Harukazu Suzuki

List of Publications by Year
in descending order

156 papers	24,534 citations	25034 57 h-index	7745 150 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. Nature, 2014, 507, 455-461.	27.8	2,269
2	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	27.8	1,838
3	Antisense Transcription in the Mammalian Transcriptome. Science, 2005, 309, 1564-1566.	12.6	1,553
4	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. Nature, 2002, 420, 563-573.	27.8	1,548
5	Genome-wide analysis of mammalian promoter architecture and evolution. Nature Genetics, 2006, 38, 626-635.	21.4	1,201
6	Structural parts involved in activation and inactivation of the sodium channel. Nature, 1989, 339, 597-603.	27.8	1,184
7	Existence of distinct sodium channel messenger RNAs in rat brain. Nature, 1986, 320, 188-192.	27.8	945
8	An atlas of human long non-coding RNAs with accurate 5â€² ends. Nature, 2017, 543, 199-204.	27.8	898
9	The regulated retrotransposon transcriptome of mammalian cells. Nature Genetics, 2009, 41, 563-571.	21.4	731
10	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. Cell, 2010, 140, 744-752.	28.9	667
11	Functional annotation of a full-length mouse cDNA collection. Nature, 2001, 409, 685-690.	27.8	653
12	High-Throughput Mapping of a Dynamic Signaling Network in Mammalian Cells. Science, 2005, 307, 1621-1625.	12.6	651
13	Expression of functional sodium channels from cloned cDNA. Nature, 1986, 322, 826-828.	27.8	525
14	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. Science, 2015, 347, 1010-1014.	12.6	517
15	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
16	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
17	Conservation and divergence in Toll-like receptor 4-regulated gene expression in primary human versus mouse macrophages. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E944-53.	7.1	332
18	Tiny RNAs associated with transcription start sites in animals. Nature Genetics, 2009, 41, 572-578.	21.4	327

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19	A single point mutation confers tetrodotoxin and saxitoxin insensitivity on the sodium channel II. FEBS Letters, 1989, 259, 213-216.	2.8	321
20	A comprehensive survey of 3′ animal miRNA modification events and a possible role for 3′ adenylation in modulating miRNA targeting effectiveness. Genome Research, 2010, 20, 1398-1410.	5.5	309
21	Primary structure of the Î±-subunit of transducin and its relationship to ras proteins. Nature, 1985, 315, 242-245.	27.8	307
22	Complex Loci in Human and Mouse Genomes. PLoS Genetics, 2006, 2, e47.	3.5	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. RNA Biology, 2011, 8, 158-177.	3.1	273
24	Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. Nature Genetics, 2014, 46, 558-566.	21.4	271
25	A predictive computational framework for direct reprogramming between human cell types. Nature Genetics, 2016, 48, 331-335.	21.4	263
26	Statin Therapy Reduces the Mycobacterium tuberculosis Burden in Human Macrophages and in Mice by Enhancing Autophagy and Phagosome Maturation. Journal of Infectious Diseases, 2014, 209, 754-763.	4.0	245
27	LPS regulates proinflammatory gene expression in macrophages by altering histone deacetylase expression. FASEB Journal, 2006, 20, 1315-1327.	0.5	210
28	FANTOM5 CAGE profiles of human and mouse samples. Scientific Data, 2017, 4, 170112.	5.3	195
29	Transcription and enhancer profiling in human monocyte subsets. Blood, 2014, 123, e90-e99.	1.4	157
30	Functional expression of cloned cDNA encoding sodium channel III. FEBS Letters, 1988, 228, 195-200.	2.8	149
31	Clusters of Internally Primed Transcripts Reveal Novel Long Noncoding RNAs. PLoS Genetics, 2006, 2, e37.	3.5	148
32	A genome-wide and nonredundant mouse transcription factor database. Biochemical and Biophysical Research Communications, 2004, 322, 787-793.	2.1	137
33	PAPD5-mediated 3′ adenylation and subsequent degradation of miR-21 is disrupted in proliferative disease. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11467-11472.	7.1	130
34	Interaction generality, a measurement to assess the reliability of a protein-protein interaction. Nucleic Acids Research, 2002, 30, 1163-1168.	14.5	128
35	Cross-mapping and the identification of editing sites in mature microRNAs in high-throughput sequencing libraries. Genome Research, 2010, 20, 257-264.	5.5	126
36	Transcriptional network dynamics in macrophage activation. Genomics, 2006, 88, 133-142.	2.9	125

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37	Doc2: A Novel Brain Protein Having Two Repeated C2-like Domains. Biochemical and Biophysical Research Communications, 1995, 206, 439-448.	2.1	123
38	Functional annotation of human long noncoding RNAs via molecular phenotyping. Genome Research, 2020, 30, 1060-1072.	5.5	109
39	Construction of reliable protein-protein interaction networks with a new interaction generality measure. Bioinformatics, 2003, 19, 756-763.	4.1	108
40	C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution. Nature Communications, 2019, 10, 360.	12.8	102
41	Protein-Protein Interaction Panel Using Mouse Full-Length cDNAs. Genome Research, 2001, 11, 1758-1765.	5.5	100
42	Next-generation sequencing-based small RNA profiling of cerebrospinal fluid exosomes. Neuroscience Letters, 2017, 636, 48-57.	2.1	93
43	Transcriptional landscape of Mycobacterium tuberculosis infection in macrophages. Scientific Reports, 2018, 8, 6758.	3.3	92
44	Transcriptional features of genomic regulatory blocks. Genome Biology, 2009, 10, R38.	9.6	90
45	Enhanced Identification of Transcriptional Enhancers Provides Mechanistic Insights into Diseases. Trends in Genetics, 2016, 32, 76-88.	6.7	87
46	The PDZ Protein Tax-interacting Protein-1 Inhibits Î²-Catenin Transcriptional Activity and Growth of Colorectal Cancer Cells. Journal of Biological Chemistry, 2003, 278, 38758-38764.	3.4	86
47	Data-driven normalization strategies for high-throughput quantitative RT-PCR. BMC Bioinformatics, 2009, 10, 110.	2.6	86
48	Batf2/Irf1 Induces Inflammatory Responses in Classically Activated Macrophages, Lipopolysaccharides, and Mycobacterial Infection. Journal of Immunology, 2015, 194, 6035-6044.	0.8	83
49	The enhancer and promoter landscape of human regulatory and conventional T-cell subpopulations. Blood, 2014, 123, e68-e78.	1.4	77
50	Identification of a Novel Kinase-like Gene Induced during Neuronal Cell Death. Biochemical and Biophysical Research Communications, 1999, 258, 260-264.	2.1	73
51	The FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. Genome Biology, 2009, 10, R40.	9.6	73
52	LRRN4 and UPK3B Are Markers of Primary Mesothelial Cells. PLoS ONE, 2011, 6, e25391.	2.5	71
53	CDS Annotation in Full-Length cDNA Sequence. Genome Research, 2003, 13, 1478-1487.	5.5	69
54	Predicting 5â€fluorouracil chemosensitivity of liver metastases from colorectal cancer using primary tumor specimens: Threeâ€gene expression model predicts clinical response. International Journal of Cancer, 2006, 119, 406-413.	5.1	68

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55	FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. Genome Biology, 2009, 10, R39.	9.6	67
56	Deciphering the transcriptional circuitry of microRNA genes expressed during human monocytic differentiation. BMC Genomics, 2009, 10, 595.	2.8	65
57	Combinatorial perturbation analysis reveals divergent regulations of mesenchymal genes during epithelial-to-mesenchymal transition. Npj Systems Biology and Applications, 2019, 5, 21.	3.0	65
58	RUNX1 regulates site specificity of DNA demethylation by recruitment of DNA demethylation machineries in hematopoietic cells. Blood Advances, 2017, 1, 1699-1711.	5.2	64
59	Genome-wide investigation of in vivo EGR-1 binding sites in monocytic differentiation. Genome Biology, 2009, 10, R41.	9.6	62
60	Global analysis of pre-mRNA subcellular localization following splicing inhibition by spliceostatin A. Rna, 2017, 23, 47-57.	3.5	61
61	T2BP, a Novel TRAF2 Binding Protein, Can Activate NF-κB and AP-1 without TNF Stimulation. Biochemical and Biophysical Research Communications, 2002, 290, 1108-1113.	2.1	60
62	LPS regulates a set of genes in primary murine macrophages by antagonising CSF-1 action. Immunobiology, 2005, 210, 97-107.	1.9	58
63	Reversible hydrogel formation driven by protein–peptide–specific interaction and chondrocyte entrapment. Biomaterials, 2010, 31, 58-66.	11.4	55
64	Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics. Nucleic Acids Research, 2015, 43, 6969-6982.	14.5	54
65	Gemin2 Plays an Important Role in Stabilizing the Survival of Motor Neuron Complex*. Journal of Biological Chemistry, 2007, 282, 11122-11134.	3.4	51
66	Solution structure of a BolA-like protein from Mus musculus. Protein Science, 2004, 13, 545-548.	7.6	49
67	Update of the FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. Nucleic Acids Research, 2011, 39, D856-D860.	14.5	49
68	A screening system to identify transcription factors that induce binding site-directed DNA demethylation. Epigenetics and Chromatin, 2017, 10, 60.	3.9	48
69	Ligand-specific sequential regulation of transcription factors for differentiation of MCF-7 cells. BMC Genomics, 2009, 10, 545.	2.8	45
70	Temporal dynamics and transcriptional control using single-cell gene expression analysis. Genome Biology, 2013, 14, R118.	9.6	43
71	Genome-wide profiling of transcribed enhancers during macrophage activation. Epigenetics and Chromatin, 2017, 10, 50.	3.9	41
72	Nuclear Pore Complex Protein Mediated Nuclear Localization of Dicer Protein in Human Cells. PLoS ONE, 2011, 6, e23385.	2.5	40

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73	Simvastatin Enhances Protection against Listeria monocytogenes Infection in Mice by Counteracting Listeria-Induced Phagosomal Escape. PLoS ONE, 2013, 8, e75490.	2.5	39
74	NF-ÎºB activator Act1 associates with IL-1/Toll pathway adaptor molecule TRAF6. FEBS Letters, 2002, 532, 241-246.	2.8	38
75	OVOL2 induces mesenchymal-to-epithelial transition in fibroblasts and enhances cell-state reprogramming towards epithelial lineages. Scientific Reports, 2019, 9, 6490.	3.3	38
76	Differential Targeting of c-Maf, Bach-1, and Elmo-1 by microRNA-143 and microRNA-365 Promotes the Intracellular Growth of Mycobacterium tuberculosis in Alternatively IL-4/IL-13 Activated Macrophages. Frontiers in Immunology, 2019, 10, 421.	4.8	37
77	Stac, a Novel Neuron-Specific Protein with Cysteine-Rich and SH3 Domains. Biochemical and Biophysical Research Communications, 1996, 229, 902-909.	2.1	36
78	Reconstruction of Monocyte Transcriptional Regulatory Network Accompanies Monocytic Functions in Human Fibroblasts. PLoS ONE, 2012, 7, e33474.	2.5	36
79	A transient disruption of fibroblastic transcriptional regulatory network facilitates<i>trans</i>-differentiation. Nucleic Acids Research, 2014, 42, 8905-8913.	14.5	35
80	Recounting the FANTOM CAGE-Associated Transcriptome. Genome Research, 2020, 30, 1073-1081.	5.5	35
81	Core promoter structure and genomic context reflect histone 3 lysine 9 acetylation patterns. BMC Genomics, 2010, 11, 257.	2.8	34
82	Restriction landmark cDNA scanning (RLCS): a novel cDNA display system using two-dimensional gel electrophoresis. Nucleic Acids Research, 1996, 24, 289-294.	14.5	33
83	Reduction of non-insert sequence reads by dimer eliminator LNA oligonucleotide for small RNA deep sequencing. BioTechniques, 2010, 49, 751-755.	1.8	32
84	Identification of ZNF395 as a novel modulator of adipogenesis. Experimental Cell Research, 2013, 319, 68-76.	2.6	32
85	The combination of gene perturbation assay and ChIP-chip reveals functional direct target genes for IRF8 in THP-1 cells. Molecular Immunology, 2010, 47, 2295-2302.	2.2	31
86	Targeting Batf2 for infectious diseases and cancer. Oncotarget, 2015, 6, 26575-26582.	1.8	31
87	Primary structure of the virus activating protease: from chick embryo Its identity with the blood clotting factor Xa. FEBS Letters, 1991, 283, 281-285.	2.8	30
88	Constructing ORFeome resources with removable termination codons. BioTechniques, 2006, 41, 44-50.	1.8	30
89	High-resolution analysis of aberrant regions in autosomal chromosomes in human leukemia THP-1 cell line. BMC Research Notes, 2009, 2, 153.	1.4	30
90	Towards defining the nuclear proteome. Genome Biology, 2008, 9, R15.	9.6	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. BioTechniques, 2008, 45, 95-97.	1.8	29
92	A framework for identification of on- and off-target transcriptional responses to drug treatment. Scientific Reports, 2019, 9, 17603.	3.3	29
93	Single-Nucleotide Resolution Mapping of Hepatitis B Virus Promoters in Infected Human Livers and Hepatocellular Carcinoma. Journal of Virology, 2016, 90, 10811-10822.	3.4	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. Journal of Virology, 2016, 90, 9058-9074.	3.4	27
95	Molecular cloning of rat GADD45Î³, gene induction and its role during neuronal cell death. FEBS Letters, 1999, 446, 313-317.	2.8	25
96	Force Measurement for Antigenâˆ’Antibody Interaction by Atomic Force Microscopy Using a Photograft-Polymer Spacer. Biomacromolecules, 2005, 6, 2776-2784.	5.4	25
97	Accessibility to tissue-specific genes from methylation profiles of mouse brain genomic DNA. Electrophoresis, 1995, 16, 218-226.	2.4	24
98	Dynamic Force Spectroscopy of the Specific Interaction between the PDZ Domain and Its Recognition Peptides. Langmuir, 2007, 23, 2668-2673.	3.5	24
99	Nanoscale elongating control of the selfâ€assembled protein filament with the cysteineâ€introduced building blocks. Protein Science, 2009, 18, 960-969.	7.6	24
100	Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. EBioMedicine, 2017, 24, 257-266.	6.1	24
101	Genomic analysis of a NF1 -related pseudogene on human chromosome 21. Gene, 1994, 147, 277-280.	2.2	23
102	A spot cloning method for restriction landmark genomic scanning. Electrophoresis, 1995, 16, 203-209.	2.4	23
103	The Mammalian Protein-Protein Interaction Database and Its Viewing System That Is Linked to the Main FANTOM2 Viewer. Genome Research, 2003, 13, 1534-1541.	5.5	23
104	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
105	IL-4RÎ±-Dependent Alternative Activation of Macrophages Is Not Decisive for Mycobacterium tuberculosis Pathology and Bacterial Burden in Mice. PLoS ONE, 2015, 10, e0121070.	2.5	23
106	Two-step cleavage of hairpin RNA with 5' overhangs by human DICER. BMC Molecular Biology, 2011, 12, 6.	3.0	21
107	CCL2 enhances pluripotency of human induced pluripotent stem cells by activating hypoxia related genes. Scientific Reports, 2014, 4, 5228.	3.3	21
108	Role of Survival Motor Neuron Complex Components in Small Nuclear Ribonucleoprotein Assembly. Journal of Biological Chemistry, 2009, 284, 14609-14617.	3.4	20

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109	Subcellular Localization of Mammalian Type II Membrane Proteins. Traffic, 2006, 7, 613-625.	2.7	19
110	Batf2 differentially regulates tissue immunopathology in Type 1 and Type 2 diseases. Mucosal Immunology, 2019, 12, 390-402.	6.0	19
111	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
112	PhosphoregDB: the tissue and sub-cellular distribution of mammalian protein kinases and phosphatases. BMC Bioinformatics, 2006, 7, 82.	2.6	18
113	Solution Structure of the Mouse Enhancer of Rudimentary Protein Reveals a Novel Fold. Journal of Biomolecular NMR, 2005, 32, 329-334.	2.8	17
114	Building promoter aware transcriptional regulatory networks using siRNA perturbation and deepCAGE. Nucleic Acids Research, 2010, 38, 8141-8148.	14.5	17
115	CC Chemokine Ligand 2 and Leukemia Inhibitory Factor Cooperatively Promote Pluripotency in Mouse Induced Pluripotent Cells. Stem Cells, 2011, 29, 1196-1205.	3.2	17
116	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease. PLoS Computational Biology, 2018, 14, e1005934.	3.2	17
117	Protein-protein interactions in the mammalian brain. Journal of Physiology, 2006, 575, 373-377.	2.9	16
118	Transcriptionally induced enhancers in the macrophage immune response to Mycobacterium tuberculosis infection. BMC Genomics, 2019, 20, 71.	2.8	16
119	Inferring Higher Functional Information for RIKEN Mouse Full-Length cDNA Clones With FACTS. Genome Research, 2003, 13, 1520-1533.	5.5	14
120	Scanning gene expression during neuronal cell death evoked by nerve growth factor depletion. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 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. Frontiers in Genetics, 2015, 6, 331.	2.3	13
122	Protein-protein interactions of the hyperthermophilic archaeon Pyrococcus horikoshii OT3. Genome Biology, 2005, 6, R98.	9.6	12
123	IRNdb: the database of immunologically relevant non-coding RNAs. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw138.	3.0	12
124	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. Nature Communications, 2021, 12, 3297.	12.8	11
125	Establishment of single-cell screening system for the rapid identification of transcriptional modulators involved in direct cell reprogramming. Nucleic Acids Research, 2012, 40, e165-e165.	14.5	10
126	Transcriptome analysis reveals inadequate spermatogenesis and immediate radical immune reactions during organ culture inÂvitro spermatogenesis. Biochemical and Biophysical Research Communications, 2020, 530, 732-738.	2.1	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. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1998, 1399, 10-18.	2.4	9
128	Expression analysis of genes responsible for serotonin signaling in the brain. Neurobiology of Disease, 2005, 19, 378-385.	4.4	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. FEBS Letters, 1993, 325, 303-308.	2.8	8
130	Correspondence of RLGS-M Spot Behavior with Tissue Expression on Mouse Homologue of DP1/TB2 Gene. Biochemical and Biophysical Research Communications, 1995, 213, 967-974.	2.1	8
131	Spliceostatin A interaction with SF3B limits U1 snRNP availability and causes premature cleavage and polyadenylation. Cell Chemical Biology, 2021, 28, 1356-1365.e4.	5.2	8
132	Evaluation of Berberine as an Adjunct to TB Treatment. Frontiers in Immunology, 2021, 12, 656419.	4.8	8
133	Human and Mouse Chromosomal Mapping of Stac, a Neuron-Specific Protein with an SH3 Domain. Genomics, 1998, 47, 140-142.	2.9	7
134	RUNX1 induces DNA replication independent active DNA demethylation at SPI1 regulatory regions. BMC Molecular Biology, 2017, 18, 9.	3.0	7
135	GATA6 is predicted to regulate DNA methylation in an in vitro model of human hepatocyte differentiation. Communications Biology, 2022, 5, 414.	4.4	7
136	In vitro pull-down assay without expression constructs. BioTechniques, 2004, 37, 918-920.	1.8	6
137	Integrative Genome-Wide Expression Analysis Bears Evidence of Estrogen Receptor-Independent Transcription in Heregulin-Stimulated MCF-7 Cells. PLoS ONE, 2008, 3, e1803.	2.5	6
138	CpG site-specific alteration of hydroxymethylcytosine to methylcytosine beyond DNA replication. Biochemical and Biophysical Research Communications, 2012, 426, 141-147.	2.1	6
139	Genome-scale regression analysis reveals a linear relationship for promoters and enhancers after combinatorial drug treatment. Bioinformatics, 2017, 33, 3696-3700.	4.1	6
140	TrkB mutant lacking the amino-terminal half of the extracellular portion acts as a functional brain-derived neurotrophic factor receptor. Biochimica Et Biophysica Acta - Biomembranes, 1999, 1420, 104-110.	2.6	5
141	Development of a high-throughput method for the systematic identification of human proteins nuclear translocation potential. BMC Cell Biology, 2009, 10, 69.	3.0	5
142	Prediction of human cDNA from its homologous mouse full-length cDNA and human shotgun database. FEBS Letters, 1999, 464, 129-132.	2.8	4
143	Loss of variation of state detected in soybean metabolic and human myelomonocytic leukaemia cell transcriptional networks under external stimuli. Scientific Reports, 2016, 6, 35946.	3.3	4
144	A Transcriptional Switch Point During Hematopoietic Stem and Progenitor Cell Ontogeny. Stem Cells and Development, 2017, 26, 314-327.	2.1	4

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145	SkewC: Identifying cells with skewed gene body coverage in single-cell RNA sequencing data. IScience, 2022, 25, 103777.	4.1	4
146	Prediction of transcription factors associated with DNA demethylation during human cellular development. Chromosome Research, 2022, 30, 109-121.	2.2	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. Scientific Reports, 2015, 5, 8283.	3.3	3
148	Asymmetric Regulation of Peripheral Genes by Two Transcriptional Regulatory Networks. PLoS ONE, 2016, 11, e0160459.	2.5	3
149	IL-4i1 Regulation of Immune Protection During <i>Mycobacterium tuberculosis</i> Infection. Journal of Infectious Diseases, 2021, 224, 2170-2180.	4.0	3
150	Global insights into protein complexes through integrated analysis of the reliable interactome and knockout lethality. Biochemical and Biophysical Research Communications, 2003, 301, 633-640.	2.1	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. FEBS Letters, 2000, 471, 261-261.	2.8	0
153	Beyond the FANTOM4. Genome Biology, 2010, 11, O11.	9.6	0
154	Development of p53 knockout U87MG cell line for unbiased drug delivery testing system using CRISPR-Cas9 and transcriptomic analysis. Journal of Biotechnology, 2021, 332, 72-82.	3.8	0
155	Repositioning Monocyte TFRN into Fibroblasts. Methods in Molecular Biology, 2014, 1164, 211-218.	0.9	0
156	Direct reprogramming based on transcriptional regulatory network analysis. Inflammation and Regeneration, 2014, 34, 224-232.	3.7	0