

Koji Hisatake

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

2,482
citations

394421

19
h-index

289244

40
g-index

40
all docs

40
docs citations

40
times ranked

3180
citing authors

#	ARTICLE	IF	CITATIONS
1	Structurally-discovered KLF4 variants accelerate and stabilize reprogramming to pluripotency. <i>IScience</i> , 2022, 25, 103525.	4.1	4
2	Early reactivation of clustered genes on the inactive X chromosome during somatic cell reprogramming. <i>Stem Cell Reports</i> , 2022, 17, 53-67.	4.8	3
3	Downregulation of Odd-Skipped Related 2, a Novel Regulator of Epithelial-Mesenchymal Transition, Enables Efficient Somatic Cell Reprogramming. <i>Stem Cells</i> , 2022, , .	3.2	2
4	Utilization of a novel Sendai virus vector in ex vivo gene therapy for hemophilia A. <i>International Journal of Hematology</i> , 2021, 113, 493-499.	1.6	5
5	Visualization of intracellular lipid metabolism in brown adipocytes by time-lapse ultra-multiplex CARS microspectroscopy with an onstage incubator. <i>Journal of Chemical Physics</i> , 2021, 155, 125102.	3.0	5
6	Mechanisms of the Metabolic Shift during Somatic Cell Reprogramming. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2254.	4.1	47
7	Live-cell imaging of subcellular structures for quantitative evaluation of pluripotent stem cells. <i>Scientific Reports</i> , 2019, 9, 1777.	3.3	17
8	Template Activating Factor-1 $\hat{\pm}$ Regulates Retroviral Silencing during Reprogramming. <i>Cell Reports</i> , 2019, 29, 1909-1922.e5.	6.4	8
9	Non-invasive in vivo imaging of UCP1 expression in live mice via near-infrared fluorescent protein iRFP720. <i>PLoS ONE</i> , 2019, 14, e0225213.	2.5	10
10	Live cell imaging of X chromosome reactivation during somatic cell reprogramming. <i>Biochemistry and Biophysics Reports</i> , 2018, 15, 86-92.	1.3	2
11	A Role for KLF4 in Promoting the Metabolic Shift via TCL1 during Induced Pluripotent Stem Cell Generation. <i>Stem Cell Reports</i> , 2017, 8, 787-801.	4.8	36
12	Simple and effective generation of transgene-free induced pluripotent stem cells using an auto-erasable Sendai virus vector responding to microRNA-302. <i>Stem Cell Research</i> , 2017, 23, 13-19.	0.7	56
13	BMP-SMAD-ID promotes reprogramming to pluripotency by inhibiting p16/INK4A-dependent senescence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13057-13062.	7.1	75
14	Association of the winged helix motif of the $\langle \text{scp} \rangle \text{TFIIE} \langle / \text{scp} \rangle \hat{\pm}$ subunit of $\langle \text{scp} \rangle \text{TFIIE} \langle / \text{scp} \rangle$ with either the $\langle \text{scp} \rangle \text{TFIIE} \langle / \text{scp} \rangle \hat{2}$ subunit or $\langle \text{scp} \rangle \text{TFIIB} \langle / \text{scp} \rangle$ distinguishes its functions in transcription. <i>Genes To Cells</i> , 2015, 20, 203-216.	1.2	3
15	The RNA Binding Complexes NF45-NF90 and NF45-NF110 Associate Dynamically with the c-fos Gene and Function as Transcriptional Coactivators. <i>Journal of Biological Chemistry</i> , 2015, 290, 26832-26845.	3.4	24
16	Manipulation of KLF4 Expression Generates iPSCs Paused at Successive Stages of Reprogramming. <i>Stem Cell Reports</i> , 2014, 3, 915-929.	4.8	42
17	The Paired-box Homeodomain Transcription Factor Pax6 Binds to the Upstream Region of the TRAP Gene Promoter and Suppresses Receptor Activator of NF- $\hat{\rho}$ B Ligand (RANKL)-induced Osteoclast Differentiation. <i>Journal of Biological Chemistry</i> , 2013, 288, 31299-31312.	3.4	20
18	Heterogeneous Nuclear Ribonucleoprotein R Cooperates with Mediator to Facilitate Transcription Reinitiation on the c-Fos Gene. <i>PLoS ONE</i> , 2013, 8, e72496.	2.5	9

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19	cAMP-response Element-binding Protein (CREB) Controls MSK1-mediated Phosphorylation of Histone H3 at the c-fos Promoter in Vitro. <i>Journal of Biological Chemistry</i> , 2010, 285, 9390-9401.	3.4	30
20	Heterogeneous Nuclear Ribonucleoprotein R Enhances Transcription from the Naturally Configured c-fos Promoter in Vitro. <i>Journal of Biological Chemistry</i> , 2009, 284, 23472-23480.	3.4	21
21	DSIF, the Paf1 complex, and Tat-SF1 have nonredundant, cooperative roles in RNA polymerase II elongation. <i>Genes and Development</i> , 2009, 23, 2765-2777.	5.9	95
22	Arginine Methylation of FOXO Transcription Factors Inhibits Their Phosphorylation by Akt. <i>Molecular Cell</i> , 2008, 32, 221-231.	9.7	375
23	The Fission Yeast Protein Ker1p Is an Ortholog of RNA Polymerase I Subunit A14 in <i>Saccharomyces cerevisiae</i> and Is Required for Stable Association of Rrn3p and RPA21 in RNA Polymerase I. <i>Journal of Biological Chemistry</i> , 2005, 280, 11467-11474.	3.4	8
24	Transcriptional Coactivator PC4 Stimulates Promoter Escape and Facilitates Transcriptional Synergy by GAL4-VP16. <i>Molecular and Cellular Biology</i> , 2004, 24, 6525-6535.	2.3	37
25	Essential Role of p38 Mitogen-activated Protein Kinase in Cathepsin K Gene Expression during Osteoclastogenesis through Association of NFATc1 and PU.1. <i>Journal of Biological Chemistry</i> , 2004, 279, 45969-45979.	3.4	365
26	ABT1-associated protein (ABTAP), a novel nuclear protein conserved from yeast to mammals, represses transcriptional activation by ABT1. <i>Journal of Cellular Biochemistry</i> , 2004, 93, 788-806.	2.6	5
27	Alleviation of PC4-mediated Transcriptional Repression by the ERCC3 Helicase Activity of General Transcription Factor TFIIH. <i>Journal of Biological Chemistry</i> , 2003, 278, 14827-14831.	3.4	17
28	The fission yeast RPA51 is a functional homolog of the budding yeast A49 subunit of RNA polymerase I and required for maximizing transcription of ribosomal DNA. <i>Genes and Genetic Systems</i> , 2003, 78, 199-209.	0.7	15
29	The regulatory role for the ERCC3 helicase of general transcription factor TFIIH during promoter escape in transcriptional activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 1206-1211.	7.1	17
30	The fission yeast RPA21 subunit of RNA polymerase I: An evolutionarily conserved subunit interacting with ribosomal DNA (rDNA) transcription factor Rrn3p for recruitment to rDNA promoter.. <i>Genes and Genetic Systems</i> , 2002, 77, 147-157.	0.7	7
31	Reconstitution of recombinant TFIIH that can mediate activator-dependent transcription. <i>Genes To Cells</i> , 2001, 6, 707-719.	1.2	20
32	Regulation of Receptor Activator of NF- κ B Ligand-induced Tartrate-resistant Acid Phosphatase Gene Expression by PU.1-interacting Protein/Interferon Regulatory Factor-4. <i>Journal of Biological Chemistry</i> , 2001, 276, 33086-33092.	3.4	20
33	The Rpb6 Subunit of Fission Yeast RNA Polymerase II Is a Contact Target of the Transcription Elongation Factor TFIIIS. <i>Molecular and Cellular Biology</i> , 2000, 20, 1263-1270.	2.3	37
34	FACT Relieves DSIF/NELF-Mediated Inhibition of Transcriptional Elongation and Reveals Functional Differences between P-TEFb and TFIIH. <i>Molecular Cell</i> , 2000, 5, 1067-1072.	9.7	98
35	Crystal structure of a TFIIIB-TBP-TATA-element ternary complex. <i>Nature</i> , 1995, 377, 119-128.	27.8	543
36	Functional dissection of TFIIIB domains required for TFIIIB-TFIID-promoter complex formation and basal transcription activity. <i>Nature</i> , 1993, 363, 744-747.	27.8	85

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37	The p250 subunit of native TATA box-binding factor TFIID is the cell-cycle regulatory protein CCG1. Nature, 1993, 362, 179-181.	27.8	202
38	Structure of the core promoter of human and mouse ribosomal RNA gene. Journal of Molecular Biology, 1991, 218, 55-67.	4.2	14
39	Cloning and structural analysis of cDNA and the gene for mouse transcription factor UBF. Nucleic Acids Research, 1991, 19, 4631-4637.	14.5	82
40	Conserved structural motifs between xenopus and human TFIIB. Nucleic Acids Research, 1991, 19, 6639-6639.	14.5	21