

Masako Suzuki

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7470984/publications.pdf>

Version: 2024-02-01

90
papers

3,935
citations

101543

36
h-index

128289

60
g-index

105
all docs

105
docs citations

105
times ranked

7547
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative isoschizomer profiling of cytosine methylation: The HELP assay. <i>Genome Research</i> , 2006, 16, 1046-1055.	5.5	355
2	Hypomethylation of Noncoding DNA Regions and Overexpression of the Long Noncoding RNA, AFAP1-AS1, in Barrett's Esophagus and Esophageal Adenocarcinoma. <i>Gastroenterology</i> , 2013, 144, 956-966.e4.	1.3	216
3	Redistribution of H3K27me3 upon DNA hypomethylation results in de-repression of Polycomb target genes. <i>Genome Biology</i> , 2013, 14, R25.	9.6	200
4	Cytosine methylation changes in enhancer regions of core pro-fibrotic genes characterize kidney fibrosis development. <i>Genome Biology</i> , 2013, 14, R108.	9.6	187
5	Equivalency of Nuclear Transferâ€Derived Embryonic Stem Cells to Those Derived from Fertilized Mouse Blastocysts. <i>Stem Cells</i> , 2006, 24, 2023-2033.	3.2	156
6	High-resolution genome-wide cytosine methylation profiling with simultaneous copy number analysis and optimization for limited cell numbers. <i>Nucleic Acids Research</i> , 2009, 37, 3829-3839.	14.5	141
7	Widespread Hypomethylation Occurs Early and Synergizes with Gene Amplification during Esophageal Carcinogenesis. <i>PLoS Genetics</i> , 2011, 7, e1001356.	3.5	112
8	Geneticâ€epigenetic interactions in cis: a major focus in the post-GWAS era. <i>Genome Biology</i> , 2017, 18, 120.	8.8	109
9	Lactate-mediated epigenetic reprogramming regulates formation of human pancreatic cancer-associated fibroblasts. <i>ELife</i> , 2019, 8, .	6.0	103
10	Epigenetic Functions of Smchd1 Repress Gene Clusters on the Inactive X Chromosome and on Autosomes. <i>Molecular and Cellular Biology</i> , 2013, 33, 3150-3165.	2.3	99
11	Differential epigenome-wide DNA methylation patterns in childhood obesity-associated asthma. <i>Scientific Reports</i> , 2013, 3, 2164.	3.3	94
12	Mosaic Epigenetic Dysregulation of Ectodermal Cells in Autism Spectrum Disorder. <i>PLoS Genetics</i> , 2014, 10, e1004402.	3.5	93
13	Myeloma Is Characterized by Stage-Specific Alterations in DNA Methylation That Occur Early during Myelomagenesis. <i>Journal of Immunology</i> , 2013, 190, 2966-2975.	0.8	90
14	Genome-wide and locus-specific DNA hypomethylation in G9a deficient mouse embryonic stem cells. <i>Genes To Cells</i> , 2007, 12, 1-11.	1.2	79
15	Optimized design and data analysis of tag-based cytosine methylation assays. <i>Genome Biology</i> , 2010, 11, R36.	9.6	76
16	Engineering a haematopoietic stem cell niche by revitalizing mesenchymal stromal cells. <i>Nature Cell Biology</i> , 2019, 21, 560-567.	10.3	74
17	DNA Methylation is Developmentally Regulated for Genes Essential for Cardiogenesis. <i>Journal of the American Heart Association</i> , 2014, 3, e000976.	3.7	71
18	Preference of DNA Methyltransferases for CpG Islands in Mouse Embryonic Stem Cells. <i>Genome Research</i> , 2004, 14, 1733-1740.	5.5	70

#	ARTICLE	IF	CITATIONS
19	A pipeline for the quantitative analysis of CG dinucleotide methylation using mass spectrometry. <i>Bioinformatics</i> , 2009, 25, 2164-2170.	4.1	69
20	Genome-wide hydroxymethylation tested using the HELP-GT assay shows redistribution in cancer. <i>Nucleic Acids Research</i> , 2013, 41, e157-e157.	14.5	69
21	Chromatin organization in the female mouse brain fluctuates across the oestrous cycle. <i>Nature Communications</i> , 2019, 10, 2851.	12.8	68
22	Whole-genome bisulfite sequencing with improved accuracy and cost. <i>Genome Research</i> , 2018, 28, 1364-1371.	5.5	64
23	Ascorbic acid-induced TET activation mitigates adverse hydroxymethylcytosine loss in renal cell carcinoma. <i>Journal of Clinical Investigation</i> , 2019, 129, 1612-1625.	8.2	64
24	Epigenetic changes in B lymphocytes associated with house dust mite allergic asthma. <i>Epigenetics</i> , 2011, 6, 1131-1137.	2.7	62
25	Post-conversion targeted capture of modified cytosines in mammalian and plant genomes. <i>Nucleic Acids Research</i> , 2015, 43, e81-e81.	14.5	62
26	Kidney Cancer Is Characterized by Aberrant Methylation of Tissue-Specific Enhancers That Are Prognostic for Overall Survival. <i>Clinical Cancer Research</i> , 2014, 20, 4349-4360.	7.0	60
27	Lsh regulates LTR retrotransposon repression independently of Dnmt3b function. <i>Genome Biology</i> , 2013, 14, R146.	9.6	54
28	Regulation of conceptus adhesion by endometrial CXC chemokines during the implantation period in sheep. <i>Molecular Reproduction and Development</i> , 2006, 73, 850-858.	2.0	52
29	Altered hydroxymethylation is seen at regulatory regions in pancreatic cancer and regulates oncogenic pathways. <i>Genome Research</i> , 2017, 27, 1830-1842.	5.5	51
30	Methylome Profiling Reveals Distinct Alterations in Phenotypic and Mutational Subgroups of Myeloproliferative Neoplasms. <i>Cancer Research</i> , 2013, 73, 1076-1085.	0.9	50
31	Fetal "Not Maternal" APOL1 Genotype Associated with Risk for Preeclampsia in Those with African Ancestry. <i>American Journal of Human Genetics</i> , 2018, 103, 367-376.	6.2	49
32	Epigenetic Silencing of the Circadian Clock Gene CRY1 is Associated with an Indolent Clinical Course in Chronic Lymphocytic Leukemia. <i>PLoS ONE</i> , 2012, 7, e34347.	2.5	44
33	Notch Pathway Is Activated via Genetic and Epigenetic Alterations and Is a Therapeutic Target in Clear Cell Renal Cancer. <i>Journal of Biological Chemistry</i> , 2017, 292, 837-846.	3.4	43
34	In Utero Exposure to a High-Fat Diet Programs Hepatic Hypermethylation and Gene Dysregulation and Development of Metabolic Syndrome in Male Mice. <i>Endocrinology</i> , 2017, 158, 2860-2872.	2.8	42
35	Cell type-specific methylation profiles occurring disproportionately in CpG-less regions that delineate developmental similarity. <i>Genes To Cells</i> , 2007, 12, 1123-1132.	1.2	41
36	Aberrant Epigenetic and Genetic Marks Are Seen in Myelodysplastic Leukocytes and Reveal Dock4 as a Candidate Pathogenic Gene on Chromosome 7q. <i>Journal of Biological Chemistry</i> , 2011, 286, 25211-25223.	3.4	41

#	ARTICLE	IF	CITATIONS
37	Functional genetic variants can mediate their regulatory effects through alteration of transcription factor binding. <i>Nature Communications</i> , 2019, 10, 3472.	12.8	39
38	Late-replicating heterochromatin is characterized by decreased cytosine methylation in the human genome. <i>Genome Research</i> , 2011, 21, 1833-1840.	5.5	38
39	DNA demethylation by 5-aza-2'-deoxycytidine is imprinted, targeted to euchromatin, and has limited transcriptional consequences. <i>Epigenetics and Chromatin</i> , 2015, 8, 11.	3.9	38
40	High Resolution Methylome Analysis Reveals Widespread Functional Hypomethylation during Adult Human Erythropoiesis. <i>Journal of Biological Chemistry</i> , 2013, 288, 8805-8814.	3.4	37
41	DNA Methylation Profiles of Donor Nuclei Cells and Tissues of Cloned Bovine Fetuses. <i>Journal of Reproduction and Development</i> , 2006, 52, 259-266.	1.4	34
42	Genome Wide Methylome Alterations in Lung Cancer. <i>PLoS ONE</i> , 2015, 10, e0143826.	2.5	30
43	A new class of tissue-specifically methylated regions involving entire CpG islands in the mouse. <i>Genes To Cells</i> , 2007, 12, 1305-1314.	1.2	27
44	DNA methylation profiling using HpaII tiny fragment enrichment by ligation-mediated PCR (HELP). <i>Methods</i> , 2010, 52, 218-222.	3.8	26
45	Interleukin 2 modulates thymic-derived regulatory T cell epigenetic landscape. <i>Nature Communications</i> , 2018, 9, 5368.	12.8	26
46	Loss of <i>MEN1</i> activates DNMT1 implicating DNA hypermethylation as a driver of MEN1 tumorigenesis. <i>Oncotarget</i> , 2016, 7, 12633-12650.	1.8	25
47	The Wasp System: An open source environment for managing and analyzing genomic data. <i>Genomics</i> , 2012, 100, 345-351.	2.9	24
48	Establishment of trophoblast stem cell lines from somatic cell nuclear-transferred embryos. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16293-16297.	7.1	23
49	Insights from deconvolution of cell subtype proportions enhance the interpretation of functional genomic data. <i>PLoS ONE</i> , 2019, 14, e0215987.	2.5	21
50	The SEQC2 epigenomics quality control (EpiQC) study. <i>Genome Biology</i> , 2021, 22, 332.	8.8	20
51	The shape of gene expression distributions matter: how incorporating distribution shape improves the interpretation of cancer transcriptomic data. <i>BMC Bioinformatics</i> , 2020, 21, 562.	2.6	19
52	Maternal gametic transmission of translocations or inversions of human chromosome 11p15.5 results in regional DNA hypermethylation and downregulation of CDKN1C expression. <i>Genomics</i> , 2012, 99, 25-35.	2.9	18
53	Functional Genomics of the Pediatric Obese Asthma Phenotype Reveal Enrichment of Rho-GTPase Pathways. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 202, 259-274.	5.6	17
54	Mechanisms of establishment and functional significance of DNA demethylation during erythroid differentiation. <i>Blood Advances</i> , 2018, 2, 1833-1852.	5.2	15

#	ARTICLE	IF	CITATIONS
55	Cell type-specific chromatin accessibility analysis in the mouse and human brain. <i>Epigenetics</i> , 2022, 17, 202-219.	2.7	13
56	Automated Computational Analysis of Genome-Wide DNA Methylation Profiling Data from HELP-Tagging Assays. <i>Methods in Molecular Biology</i> , 2012, 815, 79-87.	0.9	13
57	Tet-mediated DNA demethylation regulates specification of hematopoietic stem and progenitor cells during mammalian embryogenesis. <i>Science Advances</i> , 2022, 8, eabm3470.	10.3	13
58	DNA methylation changes in murine breast adenocarcinomas allow the identification of candidate genes for human breast carcinogenesis. <i>Mammalian Genome</i> , 2011, 22, 249-259.	2.2	11
59	Genome-wide DNA Methylation Analysis Using Massively Parallel Sequencing Technologies. <i>Seminars in Hematology</i> , 2013, 50, 70-77.	3.4	11
60	Large, Male Germ Cell-Specific Hypomethylated DNA Domains With Unique Genomic and Epigenomic Features on the Mouse X Chromosome. <i>DNA Research</i> , 2013, 20, 549-565.	3.4	10
61	Intrauterine Hyperglycemia Is Associated with an Impaired Postnatal Response to Oxidative Damage. <i>Stem Cells and Development</i> , 2018, 27, 683-691.	2.1	10
62	Amnion as a surrogate tissue reporter of the effects of maternal preeclampsia on the fetus. <i>Clinical Epigenetics</i> , 2016, 8, 67.	4.1	9
63	Disproportionate Vitamin A Deficiency in Women of Specific Ethnicities Linked to Differences in Allele Frequencies of Vitamin A-Related Polymorphisms. <i>Nutrients</i> , 2021, 13, 1743.	4.1	8
64	Genetic Variations of Vitamin A-Absorption and Storage-Related Genes, and Their Potential Contribution to Vitamin A Deficiency Risks Among Different Ethnic Groups. <i>Frontiers in Nutrition</i> , 2022, 9, 861619.	3.7	6
65	High-efficiency genomic editing in Epstein-Barr virus-transformed lymphoblastoid B cells using a single-stranded donor oligonucleotide strategy. <i>Communications Biology</i> , 2019, 2, 312.	4.4	5
66	Selective modulation of local linkages between active transcription and oxidative demethylation activity shapes cardiomyocyte-specific gene-body epigenetic status in mice. <i>BMC Genomics</i> , 2018, 19, 349.	2.8	4
67	Premature differentiation of nephron progenitor cell and dysregulation of gene pathways critical to kidney development in a model of preterm birth. <i>Scientific Reports</i> , 2021, 11, 21667.	3.3	4
68	Detecting, quantifying, and discriminating the mechanism of mosaic chromosomal aneuploidies using MAD-seq. <i>Genome Research</i> , 2018, 28, 1039-1052.	5.5	3
69	A Cellular Stress Response Induced by the CRISPR-dCas9 Activation System Is Not Heritable Through Cell Divisions. <i>CRISPR Journal</i> , 2020, 3, 188-197.	2.9	2
70	Epigenomic Profiling of Myeloproliferative Diseases Reveal Idiopathic Myelofibrosis as An Epigenetically Distinct Subgroup and Highlights the Epigenetic Effects of Jak2V617F Mutation. <i>Blood</i> , 2010, 116, 627-627.	1.4	2
71	Vitamin D Deficiency During Development Permanently Alters Liver Cell Composition and Function. <i>Frontiers in Endocrinology</i> , 2022, 13, .	3.5	2
72	Institutional Profile: The Einstein Center for Epigenomics: studying the role of epigenomic dysregulation in human disease. <i>Epigenomics</i> , 2009, 1, 33-38.	2.1	1

#	ARTICLE	IF	CITATIONS
73	DNA methylation: A link between genome variation and blood pressure. Science Translational Medicine, 2015, 7, .	12.4	1
74	Abstract 4230: Senescence reversion contributes to acquired drug resistance. , 2012, , .		1
75	Whole Methylome Explorations Of Paired Lung Tumor And Non-Tumor Clinical Samples. , 2012, , .		0
76	O10. Neuronal Chromatin Dynamics and Anxiety-Related Phenotypes Across the Estrous Cycle. Biological Psychiatry, 2018, 83, S112.	1.3	0
77	2011 - ENGINEERING A HEMATOPOIETIC STEM CELL NICHE BY REVITALIZING MESENCHYMAL STEM CELLS. Experimental Hematology, 2019, 76, S45.	0.4	0
78	The Role of Egr1 in Driving Ventral Hippocampal Gene Expression Patterns Underlying Sex Hormone-Dependent Changes in Anxiety-Like Behavior Within Females. Biological Psychiatry, 2020, 87, S453.	1.3	0
79	Abstract 4820: Whole methylome explorations of paired tumor and non-tumor clinical samples using HELP. , 2011, , .		0
80	Abstract A38: Whole methylome explorations of paired lung tumor and non-tumor clinical samples. Clinical Cancer Research, 2012, 18, A38-A38.	7.0	0
81	Abstract 4231: Genome wide hydroxymethylation tested using the HELP-GT assay shows redistribution in cancer.. , 2013, , .		0
82	Childhood memory. Science Translational Medicine, 2015, 7, .	12.4	0
83	Timing is everything. Science Translational Medicine, 2015, 7, .	12.4	0
84	Diverse diseases, diverse variants. Science Translational Medicine, 2015, 7, .	12.4	0
85	A brite idea for noncoding variants. Science Translational Medicine, 2015, 7, .	12.4	0
86	Above the landscape. Science Translational Medicine, 2015, 7, .	12.4	0
87	An integrative analysis sheds light on methylation profiles. Science Translational Medicine, 2016, 8, .	12.4	0
88	Balance of nutrients: Is more better?. Science Translational Medicine, 2016, 8, .	12.4	0
89	Abstract 1170: Notch pathway is overexpressed and is a therapeutic target in clear cell renal cancer. , 2017, , .		0
90	Engineering a Hematopoietic Stem Cell Niche By Revitalizing Mesenchymal Stem Cells with Five Transcription Factors. Blood, 2019, 134, 5004-5004.	1.4	0