

Yoshihide Hayashizaki

List of Publications by Year in descending order

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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	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
2	Landscape of transcription in human cells. <i>Nature</i> , 2012, 489, 101-108.	27.8	4,484
3	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014, 507, 455-461.	27.8	2,269
4	Genome-wide analysis of mammalian promoter architecture and evolution. <i>Nature Genetics</i> , 2006, 38, 626-635.	21.4	1,201
5	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017, 543, 199-204.	27.8	898
6	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015, 16, 22.	8.8	687
7	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
8	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , 2015, 347, 1010-1014.	12.6	517
9	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017, 35, 872-878.	17.5	456
10	An RNA-dependent RNA polymerase formed by TERT and the RMRP RNA. <i>Nature</i> , 2009, 461, 230-235.	27.8	334
11	High-Efficiency Full-Length cDNA Cloning by Biotinylated CAP Trapper. <i>Genomics</i> , 1996, 37, 327-336.	2.9	297
12	Adipose Tissue MicroRNAs as Regulators of CCL2 Production in Human Obesity. <i>Diabetes</i> , 2012, 61, 1986-1993.	0.6	263
13	A predictive computational framework for direct reprogramming between human cell types. <i>Nature Genetics</i> , 2016, 48, 331-335.	21.4	263
14	A code for transcription initiation in mammalian genomes. <i>Genome Research</i> , 2008, 18, 1-12.	5.5	237
15	TagDust—a program to eliminate artifacts from next generation sequencing data. <i>Bioinformatics</i> , 2009, 25, 2839-2840.	4.1	210
16	Unamplified cap analysis of gene expression on a single-molecule sequencer. <i>Genome Research</i> , 2011, 21, 1150-1159.	5.5	172
17	Update of the FANTOM web resource: expansion to provide additional transcriptome atlases. <i>Nucleic Acids Research</i> , 2019, 47, D752-D758.	14.5	172
18	Detecting Expressed Genes Using CAGE. <i>Methods in Molecular Biology</i> , 2014, 1164, 67-85.	0.9	170

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19	Interactive visualization and analysis of large-scale sequencing datasets using ZENBU. <i>Nature Biotechnology</i> , 2014, 32, 217-219.	17.5	163
20	Linking promoters to functional transcripts in small samples with nanoCAGE and CAGEscan. <i>Nature Methods</i> , 2010, 7, 528-534.	19.0	152
21	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
22	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
23	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
24	Complementing tissue characterization by integrating transcriptome profiling from the Human Protein Atlas and from the FANTOM5 consortium. <i>Nucleic Acids Research</i> , 2015, 43, 6787-6798.	14.5	94
25	Next-generation sequencing-based small RNA profiling of cerebrospinal fluid exosomes. <i>Neuroscience Letters</i> , 2017, 636, 48-57.	2.1	93
26	Enhanced Identification of Transcriptional Enhancers Provides Mechanistic Insights into Diseases. <i>Trends in Genetics</i> , 2016, 32, 76-88.	6.7	87
27	Batf2/Irf1 Induces Inflammatory Responses in Classically Activated Macrophages, Lipopolysaccharides, and Mycobacterial Infection. <i>Journal of Immunology</i> , 2015, 194, 6035-6044.	0.8	83
28	NET-CAGE characterizes the dynamics and topology of human transcribed cis-regulatory elements. <i>Nature Genetics</i> , 2019, 51, 1369-1379.	21.4	72
29	MOIRAI: a compact workflow system for CAGE analysis. <i>BMC Bioinformatics</i> , 2014, 15, 144.	2.6	66
30	FANTOM5 transcriptome catalog of cellular states based on Semantic MediaWiki. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw105.	3.0	64
31	Transcriptome analysis of controlled and therapy-resistant childhood asthma reveals distinct gene expression profiles. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 136, 638-648.	2.9	59
32	Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics. <i>Nucleic Acids Research</i> , 2015, 43, 6969-6982.	14.5	54
33	CDK1 dependent phosphorylation of hTERT contributes to cancer progression. <i>Nature Communications</i> , 2020, 11, 1557.	12.8	38
34	A transient disruption of fibroblastic transcriptional regulatory network facilitates trans-differentiation. <i>Nucleic Acids Research</i> , 2014, 42, 8905-8913.	14.5	35
35	Functional annotation of the vlinc class of non-coding RNAs using systems biology approach. <i>Nucleic Acids Research</i> , 2016, 44, 3233-3252.	14.5	31
36	Promoter-level expression clustering identifies time development of transcriptional regulatory cascades initiated by ErbB receptors in breast cancer cells. <i>Scientific Reports</i> , 2015, 5, 11999.	3.3	30

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37	Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution. <i>Diabetes</i> , 2017, 66, 218-230.	0.6	27
38	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
39	Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. <i>EBioMedicine</i> , 2017, 24, 257-266.	6.1	24
40	Technical Advance: Transcription factor, promoter, and enhancer utilization in human myeloid cells. <i>Journal of Leukocyte Biology</i> , 2015, 97, 985-995.	3.3	23
41	Transcriptional Dynamics Reveal Critical Roles for Non-coding RNAs in the Immediate-Early Response. <i>PLoS Computational Biology</i> , 2015, 11, e1004217.	3.2	22
42	CCL2 enhances pluripotency of human induced pluripotent stem cells by activating hypoxia related genes. <i>Scientific Reports</i> , 2014, 4, 5228.	3.3	21
43	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
44	MicroRNA-27a/b-3p and PPAR γ regulate SCAMP3 through a feed-forward loop during adipogenesis. <i>Scientific Reports</i> , 2019, 9, 13891.	3.3	17
45	<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
46	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
47	Mapping Mammalian Cell-type-specific Transcriptional Regulatory Networks Using KD-CAGE and ChIP-seq Data in the TC-YIK Cell Line. <i>Frontiers in Genetics</i> , 2015, 6, 331.	2.3	13
48	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297.	12.8	11
49	<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
50	Eprobe mediated RT-qPCR for the detection of leukemia-associated fusion genes. <i>PLoS ONE</i> , 2018, 13, e0202429.	2.5	4
51	Cap Analysis of Gene Expression (CAGE) Sequencing Reveals Alterations of the Transcript Signatures in Acute Monocytic Leukemia Cells By Fatty Acid Oxidation Inhibition. <i>Blood</i> , 2015, 126, 3631-3631.	1.4	1
52	Association between the EGFR or KRAS mutation status and the FDG-PET findings in surgically resected lung adenocarcinoma. <i>Journal of Clinical Oncology</i> , 2015, 33, 7535-7535.	1.6	0
53	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. <i>Blood</i> , 2016, 128, 1530-1530.	1.4	0
54	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

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55	CREB3L1 Overexpression Can Reliably Discriminate Ph-MPNs from Reactive Cases. Blood, 2020, 136, 41-41.	1.4	0