# Masako Suzuki

List of Publications by Year
in descending order



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|---|---|---|---|
| 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 | Cell type-specific chromatin accessibility analysis in the mouse and human brain. Epigenetics, 2022, 17, 202-219. | 2.7 | 13 |
| 2 | Tet-mediated DNA demethylation regulates specification of hematopoietic stem and progenitor cells during mammalian embryogenesis. Science Advances, 2022, 8, eabm3470. | 10.3 | 13 |
| 3 | Vitamin D Deficiency During Development Permanently Alters Liver Cell Composition and Function. Frontiers in Endocrinology, 2022, 13, . | 3.5 | 2 |
| 4 | Genetic Variations of Vitamin A-Absorption and Storage-Related Genes, and Their Potential Contribution to Vitamin A Deficiency Risks Among Different Ethnic Groups. Frontiers in Nutrition, 2022, 9, 861619. | 3.7 | 6 |
| 5 | Disproportionate Vitamin A Deficiency in Women of Specific Ethnicities Linked to Differences in Allele Frequencies of Vitamin A-Related Polymorphisms. Nutrients, 2021, 13, 1743. | 4.1 | 8 |
| 6 | Premature differentiation of nephron progenitor cell and dysregulation of gene pathways critical to kidney development in a model of preterm birth. Scientific Reports, 2021, 11, 21667. | 3.3 | 4 |
| 7 | The SEQC2 epigenomics quality control (EpiQC) study. Genome Biology, 2021, 22, 332. | 8.8 | 20 |
| 8 | 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 |
| 9 | A Cellular Stress Response Induced by the CRISPR-dCas9 Activation System Is Not Heritable Through Cell Divisions. CRISPR Journal, 2020, 3, 188-197. | 2.9 | 2 |
| 10 | Functional Genomics of the Pediatric Obese Asthma Phenotype Reveal Enrichment of Rho-GTPase Pathways. American Journal of Respiratory and Critical Care Medicine, 2020, 202, 259-274. | 5.6 | 17 |
| 11 | The shape of gene expression distributions matter: how incorporating distribution shape improves the interpretation of cancer transcriptomic data. BMC Bioinformatics, 2020, 21, 562. | 2.6 | 19 |
| 12 | Functional genetic variants can mediate their regulatory effects through alteration of transcription factor binding. Nature Communications, 2019, 10, 3472. | 12.8 | 39 |
| 13 | High-efficiency genomic editing in Epstein-Barr virus-transformed lymphoblastoid B cells using a single-stranded donor oligonucleotide strategy. Communications Biology, 2019, 2, 312. | 4.4 | 5 |
| 14 | Chromatin organization in the female mouse brain fluctuates across the oestrous cycle. Nature Communications, 2019, 10, 2851. | 12.8 | 68 |
| 15 | 2011 - ENGINEERING A HEMATOPOIETIC STEM CELL NICHE BY REVITALIZING MESENCHYMAL STEM CELLS. Experimental Hematology, 2019, 76, S45. | 0.4 | 0 |
| 16 | Insights from deconvolution of cell subtype proportions enhance the interpretation of functional genomic data. PLoS ONE, 2019, 14, e0215987. | 2.5 | 21 |
| 17 | Engineering a haematopoietic stem cell niche by revitalizing mesenchymal stromal cells. Nature Cell Biology, 2019, 21, 560-567. | 10.3 | 74 |
| 18 | Ascorbic acidâ€“induced TET activation mitigates adverse hydroxymethylcytosine loss in renal cell carcinoma. Journal of Clinical Investigation, 2019, 129, 1612-1625. | 8.2 | 64 |

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|---|---|---|---|
| 19 | Lactate-mediated epigenetic reprogramming regulates formation of human pancreatic cancer-associated fibroblasts. ELife, 2019, 8, . | 6.0 | 103 |
| 20 | Engineering a Hematopoietic Stem Cell Niche By Revitalizing Mesenchymal Stem Cells with Five Transcription Factors. Blood, 2019, 134, 5004-5004. | 1.4 | 0 |
| 21 | Intrauterine Hyperglycemia Is Associated with an Impaired Postnatal Response to Oxidative Damage. Stem Cells and Development, 2018, 27, 683-691. | 2.1 | 10 |
| 22 | Interleukin 2 modulates thymic-derived regulatory T cell epigenetic landscape. Nature Communications, 2018, 9, 5368. | 12.8 | 26 |
| 23 | Fetalâ€"Not Maternalâ€"APOL1 Genotype Associated with Risk for Preeclampsia in Those with African Ancestry. American Journal of Human Genetics, 2018, 103, 367-376. | 6.2 | 49 |
| 24 | Mechanisms of establishment and functional significance of DNA demethylation during erythroid differentiation. Blood Advances, 2018, 2, 1833-1852. | 5.2 | 15 |
| 25 | Detecting, quantifying, and discriminating the mechanism of mosaic chromosomal aneuploidies using MAD-seq. Genome Research, 2018, 28, 1039-1052. | 5.5 | 3 |
| 26 | O10. Neuronal Chromatin Dynamics and Anxiety-Related Phenotypes Across the Estrous Cycle. Biological Psychiatry, 2018, 83, S112. | 1.3 | 0 |
| 27 | Selective modulation of local linkages between active transcription and oxidative demethylation activity shapes cardiomyocyte-specific gene-body epigenetic status in mice. BMC Genomics, 2018, 19, 349. | 2.8 | 4 |
| 28 | Whole-genome bisulfite sequencing with improved accuracy and cost. Genome Research, 2018, 28, 1364-1371. | 5.5 | 64 |
| 29 | Notch Pathway Is Activated via Genetic and Epigenetic Alterations and Is a Therapeutic Target in Clear Cell Renal Cancer. Journal of Biological Chemistry, 2017, 292, 837-846. | 3.4 | 43 |
| 30 | Geneticâ€"epigenetic interactions in cis: a major focus in the post-GWAS era. Genome Biology, 2017, 18, 120. | 8.8 | 109 |
| 31 | In Utero Exposure to a High-Fat Diet Programs Hepatic Hypermethylation and Gene Dysregulation and Development of Metabolic Syndrome in Male Mice. Endocrinology, 2017, 158, 2860-2872. | 2.8 | 42 |
| 32 | Altered hydroxymethylation is seen at regulatory regions in pancreatic cancer and regulates oncogenic pathways. Genome Research, 2017, 27, 1830-1842. | 5.5 | 51 |
| 33 | Abstract 1170: Notch pathway is overexpressed and is a therapeutic target in clear cell renal cancer. , 2017, , . | | 0 |
| 34 | Loss of MEN1 activates DNMT1 implicating DNA hypermethylation as a driver of MEN1 tumorigenesis. Oncotarget, 2016, 7, 12633-12650. | 1.8 | 25 |
| 35 | Amnion as a surrogate tissue reporter of the effects of maternal preeclampsia on the fetus. Clinical Epigenetics, 2016, 8, 67. | 4.1 | 9 |
| 36 | An integrative analysis sheds light on methylation profiles. Science Translational Medicine, 2016, 8, . | 12.4 | 0 |

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|---|---|---|---|
| 37 | Balance of nutrients: Is more better?. Science Translational Medicine, 2016, 8, . | 12.4 | 0 |
| 38 | Post-conversion targeted capture of modified cytosines in mammalian and plant genomes. Nucleic Acids Research, 2015, 43, e81-e81. | 14.5 | 62 |
| 39 | DNA demethylation by 5-aza-2â€²-deoxycytidine is imprinted, targeted to euchromatin, and has limited transcriptional consequences. Epigenetics and Chromatin, 2015, 8, 11. | 3.9 | 38 |
| 40 | DNA methylation: A link between genome variation and blood pressure. Science Translational Medicine, 2015, 7, . | 12.4 | 1 |
| 41 | Genome Wide Methylome Alterations in Lung Cancer. PLoS ONE, 2015, 10, e0143826. | 2.5 | 30 |
| 42 | Childhood memory. Science Translational Medicine, 2015, 7, . | 12.4 | 0 |
| 43 | Timing is everything. Science Translational Medicine, 2015, 7, . | 12.4 | 0 |
| 44 | Diverse diseases, diverse variants. Science Translational Medicine, 2015, 7, . | 12.4 | 0 |
| 45 | A brite idea for noncoding variants. Science Translational Medicine, 2015, 7, . | 12.4 | 0 |
| 46 | Above the landscape. Science Translational Medicine, 2015, 7, . | 12.4 | 0 |
| 47 | Kidney Cancer Is Characterized by Aberrant Methylation of Tissue-Specific Enhancers That Are Prognostic for Overall Survival. Clinical Cancer Research, 2014, 20, 4349-4360. | 7.0 | 60 |
| 48 | Mosaic Epigenetic Dysregulation of Ectodermal Cells in Autism Spectrum Disorder. PLoS Genetics, 2014, 10, e1004402. | 3.5 | 93 |
| 49 | DNA Methylation is Developmentally Regulated for Genes Essential for Cardiogenesis. Journal of the American Heart Association, 2014, 3, e000976. | 3.7 | 71 |
| 50 | Redistribution of H3K27me3 upon DNA hypomethylation results in de-repression of Polycomb target genes. Genome Biology, 2013, 14, R25. | 9.6 | 200 |
| 51 | Cytosine methylation changes in enhancer regions of core pro-fibrotic genes characterize kidney fibrosis development. Genome Biology, 2013, 14, R108. | 9.6 | 187 |
| 52 | Hypomethylation of Noncoding DNA Regions and Overexpression of the Long Noncoding RNA, AFAP1-AS1, in Barrett's Esophagus and Esophageal Adenocarcinoma. Gastroenterology, 2013, 144, 956-966.e4. | 1.3 | 216 |
| 53 | Myeloma Is Characterized by Stage-Specific Alterations in DNA Methylation That Occur Early during Myelomagenesis. Journal of Immunology, 2013, 190, 2966-2975. | 0.8 | 90 |
| 54 | Genome-wide DNA Methylation Analysis Using Massively Parallel Sequencing Technologies. Seminars in Hematology, 2013, 50, 70-77. | 3.4 | 11 |

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|---|---|---|---|
| 55 | Epigenetic Functions of Smchd1 Repress Gene Clusters on the Inactive X Chromosome and on Autosomes. Molecular and Cellular Biology, 2013, 33, 3150-3165. | 2.3 | 99 |
| 56 | Large, Male Germ Cell-Specific Hypomethylated DNA Domains With Unique Genomic and Epigenomic Features on the Mouse X Chromosome. DNA Research, 2013, 20, 549-565. | 3.4 | 10 |
| 57 | Methylome Profiling Reveals Distinct Alterations in Phenotypic and Mutational Subgroups of Myeloproliferative Neoplasms. Cancer Research, 2013, 73, 1076-1085. | 0.9 | 50 |
| 58 | High Resolution Methylome Analysis Reveals Widespread Functional Hypomethylation during Adult Human Erythropoiesis. Journal of Biological Chemistry, 2013, 288, 8805-8814. | 3.4 | 37 |
| 59 | Genome-wide hydroxymethylation tested using the HELP-GT assay shows redistribution in cancer. Nucleic Acids Research, 2013, 41, e157-e157. | 14.5 | 69 |
| 60 | Differential epigenome-wide DNA methylation patterns in childhood obesity-associated asthma. Scientific Reports, 2013, 3, 2164. | 3.3 | 94 |
| 61 | Lsh regulates LTR retrotransposon repression independently of Dnmt3b function. Genome Biology, 2013, 14, R146. | 9.6 | 54 |
| 62 | Abstract 4231: Genome wide hydroxymethylation tested using the HELP-GT assay shows redistribution in cancer.. , 2013, , . | | 0 |
| 63 | The Wasp System: An open source environment for managing and analyzing genomic data. Genomics, 2012, 100, 345-351. | 2.9 | 24 |
| 64 | Maternal gametic transmission of translocations or inversions of human chromosome 11p15.5 results in regional DNA hypermethylation and downregulation of CDKN1C expression. Genomics, 2012, 99, 25-35. | 2.9 | 18 |
| 65 | Epigenetic Silencing of the Circadian Clock Gene CRY1 is Associated with an Indolent Clinical Course in Chronic Lymphocytic Leukemia. PLoS ONE, 2012, 7, e34347. | 2.5 | 44 |
| 66 | Whole Methylome Explorations Of Paired Lung Tumor And Non-Tumor Clinical Samples. , 2012, , . | | 0 |
| 67 | Automated Computational Analysis of Genome-Wide DNA Methylation Profiling Data from HELP-Tagging Assays. Methods in Molecular Biology, 2012, 815, 79-87. | 0.9 | 13 |
| 68 | Abstract 4230: Senescence reversion contributes to acquired drug resistance. , 2012, , . | | 1 |
| 69 | Abstract A38: Whole methylome explorations of paired lung tumor and non-tumor clinical samples. Clinical Cancer Research, 2012, 18, A38-A38. | 7.0 | 0 |
| 70 | DNA methylation changes in murine breast adenocarcinomas allow the identification of candidate genes for human breast carcinogenesis. Mammalian Genome, 2011, 22, 249-259. | 2.2 | 11 |
| 71 | Epigenetic changes in B lymphocytes associated with house dust mite allergic asthma. Epigenetics, 2011, 6, 1131-1137. | 2.7 | 62 |
| 72 | Late-replicating heterochromatin is characterized by decreased cytosine methylation in the human genome. Genome Research, 2011, 21, 1833-1840. | 5.5 | 38 |

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|---|---|---|---|
| 73 | Aberrant Epigenetic and Genetic Marks Are Seen in Myelodysplastic Leukocytes and Reveal Dock4 as a Candidate Pathogenic Gene on Chromosome 7q. Journal of Biological Chemistry, 2011, 286, 25211-25223. | 3.4 | 41 |
| 74 | Widespread Hypomethylation Occurs Early and Synergizes with Gene Amplification during Esophageal Carcinogenesis. PLoS Genetics, 2011, 7, e1001356. | 3.5 | 112 |
| 75 | Abstract 4820: Whole methylome explorations of paired tumor and non-tumor clinical samples using HELP. , 2011, , . | | 0 |
| 76 | DNA methylation profiling using HpaII tiny fragment enrichment by ligation-mediated PCR (HELP). Methods, 2010, 52, 218-222. | 3.8 | 26 |
| 77 | Optimized design and data analysis of tag-based cytosine methylation assays. Genome Biology, 2010, 11, R36. | 9.6 | 76 |
| 78 | Epigenomic Profiling of Myeloproliferative Diseases Reveal Idiopathic Myelofibrosis as An Epigenetically Distinct Subgroup and Highlights the Epigenetic Effects of Jak2V617F Mutation. Blood, 2010, 116, 627-627. | 1.4 | 2 |
| 79 | A pipeline for the quantitative analysis of CG dinucleotide methylation using mass spectrometry. Bioinformatics, 2009, 25, 2164-2170. | 4.1 | 69 |
| 80 | High-resolution genome-wide cytosine methylation profiling with simultaneous copy number analysis and optimization for limited cell numbers. Nucleic Acids Research, 2009, 37, 3829-3839. | 14.5 | 141 |
| 81 | Institutional Profile: The Einstein Center for Epigenomics: studying the role of epigenomic dysregulation in human disease. Epigenomics, 2009, 1, 33-38. | 2.1 | 1 |
| 82 | Establishment of trophoblast stem cell lines from somatic cell nuclear-transferred embryos. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16293-16297. | 7.1 | 23 |
| 83 | Genome-wide and locus-specific DNA hypomethylation in G9a deficient mouse embryonic stem cells. Genes To Cells, 2007, 12, 1-11. | 1.2 | 79 |
| 84 | Cell type-specific methylation profiles occurring disproportionately in CpG-less regions that delineate developmental similarity. Genes To Cells, 2007, 12, 1123-1132. | 1.2 | 41 |
| 85 | A new class of tissueâ€specifically methylated regions involving entire CpG islands in the mouse. Genes To Cells, 2007, 12, 1305-1314. | 1.2 | 27 |
| 86 | Comparative isoschizomer profiling of cytosine methylation: The HELP assay. Genome Research, 2006, 16, 1046-1055. | 5.5 | 355 |
| 87 | Equivalency of Nuclear Transferâ€Derived Embryonic Stem Cells to Those Derived from Fertilized Mouse Blastocysts. Stem Cells, 2006, 24, 2023-2033. | 3.2 | 156 |
| 88 | DNA Methylation Profiles of Donor Nuclei Cells and Tissues of Cloned Bovine Fetuses. Journal of Reproduction and Development, 2006, 52, 259-266. | 1.4 | 34 |
| 89 | Regulation of conceptus adhesion by endometrial CXC chemokines during the implantation period in sheep. Molecular Reproduction and Development, 2006, 73, 850-858. | 2.0 | 52 |
| 90 | Preference of DNA Methyltransferases for CpG Islands in Mouse Embryonic Stem Cells. Genome Research, 2004, 14, 1733-1740. | 5.5 | 70 |