

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	Regulation of RNA polymerase II activation by histone acetylation in single living cells. <i>Nature</i> , 2014, 516, 272-275.	27.8	237
2	A chromatin integration labelling method enables epigenomic profiling with lower input. <i>Nature Cell Biology</i> , 2019, 21, 287-296.	10.3	121
3	Testis-Specific Histone Variant H3t Gene Is Essential for Entry into Spermatogenesis. <i>Cell Reports</i> , 2017, 18, 593-600.	6.4	82
4	Crystal structure of the overlapping dinucleosome composed of hexasome and octasome. <i>Science</i> , 2017, 356, 205-208.	12.6	77
5	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
6	A cluster of noncoding RNAs activates the ESR1 locus during breast cancer adaptation. <i>Nature Communications</i> , 2015, 6, 6966.	12.8	60
7	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
8	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
9	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
10	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
11	Tissue-specific expression of histone H3 variants diversified after species separation. <i>Epigenetics and Chromatin</i> , 2015, 8, 35.	3.9	51
12	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
13	Chromatin-prebound Crm1 recruits Nup98-HoxA9 fusion to induce aberrant expression of Hox cluster genes. <i>ELife</i> , 2016, 5, e09540.	6.0	45
14	Structure and function of human histone H3.Y nucleosome. <i>Nucleic Acids Research</i> , 2016, 44, 6127-6141.	14.5	44
15	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
16	Histone H4 lysine 20 acetylation is associated with gene repression in human cells. <i>Scientific Reports</i> , 2016, 6, 24318.	3.3	40
17	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
18	Sustained expression of HeyL is critical for the proliferation of muscle stem cells in overloaded muscle. <i>ELife</i> , 2019, 8, .	6.0	40

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19	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
20	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
21	Incorporation of histone H3.1 suppresses the lineage potential of skeletal muscle. <i>Nucleic Acids Research</i> , 2015, 43, 775-786.	14.5	34
22	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
23	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
24	Cryo-EM structure of the nucleosome containing the <i>ALB1</i> enhancer DNA sequence. <i>Open Biology</i> , 2018, 8, .	3.6	31
25	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
26	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
27	Histone H3.3 sub-variant H3mm7 is required for normal skeletal muscle regeneration. <i>Nature Communications</i> , 2018, 9, 1400.	12.8	23
28	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
29	High-depth spatial transcriptome analysis by photo-isolation chemistry. <i>Nature Communications</i> , 2021, 12, 4416.	12.8	22
30	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
31	SraTailor: Graphical user interface software for processing and visualizing Ch<sc>IP</sc>â€œseq data. <i>Genes To Cells</i> , 2014, 19, 919-926.	1.2	16
32	agplus: a rapid and flexible tool for aggregation plots. <i>Bioinformatics</i> , 2015, 31, 3046-3047.	4.1	15
33	Exploration of nucleosome positioning patterns in transcription factor function. <i>Scientific Reports</i> , 2016, 6, 19620.	3.3	14
34	Biochemical analysis of nucleosome targeting by Tn5 transposase. <i>Open Biology</i> , 2019, 9, 190116.	3.6	14
35	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
36	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

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37	Sensitive detection of fluorescence in western blotting by merging images. PLoS ONE, 2018, 13, e0191532.	2.5	13
38	Chromatin architecture may dictate the target site for DMC1, but not for RAD51, during homologous pairing. Scientific Reports, 2016, 6, 24228.	3.3	12
39	Chromatin integration labeling for mapping DNA-binding proteins and modifications with low input. Nature Protocols, 2020, 15, 3334-3360.	12.0	12
40	Identification of Immunoglobulin Gene Sequences from a Small Read Number of mRNA-Seq Using Hybridomas. PLoS ONE, 2016, 11, e0165473.	2.5	11
41	A co-localization model of paired ChIP-seq data using a large ENCODE data set enables comparison of multiple samples. Nucleic Acids Research, 2013, 41, 54-62.	14.5	8
42	An extensive and dynamic trans-omic network illustrating prominent regulatory mechanisms in response to insulin in the liver. Cell Reports, 2021, 36, 109569.	6.4	7
43	Chromatin structure-dependent histone incorporation revealed by a genome-wide deposition assay. ELife, 2021, 10, .	6.0	6
44	Transcriptome analysis of gene expression changes upon enzymatic dissociation in skeletal myoblasts. Genes To Cells, 2021, 26, 530-540.	1.2	6
45	Tenogenic Induction From Induced Pluripotent Stem Cells Unveils the Trajectory Towards Tenocyte Differentiation. Frontiers in Cell and Developmental Biology, 2022, 10, 780038.	3.7	6
46	Thymine <scp>DNA</scp> glycosylase modulates <scp>DNA</scp> damage response and gene expression by base excision repairâ€dependent and independent mechanisms. Genes To Cells, 2017, 22, 392-405.	1.2	4
47	Photo-isolation chemistry for high-resolution and deep spatial transcriptome with mouse tissue sections. STAR Protocols, 2022, 3, 101346.	1.2	3
48	Discriminative feature of cells characterizes cell populations of interest by a small subset of genes. PLoS Computational Biology, 2021, 17, e1009579.	3.2	2
49	Modeling population size independent tissue epigenomes by ChIâ€seq with single thin sections. Molecular Systems Biology, 2021, 17, e10323.	7.2	1
50	Genome-wide analysis of chromatin structure changes upon MyoD binding in proliferative myoblasts during the cell cycle. Journal of Biochemistry, 2021, 169, 653-661.	1.7	0
51	The Deposition of H3.3 Mediated by Transcription Factors Determines Hematopoietic Cell Fate. Blood, 2012, 120, 1193-1193.	1.4	0
52	Visualization Of Normal and Malignant Epigenetic Regulation In Hematopoiesis Utilizing Newly-Developed Histone Variant H3.3 Chipseq Analysis. Blood, 2013, 122, 1189-1189.	1.4	0