

# Alistair R R Forrest

## List of Publications by Citations

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151  
papers

19,526  
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56  
h-index

139  
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161  
ext. papers

23,812  
ext. citations

12.4  
avg, IF

5.64  
L-index

#	Paper	IF	Citations
151	The transcriptional landscape of the mammalian genome. <i>Science</i> , <b>2005</b> , 309, 1559-63	33.3	2807
150	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , <b>2014</b> , 507, 455-461	50.4	1595
149	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , <b>2002</b> , 420, 563-73	50.4	1350
148	A promoter-level mammalian expression atlas. <i>Nature</i> , <b>2014</b> , 507, 462-70	50.4	1301
147	Genome-wide analysis of mammalian promoter architecture and evolution. <i>Nature Genetics</i> , <b>2006</b> , 38, 626-35	36.3	1021
146	Stem cell transcriptome profiling via massive-scale mRNA sequencing. <i>Nature Methods</i> , <b>2008</b> , 5, 613-9	21.6	841
145	Long non-coding antisense RNA controls Uchl1 translation through an embedded SINEB2 repeat. <i>Nature</i> , <b>2012</b> , 491, 454-7	50.4	684
144	The regulated retrotransposon transcriptome of mammalian cells. <i>Nature Genetics</i> , <b>2009</b> , 41, 563-71	36.3	601
143	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , <b>2017</b> , 543, 199-204	50.4	581
142	An atlas of combinatorial transcriptional regulation in mouse and man. <i>Cell</i> , <b>2010</b> , 140, 744-52	56.2	555
141	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , <b>2015</b> , 16, 22	18.3	443
140	A draft network of ligand-receptor-mediated multicellular signalling in human. <i>Nature Communications</i> , <b>2015</b> , 6, 7866	17.4	393
139	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , <b>2015</b> , 347, 1010-4	33.3	384
138	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , <b>2009</b> , 41, 553-62	36.3	356
137	Tiny RNAs associated with transcription start sites in animals. <i>Nature Genetics</i> , <b>2009</b> , 41, 572-8	36.3	302
136	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 872-878	44.5	282
135	Hierarchical folding and reorganization of chromosomes are linked to transcriptional changes in cellular differentiation. <i>Molecular Systems Biology</i> , <b>2015</b> , 11, 852	12.2	229

134	The miR-17-5p microRNA is a key regulator of the G1/S phase cell cycle transition. <i>Genome Biology</i> , <b>2008</b> , 9, R127	18.3	228
133	Induction of microRNAs, mir-155, mir-222, mir-424 and mir-503, promotes monocytic differentiation through combinatorial regulation. <i>Leukemia</i> , <b>2010</b> , 24, 460-6	10.7	205
132	Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. <i>Nature Genetics</i> , <b>2014</b> , 46, 558-66	36.3	203
131	A predictive computational framework for direct reprogramming between human cell types. <i>Nature Genetics</i> , <b>2016</b> , 48, 331-5	36.3	184
130	MiR-107 and MiR-185 can induce cell cycle arrest in human non small cell lung cancer cell lines. <i>PLoS ONE</i> , <b>2009</b> , 4, e6677	3.7	173
129	The abundance of short proteins in the mammalian proteome. <i>PLoS Genetics</i> , <b>2006</b> , 2, e52	6	159
128	Effects of cytosine methylation on transcription factor binding sites. <i>BMC Genomics</i> , <b>2014</b> , 15, 119	4.5	156
127	Unamplified cap analysis of gene expression on a single-molecule sequencer. <i>Genome Research</i> , <b>2011</b> , 21, 1150-9	9.7	143
126	Transcript annotation in FANTOM3: mouse gene catalog based on physical cDNAs. <i>PLoS Genetics</i> , <b>2006</b> , 2, e62	6	138
125	Redefinition of the human mast cell transcriptome by deep-CAGE sequencing. <i>Blood</i> , <b>2014</b> , 123, e58-67	2.2	126
124	Interactive visualization and analysis of large-scale sequencing datasets using ZENBU. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 217-9	44.5	124
123	CAGEr: precise TSS data retrieval and high-resolution promoterome mining for integrative analyses. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, e51	20.1	117
122	Systematic assessment of tissue dissociation and storage biases in single-cell and single-nucleus RNA-seq workflows. <i>Genome Biology</i> , <b>2020</b> , 21, 130	18.3	117
121	Transcription and enhancer profiling in human monocyte subsets. <i>Blood</i> , <b>2014</b> , 123, e90-9	2.2	101
120	Novel genes regulated by Sonic Hedgehog in pluripotent mesenchymal cells. <i>Oncogene</i> , <b>2002</b> , 21, 8196-205	20.5	101
119	Expression analysis of the long non-coding RNA antisense to Uchl1 (AS Uchl1) during dopaminergic cells differentiation in vitro and in neurochemical models of Parkinson's disease. <i>Frontiers in Cellular Neuroscience</i> , <b>2015</b> , 9, 114	6.1	99
118	Regulation of CDC25B phosphatases subcellular localization. <i>Oncogene</i> , <b>2000</b> , 19, 2179-85	9.2	92
117	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , <b>2017</b> , 4, 170112	8.2	88

116	Cdc25B activity is regulated by 14-3-3. <i>Oncogene</i> , <b>2001</b> , 20, 4393-401	9.2	88
115	Differential roles of epigenetic changes and Foxp3 expression in regulatory T cell-specific transcriptional regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 5289-94	11.5	85
114	Pax9 and Jagged1 act downstream of Gli3 in vertebrate limb development. <i>Mechanisms of Development</i> , <b>2005</b> , 122, 1218-33	1.7	84
113	Generation of diversity in the innate immune system: macrophage heterogeneity arises from gene-autonomous transcriptional probability of individual inducible genes. <i>Journal of Immunology</i> , <b>2002</b> , 168, 44-50	5.3	84
112	Sensitization to immune checkpoint blockade through activation of a STAT1/NK axis in the tumor microenvironment. <i>Science Translational Medicine</i> , <b>2019</b> , 11,	17.5	83
111	A rescue strategy for multimapping short sequence tags refines surveys of transcriptional activity by CAGE. <i>Genomics</i> , <b>2008</b> , 91, 281-8	4.3	82
110	Cdc25-dependent activation of cyclin A/cdk2 is blocked in G2 phase arrested cells independently of ATM/ATR. <i>Oncogene</i> , <b>2001</b> , 20, 921-32	9.2	82
109	Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D737-D743	20.1	80
108	Systematic characterization of the zinc-finger-containing proteins in the mouse transcriptome. <i>Genome Research</i> , <b>2003</b> , 13, 1430-42	9.7	79
107	Comparison of CAGE and RNA-seq transcriptome profiling using clonally amplified and single-molecule next-generation sequencing. <i>Genome Research</i> , <b>2014</b> , 24, 708-17	9.7	66
106	Stromal cell diversity associated with immune evasion in human triple-negative breast cancer. <i>EMBO Journal</i> , <b>2020</b> , 39, e104063	13	66
105	The FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. <i>Genome Biology</i> , <b>2009</b> , 10, R40	18.3	65
104	Analysis of the human monocyte-derived macrophage transcriptome and response to lipopolysaccharide provides new insights into genetic aetiology of inflammatory bowel disease. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006641	6	64
103	Alternate transcription of the Toll-like receptor signaling cascade. <i>Genome Biology</i> , <b>2006</b> , 7, R10	18.3	63
102	Complementing tissue characterization by integrating transcriptome profiling from the Human Protein Atlas and from the FANTOM5 consortium. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 6787-98	20.1	61
101	Analysis of the DNA methylome and transcriptome in granulopoiesis reveals timed changes and dynamic enhancer methylation. <i>Blood</i> , <b>2014</b> , 123, e79-89	2.2	59
100	14-3-3 acts as an intramolecular bridge to regulate cdc25B localization and activity. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 28580-7	5.4	59
99	Multiple splicing variants of cdc25B regulate G2/M progression. <i>Biochemical and Biophysical Research Communications</i> , <b>1999</b> , 260, 510-5	3.4	59

98	The enhancer and promoter landscape of human regulatory and conventional T-cell subpopulations. <i>Blood</i> , <b>2014</b> , 123, e68-78	2.2	58
97	Transcriptome Analysis of Recurrently Deregulated Genes across Multiple Cancers Identifies New Pan-Cancer Biomarkers. <i>Cancer Research</i> , <b>2016</b> , 76, 216-26	10.1	56
96	FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. <i>Genome Biology</i> , <b>2009</b> , 10, R39	18.3	56
95	A novel corepressor, BCoR-L1, represses transcription through an interaction with CtBP. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 15248-57	5.4	53
94	Pseudo-messenger RNA: phantoms of the transcriptome. <i>PLoS Genetics</i> , <b>2006</b> , 2, e23	6	51
93	scMatch: a single-cell gene expression profile annotation tool using reference datasets. <i>Bioinformatics</i> , <b>2019</b> , 35, 4688-4695	7.2	50
92	LRRN4 and UPK3B are markers of primary mesothelial cells. <i>PLoS ONE</i> , <b>2011</b> , 6, e25391	3.7	49
91	Update of the FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D856-60	20.1	45
90	FANTOM5 transcriptome catalog of cellular states based on Semantic MediaWiki. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2016</b> , 2016,	5	44
89	Whole genome transcriptome analysis. <i>RNA Biology</i> , <b>2009</b> , 6, 107-12	4.8	42
88	Transcriptional landscape of Mycobacterium tuberculosis infection in macrophages. <i>Scientific Reports</i> , <b>2018</b> , 8, 6758	4.9	41
87	Genome-wide review of transcriptional complexity in mouse protein kinases and phosphatases. <i>Genome Biology</i> , <b>2006</b> , 7, R5	18.3	41
86	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , <b>2020</b> , 30, 1060-1072	9.7	41
85	CAGE profiling of ncRNAs in hepatocellular carcinoma reveals widespread activation of retroviral LTR promoters in virus-induced tumors. <i>Genome Research</i> , <b>2015</b> , 25, 1812-24	9.7	40
84	Phosphoregulators: protein kinases and protein phosphatases of mouse. <i>Genome Research</i> , <b>2003</b> , 13, 1443-54	9.7	39
83	Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 6969-82	20.1	38
82	RECLU: a pipeline to discover reproducible transcriptional start sites and their alternative regulation using capped analysis of gene expression (CAGE). <i>BMC Genomics</i> , <b>2014</b> , 15, 269	4.5	37
81	Ceruloplasmin is a novel adipokine which is overexpressed in adipose tissue of obese subjects and in obesity-associated cancer cells. <i>PLoS ONE</i> , <b>2014</b> , 9, e80274	3.7	36

80	Mesencephalic dopaminergic neurons express a repertoire of olfactory receptors and respond to odorant-like molecules. <i>BMC Genomics</i> , <b>2014</b> , 15, 729	4.5	36
79	Tissue-specific gene expression in soybean ( <i>Glycine max</i> ) detected by cDNA microarray analysis. <i>Journal of Plant Physiology</i> , <b>2002</b> , 159, 1361-1374	3.6	36
78	The FANTOM5 collection, a data series underpinning mammalian transcriptome atlases in diverse cell types. <i>Scientific Data</i> , <b>2017</b> , 4, 170113	8.2	35
77	The frequent evolutionary birth and death of functional promoters in mouse and human. <i>Genome Research</i> , <b>2015</b> , 25, 1546-57	9.7	33
76	The statistical geometry of transcriptome divergence in cell-type evolution and cancer. <i>Nature Communications</i> , <b>2015</b> , 6, 6066	17.4	33
75	Integration of genetics and miRNA-target gene network identified disease biology implicated in tissue specificity. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 11898-11909	20.1	26
74	Transcriptional profiling of the human fibrillin/LTBP gene family, key regulators of mesenchymal cell functions. <i>Molecular Genetics and Metabolism</i> , <b>2014</b> , 112, 73-83	3.7	25
73	DeepCAGE Transcriptomics Reveal an Important Role of the Transcription Factor MAFB in the Lymphatic Endothelium. <i>Cell Reports</i> , <b>2015</b> , 13, 1493-1504	10.6	25
72	The combination of gene perturbation assay and ChIP-chip reveals functional direct target genes for IRF8 in THP-1 cells. <i>Molecular Immunology</i> , <b>2010</b> , 47, 2295-302	4.3	25
71	Predicting cell-to-cell communication networks using NATMI. <i>Nature Communications</i> , <b>2020</b> , 11, 5011	17.4	25
70	Promoter-level expression clustering identifies time development of transcriptional regulatory cascades initiated by ErbB receptors in breast cancer cells. <i>Scientific Reports</i> , <b>2015</b> , 5, 11999	4.9	24
69	Characterizing embryonic gene expression patterns in the mouse using nonredundant sequence-based selection. <i>Genome Research</i> , <b>2003</b> , 13, 2609-20	9.7	24
68	A transient disruption of fibroblastic transcriptional regulatory network facilitates trans-differentiation. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 8905-13	20.1	23
67	Systematic analysis of transcription start sites in avian development. <i>PLoS Biology</i> , <b>2017</b> , 15, e2002887	9.7	22
66	Functional annotation of the vlinc class of non-coding RNAs using systems biology approach. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 3233-52	20.1	21
65	Analysis of complementary expression profiles following WT1 induction versus repression reveals the cholesterol/fatty acid synthetic pathways as a possible major target of WT1. <i>Oncogene</i> , <b>2004</b> , 23, 3067-79	9.2	21
64	Retinoic acid potentiates inflammatory cytokines in human mast cells: identification of mast cells as prominent constituents of the skin retinoid network. <i>Molecular and Cellular Endocrinology</i> , <b>2015</b> , 406, 49-59	4.4	20
63	Integrative CAGE and DNA Methylation Profiling Identify Epigenetically Regulated Genes in NSCLC. <i>Molecular Cancer Research</i> , <b>2017</b> , 15, 1354-1365	6.6	20

62	New era in genetics of early-onset muscle disease: Breakthroughs and challenges. <i>Seminars in Cell and Developmental Biology</i> , <b>2017</b> , 64, 160-170	7.5	20
61	High-throughput transcription profiling identifies putative epigenetic regulators of hematopoiesis. <i>Blood</i> , <b>2014</b> , 123, e46-57	2.2	19
60	Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution. <i>Diabetes</i> , <b>2017</b> , 66, 218-230	0.9	19
59	Reinforcing the association between distal 1q CNVs and structural brain disorder: A case of a complex 1q43-q44 CNV and a review of the literature. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , <b>2016</b> , 171B, 458-67	3.5	18
58	Automated workflow for preparation of cDNA for cap analysis of gene expression on a single molecule sequencer. <i>PLoS ONE</i> , <b>2012</b> , 7, e30809	3.7	18
57	Technical Advance: Transcription factor, promoter, and enhancer utilization in human myeloid cells. <i>Journal of Leukocyte Biology</i> , <b>2015</b> , 97, 985-995	6.5	17
56	The Constrained Maximal Expression Level Owing to Haploidy Shapes Gene Content on the Mammalian X Chromosome. <i>PLoS Biology</i> , <b>2015</b> , 13, e1002315	9.7	17
55	A simple metric of promoter architecture robustly predicts expression breadth of human genes suggesting that most transcription factors are positive regulators. <i>Genome Biology</i> , <b>2014</b> , 15, 413	18.3	17
54	Subcellular localization of mammalian type II membrane proteins. <i>Traffic</i> , <b>2006</b> , 7, 613-25	5.7	17
53	Bi-allelic mutations in MYL1 cause a severe congenital myopathy. <i>Human Molecular Genetics</i> , <b>2018</b> , 27, 4263-4272	5.6	17
52	YY1 binding association with sex-biased transcription revealed through X-linked transcript levels and allelic binding analyses. <i>Scientific Reports</i> , <b>2016</b> , 6, 37324	4.9	16
51	CC chemokine ligand 2 and leukemia inhibitory factor cooperatively promote pluripotency in mouse induced pluripotent cells. <i>Stem Cells</i> , <b>2011</b> , 29, 1196-205	5.8	16
50	PhosphoregDB: the tissue and sub-cellular distribution of mammalian protein kinases and phosphatases. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 82	3.6	16
49	Transcriptional dynamics reveal critical roles for non-coding RNAs in the immediate-early response. <i>PLoS Computational Biology</i> , <b>2015</b> , 11, e1004217	5	15
48	Chromatin states reveal functional associations for globally defined transcription start sites in four human cell lines. <i>BMC Genomics</i> , <b>2014</b> , 15, 120	4.5	15
47	Antisense Transcription in Loci Associated to Hereditary Neurodegenerative Diseases. <i>Molecular Neurobiology</i> , <b>2019</b> , 56, 5392-5415	6.2	15
46	Unravelling the molecular basis for regulatory T-cell plasticity and loss of function in disease. <i>Clinical and Translational Immunology</i> , <b>2018</b> , 7, e1011	6.8	14
45	Specific mesothelial signature marks the heterogeneity of mesenchymal stem cells from high-grade serous ovarian cancer. <i>Stem Cells</i> , <b>2014</b> , 32, 2998-3011	5.8	14

44	CCL2 enhances pluripotency of human induced pluripotent stem cells by activating hypoxia related genes. <i>Scientific Reports</i> , <b>2014</b> , 4, 5228	4.9	14
43	Regulatory interdependence of myeloid transcription factors revealed by Matrix RNAi analysis. <i>Genome Biology</i> , <b>2009</b> , 10, R121	18.3	14
42	Transcriptome analysis of periodontitis-associated fibroblasts by CAGE sequencing identified DLX5 and RUNX2 long variant as novel regulators involved in periodontitis. <i>Scientific Reports</i> , <b>2016</b> , 6, 33666	4.9	14
41	Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. <i>EBioMedicine</i> , <b>2017</b> , 24, 257-266	8.8	13
40	The evolution of human cells in terms of protein innovation. <i>Molecular Biology and Evolution</i> , <b>2014</b> , 31, 1364-74	8.3	13
39	Exploration of the cell-cycle genes found within the RIKEN FANTOM2 data set. <i>Genome Research</i> , <b>2003</b> , 13, 1366-75	9.7	12
38	Comparative transcriptomics of primary cells in vertebrates. <i>Genome Research</i> , <b>2020</b> , 30, 951-961	9.7	12
37	On-the-fly selection of cell-specific enhancers, genes, miRNAs and proteins across the human body using SlideBase. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2016</b> , 2016,	5	12
36	CAGED-oPOSSUM: motif enrichment analysis from CAGE-derived TSSs. <i>Bioinformatics</i> , <b>2016</b> , 32, 2858-60	7.2	11
35	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> , <b>2015</b> , 6, 331	4.5	11
34	Building promoter aware transcriptional regulatory networks using siRNA perturbation and deepCAGE. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, 8141-8	20.1	11
33	DeepCAGE transcriptomics identify HOXD10 as a transcription factor regulating lymphatic endothelial responses to VEGF-C. <i>Journal of Cell Science</i> , <b>2016</b> , 129, 2573-85	5.3	11
32	Linking FANTOM5 CAGE peaks to annotations with CAGEscan. <i>Scientific Data</i> , <b>2017</b> , 4, 170147	8.2	10
31	Brain-Enriched Coding and Long Non-coding RNA Genes Are Overrepresented in Recurrent Neurodevelopmental Disorder CNVs. <i>Cell Reports</i> , <b>2020</b> , 33, 108307	10.6	10
30	Systematic assessment of tissue dissociation and storage biases in single-cell and single-nucleus RNA-seq workflows		9
29	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1005934	5	8
28	Myoglobinopathy is an adult-onset autosomal dominant myopathy with characteristic sarcoplasmic inclusions. <i>Nature Communications</i> , <b>2019</b> , 10, 1396	17.4	7
27	CAGE-defined promoter regions of the genes implicated in Rett Syndrome. <i>BMC Genomics</i> , <b>2014</b> , 15, 1177	4.5	7



26	Comprehensive Characterization of Transcriptional Activity during Influenza A Virus Infection Reveals Biases in Cap-Snatching of Host RNA Sequences. <i>Journal of Virology</i> , <b>2020</b> , 94,	6.6	6
25	Functional Annotation of Human Long Non-Coding RNAs via Molecular Phenotyping		6
24	CAGExploreR: an R package for the analysis and visualization of promoter dynamics across multiple experiments. <i>Bioinformatics</i> , <b>2014</b> , 30, 1183-1184	7.2	5
23	Annotating non-coding transcription using functional genomics strategies. <i>Briefings in Functional Genomics &amp; Proteomics</i> , <b>2009</b> , 8, 437-43		5
22	Monitoring transcription initiation activities in rat and dog. <i>Scientific Data</i> , <b>2017</b> , 4, 170173	8.2	4
21	Human genetics and genomics meetings going virtual: practical lessons learned from two international meetings in early 2020. <i>Human Genomics</i> , <b>2020</b> , 14, 27	6.8	4
20	Molecular Insights Into Regulatory T-Cell Adaptation to Self, Environment, and Host Tissues: Plasticity or Loss of Function in Autoimmune Disease. <i>Frontiers in Immunology</i> , <b>2020</b> , 11, 1269	8.4	4
19	Identification of novel cerebellar developmental transcriptional regulators with motif activity analysis. <i>BMC Genomics</i> , <b>2019</b> , 20, 718	4.5	3
18	A Transcriptional Switch Point During Hematopoietic Stem and Progenitor Cell Ontogeny. <i>Stem Cells and Development</i> , <b>2017</b> , 26, 314-327	4.4	3
17	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , <b>2010</b> , 141, 369	56.2	3
16	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , <b>2021</b> , 12, 3297	17.4	3
15	Expression Levels of Therapeutic Targets as Indicators of Sensitivity to Targeted Therapeutics. <i>Molecular Cancer Therapeutics</i> , <b>2019</b> , 18, 2480-2489	6.1	3
14	Conserved temporal ordering of promoter activation implicates common mechanisms governing the immediate early response across cell types and stimuli. <i>Open Biology</i> , <b>2018</b> , 8,	7	3
13	Transcription Factor NKX6.3 Sheds Light on Gastric Cancer Progression. <i>EBioMedicine</i> , <b>2016</b> , 9, 9-10	8.8	2
12	Transcription start site profiling of 15 anatomical regions of the Macaca mulatta central nervous system. <i>Scientific Data</i> , <b>2017</b> , 4, 170163	8.2	2
11	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease		2
10	Single-cell analysis reveals diverse stromal subsets associated with immune evasion in triple-negative breast cancer		2
9	Intra- and intertumoral heterogeneity of liver metastases in a patient with uveal melanoma revealed by single-cell RNA sequencing. <i>Journal of Physical Education and Sports Management</i> , <b>2021</b> , 7,	2.8	2

8	Discovery of Transcription Factors Novel to Mouse Cerebellar Granule Cell Development Through Laser-Capture Microdissection. <i>Cerebellum</i> , <b>2018</b> , 17, 308-325	4.3	1
7	Application of Gene Expression Trajectories Initiated from ErbB Receptor Activation Highlights the Dynamics of Divergent Promoter Usage. <i>PLoS ONE</i> , <b>2015</b> , 10, e0144176	3.7	1
6	MaxHiC: robust estimation of chromatin interaction frequency in Hi-C and capture Hi-C experiments		1
5	CAGED-oPOSSUM: motif enrichment analysis from CAGE-derived TSSs		1
4	Improved CRISPR/Cas9 gene editing in primary human myoblasts using low confluency cultures on Matrigel. <i>Skeletal Muscle</i> , <b>2021</b> , 11, 23	5.1	1
3	Functional validation of variants of unknown significance using CRISPR gene editing and transcriptomics: A Kleeftstra syndrome case study.. <i>Gene</i> , <b>2022</b> , 821, 146287	3.8	0
2	Deep sequencing blood transcriptomes. <i>Blood</i> , <b>2014</b> , 123, 2595-6	2.2	
1	Stranded RNA-Seq: Strand-Specific Shotgun Sequencing of RNA <b>2012</b> , 91-108		