

Yuko Sato

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

1,222
citations

471509

17
h-index

434195

31
g-index

38
all docs

38
docs citations

38
times ranked

1692
citing authors

#	ARTICLE	IF	CITATIONS
1	Live imaging of transcription sites using an elongating RNA polymerase IIâ€“specific probe. <i>Journal of Cell Biology</i> , 2022, 221, .	5.2	22
2	Imaging transcription elongation dynamics by new technologies unveils the organization of initiation and elongation in transcription factories. <i>Current Opinion in Cell Biology</i> , 2022, 74, 71-79.	5.4	11
3	Single-cell profiling of transcriptome and histone modifications with EpiDamID. <i>Molecular Cell</i> , 2022, 82, 1956-1970.e14.	9.7	28
4	Live-cell epigenome manipulation by synthetic histone acetylation catalyst system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	24
5	Multiplexed Imaging of Posttranslational Modifications of Endogenous Proteins in Live Cells. <i>Methods in Molecular Biology</i> , 2021, 2350, 31-41.	0.9	2
6	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
7	Transcription organizes euchromatin via microphase separation. <i>Nature Communications</i> , 2021, 12, 1360.	12.8	83
8	A live imaging system to analyze spatiotemporal dynamics of RNA polymerase II modification in <i>Arabidopsis thaliana</i> . <i>Communications Biology</i> , 2021, 4, 580.	4.4	5
9	Live-cell imaging probes to track chromatin modification dynamics. <i>Microscopy (Oxford, England)</i> , 2021, 70, 415-422.	1.5	16
10	Dynamic Behavior of Inactive X During the Cell Cycle as Revealed by H3K27me3-Specific Intracellular Antibody. <i>Methods in Molecular Biology</i> , 2021, 2329, 237-247.	0.9	0
11	Intrabody-based FRET probe to visualize endogenous histone acetylation. <i>Scientific Reports</i> , 2019, 9, 10188.	3.3	10
12	Cyclization of Single-Chain Fv Antibodies Markedly Suppressed Their Characteristic Aggregation Mediated by Inter-Chain VH-VL Interactions. <i>Molecules</i> , 2019, 24, 2620.	3.8	20
13	A genetically encoded probe for imaging nascent and mature HA-tagged proteins in vivo. <i>Nature Communications</i> , 2019, 10, 2947.	12.8	72
14	Preparation of single-chain Fv antibodies in the cytoplasm of <i>Escherichia coli</i> by simplified and systematic chaperone optimization. <i>Journal of Biochemistry</i> , 2019, 166, 455-462.	1.7	8
15	Histone H3K27 acetylation precedes active transcription during zebrafish zygotic genome activation as revealed by live-cell analysis. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	81
16	Histone H3.3 sub-variant H3mm7 is required for normal skeletal muscle regeneration. <i>Nature Communications</i> , 2018, 9, 1400.	12.8	23
17	Visualizing the Dynamics of Inactive X Chromosomes in Living Cells Using Antibody-Based Fluorescent Probes. <i>Methods in Molecular Biology</i> , 2018, 1861, 91-102.	0.9	15
18	JQ1 affects BRD2-dependent and independent transcription regulation without disrupting H4-hyperacetylated chromatin states. <i>Epigenetics</i> , 2018, 13, 410-431.	2.7	32

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19	Reduction in chromosome mobility accompanies nuclear organization during early embryogenesis in <i>Caenorhabditis elegans</i> . <i>Scientific Reports</i> , 2017, 7, 3631.	3.3	24
20	Semi-quantitative Analysis of H4K20me1 Levels in Living Cells Using Mintbody. <i>Bio-protocol</i> , 2017, 7, e2276.	0.4	3
21	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
22	A Genetically Encoded Probe for Live-Cell Imaging of H4K20 Monomethylation. <i>Journal of Molecular Biology</i> , 2016, 428, 3885-3902.	4.2	52
23	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
24	<i>In vivo</i> tracking of histone H3 lysine 9 acetylation in <i>Xenopus laevis</i> during tail regeneration. <i>Genes To Cells</i> , 2016, 21, 358-369.	1.2	29
25	Histone Acetylation on <i>Drosophila</i> Polytene Chromosomes Visualized by Mintbody. <i>Cytologia</i> , 2015, 80, 383-384.	0.6	8
26	Tissue-specific expression of histone H3 variants diversified after species separation. <i>Epigenetics and Chromatin</i> , 2015, 8, 35.	3.9	51
27	Incorporation of histone H3.1 suppresses the lineage potential of skeletal muscle. <i>Nucleic Acids Research</i> , 2015, 43, 775-786.	14.5	34
28	Visualizing posttranslational and epigenetic modifications of endogenous proteins in vivo. <i>Histochemistry and Cell Biology</i> , 2015, 144, 101-109.	1.7	49
29	Quantifying histone and RNA polymerase II post-translational modification dynamics in mother and daughter cells. <i>Methods</i> , 2014, 70, 77-88.	3.8	16
30	Regulation of RNA polymerase II activation by histone acetylation in single living cells. <i>Nature</i> , 2014, 516, 272-275.	27.8	237
31	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
32	Genetically encoded system to track histone modification in vivo. <i>Scientific Reports</i> , 2013, 3, 2436.	3.3	96