Piero Carninci

List of Publications by Year
in descending order

404 papers	95,196 citations	1536 106 h-index	303 291 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. Nature, 2012, 489, 57-74.	27.8	15,516
2	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	27.8	6,319
3	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
4	Landscape of transcription in human cells. Nature, 2012, 489, 101-108.	27.8	4,484
5	The GENCODE v7 catalog of human long noncoding RNAs: Analysis of their gene structure, evolution, and expression. Genome Research, 2012, 22, 1775-1789.	5.5	4,428
6	The Transcriptional Landscape of the Mammalian Genome. Science, 2005, 309, 1559-1563.	12.6	3,227
7	An atlas of active enhancers across human cell types and tissues. Nature, 2014, 507, 455-461.	27.8	2,269
8	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	27.8	1,838
9	Monitoring the expression profiles of 7000 Arabidopsis genes under drought, cold and high-salinity stresses using a full-length cDNA microarray. Plant Journal, 2002, 31, 279-292.	5.7	1,697
10	Insights into social insects from the genome of the honeybee Apis mellifera. Nature, 2006, 443, 931-949.	27.8	1,648
11	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16899-16903.	7.1	1,610
12	Antisense Transcription in the Mammalian Transcriptome. Science, 2005, 309, 1564-1566.	12.6	1,553
13	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. Nature, 2002, 420, 563-573.	27.8	1,548
14	The Human Cell Atlas. ELife, 2017, 6, .	6.0	1,547
15	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). PLoS Biology, 2011, 9, e1001046.	5.6	1,257
16	Genome-wide analysis of mammalian promoter architecture and evolution. Nature Genetics, 2006, 38, 626-635.	21.4	1,201
17	Monitoring the Expression Pattern of 1300 Arabidopsis Genes under Drought and Cold Stresses by Using a Full-Length cDNA Microarray. Plant Cell, 2001, 13, 61-72.	6.6	986
18	Direct generation of functional dopaminergic neurons from mouse and human fibroblasts. Nature, 2011, 476, 224-227.	27.8	941

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19	Comprehensive Analysis of NAC Family Genes in Oryza sativa and Arabidopsis thaliana. DNA Research, 2003, 10, 239-247.	3.4	911
20	An atlas of human long non-coding RNAs with accurate 5â€² ends. Nature, 2017, 543, 199-204.	27.8	898
21	Long non-coding antisense RNA controls Uchl1 translation through an embedded SINEB2 repeat. Nature, 2012, 491, 454-457.	27.8	881
22	Empirical Analysis of Transcriptional Activity in the Arabidopsis Genome. Science, 2003, 302, 842-846.	12.6	853
23	Collection, Mapping, and Annotation of Over 28,000 cDNA Clones from japonica Rice. Science, 2003, 301, 376-379.	12.6	834
24	The regulated retrotransposon transcriptome of mammalian cells. Nature Genetics, 2009, 41, 563-571.	21.4	731
25	Gateways to the FANTOM5 promoter level mammalian expression atlas. Genome Biology, 2015, 16, 22.	8.8	687
26	A draft network of ligandâ€"receptor-mediated multicellular signalling in human. Nature Communications, 2015, 6, 7866.	12.8	676
27	Cap analysis gene expression for high-throughput analysis of transcriptional starting point and identification of promoter usage. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 15776-15781.	7.1	673
28	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. Cell, 2010, 140, 744-752.	28.9	667
29	Functional annotation of a full-length mouse cDNA collection. Nature, 2001, 409, 685-690.	27.8	653
30	Diversity and dynamics of the Drosophila transcriptome. Nature, 2014, 512, 393-399.	27.8	647
31	Functional Annotation of a Full-Length Arabidopsis cDNA Collection. Science, 2002, 296, 141-145.	12.6	631
32	Somatic retrotransposition alters the genetic landscape of the human brain. Nature, 2011, 479, 534-537.	27.8	621
33	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. Science, 2015, 347, 1010-1014.	12.6	517
34	The Status, Quality, and Expansion of the NIH Full-Length cDNA Project: The Mammalian Gene Collection (MGC). Genome Research, 2004, 14, 2121-2127.	5.5	486
35	Site-specific DICER and DROSHA RNA products control the DNA-damage response. Nature, 2012, 488, 231-235.	27.8	460
36	An integrated expression atlas of miRNAs and their promoters in human and mouse. Nature Biotechnology, 2017, 35, 872-878.	17.5	456

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37	Metazoan promoters: emerging characteristics and insights into transcriptional regulation. Nature Reviews Genetics, 2012, 13, 233-245.	16.3	448
38	Mammalian RNA polymerase II core promoters: insights from genome-wide studies. Nature Reviews Genetics, 2007, 8, 424-436.	16.3	435
39	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. Nature Genetics, 2009, 41, 553-562.	21.4	408
40	CAGE: cap analysis of gene expression. Nature Methods, 2006, 3, 211-222.	19.0	397
41	Monitoring the expression pattern of around 7,000 Arabidopsis genes under ABA treatments using a full-length cDNA microarray. Functional and Integrative Genomics, 2002, 2, 282-291.	3.5	394
42	Small RNAs derived from snoRNAs. Rna, 2009, 15, 1233-1240.	3.5	384
43	The Reality of Pervasive Transcription. PLoS Biology, 2011, 9, e1000625.	5.6	380
44	Endogenous Retrotransposition Activates Oncogenic Pathways in Hepatocellular Carcinoma. Cell, 2013, 153, 101-111.	28.9	352
45	Comparative genomics of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: Implication for land plant evolution. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8007-8012.	7.1	341
46	Conservation and divergence in Toll-like receptor 4-regulated gene expression in primary human versus mouse macrophages. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E944-53.	7.1	332
47	Tiny RNAs associated with transcription start sites in animals. Nature Genetics, 2009, 41, 572-578.	21.4	327
48	Hierarchical folding and reorganization of chromosomes are linked to transcriptional changesÂin cellular differentiation. Molecular Systems Biology, 2015, 11, 852.	7.2	305
49	High-Efficiency Full-Length cDNA Cloning by Biotinylated CAP Trapper. Genomics, 1996, 37, 327-336.	2.9	297
50	Genome-wide analysis of cancer/testis gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20422-20427.	7.1	295
51	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. PLoS Biology, 2004, 2, e162.	5.6	290
52	Complex Loci in Human and Mouse Genomes. PLoS Genetics, 2006, 2, e47.	3.5	290
53	Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. Nature Genetics, 2014, 46, 558-566.	21.4	271
54	Normalization and Subtraction of Cap-Trapper-Selected cDNAs to Prepare Full-Length cDNA Libraries for Rapid Discovery of New Genes. Genome Research, 2000, 10, 1617-1630.	5.5	263

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55	Hidden layers of human small RNAs. BMC Genomics, 2008, 9, 157.	2.8	255
56	5â€² endâ€“centered expression profiling using cap-analysis gene expression and next-generation sequencing. Nature Protocols, 2012, 7, 542-561.	12.0	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.	7.1	240
58	A code for transcription initiation in mammalian genomes. Genome Research, 2008, 18, 1-12.	5.5	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.	7.1	231
60	Antisense Transcripts With FANTOM2 Clone Set and Their Implications for Gene Regulation. Genome Research, 2003, 13, 1324-1334.	5.5	224
61	Amphioxus functional genomics and the origins of vertebrate gene regulation. Nature, 2018, 564, 64-70.	27.8	224
62	High-efficiency cloning of Arabidopsis full-length cDNA by biotinylated CAP trapper. Plant Journal, 1998, 15, 707-720.	5.7	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.	7.1	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.	7.1	212
65	Genome-wide analysis of promoter architecture in Drosophila melanogaster. Genome Research, 2011, 21, 182-192.	5.5	211
66	Chromatin-associated RNA interference components contribute to transcriptional regulation in Drosophila. Nature, 2011, 480, 391-395.	27.8	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.	7.1	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.	8.2	197
69	FANTOM5 CAGE profiles of human and mouse samples. Scientific Data, 2017, 4, 170112.	5.3	195
70	CAGEr: precise TSS data retrieval and high-resolution promoterome mining for integrative analyses. Nucleic Acids Research, 2015, 43, e51-e51.	14.5	194
71	The Abundance of Short Proteins in the Mammalian Proteome. PLoS Genetics, 2006, 2, e52.	3.5	189
72	Two independent transcription initiation codes overlap on vertebrate core promoters. Nature, 2014, 507, 381-385.	27.8	182

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73	The Drosophila Gene Collection: Identification of Putative Full-Length cDNAs for 70% of D. melanogaster Genes. Genome Research, 2002, 12, 1294-1300.	5.5	180
74	Discovery and functional analysis of lncRNAs: Methodologies to investigate an uncharacterized transcriptome. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 3-15.	1.9	178
75	Long nonâ€coding RNA modifies chromatin. BioEssays, 2011, 33, 830-839.	2.5	177
76	A molecular neuroethological approach for identifying and characterizing a cascade of behaviorally regulated genes. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15212-15217.	7.1	176
77	High-fidelity promoter profiling reveals widespread alternative promoter usage and transposon-driven developmental gene expression. Genome Research, 2013, 23, 169-180.	5.5	176
78	Redefinition of the human mast cell transcriptome by deep-CAGE sequencing. Blood, 2014, 123, e58-e67.	1.4	175
79	Unamplified cap analysis of gene expression on a single-molecule sequencer. Genome Research, 2011, 21, 1150-1159.	5.5	172
80	Update of the FANTOM web resource: expansion to provide additional transcriptome atlases. Nucleic Acids Research, 2019, 47, D752-D758.	14.5	172
81	Detecting Expressed Genes Using CAGE. Methods in Molecular Biology, 2014, 1164, 67-85.	0.9	170
82	[2] High-efficiency full-length cDNA cloning. Methods in Enzymology, 1999, 303, 19-44.	1.0	169
83	Impact of Alternative Initiation, Splicing, and Termination on the Diversity of the mRNA Transcripts Encoded by the Mouse Transcriptome. Genome Research, 2003, 13, 1290-1300.	5.5	168
84	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. Genome Research, 2012, 22, 1658-1667.	5.5	166
85	Tag-based approaches for transcriptome research and genome annotation. Nature Methods, 2005, 2, 495-502.	19.0	165
86	Transcript Annotation in FANTOM3: Mouse Gene Catalog Based on Physical cDNAs. PLoS Genetics, 2006, 2, e62.	3.5	165
87	NMDA Receptor Regulation Prevents Regression of Visual Cortical Function in the Absence of Mecp2. Neuron, 2012, 76, 1078-1090.	8.1	163
88	Analysis of the human monocyte-derived macrophage transcriptome and response to lipopolysaccharide provides new insights into genetic aetiology of inflammatory bowel disease. PLoS Genetics, 2017, 13, e1006641.	3.5	161
89	Transcription and enhancer profiling in human monocyte subsets. Blood, 2014, 123, e90-e99.	1.4	157
90	Targeting a Complex Transcriptome: The Construction of the Mouse Full-Length cDNA Encyclopedia. Genome Research, 2003, 13, 1273-1289.	5.5	154

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91	Linking promoters to functional transcripts in small samples with nanoCAGE and CAGEscan. Nature Methods, 2010, 7, 528-534.	19.0	152
92	Clusters of Internally Primed Transcripts Reveal Novel Long Noncoding RNAs. PLoS Genetics, 2006, 2, e37.	3.5	148
93	Comparative validation of the D. melanogaster modENCODE transcriptome annotation. Genome Research, 2014, 24, 1209-1223.	5.5	147
94	Molecular mechanisms of pituitary organogenesis: In search of novel regulatory genes. Molecular and Cellular Endocrinology, 2010, 323, 4-19.	3.2	140
95	Genome sequence and analysis of the Japanese morning glory Ipomoea nil. Nature Communications, 2016, 7, 13295.	12.8	138
96	Methods for analyzing deep sequencing expression data: constructing the human and mouse promoterome with deepCAGE data. Genome Biology, 2009, 10, R79.	9.6	131
97	PAPD5-mediated 3â€² adenylation and subsequent degradation of miR-21 is disrupted in proliferative disease. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11467-11472.	7.1	130
98	Identification of Putative Noncoding RNAs Among the RIKEN Mouse Full-Length cDNA Collection. Genome Research, 2003, 13, 1301-1306.	5.5	129
99	Genome-wide detection and analysis of hippocampus core promoters using DeepCAGE. Genome Research, 2009, 19, 255-265.	5.5	128
100	Cross-mapping and the identification of editing sites in mature microRNAs in high-throughput sequencing libraries. Genome Research, 2010, 20, 257-264.	5.5	126
101	Transcriptional network dynamics in macrophage activation. Genomics, 2006, 88, 133-142.	2.9	125
102	Noncoding RNA transcription beyond annotated genes. Current Opinion in Genetics and Development, 2007, 17, 139-144.	3.3	125
103	Genetic control of the innate immune response. BMC Immunology, 2003, 4, 5.	2.2	119
104	Dynamic regulation of the transcription initiation landscape at single nucleotide resolution during vertebrate embryogenesis. Genome Research, 2013, 23, 1938-1950.	5.5	119
105	Discrimination of Non-Protein-Coding Transcripts from Protein-Coding mRNA. RNA Biology, 2006, 3, 40-48.	3.1	118
106	Biased Allelic Expression in Human Primary Fibroblast Single Cells. American Journal of Human Genetics, 2015, 96, 70-80.	6.2	117
107	Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. Nucleic Acids Research, 2017, 45, D737-D743.	14.5	116
108	Antisense transcripts with rice full-length cDNAs. Genome Biology, 2003, 5, R5.	9.6	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. Frontiers in Cellular Neuroscience, 2015, 9, 114.	3.7	112
110	Differential roles of epigenetic changes and Foxp3 expression in regulatory T cell-specific transcriptional regulation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5289-5294.	7.1	111
111	The ORFeome Collaboration: a genome-scale human ORF-clone resource. Nature Methods, 2016, 13, 191-192.	19.0	111
112	Functional annotation of human long noncoding RNAs via molecular phenotyping. Genome Research, 2020, 30, 1060-1072.	5.5	109
113	Comparative Analysis of Apoptosis and Inflammation Genes of Mice and Humans. Genome Research, 2003, 13, 1376-1388.	5.5	104
114	Heterotachy in Mammalian Promoter Evolution. PLoS Genetics, 2006, 2, e30.	3.5	102
115	C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution. Nature Communications, 2019, 10, 360.	12.8	102
116	Full-length cDNAs from chicken bursal lymphocytes to facilitate gene function analysis. Genome Biology, 2004, 6, R6.	9.6	101
117	Transcriptional and structural impact of TATA-initiation site spacing in mammalian core promoters. Genome Biology, 2006, 7, R78.	9.6	101
118	Comparison of CAGE and RNA-seq transcriptome profiling using clonally amplified and single-molecule next-generation sequencing. Genome Research, 2014, 24, 708-717.	5.5	99
119	RADICL-seq identifies general and cell typeâ€"specific principles of genome-wide RNA-chromatin interactions. Nature Communications, 2020, 11, 1018.	12.8	98
120	Discovery of Imprinted Transcripts in the Mouse Transcriptome Using Large-Scale Expression Profiling. Genome Research, 2003, 13, 1402-1409.	5.5	96
121	Paradigm shifts in genomics through the FANTOM projects. Mammalian Genome, 2015, 26, 391-402.	2.2	96
122	Mice and Men: Their Promoter Properties. PLoS Genetics, 2006, 2, e54.	3.5	95
123	CAGE (Cap Analysis of Gene Expression): A Protocol for the Detection of Promoter and Transcriptional Networks. Methods in Molecular Biology, 2012, 786, 181-200.	0.9	94
124	Complementing tissue characterization by integrating transcriptome profiling from the Human Protein Atlas and from the FANTOM5 consortium. Nucleic Acids Research, 2015, 43, 6787-6798.	14.5	94
125	A rescue strategy for multimapping short sequence tags refines surveys of transcriptional activity by CAGE. Genomics, 2008, 91, 281-288.	2.9	92
126	Transcriptional landscape of Mycobacterium tuberculosis infection in macrophages. Scientific Reports, 2018, 8, 6758.	3.3	92

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127	Mouse Proteome Analysis. Genome Research, 2003, 13, 1335-1344.	5.5	91
128	The complexity of the mammalian transcriptome. Journal of Physiology, 2006, 575, 321-332.	2.9	91
129	High Efficiency Selection of Full-length cDNA by Improved Biotinylated Cap Trapper. DNA Research, 1997, 4, 61-66.	3.4	90
130	A novel feature of microsatellites in plants: a distribution gradient along the direction of transcription. FEBS Letters, 2003, 554, 17-22.	2.8	89
131	Systematic Characterization of the Zinc-Finger-Containing Proteins in the Mouse Transcriptome. Genome Research, 2003, 13, 1430-1442.	5.5	89
132	A damaged genomeâ€™s transcriptional landscape through multilayered expression profiling around in situ-mapped DNA double-strand breaks. Nature Communications, 2017, 8, 15656.	12.8	89
133	Trehalose-enhanced isolation of neuronal sub-types from adult mouse brain. BioTechniques, 2012, 52, 381-385.	1.8	87
134	Tagging mammalian transcription complexity. Trends in Genetics, 2006, 22, 501-510.	6.7	85
135	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. Genome Research, 2010, 20, 791-803.	5.5	84
136	SINEUPs: A new class of natural and synthetic antisense long non-coding RNAs that activate translation. RNA Biology, 2015, 12, 771-779.	3.1	84
137	SINEUPs are modular antisense long non-coding RNAs that increase synthesis of target proteins in cells. Frontiers in Cellular Neuroscience, 2015, 9, 174.	3.7	81
138	Transcriptome Analysis of Recurrently Deregulated Genes across Multiple Cancers Identifies New Pan-Cancer Biomarkers. Cancer Research, 2016, 76, 216-226.	0.9	80
139	Transcriptional profiling of genes responsive to abscisic acid and gibberellin in rice: phenotyping and comparative analysis between rice and Arabidopsis. Physiological Genomics, 2004, 17, 87-100.	2.3	78
140	CAGE Basic/Analysis Databases: the CAGE resource for comprehensive promoter analysis. Nucleic Acids Research, 2006, 34, D632-D636.	14.5	78
141	Prevention of hepatocellular carcinoma by targeting MYCN-positive liver cancer stem cells with acyclic retinoid. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4969-4974.	7.1	78
142	Multifaceted mammalian transcriptome. Current Opinion in Cell Biology, 2008, 20, 274-280.	5.4	77
143	The enhancer and promoter landscape of human regulatory and conventional T-cell subpopulations. Blood, 2014, 123, e68-e78.	1.4	77
144	DNA damage response inhibition at dysfunctional telomeres by modulation of telomeric DNA damage response RNAs. Nature Communications, 2017, 8, 13980.	12.8	76

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145	Dynamic usage of transcription start sites within core promoters. Genome Biology, 2006, 7, R118.	9.6	75
146	Balanced-Size and Long-Size Cloning of Full-Length, Cap-Trapped cDNAs into Vectors of the Novel Î»-FLC Family Allows Enhanced Gene Discovery Rate and Functional Analysis. Genomics, 2001, 77, 79-90.	2.9	74
147	Solution Structure of the SEA Domain from the Murine Homologue of Ovarian Cancer Antigen CA125 (MUC16). Journal of Biological Chemistry, 2004, 279, 13174-13182.	3.4	74
148	Placental expression profiling in preeclampsia: local overproduction of hemoglobin may drive pathological changes. Fertility and Sterility, 2008, 90, 1834-1843.	1.0	74
149	The Mouse Secretome: Functional Classification of the Proteins Secreted Into the Extracellular Environment. Genome Research, 2003, 13, 1350-1359.	5.5	73
150	The FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. Genome Biology, 2009, 10, R40.	9.6	73
151	LOCATE: a mouse protein subcellular localization database. Nucleic Acids Research, 2006, 34, D213-D217.	14.5	72
152	Analysis of the DNA methylome and transcriptome in granulopoiesis reveals timed changes and dynamic enhancer methylation. Blood, 2014, 123, e79-e89.	1.4	72
153	NET-CAGE characterizes the dynamics and topology of human transcribed cis-regulatory elements. Nature Genetics, 2019, 51, 1369-1379.	21.4	72
154	refTSS: A Reference Data Set for Human and Mouse Transcription Start Sites. Journal of Molecular Biology, 2019, 431, 2407-2422.	4.2	72
155	Gene discovery in genetically labeled single dopaminergic neurons of the retina. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 5069-5074.	7.1	70
156	Systematic Expression Profiling of the Mouse Transcriptome Using RIKEN cDNA Microarrays. Genome Research, 2003, 13, 1318-1323.	5.5	69
157	A Simple Physical Model Predicts Small Exon Length Variations. PLoS Genetics, 2006, 2, e45.	3.5	69
158	Evolutionary turnover of mammalian transcription start sites. Genome Research, 2006, 16, 713-722.	5.5	68
159	FANTOM5 CAGE profiles of human and mouse reprocessed for GRCh38 and GRCm38 genome assemblies. Scientific Data, 2017, 4, 170107.	5.3	68
160	Systematic analysis of transcription start sites in avian development. PLoS Biology, 2017, 15, e2002887.	5.6	68
161	Comparative Analysis of Plant and Animal Calcium Signal Transduction Element Using Plant Full-Length cDNA Data. Molecular Biology and Evolution, 2004, 21, 1855-1870.	8.9	67
162	FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. Genome Biology, 2009, 10, R39.	9.6	67

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163	Solution structure of the RWD domain of the mouse GCN2 protein. Protein Science, 2004, 13, 2089-2100.	7.6	66
164	Alternate transcription of the Toll-like receptor signaling cascade. Genome Biology, 2006, 7, R10.	9.6	66
165	MOIRAI: a compact workflow system for CAGE analysis. BMC Bioinformatics, 2014, 15, 144.	2.6	66
166	Suppression of artifacts and barcode bias in high-throughput transcriptome analyses utilizing template switching. Nucleic Acids Research, 2013, 41, e44-e44.	14.5	65
167	FANTOM5 transcriptome catalog of cellular states based on Semantic MediaWiki. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw105.	3.0	64
168	From â€œCellularâ€•RNA to â€œSmartâ€•RNA: Multiple Roles of RNA in Genome Stability and Beyond. Chemical Reviews, 2018, 118, 4365-4403.	47.7	63
169	Discovery of transcriptional regulators and signaling pathways in the developing pituitary gland by bioinformatic and genomic approaches. Genomics, 2009, 93, 449-460.	2.9	61
170	NanoCAGE: A High-Resolution Technique to Discover and Interrogate Cell Transcriptomes. Cold Spring Harbor Protocols, 2011, 2011, pdb.prot5559-pdb.prot5559.	0.3	61
171	RECLU: a pipeline to discover reproducible transcriptional start sites and their alternative regulation using capped analysis of gene expression (CAGE). BMC Genomics, 2014, 15, 269.	2.8	61
172	Krimper Enforces an Antisense Bias on piRNA Pools by Binding AGO3 in the Drosophila Germline. Molecular Cell, 2015, 59, 553-563.	9.7	61
173	On biased distribution of introns in various eukaryotes. Gene, 2002, 300, 89-95.	2.2	60
174	Altruistic functions for selfish DNA. Cell Cycle, 2009, 8, 2895-2900.	2.6	60
175	Pseudoâ€“Messenger RNA: Phantoms of the Transcriptome. PLoS Genetics, 2006, 2, e23.	3.5	58
176	RNA Dust: Where are the Genes?. DNA Research, 2010, 17, 51-59.	3.4	58
177	Identification of antisense long noncoding RNAs that function as SINEUPs in human cells. Scientific Reports, 2016, 6, 33605.	3.3	58
178	Genomics Approach to Abscisic Acid- and Gibberellin-responsive Genes in Rice. DNA Research, 2003, 10, 249-261.	3.4	57
179	FANTOM enters 20th year: expansion of transcriptomic atlases and functional annotation of non-coding RNAs. Nucleic Acids Research, 2021, 49, D892-D898.	14.5	57
180	Genomic organization of transcriptomes in mammals: Coregulation and cofunctionality. Genomics, 2007, 89, 580-587.	2.9	56

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181	The frequent evolutionary birth and death of functional promoters in mouse and human. Genome Research, 2015, 25, 1546-1557.	5.5	55
182	The FANTOM5 collection, a data series underpinning mammalian transcriptome atlases in diverse cell types. Scientific Data, 2017, 4, 170113.	5.3	55
183	Multiple tissue-specific promoters control expression of the murine tartrate-resistant acid phosphatase gene. Gene, 2003, 307, 111-123.	2.2	54
184	Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics. Nucleic Acids Research, 2015, 43, 6969-6982.	14.5	54
185	A Comprehensive Transcript Map of the Mouse Gnas Imprinted Complex. Genome Research, 2003, 13, 1410-1415.	5.5	53
186	RIKEN Integrated Sequence Analysis (RISA) System---384-Format Sequencing Pipeline with 384 Multicapillary Sequencer. Genome Research, 2000, 10, 1757-1771.	5.5	52
187	Promoter architecture of mouse olfactory receptor genes. Genome Research, 2012, 22, 486-497.	5.5	52
188	Gene Organization in Rice Revealed by Full-Length cDNA Mapping and Gene Expression Analysis through Microarray. PLoS ONE, 2007, 2, e1235.	2.5	51
189	Identification and Analysis of Chromodomain-Containing Proteins Encoded in the Mouse Transcriptome. Genome Research, 2003, 13, 1416-1429.	5.5	50
190	The effect of genetic variation on promoter usage and enhancer activity. Nature Communications, 2017, 8, 1358.	12.8	50
191	Cloning Full-Length, Cap-Trapper-Selected cDNAs by Using the Single-Strand Linker Ligation Method. BioTechniques, 2001, 30, 1250-1254.	1.8	49
192	Solution structure of a BolA-like protein from Mus musculus. Protein Science, 2004, 13, 545-548.	7.6	49
193	Cytoskeletal Rearrangements in Synovial Fibroblasts as a Novel Pathophysiological Determinant of Modeled Rheumatoid Arthritis. PLoS Genetics, 2005, 1, e48.	3.5	49
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