

Harukazu Suzuki

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161
papers

19,796
citations

53
h-index

140
g-index

178
ext. papers

23,089
ext. citations

11.1
avg, IF

5.46
L-index

#	Paper	IF	Citations
161	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014 , 507, 455-461	50.4	1595
160	Antisense transcription in the mammalian transcriptome. <i>Science</i> , 2005 , 309, 1564-6	33.3	1354
159	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002 , 420, 563-73	50.4	1350
158	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014 , 507, 462-70	50.4	1301
157	Structural parts involved in activation and inactivation of the sodium channel. <i>Nature</i> , 1989 , 339, 597-603	50.4	1091
156	Genome-wide analysis of mammalian promoter architecture and evolution. <i>Nature Genetics</i> , 2006 , 38, 626-35	36.3	1021
155	Existence of distinct sodium channel messenger RNAs in rat brain. <i>Nature</i> , 1986 , 320, 188-92	50.4	880
154	The regulated retrotransposon transcriptome of mammalian cells. <i>Nature Genetics</i> , 2009 , 41, 563-71	36.3	601
153	High-throughput mapping of a dynamic signaling network in mammalian cells. <i>Science</i> , 2005 , 307, 1621-5	33.3	587
152	An atlas of human long non-coding RNAs with accurate 5Tends. <i>Nature</i> , 2017 , 543, 199-204	50.4	581
151	Functional annotation of a full-length mouse cDNA collection. <i>Nature</i> , 2001 , 409, 685-90	50.4	560
150	An atlas of combinatorial transcriptional regulation in mouse and man. <i>Cell</i> , 2010 , 140, 744-52	56.2	555
149	Expression of functional sodium channels from cloned cDNA. <i>Nature</i> , 1986 , 322, 826-8	50.4	473
148	Experimental validation of the regulated expression of large numbers of non-coding RNAs from the mouse genome. <i>Genome Research</i> , 2006 , 16, 11-9	9.7	407
147	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , 2015 , 347, 1010-4	33.3	384
146	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009 , 41, 553-62	36.3	356
145	Tiny RNAs associated with transcription start sites in animals. <i>Nature Genetics</i> , 2009 , 41, 572-8	36.3	302

144	Primary structure of the alpha-subunit of transducin and its relationship to ras proteins. <i>Nature</i> , 1985 , 315, 242-5	50.4	296
143	A single point mutation confers tetrodotoxin and saxitoxin insensitivity on the sodium channel II. <i>FEBS Letters</i> , 1989 , 259, 213-6	3.8	285
142	A comprehensive survey of 3Tanimal miRNA modification events and a possible role for 3Tadenylation in modulating miRNA targeting effectiveness. <i>Genome Research</i> , 2010 , 20, 1398-410	9.7	269
141	Complex Loci in human and mouse genomes. <i>PLoS Genetics</i> , 2006 , 2, e47	6	246
140	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, 158-77	4.8	221
139	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	11.5	212
138	Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. <i>Nature Genetics</i> , 2014 , 46, 558-66	36.3	203
137	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, 754-63	7	190
136	A predictive computational framework for direct reprogramming between human cell types. <i>Nature Genetics</i> , 2016 , 48, 331-5	36.3	184
135	LPS regulates proinflammatory gene expression in macrophages by altering histone deacetylase expression. <i>FASEB Journal</i> , 2006 , 20, 1315-27	0.9	182
134	Clusters of internally primed transcripts reveal novel long noncoding RNAs. <i>PLoS Genetics</i> , 2006 , 2, e37	6	135
133	Functional expression of cloned cDNA encoding sodium channel III. <i>FEBS Letters</i> , 1988 , 228, 195-200	3.8	130
132	Doc2: a novel brain protein having two repeated C2-like domains. <i>Biochemical and Biophysical Research Communications</i> , 1995 , 206, 439-48	3.4	115
131	Interaction generality, a measurement to assess the reliability of a protein-protein interaction. <i>Nucleic Acids Research</i> , 2002 , 30, 1163-8	20.1	114
130	PAPD5-mediated 3Tadenylation 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, 11467-72	11.5	106
129	Cross-mapping and the identification of editing sites in mature microRNAs in high-throughput sequencing libraries. <i>Genome Research</i> , 2010 , 20, 257-64	9.7	105
128	Transcriptional network dynamics in macrophage activation. <i>Genomics</i> , 2006 , 88, 133-42	4.3	104
127	Transcription and enhancer profiling in human monocyte subsets. <i>Blood</i> , 2014 , 123, e90-9	2.2	101

126	A genome-wide and nonredundant mouse transcription factor database. <i>Biochemical and Biophysical Research Communications</i> , 2004 , 322, 787-93	3.4	101
125	Construction of reliable protein-protein interaction networks with a new interaction generality measure. <i>Bioinformatics</i> , 2003 , 19, 756-63	7.2	91
124	Protein-protein interaction panel using mouse full-length cDNAs. <i>Genome Research</i> , 2001 , 11, 1758-65	9.7	89
123	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , 2017 , 4, 170112	8.2	88
122	Beyond the FANTOM4 2010 , 11, O11		78
121	Transcriptional features of genomic regulatory blocks. <i>Genome Biology</i> , 2009 , 10, R38	18.3	77
120	Data-driven normalization strategies for high-throughput quantitative RT-PCR. <i>BMC Bioinformatics</i> , 2009 , 10, 110	3.6	72
119	The FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. <i>Genome Biology</i> , 2009 , 10, R40	18.3	65
118	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, 406-13	7.5	64
117	Next-generation sequencing-based small RNA profiling of cerebrospinal fluid exosomes. <i>Neuroscience Letters</i> , 2017 , 636, 48-57	3.3	63
116	Enhanced Identification of Transcriptional Enhancers Provides Mechanistic Insights into Diseases. <i>Trends in Genetics</i> , 2016 , 32, 76-88	8.5	59
115	The PDZ protein tax-interacting protein-1 inhibits beta-catenin transcriptional activity and growth of colorectal cancer cells. <i>Journal of Biological Chemistry</i> , 2003 , 278, 38758-64	5.4	59
114	The enhancer and promoter landscape of human regulatory and conventional T-cell subpopulations. <i>Blood</i> , 2014 , 123, e68-78	2.2	58
113	Identification of a novel kinase-like gene induced during neuronal cell death. <i>Biochemical and Biophysical Research Communications</i> , 1999 , 258, 260-4	3.4	58
112	Deciphering the transcriptional circuitry of microRNA genes expressed during human monocytic differentiation. <i>BMC Genomics</i> , 2009 , 10, 595	4.5	57
111	FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. <i>Genome Biology</i> , 2009 , 10, R39	18.3	56
110	Genome-wide investigation of in vivo EGR-1 binding sites in monocytic differentiation. <i>Genome Biology</i> , 2009 , 10, R41	18.3	55
109	Reversible hydrogel formation driven by protein-peptide-specific interaction and chondrocyte entrapment. <i>Biomaterials</i> , 2010 , 31, 58-66	15.6	52

108	Batf2/Irf1 induces inflammatory responses in classically activated macrophages, lipopolysaccharides, and mycobacterial infection. <i>Journal of Immunology</i> , 2015 , 194, 6035-44	5.3	49
107	LRRN4 and UPK3B are markers of primary mesothelial cells. <i>PLoS ONE</i> , 2011 , 6, e25391	3.7	49
106	CDS annotation in full-length cDNA sequence. <i>Genome Research</i> , 2003 , 13, 1478-87	9.7	49
105	T2BP, a novel TRAF2 binding protein, can activate NF-kappaB and AP-1 without TNF stimulation. <i>Biochemical and Biophysical Research Communications</i> , 2002 , 290, 1108-13	3.4	49
104	C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution. <i>Nature Communications</i> , 2019 , 10, 360	17.4	45
103	Update of the FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. <i>Nucleic Acids Research</i> , 2011 , 39, D856-60	20.1	45
102	Gemin2 plays an important role in stabilizing the survival of motor neuron complex. <i>Journal of Biological Chemistry</i> , 2007 , 282, 11122-34	5.4	44
101	LPS regulates a set of genes in primary murine macrophages by antagonising CSF-1 action. <i>Immunobiology</i> , 2005 , 210, 97-107	3.4	43
100	Transcriptional landscape of Mycobacterium tuberculosis infection in macrophages. <i>Scientific Reports</i> , 2018 , 8, 6758	4.9	41
99	Global analysis of pre-mRNA subcellular localization following splicing inhibition by spliceostatin A. <i>Rna</i> , 2017 , 23, 47-57	5.8	41
98	Solution structure of a BOLA-like protein from <i>Mus musculus</i> . <i>Protein Science</i> , 2004 , 13, 545-8	6.3	41
97	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020 , 30, 1060-1072	9.7	41
96	RUNX1 regulates site specificity of DNA demethylation by recruitment of DNA demethylation machineries in hematopoietic cells. <i>Blood Advances</i> , 2017 , 1, 1699-1711	7.8	39
95	Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics. <i>Nucleic Acids Research</i> , 2015 , 43, 6969-82	20.1	38
94	Ligand-specific sequential regulation of transcription factors for differentiation of MCF-7 cells. <i>BMC Genomics</i> , 2009 , 10, 545	4.5	37
93	Nuclear pore complex protein mediated nuclear localization of dicer protein in human cells. <i>PLoS ONE</i> , 2011 , 6, e23385	3.7	37
92	NF-kappaB activator Act1 associates with IL-1/Toll pathway adaptor molecule TRAF6. <i>FEBS Letters</i> , 2002 , 532, 241-6	3.8	35
91	Temporal dynamics and transcriptional control using single-cell gene expression analysis. <i>Genome Biology</i> , 2013 , 14, R118	18.3	34

90	Simvastatin enhances protection against <i>Listeria monocytogenes</i> infection in mice by counteracting <i>Listeria</i> -induced phagosomal escape. <i>PLoS ONE</i> , 2013 , 8, e75490	3.7	33
89	A screening system to identify transcription factors that induce binding site-directed DNA demethylation. <i>Epigenetics and Chromatin</i> , 2017 , 10, 60	5.8	32
88	Stac, a novel neuron-specific protein with cysteine-rich and SH3 domains. <i>Biochemical and Biophysical Research Communications</i> , 1996 , 229, 902-9	3.4	32
87	Reconstruction of monocyte transcriptional regulatory network accompanies monocytic functions in human fibroblasts. <i>PLoS ONE</i> , 2012 , 7, e33474	3.7	31
86	Combinatorial perturbation analysis reveals divergent regulations of mesenchymal genes during epithelial-to-mesenchymal transition. <i>Npj Systems Biology and Applications</i> , 2019 , 5, 21	5	27
85	Reduction of non-insert sequence reads by dimer eliminator LNA oligonucleotide for small RNA deep sequencing. <i>BioTechniques</i> , 2010 , 49, 751-5	2.5	27
84	Restriction landmark cDNA scanning (RLCS): a novel cDNA display system using two-dimensional gel electrophoresis. <i>Nucleic Acids Research</i> , 1996 , 24, 289-94	20.1	27
83	Towards defining the nuclear proteome. <i>Genome Biology</i> , 2008 , 9, R15	18.3	27
82	Identification of ZNF395 as a novel modulator of adipogenesis. <i>Experimental Cell Research</i> , 2013 , 319, 68-76	4.2	25
81	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, 2295-302	4.3	25
80	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, 95-7	2.5	25
79	Core promoter structure and genomic context reflect histone 3 lysine 9 acetylation patterns. <i>BMC Genomics</i> , 2010 , 11, 257	4.5	24
78	A transient disruption of fibroblastic transcriptional regulatory network facilitates trans-differentiation. <i>Nucleic Acids Research</i> , 2014 , 42, 8905-13	20.1	23
77	Nanoscale elongating control of the self-assembled protein filament with the cysteine-introduced building blocks. <i>Protein Science</i> , 2009 , 18, 960-9	6.3	23
76	Force measurement for antigen-antibody interaction by atomic force microscopy using a photograft-polymer spacer. <i>Biomacromolecules</i> , 2005 , 6, 2776-84	6.9	23
75	Molecular cloning of rat GADD45gamma, gene induction and its role during neuronal cell death. <i>FEBS Letters</i> , 1999 , 446, 313-7	3.8	23
74	High-resolution analysis of aberrant regions in autosomal chromosomes in human leukemia THP-1 cell line. <i>BMC Research Notes</i> , 2009 , 2, 153	2.3	22
73	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, 913-21	4.3	22

72	A spot cloning method for restriction landmark genomic scanning. <i>Electrophoresis</i> , 1995 , 16, 203-9	3.6	22
71	Dynamic force spectroscopy of the specific interaction between the PDZ domain and its recognition peptides. <i>Langmuir</i> , 2007 , 23, 2668-73	4	21
70	Constructing ORFeome resources with removable termination codons. <i>BioTechniques</i> , 2006 , 41, 44, 46, 48 passim	2.5	21
69	Targeting Batf2 for infectious diseases and cancer. <i>Oncotarget</i> , 2015 , 6, 26575-82	3.3	21
68	Role of survival motor neuron complex components in small nuclear ribonucleoprotein assembly. <i>Journal of Biological Chemistry</i> , 2009 , 284, 14609-17	5.4	20
67	Genomic analysis of a NF1-related pseudogene on human chromosome 21. <i>Gene</i> , 1994 , 147, 277-80	3.8	20
66	Accessibility to tissue-specific genes from methylation profiles of mouse brain genomic DNA. <i>Electrophoresis</i> , 1995 , 16, 218-26	3.6	20
65	Primary structure of the virus activating protease from chick embryo. Its identity with the blood clotting factor Xa. <i>FEBS Letters</i> , 1991 , 283, 281-5	3.8	20
64	Two-step cleavage of hairpin RNA with 5TOverhangs by human DICER. <i>BMC Molecular Biology</i> , 2011 , 12, 6	4.5	19
63	OVOL2 induces mesenchymal-to-epithelial transition in fibroblasts and enhances cell-state reprogramming towards epithelial lineages. <i>Scientific Reports</i> , 2019 , 9, 6490	4.9	18
62	Differential Targeting of c-Maf, Bach-1, and Elmo-1 by microRNA-143 and microRNA-365 Promotes the Intracellular Growth of in Alternatively IL-4/IL-13 Activated Macrophages. <i>Frontiers in Immunology</i> , 2019 , 10, 421	8.4	18
61	The mammalian protein-protein interaction database and its viewing system that is linked to the main FANTOM2 viewer. <i>Genome Research</i> , 2003 , 13, 1534-41	9.7	18
60	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, 9058-74	6.6	18
59	Subcellular localization of mammalian type II membrane proteins. <i>Traffic</i> , 2006 , 7, 613-25	5.7	17
58	IL-4R β dependent alternative activation of macrophages is not decisive for Mycobacterium tuberculosis pathology and bacterial burden in mice. <i>PLoS ONE</i> , 2015 , 10, e0121070	3.7	16
57	CC chemokine ligand 2 and leukemia inhibitory factor cooperatively promote pluripotency in mouse induced pluripotent cells. <i>Stem Cells</i> , 2011 , 29, 1196-205	5.8	16
56	PhosphoregDB: the tissue and sub-cellular distribution of mammalian protein kinases and phosphatases. <i>BMC Bioinformatics</i> , 2006 , 7, 82	3.6	16
55	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, 214-8	3.8	16

54	CCL2 enhances pluripotency of human induced pluripotent stem cells by activating hypoxia related genes. <i>Scientific Reports</i> , 2014 , 4, 5228	4.9	14
53	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	6.6	14
52	Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. <i>EBioMedicine</i> , 2017 , 24, 257-266	8.8	13
51	Recounting the FANTOM CAGE-Associated Transcriptome. <i>Genome Research</i> , 2020 , 30, 1073-1081	9.7	13
50	Solution structure of the mouse enhancer of rudimentary protein reveals a novel fold. <i>Journal of Biomolecular NMR</i> , 2005 , 32, 329-34	3	13
49	A framework for identification of on- and off-target transcriptional responses to drug treatment. <i>Scientific Reports</i> , 2019 , 9, 17603	4.9	13
48	Transcriptionally induced enhancers in the macrophage immune response to Mycobacterium tuberculosis infection. <i>BMC Genomics</i> , 2019 , 20, 71	4.5	12
47	Genome-wide profiling of transcribed enhancers during macrophage activation. <i>Epigenetics and Chromatin</i> , 2017 , 10, 50	5.8	11
46	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	4.5	11
45	Building promoter aware transcriptional regulatory networks using siRNA perturbation and deepCAGE. <i>Nucleic Acids Research</i> , 2010 , 38, 8141-8	20.1	11
44	Protein-protein interactions of the hyperthermophilic archaeon <i>Pyrococcus horikoshii</i> OT3. <i>Genome Biology</i> , 2005 , 6, R98	18.3	11
43	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		11
42	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	20.1	10
41	Protein-protein interactions in the mammalian brain. <i>Journal of Physiology</i> , 2006 , 575, 373-7	3.9	10
40	Inferring higher functional information for RIKEN mouse full-length cDNA clones with FACTS. <i>Genome Research</i> , 2003 , 13, 1520-33	9.7	10
39	Expression analysis of genes responsible for serotonin signaling in the brain. <i>Neurobiology of Disease</i> , 2005 , 19, 378-85	7.5	9
38	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, 10-8		8
37	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	5	8

36	IRNdb: the database of immunologically relevant non-coding RNAs. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	7
35	Human and mouse chromosomal mapping of Stac, a neuron-specific protein with an SH3 domain. <i>Genomics</i> , 1998 , 47, 140-2	4.3	7
34	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, 967-74	3.4	7
33	Genome-scale regression analysis reveals a linear relationship for promoters and enhancers after combinatorial drug treatment. <i>Bioinformatics</i> , 2017 , 33, 3696-3700	7.2	6
32	CpG site-specific alteration of hydroxymethylcytosine to methylcytosine beyond DNA replication. <i>Biochemical and Biophysical Research Communications</i> , 2012 , 426, 141-7	3.4	6
31	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	3.7	6
30	In vitro pull-down assay without expression constructs. <i>BioTechniques</i> , 2004 , 37, 918, 920	2.5	6
29	Functional Annotation of Human Long Non-Coding RNAs via Molecular Phenotyping		6
28	Batf2 differentially regulates tissue immunopathology in Type 1 and Type 2 diseases. <i>Mucosal Immunology</i> , 2019 , 12, 390-402	9.2	6
27	RUNX1 induces DNA replication independent active DNA demethylation at SPI1 regulatory regions. <i>BMC Molecular Biology</i> , 2017 , 18, 9	4.5	5
26	Development of a high-throughput method for the systematic identification of human proteins nuclear translocation potential. <i>BMC Cell Biology</i> , 2009 , 10, 69		5
25	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, 104-10	3.8	4
24	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, 303-8	3.8	4
23	Single-cell transcriptomes of fluorescent, ubiquitination-based cell cycle indicator cells		4
22	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	3.4	4
21	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	4.9	3
20	A Transcriptional Switch Point During Hematopoietic Stem and Progenitor Cell Ontogeny. <i>Stem Cells and Development</i> , 2017 , 26, 314-327	4.4	3
19	Prediction of human cDNA from its homologous mouse full-length cDNA and human shotgun database. <i>FEBS Letters</i> , 1999 , 464, 129-32	3.8	3

18	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021 , 12, 3297	17.4	3
17	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	4.9	2
16	Asymmetric Regulation of Peripheral Genes by Two Transcriptional Regulatory Networks. <i>PLoS ONE</i> , 2016 , 11, e0160459	3.7	2
15	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease		2
14	Global insights into protein complexes through integrated analysis of the reliable interactome and knockout lethality. <i>Biochemical and Biophysical Research Communications</i> , 2003 , 301, 633-40	3.4	1
13	Prediction of transcription factors associated with DNA demethylation during human cellular development.. <i>Chromosome Research</i> , 2022 , 30, 109	4.4	1
12	Evaluation of Berberine as an Adjunct to TB Treatment. <i>Frontiers in Immunology</i> , 2021 , 12, 656419	8.4	1
11	Quality assessment of single-cell RNA sequencing data by coverage skewness analysis		1
10	RLCS, Restriction Landmark cDNA Scanning 1997 , 129-156		1
9	C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution		1
8	Evidence of transcription at polyT short tandem repeats		1
7	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	8.2	1
6	SkewC: Identifying cells with skewed gene body coverage in single-cell RNA sequencing data.. <i>iScience</i> , 2022 , 25, 103777	6.1	0
5	GATA6 is predicted to regulate DNA methylation in an in vitro model of human hepatocyte differentiation.. <i>Communications Biology</i> , 2022 , 5, 414	6.7	0
4	Corrigendum to: prediction of human cDNA from its homologous mouse full-length cDNA and human shotgun database. <i>FEBS Letters</i> , 2000 , 471, 261	3.8	
3	Repositioning monocyte TFRN into fibroblasts. <i>Methods in Molecular Biology</i> , 2014 , 1164, 211-8	1.4	
2	Direct reprogramming based on transcriptional regulatory network analysis. <i>Inflammation and Regeneration</i> , 2014 , 34, 224-232	10.9	
1	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	3.7	

