

Shintaro Katayama

List of Publications by Year in descending order

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48
papers

12,060
citations

257450

24
h-index

206112

48
g-index

48
all docs

48
docs citations

48
times ranked

18269
citing authors

#	ARTICLE	IF	CITATIONS
1	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	12.6	3,227
2	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	27.8	1,838
3	Antisense Transcription in the Mammalian Transcriptome. <i>Science</i> , 2005, 309, 1564-1566.	12.6	1,553
4	Genome-wide analysis of mammalian promoter architecture and evolution. <i>Nature Genetics</i> , 2006, 38, 626-635.	21.4	1,201
5	Cap analysis gene expression for high-throughput analysis of transcriptional starting point and identification of promoter usage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15776-15781.	7.1	673
6	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 140, 744-752.	28.9	667
7	Experimental validation of the regulated expression of large numbers of non-coding RNAs from the mouse genome. <i>Genome Research</i> , 2005, 16, 11-19.	5.5	461
8	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	21.4	408
9	Androgen-responsive long noncoding RNA CTBP1-AS promotes prostate cancer. <i>EMBO Journal</i> , 2013, 32, 1665-1680.	7.8	243
10	The pruritus- and TH2-associated cytokine IL-31 promotes growth of sensory nerves. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 138, 500-508.e24.	2.9	201
11	Unamplified cap analysis of gene expression on a single-molecule sequencer. <i>Genome Research</i> , 2011, 21, 1150-1159.	5.5	172
12	Transcript Annotation in FANTOM3: Mouse Gene Catalog Based on Physical cDNAs. <i>PLoS Genetics</i> , 2006, 2, e62.	3.5	165
13	miR-148a is an androgen-responsive microRNA that promotes LNCaP prostate cell growth by repressing its target CAND1 expression. <i>Prostate Cancer and Prostatic Diseases</i> , 2010, 13, 356-361.	3.9	128
14	Transcriptional network dynamics in macrophage activation. <i>Genomics</i> , 2006, 88, 133-142.	2.9	125
15	Damaging heterozygous mutations in NFKB1 lead to diverse immunologic phenotypes. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 140, 782-796.	2.9	113
16	Integration of cap analysis of gene expression and chromatin immunoprecipitation analysis on array reveals genome-wide androgen receptor signaling in prostate cancer cells. <i>Oncogene</i> , 2011, 30, 619-630.	5.9	99
17	Single-cell transcriptome analysis of endometrial tissue. <i>Human Reproduction</i> , 2016, 31, 844-853.	0.9	95
18	The complexity of the mammalian transcriptome. <i>Journal of Physiology</i> , 2006, 575, 321-332.	2.9	91

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19	NET-CAGE characterizes the dynamics and topology of human transcribed cis-regulatory elements. <i>Nature Genetics</i> , 2019, 51, 1369-1379.	21.4	72
20	MANF protects human pancreatic beta cells against stress-induced cell death. <i>Diabetologia</i> , 2018, 61, 2202-2214.	6.3	66
21	Estrogen receptor $\hat{1}^2$, a regulator of androgen receptor signaling in the mouse ventral prostate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3816-E3822.	7.1	53
22	Comprehensive mapping of the effects of azacitidine on DNA methylation, repressive/permmissive histone marks and gene expression in primary cells from patients with MDS and MDS-related disease. <i>Oncotarget</i> , 2017, 8, 28812-28825.	1.8	42
23	Aberrant splicing of genes involved in haemoglobin synthesis and impaired terminal erythroid maturation in <i><i>SF</i>3B1</i> mutated refractory anaemia with ring sideroblasts. <i>British Journal of Haematology</i>, 2015, 171, 478-490.</i>	2.5	37
24	Single-cell RNA-seq analysis reveals the platinum resistance gene COX7B and the surrogate marker CD63. <i>Cancer Medicine</i> , 2018, 7, 6193-6204.	2.8	29
25	Differences in Gene Expression between Mouse and Human for Dynamically Regulated Genes in Early Embryo. <i>PLoS ONE</i> , 2014, 9, e102949.	2.5	25
26	Fetal HLA-G mediated immune tolerance and interferon response in preeclampsia. <i>EBioMedicine</i> , 2020, 59, 102872.	6.1	25
27	Construction of representative transcript and protein sets of human, mouse, and rat as a platform for their transcriptome and proteome analysis. <i>Genomics</i> , 2004, 84, 913-921.	2.9	23
28	Gene expression analysis of skin grafts and cultured keratinocytes using synthetic RNA normalization reveals insights into differentiation and growth control. <i>BMC Genomics</i> , 2015, 16, 476.	2.8	21
29	Branched-chain amino acid metabolism is regulated by ERR $\hat{1}\pm$ in primary human myotubes and is further impaired by glucose loading in type 2 diabetes. <i>Diabetologia</i> , 2021, 64, 2077-2091.	6.3	20
30	Identification of region-specific transcription factor genes in the adult mouse brain by medium-scale real-time RT-PCR. <i>FEBS Letters</i> , 2004, 573, 214-218.	2.8	18
31	Mlh1 deficiency in normal mouse colon mucosa associates with chromosomally unstable colon cancer. <i>Carcinogenesis</i> , 2018, 39, 788-797.	2.8	18
32	Delineating the Healthy Human Skin UV Response and Early Induction of Interferon Pathway in Cutaneous Lupus Erythematosus. <i>Journal of Investigative Dermatology</i> , 2019, 139, 2058-2061.e4.	0.7	16
33	Cystatin B-deficiency triggers ectopic histone H3 tail cleavage during neurogenesis. <i>Neurobiology of Disease</i> , 2021, 156, 105418.	4.4	13
34	Integrated analysis of the genome and the transcriptome by FANTOM. <i>Briefings in Bioinformatics</i> , 2004, 5, 249-258.	6.5	12
35	Optimizing bone morphogenic protein 4-mediated human embryonic stem cell differentiation into trophoblast-like cells using fibroblast growth factor 2 and transforming growth factor- $\hat{1}^2$ /activin/nodal signalling inhibition. <i>Reproductive BioMedicine Online</i> , 2017, 35, 253-263.	2.4	11
36	Complement in Human Pre-implantation Embryos: Attack and Defense. <i>Frontiers in Immunology</i> , 2019, 10, 2234.	4.8	11

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37	Dyslexia Candidate Gene and Ciliary Gene Expression Dynamics During Human Neuronal Differentiation. <i>Molecular Neurobiology</i> , 2020, 57, 2944-2958.	4.0	11
38	Distinct whole-blood transcriptome profile of children with metabolic healthy overweight/obesity compared to metabolic unhealthy overweight/obesity. <i>Pediatric Research</i> , 2021, 89, 1687-1694.	2.3	10
39	Motor Function Deficits in the Estrogen Receptor Beta Knockout Mouse: Role on Excitatory Neurotransmission and Myelination in the Motor Cortex. <i>Neuroendocrinology</i> , 2021, 111, 27-44.	2.5	10
40	Guide for library design and bias correction for large-scale transcriptome studies using highly multiplexed RNAseq methods. <i>BMC Bioinformatics</i> , 2019, 20, 418.	2.6	9
41	Gene-Expression Profiling Suggests Impaired Signaling via the Interferon Pathway in <i>Cstb</i> ^{-/-} Microglia. <i>PLoS ONE</i> , 2016, 11, e0158195.	2.5	9
42	Nasal upregulation of <i>CST1</i> in dog-sensitised children with severe allergic airway disease. <i>ERJ Open Research</i> , 2021, 7, 00917-2020.	2.6	8
43	Embryonic LTR retrotransposons supply promoter modules to somatic tissues. <i>Genome Research</i> , 2021, 31, 1983-1993.	5.5	7
44	A preliminary transcriptome analysis suggests a transitory effect of vitamin D on mitochondrial function in obese young Finnish subjects. <i>Endocrine Connections</i> , 2019, 8, 559-570.	1.9	6
45	Differentiation of ciliated human midbrain-derived LUHMES neurons. <i>Journal of Cell Science</i> , 2020, 133, .	2.0	6
46	Generation of RNA sequencing libraries for transcriptome analysis of globin-rich tissues of the domestic dog. <i>STAR Protocols</i> , 2021, 2, 100995.	1.2	6
47	SkewC: Identifying cells with skewed gene body coverage in single-cell RNA sequencing data. <i>IScience</i> , 2022, 25, 103777.	4.1	4
48	Complex Transcription Mechanisms in Mammalian Genomes - The Transcriptome of FANTOM3. <i>Current Genomics</i> , 2005, 6, 619-625.	1.6	2