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	Towards SINEUP-based therapeutics: Design of an inÂvitro synthesized SINEUP RNA. Molecular Therapy - Nucleic Acids, 2022, 27, 1092-1102.	5.1	4
2	Complete Transcriptome Analysis by 5â€²-End Single-Cell RNA-Seq with Random Priming. Methods in Molecular Biology, 2022, 2490, 141-156.	0.9	0
3	Lessons from the functional characterization of lncRNAs: introduction to mammalian genome special issue. Mammalian Genome, 2022, , .	2.2	1
4	Multiomic atlas with functional stratification and developmental dynamics of zebrafish cis-regulatory elements. Nature Genetics, 2022, 54, 1037-1050.	21.4	26
5	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
6	LETR1 is a lymphatic endothelial-specific lncRNA governing cell proliferation and migration through KLF4 and SEMA3C. Nature Communications, 2021, 12, 925.	12.8	18
7	Antisense RNAs during early vertebrate development are divided in groups with distinct features. Genome Research, 2021, 31, 995-1010.	5.5	7
8	Decoding Neuronal Diversification by Multiplexed Single-cell RNA-Seq. Stem Cell Reports, 2021, 16, 810-824.	4.8	8
9	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. Nature Communications, 2021, 12, 3297.	12.8	11
10	The choice of negative control antisense oligonucleotides dramatically impacts downstream analysis depending on the cellular background. BMC Genomic Data, 2021, 22, 33.	1.7	0
11	Analysis of Enhancerâ€"Promoter Interactions using CAGE and RADICL-Seq Technologies. Methods in Molecular Biology, 2021, 2351, 201-210.	0.9	2
12	Low Quantity Single Strand CAGE (LQ-ssCAGE) Maps Regulatory Enhancers and Promoters. Methods in Molecular Biology, 2021, 2351, 67-90.	0.9	6
13	A field guide to cultivating computational biology. PLoS Biology, 2021, 19, e3001419.	5.6	6
14	SINEUPs: a novel toolbox for RNA therapeutics. Essays in Biochemistry, 2021, 65, 775-789.	4.7	13
15	Embryonic LTR retrotransposons supply promoter modules to somatic tissues. Genome Research, 2021, 31, 1983-1993.	5.5	7
16	Japan: prize diversity, not conformity, to boost research. Nature, 2021, 599, 201-201.	27.8	1
17	SINEUP Non-coding RNA Targeting GDNF Rescues Motor Deficits and Neurodegeneration in a Mouse Model of Parkinsonâ€™s Disease. Molecular Therapy, 2020, 28, 642-652.	8.2	41
18	Dual-initiation promoters with intertwined canonical and TCT/TOP transcription start sites diversify transcript processing. Nature Communications, 2020, 11, 168.	12.8	37

#	Article	IF	Citations
19	A human minisatellite hosts an alternative transcription start site for NPRL3 driving its expression in a repeat numberâ€dependent manner. Human Mutation, 2020, 41, 807-824.	2.5	6
20	Synthetic <i>inÂvitro</i> transcribed lncRNAs (SINEUPs) with chemical modifications enhance target mRNA translation. FEBS Letters, 2020, 594, 4357-4369.	2.8	15
21	An NMR-based approach reveals the core structure of the functional domain of SINEUP lncRNAs. Nucleic Acids Research, 2020, 48, 9346-9360.	14.5	18
22	Functional annotation of human long noncoding RNAs via molecular phenotyping. Genome Research, 2020, 30, 1060-1072.	5.5	109
23	Comparative transcriptomics of primary cells in vertebrates. Genome Research, 2020, 30, 951-961.	5.5	29
24	SINEUP long non-coding RNA acts via PTBP1 and HNRNPK to promote translational initiation assemblies. Nucleic Acids Research, 2020, 48, 11626-11644.	14.5	33
25	Use of Cap Analysis Gene Expression to detect human papillomavirus promoter activity patterns at different disease stages. Scientific Reports, 2020, 10, 17991.	3.3	1
26	Safety and efficacy of the Russian COVID-19 vaccine: more information needed. Lancet, The, 2020, 396, e53.	13.7	27
27	Analysis of splice variants of the human protein disulfide isomerase (P4HB) gene. BMC Genomics, 2020, 21, 766.	2.8	3
28	The Secret Life of lncRNAs: Conserved, yet Not Conserved. Cell, 2020, 181, 512-514.	28.9	9
29	Genome-Wide Technologies to Study RNAâ€"Chromatin Interactions. Non-coding RNA, 2020, 6, 20.	2.6	19
30	Comprehensive Characterization of Transcriptional Activity during Influenza A Virus Infection Reveals Biases in Cap-Snatching of Host RNA Sequences. Journal of Virology, 2020, 94, .	3.4	14
31	Machine-driven parameter screen of biochemical reactions. Nucleic Acids Research, 2020, 48, e37-e37.	14.5	0
32	Recounting the FANTOM CAGE-Associated Transcriptome. Genome Research, 2020, 30, 1073-1081.	5.5	35
33	RADICL-seq identifies general and cell typeâ€"specific principles of genome-wide RNA-chromatin interactions. Nature Communications, 2020, 11, 1018.	12.8	98
34	Cap Analysis of Gene Expression (CAGE): A Quantitative and Genome-Wide Assay of Transcription Start Sites. Methods in Molecular Biology, 2020, 2120, 277-301.	0.9	22
35	Expanded ENCODE delivers invaluable genomic encyclopedia. Nature, 2020, 583, 685-686.	27.8	7
36	Nuclear AGO1 Regulates Gene Expression by Affecting Chromatin Architecture in Human Cells. Cell Systems, 2019, 9, 446-458.e6.	6.2	27

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37	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
38	NET-CAGE characterizes the dynamics and topology of human transcribed cis-regulatory elements. Nature Genetics, 2019, 51, 1369-1379.	21.4	72
39	Broad Heterochromatic Domains Open in Gonocyte Development Prior to De Novo DNA Methylation. Developmental Cell, 2019, 51, 21-34.e5.	7.0	26
40	Identification of novel cerebellar developmental transcriptional regulators with motif activity analysis. BMC Genomics, 2019, 20, 718.	2.8	11
41	MicroRNA-27a/b-3p and PPARG regulate SCAMP3 through a feed- forward loop during adipogenesis. Scientific Reports, 2019, 9, 13891.	3.3	17
42	SINEUP non-coding RNAs rescue defective frataxin expression and activity in a cellular model of Friedreich's Ataxia. Nucleic Acids Research, 2019, 47, 10728-10743.	14.5	30
43	The RNAâ€binding protein ILF3 binds to transposable element sequences in SINEUP lncRNAs. FASEB Journal, 2019, 33, 13572-13589.	0.5	20
44	C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution. Nature Communications, 2019, 10, 360.	12.8	102
45	refTSS: A Reference Data Set for Human and Mouse Transcription Start Sites. Journal of Molecular Biology, 2019, 431, 2407-2422.	4.2	72
46	Cell Based Assays of SINEUP Non-coding RNAs That Can Specifically Enhance mRNA Translation. Journal of Visualized Experiments, 2019, , .	0.3	5
47	Multi-year whole-blood transcriptome data for the study of onset and progression of Parkinsonâ€™s Disease. Scientific Data, 2019, 6, 20.	5.3	8
48	Dynamics of cardiomyocyte transcriptome and chromatin landscape demarcates key events of heart development. Genome Research, 2019, 29, 506-519.	5.5	21
49	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	15
50	Look for methods, not conclusions. Cell Death and Disease, 2019, 10, 931.	6.3	1
51	Update of the FANTOM web resource: expansion to provide additional transcriptome atlases. Nucleic Acids Research, 2019, 47, D752-D758.	14.5	172
52	Antisense Transcription in Loci Associated to Hereditary Neurodegenerative Diseases. Molecular Neurobiology, 2019, 56, 5392-5415.	4.0	29
53	Tagging Transcription Starting Sites with CAGE. , 2019, , 7-20.		0
54	The Human Cell Atlas: Technical approaches and challenges. Briefings in Functional Genomics, 2018, 17, 283-294.	2.7	34

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55	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
56	Structural determinants of the SINE B2 element embedded in the long non-coding RNA activator of translation AS Uchl1. Scientific Reports, 2018, 8, 3189.	3.3	32
57	Discovery of Transcription Factors Novel to Mouse Cerebellar Granule Cell Development Through Laser-Capture Microdissection. Cerebellum, 2018, 17, 308-325.	2.5	6
58	Transcriptional landscape of Mycobacterium tuberculosis infection in macrophages. Scientific Reports, 2018, 8, 6758.	3.3	92
59	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
60	Target-enrichment sequencing for detailed characterization of small RNAs. Nature Protocols, 2018, 13, 768-786.	12.0	9
61	SCPortalen: human and mouse single-cell centric database. Nucleic Acids Research, 2018, 46, D781-D787.	14.5	48
62	Conserved temporal ordering of promoter activation implicates common mechanisms governing the immediate early response across cell types and stimuli. Open Biology, 2018, 8, 180011.	3.6	13
63	Integration of genetics and miRNAâ€"target gene network identified disease biology implicated in tissue specificity. Nucleic Acids Research, 2018, 46, 11898-11909.	14.5	39
64	SLIC-CAGE: high-resolution transcription start site mapping using nanogram-levels of total RNA. Genome Research, 2018, 28, 1943-1956.	5.5	33
65	Amphioxus functional genomics and the origins of vertebrate gene regulation. Nature, 2018, 564, 64-70.	27.8	224
66	Promoter Usage and Dynamics in Vascular Smooth Muscle Cells Exposed to Fibroblast Growth Factor-2 or Interleukin-1Î². Scientific Reports, 2018, 8, 13164.	3.3	10
67	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease. PLoS Computational Biology, 2018, 14, e1005934.	3.2	17
68	Identification of functional features of synthetic SINEUPs, antisense lncRNAs that specifically enhance protein translation. PLoS ONE, 2018, 13, e0183229.	2.5	23
69	DEIVA: a web application for interactive visual analysis of differential gene expression profiles. BMC Genomics, 2017, 18, 47.	2.8	41
70	DNA damage response inhibition at dysfunctional telomeres by modulation of telomeric DNA damage response RNAs. Nature Communications, 2017, 8, 13980.	12.8	76
71	An atlas of human long non-coding RNAs with accurate 5â€² ends. Nature, 2017, 543, 199-204.	27.8	898
72	The FANTOM5 Computation Ecosystem: Genomic Information Hub for Promoters and Active Enhancers. Methods in Molecular Biology, 2017, 1611, 199-217.	0.9	23

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73	From bench to bedside: The long journey of long non-coding RNAs. Current Opinion in Systems Biology, 2017, 3, 119-124.	2.6	22
74	A damaged genome's transcriptional landscape through multilayered expression profiling around in situ-mapped DNA double-strand breaks. Nature Communications, 2017, 8, 15656.	12.8	89
75	Linking FANTOM5 CAGE peaks to annotations with CAGEscan. Scientific Data, 2017, 4, 170147.	5.3	29
76	Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. EBioMedicine, 2017, 24, 257-266.	6.1	24
77	The FANTOM5 collection, a data series underpinning mammalian transcriptome atlases in diverse cell types. Scientific Data, 2017, 4, 170113.	5.3	55
78	An integrated expression atlas of miRNAs and their promoters in human and mouse. Nature Biotechnology, 2017, 35, 872-878.	17.5	456
79	FANTOM5 CAGE profiles of human and mouse samples. Scientific Data, 2017, 4, 170112.	5.3	195
80	FANTOM5 CAGE profiles of human and mouse reprocessed for GRCh38 and GRCm38 genome assemblies. Scientific Data, 2017, 4, 170107.	5.3	68
81	Monitoring transcription initiation activities in rat and dog. Scientific Data, 2017, 4, 170173.	5.3	6
82	The effect of genetic variation on promoter usage and enhancer activity. Nature Communications, 2017, 8, 1358.	12.8	50
83	Integrative CAGE and DNA Methylation Profiling Identify Epigenetically Regulated Genes in NSCLC. Molecular Cancer Research, 2017, 15, 1354-1365.	3.4	25
84	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
85	Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution. Diabetes, 2017, 66, 218-230.	0.6	27
86	A Transcriptional Switch Point During Hematopoietic Stem and Progenitor Cell Ontogeny. Stem Cells and Development, 2017, 26, 314-327.	2.1	4
87	Transcription start site profiling of 15 anatomical regions of the Macaca mulatta central nervous system. Scientific Data, 2017, 4, 170163.	5.3	4
88	The Human Cell Atlas. ELife, 2017, 6, .	6.0	1,547
89	RNA extraction from sorted neuronal subtypes. BioTechniques, 2017, 62, .	1.8	1
90	Systematic analysis of transcription start sites in avian development. PLoS Biology, 2017, 15, e2002887.	5.6	68

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91	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
92	On-the-fly selection of cell-specific enhancers, genes, miRNAs and proteins across the human body using SlideBase. Database: the Journal of Biological Databases and Curation, 2016, 2016, .	3.0	24
93	Transcriptome analysis of periodontitis-associated fibroblasts by CAGE sequencing identified DLX5 and RUNX2 long variant as novel regulators involved in periodontitis. Scientific Reports, 2016, 6, 33666.	3.3	18
94	DeepCAGE transcriptomics identify HOXD10 as transcription factor regulating lymphatic endothelial responses to VEGF-C. Journal of Cell Science, 2016, 129, 2573-85.	2.0	15
95	Transcriptional, post-transcriptional and chromatin-associated regulation of pri-miRNAs, pre-miRNAs and moRNAs. Nucleic Acids Research, 2016, 44, 3070-3081.	14.5	38
96	Single-Nucleotide Resolution Mapping of Hepatitis B Virus Promoters in Infected Human Livers and Hepatocellular Carcinoma. Journal of Virology, 2016, 90, 10811-10822.	3.4	27
97	Isoforms of the Erythropoietin receptor in dopaminergic neurons of the *Substantia Nigra*. Journal of Neurochemistry, 2016, 139, 596-609.	3.9	11
98	YY1 binding association with sex-biased transcription revealed through X-linked transcript levels and allelic binding analyses. Scientific Reports, 2016, 6, 37324.	3.3	32
99	Characterization of piRNAs across postnatal development in mouse brain. Scientific Reports, 2016, 6, 25039.	3.3	34
100	Genome sequence and analysis of the Japanese morning glory Ipomoea nil. Nature Communications, 2016, 7, 13295.	12.8	138
101	Identification of antisense long noncoding RNAs that function as SINEUPs in human cells. Scientific Reports, 2016, 6, 33605.	3.3	58
102	FANTOM5 transcriptome catalog of cellular states based on Semantic MediaWiki. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw105.	3.0	64
103	Transcriptome Analysis of Recurrently Deregulated Genes across Multiple Cancers Identifies New Pan-Cancer Biomarkers. Cancer Research, 2016, 76, 216-226.	0.9	80
104	Functional annotation of the vlinc class of non-coding RNAs using systems biology approach. Nucleic Acids Research, 2016, 44, 3233-3252.	14.5	31
105	The ORFeome Collaboration: a genome-scale human ORF-clone resource. Nature Methods, 2016, 13, 191-192.	19.0	111
106	Deficiency of multidrug resistance 2 contributes to cell transformation through oxidative stress. Carcinogenesis, 2016, 37, 39-48.	2.8	15
107	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
108	Epi-drivers and cancer-testis genes. Translational Cancer Research, 2016, 5, 334-336.	1.0	1

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109	Abstract 2897: Recurrent transcriptome alterations across multiple cancer types. , 2016, , .		0
110	In grateful recognition of our Editorial Board. BioEssays, 2015, 37, 1254-1255.	2.5	0
111	Promoter-level expression clustering identifies time development of transcriptional regulatory cascades initiated by ErbB receptors in breast cancer cells. Scientific Reports, 2015, 5, 11999.	3.3	30
112	Hierarchical folding and reorganization of chromosomes are linked to transcriptional changesÂin cellular differentiation. Molecular Systems Biology, 2015, 11, 852.	7.2	305
113	DeepCAGE Transcriptomics Reveal an Important Role of the Transcription Factor MAFB in the Lymphatic Endothelium. Cell Reports, 2015, 13, 1493-1504.	6.4	46
114	Remodeling of retrotransposon elements during epigenetic induction of adult visual cortical plasticityÂby HDAC inhibitors. Epigenetics and Chromatin, 2015, 8, 55.	3.9	32
115	Mapping Mammalian Cell-type-specific Transcriptional Regulatory Networks Using KD-CAGE and ChIP-seq Data in the TC-YIK Cell Line. Frontiers in Genetics, 2015, 6, 331.	2.3	13
116	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
117	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
118	HSA21 Single-Minded 2 (Sim2) Binding Sites Co-Localize with Super-Enhancers and Pioneer Transcription Factors in Pluripotent Mouse ES Cells. PLoS ONE, 2015, 10, e0126475.	2.5	9
119	The Constrained Maximal Expression Level Owing to Haploidy Shapes Gene Content on the Mammalian X Chromosome. PLoS Biology, 2015, 13, e1002315.	5.6	32
120	Application of Gene Expression Trajectories Initiated from ErbB Receptor Activation Highlights the Dynamics of Divergent Promoter Usage. PLoS ONE, 2015, 10, e0144176.	2.5	1
121	Engineering mammalian cell factories with SINEUP noncoding RNAs to improve translation of secreted proteins. Gene, 2015, 569, 287-293.	2.2	35
122	Biased Allelic Expression in Human Primary Fibroblast Single Cells. American Journal of Human Genetics, 2015, 96, 70-80.	6.2	117
123	Nuclear transcriptome profiling of induced pluripotent stem cells and embryonic stem cells identify non-coding loci resistant to reprogramming. Cell Cycle, 2015, 14, 1148-1155.	2.6	14
124	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. Science, 2015, 347, 1010-1014.	12.6	517
125	Characterization of Novel Transcripts of Human Papillomavirus Type 16 Using Cap Analysis Gene Expression Technology. Journal of Virology, 2015, 89, 2448-2452.	3.4	6
126	Gateways to the FANTOM5 promoter level mammalian expression atlas. Genome Biology, 2015, 16, 22.	8.8	687

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127	Krimper Enforces an Antisense Bias on piRNA Pools by Binding AGO3 in the Drosophila Germline. Molecular Cell, 2015, 59, 553-563.	9.7	61
128	The frequent evolutionary birth and death of functional promoters in mouse and human. Genome Research, 2015, 25, 1546-1557.	5.5	55
129	Telomerase Reverse Transcriptase Regulates microRNAs. International Journal of Molecular Sciences, 2015, 16, 1192-1208.	4.1	22
130	A draft network of ligandâ€"receptor-mediated multicellular signalling in human. Nature Communications, 2015, 6, 7866.	12.8	676
131	Transcriptional Dynamics Reveal Critical Roles for Non-coding RNAs in the Immediate-Early Response. PLoS Computational Biology, 2015, 11, e1004217.	3.2	22
132	CAGEr: precise TSS data retrieval and high-resolution promoterome mining for integrative analyses. Nucleic Acids Research, 2015, 43, e51-e51.	14.5	194
133	Technical Advance: Transcription factor, promoter, and enhancer utilization in human myeloid cells. Journal of Leukocyte Biology, 2015, 97, 985-995.	3.3	23
134	Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics. Nucleic Acids Research, 2015, 43, 6969-6982.	14.5	54
135	STAP cells are derived from ES cells. Nature, 2015, 525, E4-E5.	27.8	8
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	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
138	Expression Specificity of Disease-Associated lncRNAs: Toward Personalized Medicine. Current Topics in Microbiology and Immunology, 2015, 394, 237-258.	1.1	33
139	Complexity of Mammalian Transcriptome Analyzed by RNA Deep Sequencing. , 2015, , 3-22.		2
140	CAGE profiling of ncRNAs in hepatocellular carcinoma reveals widespread activation of retroviral LTR promoters in virus-induced tumors. Genome Research, 2015, 25, 1812-1824.	5.5	49
141	Paradigm shifts in genomics through the FANTOM projects. Mammalian Genome, 2015, 26, 391-402.	2.2	96
142	A new approach for screening cervical cancer by characterization of transcripts using CAGE technology.. Journal of Clinical Oncology, 2015, 33, e16514-e16514.	1.6	1
143	NanoCAGE analysis of the mouse olfactory epithelium identifies the expression of vomeronasal receptors and of proximal LINE elements. Frontiers in Cellular Neuroscience, 2014, 8, 41.	3.7	11
144	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

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145	Digital expression profiling of the compartmentalized translatome of Purkinje neurons. Genome Research, 2014, 24, 1396-1410.	5.5	49
146	PAPD5-mediated 3′ 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
147	Mesencephalic dopaminergic neurons express a repertoire of olfactory receptors and respond to odorant-like molecules. BMC Genomics, 2014, 15, 729.	2.8	46
148	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	27.8	1,838
149	Diversity and dynamics of the Drosophila transcriptome. Nature, 2014, 512, 393-399.	27.8	647
150	Two independent transcription initiation codes overlap on vertebrate core promoters. Nature, 2014, 507, 381-385.	27.8	182
151	An atlas of active enhancers across human cell types and tissues. Nature, 2014, 507, 455-461.	27.8	2,269
152	The enhancer and promoter landscape of human regulatory and conventional T-cell subpopulations. Blood, 2014, 123, e68-e78.	1.4	77
153	Systemic identification of estrogen-regulated genes in breast cancer cells through cap analysis of gene expression mapping. Biochemical and Biophysical Research Communications, 2014, 447, 531-536.	2.1	14
154	Analysis of the DNA methylome and transcriptome in granulopoiesis reveals timed changes and dynamic enhancer methylation. Blood, 2014, 123, e79-e89.	1.4	72
155	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
156	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
157	Transcription and enhancer profiling in human monocyte subsets. Blood, 2014, 123, e90-e99.	1.4	157
158	Mice in the ENCODE spotlight. Nature, 2014, 515, 346-347.	27.8	11
159	Specific Mesothelial Signature Marks the Heterogeneity of Mesenchymal Stem Cells From High-Grade Serous Ovarian Cancer. Stem Cells, 2014, 32, 2998-3011.	3.2	16
160	Widespread genome transcription: New possibilities for RNA therapies. Biochemical and Biophysical Research Communications, 2014, 452, 294-301.	2.1	37
161	Comparative validation of the <i>D. melanogaster</i> modENCODE transcriptome annotation. Genome Research, 2014, 24, 1209-1223.	5.5	147
162	The devil in the details of RNA-seq. Nature Biotechnology, 2014, 32, 882-884.	17.5	35

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163	MOIRAI: a compact workflow system for CAGE analysis. BMC Bioinformatics, 2014, 15, 144.	2.6	66
164	Chromatin states reveal functional associations for globally defined transcription start sites in four human cell lines. BMC Genomics, 2014, 15, 120.	2.8	17
165	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
166	CAGE-defined promoter regions of the genes implicated in Rett Syndrome. BMC Genomics, 2014, 15, 1177.	2.8	10
167	Redefinition of the human mast cell transcriptome by deep-CAGE sequencing. Blood, 2014, 123, e58-e67.	1.4	175
168	Detecting Expressed Genes Using CAGE. Methods in Molecular Biology, 2014, 1164, 67-85.	0.9	170
169	Multiplicity of 5â€² Cap Structures Present on Short RNAs. PLoS ONE, 2014, 9, e102895.	2.5	29
170	Dynamic regulation of the transcription initiation landscape at single nucleotide resolution during vertebrate embryogenesis. Genome Research, 2013, 23, 1938-1950.	5.5	119
171	Comparison of RNA- or LNA-hybrid oligonucleotides in template-switching reactions for high-speed sequencing library preparation. BMC Genomics, 2013, 14, 665.	2.8	23
172	Population transcriptomics with singleâ€cell resolution: A new field made possible by microfluidics. BioEssays, 2013, 35, 131-140.	2.5	20
173	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
174	High-fidelity promoter profiling reveals widespread alternative promoter usage and transposon-driven developmental gene expression. Genome Research, 2013, 23, 169-180.	5.5	176
175	Regional differences in gene expression and promoter usage in aged human brains. Neurobiology of Aging, 2013, 34, 1825-1836.	3.1	30
176	Endogenous Retrotransposition Activates Oncogenic Pathways in Hepatocellular Carcinoma. Cell, 2013, 153, 101-111.	28.9	352
177	Suppression of artifacts and barcode bias in high-throughput transcriptome analyses utilizing template switching. Nucleic Acids Research, 2013, 41, e44-e44.	14.5	65
178	Temporal dynamics and transcriptional control using single-cell gene expression analysis. Genome Biology, 2013, 14, R118.	9.6	43
179	A comprehensive promoter landscape identifies a novel promoter for CD133 in restricted tissues, cancers, and stem cells. Frontiers in Genetics, 2013, 4, 209.	2.3	10
180	Promoter architecture of mouse olfactory receptor genes. Genome Research, 2012, 22, 486-497.	5.5	52

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181	5′ end–centered expression profiling using cap-analysis gene expression and next-generation sequencing. Nature Protocols, 2012, 7, 542-561.	12.0	246
182	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	27.8	15,516
183	NMDA Receptor Regulation Prevents Regression of Visual Cortical Function in the Absence of Mecp2. Neuron, 2012, 76, 1078-1090.	8.1	163
184	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
185	Long non-coding antisense RNA controls Uchl1 translation through an embedded SINEB2 repeat. Nature, 2012, 491, 454-457.	27.8	881
186	Metazoan promoters: emerging characteristics and insights into transcriptional regulation. Nature Reviews Genetics, 2012, 13, 233-245.	16.3	448
187	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
188	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. Genome Research, 2012, 22, 1658-1667.	5.5	166
189	Landscape of transcription in human cells. Nature, 2012, 489, 101-108.	27.8	4,484
190	Structure by Sequencing: Discovery of Hidden Messages in the Noncoding RNA Fraction. Molecular Cell, 2012, 48, 153-155.	9.7	4
191	Automated Workflow for Preparation of cDNA for Cap Analysis of Gene Expression on a Single Molecule Sequencer. PLoS ONE, 2012, 7, e30809.	2.5	22
192	piRNAs Warrant Investigation in Rett Syndrome: An Omics Perspective. Disease Markers, 2012, 33, 261-275.	1.3	23
193	Trehalose-enhanced isolation of neuronal sub-types from adult mouse brain. BioTechniques, 2012, 52, 381-385.	1.8	87
194	Site-specific DICER and DROSHA RNA products control the DNA-damage response. Nature, 2012, 488, 231-235.	27.8	460
195	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
196	piRNAs warrant investigation in Rett Syndrome: an omics perspective. Disease Markers, 2012, 33, 261-75.	1.3	13
197	FXYD6, a Na,K-ATPase Regulator, Is Expressed in Type II Taste Cells. Bioscience, Biotechnology and Biochemistry, 2011, 75, 1061-1066.	1.3	11
198	Unamplified cap analysis of gene expression on a single-molecule sequencer. Genome Research, 2011, 21, 1150-1159.	5.5	172

#	Article	IF	Citations
199	Chromatin-associated RNA interference components contribute to transcriptional regulation in Drosophila. Nature, 2011, 480, 391-395.	27.8	203
200	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). PLoS Biology, 2011, 9, e1001046.	5.6	1,257
201	Somatic retrotransposition alters the genetic landscape of the human brain. Nature, 2011, 479, 534-537.	27.8	621
202	Direct generation of functional dopaminergic neurons from mouse and human fibroblasts. Nature, 2011, 476, 224-227.	27.8	941
203	Profiling transcription initiation in human aged brain using deep-CAGE. BMC Bioinformatics, 2011, 12, .	2.6	3
204	Whole transcriptome analysis: what are we still missing?. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2011, 3, 527-543.	6.6	22
205	Long nonâ€coding RNA modifies chromatin. BioEssays, 2011, 33, 830-839.	2.5	177
206	NanoCAGE: A High-Resolution Technique to Discover and Interrogate Cell Transcriptomes. Cold Spring Harbor Protocols, 2011, 2011, pdb.prot5559-pdb.prot5559.	0.3	61
207	Update of the FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. Nucleic Acids Research, 2011, 39, D856-D860.	14.5	49
208	The Reality of Pervasive Transcription. PLoS Biology, 2011, 9, e1000625.	5.6	380
209	Genome-wide analysis of promoter architecture in <i>Drosophila melanogaster</i>. Genome Research, 2011, 21, 182-192.	5.5	211
210	The Short Non-Coding Transcriptome of the Protozoan Parasite Trypanosoma cruzi. PLoS Neglected Tropical Diseases, 2011, 5, e1283.	3.0	35
211	Nuclear Pore Complex Protein Mediated Nuclear Localization of Dicer Protein in Human Cells. PLoS ONE, 2011, 6, e23385.	2.5	40
212	Core promoter structure and genomic context reflect histone 3 lysine 9 acetylation patterns. BMC Genomics, 2010, 11, 257.	2.8	34
213	Linking promoters to functional transcripts in small samples with nanoCAGE and CAGEscan. Nature Methods, 2010, 7, 528-534.	19.0	152
214	Reduction of non-insert sequence reads by dimer eliminator LNA oligonucleotide for small RNA deep sequencing. BioTechniques, 2010, 49, 751-755.	1.8	32
215	High Sensitivity TSS Prediction: Estimates of Locations Where TSS Cannot Occur. PLoS ONE, 2010, 5, e13934.	2.5	8
216	RNA Dust: Where are the Genes?. DNA Research, 2010, 17, 209-209.	3.4	0

#	ARTICLE	IF	CITATIONS
217	Building promoter aware transcriptional regulatory networks using siRNA perturbation and deepCAGE. Nucleic Acids Research, 2010, 38, 8141-8148.	14.5	17
218	RNA Dust: Where are the Genes?. DNA Research, 2010, 17, 51-59.	3.4	58
219	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. Genome Research, 2010, 20, 791-803.	5.5	84
220	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
221	Molecular mechanisms of pituitary organogenesis: In search of novel regulatory genes. Molecular and Cellular Endocrinology, 2010, 323, 4-19.	3.2	140
222	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. Cell, 2010, 140, 744-752.	28.9	667
223	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. Cell, 2010, 141, 369.	28.9	4
224	From identification to validation to gene count. Genome Biology, 2010, 11, .	8.8	1
225	Beyond the FANTOM4. Genome Biology, 2010, 11, O11.	9.6	0
226	Genome-wide detection and analysis of hippocampus core promoters using DeepCAGE. Genome Research, 2009, 19, 255-265.	5.5	128
227	High-throughput verification of transcriptional starting sites by Deep-RACE. BioTechniques, 2009, 46, 130-132.	1.8	33
228	Tunable fractionation of nucleic acids. BioTechniques, 2009, 47, 1041-1043.	1.8	4
229	Whole genome transcriptome analysis. RNA Biology, 2009, 6, 107-112.	3.1	44
230	Annotating non-coding transcription using functional genomics strategies. Briefings in Functional Genomics & Proteomics, 2009, 8, 437-443.	3.8	5
231	The long and short of RNAs. Nature, 2009, 457, 974-975.	27.8	45
232	Tiny RNAs associated with transcription start sites in animals. Nature Genetics, 2009, 41, 572-578.	21.4	327
233	The regulated retrotransposon transcriptome of mammalian cells. Nature Genetics, 2009, 41, 563-571.	21.4	731
234	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

#	Article	IF	Citations
235	Is sequencing enlightenment ending the dark age of the transcriptome?. Nature Methods, 2009, 6, 711-713.	19.0	28
236	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
237	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
238	Altruistic functions for selfish DNA. Cell Cycle, 2009, 8, 2895-2900.	2.6	60
239	Small RNAs derived from snoRNAs. Rna, 2009, 15, 1233-1240.	3.5	384
240	Genetics, Gene Expression and Bioinformatics of the Pituitary Gland. Hormone Research in Paediatrics, 2009, 71, 101-115.	1.8	11
241	Generation of Full-Length cDNA Libraries: Focus on Plants. Methods in Molecular Biology, 2009, 533, 49-68.	0.9	2
242	Methods for analyzing deep sequencing expression data: constructing the human and mouse promoterome with deepCAGE data. Genome Biology, 2009, 10, R79.	9.6	131
243	FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. Genome Biology, 2009, 10, R39.	9.6	67
244	The FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. Genome Biology, 2009, 10, R40.	9.6	73
245	Tagging Transcription Starting Sites with CAGE. , 2009, , 7-20.		1
246	Construction of CAGE Libraries. , 2009, , 21-39.		0
247	A code for transcription initiation in mammalian genomes. Genome Research, 2008, 18, 1-12.	5.5	237
248	Non-coding RNA transcription: turning on neighbours. Nature Cell Biology, 2008, 10, 1023-1024.	10.3	32
249	Rapidly evolving human promoter regions. Nature Genetics, 2008, 40, 1262-1263.	21.4	18
250	Hunting hidden transcripts. Nature Methods, 2008, 5, 587-589.	19.0	8
251	Hidden layers of human small RNAs. BMC Genomics, 2008, 9, 157.	2.8	255
252	Multifaceted mammalian transcriptome. Current Opinion in Cell Biology, 2008, 20, 274-280.	5.4	77

#	Article	IF	Citations
253	A rescue strategy for multimapping short sequence tags refines surveys of transcriptional activity by CAGE. Genomics, 2008, 91, 281-288.	2.9	92
254	Placental expression profiling in preeclampsia: local overproduction of hemoglobin may drive pathological changes. Fertility and Sterility, 2008, 90, 1834-1843.	1.0	74
255	GÎ±14 is a candidate mediator of sweet/umami signal transduction in the posterior region of the mouse tongue. Biochemical and Biophysical Research Communications, 2008, 376, 504-508.	2.1	39
256	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
257	A Resource for Transcriptomic Analysis in the Mouse Brain. PLoS ONE, 2008, 3, e3012.	2.5	11
258	Development of a DNA barcode tagging method for monitoring dynamic changes in gene expression by using an ultra high-throughput sequencer. BioTechniques, 2008, 45, 95-97.	1.8	29
259	Transcriptomics resources for functional genomics. Briefings in Functional Genomics & Proteomics, 2007, 6, 171-179.	3.8	0
260	Constructing the landscape of the mammalian transcriptome. Journal of Experimental Biology, 2007, 210, 1497-1506.	1.7	40
261	Genomic organization of transcriptomes in mammals: Coregulation and cofunctionality. Genomics, 2007, 89, 580-587.	2.9	56
262	Noncoding RNA transcription beyond annotated genes. Current Opinion in Genetics and Development, 2007, 17, 139-144.	3.3	125
263	Diversity of Ca2+-activated K+ channel transcripts in inner ear hair cells. Gene, 2007, 386, 11-23.	2.2	27
264	Splicing bypasses 3â€² end formation signals to allow complex gene architectures. Gene, 2007, 403, 188-193.	2.2	7
265	Epigenetic regulation of critical period plasticity in visual cortex. Neuroscience Research, 2007, 58, S66.	1.9	0
266	Simplified ontologies allowing comparison of developmental mammalian gene expression. Genome Biology, 2007, 8, R229.	9.6	12
267	CAGE-TSSchip: promoter-based expression profiling using the 5'-leading label of capped transcripts. Genome Biology, 2007, 8, R42.	9.6	3
268	Gene Organization in Rice Revealed by Full-Length cDNA Mapping and Gene Expression Analysis through Microarray. PLoS ONE, 2007, 2, e1235.	2.5	51
269	Mammalian RNA polymerase II core promoters: insights from genome-wide studies. Nature Reviews Genetics, 2007, 8, 424-436.	16.3	435
270	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

#	ARTICLE	IF	CITATIONS
271	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.	3.6	3
272	Large-scale clustering of CAGE tag expression data. BMC Bioinformatics, 2007, 8, 161.	2.6	8
273	Dynamic usage of transcription start sites within core promoters. Genome Biology, 2006, 7, R118.	9.6	75
274	Transcriptional and structural impact of TATA-initiation site spacing in mammalian core promoters. Genome Biology, 2006, 7, R78.	9.6	101
275	Alternate transcription of the Toll-like receptor signaling cascade. Genome Biology, 2006, 7, R10.	9.6	66
276	Genome-wide review of transcriptional complexity in mouse protein kinases and phosphatases. Genome Biology, 2006, 7, R5.	9.6	48
277	CAGE Basic/Analysis Databases: the CAGE resource for comprehensive promoter analysis. Nucleic Acids Research, 2006, 34, D632-D636.	14.5	78
278	Transcriptional network dynamics in macrophage activation. Genomics, 2006, 88, 133-142.	2.9	125
279	Constructing ORFeome resources with removable termination codons. BioTechniques, 2006, 41, 44-50.	1.8	30
280	Subcellular Localization of Mammalian Type II Membrane Proteins. Traffic, 2006, 7, 613-625.	2.7	19
281	Genome-wide analysis of mammalian promoter architecture and evolution. Nature Genetics, 2006, 38, 626-635.	21.4	1,201
282	CAGE: cap analysis of gene expression. Nature Methods, 2006, 3, 211-222.	19.0	397
283	Insights into social insects from the genome of the honeybee Apis mellifera. Nature, 2006, 443, 931-949.	27.8	1,648
284	The complexity of the mammalian transcriptome. Journal of Physiology, 2006, 575, 321-332.	2.9	91
285	Tagging mammalian transcription complexity. Trends in Genetics, 2006, 22, 501-510.	6.7	85
286	Computational promoter analysis of mouse, rat and human antimicrobial peptide-coding genes. BMC Bioinformatics, 2006, 7, S8.	2.6	26
287	LOCATE: a mouse protein subcellular localization database. Nucleic Acids Research, 2006, 34, D213-D217.	14.5	72
288	Evolutionary turnover of mammalian transcription start sites. Genome Research, 2006, 16, 713-722.	5.5	68

#	Article	IF	Citations
289	Mice and Men: Their Promoter Properties. PLoS Genetics, 2006, 2, e54.	3.5	95
290	Clusters of Internally Primed Transcripts Reveal Novel Long Noncoding RNAs. PLoS Genetics, 2006, 2, e37.	3.5	148
291	Pseudoâ€"Messenger RNA: Phantoms of the Transcriptome. PLoS Genetics, 2006, 2, e23.	3.5	58
292	The Abundance of Short Proteins in the Mammalian Proteome. PLoS Genetics, 2006, 2, e52.	3.5	189
293	Genome Network and FANTOM3: Assessing the Complexity of the Transcriptome. PLoS Genetics, 2006, 2, e63.	3.5	26
294	Complex Loci in Human and Mouse Genomes. PLoS Genetics, 2006, 2, e47.	3.5	290
295	Heterotachy in Mammalian Promoter Evolution. PLoS Genetics, 2006, 2, e30.	3.5	102
296	A Method for Similarity Search of Genomic Positional Expression Using CAGE. PLoS Genetics, 2006, 2, e44.	3.5	4
297	Differential Use of Signal Peptides and Membrane Domains Is a Common Occurrence in the Protein Output of Transcriptional Units. PLoS Genetics, 2006, 2, e46.	3.5	34
298	A Simple Physical Model Predicts Small Exon Length Variations. PLoS Genetics, 2006, 2, e45.	3.5	69
299	Transcript Annotation in FANTOM3: Mouse Gene Catalog Based on Physical cDNAs. PLoS Genetics, 2006, 2, e62.	3.5	165
300	Discrimination of Non-Protein-Coding Transcripts from Protein-Coding mRNA. RNA Biology, 2006, 3, 40-48.	3.1	118
301	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
302	Antisense Transcription in the Mammalian Transcriptome. Science, 2005, 309, 1564-1566.	12.6	1,553
303	Tag-based approaches for transcriptome research and genome annotation. Nature Methods, 2005, 2, 495-502.	19.0	165
304	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.	1.8	38
305	Cytoskeletal Rearrangements in Synovial Fibroblasts as a Novel Pathophysiological Determinant of Modeled Rheumatoid Arthritis. PLoS Genetics, 2005, 1, e48.	3.5	49
306	Computational analysis suggests that alternative first exons are involved in tissue-specific transcription in rice (Oryza sativa). Bioinformatics, 2005, 21, 1758-1763.	4.1	26

#	Article	IF	Citations
307	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
308	The Transcriptional Landscape of the Mammalian Genome. Science, 2005, 309, 1559-1563.	12.6	3,227
309	Protein-protein interactions of the hyperthermophilic archaeon Pyrococcus horikoshii OT3. Genome Biology, 2005, 6, R98.	9.6	12
310	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
311	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
312	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
313	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
314	FREP: a database of functional repeats in mouse cDNAs. Nucleic Acids Research, 2004, 32, 471D-475.	14.5	6
315	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
316	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. PLoS Biology, 2004, 2, e162.	5.6	290
317	CTAB-Urea Method Purifies RNA from Melanin for cDNA Microarray Analysis. Pigment Cell & Melanoma Research, 2004, 17, 312-315.	3.6	26
318	Libraries enriched for alternatively spliced exons reveal splicing patterns in melanocytes and melanomas. Nature Methods, 2004, 1, 233-239.	19.0	45
319	Solution structure of the RWD domain of the mouse GCN2 protein. Protein Science, 2004, 13, 2089-2100.	7.6	66
320	Full-length cDNAs from chicken bursal lymphocytes to facilitate gene function analysis. Genome Biology, 2004, 6, R6.	9.6	101
321	Identification of unique transcripts from a mouse full-length, subtracted inner ear cDNA library. Genomics, 2004, 83, 1012-1023.	2.9	23
322	Absolute expression values for mouse transcripts: re-annotation of the READ expression database by the use of CAGE and EST sequence tags. FEBS Letters, 2004, 559, 22-26.	2.8	21
323	Solution structure of a BolA-like protein from Mus musculus. Protein Science, 2004, 13, 545-548.	7.6	49
324	Construction of a full-length cDNA library from young spikelets of hexaploid wheat and its characterization by large-scale sequencing of expressed sequence tags. Genes and Genetic Systems, 2004, 79, 227-232.	0.7	47

#	ARTICLE	IF	CITATIONS
325	Large-scale collection and characterization of promoters of human and mouse genes. In Silico Biology, 2004, 4, 429-44.	0.9	14
326	Genetic control of the innate immune response. BMC Immunology, 2003, 4, 5.	2.2	119
327	Comprehensive Analysis of NAC Family Genes in Oryza sativa and Arabidopsis thaliana. DNA Research, 2003, 10, 239-247.	3.4	911
328	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
329	Empirical Analysis of Transcriptional Activity in the Arabidopsis Genome. Science, 2003, 302, 842-846.	12.6	853
330	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
331	A novel feature of microsatellites in plants: a distribution gradient along the direction of transcription. FEBS Letters, 2003, 554, 17-22.	2.8	89
332	Multiple tissue-specific promoters control expression of the murine tartrate-resistant acid phosphatase gene. Gene, 2003, 307, 111-123.	2.2	54
333	Antisense transcripts with rice full-length cDNAs. Genome Biology, 2003, 5, R5.	9.6	112
334	Targeting a Complex Transcriptome: The Construction of the Mouse Full-Length cDNA Encyclopedia. Genome Research, 2003, 13, 1273-1289.	5.5	154
335	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
336	A Comprehensive Transcript Map of the Mouse *Gnas* Imprinted Complex. Genome Research, 2003, 13, 1410-1415.	5.5	53
337	Comparative Analysis of Apoptosis and Inflammation Genes of Mice and Humans. Genome Research, 2003, 13, 1376-1388.	5.5	104
338	Cytokine-Related Genes Identified From the RIKEN Full-Length Mouse cDNA Data Set. Genome Research, 2003, 13, 1307-1317.	5.5	2
339	Identification and Analysis of Chromodomain-Containing Proteins Encoded in the Mouse Transcriptome. Genome Research, 2003, 13, 1416-1429.	5.5	50
340	Systematic Expression Profiling of the Mouse Transcriptome Using RIKEN cDNA Microarrays. Genome Research, 2003, 13, 1318-1323.	5.5	69
341	Mouse Proteome Analysis. Genome Research, 2003, 13, 1335-1344.	5.5	91
342	Discovery of Imprinted Transcripts in the Mouse Transcriptome Using Large-Scale Expression Profiling. Genome Research, 2003, 13, 1402-1409.	5.5	96

#	ARTICLE	IF	CITATIONS
343	Systematic Characterization of the Zinc-Finger-Containing Proteins in the Mouse Transcriptome. Genome Research, 2003, 13, 1430-1442.	5.5	89
344	Comprehensive Analysis of the Mouse Metabolome Based on the Transcriptome. Genome Research, 2003, 13, 1345-1349.	5.5	27
345	Human Disease Genes and Their Cloned Mouse Orthologs: Exploration of the FANTOM2 cDNA Sequence Data Set. Genome Research, 2003, 13, 1496-1500.	5.5	7
346	Genomics Approach to Abscisic Acid- and Gibberellin-responsive Genes in Rice. DNA Research, 2003, 10, 249-261.	3.4	57
347	Analysis of the Mouse Transcriptome for Genes Involved in the Function of the Nervous System. Genome Research, 2003, 13, 1395-1401.	5.5	30
348	Kinesin Superfamily Proteins (KIFs) in the Mouse Transcriptome. Genome Research, 2003, 13, 1455-1465.	5.5	44
349	G Protein-Coupled Receptor Genes in the FANTOM2 Database. Genome Research, 2003, 13, 1466-1477.	5.5	32
350	Continued Discovery of Transcriptional Units Expressed in Cells of the Mouse Mononuclear Phagocyte Lineage. Genome Research, 2003, 13, 1360-1365.	5.5	41
351	Phosphoregulators: Protein Kinases and Protein Phosphatases of Mouse. Genome Research, 2003, 13, 1443-1454.	5.5	43
352	Collection, Mapping, and Annotation of Over 28,000 cDNA Clones from japonica Rice. Science, 2003, 301, 376-379.	12.6	834
353	Antisense Transcripts With FANTOM2 Clone Set and Their Implications for Gene Regulation. Genome Research, 2003, 13, 1324-1334.	5.5	224
354	Identification of Putative Noncoding RNAs Among the RIKEN Mouse Full-Length cDNA Collection. Genome Research, 2003, 13, 1301-1306.	5.5	129
355	The Mouse Secretome: Functional Classification of the Proteins Secreted Into the Extracellular Environment. Genome Research, 2003, 13, 1350-1359.	5.5	73
356	Exploration of the Cell-Cycle Genes Found Within the RIKEN FANTOM2 Data Set. Genome Research, 2003, 13, 1366-1375.	5.5	16
357	Subtraction of cap-trapped full-length cDNA libraries to select rare transcripts. BioTechniques, 2003, 35, 510-518.	1.8	12
358	A Computer-Based Method of Selecting Clones for a Full-Length cDNA Project: Simultaneous Collection of Negligibly Redundant and Variant cDNAs. Genome Research, 2002, 12, 1127-1134.	5.5	28
359	The DT40 web site: sampling and connecting the genes of a B cell line. Nucleic Acids Research, 2002, 30, 230-231.	14.5	26
360	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

#	Article	IF	Citations
361	Inferring Alternative Splicing Patterns in Mouse from a Full-Length cDNA Library and Microarray Data. Genome Research, 2002, 12, 1286-1293.	5.5	21
362	Functional Annotation of a Full-Length Arabidopsis cDNA Collection. Science, 2002, 296, 141-145.	12.6	631
363	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
364	On biased distribution of introns in various eukaryotes. Gene, 2002, 300, 89-95.	2.2	60
365	Comprehensive sequence analysis of translation termination sites in various eukaryotes. Gene, 2002, 300, 79-87.	2.2	15
366	Extra-Long First-Strand cDNA Synthesis. BioTechniques, 2002, 32, 984-985.	1.8	29
367	Cytoplasmic RNA Extraction from Fresh and Frozen Mammalian Tissues. BioTechniques, 2002, 33, 306-309.	1.8	12
368	A framework for integrating the songbird brain. Journal of Comparative Physiology A: Neuroethology, Sensory, Neural, and Behavioral Physiology, 2002, 188, 961-980.	1.6	31
369	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
370	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
371	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	27.8	6,319
372	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. Nature, 2002, 420, 563-573.	27.8	1,548
373	Mapping of 19032 mouse cDNAs on mouse chromosomes. Journal of Structural and Functional Genomics, 2002, 2, 23-28.	1.2	2
374	Functional annotation of a full-length mouse cDNA collection. Nature, 2001, 409, 685-690.	27.8	653
375	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
376	Comparative evaluation of 5â€²-end-sequence quality of clones in CAP trapper and other full-length-cDNA libraries. Gene, 2001, 263, 93-102.	2.2	37
377	Correlation between sequence conservation of the 5â€² untranslated region and codon usage bias in Mus musculus genes. Gene, 2001, 276, 101-105.	2.2	34
378	Removal of PolyA Tails from Full-Length cDNA Libraries for High-Efficiency Sequencing. BioTechniques, 2001, 31, 1042-1049.	1.8	13

#	Article	IF	Citations
379	Cloning Full-Length, Cap-Trapper-Selected cDNAs by Using the Single-Strand Linker Ligation Method. BioTechniques, 2001, 30, 1250-1254.	1.8	49
380	Meeting Report: 14th International Mouse Genome Conference. Mammalian Genome, 2001, 12, 401-405.	2.2	0
381	Arabidopsis encyclopedia using full-length cDNAs and its application. Plant Physiology and Biochemistry, 2001, 39, 211-220.	5.8	34
382	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
383	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.	6.6	19
384	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
385	Computer-Based Methods for the Mouse Full-Length cDNA Encyclopedia: Real-Time Sequence Clustering for Construction of a Nonredundant cDNA Library. Genome Research, 2001, 11, 281-289.	5.5	25
386	Computer-Based Methods for the Mouse Full-Length cDNA Encyclopedia: Real-Time Sequence Clustering for Construction of a Nonredundant cDNA Library. Genome Research, 2001, 11, 281-289.	5.5	19
387	RIKEN Integrated Sequence Analysis (RISA) System---384-Format Sequencing Pipeline with 384 Multicapillary Sequencer. Genome Research, 2000, 10, 1757-1771.	5.5	52
388	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
389	Increased specificity of reverse transcription priming by trehalose and oligo-blockers allows high-efficiency window separation of mRNA display. Nucleic Acids Research, 1999, 27, 1345-1349.	14.5	39
390	[2] High-efficiency full-length cDNA cloning. Methods in Enzymology, 1999, 303, 19-44.	1.0	169
391	Automated Filtration-Based High-Throughput Plasmid Preparation System. Genome Research, 1999, 9, 463-470.	5.5	28
392	High-efficiency cloning of Arabidopsis full-length cDNA by biotinylated CAP trapper. Plant Journal, 1998, 15, 707-720.	5.7	217
393	Characterization of Gene Expression in Mouse Blastocyst Using Single-Pass Sequencing of 3995 Clones. Genomics, 1998, 49, 167-179.	2.9	47
394	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
395	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.	7.1	38
396	High Efficiency Selection of Full-length cDNA by Improved Biotinylated Cap Trapper. DNA Research, 1997, 4, 61-66.	3.4	90

#	Article	IF	Citations
397	Simple and rapid preparation of plasmid template by a filtration method using microtiter filter plates. Nucleic Acids Research, 1997, 25, 1315-1316.	14.5	29
398	A Novel Control System for Polymerase Chain Reaction Using a RIKEN GS384 Thermalcycler. DNA Research, 1997, 4, 387-391.	3.4	6
399	High-Efficiency Full-Length cDNA Cloning by Biotinylated CAP Trapper. Genomics, 1996, 37, 327-336.	2.9	297
400	A discontinuous buffer system increasing resolution and reproducibility in DNA sequencing on high voltage horizontal ultrathin-layer electrophoresis. Electrophoresis, 1995, 16, 1836-1845.	2.4	13
401	A simple discontinuous buffer system for increased resolution and speed in gel electrophoretic analysis of DNA sequence. Nucleic Acids Research, 1990, 18, 204-204.	14.5	15
402	Wavelet profiles: their application in Oryza sativa DNA sequence analysis. , 0, , .		4
403	From CAGE to DeepCAGE: High-Throughput Transcription Start Site and Promoter Identification for Gene Network Analysis. , 0, , 55-75.		0
404	Single-Cell Convert-Seq Decodes Regulatory Factors Driving Neuronal Diversity. SSRN Electronic Journal, 0, , .	0.4	1