

Harukazu Suzuki

List of Publications by Year in descending order

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156
papers

24,534
citations

24978

57
h-index

7931

149
g-index

178
all docs

178
docs citations

178
times ranked

32002
citing authors

#	ARTICLE	IF	CITATIONS
1	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014, 507, 455-461.	13.7	2,269
2	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	13.7	1,838
3	Antisense Transcription in the Mammalian Transcriptome. <i>Science</i> , 2005, 309, 1564-1566.	6.0	1,553
4	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002, 420, 563-573.	13.7	1,548
5	Genome-wide analysis of mammalian promoter architecture and evolution. <i>Nature Genetics</i> , 2006, 38, 626-635.	9.4	1,201
6	Structural parts involved in activation and inactivation of the sodium channel. <i>Nature</i> , 1989, 339, 597-603.	13.7	1,184
7	Existence of distinct sodium channel messenger RNAs in rat brain. <i>Nature</i> , 1986, 320, 188-192.	13.7	945
8	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017, 543, 199-204.	13.7	898
9	The regulated retrotransposon transcriptome of mammalian cells. <i>Nature Genetics</i> , 2009, 41, 563-571.	9.4	731
10	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 140, 744-752.	13.5	667
11	Functional annotation of a full-length mouse cDNA collection. <i>Nature</i> , 2001, 409, 685-690.	13.7	653
12	High-Throughput Mapping of a Dynamic Signaling Network in Mammalian Cells. <i>Science</i> , 2005, 307, 1621-1625.	6.0	651
13	Expression of functional sodium channels from cloned cDNA. <i>Nature</i> , 1986, 322, 826-828.	13.7	525
14	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , 2015, 347, 1010-1014.	6.0	517
15	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.	2.4	461
16	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	9.4	408
17	Conservation and divergence in Toll-like receptor 4-regulated gene expression in primary human versus mouse macrophages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E944-53.	3.3	332
18	Tiny RNAs associated with transcription start sites in animals. <i>Nature Genetics</i> , 2009, 41, 572-578.	9.4	327

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19	A single point mutation confers tetrodotoxin and saxitoxin insensitivity on the sodium channel II. <i>FEBS Letters</i> , 1989, 259, 213-216.	1.3	321
20	A comprehensive survey of 3'â€² animal miRNA modification events and a possible role for 3'â€² adenylation in modulating miRNA targeting effectiveness. <i>Genome Research</i> , 2010, 20, 1398-1410.	2.4	309
21	Primary structure of the $\hat{\pm}$ -subunit of transducin and its relationship to ras proteins. <i>Nature</i> , 1985, 315, 242-245.	13.7	307
22	Complex Loci in Human and Mouse Genomes. <i>PLoS Genetics</i> , 2006, 2, e47.	1.5	290
23	Deep-sequencing of human Argonaute-associated small RNAs provides insight into miRNA sorting and reveals Argonaute association with RNA fragments of diverse origin. <i>RNA Biology</i> , 2011, 8, 158-177.	1.5	273
24	Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. <i>Nature Genetics</i> , 2014, 46, 558-566.	9.4	271
25	A predictive computational framework for direct reprogramming between human cell types. <i>Nature Genetics</i> , 2016, 48, 331-335.	9.4	263
26	Statin Therapy Reduces the Mycobacterium tuberculosis Burden in Human Macrophages and in Mice by Enhancing Autophagy and Phagosome Maturation. <i>Journal of Infectious Diseases</i> , 2014, 209, 754-763.	1.9	245
27	LPS regulates proinflammatory gene expression in macrophages by altering histone deacetylase expression. <i>FASEB Journal</i> , 2006, 20, 1315-1327.	0.2	210
28	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , 2017, 4, 170112.	2.4	195
29	Transcription and enhancer profiling in human monocyte subsets. <i>Blood</i> , 2014, 123, e90-e99.	0.6	157
30	Functional expression of cloned cDNA encoding sodium channel III. <i>FEBS Letters</i> , 1988, 228, 195-200.	1.3	149
31	Clusters of Internally Primed Transcripts Reveal Novel Long Noncoding RNAs. <i>PLoS Genetics</i> , 2006, 2, e37.	1.5	148
32	A genome-wide and nonredundant mouse transcription factor database. <i>Biochemical and Biophysical Research Communications</i> , 2004, 322, 787-793.	1.0	137
33	PAPD5-mediated 3'â€² 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.	3.3	130
34	Interaction generality, a measurement to assess the reliability of a protein-protein interaction. <i>Nucleic Acids Research</i> , 2002, 30, 1163-1168.	6.5	128
35	Cross-mapping and the identification of editing sites in mature microRNAs in high-throughput sequencing libraries. <i>Genome Research</i> , 2010, 20, 257-264.	2.4	126
36	Transcriptional network dynamics in macrophage activation. <i>Genomics</i> , 2006, 88, 133-142.	1.3	125

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37	Doc2: A Novel Brain Protein Having Two Repeated C2-like Domains. <i>Biochemical and Biophysical Research Communications</i> , 1995, 206, 439-448.	1.0	123
38	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	2.4	109
39	Construction of reliable protein-protein interaction networks with a new interaction generality measure. <i>Bioinformatics</i> , 2003, 19, 756-763.	1.8	108
40	C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution. <i>Nature Communications</i> , 2019, 10, 360.	5.8	102
41	Protein-Protein Interaction Panel Using Mouse Full-Length cDNAs. <i>Genome Research</i> , 2001, 11, 1758-1765.	2.4	100
42	Next-generation sequencing-based small RNA profiling of cerebrospinal fluid exosomes. <i>Neuroscience Letters</i> , 2017, 636, 48-57.	1.0	93
43	Transcriptional landscape of <i>Mycobacterium tuberculosis</i> infection in macrophages. <i>Scientific Reports</i> , 2018, 8, 6758.	1.6	92
44	Transcriptional features of genomic regulatory blocks. <i>Genome Biology</i> , 2009, 10, R38.	13.9	90
45	Enhanced Identification of Transcriptional Enhancers Provides Mechanistic Insights into Diseases. <i>Trends in Genetics</i> , 2016, 32, 76-88.	2.9	87
46	The PDZ Protein Tax-interacting Protein-1 Inhibits β -Catenin Transcriptional Activity and Growth of Colorectal Cancer Cells. <i>Journal of Biological Chemistry</i> , 2003, 278, 38758-38764.	1.6	86
47	Data-driven normalization strategies for high-throughput quantitative RT-PCR. <i>BMC Bioinformatics</i> , 2009, 10, 110.	1.2	86
48	Batf2/Irf1 Induces Inflammatory Responses in Classically Activated Macrophages, Lipopolysaccharides, and Mycobacterial Infection. <i>Journal of Immunology</i> , 2015, 194, 6035-6044.	0.4	83
49	The enhancer and promoter landscape of human regulatory and conventional T-cell subpopulations. <i>Blood</i> , 2014, 123, e68-e78.	0.6	77
50	Identification of a Novel Kinase-like Gene Induced during Neuronal Cell Death. <i>Biochemical and Biophysical Research Communications</i> , 1999, 258, 260-264.	1.0	73
51	The FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. <i>Genome Biology</i> , 2009, 10, R40.	13.9	73
52	LRRN4 and UPK3B Are Markers of Primary Mesothelial Cells. <i>PLoS ONE</i> , 2011, 6, e25391.	1.1	71
53	CDS Annotation in Full-Length cDNA Sequence. <i>Genome Research</i> , 2003, 13, 1478-1487.	2.4	69
54	Predicting 5-fluorouracil chemosensitivity of liver metastases from colorectal cancer using primary tumor specimens: Three-gene expression model predicts clinical response. <i>International Journal of Cancer</i> , 2006, 119, 406-413.	2.3	68

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55	FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. <i>Genome Biology</i> , 2009, 10, R39.	13.9	67
56	Deciphering the transcriptional circuitry of microRNA genes expressed during human monocytic differentiation. <i>BMC Genomics</i> , 2009, 10, 595.	1.2	65
57	Combinatorial perturbation analysis reveals divergent regulations of mesenchymal genes during epithelial-to-mesenchymal transition. <i>Npj Systems Biology and Applications</i> , 2019, 5, 21.	1.4	65
58	RUNX1 regulates site specificity of DNA demethylation by recruitment of DNA demethylation machineries in hematopoietic cells. <i>Blood Advances</i> , 2017, 1, 1699-1711.	2.5	64
59	Genome-wide investigation of in vivo EGR-1 binding sites in monocytic differentiation. <i>Genome Biology</i> , 2009, 10, R41.	13.9	62
60	Global analysis of pre-mRNA subcellular localization following splicing inhibition by spliceostatin A. <i>Rna</i> , 2017, 23, 47-57.	1.6	61
61	T2BP, a Novel TRAF2 Binding Protein, Can Activate NF- κ B and AP-1 without TNF Stimulation. <i>Biochemical and Biophysical Research Communications</i> , 2002, 290, 1108-1113.	1.0	60
62	LPS regulates a set of genes in primary murine macrophages by antagonising CSF-1 action. <i>Immunobiology</i> , 2005, 210, 97-107.	0.8	58
63	Reversible hydrogel formation driven by protein-peptide specific interaction and chondrocyte entrapment. <i>Biomaterials</i> , 2010, 31, 58-66.	5.7	55
64	Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics. <i>Nucleic Acids Research</i> , 2015, 43, 6969-6982.	6.5	54
65	Gemin2 Plays an Important Role in Stabilizing the Survival of Motor Neuron Complex*. <i>Journal of Biological Chemistry</i> , 2007, 282, 11122-11134.	1.6	51
66	Solution structure of a BOLA-like protein from <i>Mus musculus</i> . <i>Protein Science</i> , 2004, 13, 545-548.	3.1	49
67	Update of the FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. <i>Nucleic Acids Research</i> , 2011, 39, D856-D860.	6.5	49
68	A screening system to identify transcription factors that induce binding site-directed DNA demethylation. <i>Epigenetics and Chromatin</i> , 2017, 10, 60.	1.8	48
69	Ligand-specific sequential regulation of transcription factors for differentiation of MCF-7 cells. <i>BMC Genomics</i> , 2009, 10, 545.	1.2	45
70	Temporal dynamics and transcriptional control using single-cell gene expression analysis. <i>Genome Biology</i> , 2013, 14, R118.	13.9	43
71	Genome-wide profiling of transcribed enhancers during macrophage activation. <i>Epigenetics and Chromatin</i> , 2017, 10, 50.	1.8	41
72	Nuclear Pore Complex Protein Mediated Nuclear Localization of Dicer Protein in Human Cells. <i>PLoS ONE</i> , 2011, 6, e23385.	1.1	40

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73	Simvastatin Enhances Protection against <i>Listeria monocytogenes</i> Infection in Mice by Counteracting Listeria-Induced Phagosomal Escape. <i>PLoS ONE</i> , 2013, 8, e75490.	1.1	39
74	NF- κ B activator Act1 associates with IL-1/Toll pathway adaptor molecule TRAF6. <i>FEBS Letters</i> , 2002, 532, 241-246.	1.3	38
75	OVOL2 induces mesenchymal-to-epithelial transition in fibroblasts and enhances cell-state reprogramming towards epithelial lineages. <i>Scientific Reports</i> , 2019, 9, 6490.	1.6	38
76	Differential Targeting of c-Maf, Bach-1, and Elmo-1 by microRNA-143 and microRNA-365 Promotes the Intracellular Growth of <i>Mycobacterium tuberculosis</i> in Alternatively IL-4/IL-13 Activated Macrophages. <i>Frontiers in Immunology</i> , 2019, 10, 421.	2.2	37
77	Stac, a Novel Neuron-Specific Protein with Cysteine-Rich and SH3 Domains. <i>Biochemical and Biophysical Research Communications</i> , 1996, 229, 902-909.	1.0	36
78	Reconstruction of Monocyte Transcriptional Regulatory Network Accompanies Monocytic Functions in Human Fibroblasts. <i>PLoS ONE</i> , 2012, 7, e33474.	1.1	36
79	A transient disruption of fibroblastic transcriptional regulatory network facilitates <i>trans</i> -differentiation. <i>Nucleic Acids Research</i> , 2014, 42, 8905-8913.	6.5	35
80	Recounting the FANTOM CAGE-Associated Transcriptome. <i>Genome Research</i> , 2020, 30, 1073-1081.	2.4	35
81	Core promoter structure and genomic context reflect histone 3 lysine 9 acetylation patterns. <i>BMC Genomics</i> , 2010, 11, 257.	1.2	34
82	Restriction landmark cDNA scanning (RLCS): a novel cDNA display system using two-dimensional gel electrophoresis. <i>Nucleic Acids Research</i> , 1996, 24, 289-294.	6.5	33
83	Reduction of non-insert sequence reads by dimer eliminator LNA oligonucleotide for small RNA deep sequencing. <i>BioTechniques</i> , 2010, 49, 751-755.	0.8	32
84	Identification of ZNF395 as a novel modulator of adipogenesis. <i>Experimental Cell Research</i> , 2013, 319, 68-76.	1.2	32
85	The combination of gene perturbation assay and ChIP-chip reveals functional direct target genes for IRF8 in THP-1 cells. <i>Molecular Immunology</i> , 2010, 47, 2295-2302.	1.0	31
86	Targeting Batf2 for infectious diseases and cancer. <i>Oncotarget</i> , 2015, 6, 26575-26582.	0.8	31
87	Primary structure of the virus activating protease: from chick embryo Its identity with the blood clotting factor Xa. <i>FEBS Letters</i> , 1991, 283, 281-285.	1.3	30
88	Constructing ORFeome resources with removable termination codons. <i>BioTechniques</i> , 2006, 41, 44-50.	0.8	30
89	High-resolution analysis of aberrant regions in autosomal chromosomes in human leukemia THP-1 cell line. <i>BMC Research Notes</i> , 2009, 2, 153.	0.6	30
90	Towards defining the nuclear proteome. <i>Genome Biology</i> , 2008, 9, R15.	13.9	29

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91	Development of a DNA barcode tagging method for monitoring dynamic changes in gene expression by using an ultra high-throughput sequencer. <i>BioTechniques</i> , 2008, 45, 95-97.	0.8	29
92	A framework for identification of on- and off-target transcriptional responses to drug treatment. <i>Scientific Reports</i> , 2019, 9, 17603.	1.6	29
93	Single-Nucleotide Resolution Mapping of Hepatitis B Virus Promoters in Infected Human Livers and Hepatocellular Carcinoma. <i>Journal of Virology</i> , 2016, 90, 10811-10822.	1.5	27
94	Fungus-Derived Neoechinulin B as a Novel Antagonist of Liver X Receptor, Identified by Chemical Genetics Using a Hepatitis C Virus Cell Culture System. <i>Journal of Virology</i> , 2016, 90, 9058-9074.	1.5	27
95	Molecular cloning of rat GADD45 ¹³ , gene induction and its role during neuronal cell death. <i>FEBS Letters</i> , 1999, 446, 313-317.	1.3	25
96	Force Measurement for Antigen-Antibody Interaction by Atomic Force Microscopy Using a Photograft-Polymer Spacer. <i>Biomacromolecules</i> , 2005, 6, 2776-2784.	2.6	25
97	Accessibility to tissue-specific genes from methylation profiles of mouse brain genomic DNA. <i>Electrophoresis</i> , 1995, 16, 218-226.	1.3	24
98	Dynamic Force Spectroscopy of the Specific Interaction between the PDZ Domain and Its Recognition Peptides. <i>Langmuir</i> , 2007, 23, 2668-2673.	1.6	24
99	Nanoscale elongating control of the self-assembled protein filament with the cysteine-introduced building blocks. <i>Protein Science</i> , 2009, 18, 960-969.	3.1	24
100	Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. <i>EBioMedicine</i> , 2017, 24, 257-266.	2.7	24
101	Genomic analysis of a NF1-related pseudogene on human chromosome 21. <i>Gene</i> , 1994, 147, 277-280.	1.0	23
102	A spot cloning method for restriction landmark genomic scanning. <i>Electrophoresis</i> , 1995, 16, 203-209.	1.3	23
103	The Mammalian Protein-Protein Interaction Database and Its Viewing System That Is Linked to the Main FANTOM2 Viewer. <i>Genome Research</i> , 2003, 13, 1534-1541.	2.4	23
104	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.	1.3	23
105	IL-4-Dependent Alternative Activation of Macrophages Is Not Decisive for Mycobacterium tuberculosis Pathology and Bacterial Burden in Mice. <i>PLoS ONE</i> , 2015, 10, e0121070.	1.1	23
106	Two-step cleavage of hairpin RNA with 5' overhangs by human DICER. <i>BMC Molecular Biology</i> , 2011, 12, 6.	3.0	21
107	CCL2 enhances pluripotency of human induced pluripotent stem cells by activating hypoxia related genes. <i>Scientific Reports</i> , 2014, 4, 5228.	1.6	21
108	Role of Survival Motor Neuron Complex Components in Small Nuclear Ribonucleoprotein Assembly. <i>Journal of Biological Chemistry</i> , 2009, 284, 14609-14617.	1.6	20

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109	Subcellular Localization of Mammalian Type II Membrane Proteins. <i>Traffic</i> , 2006, 7, 613-625.	1.3	19
110	Batf2 differentially regulates tissue immunopathology in Type 1 and Type 2 diseases. <i>Mucosal Immunology</i> , 2019, 12, 390-402.	2.7	19
111	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.	1.3	18
112	PhosphoregDB: the tissue and sub-cellular distribution of mammalian protein kinases and phosphatases. <i>BMC Bioinformatics</i> , 2006, 7, 82.	1.2	18
113	Solution Structure of the Mouse Enhancer of Rudimentary Protein Reveals a Novel Fold. <i>Journal of Biomolecular NMR</i> , 2005, 32, 329-334.	1.6	17
114	Building promoter aware transcriptional regulatory networks using siRNA perturbation and deepCAGE. <i>Nucleic Acids Research</i> , 2010, 38, 8141-8148.	6.5	17
115	CC Chemokine Ligand 2 and Leukemia Inhibitory Factor Cooperatively Promote Pluripotency in Mouse Induced Pluripotent Cells. <i>Stem Cells</i> , 2011, 29, 1196-1205.	1.4	17
116	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease. <i>PLoS Computational Biology</i> , 2018, 14, e1005934.	1.5	17
117	Protein-protein interactions in the mammalian brain. <i>Journal of Physiology</i> , 2006, 575, 373-377.	1.3	16
118	Transcriptionally induced enhancers in the macrophage immune response to <i>Mycobacterium tuberculosis</i> infection. <i>BMC Genomics</i> , 2019, 20, 71.	1.2	16
119	Inferring Higher Functional Information for RIKEN Mouse Full-Length cDNA Clones With FACTS. <i>Genome Research</i> , 2003, 13, 1520-1533.	2.4	14
120	Scanning gene expression during neuronal cell death evoked by nerve growth factor depletion. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1999, 1489, 293-302.	2.4	13
121	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.	1.1	13
122	Protein-protein interactions of the hyperthermophilic archaeon <i>Pyrococcus horikoshii</i> OT3. <i>Genome Biology</i> , 2005, 6, R98.	13.9	12
123	IRNdb: the database of immunologically relevant non-coding RNAs. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw138.	1.4	12
124	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297.	5.8	11
125	Establishment of single-cell screening system for the rapid identification of transcriptional modulators involved in direct cell reprogramming. <i>Nucleic Acids Research</i> , 2012, 40, e165-e165.	6.5	10
126	Transcriptome analysis reveals inadequate spermatogenesis and immediate radical immune reactions during organ culture in vitro spermatogenesis. <i>Biochemical and Biophysical Research Communications</i> , 2020, 530, 732-738.	1.0	10

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127	Improved restriction landmark cDNA scanning and its application to global analysis of genes regulated by nerve growth factor in PC12 cells. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1998, 1399, 10-18.	2.4	9
128	Expression analysis of genes responsible for serotonin signaling in the brain. <i>Neurobiology of Disease</i> , 2005, 19, 378-385.	2.1	9
129	An exon-trapping system with a newly constructed trapping vector pEXT2; its application to the proximal region of the human chromosome 21 long arm. <i>FEBS Letters</i> , 1993, 325, 303-308.	1.3	8
130	Correspondence of RLGS-M Spot Behavior with Tissue Expression on Mouse Homologue of DP1/TB2 Gene. <i>Biochemical and Biophysical Research Communications</i> , 1995, 213, 967-974.	1.0	8
131	Spliceostatin A interaction with SF3B limits U1 snRNP availability and causes premature cleavage and polyadenylation. <i>Cell Chemical Biology</i> , 2021, 28, 1356-1365.e4.	2.5	8
132	Evaluation of Berberine as an Adjunct to TB Treatment. <i>Frontiers in Immunology</i> , 2021, 12, 656419.	2.2	8
133	Human and Mouse Chromosomal Mapping of Stac, a Neuron-Specific Protein with an SH3 Domain. <i>Genomics</i> , 1998, 47, 140-142.	1.3	7
134	RUNX1 induces DNA replication independent active DNA demethylation at SPI1 regulatory regions. <i>BMC Molecular Biology</i> , 2017, 18, 9.	3.0	7
135	GATA6 is predicted to regulate DNA methylation in an in vitro model of human hepatocyte differentiation. <i>Communications Biology</i> , 2022, 5, 414.	2.0	7
136	In vitro pull-down assay without expression constructs. <i>BioTechniques</i> , 2004, 37, 918-920.	0.8	6
137	Integrative Genome-Wide Expression Analysis Bears Evidence of Estrogen Receptor-Independent Transcription in Heregulin-Stimulated MCF-7 Cells. <i>PLoS ONE</i> , 2008, 3, e1803.	1.1	6
138	CpG site-specific alteration of hydroxymethylcytosine to methylcytosine beyond DNA replication. <i>Biochemical and Biophysical Research Communications</i> , 2012, 426, 141-147.	1.0	6
139	Genome-scale regression analysis reveals a linear relationship for promoters and enhancers after combinatorial drug treatment. <i>Bioinformatics</i> , 2017, 33, 3696-3700.	1.8	6
140	TrkB mutant lacking the amino-terminal half of the extracellular portion acts as a functional brain-derived neurotrophic factor receptor. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1999, 1420, 104-110.	1.4	5
141	Development of a high-throughput method for the systematic identification of human proteins nuclear translocation potential. <i>BMC Cell Biology</i> , 2009, 10, 69.	3.0	5
142	Prediction of human cDNA from its homologous mouse full-length cDNA and human shotgun database. <i>FEBS Letters</i> , 1999, 464, 129-132.	1.3	4
143	Loss of variation of state detected in soybean metabolic and human myelomonocytic leukaemia cell transcriptional networks under external stimuli. <i>Scientific Reports</i> , 2016, 6, 35946.	1.6	4
144	A Transcriptional Switch Point During Hematopoietic Stem and Progenitor Cell Ontogeny. <i>Stem Cells and Development</i> , 2017, 26, 314-327.	1.1	4

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145	SkewC: Identifying cells with skewed gene body coverage in single-cell RNA sequencing data. <i>IScience</i> , 2022, 25, 103777.	1.9	4
146	Prediction of transcription factors associated with DNA demethylation during human cellular development. <i>Chromosome Research</i> , 2022, 30, 109-121.	1.0	4
147	System-wide analysis of the transcriptional network of human myelomonocytic leukemia cells predicts attractor structure and phorbol-ester-induced differentiation and dedifferentiation transitions. <i>Scientific Reports</i> , 2015, 5, 8283.	1.6	3
148	Asymmetric Regulation of Peripheral Genes by Two Transcriptional Regulatory Networks. <i>PLoS ONE</i> , 2016, 11, e0160459.	1.1	3
149	IL-4i1 Regulation of Immune Protection During <i>Mycobacterium tuberculosis</i> Infection. <i>Journal of Infectious Diseases</i> , 2021, 224, 2170-2180.	1.9	3
150	Global insights into protein complexes through integrated analysis of the reliable interactome and knockout lethality. <i>Biochemical and Biophysical Research Communications</i> , 2003, 301, 633-640.	1.0	2
151	RLCS, Restriction Landmark cDNA Scanning. , 1997, , 129-156.		1
152	Corrigendum to: Prediction of human cDNA from its homologous mouse full-length cDNA and human shotgun database. <i>FEBS Letters</i> , 2000, 471, 261-261.	1.3	0
153	Beyond the FANTOM4. <i>Genome Biology</i> , 2010, 11, O11.	13.9	0
154	Development of p53 knockout U87MG cell line for unbiased drug delivery testing system using CRISPR-Cas9 and transcriptomic analysis. <i>Journal of Biotechnology</i> , 2021, 332, 72-82.	1.9	0
155	Repositioning Monocyte TFRN into Fibroblasts. <i>Methods in Molecular Biology</i> , 2014, 1164, 211-218.	0.4	0
156	Direct reprogramming based on transcriptional regulatory network analysis. <i>Inflammation and Regeneration</i> , 2014, 34, 224-232.	1.5	0