

# Piero Carninci

## List of Publications by Year in Descending Order

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**Version:** 2024-04-19

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

412  
papers

75,687  
citations

98  
h-index

273  
g-index

460  
ext. papers

88,352  
ext. citations

12.5  
avg, IF

8.41  
L-index

#	Paper	IF	Citations
4 <sup>12</sup>	Towards SINEUP-based therapeutics: Design of an synthesized SINEUP RNA.. <i>Molecular Therapy - Nucleic Acids</i> , <b>2022</b> , 27, 1092-1102	10.7	0
4 <sup>11</sup>	Complete Transcriptome Analysis by 5CEnd Single-Cell RNA-Seq with Random Priming.. <i>Methods in Molecular Biology</i> , <b>2022</b> , 2490, 141-156	1.4	
4 <sup>10</sup>	A field guide to cultivating computational biology. <i>PLoS Biology</i> , <b>2021</b> , 19, e3001419	9.7	2
4 <sup>09</sup>	SINEUPs: a novel toolbox for RNA therapeutics. <i>Essays in Biochemistry</i> , <b>2021</b> , 65, 775-789	7.6	3
4 <sup>08</sup>	Embryonic LTR retrotransposons supply promoter modules to somatic tissues. <i>Genome Research</i> , <b>2021</b> , 31, 1983-1993	9.7	1
4 <sup>07</sup>	Antisense RNAs during early vertebrate development are divided in groups with distinct features. <i>Genome Research</i> , <b>2021</b> , 31, 995-1010	9.7	3
4 <sup>06</sup>	Decoding Neuronal Diversification by Multiplexed Single-cell RNA-Seq. <i>Stem Cell Reports</i> , <b>2021</b> , 16, 810-824		4
4 <sup>05</sup>	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , <b>2021</b> , 12, 3297	17.4	3
4 <sup>04</sup>	FANTOM enters 20th year: expansion of transcriptomic atlases and functional annotation of non-coding RNAs. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D892-D898	20.1	19
4 <sup>03</sup>	LETR1 is a lymphatic endothelial-specific lncRNA governing cell proliferation and migration through KLF4 and SEMA3C. <i>Nature Communications</i> , <b>2021</b> , 12, 925	17.4	4
4 <sup>02</sup>	The choice of negative control antisense oligonucleotides dramatically impacts downstream analysis depending on the cellular background. <i>BMC Genomic Data</i> , <b>2021</b> , 22, 33	0	
4 <sup>01</sup>	Analysis of Enhancer-Promoter Interactions using CAGE and RADICL-Seq Technologies. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2351, 201-210	1.4	2
4 <sup>00</sup>	Low Quantity Single Strand CAGE (LQ-ssCAGE) Maps Regulatory Enhancers and Promoters. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2351, 67-90	1.4	1
399	Analysis of splice variants of the human protein disulfide isomerase (P4HB) gene. <i>BMC Genomics</i> , <b>2020</b> , 21, 766	4.5	1
398	The Secret Life of lncRNAs: Conserved, yet Not Conserved. <i>Cell</i> , <b>2020</b> , 181, 512-514	56.2	6
397	Genome-Wide Technologies to Study RNA-Chromatin Interactions. <i>Non-coding RNA</i> , <b>2020</b> , 6,	7.1	7
396	Comprehensive Characterization of Transcriptional Activity during Influenza A Virus Infection Reveals Biases in Cap-Snatching of Host RNA Sequences. <i>Journal of Virology</i> , <b>2020</b> , 94,	6.6	6

395	Machine-driven parameter screen of biochemical reactions. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, e37	20.1	
394	Recounting the FANTOM CAGE-Associated Transcriptome. <i>Genome Research</i> , <b>2020</b> , 30, 1073-1081	9.7	13
393	RADICL-seq identifies general and cell type-specific principles of genome-wide RNA-chromatin interactions. <i>Nature Communications</i> , <b>2020</b> , 11, 1018	17.4	48
392	Dual-initiation promoters with intertwined canonical and TCT/TOP transcription start sites diversify transcript processing. <i>Nature Communications</i> , <b>2020</b> , 11, 168	17.4	17
391	A human minisatellite hosts an alternative transcription start site for NPRL3 driving its expression in a repeat number-dependent manner. <i>Human Mutation</i> , <b>2020</b> , 41, 807-824	4.7	4
390	Synthetic in vitro transcribed lncRNAs (SINEUPs) with chemical modifications enhance target mRNA translation. <i>FEBS Letters</i> , <b>2020</b> , 594, 4357-4369	3.8	7
389	An NMR-based approach reveals the core structure of the functional domain of SINEUP lncRNAs. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 9346-9360	20.1	8
388	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , <b>2020</b> , 30, 1060-1072	9.7	41
387	Comparative transcriptomics of primary cells in vertebrates. <i>Genome Research</i> , <b>2020</b> , 30, 951-961	9.7	12
386	SINEUP long non-coding RNA acts via PTBP1 and HNRNPK to promote translational initiation assemblies. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 11626-11644	20.1	8
385	Use of Cap Analysis Gene Expression to detect human papillomavirus promoter activity patterns at different disease stages. <i>Scientific Reports</i> , <b>2020</b> , 10, 17991	4.9	0
384	Safety and efficacy of the Russian COVID-19 vaccine: more information needed. <i>Lancet, The</i> , <b>2020</b> , 396, e53	40	20
383	SINEUP Non-coding RNA Targeting GDNF Rescues Motor Deficits and Neurodegeneration in a Mouse Model of Parkinson Disease. <i>Molecular Therapy</i> , <b>2020</b> , 28, 642-652	11.7	20
382	Cap Analysis of Gene Expression (CAGE): A Quantitative and Genome-Wide Assay of Transcription Start Sites. <i>Methods in Molecular Biology</i> , <b>2020</b> , 2120, 277-301	1.4	7
381	NET-CAGE characterizes the dynamics and topology of human transcribed cis-regulatory elements. <i>Nature Genetics</i> , <b>2019</b> , 51, 1369-1379	36.3	33
380	Broad Heterochromatic Domains Open in Gonocyte Development Prior to De Novo DNA Methylation. <i>Developmental Cell</i> , <b>2019</b> , 51, 21-34.e5	10.2	17
379	Identification of novel cerebellar developmental transcriptional regulators with motif activity analysis. <i>BMC Genomics</i> , <b>2019</b> , 20, 718	4.5	3
378	MicroRNA-27a/b-3p and PPARG regulate SCAMP3 through a feed-forward loop during adipogenesis. <i>Scientific Reports</i> , <b>2019</b> , 9, 13891	4.9	12

377	SINEUP non-coding RNAs rescue defective frataxin expression and activity in a cellular model of Friedreich's Ataxia. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 10728-10743	20.1	18
376	The RNA-binding protein ILF3 binds to transposable element sequences in SINEUP lncRNAs. <i>FASEB Journal</i> , <b>2019</b> , 33, 13572-13589	0.9	14
375	C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution. <i>Nature Communications</i> , <b>2019</b> , 10, 360	17.4	45
374	refTSS: A Reference Data Set for Human and Mouse Transcription Start Sites. <i>Journal of Molecular Biology</i> , <b>2019</b> , 431, 2407-2422	6.5	20
373	Cell Based Assays of SINEUP Non-coding RNAs That Can Specifically Enhance mRNA Translation. <i>Journal of Visualized Experiments</i> , <b>2019</b> ,	1.6	4
372	Multi-year whole-blood transcriptome data for the study of onset and progression of Parkinson's Disease. <i>Scientific Data</i> , <b>2019</b> , 6, 20	8.2	5
371	Dynamics of cardiomyocyte transcriptome and chromatin landscape demarcates key events of heart development. <i>Genome Research</i> , <b>2019</b> , 29, 506-519	9.7	14
370	Nuclear AGO1 Regulates Gene Expression by Affecting Chromatin Architecture in Human Cells. <i>Cell Systems</i> , <b>2019</b> , 9, 446-458.e6	10.6	10
369	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> , <b>2019</b> , 116, 24242-24251	11.5	90
368	Tagging Transcription Starting Sites with CAGE <b>2019</b> , 7-20		
367	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2019</b> , 2019,	5	4
366	Look for methods, not conclusions. <i>Cell Death and Disease</i> , <b>2019</b> , 10, 931	9.8	
365	Update of the FANTOM web resource: expansion to provide additional transcriptome atlases. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D752-D758	20.1	80
364	Antisense Transcription in Loci Associated to Hereditary Neurodegenerative Diseases. <i>Molecular Neurobiology</i> , <b>2019</b> , 56, 5392-5415	6.2	15
363	The Human Cell Atlas: Technical approaches and challenges. <i>Briefings in Functional Genomics</i> , <b>2018</b> , 17, 283-294	4.9	22
362	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> , <b>2018</b> , 115, 4969-4974	11.5	50
361	Structural determinants of the SINE B2 element embedded in the long non-coding RNA activator of translation AS Uchl1. <i>Scientific Reports</i> , <b>2018</b> , 8, 3189	4.9	24
360	Discovery of Transcription Factors Novel to Mouse Cerebellar Granule Cell Development Through Laser-Capture Microdissection. <i>Cerebellum</i> , <b>2018</b> , 17, 308-325	4.3	1

359	Transcriptional landscape of Mycobacterium tuberculosis infection in macrophages. <i>Scientific Reports</i> , <b>2018</b> , 8, 6758	4.9	41
358	From "Cellular" RNA to "Smart" RNA: Multiple Roles of RNA in Genome Stability and Beyond. <i>Chemical Reviews</i> , <b>2018</b> , 118, 4365-4403	68.1	44
357	Target-enrichment sequencing for detailed characterization of small RNAs. <i>Nature Protocols</i> , <b>2018</b> , 13, 768-786	18.8	8
356	SCPortalen: human and mouse single-cell centric database. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D781-D787	20.1	25
355	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1005934	5	8
354	Identification of functional features of synthetic SINEUPs, antisense lncRNAs that specifically enhance protein translation. <i>PLoS ONE</i> , <b>2018</b> , 13, e0183229	3.7	16
353	Conserved temporal ordering of promoter activation implicates common mechanisms governing the immediate early response across cell types and stimuli. <i>Open Biology</i> , <b>2018</b> , 8,	7	3
352	Integration of genetics and miRNA-target gene network identified disease biology implicated in tissue specificity. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 11898-11909	20.1	26
351	SLIC-CAGE: high-resolution transcription start site mapping using nanogram-levels of total RNA. <i>Genome Research</i> , <b>2018</b> , 28, 1943-1956	9.7	17
350	Amphioxus functional genomics and the origins of vertebrate gene regulation. <i>Nature</i> , <b>2018</b> , 564, 64-70	50.4	120
349	Promoter Usage and Dynamics in Vascular Smooth Muscle Cells Exposed to Fibroblast Growth Factor-2 or Interleukin-1. <i>Scientific Reports</i> , <b>2018</b> , 8, 13164	4.9	6
348	DEIVA: a web application for interactive visual analysis of differential gene expression profiles. <i>BMC Genomics</i> , <b>2017</b> , 18, 47	4.5	33
347	DNA damage response inhibition at dysfunctional telomeres by modulation of telomeric DNA damage response RNAs. <i>Nature Communications</i> , <b>2017</b> , 8, 13980	17.4	53
346	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , <b>2017</b> , 543, 199-204	50.4	581
345	The FANTOM5 Computation Ecosystem: Genomic Information Hub for Promoters and Active Enhancers. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1611, 199-217	1.4	13
344	From bench to bedside: The long journey of long non-coding RNAs. <i>Current Opinion in Systems Biology</i> , <b>2017</b> , 3, 119-124	3.2	17
343	A damaged genome's transcriptional landscape through multilayered expression profiling around in situ-mapped DNA double-strand breaks. <i>Nature Communications</i> , <b>2017</b> , 8, 15656	17.4	53
342	The Human Cell Atlas <b>2017</b> ,		41

341	Linking FANTOM5 CAGE peaks to annotations with CAGEscan. <i>Scientific Data</i> , <b>2017</b> , 4, 170147	8.2	10
340	Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. <i>EBioMedicine</i> , <b>2017</b> , 24, 257-266	8.8	13
339	The FANTOM5 collection, a data series underpinning mammalian transcriptome atlases in diverse cell types. <i>Scientific Data</i> , <b>2017</b> , 4, 170113	8.2	35
338	Systematic analysis of transcription start sites in avian development. <i>PLoS Biology</i> , <b>2017</b> , 15, e2002887	9.7	22
337	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> , <b>2017</b> , 13, e1006641	6	64
336	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 872-878	44.5	282
335	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , <b>2017</b> , 4, 170112	8.2	88
334	FANTOM5 CAGE profiles of human and mouse reprocessed for GRCh38 and GRCm38 genome assemblies. <i>Scientific Data</i> , <b>2017</b> , 4, 170107	8.2	29
333	Monitoring transcription initiation activities in rat and dog. <i>Scientific Data</i> , <b>2017</b> , 4, 170173	8.2	4
332	The effect of genetic variation on promoter usage and enhancer activity. <i>Nature Communications</i> , <b>2017</b> , 8, 1358	17.4	26
331	Integrative CAGE and DNA Methylation Profiling Identify Epigenetically Regulated Genes in NSCLC. <i>Molecular Cancer Research</i> , <b>2017</b> , 15, 1354-1365	6.6	20
330	Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D737-D743	20.1	80
329	Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution. <i>Diabetes</i> , <b>2017</b> , 66, 218-230	0.9	19
328	A Transcriptional Switch Point During Hematopoietic Stem and Progenitor Cell Ontogeny. <i>Stem Cells and Development</i> , <b>2017</b> , 26, 314-327	4.4	3
327	Transcription start site profiling of 15 anatomical regions of the Macaca mulatta central nervous system. <i>Scientific Data</i> , <b>2017</b> , 4, 170163	8.2	2
326	The Human Cell Atlas. <i>ELife</i> , <b>2017</b> , 6,	8.9	937
325	Author response: The Human Cell Atlas <b>2017</b> ,		10
324	Discovery and functional analysis of lncRNAs: Methodologies to investigate an uncharacterized transcriptome. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , <b>2016</b> , 1859, 3-15	6	138

323	Expression Specificity of Disease-Associated lncRNAs: Toward Personalized Medicine. <i>Current Topics in Microbiology and Immunology</i> , <b>2016</b> , 394, 237-58	3.3	27
322	YY1 binding association with sex-biased transcription revealed through X-linked transcript levels and allelic binding analyses. <i>Scientific Reports</i> , <b>2016</b> , 6, 37324	4.9	16
321	Characterization of piRNAs across postnatal development in mouse brain. <i>Scientific Reports</i> , <b>2016</b> , 6, 25039	4.9	25
320	Genome sequence and analysis of the Japanese morning glory <i>Ipomoea nil</i> . <i>Nature Communications</i> , <b>2016</b> , 7, 13295	17.4	91
319	Identification of antisense long noncoding RNAs that function as SINEUPs in human cells. <i>Scientific Reports</i> , <b>2016</b> , 6, 33605	4.9	42
318	FANTOM5 transcriptome catalog of cellular states based on Semantic MediaWiki. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2016</b> , 2016,	5	44
317	Transcriptome Analysis of Recurrently Deregulated Genes across Multiple Cancers Identifies New Pan-Cancer Biomarkers. <i>Cancer Research</i> , <b>2016</b> , 76, 216-26	10.1	56
316	Functional annotation of the vlinc class of non-coding RNAs using systems biology approach. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 3233-52	20.1	21
315	The ORFeome Collaboration: a genome-scale human ORF-clone resource. <i>Nature Methods</i> , <b>2016</b> , 13, 191-2	21.6	80
314	Deficiency of multidrug resistance 2 contributes to cell transformation through oxidative stress. <i>Carcinogenesis</i> , <b>2016</b> , 37, 39-48	4.6	13
313	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> , <b>2016</b> , 2016,	5	12
312	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> , <b>2016</b> , 6, 33666	4.9	14
311	DeepCAGE transcriptomics identify HOXD10 as a transcription factor regulating lymphatic endothelial responses to VEGF-C. <i>Journal of Cell Science</i> , <b>2016</b> , 129, 2573-85	5.3	11
310	Transcriptional, post-transcriptional and chromatin-associated regulation of pri-miRNAs, pre-miRNAs and moRNAs. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 3070-81	20.1	25
309	Single-Nucleotide Resolution Mapping of Hepatitis B Virus Promoters in Infected Human Livers and Hepatocellular Carcinoma. <i>Journal of Virology</i> , <b>2016</b> , 90, 10811-10822	6.6	14
308	Isoforms of the Erythropoietin receptor in dopaminergic neurons of the Substantia Nigra. <i>Journal of Neurochemistry</i> , <b>2016</b> , 139, 596-609	6	8
307	Characterization of novel transcripts of human papillomavirus type 16 using cap analysis gene expression technology. <i>Journal of Virology</i> , <b>2015</b> , 89, 2448-52	6.6	5
306	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , <b>2015</b> , 16, 22	18.3	443

305	Krimper Enforces an Antisense Bias on piRNA Pools by Binding AGO3 in the Drosophila Germline. <i>Molecular Cell</i> , <b>2015</b> , 59, 553-63	17.6	47
304	The frequent evolutionary birth and death of functional promoters in mouse and human. <i>Genome Research</i> , <b>2015</b> , 25, 1546-57	9.7	33
303	Telomerase reverse transcriptase regulates microRNAs. <i>International Journal of Molecular Sciences</i> , <b>2015</b> , 16, 1192-208	6.3	15
302	A draft network of ligand-receptor-mediated multicellular signalling in human. <i>Nature Communications</i> , <b>2015</b> , 6, 7866	17.4	393
301	Transcriptional dynamics reveal critical roles for non-coding RNAs in the immediate-early response. <i>PLoS Computational Biology</i> , <b>2015</b> , 11, e1004217	5	15
300	CAGEr: precise TSS data retrieval and high-resolution promoterome mining for integrative analyses. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, e51	20.1	117
299	Technical Advance: Transcription factor, promoter, and enhancer utilization in human myeloid cells. <i>Journal of Leukocyte Biology</i> , <b>2015</b> , 97, 985-995	6.5	17
298	Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 6969-82	20.1	38
297	STAP cells are derived from ES cells. <i>Nature</i> , <b>2015</b> , 525, E4-5	50.4	6
296	SINEUPS: A new class of natural and synthetic antisense long non-coding RNAs that activate translation. <i>RNA Biology</i> , <b>2015</b> , 12, 771-9	4.8	51
295	Complementing tissue characterization by integrating transcriptome profiling from the Human Protein Atlas and from the FANTOM5 consortium. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 6787-98	20.1	61
294	Complexity of Mammalian Transcriptome Analyzed by RNA Deep Sequencing <b>2015</b> , 3-22		0
293	CAGE profiling of ncRNAs in hepatocellular carcinoma reveals widespread activation of retroviral LTR promoters in virus-induced tumors. <i>Genome Research</i> , <b>2015</b> , 25, 1812-24	9.7	40
292	Paradigm shifts in genomics through the FANTOM projects. <i>Mammalian Genome</i> , <b>2015</b> , 26, 391-402	3.2	73
291	Promoter-level expression clustering identifies time development of transcriptional regulatory cascades initiated by ErbB receptors in breast cancer cells. <i>Scientific Reports</i> , <b>2015</b> , 5, 11999	4.9	24
290	Hierarchical folding and reorganization of chromosomes are linked to transcriptional changes in cellular differentiation. <i>Molecular Systems Biology</i> , <b>2015</b> , 11, 852	12.2	229
289	DeepCAGE Transcriptomics Reveal an Important Role of the Transcription Factor MAFB in the Lymphatic Endothelium. <i>Cell Reports</i> , <b>2015</b> , 13, 1493-1504	10.6	25
288	Remodeling of retrotransposon elements during epigenetic induction of adult visual cortical plasticity by HDAC inhibitors. <i>Epigenetics and Chromatin</i> , <b>2015</b> , 8, 55	5.8	27



287	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> , <b>2015</b> , 6, 331	4.5	11
286	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 disease. <i>Frontiers in Cellular Neuroscience</i> , <b>2015</b> , 9, 114	6.1	99
285	SINEUPs are modular antisense long non-coding RNAs that increase synthesis of target proteins in cells. <i>Frontiers in Cellular Neuroscience</i> , <b>2015</b> , 9, 174	6.1	60
284	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> , <b>2015</b> , 10, e0126475	3.7	5
283	The Constrained Maximal Expression Level Owing to Haploidy Shapes Gene Content on the Mammalian X Chromosome. <i>PLoS Biology</i> , <b>2015</b> , 13, e1002315	9.7	17
282	Application of Gene Expression Trajectories Initiated from ErbB Receptor Activation Highlights the Dynamics of Divergent Promoter Usage. <i>PLoS ONE</i> , <b>2015</b> , 10, e0144176	3.7	1
281	Engineering mammalian cell factories with SINEUP noncoding RNAs to improve translation of secreted proteins. <i>Gene</i> , <b>2015</b> , 569, 287-93	3.8	31
280	Biased allelic expression in human primary fibroblast single cells. <i>American Journal of Human Genetics</i> , <b>2015</b> , 96, 70-80	11	88
279	Nuclear transcriptome profiling of induced pluripotent stem cells and embryonic stem cells identify non-coding loci resistant to reprogramming. <i>Cell Cycle</i> , <b>2015</b> , 14, 1148-55	4.7	11
278	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , <b>2015</b> , 347, 1010-4	33.3	384
277	A new approach for screening cervical cancer by characterization of transcripts using CAGE technology.. <i>Journal of Clinical Oncology</i> , <b>2015</b> , 33, e16514-e16514	2.2	
276	A promoter-level mammalian expression atlas. <i>Nature</i> , <b>2014</b> , 507, 462-70	50.4	1301
275	Diversity and dynamics of the Drosophila transcriptome. <i>Nature</i> , <b>2014</b> , 512, 393-9	50.4	418
274	Two independent transcription initiation codes overlap on vertebrate core promoters. <i>Nature</i> , <b>2014</b> , 507, 381-385	50.4	121
273	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , <b>2014</b> , 507, 455-461	50.4	1595
272	The enhancer and promoter landscape of human regulatory and conventional T-cell subpopulations. <i>Blood</i> , <b>2014</b> , 123, e68-78	2.2	58
271	Systemic identification of estrogen-regulated genes in breast cancer cells through cap analysis of gene expression mapping. <i>Biochemical and Biophysical Research Communications</i> , <b>2014</b> , 447, 531-6	3.4	10
270	Analysis of the DNA methylome and transcriptome in granulopoiesis reveals timed changes and dynamic enhancer methylation. <i>Blood</i> , <b>2014</b> , 123, e79-89	2.2	59

269	Comparison of CAGE and RNA-seq transcriptome profiling using clonally amplified and single-molecule next-generation sequencing. <i>Genome Research</i> , <b>2014</b> , 24, 708-17	9.7	66
268	Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. <i>Nature Genetics</i> , <b>2014</b> , 46, 558-66	36.3	203
267	Transcription and enhancer profiling in human monocyte subsets. <i>Blood</i> , <b>2014</b> , 123, e90-9	2.2	101
266	Genomics: mice in the ENCODE spotlight. <i>Nature</i> , <b>2014</b> , 515, 346-7	50.4	10
265	Specific mesothelial signature marks the heterogeneity of mesenchymal stem cells from high-grade serous ovarian cancer. <i>Stem Cells</i> , <b>2014</b> , 32, 2998-3011	5.8	14
264	Widespread genome transcription: new possibilities for RNA therapies. <i>Biochemical and Biophysical Research Communications</i> , <b>2014</b> , 452, 294-301	3.4	27
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