

# Alistair R R Forrest

## List of Publications by Year in descending order

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146  
papers

25,863  
citations

19608

61  
h-index

8370

147  
g-index

161  
all docs

161  
docs citations

161  
times ranked

36985  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	6.0	3,227
2	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014, 507, 455-461.	13.7	2,269
3	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	13.7	1,838
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	Stem cell transcriptome profiling via massive-scale mRNA sequencing. <i>Nature Methods</i> , 2008, 5, 613-619.	9.0	952
7	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017, 543, 199-204.	13.7	898
8	Long non-coding antisense RNA controls Uchl1 translation through an embedded SINEB2 repeat. <i>Nature</i> , 2012, 491, 454-457.	13.7	881
9	The regulated retrotransposon transcriptome of mammalian cells. <i>Nature Genetics</i> , 2009, 41, 563-571.	9.4	731
10	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015, 16, 22.	3.8	687
11	A draft network of ligand-receptor-mediated multicellular signalling in human. <i>Nature Communications</i> , 2015, 6, 7866.	5.8	676
12	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 140, 744-752.	13.5	667
13	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , 2015, 347, 1010-1014.	6.0	517
14	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017, 35, 872-878.	9.4	456
15	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
16	Systematic assessment of tissue dissociation and storage biases in single-cell and single-nucleus RNA-seq workflows. <i>Genome Biology</i> , 2020, 21, 130.	3.8	342
17	Tiny RNAs associated with transcription start sites in animals. <i>Nature Genetics</i> , 2009, 41, 572-578.	9.4	327
18	Hierarchical folding and reorganization of chromosomes are linked to transcriptional changes in cellular differentiation. <i>Molecular Systems Biology</i> , 2015, 11, 852.	3.2	305

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19	The miR-17-5p microRNA is a key regulator of the G1/S phase cell cycle transition. <i>Genome Biology</i> , 2008, 9, R127.	13.9	278
20	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
21	A predictive computational framework for direct reprogramming between human cell types. <i>Nature Genetics</i> , 2016, 48, 331-335.	9.4	263
22	Induction of microRNAs, mir-155, mir-222, mir-424 and mir-503, promotes monocytic differentiation through combinatorial regulation. <i>Leukemia</i> , 2010, 24, 460-466.	3.3	229
23	Stromal cell diversity associated with immune evasion in human triple-negative breast cancer. <i>EMBO Journal</i> , 2020, 39, e104063.	3.5	224
24	Effects of cytosine methylation on transcription factor binding sites. <i>BMC Genomics</i> , 2014, 15, 119.	1.2	214
25	MiR-107 and MiR-185 Can Induce Cell Cycle Arrest in Human Non Small Cell Lung Cancer Cell Lines. <i>PLoS ONE</i> , 2009, 4, e6677.	1.1	200
26	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , 2017, 4, 170112.	2.4	195
27	CAGE: precise TSS data retrieval and high-resolution promoterome mining for integrative analyses. <i>Nucleic Acids Research</i> , 2015, 43, e51-e51.	6.5	194
28	The Abundance of Short Proteins in the Mammalian Proteome. <i>PLoS Genetics</i> , 2006, 2, e52.	1.5	189
29	Redefinition of the human mast cell transcriptome by deep-CAGE sequencing. <i>Blood</i> , 2014, 123, e58-e67.	0.6	175
30	Unamplified cap analysis of gene expression on a single-molecule sequencer. <i>Genome Research</i> , 2011, 21, 1150-1159.	2.4	172
31	Transcript Annotation in FANTOM3: Mouse Gene Catalog Based on Physical cDNAs. <i>PLoS Genetics</i> , 2006, 2, e62.	1.5	165
32	Interactive visualization and analysis of large-scale sequencing datasets using ZENBU. <i>Nature Biotechnology</i> , 2014, 32, 217-219.	9.4	163
33	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> , 2017, 13, e1006641.	1.5	161
34	Transcription and enhancer profiling in human monocyte subsets. <i>Blood</i> , 2014, 123, e90-e99.	0.6	157
35	Sensitization to immune checkpoint blockade through activation of a STAT1/NK axis in the tumor microenvironment. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	147
36	Predicting cell-to-cell communication networks using NATMI. <i>Nature Communications</i> , 2020, 11, 5011.	5.8	137

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37	Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. <i>Nucleic Acids Research</i> , 2017, 45, D737-D743.	6.5	116
38	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> , 2015, 9, 114.	1.8	112
39	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> , 2014, 111, 5289-5294.	3.3	111
40	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	2.4	109
41	Novel genes regulated by Sonic Hedgehog in pluripotent mesenchymal cells. <i>Oncogene</i> , 2002, 21, 8196-8205.	2.6	108
42	scMatch: a single-cell gene expression profile annotation tool using reference datasets. <i>Bioinformatics</i> , 2019, 35, 4688-4695.	1.8	108
43	Comparison of CAGE and RNA-seq transcriptome profiling using clonally amplified and single-molecule next-generation sequencing. <i>Genome Research</i> , 2014, 24, 708-717.	2.4	99
44	Regulation of CDC25B phosphatases subcellular localization. <i>Oncogene</i> , 2000, 19, 2179-2185.	2.6	98
45	Cdc25B activity is regulated by 14-3-3. <i>Oncogene</i> , 2001, 20, 4393-4401.	2.6	96
46	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> , 2002, 168, 44-50.	0.4	94
47	Complementing tissue characterization by integrating transcriptome profiling from the Human Protein Atlas and from the FANTOM5 consortium. <i>Nucleic Acids Research</i> , 2015, 43, 6787-6798.	6.5	94
48	A rescue strategy for multimapping short sequence tags refines surveys of transcriptional activity by CAGE. <i>Genomics</i> , 2008, 91, 281-288.	1.3	92
49	Transcriptional landscape of Mycobacterium tuberculosis infection in macrophages. <i>Scientific Reports</i> , 2018, 8, 6758.	1.6	92
50	Systematic Characterization of the Zinc-Finger-Containing Proteins in the Mouse Transcriptome. <i>Genome Research</i> , 2003, 13, 1430-1442.	2.4	89
51	Pax9 and Jagged1 act downstream of Gli3 in vertebrate limb development. <i>Mechanisms of Development</i> , 2005, 122, 1218-1233.	1.7	89
52	Cdc25-dependent activation of cyclin A/cdk2 is blocked in G2 phase arrested cells independently of ATM/ATR. <i>Oncogene</i> , 2001, 20, 921-932.	2.6	84
53	Transcriptome Analysis of Recurrently Deregulated Genes across Multiple Cancers Identifies New Pan-Cancer Biomarkers. <i>Cancer Research</i> , 2016, 76, 216-226.	0.4	80
54	The enhancer and promoter landscape of human regulatory and conventional T-cell subpopulations. <i>Blood</i> , 2014, 123, e68-e78.	0.6	77

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55	The FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. <i>Genome Biology</i> , 2009, 10, R40.	13.9	73
56	A Novel Corepressor, BCoR-L1, Represses Transcription through an Interaction with CtBP. <i>Journal of Biological Chemistry</i> , 2007, 282, 15248-15257.	1.6	72
57	Analysis of the DNA methylome and transcriptome in granulopoiesis reveals timed changes and dynamic enhancer methylation. <i>Blood</i> , 2014, 123, e79-e89.	0.6	72
58	LRRN4 and UPK3B Are Markers of Primary Mesothelial Cells. <i>PLoS ONE</i> , 2011, 6, e25391.	1.1	71
59	14-3-3 Acts as an Intramolecular Bridge to Regulate cdc25B Localization and Activity. <i>Journal of Biological Chemistry</i> , 2003, 278, 28580-28587.	1.6	69
60	Systematic analysis of transcription start sites in avian development. <i>PLoS Biology</i> , 2017, 15, e2002887.	2.6	68
61	FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. <i>Genome Biology</i> , 2009, 10, R39.	13.9	67
62	Alternate transcription of the Toll-like receptor signaling cascade. <i>Genome Biology</i> , 2006, 7, R10.	13.9	66
63	FANTOM5 transcriptome catalog of cellular states based on Semantic MediaWiki. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw105.	1.4	64
64	Multiple Splicing Variants of cdc25B Regulate G2/M Progression. <i>Biochemical and Biophysical Research Communications</i> , 1999, 260, 510-515.	1.0	61
65	RECLU: a pipeline to discover reproducible transcriptional start sites and their alternative regulation using capped analysis of gene expression (CAGE). <i>BMC Genomics</i> , 2014, 15, 269.	1.2	61
66	Pseudoâ€“Messenger RNA: Phantoms of the Transcriptome. <i>PLoS Genetics</i> , 2006, 2, e23.	1.5	58
67	The frequent evolutionary birth and death of functional promoters in mouse and human. <i>Genome Research</i> , 2015, 25, 1546-1557.	2.4	55
68	The FANTOM5 collection, a data series underpinning mammalian transcriptome atlases in diverse cell types. <i>Scientific Data</i> , 2017, 4, 170113.	2.4	55
69	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
70	Ceruloplasmin Is a Novel Adipokine Which Is Overexpressed in Adipose Tissue of Obese Subjects and in Obesity-Associated Cancer Cells. <i>PLoS ONE</i> , 2014, 9, e80274.	1.1	50
71	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
72	The statistical geometry of transcriptome divergence in cell-type evolution and cancer. <i>Nature Communications</i> , 2015, 6, 6066.	5.8	49

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73	CAGE profiling of ncRNAs in hepatocellular carcinoma reveals widespread activation of retroviral LTR promoters in virus-induced tumors. <i>Genome Research</i> , 2015, 25, 1812-1824.	2.4	49
74	Genome-wide review of transcriptional complexity in mouse protein kinases and phosphatases. <i>Genome Biology</i> , 2006, 7, R5.	13.9	48
75	Mesencephalic dopaminergic neurons express a repertoire of olfactory receptors and respond to odorant-like molecules. <i>BMC Genomics</i> , 2014, 15, 729.	1.2	46
76	DeepCAGE Transcriptomics Reveal an Important Role of the Transcription Factor MAFB in the Lymphatic Endothelium. <i>Cell Reports</i> , 2015, 13, 1493-1504.	2.9	46
77	Whole genome transcriptome analysis. <i>RNA Biology</i> , 2009, 6, 107-112.	1.5	44
78	Phosphoregulators: Protein Kinases and Protein Phosphatases of Mouse. <i>Genome Research</i> , 2003, 13, 1443-1454.	2.4	43
79	Tissue-specific gene expression in soybean ( <i>Glycine max</i> ) detected by cDNA microarray analysis. <i>Journal of Plant Physiology</i> , 2002, 159, 1361-1374.	1.6	39
80	Transcriptional profiling of the human fibrillin/LTBP gene family, key regulators of mesenchymal cell functions. <i>Molecular Genetics and Metabolism</i> , 2014, 112, 73-83.	0.5	39
81	Integration of genetics and miRNA target gene network identified disease biology implicated in tissue specificity. <i>Nucleic Acids Research</i> , 2018, 46, 11898-11909.	6.5	39
82	A transient disruption of fibroblastic transcriptional regulatory network facilitates trans-differentiation. <i>Nucleic Acids Research</i> , 2014, 42, 8905-8913.	6.5	35
83	The Constrained Maximal Expression Level Owing to Haploidy Shapes Gene Content on the Mammalian X Chromosome. <i>PLoS Biology</i> , 2015, 13, e1002315.	2.6	32
84	YY1 binding association with sex-biased transcription revealed through X-linked transcript levels and allelic binding analyses. <i>Scientific Reports</i> , 2016, 6, 37324.	1.6	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	Functional annotation of the vlinc class of non-coding RNAs using systems biology approach. <i>Nucleic Acids Research</i> , 2016, 44, 3233-3252.	6.5	31
87	Bi-allelic mutations in MYL1 cause a severe congenital myopathy. <i>Human Molecular Genetics</i> , 2018, 27, 4263-4272.	1.4	31
88	Promoter-level expression clustering identifies time development of transcriptional regulatory cascades initiated by ErbB receptors in breast cancer cells. <i>Scientific Reports</i> , 2015, 5, 11999.	1.6	30
89	Linking FANTOM5 CAGE peaks to annotations with CAGEscan. <i>Scientific Data</i> , 2017, 4, 170147.	2.4	29
90	Antisense Transcription in Loci Associated to Hereditary Neurodegenerative Diseases. <i>Molecular Neurobiology</i> , 2019, 56, 5392-5415.	1.9	29

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91	Comparative transcriptomics of primary cells in vertebrates. <i>Genome Research</i> , 2020, 30, 951-961.	2.4	29
92	Characterizing Embryonic Gene Expression Patterns in the Mouse Using Nonredundant Sequence-Based Selection. <i>Genome Research</i> , 2003, 13, 2609-2620.	2.4	27
93	Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution. <i>Diabetes</i> , 2017, 66, 218-230.	0.3	27
94	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> , 2004, 23, 3067-3079.	2.6	25
95	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> , 2015, 406, 49-59.	1.6	25
96	Integrative CAGE and DNA Methylation Profiling Identify Epigenetically Regulated Genes in NSCLC. <i>Molecular Cancer Research</i> , 2017, 15, 1354-1365.	1.5	25
97	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> , 2016, 2016, .	1.4	24
98	Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. <i>EBioMedicine</i> , 2017, 24, 257-266.	2.7	24
99	New era in genetics of early-onset muscle disease: Breakthroughs and challenges. <i>Seminars in Cell and Developmental Biology</i> , 2017, 64, 160-170.	2.3	24
100	Technical Advance: Transcription factor, promoter, and enhancer utilization in human myeloid cells. <i>Journal of Leukocyte Biology</i> , 2015, 97, 985-995.	1.5	23
101	Reinforcing the association between distal 1q43 CNVs and structural brain disorder: A case of a complex 1q43 CNV and a review of the literature. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2016, 171, 458-467.	1.1	23
102	Unravelling the molecular basis for regulatory T cell plasticity and loss of function in disease. <i>Clinical and Translational Immunology</i> , 2018, 7, e1011.	1.7	23
103	Automated Workflow for Preparation of cDNA for Cap Analysis of Gene Expression on a Single Molecule Sequencer. <i>PLoS ONE</i> , 2012, 7, e30809.	1.1	22
104	Transcriptional Dynamics Reveal Critical Roles for Non-coding RNAs in the Immediate-Early Response. <i>PLoS Computational Biology</i> , 2015, 11, e1004217.	1.5	22
105	CCL2 enhances pluripotency of human induced pluripotent stem cells by activating hypoxia related genes. <i>Scientific Reports</i> , 2014, 4, 5228.	1.6	21
106	High-throughput transcription profiling identifies putative epigenetic regulators of hematopoiesis. <i>Blood</i> , 2014, 123, e46-e57.	0.6	21
107	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> , 2014, 15, 413.	3.8	20
108	Brain-Enriched Coding and Long Non-coding RNA Genes Are Overrepresented in Recurrent Neurodevelopmental Disorder CNVs. <i>Cell Reports</i> , 2020, 33, 108307.	2.9	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	PhosphoregDB: the tissue and sub-cellular distribution of mammalian protein kinases and phosphatases. <i>BMC Bioinformatics</i> , 2006, 7, 82.	1.2	18
111	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> , 2016, 6, 33666.	1.6	18
112	Building promoter aware transcriptional regulatory networks using siRNA perturbation and deepCAGE. <i>Nucleic Acids Research</i> , 2010, 38, 8141-8148.	6.5	17
113	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
114	Chromatin states reveal functional associations for globally defined transcription start sites in four human cell lines. <i>BMC Genomics</i> , 2014, 15, 120.	1.2	17
115	Expression Levels of Therapeutic Targets as Indicators of Sensitivity to Targeted Therapeutics. <i>Molecular Cancer Therapeutics</i> , 2019, 18, 2480-2489.	1.9	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	Exploration of the Cell-Cycle Genes Found Within the RIKEN FANTOM2 Data Set. <i>Genome Research</i> , 2003, 13, 1366-1375.	2.4	16
118	Regulatory interdependence of myeloid transcription factors revealed by Matrix RNAi analysis. <i>Genome Biology</i> , 2009, 10, R121.	13.9	16
119	Specific Mesothelial Signature Marks the Heterogeneity of Mesenchymal Stem Cells From High-Grade Serous Ovarian Cancer. <i>Stem Cells</i> , 2014, 32, 2998-3011.	1.4	16
120	DeepCAGE transcriptomics identify HOXD10 as transcription factor regulating lymphatic endothelial responses to VEGF-C. <i>Journal of Cell Science</i> , 2016, 129, 2573-85.	1.2	15
121	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> , 2020, 11, 1269.	2.2	14
122	Comprehensive Characterization of Transcriptional Activity during Influenza A Virus Infection Reveals Biases in Cap-Snatching of Host RNA Sequences. <i>Journal of Virology</i> , 2020, 94, .	1.5	14
123	The Evolution of Human Cells in Terms of Protein Innovation. <i>Molecular Biology and Evolution</i> , 2014, 31, 1364-1374.	3.5	13
124	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
125	CAGEd-oPOSSUM: motif enrichment analysis from CAGE-derived TSSs. <i>Bioinformatics</i> , 2016, 32, 2858-2860.	1.8	13
126	Conserved temporal ordering of promoter activation implicates common mechanisms governing the immediate early response across cell types and stimuli. <i>Open Biology</i> , 2018, 8, 180011.	1.5	13



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127	Identification of novel cerebellar developmental transcriptional regulators with motif activity analysis. BMC Genomics, 2019, 20, 718.	1.2	11
128	Myoglobinopathy is an adult-onset autosomal dominant myopathy with characteristic sarcoplasmic inclusions. Nature Communications, 2019, 10, 1396.	5.8	11
129	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. Nature Communications, 2021, 12, 3297.	5.8	11
130	Intra- and intertumoral heterogeneity of liver metastases in a patient with uveal melanoma revealed by single-cell RNA sequencing. Journal of Physical Education and Sports Management, 2021, 7, a006111.	0.5	11
131	CAGE-defined promoter regions of the genes implicated in Rett Syndrome. BMC Genomics, 2014, 15, 1177.	1.2	10
132	Human genetics and genomics meetings going virtual: practical lessons learned from two international meetings in early 2020. Human Genomics, 2020, 14, 27.	1.4	8
133	MaxHiC: A robust background correction model to identify biologically relevant chromatin interactions in Hi-C and capture Hi-C experiments. PLoS Computational Biology, 2022, 18, e1010241.	1.5	7
134	Monitoring transcription initiation activities in rat and dog. Scientific Data, 2017, 4, 170173.	2.4	6
135	Discovery of Transcription Factors Novel to Mouse Cerebellar Granule Cell Development Through Laser-Capture Microdissection. Cerebellum, 2018, 17, 308-325.	1.4	6
136	Functional validation of variants of unknown significance using CRISPR gene editing and transcriptomics: A Kleefstra syndrome case study. Gene, 2022, 821, 146287.	1.0	6
137	Bi-allelic loss-of-function OBSCN variants predispose individuals to severe recurrent rhabdomyolysis. Brain, 2022, 145, 3985-3998.	3.7	6
138	Annotating non-coding transcription using functional genomics strategies. Briefings in Functional Genomics & Proteomics, 2009, 8, 437-443.	3.8	5
139	CAGExploreR: an R package for the analysis and visualization of promoter dynamics across multiple experiments. Bioinformatics, 2014, 30, 1183-1184.	1.8	5
140	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. Cell, 2010, 141, 369.	13.5	4
141	A Transcriptional Switch Point During Hematopoietic Stem and Progenitor Cell Ontogeny. Stem Cells and Development, 2017, 26, 314-327.	1.1	4
142	Transcription start site profiling of 15 anatomical regions of the Macaca mulatta central nervous system. Scientific Data, 2017, 4, 170163.	2.4	4
143	Improved CRISPR/Cas9 gene editing in primary human myoblasts using low confluency cultures on Matrigel. Skeletal Muscle, 2021, 11, 23.	1.9	4
144	Transcription Factor NKX6.3 Sheds Light on Gastric Cancer Progression. EBioMedicine, 2016, 9, 9-10.	2.7	2

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145	Application of Gene Expression Trajectories Initiated from ErbB Receptor Activation Highlights the Dynamics of Divergent Promoter Usage. PLoS ONE, 2015, 10, e0144176.	1.1	1
146	Deep sequencing blood transcriptomes. Blood, 2014, 123, 2595-2596.	0.6	0