

Piero Carninci

List of Publications by Year in descending order

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389
papers

76,823
citations

1447

104
h-index

529

260
g-index

470
all docs

470
docs citations

470
times ranked

68748
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	35.3	6,401
2	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	35.3	4,757
3	Landscape of transcription in human cells. <i>Nature</i> , 2012, 489, 101-108.	35.3	4,661
4	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.	5.5	4,551
5	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	19.6	3,268
6	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014, 507, 455-461.	35.3	2,342
7	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.	5.8	1,712
8	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	5.8	1,677
9	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.	7.4	1,628
10	Antisense Transcription in the Mammalian Transcriptome. <i>Science</i> , 2005, 309, 1564-1566.	19.6	1,574
11	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002, 420, 563-573.	35.3	1,563
12	Genome-wide analysis of mammalian promoter architecture and evolution. <i>Nature Genetics</i> , 2006, 38, 626-635.	20.1	1,227
13	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.	6.6	992
14	Direct generation of functional dopaminergic neurons from mouse and human fibroblasts. <i>Nature</i> , 2011, 476, 224-227.	35.3	953
15	Comprehensive Analysis of NAC Family Genes in <i>Oryza sativa</i> and <i>Arabidopsis thaliana</i> . <i>DNA Research</i> , 2003, 10, 239-247.	3.4	950
16	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017, 543, 199-204.	35.3	930
17	Long non-coding antisense RNA controls Uchl1 translation through an embedded SINEB2 repeat. <i>Nature</i> , 2012, 491, 454-457.	35.3	908
18	Collection, Mapping, and Annotation of Over 28,000 cDNA Clones from japonica Rice. <i>Science</i> , 2003, 301, 376-379.	19.6	837

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19	The regulated retrotransposon transcriptome of mammalian cells. <i>Nature Genetics</i> , 2009, 41, 563-571.	20.1	746
20	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015, 16, 22.	8.5	713
21	A draft network of ligand-receptor-mediated multicellular signalling in human. <i>Nature Communications</i> , 2015, 6, 7866.	12.8	701
22	Diversity and dynamics of the <i>Drosophila</i> transcriptome. <i>Nature</i> , 2014, 512, 393-399.	35.3	682
23	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.	7.4	681
24	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 140, 744-752.	27.3	671
25	Functional annotation of a full-length mouse cDNA collection. <i>Nature</i> , 2001, 409, 685-690.	35.3	655
26	Somatic retrotransposition alters the genetic landscape of the human brain. <i>Nature</i> , 2011, 479, 534-537.	35.3	637
27	Functional Annotation of a Full-Length Arabidopsis cDNA Collection. <i>Science</i> , 2002, 296, 141-145.	19.6	634
28	Long non-coding RNAs: definitions, functions, challenges and recommendations. <i>Nature Reviews Molecular Cell Biology</i> , 2023, 24, 430-447.	36.5	571
29	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.	5.5	491
30	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017, 35, 872-878.	20.4	477
31	Site-specific DICER and DROSHA RNA products control the DNA-damage response. <i>Nature</i> , 2012, 488, 231-235.	35.3	471
32	Metazoan promoters: emerging characteristics and insights into transcriptional regulation. <i>Nature Reviews Genetics</i> , 2012, 13, 233-245.	16.4	462
33	Mammalian RNA polymerase II core promoters: insights from genome-wide studies. <i>Nature Reviews Genetics</i> , 2007, 8, 424-436.	16.4	443
34	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	20.1	408
35	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.	3.4	402
36	Small RNAs derived from snoRNAs. <i>Rna</i> , 2009, 15, 1233-1240.	3.5	389

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37	The Reality of Pervasive Transcription. <i>PLoS Biology</i> , 2011, 9, e1000625.	5.3	389
38	Endogenous Retrotransposition Activates Oncogenic Pathways in Hepatocellular Carcinoma. <i>Cell</i> , 2013, 153, 101-111.	27.3	359
39	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.	7.4	341
40	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.	7.4	336
41	Tiny RNAs associated with transcription start sites in animals. <i>Nature Genetics</i> , 2009, 41, 572-578.	20.1	328
42	Hierarchical folding and reorganization of chromosomes are linked to transcriptional changes in cellular differentiation. <i>Molecular Systems Biology</i> , 2015, 11, 852.	7.2	316
43	High-Efficiency Full-Length cDNA Cloning by Biotinylated CAP Trapper. <i>Genomics</i> , 1996, 37, 327-336.	2.9	303
44	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.	7.4	301
45	Complex Loci in Human and Mouse Genomes. <i>PLoS Genetics</i> , 2006, 2, e47.	3.3	293
46	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	5.3	290
47	Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. <i>Nature Genetics</i> , 2014, 46, 558-566.	20.1	275
48	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.	5.5	264
49	Hidden layers of human small RNAs. <i>BMC Genomics</i> , 2008, 9, 157.	2.9	258
50	A code for transcription initiation in mammalian genomes. <i>Genome Research</i> , 2008, 18, 1-12.	5.5	246
51	Unexpected expression of β - and β -globin in mesencephalic dopaminergic neurons and glial cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15454-15459.	7.4	245
52	Amphioxus functional genomics and the origins of vertebrate gene regulation. <i>Nature</i> , 2018, 564, 64-70.	35.3	239
53	Single-cell transcriptomics reveals expansion of cytotoxic CD4 T cells in supercentenarians. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24242-24251.	7.4	239
54	Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 520-524.	7.4	232

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55	Intrinsically disordered proteins drive membrane curvature. <i>Nature Communications</i> , 2015, 6, 7875.	12.8	232
56	High-efficiency cloning of Arabidopsis full-length cDNA by biotinylated CAP trapper. <i>Plant Journal</i> , 1998, 15, 707-720.	5.8	220
57	Transcriptome analysis of the aphid bacteriocyte, the symbiotic host cell that harbors an endocellular mutualistic bacterium, <i>Buchnera</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5477-5482.	7.4	220
58	Genome-wide analysis of promoter architecture in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2011, 21, 182-192.	5.5	220
59	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , 2017, 4, 170112.	5.3	210
60	Chromatin-associated RNA interference components contribute to transcriptional regulation in <i>Drosophila</i> . <i>Nature</i> , 2011, 480, 391-395.	35.3	206
61	CAGE: precise TSS data retrieval and high-resolution promoterome mining for integrative analyses. <i>Nucleic Acids Research</i> , 2015, 43, e51-e51.	13.8	206
62	Chromatin signatures and retrotransposon profiling in mouse embryos reveal regulation of LINE-1 by RNA. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 332-338.	7.8	203
63	Delineating developmental and metabolic pathways in vivo by expression profiling using the RIKEN set of 18,816 full-length enriched mouse cDNA arrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 2199-2204.	7.4	197
64	The Abundance of Short Proteins in the Mammalian Proteome. <i>PLoS Genetics</i> , 2006, 2, e52.	3.3	194
65	Update of the FANTOM web resource: expansion to provide additional transcriptome atlases. <i>Nucleic Acids Research</i> , 2019, 47, D752-D758.	13.8	185
66	Long non-coding RNA modifies chromatin. <i>BioEssays</i> , 2011, 33, 830-839.	2.5	183
67	High-fidelity promoter profiling reveals widespread alternative promoter usage and transposon-driven developmental gene expression. <i>Genome Research</i> , 2013, 23, 169-180.	5.5	183
68	Two independent transcription initiation codes overlap on vertebrate core promoters. <i>Nature</i> , 2014, 507, 381-385.	35.3	183
69	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.	1.9	182
70	The <i>Drosophila</i> Gene Collection: Identification of Putative Full-Length cDNAs for 70% of <i>D. melanogaster</i> Genes. <i>Genome Research</i> , 2002, 12, 1294-1300.	5.5	181
71	Redefinition of the human mast cell transcriptome by deep-CAGE sequencing. <i>Blood</i> , 2014, 123, e58-e67.	1.4	180
72	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.	7.4	178

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73	Detecting Expressed Genes Using CAGE. <i>Methods in Molecular Biology</i> , 2014, 1164, 67-85.	0.7	177
74	Unamplified cap analysis of gene expression on a single-molecule sequencer. <i>Genome Research</i> , 2011, 21, 1150-1159.	5.5	176
75	[2] High-efficiency full-length cDNA cloning. <i>Methods in Enzymology</i> , 1999, 303, 19-44.	1.7	170
76	NMDA Receptor Regulation Prevents Regression of Visual Cortical Function in the Absence of Mecp2. <i>Neuron</i> , 2012, 76, 1078-1090.	7.9	169
77	Sulfenome mining in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11545-11550.	7.4	168
78	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012, 22, 1658-1667.	5.5	167
79	Transcript Annotation in FANTOM3: Mouse Gene Catalog Based on Physical cDNAs. <i>PLoS Genetics</i> , 2006, 2, e62.	3.3	166
80	Transcription and enhancer profiling in human monocyte subsets. <i>Blood</i> , 2014, 123, e90-e99.	1.4	166
81	Tag-based approaches for transcriptome research and genome annotation. <i>Nature Methods</i> , 2005, 2, 495-502.	19.2	165
82	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.	3.3	165
83	Comparative validation of the <i>D. melanogaster</i> modENCODE transcriptome annotation. <i>Genome Research</i> , 2014, 24, 1209-1223.	5.5	160
84	Linking promoters to functional transcripts in small samples with nanoCAGE and CAGEscan. <i>Nature Methods</i> , 2010, 7, 528-534.	19.2	155
85	Targeting a Complex Transcriptome: The Construction of the Mouse Full-Length cDNA Encyclopedia. <i>Genome Research</i> , 2003, 13, 1273-1289.	5.5	154
86	Clusters of Internally Primed Transcripts Reveal Novel Long Noncoding RNAs. <i>PLoS Genetics</i> , 2006, 2, e37.	3.3	149
87	Molecular mechanisms of pituitary organogenesis: In search of novel regulatory genes. <i>Molecular and Cellular Endocrinology</i> , 2010, 323, 4-19.	3.2	142
88	Genome sequence and analysis of the Japanese morning glory <i>Ipomoea nil</i> . <i>Nature Communications</i> , 2016, 7, 13295.	12.8	140
89	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.	7.4	133
90	Methods for analyzing deep sequencing expression data: constructing the human and mouse promoterome with deepCAGE data. <i>Genome Biology</i> , 2009, 10, R79.	9.1	132

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91	Genome-wide detection and analysis of hippocampus core promoters using DeepCAGE. <i>Genome Research</i> , 2009, 19, 255-265.	5.5	129
92	Cross-mapping and the identification of editing sites in mature microRNAs in high-throughput sequencing libraries. <i>Genome Research</i> , 2010, 20, 257-264.	5.5	127
93	Transcriptional network dynamics in macrophage activation. <i>Genomics</i> , 2006, 88, 133-142.	2.9	125
94	Noncoding RNA transcription beyond annotated genes. <i>Current Opinion in Genetics and Development</i> , 2007, 17, 139-144.	3.3	125
95	Neuroendocrine tumours: the role of imaging for diagnosis and therapy. <i>Nature Reviews Endocrinology</i> , 2014, 10, 102-114.	9.4	125
96	Dynamic regulation of the transcription initiation landscape at single nucleotide resolution during vertebrate embryogenesis. <i>Genome Research</i> , 2013, 23, 1938-1950.	5.5	122
97	Genetic control of the innate immune response. <i>BMC Immunology</i> , 2003, 4, 5.	2.2	120
98	Discrimination of Non-Protein-Coding Transcripts from Protein-Coding mRNA. <i>RNA Biology</i> , 2006, 3, 40-48.	3.3	120
99	Biased Allelic Expression in Human Primary Fibroblast Single Cells. <i>American Journal of Human Genetics</i> , 2015, 96, 70-80.	6.0	120
100	Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. <i>Nucleic Acids Research</i> , 2017, 45, D737-D743.	13.8	120
101	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	5.5	119
102	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.	3.8	116
103	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.	7.4	114
104	Antisense transcripts with rice full-length cDNAs. <i>Genome Biology</i> , 2003, 5, R5.	9.1	113
105	RADICL-seq identifies general and cell type-specific principles of genome-wide RNA-chromatin interactions. <i>Nature Communications</i> , 2020, 11, 1018.	12.8	113
106	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.	13.8	106
107	C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution. <i>Nature Communications</i> , 2019, 10, 360.	12.8	106
108	Full-length cDNAs from chicken bursal lymphocytes to facilitate gene function analysis. <i>Genome Biology</i> , 2004, 6, R6.	9.1	105

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109	Transcriptional and structural impact of TATA-initiation site spacing in mammalian core promoters. <i>Genome Biology</i> , 2006, 7, R78.	9.1	104
110	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.	5.5	104
111	Heterotachy in Mammalian Promoter Evolution. <i>PLoS Genetics</i> , 2006, 2, e30.	3.3	103
112	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.	12.8	100
113	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.	0.7	98
114	Paradigm shifts in genomics through the FANTOM projects. <i>Mammalian Genome</i> , 2015, 26, 391-402.	2.2	98
115	Mice and Men: Their Promoter Properties. <i>PLoS Genetics</i> , 2006, 2, e54.	3.3	95
116	Transcriptional landscape of Mycobacterium tuberculosis infection in macrophages. <i>Scientific Reports</i> , 2018, 8, 6758.	3.4	94
117	A rescue strategy for multimapping short sequence tags refines surveys of transcriptional activity by CAGE. <i>Genomics</i> , 2008, 91, 281-288.	2.9	93
118	The complexity of the mammalian transcriptome. <i>Journal of Physiology</i> , 2006, 575, 321-332.	2.8	92
119	High Efficiency Selection of Full-length cDNA by Improved Biotinylated Cap Trapper. <i>DNA Research</i> , 1997, 4, 61-66.	3.4	90
120	Trehalose-Enhanced Isolation of Neuronal Sub-Types from Adult Mouse Brain. <i>BioTechniques</i> , 2012, 52, 381-385.	1.7	90
121	Tagging mammalian transcription complexity. <i>Trends in Genetics</i> , 2006, 22, 501-510.	6.7	85
122	SINEUPs: A new class of natural and synthetic antisense long non-coding RNAs that activate translation. <i>RNA Biology</i> , 2015, 12, 771-779.	3.3	85
123	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. <i>Genome Research</i> , 2010, 20, 791-803.	5.5	84
124	Transcriptome-wide sites of collided ribosomes reveal principles of translational pausing. <i>Genome Research</i> , 2020, 30, 985-999.	5.5	83
125	Transcriptome Analysis of Recurrently Deregulated Genes across Multiple Cancers Identifies New Pan-Cancer Biomarkers. <i>Cancer Research</i> , 2016, 76, 216-226.	0.9	82
126	NET-CAGE characterizes the dynamics and topology of human transcribed cis-regulatory elements. <i>Nature Genetics</i> , 2019, 51, 1369-1379.	20.1	82

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127	refTSS: A Reference Data Set for Human and Mouse Transcription Start Sites. <i>Journal of Molecular Biology</i> , 2019, 431, 2407-2422.	4.2	82
128	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.	3.8	81
129	CAGE Basic/Analysis Databases: the CAGE resource for comprehensive promoter analysis. <i>Nucleic Acids Research</i> , 2006, 34, D632-D636.	13.8	80
130	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.	7.4	80
131	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.	2.2	78
132	The enhancer and promoter landscape of human regulatory and conventional T-cell subpopulations. <i>Blood</i> , 2014, 123, e68-e78.	1.4	78
133	DNA damage response inhibition at dysfunctional telomeres by modulation of telomeric DNA damage response RNAs. <i>Nature Communications</i> , 2017, 8, 13980.	12.8	78
134	Multifaceted mammalian transcriptome. <i>Current Opinion in Cell Biology</i> , 2008, 20, 274-280.	5.4	77
135	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.	3.4	75
136	Dynamic usage of transcription start sites within core promoters. <i>Genome Biology</i> , 2006, 7, R118.	9.1	75
137	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.	2.9	74
138	Placental expression profiling in preeclampsia: local overproduction of hemoglobin may drive pathological changes. <i>Fertility and Sterility</i> , 2008, 90, 1834-1843.	0.9	74
139	Analysis of the DNA methylome and transcriptome in granulopoiesis reveals timed changes and dynamic enhancer methylation. <i>Blood</i> , 2014, 123, e79-e89.	1.4	74
140	Gut microbial carbohydrate metabolism contributes to insulin resistance. <i>Nature</i> , 2023, 621, 389-395.	35.3	74
141	The FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. <i>Genome Biology</i> , 2009, 10, R40.	9.1	73
142	LOCATE: a mouse protein subcellular localization database. <i>Nucleic Acids Research</i> , 2006, 34, D213-D217.	13.8	72
143	FANTOM5 CAGE profiles of human and mouse reprocessed for GRCh38 and GRCm38 genome assemblies. <i>Scientific Data</i> , 2017, 4, 170107.	5.3	72
144	Systematic analysis of transcription start sites in avian development. <i>PLoS Biology</i> , 2017, 15, e2002887.	5.3	72

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145	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.	7.4	70
146	Evolutionary turnover of mammalian transcription start sites. Genome Research, 2006, 16, 713-722.	5.5	70
147	Comparative Analysis of Plant and Animal Calcium Signal Transduction Element Using Plant Full-Length cDNA Data. Molecular Biology and Evolution, 2004, 21, 1855-1870.	9.0	69
148	A Simple Physical Model Predicts Small Exon Length Variations. PLoS Genetics, 2006, 2, e45.	3.3	69
149	Solution structure of the RWD domain of the mouse GCN2 protein. Protein Science, 2004, 13, 2089-2100.	7.7	68
150	Alternate transcription of the Toll-like receptor signaling cascade. Genome Biology, 2006, 7, R10.	9.1	67
151	FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. Genome Biology, 2009, 10, R39.	9.1	67
152	Suppression of artifacts and barcode bias in high-throughput transcriptome analyses utilizing template switching. Nucleic Acids Research, 2013, 41, e44-e44.	13.8	67
153	MOIRAI: a compact workflow system for CAGE analysis. BMC Bioinformatics, 2014, 15, 144.	2.6	67
154	FANTOM enters 20th year: expansion of transcriptomic atlases and functional annotation of non-coding RNAs. Nucleic Acids Research, 2021, 49, D892-D898.	13.8	66
155	Krimper Enforces an Antisense Bias on piRNA Pools by Binding AGO3 in the Drosophila Germline. Molecular Cell, 2015, 59, 553-563.	9.4	65
156	From "Cellular" RNA to "Smart" RNA: Multiple Roles of RNA in Genome Stability and Beyond. Chemical Reviews, 2018, 118, 4365-4403.	49.4	65
157	FANTOM5 transcriptome catalog of cellular states based on Semantic MediaWiki. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw105.	3.1	64
158	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.	2.9	62
159	Identification of antisense long noncoding RNAs that function as SINEUIPs in human cells. Scientific Reports, 2016, 6, 33605.	3.4	62
160	On biased distribution of introns in various eukaryotes. Gene, 2002, 300, 89-95.	2.3	61
161	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
162	NanoCAGE: A High-Resolution Technique to Discover and Interrogate Cell Transcriptomes. Cold Spring Harbor Protocols, 2011, 2011, pdb.prot5559-pdb.prot5559.	0.3	61

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163	Genomics Approach to Abscisic Acid- and Gibberellin-responsive Genes in Rice. <i>DNA Research</i> , 2003, 10, 249-261.	3.4	58
164	Pseudoâ€‘Messenger RNA: Phantoms of the Transcriptome. <i>PLoS Genetics</i> , 2006, 2, e23.	3.3	58
165	RNA Dust: Where are the Genes?. <i>DNA Research</i> , 2010, 17, 51-59.	3.4	58
166	Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics. <i>Nucleic Acids Research</i> , 2015, 43, 6969-6982.	13.8	58
167	The FANTOM5 collection, a data series underpinning mammalian transcriptome atlases in diverse cell types. <i>Scientific Data</i> , 2017, 4, 170113.	5.3	58
168	Genomic organization of transcriptomes in mammals: Coregulation and cofunctionality. <i>Genomics</i> , 2007, 89, 580-587.	2.9	56
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