

Piero Carninci

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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
412	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012 , 489, 57-74	50.4	11449
411	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002 , 420, 520-62	50.4	5376
410	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007 , 447, 799-816	50.4	4121
409	Landscape of transcription in human cells. <i>Nature</i> , 2012 , 489, 101-8	50.4	3544
408	The GENCODE v7 catalog of human long noncoding RNAs: analysis of their gene structure, evolution, and expression. <i>Genome Research</i> , 2012 , 22, 1775-89	9.7	3408
407	The transcriptional landscape of the mammalian genome. <i>Science</i> , 2005 , 309, 1559-63	33.3	2807
406	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014 , 507, 455-461	50.4	1595
405	Monitoring the expression profiles of 7000 Arabidopsis genes under drought, cold and high-salinity stresses using a full-length cDNA microarray. <i>Plant Journal</i> , 2002 , 31, 279-92	6.9	1501
404	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 16899-903	11.5	1457
403	Insights into social insects from the genome of the honeybee <i>Apis mellifera</i> . <i>Nature</i> , 2006 , 443, 931-49	50.4	1414
402	Antisense transcription in the mammalian transcriptome. <i>Science</i> , 2005 , 309, 1564-6	33.3	1354
401	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002 , 420, 563-73	50.4	1350
400	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014 , 507, 462-70	50.4	1301
399	A user@ guide to the encyclopedia of DNA elements (ENCODE). <i>PLoS Biology</i> , 2011 , 9, e1001046	9.7	1060
398	Genome-wide analysis of mammalian promoter architecture and evolution. <i>Nature Genetics</i> , 2006 , 38, 626-35	36.3	1021
397	The Human Cell Atlas. <i>ELife</i> , 2017 , 6,	8.9	937
396	Monitoring the expression pattern of 1300 Arabidopsis genes under drought and cold stresses by using a full-length cDNA microarray. <i>Plant Cell</i> , 2001 , 13, 61-72	11.6	910

395	Direct generation of functional dopaminergic neurons from mouse and human fibroblasts. <i>Nature</i> , 2011 , 476, 224-7	50.4	784
394	Empirical analysis of transcriptional activity in the Arabidopsis genome. <i>Science</i> , 2003 , 302, 842-6	33.3	782
393	Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice. <i>Science</i> , 2003 , 301, 376-9	33.3	772
392	Long non-coding antisense RNA controls Uchl1 translation through an embedded SINEB2 repeat. <i>Nature</i> , 2012 , 491, 454-7	50.4	684
391	Comprehensive analysis of NAC family genes in <i>Oryza sativa</i> and <i>Arabidopsis thaliana</i> . <i>DNA Research</i> , 2003 , 10, 239-47	4.5	684
390	The regulated retrotransposon transcriptome of mammalian cells. <i>Nature Genetics</i> , 2009 , 41, 563-71	36.3	601
389	Functional annotation of a full-length Arabidopsis cDNA collection. <i>Science</i> , 2002 , 296, 141-5	33.3	588
388	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017 , 543, 199-204	50.4	581
387	Functional annotation of a full-length mouse cDNA collection. <i>Nature</i> , 2001 , 409, 685-90	50.4	560
386	An atlas of combinatorial transcriptional regulation in mouse and man. <i>Cell</i> , 2010 , 140, 744-52	56.2	555
385	Cap analysis gene expression for high-throughput analysis of transcriptional starting point and identification of promoter usage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 15776-81	11.5	554
384	Somatic retrotransposition alters the genetic landscape of the human brain. <i>Nature</i> , 2011 , 479, 534-7	50.4	519
383	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015 , 16, 22	18.3	443
382	Diversity and dynamics of the <i>Drosophila</i> transcriptome. <i>Nature</i> , 2014 , 512, 393-9	50.4	418
381	The status, quality, and expansion of the NIH full-length cDNA project: the Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2004 , 14, 2121-7	9.7	404
380	Mammalian RNA polymerase II core promoters: insights from genome-wide studies. <i>Nature Reviews Genetics</i> , 2007 , 8, 424-36	30.1	394
379	A draft network of ligand-receptor-mediated multicellular signalling in human. <i>Nature Communications</i> , 2015 , 6, 7866	17.4	393
378	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , 2015 , 347, 1010-4	33.3	384

377	Site-specific DICER and DROSHA RNA products control the DNA-damage response. <i>Nature</i> , 2012 , 488, 231-5	50.4	380
376	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009 , 41, 553-62	36.3	356
375	Monitoring the expression pattern of around 7,000 Arabidopsis genes under ABA treatments using a full-length cDNA microarray. <i>Functional and Integrative Genomics</i> , 2002 , 2, 282-91	3.8	353
374	Metazoan promoters: emerging characteristics and insights into transcriptional regulation. <i>Nature Reviews Genetics</i> , 2012 , 13, 233-45	30.1	347
373	CAGE: cap analysis of gene expression. <i>Nature Methods</i> , 2006 , 3, 211-22	21.6	328
372	The reality of pervasive transcription. <i>PLoS Biology</i> , 2011 , 9, e1000625; discussion e1001102	9.7	325
371	Small RNAs derived from snoRNAs. <i>Rna</i> , 2009 , 15, 1233-40	5.8	325
370	Tiny RNAs associated with transcription start sites in animals. <i>Nature Genetics</i> , 2009 , 41, 572-8	36.3	302
369	Comparative genomics of <i>Physcomitrella patens</i> gametophytic transcriptome and <i>Arabidopsis thaliana</i> : implication for land plant evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 8007-12	11.5	301
368	Endogenous retrotransposition activates oncogenic pathways in hepatocellular carcinoma. <i>Cell</i> , 2013 , 153, 101-11	56.2	291
367	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017 , 35, 872-878	44.5	282
366	High-efficiency full-length cDNA cloning by biotinylated CAP trapper. <i>Genomics</i> , 1996 , 37, 327-36	4.3	266
365	Integrative annotation of 21,037 human genes validated by full-length cDNA clones. <i>PLoS Biology</i> , 2004 , 2, e162	9.7	255
364	Genome-wide analysis of cancer/testis gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 20422-7	11.5	254
363	Complex Loci in human and mouse genomes. <i>PLoS Genetics</i> , 2006 , 2, e47	6	246
362	Hierarchical folding and reorganization of chromosomes are linked to transcriptional changes in cellular differentiation. <i>Molecular Systems Biology</i> , 2015 , 11, 852	12.2	229
361	Hidden layers of human small RNAs. <i>BMC Genomics</i> , 2008 , 9, 157	4.5	226
360	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. <i>Genome Research</i> , 2000 , 10, 1617-30	9.7	221

359	Conservation and divergence in Toll-like receptor 4-regulated gene expression in primary human versus mouse macrophages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, E944-53	11.5	212
358	Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998 , 95, 520-4	11.5	205
357	Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. <i>Nature Genetics</i> , 2014 , 46, 558-66	36.3	203
356	Unexpected expression of alpha- and beta-globin in mesencephalic dopaminergic neurons and glial cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 15454-9	11.5	193
355	Antisense transcripts with FANTOM2 clone set and their implications for gene regulation. <i>Genome Research</i> , 2003 , 13, 1324-34	9.7	192
354	High-efficiency cloning of Arabidopsis full-length cDNA by biotinylated CAP trapper. <i>Plant Journal</i> , 1998 , 15, 707-20	6.9	189
353	5' end-centered expression profiling using cap-analysis gene expression and next-generation sequencing. <i>Nature Protocols</i> , 2012 , 7, 542-61	18.8	182
352	Delineating developmental and metabolic pathways in vivo by expression profiling using the RIKEN set of 18,816 full-length enriched mouse cDNA arrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 2199-204	11.5	182
351	Chromatin-associated RNA interference components contribute to transcriptional regulation in <i>Drosophila</i> . <i>Nature</i> , 2011 , 480, 391-5	50.4	180
350	A code for transcription initiation in mammalian genomes. <i>Genome Research</i> , 2008 , 18, 1-12	9.7	179
349	Genome-wide analysis of promoter architecture in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2011 , 21, 182-92	9.7	178
348	Transcriptome analysis of the aphid bacteriocyte, the symbiotic host cell that harbors an endocellular mutualistic bacterium, <i>Buchnera</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 5477-82	11.5	168
347	The <i>Drosophila</i> gene collection: identification of putative full-length cDNAs for 70% of <i>D. melanogaster</i> genes. <i>Genome Research</i> , 2002 , 12, 1294-300	9.7	167
346	Chromatin signatures and retrotransposon profiling in mouse embryos reveal regulation of LINE-1 by RNA. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 332-8	17.6	160
345	The abundance of short proteins in the mammalian proteome. <i>PLoS Genetics</i> , 2006 , 2, e52	6	159
344	A molecular neuroethological approach for identifying and characterizing a cascade of behaviorally regulated genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 15212-7	11.5	156
343	Long non-coding RNA modifies chromatin: epigenetic silencing by long non-coding RNAs. <i>BioEssays</i> , 2011 , 33, 830-9	4.1	148
342	Impact of alternative initiation, splicing, and termination on the diversity of the mRNA transcripts encoded by the mouse transcriptome. <i>Genome Research</i> , 2003 , 13, 1290-300	9.7	148

341	Tag-based approaches for transcriptome research and genome annotation. <i>Nature Methods</i> , 2005 , 2, 495-502	21.6	148
340	High-efficiency full-length cDNA cloning. <i>Methods in Enzymology</i> , 1999 , 303, 19-44	1.7	147
339	Unamplified cap analysis of gene expression on a single-molecule sequencer. <i>Genome Research</i> , 2011 , 21, 1150-9	9.7	143
338	Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia. <i>Genome Research</i> , 2003 , 13, 1273-89	9.7	141
337	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	6	138
336	Transcript annotation in FANTOM3: mouse gene catalog based on physical cDNAs. <i>PLoS Genetics</i> , 2006 , 2, e2	6	138
335	Clusters of internally primed transcripts reveal novel long noncoding RNAs. <i>PLoS Genetics</i> , 2006 , 2, e37	6	135
334	High-fidelity promoter profiling reveals widespread alternative promoter usage and transposon-driven developmental gene expression. <i>Genome Research</i> , 2013 , 23, 169-80	9.7	133
333	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012 , 22, 1658-67	9.7	133
332	NMDA receptor regulation prevents regression of visual cortical function in the absence of Mecp2. <i>Neuron</i> , 2012 , 76, 1078-90	13.9	129
331	Redefinition of the human mast cell transcriptome by deep-CAGE sequencing. <i>Blood</i> , 2014 , 123, e58-67	2.2	126
330	Linking promoters to functional transcripts in small samples with nanoCAGE and CAGEscan. <i>Nature Methods</i> , 2010 , 7, 528-34	21.6	123
329	Molecular mechanisms of pituitary organogenesis: In search of novel regulatory genes. <i>Molecular and Cellular Endocrinology</i> , 2010 , 323, 4-19	4.4	122
328	Two independent transcription initiation codes overlap on vertebrate core promoters. <i>Nature</i> , 2014 , 507, 381-385	50.4	121
327	Amphioxus functional genomics and the origins of vertebrate gene regulation. <i>Nature</i> , 2018 , 564, 64-70	50.4	120
326	Identification of putative noncoding RNAs among the RIKEN mouse full-length cDNA collection. <i>Genome Research</i> , 2003 , 13, 1301-6	9.7	119
325	CAGEr: precise TSS data retrieval and high-resolution promoterome mining for integrative analyses. <i>Nucleic Acids Research</i> , 2015 , 43, e51	20.1	117
324	Genome-wide detection and analysis of hippocampus core promoters using DeepCAGE. <i>Genome Research</i> , 2009 , 19, 255-65	9.7	116

323	Noncoding RNA transcription beyond annotated genes. <i>Current Opinion in Genetics and Development</i> , 2007 , 17, 139-44	4.9	112
322	Genetic control of the innate immune response. <i>BMC Immunology</i> , 2003 , 4, 5	3.7	109
321	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, 11467-72	11.5	106
320	Cross-mapping and the identification of editing sites in mature microRNAs in high-throughput sequencing libraries. <i>Genome Research</i> , 2010 , 20, 257-64	9.7	105
319	Methods for analyzing deep sequencing expression data: constructing the human and mouse promoterome with deepCAGE data. <i>Genome Biology</i> , 2009 , 10, R79	18.3	105
318	Transcriptional network dynamics in macrophage activation. <i>Genomics</i> , 2006 , 88, 133-42	4.3	104
317	Transcription and enhancer profiling in human monocyte subsets. <i>Blood</i> , 2014 , 123, e90-9	2.2	101
316	Detecting expressed genes using CAGE. <i>Methods in Molecular Biology</i> , 2014 , 1164, 67-85	1.4	100
315	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> , 2015 , 9, 114	6.1	99
314	Antisense transcripts with rice full-length cDNAs. <i>Genome Biology</i> , 2003 , 5, R5	18.3	96
313	Comparative validation of the D. melanogaster modENCODE transcriptome annotation. <i>Genome Research</i> , 2014 , 24, 1209-23	9.7	95
312	Genome sequence and analysis of the Japanese morning glory Ipomoea nil. <i>Nature Communications</i> , 2016 , 7, 13295	17.4	91
311	Single-cell transcriptomics reveals expansion of cytotoxic CD4 T cells in supercentenarians. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 24242-24251	11.5	90
310	Heterotachy in mammalian promoter evolution. <i>PLoS Genetics</i> , 2006 , 2, e30	6	90
309	Discrimination of non-protein-coding transcripts from protein-coding mRNA. <i>RNA Biology</i> , 2006 , 3, 40-8	4.8	90
308	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , 2017 , 4, 170112	8.2	88
307	Biased allelic expression in human primary fibroblast single cells. <i>American Journal of Human Genetics</i> , 2015 , 96, 70-80	11	88
306	Comparative analysis of apoptosis and inflammation genes of mice and humans. <i>Genome Research</i> , 2003 , 13, 1376-88	9.7	88

305	Discovery of imprinted transcripts in the mouse transcriptome using large-scale expression profiling. <i>Genome Research</i> , 2003 , 13, 1402-9	9.7	87
304	Full-length cDNAs from chicken bursal lymphocytes to facilitate gene function analysis. <i>Genome Biology</i> , 2005 , 6, R6	18.3	86
303	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, 5289-94	11.5	85
302	Transcriptional and structural impact of TATA-initiation site spacing in mammalian core promoters. <i>Genome Biology</i> , 2006 , 7, R78	18.3	85
301	A rescue strategy for multimapping short sequence tags refines surveys of transcriptional activity by CAGE. <i>Genomics</i> , 2008 , 91, 281-8	4.3	82
300	Tagging mammalian transcription complexity. <i>Trends in Genetics</i> , 2006 , 22, 501-10	8.5	81
299	The ORFeome Collaboration: a genome-scale human ORF-clone resource. <i>Nature Methods</i> , 2016 , 13, 191-2	21.6	80
298	Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. <i>Nucleic Acids Research</i> , 2017 , 45, D737-D743	20.1	80
297	Update of the FANTOM web resource: expansion to provide additional transcriptome atlases. <i>Nucleic Acids Research</i> , 2019 , 47, D752-D758	20.1	80
296	High efficiency selection of full-length cDNA by improved biotinylated cap trapper. <i>DNA Research</i> , 1997 , 4, 61-6	4.5	79
295	A novel feature of microsatellites in plants: a distribution gradient along the direction of transcription. <i>FEBS Letters</i> , 2003 , 554, 17-22	3.8	79
294	Systematic characterization of the zinc-finger-containing proteins in the mouse transcriptome. <i>Genome Research</i> , 2003 , 13, 1430-42	9.7	79
293	RNA Dust: Where are the Genes?. <i>DNA Research</i> , 2010 , 17, 209-209	4.5	78
292	Beyond the FANTOM4 2010 , 11, O11		78
291	Dynamic regulation of the transcription initiation landscape at single nucleotide resolution during vertebrate embryogenesis. <i>Genome Research</i> , 2013 , 23, 1938-50	9.7	77
290	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. <i>Genome Research</i> , 2010 , 20, 791-803	9.7	77
289	The complexity of the mammalian transcriptome. <i>Journal of Physiology</i> , 2006 , 575, 321-32	3.9	77
288	Mice and men: their promoter properties. <i>PLoS Genetics</i> , 2006 , 2, e54	6	75

287	Mouse proteome analysis. <i>Genome Research</i> , 2003 , 13, 1335-44	9.7	75
286	Paradigm shifts in genomics through the FANTOM projects. <i>Mammalian Genome</i> , 2015 , 26, 391-402	3.2	73
285	Transcriptional profiling of genes responsive to abscisic acid and gibberellin in rice: phenotyping and comparative analysis between rice and Arabidopsis. <i>Physiological Genomics</i> , 2004 , 17, 87-100	3.6	70
284	Balanced-size and long-size cloning of full-length, cap-trapped cDNAs into vectors of the novel lambda-FLC family allows enhanced gene discovery rate and functional analysis. <i>Genomics</i> , 2001 , 77, 79-90	4.3	70
283	CAGE Basic/Analysis Databases: the CAGE resource for comprehensive promoter analysis. <i>Nucleic Acids Research</i> , 2006 , 34, D632-6	20.1	69
282	Multifaceted mammalian transcriptome. <i>Current Opinion in Cell Biology</i> , 2008 , 20, 274-80	9	68
281	Placental expression profiling in preeclampsia: local overproduction of hemoglobin may drive pathological changes. <i>Fertility and Sterility</i> , 2008 , 90, 1834-43	4.8	67
280	Comparison of CAGE and RNA-seq transcriptome profiling using clonally amplified and single-molecule next-generation sequencing. <i>Genome Research</i> , 2014 , 24, 708-17	9.7	66
279	The FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. <i>Genome Biology</i> , 2009 , 10, R40	18.3	65
278	LOCATE: a mouse protein subcellular localization database. <i>Nucleic Acids Research</i> , 2006 , 34, D213-7	20.1	65
277	The mouse secretome: functional classification of the proteins secreted into the extracellular environment. <i>Genome Research</i> , 2003 , 13, 1350-9	9.7	65
276	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	6	64
275	Evolutionary turnover of mammalian transcription start sites. <i>Genome Research</i> , 2006 , 16, 713-22	9.7	64
274	Dynamic usage of transcription start sites within core promoters. <i>Genome Biology</i> , 2006 , 7, R118	18.3	64
273	Gene discovery in genetically labeled single dopaminergic neurons of the retina. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 5069-74	11.5	64
272	Alternate transcription of the Toll-like receptor signaling cascade. <i>Genome Biology</i> , 2006 , 7, R10	18.3	63
271	Solution structure of the SEA domain from the murine homologue of ovarian cancer antigen CA125 (MUC16). <i>Journal of Biological Chemistry</i> , 2004 , 279, 13174-82	5.4	62
270	Systematic expression profiling of the mouse transcriptome using RIKEN cDNA microarrays. <i>Genome Research</i> , 2003 , 13, 1318-23	9.7	62

269	Complementing tissue characterization by integrating transcriptome profiling from the Human Protein Atlas and from the FANTOM5 consortium. <i>Nucleic Acids Research</i> , 2015 , 43, 6787-98	20.1	61
268	CAGE (cap analysis of gene expression): a protocol for the detection of promoter and transcriptional networks. <i>Methods in Molecular Biology</i> , 2012 , 786, 181-200	1.4	61
267	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	6.1	60
266	Analysis of the DNA methylome and transcriptome in granulopoiesis reveals timed changes and dynamic enhancer methylation. <i>Blood</i> , 2014 , 123, e79-89	2.2	59
265	The enhancer and promoter landscape of human regulatory and conventional T-cell subpopulations. <i>Blood</i> , 2014 , 123, e68-78	2.2	58
264	Discovery of transcriptional regulators and signaling pathways in the developing pituitary gland by bioinformatic and genomic approaches. <i>Genomics</i> , 2009 , 93, 449-60	4.3	58
263	A simple physical model predicts small exon length variations. <i>PLoS Genetics</i> , 2006 , 2, e45	6	58
262	Comparative analysis of plant and animal calcium signal transduction element using plant full-length cDNA data. <i>Molecular Biology and Evolution</i> , 2004 , 21, 1855-70	8.3	58
261	Transcriptome Analysis of Recurrently Deregulated Genes across Multiple Cancers Identifies New Pan-Cancer Biomarkers. <i>Cancer Research</i> , 2016 , 76, 216-26	10.1	56
260	FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. <i>Genome Biology</i> , 2009 , 10, R39	18.3	56
259	Solution structure of the RWD domain of the mouse GCN2 protein. <i>Protein Science</i> , 2004 , 13, 2089-100	6.3	56
258	RNA dust: where are the genes?. <i>DNA Research</i> , 2010 , 17, 51-9	4.5	55
257	Altruistic functions for selfish DNA. <i>Cell Cycle</i> , 2009 , 8, 2895-900	4.7	55
256	DNA damage response inhibition at dysfunctional telomeres by modulation of telomeric DNA damage response RNAs. <i>Nature Communications</i> , 2017 , 8, 13980	17.4	53
255	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	17.4	53
254	On biased distribution of introns in various eukaryotes. <i>Gene</i> , 2002 , 300, 89-95	3.8	53
253	Genomics approach to abscisic acid- and gibberellin-responsive genes in rice. <i>DNA Research</i> , 2003 , 10, 249-61	4.5	52
252	SINEUPs: A new class of natural and synthetic antisense long non-coding RNAs that activate translation. <i>RNA Biology</i> , 2015 , 12, 771-9	4.8	51

251	NanoCAGE: a high-resolution technique to discover and interrogate cell transcriptomes. <i>Cold Spring Harbor Protocols</i> , 2011 , 2011, pdb.prot5559	1.2	51
250	Pseudo-messenger RNA: phantoms of the transcriptome. <i>PLoS Genetics</i> , 2006 , 2, e23	6	51
249	Multiple tissue-specific promoters control expression of the murine tartrate-resistant acid phosphatase gene. <i>Gene</i> , 2003 , 307, 111-23	3.8	51
248	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	11.5	50
247	Gene organization in rice revealed by full-length cDNA mapping and gene expression analysis through microarray. <i>PLoS ONE</i> , 2007 , 2, e1235	3.7	50
246	Genomic organization of transcriptomes in mammals: Coregulation and cofunctionality. <i>Genomics</i> , 2007 , 89, 580-7	4.3	50
245	MOIRAI: a compact workflow system for CAGE analysis. <i>BMC Bioinformatics</i> , 2014 , 15, 144	3.6	49
244	Trehalose-enhanced isolation of neuronal sub-types from adult mouse brain. <i>BioTechniques</i> , 2012 , 52, 381-5	2.5	49
243	A comprehensive transcript map of the mouse Gnas imprinted complex. <i>Genome Research</i> , 2003 , 13, 1410-5	9.7	49
242	RADICL-seq identifies general and cell type-specific principles of genome-wide RNA-chromatin interactions. <i>Nature Communications</i> , 2020 , 11, 1018	17.4	48
241	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. <i>Genome Research</i> , 2000 , 10, 1757-71	9.7	48
240	Krimper Enforces an Antisense Bias on piRNA Pools by Binding AGO3 in the Drosophila Germline. <i>Molecular Cell</i> , 2015 , 59, 553-63	17.6	47
239	Cloning full-length, cap-trapper-selected cDNAs by using the single-strand linker ligation method. <i>BioTechniques</i> , 2001 , 30, 1250-4	2.5	47
238	Suppression of artifacts and barcode bias in high-throughput transcriptome analyses utilizing template switching. <i>Nucleic Acids Research</i> , 2013 , 41, e44	20.1	46
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