

# Piero Carninci

## List of Publications by Year in descending order

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404  
papers

95,196  
citations

1606

105  
h-index

300

291  
g-index

460  
all docs

460  
docs citations

460  
times ranked

95473  
citing authors

#	ARTICLE	IF	CITATIONS
1	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	13.7	15,516
2	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	13.7	6,319
3	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	13.7	4,709
4	Landscape of transcription in human cells. <i>Nature</i> , 2012, 489, 101-108.	13.7	4,484
5	The GENCODE v7 catalog of human long noncoding RNAs: Analysis of their gene structure, evolution, and expression. <i>Genome Research</i> , 2012, 22, 1775-1789.	2.4	4,428
6	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	6.0	3,227
7	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014, 507, 455-461.	13.7	2,269
8	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	13.7	1,838
9	Monitoring the expression profiles of 7000 Arabidopsis genes under drought, cold and high-salinity stresses using a full-length cDNA microarray. <i>Plant Journal</i> , 2002, 31, 279-292.	2.8	1,697
10	Insights into social insects from the genome of the honeybee <i>Apis mellifera</i> . <i>Nature</i> , 2006, 443, 931-949.	13.7	1,648
11	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16899-16903.	3.3	1,610
12	Antisense Transcription in the Mammalian Transcriptome. <i>Science</i> , 2005, 309, 1564-1566.	6.0	1,553
13	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
14	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	2.8	1,547
15	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). <i>PLoS Biology</i> , 2011, 9, e1001046.	2.6	1,257
16	Genome-wide analysis of mammalian promoter architecture and evolution. <i>Nature Genetics</i> , 2006, 38, 626-635.	9.4	1,201
17	Monitoring the Expression Pattern of 1300 Arabidopsis Genes under Drought and Cold Stresses by Using a Full-Length cDNA Microarray. <i>Plant Cell</i> , 2001, 13, 61-72.	3.1	986
18	Direct generation of functional dopaminergic neurons from mouse and human fibroblasts. <i>Nature</i> , 2011, 476, 224-227.	13.7	941

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19	Comprehensive Analysis of NAC Family Genes in <i>Oryza sativa</i> and <i>Arabidopsis thaliana</i> . <i>DNA Research</i> , 2003, 10, 239-247.	1.5	911
20	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017, 543, 199-204.	13.7	898
21	Long non-coding antisense RNA controls Uchl1 translation through an embedded SINEB2 repeat. <i>Nature</i> , 2012, 491, 454-457.	13.7	881
22	Empirical Analysis of Transcriptional Activity in the <i>Arabidopsis</i> Genome. <i>Science</i> , 2003, 302, 842-846.	6.0	853
23	Collection, Mapping, and Annotation of Over 28,000 cDNA Clones from japonica Rice. <i>Science</i> , 2003, 301, 376-379.	6.0	834
24	The regulated retrotransposon transcriptome of mammalian cells. <i>Nature Genetics</i> , 2009, 41, 563-571.	9.4	731
25	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015, 16, 22.	3.8	687
26	A draft network of ligand-receptor-mediated multicellular signalling in human. <i>Nature Communications</i> , 2015, 6, 7866.	5.8	676
27	Cap analysis gene expression for high-throughput analysis of transcriptional starting point and identification of promoter usage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15776-15781.	3.3	673
28	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 140, 744-752.	13.5	667
29	Functional annotation of a full-length mouse cDNA collection. <i>Nature</i> , 2001, 409, 685-690.	13.7	653
30	Diversity and dynamics of the <i>Drosophila</i> transcriptome. <i>Nature</i> , 2014, 512, 393-399.	13.7	647
31	Functional Annotation of a Full-Length <i>Arabidopsis</i> cDNA Collection. <i>Science</i> , 2002, 296, 141-145.	6.0	631
32	Somatic retrotransposition alters the genetic landscape of the human brain. <i>Nature</i> , 2011, 479, 534-537.	13.7	621
33	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , 2015, 347, 1010-1014.	6.0	517
34	The Status, Quality, and Expansion of the NIH Full-Length cDNA Project: The Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2004, 14, 2121-2127.	2.4	486
35	Site-specific DICER and DROSHA RNA products control the DNA-damage response. <i>Nature</i> , 2012, 488, 231-235.	13.7	460
36	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017, 35, 872-878.	9.4	456

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37	Metazoan promoters: emerging characteristics and insights into transcriptional regulation. <i>Nature Reviews Genetics</i> , 2012, 13, 233-245.	7.7	448
38	Mammalian RNA polymerase II core promoters: insights from genome-wide studies. <i>Nature Reviews Genetics</i> , 2007, 8, 424-436.	7.7	435
39	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
40	CAGE: cap analysis of gene expression. <i>Nature Methods</i> , 2006, 3, 211-222.	9.0	397
41	Monitoring the expression pattern of around 7,000 Arabidopsis genes under ABA treatments using a full-length cDNA microarray. <i>Functional and Integrative Genomics</i> , 2002, 2, 282-291.	1.4	394
42	Small RNAs derived from snoRNAs. <i>Rna</i> , 2009, 15, 1233-1240.	1.6	384
43	The Reality of Pervasive Transcription. <i>PLoS Biology</i> , 2011, 9, e1000625.	2.6	380
44	Endogenous Retrotransposition Activates Oncogenic Pathways in Hepatocellular Carcinoma. <i>Cell</i> , 2013, 153, 101-111.	13.5	352
45	Comparative genomics of <i>Physcomitrella patens</i> gametophytic transcriptome and <i>Arabidopsis thaliana</i> : Implication for land plant evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 8007-8012.	3.3	341
46	Conservation and divergence in Toll-like receptor 4-regulated gene expression in primary human versus mouse macrophages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E944-53.	3.3	332
47	Tiny RNAs associated with transcription start sites in animals. <i>Nature Genetics</i> , 2009, 41, 572-578.	9.4	327
48	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
49	High-Efficiency Full-Length cDNA Cloning by Biotinylated CAP Trapper. <i>Genomics</i> , 1996, 37, 327-336.	1.3	297
50	Genome-wide analysis of cancer/testis gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20422-20427.	3.3	295
51	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	2.6	290
52	Complex Loci in Human and Mouse Genomes. <i>PLoS Genetics</i> , 2006, 2, e47.	1.5	290
53	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
54	Normalization and Subtraction of Cap-Trapper-Selected cDNAs to Prepare Full-Length cDNA Libraries for Rapid Discovery of New Genes. <i>Genome Research</i> , 2000, 10, 1617-1630.	2.4	263

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55	Hidden layers of human small RNAs. BMC Genomics, 2008, 9, 157.	1.2	255
56	5â€² endâ€²-centered expression profiling using cap-analysis gene expression and next-generation sequencing. Nature Protocols, 2012, 7, 542-561.	5.5	246
57	Unexpected expression of Î±- and Î²-globin in mesencephalic dopaminergic neurons and glial cells. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 15454-15459.	3.3	240
58	A code for transcription initiation in mammalian genomes. Genome Research, 2008, 18, 1-12.	2.4	237
59	Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 520-524.	3.3	231
60	Antisense Transcripts With FANTOM2 Clone Set and Their Implications for Gene Regulation. Genome Research, 2003, 13, 1324-1334.	2.4	224
61	Amphioxus functional genomics and the origins of vertebrate gene regulation. Nature, 2018, 564, 64-70.	13.7	224
62	High-efficiency cloning of Arabidopsis full-length cDNA by biotinylated CAP trapper. Plant Journal, 1998, 15, 707-720.	2.8	217
63	Single-cell transcriptomics reveals expansion of cytotoxic CD4 T cells in supercentenarians. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 24242-24251.	3.3	215
64	Transcriptome analysis of the aphid bacteriocyte, the symbiotic host cell that harbors an endocellular mutualistic bacterium, Buchnera. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 5477-5482.	3.3	212
65	Genome-wide analysis of promoter architecture in <i>Drosophila melanogaster</i> . Genome Research, 2011, 21, 182-192.	2.4	211
66	Chromatin-associated RNA interference components contribute to transcriptional regulation in <i>Drosophila</i> . Nature, 2011, 480, 391-395.	13.7	203
67	Delineating developmental and metabolic pathways in vivo by expression profiling using the RIKEN set of 18,816 full-length enriched mouse cDNA arrays. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 2199-2204.	3.3	197
68	Chromatin signatures and retrotransposon profiling in mouse embryos reveal regulation of LINE-1 by RNA. Nature Structural and Molecular Biology, 2013, 20, 332-338.	3.6	197
69	FANTOM5 CAGE profiles of human and mouse samples. Scientific Data, 2017, 4, 170112.	2.4	195
70	CAGEr: precise TSS data retrieval and high-resolution promoterome mining for integrative analyses. Nucleic Acids Research, 2015, 43, e51-e51.	6.5	194
71	The Abundance of Short Proteins in the Mammalian Proteome. PLoS Genetics, 2006, 2, e52.	1.5	189
72	Two independent transcription initiation codes overlap on vertebrate core promoters. Nature, 2014, 507, 381-385.	13.7	182

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73	The Drosophila Gene Collection: Identification of Putative Full-Length cDNAs for 70% of D. melanogaster Genes. <i>Genome Research</i> , 2002, 12, 1294-1300.	2.4	180
74	Discovery and functional analysis of lncRNAs: Methodologies to investigate an uncharacterized transcriptome. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 3-15.	0.9	178
75	Long non-coding RNA modifies chromatin. <i>BioEssays</i> , 2011, 33, 830-839.	1.2	177
76	A molecular neuroethological approach for identifying and characterizing a cascade of behaviorally regulated genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15212-15217.	3.3	176
77	High-fidelity promoter profiling reveals widespread alternative promoter usage and transposon-driven developmental gene expression. <i>Genome Research</i> , 2013, 23, 169-180.	2.4	176
78	Redefinition of the human mast cell transcriptome by deep-CAGE sequencing. <i>Blood</i> , 2014, 123, e58-e67.	0.6	175
79	Unamplified cap analysis of gene expression on a single-molecule sequencer. <i>Genome Research</i> , 2011, 21, 1150-1159.	2.4	172
80	Update of the FANTOM web resource: expansion to provide additional transcriptome atlases. <i>Nucleic Acids Research</i> , 2019, 47, D752-D758.	6.5	172
81	Detecting Expressed Genes Using CAGE. <i>Methods in Molecular Biology</i> , 2014, 1164, 67-85.	0.4	170
82	[2] High-efficiency full-length cDNA cloning. <i>Methods in Enzymology</i> , 1999, 303, 19-44.	0.4	169
83	Impact of Alternative Initiation, Splicing, and Termination on the Diversity of the mRNA Transcripts Encoded by the Mouse Transcriptome. <i>Genome Research</i> , 2003, 13, 1290-1300.	2.4	168
84	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012, 22, 1658-1667.	2.4	166
85	Tag-based approaches for transcriptome research and genome annotation. <i>Nature Methods</i> , 2005, 2, 495-502.	9.0	165
86	Transcript Annotation in FANTOM3: Mouse Gene Catalog Based on Physical cDNAs. <i>PLoS Genetics</i> , 2006, 2, e62.	1.5	165
87	NMDA Receptor Regulation Prevents Regression of Visual Cortical Function in the Absence of Mecp2. <i>Neuron</i> , 2012, 76, 1078-1090.	3.8	163
88	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
89	Transcription and enhancer profiling in human monocyte subsets. <i>Blood</i> , 2014, 123, e90-e99.	0.6	157
90	Targeting a Complex Transcriptome: The Construction of the Mouse Full-Length cDNA Encyclopedia. <i>Genome Research</i> , 2003, 13, 1273-1289.	2.4	154

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91	Linking promoters to functional transcripts in small samples with nanoCAGE and CAGEscan. <i>Nature Methods</i> , 2010, 7, 528-534.	9.0	152
92	Clusters of Internally Primed Transcripts Reveal Novel Long Noncoding RNAs. <i>PLoS Genetics</i> , 2006, 2, e37.	1.5	148
93	Comparative validation of the <i>D. melanogaster</i> modENCODE transcriptome annotation. <i>Genome Research</i> , 2014, 24, 1209-1223.	2.4	147
94	Molecular mechanisms of pituitary organogenesis: In search of novel regulatory genes. <i>Molecular and Cellular Endocrinology</i> , 2010, 323, 4-19.	1.6	140
95	Genome sequence and analysis of the Japanese morning glory <i>Ipomoea nil</i> . <i>Nature Communications</i> , 2016, 7, 13295.	5.8	138
96	Methods for analyzing deep sequencing expression data: constructing the human and mouse promoterome with deepCAGE data. <i>Genome Biology</i> , 2009, 10, R79.	13.9	131
97	PAPD5-mediated 3' adenylation and subsequent degradation of miR-21 is disrupted in proliferative disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11467-11472.	3.3	130
98	Identification of Putative Noncoding RNAs Among the RIKEN Mouse Full-Length cDNA Collection. <i>Genome Research</i> , 2003, 13, 1301-1306.	2.4	129
99	Genome-wide detection and analysis of hippocampus core promoters using DeepCAGE. <i>Genome Research</i> , 2009, 19, 255-265.	2.4	128
100	Cross-mapping and the identification of editing sites in mature microRNAs in high-throughput sequencing libraries. <i>Genome Research</i> , 2010, 20, 257-264.	2.4	126
101	Transcriptional network dynamics in macrophage activation. <i>Genomics</i> , 2006, 88, 133-142.	1.3	125
102	Noncoding RNA transcription beyond annotated genes. <i>Current Opinion in Genetics and Development</i> , 2007, 17, 139-144.	1.5	125
103	Genetic control of the innate immune response. <i>BMC Immunology</i> , 2003, 4, 5.	0.9	119
104	Dynamic regulation of the transcription initiation landscape at single nucleotide resolution during vertebrate embryogenesis. <i>Genome Research</i> , 2013, 23, 1938-1950.	2.4	119
105	Discrimination of Non-Protein-Coding Transcripts from Protein-Coding mRNA. <i>RNA Biology</i> , 2006, 3, 40-48.	1.5	118
106	Biased Allelic Expression in Human Primary Fibroblast Single Cells. <i>American Journal of Human Genetics</i> , 2015, 96, 70-80.	2.6	117
107	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
108	Antisense transcripts with rice full-length cDNAs. <i>Genome Biology</i> , 2003, 5, R5.	13.9	112

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109	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
110	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
111	The ORFeome Collaboration: a genome-scale human ORF-clone resource. <i>Nature Methods</i> , 2016, 13, 191-192.	9.0	111
112	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	2.4	109
113	Comparative Analysis of Apoptosis and Inflammation Genes of Mice and Humans. <i>Genome Research</i> , 2003, 13, 1376-1388.	2.4	104
114	Heterotachy in Mammalian Promoter Evolution. <i>PLoS Genetics</i> , 2006, 2, e30.	1.5	102
115	C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution. <i>Nature Communications</i> , 2019, 10, 360.	5.8	102
116	Full-length cDNAs from chicken bursal lymphocytes to facilitate gene function analysis. <i>Genome Biology</i> , 2004, 6, R6.	13.9	101
117	Transcriptional and structural impact of TATA-initiation site spacing in mammalian core promoters. <i>Genome Biology</i> , 2006, 7, R78.	13.9	101
118	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
119	RADICL-seq identifies general and cell type-specific principles of genome-wide RNA-chromatin interactions. <i>Nature Communications</i> , 2020, 11, 1018.	5.8	98
120	Discovery of Imprinted Transcripts in the Mouse Transcriptome Using Large-Scale Expression Profiling. <i>Genome Research</i> , 2003, 13, 1402-1409.	2.4	96
121	Paradigm shifts in genomics through the FANTOM projects. <i>Mammalian Genome</i> , 2015, 26, 391-402.	1.0	96
122	Mice and Men: Their Promoter Properties. <i>PLoS Genetics</i> , 2006, 2, e54.	1.5	95
123	CAGE (Cap Analysis of Gene Expression): A Protocol for the Detection of Promoter and Transcriptional Networks. <i>Methods in Molecular Biology</i> , 2012, 786, 181-200.	0.4	94
124	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
125	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
126	Transcriptional landscape of Mycobacterium tuberculosis infection in macrophages. <i>Scientific Reports</i> , 2018, 8, 6758.	1.6	92



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127	Mouse Proteome Analysis. <i>Genome Research</i> , 2003, 13, 1335-1344.	2.4	91
128	The complexity of the mammalian transcriptome. <i>Journal of Physiology</i> , 2006, 575, 321-332.	1.3	91
129	High Efficiency Selection of Full-length cDNA by Improved Biotinylated Cap Trapper. <i>DNA Research</i> , 1997, 4, 61-66.	1.5	90
130	A novel feature of microsatellites in plants: a distribution gradient along the direction of transcription. <i>FEBS Letters</i> , 2003, 554, 17-22.	1.3	89
131	Systematic Characterization of the Zinc-Finger-Containing Proteins in the Mouse Transcriptome. <i>Genome Research</i> , 2003, 13, 1430-1442.	2.4	89
132	A damaged genome's transcriptional landscape through multilayered expression profiling around in situ-mapped DNA double-strand breaks. <i>Nature Communications</i> , 2017, 8, 15656.	5.8	89
133	Trehalose-enhanced isolation of neuronal sub-types from adult mouse brain. <i>BioTechniques</i> , 2012, 52, 381-385.	0.8	87
134	Tagging mammalian transcription complexity. <i>Trends in Genetics</i> , 2006, 22, 501-510.	2.9	85
135	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. <i>Genome Research</i> , 2010, 20, 791-803.	2.4	84
136	SINEUPs: A new class of natural and synthetic antisense long non-coding RNAs that activate translation. <i>RNA Biology</i> , 2015, 12, 771-779.	1.5	84
137	SINEUPs are modular antisense long non-coding RNAs that increase synthesis of target proteins in cells. <i>Frontiers in Cellular Neuroscience</i> , 2015, 9, 174.	1.8	81
138	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
139	Transcriptional profiling of genes responsive to abscisic acid and gibberellin in rice: phenotyping and comparative analysis between rice and Arabidopsis. <i>Physiological Genomics</i> , 2004, 17, 87-100.	1.0	78
140	CAGE Basic/Analysis Databases: the CAGE resource for comprehensive promoter analysis. <i>Nucleic Acids Research</i> , 2006, 34, D632-D636.	6.5	78
141	Prevention of hepatocellular carcinoma by targeting MYCN-positive liver cancer stem cells with acyclic retinoid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4969-4974.	3.3	78
142	Multifaceted mammalian transcriptome. <i>Current Opinion in Cell Biology</i> , 2008, 20, 274-280.	2.6	77
143	The enhancer and promoter landscape of human regulatory and conventional T-cell subpopulations. <i>Blood</i> , 2014, 123, e68-e78.	0.6	77
144	DNA damage response inhibition at dysfunctional telomeres by modulation of telomeric DNA damage response RNAs. <i>Nature Communications</i> , 2017, 8, 13980.	5.8	76

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145	Dynamic usage of transcription start sites within core promoters. <i>Genome Biology</i> , 2006, 7, R118.	13.9	75
146	Balanced-Size and Long-Size Cloning of Full-Length, Cap-Trapped cDNAs into Vectors of the Novel $\hat{\iota}$ -FLC Family Allows Enhanced Gene Discovery Rate and Functional Analysis. <i>Genomics</i> , 2001, 77, 79-90.	1.3	74
147	Solution Structure of the SEA Domain from the Murine Homologue of Ovarian Cancer Antigen CA125 (MUC16). <i>Journal of Biological Chemistry</i> , 2004, 279, 13174-13182.	1.6	74
148	Placental expression profiling in preeclampsia: local overproduction of hemoglobin may drive pathological changes. <i>Fertility and Sterility</i> , 2008, 90, 1834-1843.	0.5	74
149	The Mouse Secretome: Functional Classification of the Proteins Secreted Into the Extracellular Environment. <i>Genome Research</i> , 2003, 13, 1350-1359.	2.4	73
150	The FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. <i>Genome Biology</i> , 2009, 10, R40.	13.9	73
151	LOCATE: a mouse protein subcellular localization database. <i>Nucleic Acids Research</i> , 2006, 34, D213-D217.	6.5	72
152	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
153	NET-CAGE characterizes the dynamics and topology of human transcribed cis-regulatory elements. <i>Nature Genetics</i> , 2019, 51, 1369-1379.	9.4	72
154	refTSS: A Reference Data Set for Human and Mouse Transcription Start Sites. <i>Journal of Molecular Biology</i> , 2019, 431, 2407-2422.	2.0	72
155	Gene discovery in genetically labeled single dopaminergic neurons of the retina. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 5069-5074.	3.3	70
156	Systematic Expression Profiling of the Mouse Transcriptome Using RIKEN cDNA Microarrays. <i>Genome Research</i> , 2003, 13, 1318-1323.	2.4	69
157	A Simple Physical Model Predicts Small Exon Length Variations. <i>PLoS Genetics</i> , 2006, 2, e45.	1.5	69
158	Evolutionary turnover of mammalian transcription start sites. <i>Genome Research</i> , 2006, 16, 713-722.	2.4	68
159	FANTOM5 CAGE profiles of human and mouse reprocessed for GRCh38 and GRCm38 genome assemblies. <i>Scientific Data</i> , 2017, 4, 170107.	2.4	68
160	Systematic analysis of transcription start sites in avian development. <i>PLoS Biology</i> , 2017, 15, e2002887.	2.6	68
161	Comparative Analysis of Plant and Animal Calcium Signal Transduction Element Using Plant Full-Length cDNA Data. <i>Molecular Biology and Evolution</i> , 2004, 21, 1855-1870.	3.5	67
162	FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. <i>Genome Biology</i> , 2009, 10, R39.	13.9	67

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163	Solution structure of the RWD domain of the mouse GCN2 protein. <i>Protein Science</i> , 2004, 13, 2089-2100.	3.1	66
164	Alternate transcription of the Toll-like receptor signaling cascade. <i>Genome Biology</i> , 2006, 7, R10.	13.9	66
165	MOIRAI: a compact workflow system for CAGE analysis. <i>BMC Bioinformatics</i> , 2014, 15, 144.	1.2	66
166	Suppression of artifacts and barcode bias in high-throughput transcriptome analyses utilizing template switching. <i>Nucleic Acids Research</i> , 2013, 41, e44-e44.	6.5	65
167	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
168	From "Cellular" RNA to "Smart" RNA: Multiple Roles of RNA in Genome Stability and Beyond. <i>Chemical Reviews</i> , 2018, 118, 4365-4403.	23.0	63
169	Discovery of transcriptional regulators and signaling pathways in the developing pituitary gland by bioinformatic and genomic approaches. <i>Genomics</i> , 2009, 93, 449-460.	1.3	61
170	NanoCAGE: A High-Resolution Technique to Discover and Interrogate Cell Transcriptomes. <i>Cold Spring Harbor Protocols</i> , 2011, 2011, pdb.prot5559-pdb.prot5559.	0.2	61
171	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
172	Krimper Enforces an Antisense Bias on piRNA Pools by Binding AGO3 in the Drosophila Germline. <i>Molecular Cell</i> , 2015, 59, 553-563.	4.5	61
173	On biased distribution of introns in various eukaryotes. <i>Gene</i> , 2002, 300, 89-95.	1.0	60
174	Altruistic functions for selfish DNA. <i>Cell Cycle</i> , 2009, 8, 2895-2900.	1.3	60
175	Pseudo" Messenger RNA: Phantoms of the Transcriptome. <i>PLoS Genetics</i> , 2006, 2, e23.	1.5	58
176	RNA Dust: Where are the Genes?. <i>DNA Research</i> , 2010, 17, 51-59.	1.5	58
177	Identification of antisense long noncoding RNAs that function as SINEUIPs in human cells. <i>Scientific Reports</i> , 2016, 6, 33605.	1.6	58
178	Genomics Approach to Abscisic Acid- and Gibberellin-responsive Genes in Rice. <i>DNA Research</i> , 2003, 10, 249-261.	1.5	57
179	FANTOM enters 20th year: expansion of transcriptomic atlases and functional annotation of non-coding RNAs. <i>Nucleic Acids Research</i> , 2021, 49, D892-D898.	6.5	57
180	Genomic organization of transcriptomes in mammals: Coregulation and cofunctionality. <i>Genomics</i> , 2007, 89, 580-587.	1.3	56

#	ARTICLE	IF	CITATIONS
181	The frequent evolutionary birth and death of functional promoters in mouse and human. <i>Genome Research</i> , 2015, 25, 1546-1557.	2.4	55
182	The FANTOM5 collection, a data series underpinning mammalian transcriptome atlases in diverse cell types. <i>Scientific Data</i> , 2017, 4, 170113.	2.4	55
183	Multiple tissue-specific promoters control expression of the murine tartrate-resistant acid phosphatase gene. <i>Gene</i> , 2003, 307, 111-123.	1.0	54
184	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
185	A Comprehensive Transcript Map of the Mouse Gnas Imprinted Complex. <i>Genome Research</i> , 2003, 13, 1410-1415.	2.4	53
186	RIKEN Integrated Sequence Analysis (RISA) System--384-Format Sequencing Pipeline with 384 Multicapillary Sequencer. <i>Genome Research</i> , 2000, 10, 1757-1771.	2.4	52
187	Promoter architecture of mouse olfactory receptor genes. <i>Genome Research</i> , 2012, 22, 486-497.	2.4	52
188	Gene Organization in Rice Revealed by Full-Length cDNA Mapping and Gene Expression Analysis through Microarray. <i>PLoS ONE</i> , 2007, 2, e1235.	1.1	51
189	Identification and Analysis of Chromodomain-Containing Proteins Encoded in the Mouse Transcriptome. <i>Genome Research</i> , 2003, 13, 1416-1429.	2.4	50
190	The effect of genetic variation on promoter usage and enhancer activity. <i>Nature Communications</i> , 2017, 8, 1358.	5.8	50
191	Cloning Full-Length, Cap-Trapper-Selected cDNAs by Using the Single-Strand Linker Ligation Method. <i>BioTechniques</i> , 2001, 30, 1250-1254.	0.8	49
192	Solution structure of a BOLA-like protein from <i>Mus musculus</i> . <i>Protein Science</i> , 2004, 13, 545-548.	3.1	49
193	Cytoskeletal Rearrangements in Synovial Fibroblasts as a Novel Pathophysiological Determinant of Modeled Rheumatoid Arthritis. <i>PLoS Genetics</i> , 2005, 1, e48.	1.5	49
194	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
195	Digital expression profiling of the compartmentalized translome of Purkinje neurons. <i>Genome Research</i> , 2014, 24, 1396-1410.	2.4	49
196	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
197	Genome-wide review of transcriptional complexity in mouse protein kinases and phosphatases. <i>Genome Biology</i> , 2006, 7, R5.	13.9	48
198	SCP Portalen: human and mouse single-cell centric database. <i>Nucleic Acids Research</i> , 2018, 46, D781-D787.	6.5	48

#	ARTICLE	IF	CITATIONS
199	Characterization of Gene Expression in Mouse Blastocyst Using Single-Pass Sequencing of 3995 Clones. <i>Genomics</i> , 1998, 49, 167-179.	1.3	47
200	Construction of a full-length cDNA library from young spikelets of hexaploid wheat and its characterization by large-scale sequencing of expressed sequence tags. <i>Genes and Genetic Systems</i> , 2004, 79, 227-232.	0.2	47
201	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
202	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
203	Libraries enriched for alternatively spliced exons reveal splicing patterns in melanocytes and melanomas. <i>Nature Methods</i> , 2004, 1, 233-239.	9.0	45
204	The long and short of RNAs. <i>Nature</i> , 2009, 457, 974-975.	13.7	45
205	Kinesin Superfamily Proteins (KIFs) in the Mouse Transcriptome. <i>Genome Research</i> , 2003, 13, 1455-1465.	2.4	44
206	Whole genome transcriptome analysis. <i>RNA Biology</i> , 2009, 6, 107-112.	1.5	44
207	Phosphoregulators: Protein Kinases and Protein Phosphatases of Mouse. <i>Genome Research</i> , 2003, 13, 1443-1454.	2.4	43
208	Temporal dynamics and transcriptional control using single-cell gene expression analysis. <i>Genome Biology</i> , 2013, 14, R118.	13.9	43
209	Continued Discovery of Transcriptional Units Expressed in Cells of the Mouse Mononuclear Phagocyte Lineage. <i>Genome Research</i> , 2003, 13, 1360-1365.	2.4	41
210	DEIVA: a web application for interactive visual analysis of differential gene expression profiles. <i>BMC Genomics</i> , 2017, 18, 47.	1.2	41
211	SINEUP Non-coding RNA Targeting GDNF Rescues Motor Deficits and Neurodegeneration in a Mouse Model of Parkinson's Disease. <i>Molecular Therapy</i> , 2020, 28, 642-652.	3.7	41
212	Constructing the landscape of the mammalian transcriptome. <i>Journal of Experimental Biology</i> , 2007, 210, 1497-1506.	0.8	40
213	Nuclear Pore Complex Protein Mediated Nuclear Localization of Dicer Protein in Human Cells. <i>PLoS ONE</i> , 2011, 6, e23385.	1.1	40
214	Increased specificity of reverse transcription priming by trehalose and oligo-blockers allows high-efficiency window separation of mRNA display. <i>Nucleic Acids Research</i> , 1999, 27, 1345-1349.	6.5	39
215	Cl $\pm$ 14 is a candidate mediator of sweet/umami signal transduction in the posterior region of the mouse tongue. <i>Biochemical and Biophysical Research Communications</i> , 2008, 376, 504-508.	1.0	39
216	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

#	ARTICLE	IF	CITATIONS
217	Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 3455-3460.	3.3	38
218	Differential Expression of Genes within the Cochlea as Defined by a Custom Mouse Inner Ear Microarray. JARO - Journal of the Association for Research in Otolaryngology, 2005, 6, 75-89.	0.9	38
219	Transcriptional, post-transcriptional and chromatin-associated regulation of pri-miRNAs, pre-miRNAs and moRNAs. Nucleic Acids Research, 2016, 44, 3070-3081.	6.5	38
220	Comparative evaluation of 5' end-sequence quality of clones in CAP trapper and other full-length-cDNA libraries. Gene, 2001, 263, 93-102.	1.0	37
221	Widespread genome transcription: New possibilities for RNA therapies. Biochemical and Biophysical Research Communications, 2014, 452, 294-301.	1.0	37
222	Dual-initiation promoters with intertwined canonical and TCT/TOP transcription start sites diversify transcript processing. Nature Communications, 2020, 11, 168.	5.8	37
223	The devil in the details of RNA-seq. Nature Biotechnology, 2014, 32, 882-884.	9.4	35
224	Engineering mammalian cell factories with SINEUP noncoding RNAs to improve translation of secreted proteins. Gene, 2015, 569, 287-293.	1.0	35
225	Recounting the FANTOM CAGE-Associated Transcriptome. Genome Research, 2020, 30, 1073-1081.	2.4	35
226	The Short Non-Coding Transcriptome of the Protozoan Parasite Trypanosoma cruzi. PLoS Neglected Tropical Diseases, 2011, 5, e1283.	1.3	35
227	Correlation between sequence conservation of the 5' untranslated region and codon usage bias in Mus musculus genes. Gene, 2001, 276, 101-105.	1.0	34
228	Arabidopsis encyclopedia using full-length cDNAs and its application. Plant Physiology and Biochemistry, 2001, 39, 211-220.	2.8	34
229	Differential Use of Signal Peptides and Membrane Domains Is a Common Occurrence in the Protein Output of Transcriptional Units. PLoS Genetics, 2006, 2, e46.	1.5	34
230	Core promoter structure and genomic context reflect histone 3 lysine 9 acetylation patterns. BMC Genomics, 2010, 11, 257.	1.2	34
231	Characterization of piRNAs across postnatal development in mouse brain. Scientific Reports, 2016, 6, 25039.	1.6	34
232	The Human Cell Atlas: Technical approaches and challenges. Briefings in Functional Genomics, 2018, 17, 283-294.	1.3	34
233	High-throughput verification of transcriptional starting sites by Deep-RACE. BioTechniques, 2009, 46, 130-132.	0.8	33
234	Expression Specificity of Disease-Associated lncRNAs: Toward Personalized Medicine. Current Topics in Microbiology and Immunology, 2015, 394, 237-258.	0.7	33

#	ARTICLE	IF	CITATIONS
235	SLIC-CAGE: high-resolution transcription start site mapping using nanogram-levels of total RNA. <i>Genome Research</i> , 2018, 28, 1943-1956.	2.4	33
236	SINEUP long non-coding RNA acts via PTBP1 and HNRNPK to promote translational initiation assemblies. <i>Nucleic Acids Research</i> , 2020, 48, 11626-11644.	6.5	33
237	G Protein-Coupled Receptor Genes in the FANTOM2 Database. <i>Genome Research</i> , 2003, 13, 1466-1477.	2.4	32
238	Non-coding RNA transcription: turning on neighbours. <i>Nature Cell Biology</i> , 2008, 10, 1023-1024.	4.6	32
239	Reduction of non-insert sequence reads by dimer eliminator LNA oligonucleotide for small RNA deep sequencing. <i>BioTechniques</i> , 2010, 49, 751-755.	0.8	32
240	Remodeling of retrotransposon elements during epigenetic induction of adult visual cortical plasticity by HDAC inhibitors. <i>Epigenetics and Chromatin</i> , 2015, 8, 55.	1.8	32
241	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
242	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
243	Structural determinants of the SINE B2 element embedded in the long non-coding RNA activator of translation AS Uchl1. <i>Scientific Reports</i> , 2018, 8, 3189.	1.6	32
244	A framework for integrating the songbird brain. <i>Journal of Comparative Physiology A: Neuroethology, Sensory, Neural, and Behavioral Physiology</i> , 2002, 188, 961-980.	0.7	31
245	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
246	Analysis of the Mouse Transcriptome for Genes Involved in the Function of the Nervous System. <i>Genome Research</i> , 2003, 13, 1395-1401.	2.4	30
247	Constructing ORFeome resources with removable termination codons. <i>BioTechniques</i> , 2006, 41, 44-50.	0.8	30
248	Regional differences in gene expression and promoter usage in aged human brains. <i>Neurobiology of Aging</i> , 2013, 34, 1825-1836.	1.5	30
249	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
250	SINEUP non-coding RNAs rescue defective frataxin expression and activity in a cellular model of Friedreich's Ataxia. <i>Nucleic Acids Research</i> , 2019, 47, 10728-10743.	6.5	30
251	Simple and rapid preparation of plasmid template by a filtration method using microtiter filter plates. <i>Nucleic Acids Research</i> , 1997, 25, 1315-1316.	6.5	29
252	Extra-Long First-Strand cDNA Synthesis. <i>BioTechniques</i> , 2002, 32, 984-985.	0.8	29

#	ARTICLE	IF	CITATIONS
253	Development of a DNA barcode tagging method for monitoring dynamic changes in gene expression by using an ultra high-throughput sequencer. <i>BioTechniques</i> , 2008, 45, 95-97.	0.8	29
254	Linking FANTOM5 CAGE peaks to annotations with CAGEscan. <i>Scientific Data</i> , 2017, 4, 170147.	2.4	29
255	Antisense Transcription in Loci Associated to Hereditary Neurodegenerative Diseases. <i>Molecular Neurobiology</i> , 2019, 56, 5392-5415.	1.9	29
256	Comparative transcriptomics of primary cells in vertebrates. <i>Genome Research</i> , 2020, 30, 951-961.	2.4	29
257	Multiplicity of 5â€² Cap Structures Present on Short RNAs. <i>PLoS ONE</i> , 2014, 9, e102895.	1.1	29
258	A Computer-Based Method of Selecting Clones for a Full-Length cDNA Project: Simultaneous Collection of Negligibly Redundant and Variant cDNAs. <i>Genome Research</i> , 2002, 12, 1127-1134.	2.4	28
259	Is sequencing enlightenment ending the dark age of the transcriptome?. <i>Nature Methods</i> , 2009, 6, 711-713.	9.0	28
260	Automated Filtration-Based High-Throughput Plasmid Preparation System. <i>Genome Research</i> , 1999, 9, 463-470.	2.4	28
261	Comprehensive Analysis of the Mouse Metabolome Based on the Transcriptome. <i>Genome Research</i> , 2003, 13, 1345-1349.	2.4	27
262	Diversity of Ca <sup>2+</sup> -activated K <sup>+</sup> channel transcripts in inner ear hair cells. <i>Gene</i> , 2007, 386, 11-23.	1.0	27
263	Single-Nucleotide Resolution Mapping of Hepatitis B Virus Promoters in Infected Human Livers and Hepatocellular Carcinoma. <i>Journal of Virology</i> , 2016, 90, 10811-10822.	1.5	27
264	Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution. <i>Diabetes</i> , 2017, 66, 218-230.	0.3	27
265	Nuclear AGO1 Regulates Gene Expression by Affecting Chromatin Architecture in Human Cells. <i>Cell Systems</i> , 2019, 9, 446-458.e6.	2.9	27
266	Safety and efficacy of the Russian COVID-19 vaccine: more information needed. <i>Lancet</i> , The, 2020, 396, e53.	6.3	27
267	The DT40 web site: sampling and connecting the genes of a B cell line. <i>Nucleic Acids Research</i> , 2002, 30, 230-231.	6.5	26
268	CTAB-Urea Method Purifies RNA from Melanin for cDNA Microarray Analysis. <i>Pigment Cell &amp; Melanoma Research</i> , 2004, 17, 312-315.	4.0	26
269	Computational analysis suggests that alternative first exons are involved in tissue-specific transcription in rice ( <i>Oryza sativa</i> ). <i>Bioinformatics</i> , 2005, 21, 1758-1763.	1.8	26
270	Computational promoter analysis of mouse, rat and human antimicrobial peptide-coding genes. <i>BMC Bioinformatics</i> , 2006, 7, S8.	1.2	26



#	ARTICLE	IF	CITATIONS
271	Genome Network and FANTOM3: Assessing the Complexity of the Transcriptome. <i>PLoS Genetics</i> , 2006, 2, e63.	1.5	26
272	Broad Heterochromatic Domains Open in Gonocyte Development Prior to De Novo DNA Methylation. <i>Developmental Cell</i> , 2019, 51, 21-34.e5.	3.1	26
273	Multimic atlas with functional stratification and developmental dynamics of zebrafish cis-regulatory elements. <i>Nature Genetics</i> , 2022, 54, 1037-1050.	9.4	26
274	Integrative CAGE and DNA Methylation Profiling Identify Epigenetically Regulated Genes in NSCLC. <i>Molecular Cancer Research</i> , 2017, 15, 1354-1365.	1.5	25
275	Computer-Based Methods for the Mouse Full-Length cDNA Encyclopedia: Real-Time Sequence Clustering for Construction of a Nonredundant cDNA Library. <i>Genome Research</i> , 2001, 11, 281-289.	2.4	25
276	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
277	Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. <i>EBioMedicine</i> , 2017, 24, 257-266.	2.7	24
278	Identification of unique transcripts from a mouse full-length, subtracted inner ear cDNA library. <i>Genomics</i> , 2004, 83, 1012-1023.	1.3	23
279	piRNAs Warrant Investigation in Rett Syndrome: An Omics Perspective. <i>Disease Markers</i> , 2012, 33, 261-275.	0.6	23
280	Comparison of RNA- or LNA-hybrid oligonucleotides in template-switching reactions for high-speed sequencing library preparation. <i>BMC Genomics</i> , 2013, 14, 665.	1.2	23
281	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
282	The FANTOM5 Computation Ecosystem: Genomic Information Hub for Promoters and Active Enhancers. <i>Methods in Molecular Biology</i> , 2017, 1611, 199-217.	0.4	23
283	Identification of functional features of synthetic SINEUPs, antisense lncRNAs that specifically enhance protein translation. <i>PLoS ONE</i> , 2018, 13, e0183229.	1.1	23
284	Whole transcriptome analysis: what are we still missing?. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2011, 3, 527-543.	6.6	22
285	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
286	Telomerase Reverse Transcriptase Regulates microRNAs. <i>International Journal of Molecular Sciences</i> , 2015, 16, 1192-1208.	1.8	22
287	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
288	From bench to bedside: The long journey of long non-coding RNAs. <i>Current Opinion in Systems Biology</i> , 2017, 3, 119-124.	1.3	22

#	ARTICLE	IF	CITATIONS
289	Cap Analysis of Gene Expression (CAGE): A Quantitative and Genome-Wide Assay of Transcription Start Sites. <i>Methods in Molecular Biology</i> , 2020, 2120, 277-301.	0.4	22
290	Inferring Alternative Splicing Patterns in Mouse from a Full-Length cDNA Library and Microarray Data. <i>Genome Research</i> , 2002, 12, 1286-1293.	2.4	21
291	Absolute expression values for mouse transcripts: re-annotation of the READ expression database by the use of CAGE and EST sequence tags. <i>FEBS Letters</i> , 2004, 559, 22-26.	1.3	21
292	Dynamics of cardiomyocyte transcriptome and chromatin landscape demarcates key events of heart development. <i>Genome Research</i> , 2019, 29, 506-519.	2.4	21
293	Population transcriptomics with single-cell resolution: A new field made possible by microfluidics. <i>BioEssays</i> , 2013, 35, 131-140.	1.2	20
294	The RNA-binding protein ILF3 binds to transposable element sequences in SINEUP lncRNAs. <i>FASEB Journal</i> , 2019, 33, 13572-13589.	0.2	20
295	Monitoring the Expression Pattern of 1300 Arabidopsis Genes under Drought and Cold Stresses by Using a Full-Length cDNA Microarray. <i>Plant Cell</i> , 2001, 13, 61.	3.1	19
296	Subcellular Localization of Mammalian Type II Membrane Proteins. <i>Traffic</i> , 2006, 7, 613-625.	1.3	19
297	Genome-Wide Technologies to Study RNA-Chromatin Interactions. <i>Non-coding RNA</i> , 2020, 6, 20.	1.3	19
298	Computer-Based Methods for the Mouse Full-Length cDNA Encyclopedia: Real-Time Sequence Clustering for Construction of a Nonredundant cDNA Library. <i>Genome Research</i> , 2001, 11, 281-289.	2.4	19
299	Rapidly evolving human promoter regions. <i>Nature Genetics</i> , 2008, 40, 1262-1263.	9.4	18
300	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
301	An NMR-based approach reveals the core structure of the functional domain of SINEUP lncRNAs. <i>Nucleic Acids Research</i> , 2020, 48, 9346-9360.	6.5	18
302	LETR1 is a lymphatic endothelial-specific lncRNA governing cell proliferation and migration through KLF4 and SEMA3C. <i>Nature Communications</i> , 2021, 12, 925.	5.8	18
303	Building promoter aware transcriptional regulatory networks using siRNA perturbation and deepCAGE. <i>Nucleic Acids Research</i> , 2010, 38, 8141-8148.	6.5	17
304	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
305	MicroRNA-27a/b-3p and PPAR $\gamma$ regulate SCAMP3 through a feed-forward loop during adipogenesis. <i>Scientific Reports</i> , 2019, 9, 13891.	1.6	17
306	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

#	ARTICLE	IF	CITATIONS
307	Exploration of the Cell-Cycle Genes Found Within the RIKEN FANTOM2 Data Set. <i>Genome Research</i> , 2003, 13, 1366-1375.	2.4	16
308	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
309	A simple discontinuous buffer system for increased resolution and speed in gel electrophoretic analysis of DNA sequence. <i>Nucleic Acids Research</i> , 1990, 18, 204-204.	6.5	15
310	Comprehensive sequence analysis of translation termination sites in various eukaryotes. <i>Gene</i> , 2002, 300, 79-87.	1.0	15
311	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
312	Deficiency of multidrug resistance 2 contributes to cell transformation through oxidative stress. <i>Carcinogenesis</i> , 2016, 37, 39-48.	1.3	15
313	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	15
314	Synthetic <i>in vitro</i> transcribed lncRNAs (SINEUPs) with chemical modifications enhance target mRNA translation. <i>FEBS Letters</i> , 2020, 594, 4357-4369.	1.3	15
315	Systemic identification of estrogen-regulated genes in breast cancer cells through cap analysis of gene expression mapping. <i>Biochemical and Biophysical Research Communications</i> , 2014, 447, 531-536.	1.0	14
316	Nuclear transcriptome profiling of induced pluripotent stem cells and embryonic stem cells identify non-coding loci resistant to reprogramming. <i>Cell Cycle</i> , 2015, 14, 1148-1155.	1.3	14
317	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
318	Large-scale collection and characterization of promoters of human and mouse genes. <i>In Silico Biology</i> , 2004, 4, 429-44.	0.4	14
319	A discontinuous buffer system increasing resolution and reproducibility in DNA sequencing on high voltage horizontal ultrathin-layer electrophoresis. <i>Electrophoresis</i> , 1995, 16, 1836-1845.	1.3	13
320	Removal of PolyA Tails from Full-Length cDNA Libraries for High-Efficiency Sequencing. <i>BioTechniques</i> , 2001, 31, 1042-1049.	0.8	13
321	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
322	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
323	piRNAs warrant investigation in Rett Syndrome: an omics perspective. <i>Disease Markers</i> , 2012, 33, 261-75.	0.6	13
324	SINEUPs: a novel toolbox for RNA therapeutics. <i>Essays in Biochemistry</i> , 2021, 65, 775-789.	2.1	13

#	ARTICLE	IF	CITATIONS
325	Cytoplasmic RNA Extraction from Fresh and Frozen Mammalian Tissues. <i>BioTechniques</i> , 2002, 33, 306-309.	0.8	12
326	Subtraction of cap-trapped full-length cDNA libraries to select rare transcripts. <i>BioTechniques</i> , 2003, 35, 510-518.	0.8	12
327	Protein-protein interactions of the hyperthermophilic archaeon <i>Pyrococcus horikoshii</i> OT3. <i>Genome Biology</i> , 2005, 6, R98.	13.9	12
328	Simplified ontologies allowing comparison of developmental mammalian gene expression. <i>Genome Biology</i> , 2007, 8, R229.	13.9	12
329	A Resource for Transcriptomic Analysis in the Mouse Brain. <i>PLoS ONE</i> , 2008, 3, e3012.	1.1	11
330	Genetics, Gene Expression and Bioinformatics of the Pituitary Gland. <i>Hormone Research in Paediatrics</i> , 2009, 71, 101-115.	0.8	11
331	FXVD6, a Na,K-ATPase Regulator, Is Expressed in Type II Taste Cells. <i>Bioscience, Biotechnology and Biochemistry</i> , 2011, 75, 1061-1066.	0.6	11
332	NanoCAGE analysis of the mouse olfactory epithelium identifies the expression of vomeronasal receptors and of proximal LINE elements. <i>Frontiers in Cellular Neuroscience</i> , 2014, 8, 41.	1.8	11
333	Mice in the ENCODE spotlight. <i>Nature</i> , 2014, 515, 346-347.	13.7	11
334	Isoforms of the Erythropoietin receptor in dopaminergic neurons of the <i>Substantia Nigra</i> . <i>Journal of Neurochemistry</i> , 2016, 139, 596-609.	2.1	11
335	Identification of novel cerebellar developmental transcriptional regulators with motif activity analysis. <i>BMC Genomics</i> , 2019, 20, 718.	1.2	11
336	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297.	5.8	11
337	A comprehensive promoter landscape identifies a novel promoter for CD133 in restricted tissues, cancers, and stem cells. <i>Frontiers in Genetics</i> , 2013, 4, 209.	1.1	10
338	CAGE-defined promoter regions of the genes implicated in Rett Syndrome. <i>BMC Genomics</i> , 2014, 15, 1177.	1.2	10
339	Promoter Usage and Dynamics in Vascular Smooth Muscle Cells Exposed to Fibroblast Growth Factor-2 or Interleukin-1 $\beta$ . <i>Scientific Reports</i> , 2018, 8, 13164.	1.6	10
340	HSA21 Single-Minded 2 (Sim2) Binding Sites Co-Localize with Super-Enhancers and Pioneer Transcription Factors in Pluripotent Mouse ES Cells. <i>PLoS ONE</i> , 2015, 10, e0126475.	1.1	9
341	Target-enrichment sequencing for detailed characterization of small RNAs. <i>Nature Protocols</i> , 2018, 13, 768-786.	5.5	9
342	The Secret Life of lncRNAs: Conserved, yet Not Conserved. <i>Cell</i> , 2020, 181, 512-514.	13.5	9

#	ARTICLE	IF	CITATIONS
343	Large-scale clustering of CAGE tag expression data. BMC Bioinformatics, 2007, 8, 161.	1.2	8
344	Hunting hidden transcripts. Nature Methods, 2008, 5, 587-589.	9.0	8
345	High Sensitivity TSS Prediction: Estimates of Locations Where TSS Cannot Occur. PLoS ONE, 2010, 5, e13934.	1.1	8
346	STAP cells are derived from ES cells. Nature, 2015, 525, E4-E5.	13.7	8
347	Multi-year whole-blood transcriptome data for the study of onset and progression of Parkinson's Disease. Scientific Data, 2019, 6, 20.	2.4	8
348	Decoding Neuronal Diversification by Multiplexed Single-cell RNA-Seq. Stem Cell Reports, 2021, 16, 810-824.	2.3	8
349	Human Disease Genes and Their Cloned Mouse Orthologs: Exploration of the FANTOM2 cDNA Sequence Data Set. Genome Research, 2003, 13, 1496-1500.	2.4	7
350	Splicing bypasses 3' end formation signals to allow complex gene architectures. Gene, 2007, 403, 188-193.	1.0	7
351	Antisense RNAs during early vertebrate development are divided in groups with distinct features. Genome Research, 2021, 31, 995-1010.	2.4	7
352	Expanded ENCODE delivers invaluable genomic encyclopedia. Nature, 2020, 583, 685-686.	13.7	7
353	Embryonic LTR retrotransposons supply promoter modules to somatic tissues. Genome Research, 2021, 31, 1983-1993.	2.4	7
354	A Novel Control System for Polymerase Chain Reaction Using a RIKEN GS384 Thermalcycler. DNA Research, 1997, 4, 387-391.	1.5	6
355	FREP: a database of functional repeats in mouse cDNAs. Nucleic Acids Research, 2004, 32, 471D-475.	6.5	6
356	Characterization of Novel Transcripts of Human Papillomavirus Type 16 Using Cap Analysis Gene Expression Technology. Journal of Virology, 2015, 89, 2448-2452.	1.5	6
357	Monitoring transcription initiation activities in rat and dog. Scientific Data, 2017, 4, 170173.	2.4	6
358	Discovery of Transcription Factors Novel to Mouse Cerebellar Granule Cell Development Through Laser-Capture Microdissection. Cerebellum, 2018, 17, 308-325.	1.4	6
359	A human minisatellite hosts an alternative transcription start site for NPRL3 driving its expression in a repeat number-dependent manner. Human Mutation, 2020, 41, 807-824.	1.1	6
360	Low Quantity Single Strand CAGE (LQ-ssCAGE) Maps Regulatory Enhancers and Promoters. Methods in Molecular Biology, 2021, 2351, 67-90.	0.4	6

#	ARTICLE	IF	CITATIONS
361	A field guide to cultivating computational biology. PLoS Biology, 2021, 19, e3001419.	2.6	6
362	Annotating non-coding transcription using functional genomics strategies. Briefings in Functional Genomics & Proteomics, 2009, 8, 437-443.	3.8	5
363	Cell Based Assays of SINEUP Non-coding RNAs That Can Specifically Enhance mRNA Translation. Journal of Visualized Experiments, 2019, , .	0.2	5
364	Wavelet profiles: their application in Oryza sativa DNA sequence analysis. , 0, , .		4
365	A Method for Similarity Search of Genomic Positional Expression Using CAGE. PLoS Genetics, 2006, 2, e44.	1.5	4
366	Tunable fractionation of nucleic acids. BioTechniques, 2009, 47, 1041-1043.	0.8	4
367	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. Cell, 2010, 141, 369.	13.5	4
368	Structure by Sequencing: Discovery of Hidden Messages in the Noncoding RNA Fraction. Molecular Cell, 2012, 48, 153-155.	4.5	4
369	A Transcriptional Switch Point During Hematopoietic Stem and Progenitor Cell Ontogeny. Stem Cells and Development, 2017, 26, 314-327.	1.1	4
370	Transcription start site profiling of 15 anatomical regions of the Macaca mulatta central nervous system. Scientific Data, 2017, 4, 170163.	2.4	4
371	Towards SINEUP-based therapeutics: Design of an in vitro synthesized SINEUP RNA. Molecular Therapy - Nucleic Acids, 2022, 27, 1092-1102.	2.3	4
372	CAGE-TSSchip: promoter-based expression profiling using the 5'-leading label of capped transcripts. Genome Biology, 2007, 8, R42.	13.9	3
373	Informatic and genomic analysis of melanocyte cDNA libraries as a resource for the study of melanocyte development and function. Pigment Cell & Melanoma Research, 2007, 20, 201-209.	4.0	3
374	Profiling transcription initiation in human aged brain using deep-CAGE. BMC Bioinformatics, 2011, 12, .	1.2	3
375	Analysis of splice variants of the human protein disulfide isomerase (P4HB) gene. BMC Genomics, 2020, 21, 766.	1.2	3
376	Mapping of 19032 mouse cDNAs on mouse chromosomes. Journal of Structural and Functional Genomics, 2002, 2, 23-28.	1.2	2
377	Cytokine-Related Genes Identified From the RIKEN Full-Length Mouse cDNA Data Set. Genome Research, 2003, 13, 1307-1317.	2.4	2
378	Generation of Full-Length cDNA Libraries: Focus on Plants. Methods in Molecular Biology, 2009, 533, 49-68.	0.4	2

#	ARTICLE	IF	CITATIONS
379	Complexity of Mammalian Transcriptome Analyzed by RNA Deep Sequencing. , 2015, , 3-22.		2
380	Analysis of Enhancerâ€“Promoter Interactions using CAGE and RADICL-Seq Technologies. Methods in Molecular Biology, 2021, 2351, 201-210.	0.4	2
381	Tagging Transcription Starting Sites with CAGE. , 2009, , 7-20.		1
382	From identification to validation to gene count. Genome Biology, 2010, 11, .	3.8	1
383	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
384	RNA extraction from sorted neuronal subtypes. BioTechniques, 2017, 62, .	0.8	1
385	Look for methods, not conclusions. Cell Death and Disease, 2019, 10, 931.	2.7	1
386	Use of Cap Analysis Gene Expression to detect human papillomavirus promoter activity patterns at different disease stages. Scientific Reports, 2020, 10, 17991.	1.6	1
387	A new approach for screening cervical cancer by characterization of transcripts using CAGE technology.. Journal of Clinical Oncology, 2015, 33, e16514-e16514.	0.8	1
388	Epi-drivers and cancer-testis genes. Translational Cancer Research, 2016, 5, 334-336.	0.4	1
389	Single-Cell Convert-Seq Decodes Regulatory Factors Driving Neuronal Diversity. SSRN Electronic Journal, 0, , .	0.4	1
390	Japan: prize diversity, not conformity, to boost research. Nature, 2021, 599, 201-201.	13.7	1
391	Lessons from the functional characterization of lncRNAs: introduction to mammalian genome special issue. Mammalian Genome, 2022, , .	1.0	1
392	Meeting Report: 14th International Mouse Genome Conference. Mammalian Genome, 2001, 12, 401-405.	1.0	0
393	Transcriptomics resources for functional genomics. Briefings in Functional Genomics & Proteomics, 2007, 6, 171-179.	3.8	0
394	Epigenetic regulation of critical period plasticity in visual cortex. Neuroscience Research, 2007, 58, S66.	1.0	0
395	From CAGE to DeepCAGE: High-Throughput Transcription Start Site and Promoter Identification for Gene Network Analysis. , 0, , 55-75.		0
396	Construction of CAGE Libraries. , 2009, , 21-39.		0

#	ARTICLE	IF	CITATIONS
397	RNA Dust: Where are the Genes?. DNA Research, 2010, 17, 209-209.	1.5	0
398	Beyond the FANTOM4. Genome Biology, 2010, 11, O11.	13.9	0
399	In grateful recognition of our Editorial Board. BioEssays, 2015, 37, 1254-1255.	1.2	0
400	Machine-driven parameter screen of biochemical reactions. Nucleic Acids Research, 2020, 48, e37-e37.	6.5	0
401	The choice of negative control antisense oligonucleotides dramatically impacts downstream analysis depending on the cellular background. BMC Genomic Data, 2021, 22, 33.	0.7	0
402	Abstract 2897: Recurrent transcriptome alterations across multiple cancer types. , 2016, , .		0
403	Tagging Transcription Starting Sites with CAGE. , 2019, , 7-20.		0
404	Complete Transcriptome Analysis by 5â€²-End Single-Cell RNA-Seq with Random Priming. Methods in Molecular Biology, 2022, 2490, 141-156.	0.4	0