

# Yoshihide Hayashizaki

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2663339/publications.pdf>

Version: 2024-02-01

55  
papers

19,752  
citations

136950

32  
h-index

182427

51  
g-index

61  
all docs

61  
docs citations

61  
times ranked

30229  
citing authors

#	ARTICLE	IF	CITATIONS
1	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297.	12.8	11
2	<i>CREB3L1</i> overexpression as a potential diagnostic marker of Philadelphia chromosome-negative myeloproliferative neoplasms. <i>Cancer Science</i> , 2021, 112, 884-892.	3.9	10
3	CDK1 dependent phosphorylation of hTERT contributes to cancer progression. <i>Nature Communications</i> , 2020, 11, 1557.	12.8	38
4	BCL2A1: A Novel Target in Refractory Acute Myeloid Leukemia with FLT3-ITD/D835 Dual Mutations. <i>Blood</i> , 2020, 136, 32-33.	1.4	0
5	CREB3L1 Overexpression Can Reliably Discriminate Ph-MPNs from Reactive Cases. <i>Blood</i> , 2020, 136, 41-41.	1.4	0
6	NET-CAGE characterizes the dynamics and topology of human transcribed cis-regulatory elements. <i>Nature Genetics</i> , 2019, 51, 1369-1379.	21.4	72
7	MicroRNA-27a/b-3p and PPARC regulate SCAMP3 through a feed-forward loop during adipogenesis. <i>Scientific Reports</i> , 2019, 9, 13891.	3.3	17
8	Update of the FANTOM web resource: expansion to provide additional transcriptome atlases. <i>Nucleic Acids Research</i> , 2019, 47, D752-D758.	14.5	172
9	Eprobe mediated RT-qPCR for the detection of leukemia-associated fusion genes. <i>PLoS ONE</i> , 2018, 13, e0202429.	2.5	4
10	Bone Marrow Adipocytes Facilitate Fatty Acid Oxidation Activating AMPK and a Transcriptional Network Supporting Survival of Acute Monocytic Leukemia Cells. <i>Cancer Research</i> , 2017, 77, 1453-1464.	0.9	123
11	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017, 543, 199-204.	27.8	898
12	Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. <i>EBioMedicine</i> , 2017, 24, 257-266.	6.1	24
13	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017, 35, 872-878.	17.5	456
14	Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. <i>Nucleic Acids Research</i> , 2017, 45, D737-D743.	14.5	116
15	Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution. <i>Diabetes</i> , 2017, 66, 218-230.	0.6	27
16	<i>TSHR</i> Gene Polymorphisms in the Enhancer Regions Are Most Strongly Associated with the Development of Graves' Disease, Especially Intractable Disease, and of Hashimoto's Disease. <i>Thyroid</i> , 2017, 27, 111-119.	4.5	15
17	Next-generation sequencing-based small RNA profiling of cerebrospinal fluid exosomes. <i>Neuroscience Letters</i> , 2017, 636, 48-57.	2.1	93
18	Correlation of EGFR or KRAS mutation status with 18F-FDG uptake on PET-CT scan in lung adenocarcinoma. <i>PLoS ONE</i> , 2017, 12, e0175622.	2.5	20

#	ARTICLE	IF	CITATIONS
19	FANTOM5 transcriptome catalog of cellular states based on Semantic MediaWiki. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw105.	3.0	64
20	Enhanced Identification of Transcriptional Enhancers Provides Mechanistic Insights into Diseases. Trends in Genetics, 2016, 32, 76-88.	6.7	87
21	A predictive computational framework for direct reprogramming between human cell types. Nature Genetics, 2016, 48, 331-335.	21.4	263
22	Functional annotation of the vlinc class of non-coding RNAs using systems biology approach. Nucleic Acids Research, 2016, 44, 3233-3252.	14.5	31
23	Cap Analysis of Gene Expression (CAGE) Sequencing Reveals Alterations of the Transcriptional Signatures of FLT3-ITD with Secondary D835 TKD Mutations in Acute Myeloid Leukemia. Blood, 2016, 128, 1530-1530.	1.4	0
24	Promoter-level expression clustering identifies time development of transcriptional regulatory cascades initiated by ErbB receptors in breast cancer cells. Scientific Reports, 2015, 5, 11999.	3.3	30
25	Mapping Mammalian Cell-type-specific Transcriptional Regulatory Networks Using KD-CAGE and ChIP-seq Data in the TC-YIK Cell Line. Frontiers in Genetics, 2015, 6, 331.	2.3	13
26	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. Science, 2015, 347, 1010-1014.	12.6	517
27	Gateways to the FANTOM5 promoter level mammalian expression atlas. Genome Biology, 2015, 16, 22.	8.8	687
28	Transcriptional Dynamics Reveal Critical Roles for Non-coding RNAs in the Immediate-Early Response. PLoS Computational Biology, 2015, 11, e1004217.	3.2	22
29	Transcriptome analysis of controlled and therapy-resistant childhood asthma reveals distinct gene expression profiles. Journal of Allergy and Clinical Immunology, 2015, 136, 638-648.	2.9	59
30	Batf2/Irf1 Induces Inflammatory Responses in Classically Activated Macrophages, Lipopolysaccharides, and Mycobacterial Infection. Journal of Immunology, 2015, 194, 6035-6044.	0.8	83
31	Technical Advance: Transcription factor, promoter, and enhancer utilization in human myeloid cells. Journal of Leukocyte Biology, 2015, 97, 985-995.	3.3	23
32	Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics. Nucleic Acids Research, 2015, 43, 6969-6982.	14.5	54
33	Complementing tissue characterization by integrating transcriptome profiling from the Human Protein Atlas and from the FANTOM5 consortium. Nucleic Acids Research, 2015, 43, 6787-6798.	14.5	94
34	Association between the EGFR or KRAS mutation status and the FDG-PET findings in surgically resected lung adenocarcinoma.. Journal of Clinical Oncology, 2015, 33, 7535-7535.	1.6	0
35	Cap Analysis of Gene Expression (CAGE) Sequencing Reveals Alterations of the Transcript Signatures in Acute Monocytic Leukemia Cells By Fatty Acid Oxidation Inhibition. Blood, 2015, 126, 3631-3631.	1.4	1
36	A transient disruption of fibroblastic transcriptional regulatory network facilitates trans<i>-differentiation. Nucleic Acids Research, 2014, 42, 8905-8913.	14.5	35

#	ARTICLE	IF	CITATIONS
37	PAPD5-mediated 3' adenylation and subsequent degradation of miR-21 is disrupted in proliferative disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11467-11472.	7.1	130
38	Interactive visualization and analysis of large-scale sequencing datasets using ZENBU. <i>Nature Biotechnology</i> , 2014, 32, 217-219.	17.5	163
39	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014, 507, 455-461.	27.8	2,269
40	Systemic identification of estrogen-regulated genes in breast cancer cells through cap analysis of gene expression mapping. <i>Biochemical and Biophysical Research Communications</i> , 2014, 447, 531-536.	2.1	14
41	CCL2 enhances pluripotency of human induced pluripotent stem cells by activating hypoxia related genes. <i>Scientific Reports</i> , 2014, 4, 5228.	3.3	21
42	MOIRAI: a compact workflow system for CAGE analysis. <i>BMC Bioinformatics</i> , 2014, 15, 144.	2.6	66
43	Detecting Expressed Genes Using CAGE. <i>Methods in Molecular Biology</i> , 2014, 1164, 67-85.	0.9	170
44	Adipose Tissue MicroRNAs as Regulators of CCL2 Production in Human Obesity. <i>Diabetes</i> , 2012, 61, 1986-1993.	0.6	263
45	Landscape of transcription in human cells. <i>Nature</i> , 2012, 489, 101-108.	27.8	4,484
46	One-Step Detection of the 2009 Pandemic Influenza A(H1N1) Virus by the RT-SmartAmp Assay and Its Clinical Validation. <i>PLoS ONE</i> , 2012, 7, e30236.	2.5	24
47	Unamplified cap analysis of gene expression on a single-molecule sequencer. <i>Genome Research</i> , 2011, 21, 1150-1159.	5.5	172
48	Linking promoters to functional transcripts in small samples with nanoCAGE and CAGEscan. <i>Nature Methods</i> , 2010, 7, 528-534.	19.0	152
49	TagDust—a program to eliminate artifacts from next generation sequencing data. <i>Bioinformatics</i> , 2009, 25, 2839-2840.	4.1	210
50	An RNA-dependent RNA polymerase formed by TERT and the RMRP RNA. <i>Nature</i> , 2009, 461, 230-235.	27.8	334
51	A code for transcription initiation in mammalian genomes. <i>Genome Research</i> , 2008, 18, 1-12.	5.5	237
52	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	27.8	4,709
53	Genome-wide analysis of mammalian promoter architecture and evolution. <i>Nature Genetics</i> , 2006, 38, 626-635.	21.4	1,201
54	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

#	ARTICLE	IF	CITATIONS
55	High-Efficiency Full-Length cDNA Cloning by Biotinylated CAP Trapper. <i>Genomics</i> , 1996, 37, 327-336.	2.9	297