Shintaro Katayama

List of Publications by Year
in descending order

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	SkewC: Identifying cells with skewed gene body coverage in single-cell RNA sequencing data. IScience, 2022, 25, 103777.	4.1	4
2	Distinct whole-blood transcriptome profile of children with metabolic healthy overweight/obesity compared to metabolic unhealthy overweight/obesity. Pediatric Research, 2021, 89, 1687-1694.	2.3	10
3	Nasal upregulation of <i>CST1</i> in dog-sensitised children with severe allergic airway disease. ERJ Open Research, 2021, 7, 00917-2020.	2.6	8
4	Branched-chain amino acid metabolism is regulated by ERRÎ± in primary human myotubes and is further impaired by glucose loading in type 2 diabetes. Diabetologia, 2021, 64, 2077-2091.	6.3	20
5	Cystatin B-deficiency triggers ectopic histone H3 tail cleavage during neurogenesis. Neurobiology of Disease, 2021, 156, 105418.	4.4	13
6	Motor Function Deficits in the Estrogen Receptor Beta Knockout Mouse: Role on Excitatory Neurotransmission and Myelination in the Motor Cortex. Neuroendocrinology, 2021, 111, 27-44.	2.5	10
7	Embryonic LTR retrotransposons supply promoter modules to somatic tissues. Genome Research, 2021, 31, 1983-1993.	5.5	7
8	Generation of RNA sequencing libraries for transcriptome analysis of globin-rich tissues of the domestic dog. STAR Protocols, 2021, 2, 100995.	1.2	6
9	Fetal HLA-G mediated immune tolerance and interferon response in preeclampsia. EBioMedicine, 2020, 59, 102872.	6.1	25
10	Differentiation of ciliated human midbrain-derived LUHMES neurons. Journal of Cell Science, 2020, 133, .	2.0	6
11	Dyslexia Candidate Gene and Ciliary Gene Expression Dynamics During Human Neuronal Differentiation. Molecular Neurobiology, 2020, 57, 2944-2958.	4.0	11
12	Guide for library design and bias correction for large-scale transcriptome studies using highly multiplexed RNAseq methods. BMC Bioinformatics, 2019, 20, 418.	2.6	9
13	Delineating the Healthy Human Skin UV ResponseÂand Early Induction of Interferon PathwayÂin Cutaneous Lupus Erythematosus. Journal of Investigative Dermatology, 2019, 139, 2058-2061.e4.	0.7	16
14	NET-CAGE characterizes the dynamics and topology of human transcribed cis-regulatory elements. Nature Genetics, 2019, 51, 1369-1379.	21.4	72
15	Complement in Human Pre-implantation Embryos: Attack and Defense. Frontiers in Immunology, 2019, 10, 2234.	4.8	11
16	A preliminary transcriptome analysis suggests a transitory effect of vitamin D on mitochondrial function in obese young Finnish subjects. Endocrine Connections, 2019, 8, 559-570.	1.9	6
17	Mlh1 deficiency in normal mouse colon mucosa associates with chromosomally unstable colon cancer. Carcinogenesis, 2018, 39, 788-797.	2.8	18
18	Singleâ€cell RNAâ€seq analysis reveals the platinum resistance gene COX7B and the surrogate marker CD63. Cancer Medicine, 2018, 7, 6193-6204.	2.8	29

#	ARTICLE	IF	CITATIONS
19	MANF protects human pancreatic beta cells against stress-induced cell death. Diabetologia, 2018, 61, 2202-2214.	6.3	66
20	Damaging heterozygous mutations in NFKB1 lead to diverse immunologic phenotypes. Journal of Allergy and Clinical Immunology, 2017, 140, 782-796.	2.9	113
21	Estrogen receptor β, a regulator of androgen receptor signaling in the mouse ventral prostate. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E3816-E3822.	7.1	53
22	Optimizing bone morphogenic protein 4-mediated human embryonic stem cell differentiation into trophoblast-like cells using fibroblast growth factor 2 and transforming growth factor-β/activin/nodal signalling inhibition. Reproductive BioMedicine Online, 2017, 35, 253-263.	2.4	11
23	Comprehensive mapping of the effects of azacitidine on DNA methylation, repressive/permissive histone marks and gene expression in primary cells from patients with MDS and MDS-related disease. Oncotarget, 2017, 8, 28812-28825.	1.8	42
24	The pruritus- and TH2-associated cytokine IL-31 promotes growth of sensory nerves. Journal of Allergy and Clinical Immunology, 2016, 138, 500-508.e24.	2.9	201
25	Single-cell transcriptome analysis of endometrial tissue. Human Reproduction, 2016, 31, 844-853.	0.9	95
26	Gene-Expression Profiling Suggests Impaired Signaling via the Interferon Pathway in Cstb-/- Microglia. PLoS ONE, 2016, 11, e0158195.	2.5	9
27	Aberrant splicing of genes involved in haemoglobin synthesis and impaired terminal erythroid maturation in <i><scp>SF</scp>3B1</i> mutated refractory anaemia with ring sideroblasts. British Journal of Haematology, 2015, 171, 478-490.	2.5	37
28	Gene expression analysis of skin grafts and cultured keratinocytes using synthetic RNA normalization reveals insights into differentiation and growth control. BMC Genomics, 2015, 16, 476.	2.8	21
29	Differences in Gene Expression between Mouse and Human for Dynamically Regulated Genes in Early Embryo. PLoS ONE, 2014, 9, e102949.	2.5	25
30	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	27.8	1,838
31	Androgen-responsive long noncoding RNA CTBP1-AS promotes prostate cancer. EMBO Journal, 2013, 32, 1665-1680.	7.8	243
32	Unamplified cap analysis of gene expression on a single-molecule sequencer. Genome Research, 2011, 21, 1150-1159.	5.5	172
33	Integration of cap analysis of gene expression and chromatin immunoprecipitation analysis on array reveals genome-wide androgen receptor signaling in prostate cancer cells. Oncogene, 2011, 30, 619-630.	5.9	99
34	miR-148a is an androgen-responsive microRNA that promotes LNCaP prostate cell growth by repressing its target CAND1 expression. Prostate Cancer and Prostatic Diseases, 2010, 13, 356-361.	3.9	128
35	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. Cell, 2010, 140, 744-752.	28.9	667
36	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. Nature Genetics, 2009, 41, 553-562.	21.4	408

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37	Transcriptional network dynamics in macrophage activation. Genomics, 2006, 88, 133-142.	2.9	125
38	Genome-wide analysis of mammalian promoter architecture and evolution. Nature Genetics, 2006, 38, 626-635.	21.4	1,201
39	The complexity of the mammalian transcriptome. Journal of Physiology, 2006, 575, 321-332.	2.9	91
40	Transcript Annotation in FANTOM3: Mouse Gene Catalog Based on Physical cDNAs. PLoS Genetics, 2006, 2, e62.	3.5	165
41	Antisense Transcription in the Mammalian Transcriptome. Science, 2005, 309, 1564-1566.	12.6	1,553
42	Complex Transcription Mechanisms in Mammalian Genomes - The Transcriptome of FANTOM3. Current Genomics, 2005, 6, 619-625.	1.6	2
43	Experimental validation of the regulated expression of large numbers of non-coding RNAs from the mouse genome. Genome Research, 2005, 16, 11-19.	5.5	461
44	The Transcriptional Landscape of the Mammalian Genome. Science, 2005, 309, 1559-1563.	12.6	3,227
45	Integrated analysis of the genome and the transcriptome by FANTOM. Briefings in Bioinformatics, 2004, 5, 249-258.	6.5	12
46	Identification of region-specific transcription factor genes in the adult mouse brain by medium-scale real-time RT-PCR. FEBS Letters, 2004, 573, 214-218.	2.8	18
47	Construction of representative transcript and protein sets of human, mouse, and rat as a platform for their transcriptome and proteome analysis. Genomics, 2004, 84, 913-921.	2.9	23
48	Cap analysis gene expression for high-throughput analysis of transcriptional starting point and identification of promoter usage. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 15776-15781.	7.1	673