

# Piero Carninci

## List of Publications by Year in descending order

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Version: 2024-02-01

404  
papers

95,196  
citations

1877

105  
h-index

351

291  
g-index

460  
all docs

460  
docs citations

460  
times ranked

105862  
citing authors

#	ARTICLE	IF	CITATIONS
1	Towards SINEUP-based therapeutics: Design of an in vitro synthesized SINEUP RNA. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 27, 1092-1102.	2.3	4
2	Complete Transcriptome Analysis by 5'-End Single-Cell RNA-Seq with Random Priming. <i>Methods in Molecular Biology</i> , 2022, 2490, 141-156.	0.4	0
3	Lessons from the functional characterization of lncRNAs: introduction to mammalian genome special issue. <i>Mammalian Genome</i> , 2022, , .	1.0	1
4	Multioomic atlas with functional stratification and developmental dynamics of zebrafish cis-regulatory elements. <i>Nature Genetics</i> , 2022, 54, 1037-1050.	9.4	26
5	FANTOM enters 20th year: expansion of transcriptomic atlases and functional annotation of non-coding RNAs. <i>Nucleic Acids Research</i> , 2021, 49, D892-D898.	6.5	57
6	LETR1 is a lymphatic endothelial-specific lncRNA governing cell proliferation and migration through KLF4 and SEMA3C. <i>Nature Communications</i> , 2021, 12, 925.	5.8	18
7	Antisense RNAs during early vertebrate development are divided in groups with distinct features. <i>Genome Research</i> , 2021, 31, 995-1010.	2.4	7
8	Decoding Neuronal Diversification by Multiplexed Single-cell RNA-Seq. <i>Stem Cell Reports</i> , 2021, 16, 810-824.	2.3	8
9	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297.	5.8	11
10	The choice of negative control antisense oligonucleotides dramatically impacts downstream analysis depending on the cellular background. <i>BMC Genomic Data</i> , 2021, 22, 33.	0.7	0
11	Analysis of Enhancer-Promoter Interactions using CAGE and RADICL-Seq Technologies. <i>Methods in Molecular Biology</i> , 2021, 2351, 201-210.	0.4	2
12	Low Quantity Single Strand CAGE (LQ-ssCAGE) Maps Regulatory Enhancers and Promoters. <i>Methods in Molecular Biology</i> , 2021, 2351, 67-90.	0.4	6
13	A field guide to cultivating computational biology. <i>PLoS Biology</i> , 2021, 19, e3001419.	2.6	6
14	SINEUPs: a novel toolbox for RNA therapeutics. <i>Essays in Biochemistry</i> , 2021, 65, 775-789.	2.1	13
15	Embryonic LTR retrotransposons supply promoter modules to somatic tissues. <i>Genome Research</i> , 2021, 31, 1983-1993.	2.4	7
16	Japan: prize diversity, not conformity, to boost research. <i>Nature</i> , 2021, 599, 201-201.	13.7	1
17	SINEUP Non-coding RNA Targeting GDNF Rescues Motor Deficits and Neurodegeneration in a Mouse Model of Parkinson's Disease. <i>Molecular Therapy</i> , 2020, 28, 642-652.	3.7	41
18	Dual-initiation promoters with intertwined canonical and TCT/TOP transcription start sites diversify transcript processing. <i>Nature Communications</i> , 2020, 11, 168.	5.8	37

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19	A human minisatellite hosts an alternative transcription start site for NPRL3 driving its expression in a repeat number-dependent manner. <i>Human Mutation</i> , 2020, 41, 807-824.	1.1	6
20	Synthetic <i>in vitro</i> transcribed lncRNAs (SINEUPs) with chemical modifications enhance target mRNA translation. <i>FEBS Letters</i> , 2020, 594, 4357-4369.	1.3	15
21	An NMR-based approach reveals the core structure of the functional domain of SINEUP lncRNAs. <i>Nucleic Acids Research</i> , 2020, 48, 9346-9360.	6.5	18
22	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	2.4	109
23	Comparative transcriptomics of primary cells in vertebrates. <i>Genome Research</i> , 2020, 30, 951-961.	2.4	29
24	SINEUP long non-coding RNA acts via PTBP1 and HNRNPK to promote translational initiation assemblies. <i>Nucleic Acids Research</i> , 2020, 48, 11626-11644.	6.5	33
25	Use of Cap Analysis Gene Expression to detect human papillomavirus promoter activity patterns at different disease stages. <i>Scientific Reports</i> , 2020, 10, 17991.	1.6	1
26	Safety and efficacy of the Russian COVID-19 vaccine: more information needed. <i>Lancet</i> , The, 2020, 396, e53.	6.3	27
27	Analysis of splice variants of the human protein disulfide isomerase (P4HB) gene. <i>BMC Genomics</i> , 2020, 21, 766.	1.2	3
28	The Secret Life of lncRNAs: Conserved, yet Not Conserved. <i>Cell</i> , 2020, 181, 512-514.	13.5	9
29	Genome-Wide Technologies to Study RNA-Chromatin Interactions. <i>Non-coding RNA</i> , 2020, 6, 20.	1.3	19
30	Comprehensive Characterization of Transcriptional Activity during Influenza A Virus Infection Reveals Biases in Cap-Snatching of Host RNA Sequences. <i>Journal of Virology</i> , 2020, 94, .	1.5	14
31	Machine-driven parameter screen of biochemical reactions. <i>Nucleic Acids Research</i> , 2020, 48, e37-e37.	6.5	0
32	Recounting the FANTOM CAGE-Associated Transcriptome. <i>Genome Research</i> , 2020, 30, 1073-1081.	2.4	35
33	RADICL-seq identifies general and cell type-specific principles of genome-wide RNA-chromatin interactions. <i>Nature Communications</i> , 2020, 11, 1018.	5.8	98
34	Cap Analysis of Gene Expression (CAGE): A Quantitative and Genome-Wide Assay of Transcription Start Sites. <i>Methods in Molecular Biology</i> , 2020, 2120, 277-301.	0.4	22
35	Expanded ENCODE delivers invaluable genomic encyclopedia. <i>Nature</i> , 2020, 583, 685-686.	13.7	7
36	Nuclear AGO1 Regulates Gene Expression by Affecting Chromatin Architecture in Human Cells. <i>Cell Systems</i> , 2019, 9, 446-458.e6.	2.9	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.	3.3	215
38	NET-CAGE characterizes the dynamics and topology of human transcribed cis-regulatory elements. Nature Genetics, 2019, 51, 1369-1379.	9.4	72
39	Broad Heterochromatic Domains Open in Gonocyte Development Prior to De Novo DNA Methylation. Developmental Cell, 2019, 51, 21-34.e5.	3.1	26
40	Identification of novel cerebellar developmental transcriptional regulators with motif activity analysis. BMC Genomics, 2019, 20, 718.	1.2	11
41	MicroRNA-27a/b-3p and PPAR $\gamma$ regulate SCAMP3 through a feed-forward loop during adipogenesis. Scientific Reports, 2019, 9, 13891.	1.6	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.	6.5	30
43	The RNA-binding protein ILF3 binds to transposable element sequences in SINEUP lncRNAs. FASEB Journal, 2019, 33, 13572-13589.	0.2	20
44	C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution. Nature Communications, 2019, 10, 360.	5.8	102
45	refTSS: A Reference Data Set for Human and Mouse Transcription Start Sites. Journal of Molecular Biology, 2019, 431, 2407-2422.	2.0	72
46	Cell Based Assays of SINEUP Non-coding RNAs That Can Specifically Enhance mRNA Translation. Journal of Visualized Experiments, 2019, , .	0.2	5
47	Multi-year whole-blood transcriptome data for the study of onset and progression of Parkinson's Disease. Scientific Data, 2019, 6, 20.	2.4	8
48	Dynamics of cardiomyocyte transcriptome and chromatin landscape demarcates key events of heart development. Genome Research, 2019, 29, 506-519.	2.4	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, .	1.4	15
50	Look for methods, not conclusions. Cell Death and Disease, 2019, 10, 931.	2.7	1
51	Update of the FANTOM web resource: expansion to provide additional transcriptome atlases. Nucleic Acids Research, 2019, 47, D752-D758.	6.5	172
52	Antisense Transcription in Loci Associated to Hereditary Neurodegenerative Diseases. Molecular Neurobiology, 2019, 56, 5392-5415.	1.9	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.	1.3	34

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55	Prevention of hepatocellular carcinoma by targeting MYCN-positive liver cancer stem cells with acyclic retinoid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4969-4974.	3.3	78
56	Structural determinants of the SINE B2 element embedded in the long non-coding RNA activator of translation AS Uchl1. <i>Scientific Reports</i> , 2018, 8, 3189.	1.6	32
57	Discovery of Transcription Factors Novel to Mouse Cerebellar Granule Cell Development Through Laser-Capture Microdissection. <i>Cerebellum</i> , 2018, 17, 308-325.	1.4	6
58	Transcriptional landscape of Mycobacterium tuberculosis infection in macrophages. <i>Scientific Reports</i> , 2018, 8, 6758.	1.6	92
59	From "Cellular" RNA to "Smart" RNA: Multiple Roles of RNA in Genome Stability and Beyond. <i>Chemical Reviews</i> , 2018, 118, 4365-4403.	23.0	63
60	Target-enrichment sequencing for detailed characterization of small RNAs. <i>Nature Protocols</i> , 2018, 13, 768-786.	5.5	9
61	SCP Portalen: human and mouse single-cell centric database. <i>Nucleic Acids Research</i> , 2018, 46, D781-D787.	6.5	48
62	Conserved temporal ordering of promoter activation implicates common mechanisms governing the immediate early response across cell types and stimuli. <i>Open Biology</i> , 2018, 8, 180011.	1.5	13
63	Integration of genetics and miRNA target gene network identified disease biology implicated in tissue specificity. <i>Nucleic Acids Research</i> , 2018, 46, 11898-11909.	6.5	39
64	SLIC-CAGE: high-resolution transcription start site mapping using nanogram-levels of total RNA. <i>Genome Research</i> , 2018, 28, 1943-1956.	2.4	33
65	Amphioxus functional genomics and the origins of vertebrate gene regulation. <i>Nature</i> , 2018, 564, 64-70.	13.7	224
66	Promoter Usage and Dynamics in Vascular Smooth Muscle Cells Exposed to Fibroblast Growth Factor-2 or Interleukin-1 $\beta$ . <i>Scientific Reports</i> , 2018, 8, 13164.	1.6	10
67	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease. <i>PLoS Computational Biology</i> , 2018, 14, e1005934.	1.5	17
68	Identification of functional features of synthetic SINEUPs, antisense lncRNAs that specifically enhance protein translation. <i>PLoS ONE</i> , 2018, 13, e0183229.	1.1	23
69	DEIVA: a web application for interactive visual analysis of differential gene expression profiles. <i>BMC Genomics</i> , 2017, 18, 47.	1.2	41
70	DNA damage response inhibition at dysfunctional telomeres by modulation of telomeric DNA damage response RNAs. <i>Nature Communications</i> , 2017, 8, 13980.	5.8	76
71	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017, 543, 199-204.	13.7	898
72	The FANTOM5 Computation Ecosystem: Genomic Information Hub for Promoters and Active Enhancers. <i>Methods in Molecular Biology</i> , 2017, 1611, 199-217.	0.4	23

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73	From bench to bedside: The long journey of long non-coding RNAs. <i>Current Opinion in Systems Biology</i> , 2017, 3, 119-124.	1.3	22
74	A damaged genome's transcriptional landscape through multilayered expression profiling around in situ-mapped DNA double-strand breaks. <i>Nature Communications</i> , 2017, 8, 15656.	5.8	89
75	Linking FANTOM5 CAGE peaks to annotations with CAGEscan. <i>Scientific Data</i> , 2017, 4, 170147.	2.4	29
76	Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. <i>EBioMedicine</i> , 2017, 24, 257-266.	2.7	24
77	The FANTOM5 collection, a data series underpinning mammalian transcriptome atlases in diverse cell types. <i>Scientific Data</i> , 2017, 4, 170113.	2.4	55
78	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017, 35, 872-878.	9.4	456
79	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , 2017, 4, 170112.	2.4	195
80	FANTOM5 CAGE profiles of human and mouse reprocessed for GRCh38 and GRCm38 genome assemblies. <i>Scientific Data</i> , 2017, 4, 170107.	2.4	68
81	Monitoring transcription initiation activities in rat and dog. <i>Scientific Data</i> , 2017, 4, 170173.	2.4	6
82	The effect of genetic variation on promoter usage and enhancer activity. <i>Nature Communications</i> , 2017, 8, 1358.	5.8	50
83	Integrative CAGE and DNA Methylation Profiling Identify Epigenetically Regulated Genes in NSCLC. <i>Molecular Cancer Research</i> , 2017, 15, 1354-1365.	1.5	25
84	Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. <i>Nucleic Acids Research</i> , 2017, 45, D737-D743.	6.5	116
85	Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution. <i>Diabetes</i> , 2017, 66, 218-230.	0.3	27
86	A Transcriptional Switch Point During Hematopoietic Stem and Progenitor Cell Ontogeny. <i>Stem Cells and Development</i> , 2017, 26, 314-327.	1.1	4
87	Transcription start site profiling of 15 anatomical regions of the <i>Macaca mulatta</i> central nervous system. <i>Scientific Data</i> , 2017, 4, 170163.	2.4	4
88	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	2.8	1,547
89	RNA extraction from sorted neuronal subtypes. <i>BioTechniques</i> , 2017, 62, .	0.8	1
90	Systematic analysis of transcription start sites in avian development. <i>PLoS Biology</i> , 2017, 15, e2002887.	2.6	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. <i>PLoS Genetics</i> , 2017, 13, e1006641.	1.5	161
92	On-the-fly selection of cell-specific enhancers, genes, miRNAs and proteins across the human body using SlideBase. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, .	1.4	24
93	Transcriptome analysis of periodontitis-associated fibroblasts by CAGE sequencing identified DLX5 and RUNX2 long variant as novel regulators involved in periodontitis. <i>Scientific Reports</i> , 2016, 6, 33666.	1.6	18
94	DeepCAGE transcriptomics identify HOXD10 as transcription factor regulating lymphatic endothelial responses to VEGF-C. <i>Journal of Cell Science</i> , 2016, 129, 2573-85.	1.2	15
95	Transcriptional, post-transcriptional and chromatin-associated regulation of pri-miRNAs, pre-miRNAs and moRNAs. <i>Nucleic Acids Research</i> , 2016, 44, 3070-3081.	6.5	38
96	Single-Nucleotide Resolution Mapping of Hepatitis B Virus Promoters in Infected Human Livers and Hepatocellular Carcinoma. <i>Journal of Virology</i> , 2016, 90, 10811-10822.	1.5	27
97	Isoforms of the Erythropoietin receptor in dopaminergic neurons of the <i>Substantia Nigra</i> . <i>Journal of Neurochemistry</i> , 2016, 139, 596-609.	2.1	11
98	YY1 binding association with sex-biased transcription revealed through X-linked transcript levels and allelic binding analyses. <i>Scientific Reports</i> , 2016, 6, 37324.	1.6	32
99	Characterization of piRNAs across postnatal development in mouse brain. <i>Scientific Reports</i> , 2016, 6, 25039.	1.6	34
100	Genome sequence and analysis of the Japanese morning glory <i>Ipomoea nil</i> . <i>Nature Communications</i> , 2016, 7, 13295.	5.8	138
101	Identification of antisense long noncoding RNAs that function as SINEUPs in human cells. <i>Scientific Reports</i> , 2016, 6, 33605.	1.6	58
102	FANTOM5 transcriptome catalog of cellular states based on Semantic MediaWiki. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw105.	1.4	64
103	Transcriptome Analysis of Recurrently Deregulated Genes across Multiple Cancers Identifies New Pan-Cancer Biomarkers. <i>Cancer Research</i> , 2016, 76, 216-226.	0.4	80
104	Functional annotation of the vlinc class of non-coding RNAs using systems biology approach. <i>Nucleic Acids Research</i> , 2016, 44, 3233-3252.	6.5	31
105	The ORFeome Collaboration: a genome-scale human ORF-clone resource. <i>Nature Methods</i> , 2016, 13, 191-192.	9.0	111
106	Deficiency of multidrug resistance 2 contributes to cell transformation through oxidative stress. <i>Carcinogenesis</i> , 2016, 37, 39-48.	1.3	15
107	Discovery and functional analysis of lncRNAs: Methodologies to investigate an uncharacterized transcriptome. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 3-15.	0.9	178
108	Epi-drivers and cancer-testis genes. <i>Translational Cancer Research</i> , 2016, 5, 334-336.	0.4	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. <i>BioEssays</i> , 2015, 37, 1254-1255.	1.2	0
111	Promoter-level expression clustering identifies time development of transcriptional regulatory cascades initiated by ErbB receptors in breast cancer cells. <i>Scientific Reports</i> , 2015, 5, 11999.	1.6	30
112	Hierarchical folding and reorganization of chromosomes are linked to transcriptional changes in cellular differentiation. <i>Molecular Systems Biology</i> , 2015, 11, 852.	3.2	305
113	DeepCAGE Transcriptomics Reveal an Important Role of the Transcription Factor MAFB in the Lymphatic Endothelium. <i>Cell Reports</i> , 2015, 13, 1493-1504.	2.9	46
114	Remodeling of retrotransposon elements during epigenetic induction of adult visual cortical plasticity by HDAC inhibitors. <i>Epigenetics and Chromatin</i> , 2015, 8, 55.	1.8	32
115	Mapping Mammalian Cell-type-specific Transcriptional Regulatory Networks Using KD-CAGE and ChIP-seq Data in the TC-YIK Cell Line. <i>Frontiers in Genetics</i> , 2015, 6, 331.	1.1	13
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. <i>Frontiers in Cellular Neuroscience</i> , 2015, 9, 114.	1.8	112
117	SINEUPs are modular antisense long non-coding RNAs that increase synthesis of target proteins in cells. <i>Frontiers in Cellular Neuroscience</i> , 2015, 9, 174.	1.8	81
118	HSA21 Single-Minded 2 (Sim2) Binding Sites Co-Localize with Super-Enhancers and Pioneer Transcription Factors in Pluripotent Mouse ES Cells. <i>PLoS ONE</i> , 2015, 10, e0126475.	1.1	9
119	The Constrained Maximal Expression Level Owing to Haploidy Shapes Gene Content on the Mammalian X Chromosome. <i>PLoS Biology</i> , 2015, 13, e1002315.	2.6	32
120	Application of Gene Expression Trajectories Initiated from ErbB Receptor Activation Highlights the Dynamics of Divergent Promoter Usage. <i>PLoS ONE</i> , 2015, 10, e0144176.	1.1	1
121	Engineering mammalian cell factories with SINEUP noncoding RNAs to improve translation of secreted proteins. <i>Gene</i> , 2015, 569, 287-293.	1.0	35
122	Biased Allelic Expression in Human Primary Fibroblast Single Cells. <i>American Journal of Human Genetics</i> , 2015, 96, 70-80.	2.6	117
123	Nuclear transcriptome profiling of induced pluripotent stem cells and embryonic stem cells identify non-coding loci resistant to reprogramming. <i>Cell Cycle</i> , 2015, 14, 1148-1155.	1.3	14
124	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , 2015, 347, 1010-1014.	6.0	517
125	Characterization of Novel Transcripts of Human Papillomavirus Type 16 Using Cap Analysis Gene Expression Technology. <i>Journal of Virology</i> , 2015, 89, 2448-2452.	1.5	6
126	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015, 16, 22.	3.8	687



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127	Krimper Enforces an Antisense Bias on piRNA Pools by Binding AGO3 in the Drosophila Germline. <i>Molecular Cell</i> , 2015, 59, 553-563.	4.5	61
128	The frequent evolutionary birth and death of functional promoters in mouse and human. <i>Genome Research</i> , 2015, 25, 1546-1557.	2.4	55
129	Telomerase Reverse Transcriptase Regulates microRNAs. <i>International Journal of Molecular Sciences</i> , 2015, 16, 1192-1208.	1.8	22
130	A draft network of ligandâ€“receptor-mediated multicellular signalling in human. <i>Nature Communications</i> , 2015, 6, 7866.	5.8	676
131	Transcriptional Dynamics Reveal Critical Roles for Non-coding RNAs in the Immediate-Early Response. <i>PLoS Computational Biology</i> , 2015, 11, e1004217.	1.5	22
132	CAGE: precise TSS data retrieval and high-resolution promoterome mining for integrative analyses. <i>Nucleic Acids Research</i> , 2015, 43, e51-e51.	6.5	194
133	Technical Advance: Transcription factor, promoter, and enhancer utilization in human myeloid cells. <i>Journal of Leukocyte Biology</i> , 2015, 97, 985-995.	1.5	23
134	Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics. <i>Nucleic Acids Research</i> , 2015, 43, 6969-6982.	6.5	54
135	STAP cells are derived from ES cells. <i>Nature</i> , 2015, 525, E4-E5.	13.7	8
136	SINEUPs: A new class of natural and synthetic antisense long non-coding RNAs that activate translation. <i>RNA Biology</i> , 2015, 12, 771-779.	1.5	84
137	Complementing tissue characterization by integrating transcriptome profiling from the Human Protein Atlas and from the FANTOM5 consortium. <i>Nucleic Acids Research</i> , 2015, 43, 6787-6798.	6.5	94
138	Expression Specificity of Disease-Associated lncRNAs: Toward Personalized Medicine. <i>Current Topics in Microbiology and Immunology</i> , 2015, 394, 237-258.	0.7	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. <i>Genome Research</i> , 2015, 25, 1812-1824.	2.4	49
141	Paradigm shifts in genomics through the FANTOM projects. <i>Mammalian Genome</i> , 2015, 26, 391-402.	1.0	96
142	A new approach for screening cervical cancer by characterization of transcripts using CAGE technology.. <i>Journal of Clinical Oncology</i> , 2015, 33, e16514-e16514.	0.8	1
143	NanoCAGE analysis of the mouse olfactory epithelium identifies the expression of vomeronasal receptors and of proximal LINE elements. <i>Frontiers in Cellular Neuroscience</i> , 2014, 8, 41.	1.8	11
144	Differential roles of epigenetic changes and Foxp3 expression in regulatory T cell-specific transcriptional regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5289-5294.	3.3	111

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145	Digital expression profiling of the compartmentalized transcriptome of Purkinje neurons. <i>Genome Research</i> , 2014, 24, 1396-1410.	2.4	49
146	PAPD5-mediated 3' adenylation and subsequent degradation of miR-21 is disrupted in proliferative disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11467-11472.	3.3	130
147	Mesencephalic dopaminergic neurons express a repertoire of olfactory receptors and respond to odorant-like molecules. <i>BMC Genomics</i> , 2014, 15, 729.	1.2	46
148	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	13.7	1,838
149	Diversity and dynamics of the <i>Drosophila</i> transcriptome. <i>Nature</i> , 2014, 512, 393-399.	13.7	647
150	Two independent transcription initiation codes overlap on vertebrate core promoters. <i>Nature</i> , 2014, 507, 381-385.	13.7	182
151	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014, 507, 455-461.	13.7	2,269
152	The enhancer and promoter landscape of human regulatory and conventional T-cell subpopulations. <i>Blood</i> , 2014, 123, e68-e78.	0.6	77
153	Systemic identification of estrogen-regulated genes in breast cancer cells through cap analysis of gene expression mapping. <i>Biochemical and Biophysical Research Communications</i> , 2014, 447, 531-536.	1.0	14
154	Analysis of the DNA methylome and transcriptome in granulopoiesis reveals timed changes and dynamic enhancer methylation. <i>Blood</i> , 2014, 123, e79-e89.	0.6	72
155	Comparison of CAGE and RNA-seq transcriptome profiling using clonally amplified and single-molecule next-generation sequencing. <i>Genome Research</i> , 2014, 24, 708-717.	2.4	99
156	Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. <i>Nature Genetics</i> , 2014, 46, 558-566.	9.4	271
157	Transcription and enhancer profiling in human monocyte subsets. <i>Blood</i> , 2014, 123, e90-e99.	0.6	157
158	Mice in the ENCODE spotlight. <i>Nature</i> , 2014, 515, 346-347.	13.7	11
159	Specific Mesothelial Signature Marks the Heterogeneity of Mesenchymal Stem Cells From High-Grade Serous Ovarian Cancer. <i>Stem Cells</i> , 2014, 32, 2998-3011.	1.4	16
160	Widespread genome transcription: New possibilities for RNA therapies. <i>Biochemical and Biophysical Research Communications</i> , 2014, 452, 294-301.	1.0	37
161	Comparative validation of the <i>D. melanogaster</i> modENCODE transcriptome annotation. <i>Genome Research</i> , 2014, 24, 1209-1223.	2.4	147
162	The devil in the details of RNA-seq. <i>Nature Biotechnology</i> , 2014, 32, 882-884.	9.4	35

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163	MOIRAI: a compact workflow system for CAGE analysis. BMC Bioinformatics, 2014, 15, 144.	1.2	66
164	Chromatin states reveal functional associations for globally defined transcription start sites in four human cell lines. BMC Genomics, 2014, 15, 120.	1.2	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.	1.2	61
166	CAGE-defined promoter regions of the genes implicated in Rett Syndrome. BMC Genomics, 2014, 15, 1177.	1.2	10
167	Redefinition of the human mast cell transcriptome by deep-CAGE sequencing. Blood, 2014, 123, e58-e67.	0.6	175
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