

Kazumitsu Maehara

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

1,759
citations

236925

25
h-index

315739

38
g-index

62
all docs

62
docs citations

62
times ranked

3014
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Relayed signaling between mesenchymal progenitors and muscle stem cells ensures adaptive stem cell response to increased mechanical load. <i>Cell Stem Cell</i> , 2022, 29, 265-280.e6. | 11.1 | 36 |
| 2 | Tenogenic Induction From Induced Pluripotent Stem Cells Unveils the Trajectory Towards Tenocyte Differentiation. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 780038. | 3.7 | 6 |
| 3 | Photo-isolation chemistry for high-resolution and deep spatial transcriptome with mouse tissue sections. <i>STAR Protocols</i> , 2022, 3, 101346. | 1.2 | 3 |
| 4 | Genome-wide analysis of chromatin structure changes upon MyoD binding in proliferative myoblasts during the cell cycle. <i>Journal of Biochemistry</i> , 2021, 169, 653-661. | 1.7 | 0 |
| 5 | H4K20me1 and H3K27me3 are concurrently loaded onto the inactive X chromosome but dispensable for inducing gene silencing. <i>EMBO Reports</i> , 2021, 22, e51989. | 4.5 | 40 |
| 6 | Chromatin structure-dependent histone incorporation revealed by a genome-wide deposition assay. <i>ELife</i> , 2021, 10, . | 6.0 | 6 |
| 7 | Transcriptome analysis of gene expression changes upon enzymatic dissociation in skeletal myoblasts. <i>Genes To Cells</i> , 2021, 26, 530-540. | 1.2 | 6 |
| 8 | High-depth spatial transcriptome analysis by photo-isolation chemistry. <i>Nature Communications</i> , 2021, 12, 4416. | 12.8 | 22 |
| 9 | An extensive and dynamic trans-omic network illustrating prominent regulatory mechanisms in response to insulin in the liver. <i>Cell Reports</i> , 2021, 36, 109569. | 6.4 | 7 |
| 10 | Modeling population size independent tissue epigenomes by ChILâ€seq with single thin sections. <i>Molecular Systems Biology</i> , 2021, 17, e10323. | 7.2 | 1 |
| 11 | Discriminative feature of cells characterizes cell populations of interest by a small subset of genes. <i>PLoS Computational Biology</i> , 2021, 17, e1009579. | 3.2 | 2 |
| 12 | Chromatin integration labeling for mapping DNA-binding proteins and modifications with low input. <i>Nature Protocols</i> , 2020, 15, 3334-3360. | 12.0 | 12 |
| 13 | Biochemical analysis of nucleosome targeting by Tn5 transposase. <i>Open Biology</i> , 2019, 9, 190116. | 3.6 | 14 |
| 14 | The Eleanor ncRNAs activate the topological domain of the ESR1 locus to balance against apoptosis. <i>Nature Communications</i> , 2019, 10, 3778. | 12.8 | 28 |
| 15 | Calcineurin Broadly Regulates the Initiation of Skeletal Muscle-Specific Gene Expression by Binding Target Promoters and Facilitating the Interaction of the SWI/SNF Chromatin Remodeling Enzyme. <i>Molecular and Cellular Biology</i> , 2019, 39, . | 2.3 | 14 |
| 16 | Dmrt factors determine the positional information of cerebral cortical progenitors via differential suppression of homeobox genes. <i>Development (Cambridge)</i> , 2019, 146, . | 2.5 | 14 |
| 17 | A chromatin integration labelling method enables epigenomic profiling with lower input. <i>Nature Cell Biology</i> , 2019, 21, 287-296. | 10.3 | 121 |
| 18 | Chromatin-bound CRM1 recruits SET-Nup214 and NPM1c onto HOX clusters causing aberrant HOX expression in leukemia cells. <i>ELife</i> , 2019, 8, . | 6.0 | 34 |

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|----|--|------|-----------|
| 19 | Sustained expression of HeyL is critical for the proliferation of muscle stem cells in overloaded muscle. <i>ELife</i> , 2019, 8, . | 6.0 | 40 |
| 20 | Histone H3.3 sub-variant H3mm7 is required for normal skeletal muscle regeneration. <i>Nature Communications</i> , 2018, 9, 1400. | 12.8 | 23 |
| 21 | Cryo-EM structure of the nucleosome containing the <i>ALB1</i> enhancer DNA sequence. <i>Open Biology</i> , 2018, 8, . | 3.6 | 31 |
| 22 | Genome-wide analysis of the spatiotemporal regulation of firing and dormant replication origins in human cells. <i>Nucleic Acids Research</i> , 2018, 46, 6683-6696. | 14.5 | 60 |
| 23 | Sensitive detection of fluorescence in western blotting by merging images. <i>PLoS ONE</i> , 2018, 13, e0191532. | 2.5 | 13 |
| 24 | Testis-Specific Histone Variant H3t Gene Is Essential for Entry into Spermatogenesis. <i>Cell Reports</i> , 2017, 18, 593-600. | 6.4 | 82 |
| 25 | Crystal structure of the overlapping dinucleosome composed of hexasome and octasome. <i>Science</i> , 2017, 356, 205-208. | 12.6 | 77 |
| 26 | Chd2 regulates chromatin for proper gene expression toward differentiation in mouse embryonic stem cells. <i>Nucleic Acids Research</i> , 2017, 45, 8758-8772. | 14.5 | 31 |
| 27 | Crystal Structure and Characterization of Novel Human Histone H3 Variants, H3.6, H3.7, and H3.8. <i>Biochemistry</i> , 2017, 56, 2184-2196. | 2.5 | 20 |
| 28 | Thymine <i>DNA</i> glycosylase modulates <i>DNA</i> damage response and gene expression by base excision repair-dependent and independent mechanisms. <i>Genes To Cells</i> , 2017, 22, 392-405. | 1.2 | 4 |
| 29 | The requirement of Mettl3-promoted <i>MyoD</i> mRNA maintenance in proliferative myoblasts for skeletal muscle differentiation. <i>Open Biology</i> , 2017, 7, 170119. | 3.6 | 71 |
| 30 | Identification of Immunoglobulin Gene Sequences from a Small Read Number of mRNA-Seq Using Hybridomas. <i>PLoS ONE</i> , 2016, 11, e0165473. | 2.5 | 11 |
| 31 | Chd5 Regulates MuERV-L/MERVL Expression in Mouse Embryonic Stem Cells Via H3K27me3 Modification and Histone H3.1/H3.2. <i>Journal of Cellular Biochemistry</i> , 2016, 117, 780-792. | 2.6 | 29 |
| 32 | Chromatin architecture may dictate the target site for DMC1, but not for RAD51, during homologous pairing. <i>Scientific Reports</i> , 2016, 6, 24228. | 3.3 | 12 |
| 33 | Structure and function of human histone H3.Y nucleosome. <i>Nucleic Acids Research</i> , 2016, 44, 6127-6141. | 14.5 | 44 |
| 34 | Exploration of nucleosome positioning patterns in transcription factor function. <i>Scientific Reports</i> , 2016, 6, 19620. | 3.3 | 14 |
| 35 | Histone H4 lysine 20 acetylation is associated with gene repression in human cells. <i>Scientific Reports</i> , 2016, 6, 24318. | 3.3 | 40 |
| 36 | Histone H3.5 forms an unstable nucleosome and accumulates around transcription start sites in human testis. <i>Epigenetics and Chromatin</i> , 2016, 9, 2. | 3.9 | 53 |

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|----|--|------|-----------|
| 37 | Chromatin-prebound Crm1 recruits Nup98-HoxA9 fusion to induce aberrant expression of Hox cluster genes. <i>ELife</i> , 2016, 5, e09540. | 6.0 | 45 |
| 38 | Tissue-specific expression of histone H3 variants diversified after species separation. <i>Epigenetics and Chromatin</i> , 2015, 8, 35. | 3.9 | 51 |
| 39 | A cluster of noncoding RNAs activates the ESR1 locus during breast cancer adaptation. <i>Nature Communications</i> , 2015, 6, 6966. | 12.8 | 60 |
| 40 | agplus: a rapid and flexible tool for aggregation plots. <i>Bioinformatics</i> , 2015, 31, 3046-3047. | 4.1 | 15 |
| 41 | Incorporation of histone H3.1 suppresses the lineage potential of skeletal muscle. <i>Nucleic Acids Research</i> , 2015, 43, 775-786. | 14.5 | 34 |
| 42 | Cdt1-binding protein GRWD1 is a novel histone-binding protein that facilitates MCM loading through its influence on chromatin architecture. <i>Nucleic Acids Research</i> , 2015, 43, 5898-5911. | 14.5 | 59 |
| 43 | Influence of DNA methylation on positioning and DNA flexibility of nucleosomes with pericentric satellite DNA. <i>Open Biology</i> , 2015, 5, 150128. | 3.6 | 22 |
| 44 | Distribution of histone H4 modifications as revealed by a panel of specific monoclonal antibodies. <i>Chromosome Research</i> , 2015, 23, 753-766. | 2.2 | 49 |
| 45 | SraTailor: Graphical user interface software for processing and visualizing ChIP-seq data. <i>Genes To Cells</i> , 2014, 19, 919-926. | 1.2 | 16 |
| 46 | Regulation of RNA polymerase II activation by histone acetylation in single living cells. <i>Nature</i> , 2014, 516, 272-275. | 27.8 | 237 |
| 47 | Heterochromatin Dynamics during the Differentiation Process Revealed by the DNA Methylation Reporter Mouse, MethylRO. <i>Stem Cell Reports</i> , 2014, 2, 910-924. | 4.8 | 40 |
| 48 | Human TREX component Thoc5 affects alternative polyadenylation site choice by recruiting mammalian cleavage factor I. <i>Nucleic Acids Research</i> , 2013, 41, 7060-7072. | 14.5 | 57 |
| 49 | A co-localization model of paired ChIP-seq data using a large ENCODE data set enables comparison of multiple samples. <i>Nucleic Acids Research</i> , 2013, 41, 54-62. | 14.5 | 8 |
| 50 | Visualization Of Normal and Malignant Epigenetic Regulation In Hematopoiesis Utilizing Newly-Developed Histone Variant H3.3 ChIPseq Analysis. <i>Blood</i> , 2013, 122, 1189-1189. | 1.4 | 0 |
| 51 | The Deposition of H3.3 Mediated by Transcription Factors Determines Hematopoietic Cell Fate. <i>Blood</i> , 2012, 120, 1193-1193. | 1.4 | 0 |
| 52 | The classification of mRNA expression levels by the phosphorylation state of RNAPII CTD based on a combined genome-wide approach. <i>BMC Genomics</i> , 2011, 12, 516. | 2.8 | 36 |