8	263

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19	Homology of perforin to the ninth component of complement (C9). Nature, 1988, 334, 525-527.	27.8	260
20	Cloning of mice to six generations. Nature, 2000, 407, 318-319.	27.8	242
21	Methyl-CpG Binding Domain 1 (MBD1) Interacts with the Suv39h1-HP1 Heterochromatic Complex for DNA Methylation-based Transcriptional Repression. Journal of Biological Chemistry, 2003, 278, 24132-24138.	3.4	237
22	<i>Setdb1</i> 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
23	Nonlinear partial differential equations and applications: Pol protects mammalian cells against the lethal and mutagenic effects of benzo[a]pyrene. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 15548-15553.	7.1	222
24	Tracking epigenetic histone modifications in single cells using Fab-based live endogenous modification labeling. Nucleic Acids Research, 2011, 39, 6475-6488.	14.5	219
25	Epigenetic Regulation of Mouse Sex Determination by the Histone Demethylase Jmjd1a. Science, 2013, 341, 1106-1109.	12.6	217
26	Genetic and epigenetic properties of mouse male germline stem cells during long-term culture. Development (Cambridge), 2005, 132, 4155-4163.	2.5	210
27	DNA methylation in ES cells requires the lysine methyltransferase G9a but not its catalytic activity. EMBO Journal, 2008, 27, 2691-2701.	7.8	207
28	Hypoxic Stress Induces Dimethylated Histone H3 Lysine 9 through Histone Methyltransferase G9a in Mammalian Cells. Cancer Research, 2006, 66, 9009-9016.	0.9	200
29	CD3ε-mediated signals rescue the development of CD4+CD8+ thymocytes in RAG-2â°'/â^' mice in the absence of TCR β chain expression. International Immunology, 1994, 6, 995-1001.	4.0	194
30	Crucial functions of the Rap1 effector molecule RAPL in lymphocyte and dendritic cell trafficking. Nature Immunology, 2004, 5, 1045-1051.	14.5	184
31	Obesity and metabolic syndrome in histone demethylase JHDM2aâ€deficient mice. Genes To Cells, 2009, 14, 991-1001.	1.2	167
32	In Vitro and in Vivo Analyses of a Phe/Tyr Switch Controlling Product Specificity of Histone Lysine Methyltransferases. Journal of Biological Chemistry, 2005, 280, 5563-5570.	3.4	166
33	Severe growth defect in mouse cells lacking the telomerase RNA component. Nature Genetics, 1998, 19, 203-206.	21.4	159
34	DNA Damage Signaling Triggers Degradation of Histone Methyltransferases through APC/CCdh1 in Senescent Cells. Molecular Cell, 2012, 45, 123-131.	9.7	159
35	Methylation of DNA Ligase 1 by G9a/GLP Recruits UHRF1 to Replicating DNA and Regulates DNA Methylation. Molecular Cell, 2017, 67, 550-565.e5.	9.7	151
36	Role of Histone Methyltransferase G9a in CpG Methylation of the Prader-Willi Syndrome Imprinting Center. Journal of Biological Chemistry, 2003, 278, 14996-15000.	3.4	149

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37	G9a selectively represses a class of late-replicating genes at the nuclear periphery. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 19363-19368.	7.1	134
38	MPP8 mediates the interactions between DNA methyltransferase Dnmt3a and H3K9 methyltransferase GLP/G9a. Nature Communications, 2011, 2, 533.	12.8	132
39	Telomere Maintenance in Telomerase-Deficient Mouse Embryonic Stem Cells: Characterization of an Amplified Telomeric DNA. Molecular and Cellular Biology, 2000, 20, 4115-4127.	2.3	129
40	Reduced exploration, increased anxiety, and altered social behavior: Autistic-like features of euchromatin histone methyltransferase 1 heterozygous knockout mice. Behavioural Brain Research, 2010, 208, 47-55.	2.2	126
41	Essential roles of the histone methyltransferase ESET in the epigenetic control of neural progenitor cells during development. Development (Cambridge), 2012, 139, 3806-3816.	2.5	121
42	Zinc Finger Protein Wiz Links G9a/GLP Histone Methyltransferases to the Co-repressor Molecule CtBP*. Journal of Biological Chemistry, 2006, 281, 20120-20128.	3.4	108
43	Adding a Lysine Mimic in the Design of Potent Inhibitors of Histone Lysine Methyltransferases. Journal of Molecular Biology, 2010, 400, 1-7.	4.2	108
44	Lysine methyltransferase G9a is required for de novo DNA methylation and the establishment, but not the maintenance, of proviral silencing. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5718-5723.	7.1	105
45	Targeted inhibition of V(D)J recombination by a histone methyltransferase. Nature Immunology, 2004, 5, 309-316.	14.5	101
46	Importance of TRF1 for Functional Telomere Structure. Journal of Biological Chemistry, 2004, 279, 1442-1448.	3.4	91
47	Abnormalities in cloned mice are not transmitted to the progeny. Genesis, 2002, 34, 203-207.	1.6	85
48	Activation of Heat Shock Genes Is Not Necessary for Protection by Heat Shock Transcription Factor 1 against Cell Death Due to a Single Exposure to High Temperatures. Molecular and Cellular Biology, 2003, 23, 5882-5895.	2.3	84
49	Role of Perforin in Lymphocyte-Mediated Cytolysis. Advances in Immunology, 1992, 51, 215-242.	2.2	83
50	Selenium-Based S-Adenosylmethionine Analog Reveals the Mammalian Seven-Beta-Strand Methyltransferase METTL10 to Be an EF1A1 Lysine Methyltransferase. PLoS ONE, 2014, 9, e105394.	2.5	80
51	Genome-wide and locus-specific DNA hypomethylation in G9a deficient mouse embryonic stem cells. Genes To Cells, 2007, 12, 1-11.	1.2	79
52	The histone methyltransferase SETDB1 represses endogenous and exogenous retroviruses in B lymphocytes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 8367-8372.	7.1	78
53	Activation of Endogenous Retroviruses in Dnmt1 \hat{a} °/ \hat{a} ° ESCs Involves Disruption of SETDB1-Mediated Repression by NP95 Binding to Hemimethylated DNA. Cell Stem Cell, 2016, 19, 81-94.	11.1	77
54	A Jumonji (Jarid2) Protein Complex Represses cyclin D1 Expression by Methylation of Histone H3-K9. Journal of Biological Chemistry, 2009, 284, 733-739.	3.4	68

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55	Hippocampal dysfunction in the Euchromatin histone methyltransferase 1 heterozygous knockout mouse model for Kleefstra syndrome. Human Molecular Genetics, 2013, 22, 852-866.	2.9	68
56	A somatic role for the histone methyltransferase Setdb1 in endogenous retrovirus silencing. Nature Communications, 2018, 9, 1683.	12.8	67
57	Expression of perforin and cytolytic potential of human peripheral blood lymphocyte subpopulations. International Immunology, 1992, 4, 1049-1054.	4.0	66
58	JMJD1C, a JmjC Domain-Containing Protein, Is Required for Long-Term Maintenance of Male Germ Cells in Mice1. Biology of Reproduction, 2013, 89, 93.	2.7	62
59	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
60	Functional Analysis of Histone Methyltransferase G9a in B and T Lymphocytes. Journal of Immunology, 2008, 181, 485-493.	0.8	61
61	Setdb1 maintains hematopoietic stem and progenitor cells by restricting the ectopic activation of nonhematopoietic genes. Blood, 2016, 128, 638-649.	1.4	61
62	Impact of nucleic acid and methylated H3K9 binding activities of Suv39h1 on its heterochromatin assembly. ELife, 2017, 6, .	6.0	61
63	Molecular cloning and chromosomal assignment of a human perforin (PFP) gene. Immunogenetics, 1989, 30, 452-457.	2.4	55
64	SETDB1-Mediated Silencing of Retroelements. Viruses, 2020, 12, 596.	3.3	55
65	A CRISPR knockout screen identifies SETDB1-target retroelement silencing factors in embryonic stem cells. Genome Research, 2018, 28, 846-858.	5.5	54
66	The methyltransferase METTL9 mediates pervasive 1-methylhistidine modification in mammalian proteomes. Nature Communications, 2021, 12, 891.	12.8	54
67	Effect of a null mutation of the oviduct-specific glycoprotein gene on mouse fertilization. Biochemical Journal, 2003, 374, 551-557.	3.7	50
68	Distinct Roles for Histone Methyltransferases G9a and GLP in Cancer Germ-Line Antigen Gene Regulation in Human Cancer Cells and Murine Embryonic Stem Cells. Molecular Cancer Research, 2009, 7, 851-862.	3.4	50
69	Evidence of perforin-mediated cardiac myocyte injury in acute murine myocarditis caused by coxsackie virus B3. Journal of Pathology, 1993, 170, 53-58.	4.5	49
70	Distinct Roles of TRF1 in the Regulation of Telomere Structure and Lengthening. Journal of Biological Chemistry, 2008, 283, 23981-23988.	3.4	48
71	Histone H1 null vertebrate cells exhibit altered nucleosome architecture. Nucleic Acids Research, 2010, 38, 3533-3545.	14.5	47
72	The Hypoxia-Inducible Epigenetic Regulators Jmjd1a and G9a Provide a Mechanistic Link between Angiogenesis and Tumor Growth. Molecular and Cellular Biology, 2014, 34, 3702-3720.	2.3	47

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73	ATF7IP regulates SETDB1 nuclear localization and increases its ubiquitination. EMBO Reports, 2019, 20, e48297.	4.5	46
74	Tri-methylation of ATF7IP by G9a/GLP recruits the chromodomain protein MPP8. Epigenetics and Chromatin, 2018, 11, 56.	3.9	43
75	A Testicular Germ Cell-Associated Serine-Threonine Kinase, MAK, Is Dispensable for Sperm Formation. Molecular and Cellular Biology, 2002, 22, 3276-3280.	2.3	42
76	The absence of DNA polymerase \hat{I}^o does not affect somatic hypermutation of the mouse immunoglobulin heavy chain gene. Immunology Letters, 2003, 86, 265-270.	2.5	41
77	Structure of the UHRF1 Tandem Tudor Domain Bound to a Methylated Non-histone Protein, LIG1, Reveals Rules for Binding and Regulation. Structure, 2019, 27, 485-496.e7.	3.3	41
78	Histone H3 lysine 9 methyltransferases, G9a and GLP are essential for cardiac morphogenesis. Mechanisms of Development, 2013, 130, 519-531.	1.7	39
79	The Wnt–NLK Signaling Pathway Inhibits A-Myb Activity by Inhibiting the Association with Coactivator CBP and Methylating Histone H3. Molecular Biology of the Cell, 2005, 16, 4705-4713.	2.1	38
80	Histone H1 variant, H1R is involved in DNA damage response. DNA Repair, 2007, 6, 1584-1595.	2.8	38
81	Prdm12 Is Induced by Retinoic Acid and Exhibits Anti-proliferative Properties through the Cell Cycle Modulation of P19 Embryonic Carcinoma Cells. Cell Structure and Function, 2013, 38, 197-206.	1.1	36
82	Histone H3 Methylated at Arginine 17 Is Essential for Reprogramming the Paternal Genome in Zygotes. Cell Reports, 2017, 20, 2756-2765.	6.4	35
83	A Histone Methyltransferase ESET Is Critical for T Cell Development. Journal of Immunology, 2016, 197, 2269-2279.	0.8	33
84	Reply to "Reassessing the abundance of H3K9me2 chromatin domains in embryonic stem cells― Nature Genetics, 2010, 42, 5-6.	21.4	32
85	Prdm8 Regulates the Morphological Transition at Multipolar Phase during Neocortical Development. PLoS ONE, 2014, 9, e86356.	2.5	32
86	Expression of perforin in murine natural killer cells and cytotoxic T lymphocytesin vivo. European Journal of Immunology, 1992, 22, 1215-1219.	2.9	31
87	Inhibition of histone H3K9 methyltransferases by gliotoxin and related epipolythiodioxopiperazines. Journal of Antibiotics, 2012, 65, 263-265.	2.0	31
88	Is there a role for endogenous retroviruses to mediate long-term adaptive phenotypic response upon environmental inputs?. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20110340.	4.0	30
89	Expression of the mouse PR domain protein Prdm8 in the developing central nervous system. Gene Expression Patterns, 2009, 9, 503-514.	0.8	29
90	Pericentric Heterochromatin Generated by HP1 Protein Interaction-defective Histone Methyltransferase Suv39h1. Journal of Biological Chemistry, 2013, 288, 25285-25296.	3.4	28

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91	Exon resequencing of H3K9 methyltransferase complex genes, EHMT1, EHTM2 and WIZ, in Japanese autism subjects. Molecular Autism, 2014, 5, 49.	4.9	26
92	Increase of TCR \hat{V}^2 Accessibility within \hat{E}^2 Regulatory Region Influences its Recombination Frequency But Not Allelic Exclusion. Journal of Immunology, 2003, 171, 829-835.	0.8	25
93	X-inactivation is stably maintained in mouse embryos deficient for histone methyl transferase G9a. Genesis, 2004, 40, 151-156.	1.6	24
94	Combined Loss of JMJD1A and JMJD1B Reveals Critical Roles for H3K9 Demethylation in the Maintenance of Embryonic Stem Cells and Early Embryogenesis. Stem Cell Reports, 2018, 10, 1340-1354.	4.8	23
95	Thy-1 -positive dendritic epidermal cells contain a killer protein perforin. International Immunology, 1990, 2, 1113-1116.	4.0	21
96	Characterization of <i>Drosophila</i> G9a <i>in vivo</i> and identification of genetic interactants. Genes To Cells, 2008, 13, 703-722.	1.2	21
97	$\hat{l}\pm 1,3$ -Galactosyltransferase-Gene Knockout in Cattle using a Single Targeting Vector with loxP Sequences and Cre-Expressing Adenovirus. Transplantation, 2006, 81, 760-766.	1.0	19
98	Inhibition of histone methyltransferase G9a attenuates liver cancer initiation by sensitizing DNA-damaged hepatocytes to p53-induced apoptosis. Cell Death and Disease, 2021, 12, 99.	6.3	19
99	Role of METTL20 in regulating \hat{l}^2 -oxidation and heat production in mice under fasting or ketogenic conditions. Scientific Reports, 2018, 8, 1179.	3.3	18
100	Limited effect of chromatin remodeling on $D\hat{l}^2$ -to- $J\hat{l}^2$ recombination in CD4+CD8+ thymocyte: implications for a new aspect in the regulation of TCR \hat{l}^2 gene recombination. International Immunology, 2001, 13, 1405-1414.	4.0	17
101	Commitment of Immature CD4+8+ Thymocytes to the CD4 Lineage Requires CD3 Signaling but Does Not Require Expression of Clonotypic T Cell Receptor (TCR) Chains. Journal of Experimental Medicine, 1997, 186, 17-23.	8.5	16
102	Identification of ZNF200 as a novel binding partner of histone H3 methyltransferase G9a. Genes To Cells, 2007, 12, 877-888.	1.2	16
103	Pericentric H3K9me3 Formation by HP1 Interaction-defective Histone Methyltransferase Suv39h1. Cell Structure and Function, 2016, 41, 145-152.	1.1	15
104	G9a is involved in the regulation of cranial bone formation through activation of Runx2 function during development. Bone, 2020, 137, 115332.	2.9	15
105	Propargylic <i>Se</i> -adenosyl- <scp> </scp> -selenomethionine: A Chemical Tool for Methylome Analysis. Accounts of Chemical Research, 2021, 54, 3818-3827.	15.6	15
106	Direct Production of Gene-targeted Mice from ES Cells by Nuclear Transfer and Gene Transmission to their Progeny Experimental Animals, 2002, 51, 375-381.	1.1	14
107	H3K9MTase G9a is essential for the differentiation and growth of tenocytes in vitro. Histochemistry and Cell Biology, 2015, 144, 13-20.	1.7	14
108	Cutting Edge: The Histone Methyltransferase G9a Is Required for Silencing of Helper T Lineage–Associated Genes in Proliferating CD8 T Cells. Journal of Immunology, 2018, 200, 3891-3896.	0.8	14

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109	The fibronectin type-III (FNIII) domain of ATF7IP contributes to efficient transcriptional silencing mediated by the SETDB1 complex. Epigenetics and Chromatin, 2020, 13, 52.	3.9	13
110	H3K9 Demethylases JMJD1A and JMJD1B Control Prospermatogonia to Spermatogonia Transition in Mouse Germline. Stem Cell Reports, 2020, 15, 424-438.	4.8	13
111	Unveiling epidithiodiketopiperazine as a non-histone arginine methyltransferase inhibitor by chemical protein methylome analyses. Chemical Communications, 2018, 54, 9202-9205.	4.1	12
112	Regulation of mammalian 3D genome organization and histone H3K9 dimethylation by H3K9 methyltransferases. Communications Biology, 2021, 4, 571.	4.4	12
113	Essential roles of G9a in cell proliferation and differentiation during tooth development. Experimental Cell Research, 2017, 357, 202-210.	2.6	11
114	A loss-of-function variant in SUV39H2 identified in autism-spectrum disorder causes altered H3K9 trimethylation and dysregulation of protocadherin \hat{l}^2 -cluster genes in the developing brain. Molecular Psychiatry, 2021, 26, 7550-7559.	7.9	11
115	METTL18-mediated histidine methylation of RPL3 modulates translation elongation for proteostasis maintenance. ELife, 0, 11 , .	6.0	11
116	Posttranscriptional Regulation of Histone Lysine Methyltransferase GLP in Embryonic Male Mouse Germ Cells1. Biology of Reproduction, 2013, 88, 36.	2.7	10
117	Biochemical validation of EHMT1 missense mutations in Kleefstra syndrome. Journal of Human Genetics, 2018, 63, 555-562.	2.3	10
118	Deletion of Histone Methyltransferase G9a Suppresses Mutant Kras-driven Pancreatic Carcinogenesis. Cancer Genomics and Proteomics, 2020, 17, 695-705.	2.0	9
119	Rad54 is dispensable for the ALT pathway. Genes To Cells, 2006, 11, 1305-1315.	1.2	7
120	Regulation And Function Of H3K9 Methylation., 2007,, 341-354.		7
121	Regulation and function of H3K9 methylation. Sub-Cellular Biochemistry, 2007, 41, 337-50.	2.4	7
122	G9a-dependent histone methylation can be induced in G1 phase of cell cycle. Scientific Reports, 2019, 9, 956.	3.3	6
123	Derepression of inflammation-related genes link to microglia activation and neural maturation defect in a mouse model of Kleefstra syndrome. IScience, 2021, 24, 102741.	4.1	5
124	Histone H1 quantity determines the efficiency of chromatin condensation in both apoptotic and live cells. Biochemical and Biophysical Research Communications, 2019, 512, 202-207.	2.1	4
125	Heterozygous disruption of the ??1,3-galactosyltransferase gene in cattle. Transplantation, 2003, 76, 900-902.	1.0	3
126	Mammalian epigenetics in biology and medicine. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120386.	4.0	3

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127	Knockout mouse production assisted by <i>Blm</i> knockdown. Journal of Reproduction and Development, 2016, 62, 121-125.	1.4	2
128	A Simple Method for Visualization of Locus-Specific H4K20me1 Modifications in Living Caenorhabditis elegans Single Cells. G3: Genes, Genomes, Genetics, 2018, 8, 2249-2255.	1.8	2
129	Mammalian HEMK1 methylates glutamine residue of the GGQ motif of mitochondrial release factors. Scientific Reports, 2022, 12, 4104.	3.3	2