

Piero Carninci

List of Publications by Year in descending order

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389
papers

76,823
citations

1447

104
h-index

529

260
g-index

470
all docs

470
docs citations

470
times ranked

68748
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Decryption of sequence, structure, and functional features of SINE repeat elements in SINEUP non-coding RNA-mediated post-transcriptional gene regulation. <i>Nature Communications</i> , 2024, 15, . | 12.8 | 1 |
| 2 | Systematic assessment of long-read RNA-seq methods for transcript identification and quantification. <i>Nature Methods</i> , 2024, 21, 1349-1363. | 19.2 | 3 |
| 3 | CapTrap-seq: a platform-agnostic and quantitative approach for high-fidelity full-length RNA sequencing. <i>Nature Communications</i> , 2024, 15, . | 12.8 | 0 |
| 4 | Prediction of the cell-type-specific transcription of non-coding RNAs from genome sequences via machine learning. <i>Nature Biomedical Engineering</i> , 2023, 7, 830-844. | 21.9 | 12 |
| 5 | Piwil2 (Mili) sustains neurogenesis and prevents cellular senescence in the postnatal hippocampus. <i>EMBO Reports</i> , 2023, 24, . | 4.5 | 6 |
| 6 | Long non-coding RNAs: definitions, functions, challenges and recommendations. <i>Nature Reviews Molecular Cell Biology</i> , 2023, 24, 430-447. | 36.5 | 571 |
| 7 | A new layer of complexity in the human genome: Somatic recombination of repeat elements. <i>Clinical and Translational Medicine</i> , 2023, 13, . | 4.1 | 1 |
| 8 | Gut microbial carbohydrate metabolism contributes to insulin resistance. <i>Nature</i> , 2023, 621, 389-395. | 35.3 | 74 |
| 9 | The status of the human gene catalogue. <i>Nature</i> , 2023, 622, 41-47. | 35.3 | 37 |
| 10 | Towards SINEUP-based therapeutics: Design of an in vitro synthesized SINEUP RNA. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 27, 1092-1102. | 5.0 | 4 |
| 11 | Complete Transcriptome Analysis by 5' End Single-Cell RNA-Seq with Random Priming. <i>Methods in Molecular Biology</i> , 2022, 2490, 141-156. | 0.7 | 3 |
| 12 | Lessons from the functional characterization of lncRNAs: introduction to mammalian genome special issue. <i>Mammalian Genome</i> , 2022, , . | 2.2 | 1 |
| 13 | Multiomic atlas with functional stratification and developmental dynamics of zebrafish cis-regulatory elements. <i>Nature Genetics</i> , 2022, 54, 1037-1050. | 20.1 | 36 |
| 14 | Deep sequencing of short capped RNAs reveals novel families of noncoding RNAs. <i>Genome Research</i> , 2022, 32, 1727-1735. | 5.5 | 1 |
| 15 | Distinctive exercise-induced inflammatory response and exerkine induction in skeletal muscle of people with type 2 diabetes. <i>Science Advances</i> , 2022, 8, . | 10.7 | 19 |
| 16 | SCAFE: a software suite for analysis of transcribed cis-regulatory elements in single cells. <i>Bioinformatics</i> , 2022, 38, 5126-5128. | 4.2 | 7 |
| 17 | FANTOM enters 20th year: expansion of transcriptomic atlases and functional annotation of non-coding RNAs. <i>Nucleic Acids Research</i> , 2021, 49, D892-D898. | 13.8 | 66 |
| 18 | LETR1 is a lymphatic endothelial-specific lncRNA governing cell proliferation and migration through KLF4 and SEMA3C. <i>Nature Communications</i> , 2021, 12, 925. | 12.8 | 24 |

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|----|---|------|-----------|
| 19 | Antisense RNAs during early vertebrate development are divided in groups with distinct features. <i>Genome Research</i> , 2021, 31, 995-1010. | 5.5 | 10 |
| 20 | Decoding Neuronal Diversification by Multiplexed Single-cell RNA-Seq. <i>Stem Cell Reports</i> , 2021, 16, 810-824. | 4.7 | 11 |
| 21 | Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297. | 12.8 | 14 |
| 22 | The choice of negative control antisense oligonucleotides dramatically impacts downstream analysis depending on the cellular background. <i>BMC Genomic Data</i> , 2021, 22, 33. | 1.6 | 0 |
| 23 | Low Quantity Single Strand CAGE (LQ-ssCAGE) Maps Regulatory Enhancers and Promoters. <i>Methods in Molecular Biology</i> , 2021, 2351, 67-90. | 0.7 | 6 |
| 24 | A field guide to cultivating computational biology. <i>PLoS Biology</i> , 2021, 19, e3001419. | 5.3 | 9 |
| 25 | SINEUPs: a novel toolbox for RNA therapeutics. <i>Essays in Biochemistry</i> , 2021, 65, 775-789. | 4.5 | 16 |
| 26 | Embryonic LTR retrotransposons supply promoter modules to somatic tissues. <i>Genome Research</i> , 2021, 31, 1983-1993. | 5.5 | 11 |
| 27 | Japan: prize diversity, not conformity, to boost research. <i>Nature</i> , 2021, 599, 201-201. | 35.3 | 1 |
| 28 | 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. | 8.0 | 49 |
| 29 | Dual-initiation promoters with intertwined canonical and TCT/TOP transcription start sites diversify transcript processing. <i>Nature Communications</i> , 2020, 11, 168. | 12.8 | 41 |
| 30 | A human minisatellite hosts an alternative transcription start site for <i>NPRL3</i> driving its expression in a repeat number-dependent manner. <i>Human Mutation</i> , 2020, 41, 807-824. | 2.7 | 6 |
| 31 | An NMR-based approach reveals the core structure of the functional domain of SINEUP lncRNAs. <i>Nucleic Acids Research</i> , 2020, 48, 9346-9360. | 13.8 | 18 |
| 32 | Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072. | 5.5 | 119 |
| 33 | Comparative transcriptomics of primary cells in vertebrates. <i>Genome Research</i> , 2020, 30, 951-961. | 5.5 | 33 |
| 34 | Transcriptome-wide sites of collided ribosomes reveal principles of translational pausing. <i>Genome Research</i> , 2020, 30, 985-999. | 5.5 | 83 |
| 35 | SINEUP long non-coding RNA acts via PTBP1 and HNRNPK to promote translational initiation assemblies. <i>Nucleic Acids Research</i> , 2020, 48, 11626-11644. | 13.8 | 36 |
| 36 | Use of Cap Analysis Gene Expression to detect human papillomavirus promoter activity patterns at different disease stages. <i>Scientific Reports</i> , 2020, 10, 17991. | 3.4 | 2 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 37 | Safety and efficacy of the Russian COVID-19 vaccine: more information needed. <i>Lancet</i> , The, 2020, 396, e53. | 11.9 | 27 |
| 38 | Analysis of splice variants of the human protein disulfide isomerase (P4HB) gene. <i>BMC Genomics</i> , 2020, 21, 766. | 2.9 | 5 |
| 39 | The Secret Life of lncRNAs: Conserved, yet Not Conserved. <i>Cell</i> , 2020, 181, 512-514. | 27.3 | 9 |
| 40 | Genome-Wide Technologies to Study RNA-Chromatin Interactions. <i>Non-coding RNA</i> , 2020, 6, 20. | 2.7 | 21 |
| 41 | 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, . | 3.4 | 15 |
| 42 | Machine-driven parameter screen of biochemical reactions. <i>Nucleic Acids Research</i> , 2020, 48, e37-e37. | 13.8 | 0 |
| 43 | Recounting the FANTOM CAGE-Associated Transcriptome. <i>Genome Research</i> , 2020, 30, 1073-1081. | 5.5 | 37 |
| 44 | RADICL-seq identifies general and cell type-specific principles of genome-wide RNA-chromatin interactions. <i>Nature Communications</i> , 2020, 11, 1018. | 12.8 | 113 |
| 45 | 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. | 0.7 | 25 |
| 46 | Expanded ENCODE delivers invaluable genomic encyclopedia. <i>Nature</i> , 2020, 583, 685-686. | 35.3 | 8 |
| 47 | Nuclear AGO1 Regulates Gene Expression by Affecting Chromatin Architecture in Human Cells. <i>Cell Systems</i> , 2019, 9, 446-458.e6. | 6.1 | 29 |
| 48 | Single-cell transcriptomics reveals expansion of cytotoxic CD4 T cells in supercentenarians. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24242-24251. | 7.4 | 239 |
| 49 | NET-CAGE characterizes the dynamics and topology of human transcribed cis-regulatory elements. <i>Nature Genetics</i> , 2019, 51, 1369-1379. | 20.1 | 82 |
| 50 | Broad Heterochromatic Domains Open in Gonocyte Development Prior to De Novo DNA Methylation. <i>Developmental Cell</i> , 2019, 51, 21-34.e5. | 6.9 | 27 |
| 51 | Identification of novel cerebellar developmental transcriptional regulators with motif activity analysis. <i>BMC Genomics</i> , 2019, 20, 718. | 2.9 | 12 |
| 52 | MicroRNA-27a/b-3p and PPARC regulate SCAMP3 through a feed-forward loop during adipogenesis. <i>Scientific Reports</i> , 2019, 9, 13891. | 3.4 | 17 |
| 53 | SINEUP non-coding RNAs rescue defective frataxin expression and activity in a cellular model of Friedreich's Ataxia. <i>Nucleic Acids Research</i> , 2019, 47, 10728-10743. | 13.8 | 31 |
| 54 | The RNA-binding protein ILF3 binds to transposable element sequences in SINEUP lncRNAs. <i>FASEB Journal</i> , 2019, 33, 13572-13589. | 0.4 | 21 |

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|----|---|------|-----------|
| 55 | C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution. <i>Nature Communications</i> , 2019, 10, 360. | 12.8 | 106 |
| 56 | refTSS: A Reference Data Set for Human and Mouse Transcription Start Sites. <i>Journal of Molecular Biology</i> , 2019, 431, 2407-2422. | 4.2 | 82 |
| 57 | Cell Based Assays of SINE/UP Non-coding RNAs That Can Specifically Enhance mRNA Translation. <i>Journal of Visualized Experiments</i> , 2019, , . | 0.3 | 5 |
| 58 | Multi-year whole-blood transcriptome data for the study of onset and progression of Parkinson's Disease. <i>Scientific Data</i> , 2019, 6, 20. | 5.3 | 10 |
| 59 | Dynamics of cardiomyocyte transcriptome and chromatin landscape demarcates key events of heart development. <i>Genome Research</i> , 2019, 29, 506-519. | 5.5 | 21 |
| 60 | Large expert-curated database for benchmarking document similarity detection in biomedical literature search. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, . | 3.1 | 16 |
| 61 | Look for methods, not conclusions. <i>Cell Death and Disease</i> , 2019, 10, 931. | 6.3 | 1 |
| 62 | Update of the FANTOM web resource: expansion to provide additional transcriptome atlases. <i>Nucleic Acids Research</i> , 2019, 47, D752-D758. | 13.8 | 185 |
| 63 | Antisense Transcription in Loci Associated to Hereditary Neurodegenerative Diseases. <i>Molecular Neurobiology</i> , 2019, 56, 5392-5415. | 4.1 | 31 |
| 64 | Mapping magnetic lineaments and subsurface basement beneath parts of Lower Benue Trough (LBT), Nigeria: Insights from integrating gravity, magnetic and geologic data. <i>Journal of Earth System Science</i> , 2019, 128, 1. | 1.3 | 15 |
| 65 | Optimizing Fixed-Ratio Combination Therapy in Type 2 Diabetes. <i>Advances in Therapy</i> , 2019, 36, 265-277. | 2.9 | 30 |
| 66 | Tagging Transcription Starting Sites with CAGE. , 2019, , 7-20. | | 0 |
| 67 | The Human Cell Atlas: Technical approaches and challenges. <i>Briefings in Functional Genomics</i> , 2018, 17, 283-294. | 2.9 | 35 |
| 68 | Prevention of hepatocellular carcinoma by targeting MYCN-positive liver cancer stem cells with acyclic retinoid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4969-4974. | 7.4 | 80 |
| 69 | 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. | 3.4 | 33 |
| 70 | Discovery of Transcription Factors Novel to Mouse Cerebellar Granule Cell Development Through Laser-Capture Microdissection. <i>Cerebellum</i> , 2018, 17, 308-325. | 2.7 | 6 |
| 71 | Transcriptional landscape of <i>Mycobacterium tuberculosis</i> infection in macrophages. <i>Scientific Reports</i> , 2018, 8, 6758. | 3.4 | 94 |
| 72 | From "Cellular" RNA to "Smart" RNA: Multiple Roles of RNA in Genome Stability and Beyond. <i>Chemical Reviews</i> , 2018, 118, 4365-4403. | 49.4 | 65 |

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|----|---|------|-----------|
| 73 | SCPortalen: human and mouse single-cell centric database. <i>Nucleic Acids Research</i> , 2018, 46, D781-D787. | 13.8 | 50 |
| 74 | 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, . | 3.7 | 15 |
| 75 | Integration of genetics and miRNA target gene network identified disease biology implicated in tissue specificity. <i>Nucleic Acids Research</i> , 2018, 46, 11898-11909. | 13.8 | 39 |
| 76 | SLIC-CAGE: high-resolution transcription start site mapping using nanogram-levels of total RNA. <i>Genome Research</i> , 2018, 28, 1943-1956. | 5.5 | 35 |
| 77 | Amphioxus functional genomics and the origins of vertebrate gene regulation. <i>Nature</i> , 2018, 564, 64-70. | 35.3 | 239 |
| 78 | Promoter Usage and Dynamics in Vascular Smooth Muscle Cells Exposed to Fibroblast Growth Factor-2 or Interleukin-1 β . <i>Scientific Reports</i> , 2018, 8, 13164. | 3.4 | 10 |
| 79 | 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. | 3.0 | 17 |
| 80 | Identification of functional features of synthetic SINEUPs, antisense lncRNAs that specifically enhance protein translation. <i>PLoS ONE</i> , 2018, 13, e0183229. | 2.5 | 23 |
| 81 | DEIVA: a web application for interactive visual analysis of differential gene expression profiles. <i>BMC Genomics</i> , 2017, 18, 47. | 2.9 | 41 |
| 82 | DNA damage response inhibition at dysfunctional telomeres by modulation of telomeric DNA damage response RNAs. <i>Nature Communications</i> , 2017, 8, 13980. | 12.8 | 78 |
| 83 | An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017, 543, 199-204. | 35.3 | 930 |
| 84 | The FANTOM5 Computation Ecosystem: Genomic Information Hub for Promoters and Active Enhancers. <i>Methods in Molecular Biology</i> , 2017, 1611, 199-217. | 0.7 | 23 |
| 85 | From bench to bedside: The long journey of long non-coding RNAs. <i>Current Opinion in Systems Biology</i> , 2017, 3, 119-124. | 2.7 | 22 |
| 86 | A damaged genome's transcriptional landscape through multilayered expression profiling around in situ-mapped DNA double-strand breaks. <i>Nature Communications</i> , 2017, 8, 15656. | 12.8 | 100 |
| 87 | Linking FANTOM5 CAGE peaks to annotations with CAGEscan. <i>Scientific Data</i> , 2017, 4, 170147. | 5.3 | 29 |
| 88 | Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. <i>EBioMedicine</i> , 2017, 24, 257-266. | 5.9 | 27 |
| 89 | The FANTOM5 collection, a data series underpinning mammalian transcriptome atlases in diverse cell types. <i>Scientific Data</i> , 2017, 4, 170113. | 5.3 | 58 |
| 90 | An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017, 35, 872-878. | 20.4 | 477 |

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|-----|---|------|-----------|
| 91 | FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , 2017, 4, 170112. | 5.3 | 210 |
| 92 | FANTOM5 CAGE profiles of human and mouse reprocessed for GRCh38 and GRCm38 genome assemblies. <i>Scientific Data</i> , 2017, 4, 170107. | 5.3 | 72 |
| 93 | Monitoring transcription initiation activities in rat and dog. <i>Scientific Data</i> , 2017, 4, 170173. | 5.3 | 6 |
| 94 | The effect of genetic variation on promoter usage and enhancer activity. <i>Nature Communications</i> , 2017, 8, 1358. | 12.8 | 53 |
| 95 | Integrative CAGE and DNA Methylation Profiling Identify Epigenetically Regulated Genes in NSCLC. <i>Molecular Cancer Research</i> , 2017, 15, 1354-1365. | 3.4 | 25 |
| 96 | Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. <i>Nucleic Acids Research</i> , 2017, 45, D737-D743. | 13.8 | 120 |
| 97 | Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution. <i>Diabetes</i> , 2017, 66, 218-230. | 0.9 | 28 |
| 98 | A Transcriptional Switch Point During Hematopoietic Stem and Progenitor Cell Ontogeny. <i>Stem Cells and Development</i> , 2017, 26, 314-327. | 2.1 | 4 |
| 99 | Transcription start site profiling of 15 anatomical regions of the <i>Macaca mulatta</i> central nervous system. <i>Scientific Data</i> , 2017, 4, 170163. | 5.3 | 4 |
| 100 | The Human Cell Atlas. <i>ELife</i> , 2017, 6, . | 5.8 | 1,677 |
| 101 | Systematic analysis of transcription start sites in avian development. <i>PLoS Biology</i> , 2017, 15, e2002887. | 5.3 | 72 |
| 102 | Analysis of the human monocyte-derived macrophage transcriptome and response to lipopolysaccharide provides new insights into genetic aetiology of inflammatory bowel disease. <i>PLoS Genetics</i> , 2017, 13, e1006641. | 3.3 | 165 |
| 103 | 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, . | 3.1 | 25 |
| 104 | Changes in sleep duration and risk of metabolic syndrome: the Kailuan prospective study. <i>Scientific Reports</i> , 2016, 6, 36861. | 3.4 | 34 |
| 105 | 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. | 3.4 | 18 |
| 106 | DeepCAGE transcriptomics identify HOXD10 as a transcription factor regulating lymphatic endothelial responses to VEGF-C. <i>Journal of Cell Science</i> , 2016, 129, 2573-2585. | 2.0 | 15 |
| 107 | Transcriptional, post-transcriptional and chromatin-associated regulation of pri-miRNAs, pre-miRNAs and moRNAs. <i>Nucleic Acids Research</i> , 2016, 44, 3070-3081. | 13.8 | 39 |
| 108 | Recombination in <i>Streptococcus pneumoniae</i> Lineages Increase with Carriage Duration and Size of the Polysaccharide Capsule. <i>MBio</i> , 2016, 7, . | 4.2 | 51 |

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|-----|--|------|-----------|
| 109 | Acute Simian Varicella Virus Infection Causes Robust and Sustained Changes in Gene Expression in the Sensory Ganglia. <i>Journal of Virology</i> , 2016, 90, 10823-10843. | 3.4 | 20 |
| 110 | Isoforms of the Erythropoietin receptor in dopaminergic neurons of the <i>Substantia Nigra</i> . <i>Journal of Neurochemistry</i> , 2016, 139, 596-609. | 4.0 | 11 |
| 111 | YY1 binding association with sex-biased transcription revealed through X-linked transcript levels and allelic binding analyses. <i>Scientific Reports</i> , 2016, 6, 37324. | 3.4 | 34 |
| 112 | Characterization of piRNAs across postnatal development in mouse brain. <i>Scientific Reports</i> , 2016, 6, 25039. | 3.4 | 35 |
| 113 | Genome sequence and analysis of the Japanese morning glory <i>Ipomoea nil</i> . <i>Nature Communications</i> , 2016, 7, 13295. | 12.8 | 140 |
| 114 | Identification of antisense long noncoding RNAs that function as SINEUPs in human cells. <i>Scientific Reports</i> , 2016, 6, 33605. | 3.4 | 62 |
| 115 | FANTOM5 transcriptome catalog of cellular states based on Semantic MediaWiki. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw105. | 3.1 | 64 |
| 116 | Transcriptome Analysis of Recurrently Deregulated Genes across Multiple Cancers Identifies New Pan-Cancer Biomarkers. <i>Cancer Research</i> , 2016, 76, 216-226. | 0.9 | 82 |
| 117 | Functional annotation of the vlinc class of non-coding RNAs using systems biology approach. <i>Nucleic Acids Research</i> , 2016, 44, 3233-3252. | 13.8 | 35 |
| 118 | Deficiency of multidrug resistance 2 contributes to cell transformation through oxidative stress. <i>Carcinogenesis</i> , 2016, 37, 39-48. | 2.7 | 15 |
| 119 | Discovery and functional analysis of lncRNAs: Methodologies to investigate an uncharacterized transcriptome. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 3-15. | 1.9 | 182 |
| 120 | Epi-drivers and cancer-testis genes. <i>Translational Cancer Research</i> , 2016, 5, 334-336. | 1.1 | 1 |
| 121 | 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. | 3.4 | 30 |
| 122 | Hierarchical folding and reorganization of chromosomes are linked to transcriptional changes in cellular differentiation. <i>Molecular Systems Biology</i> , 2015, 11, 852. | 7.2 | 316 |
| 123 | DeepCAGE Transcriptomics Reveal an Important Role of the Transcription Factor MAFB in the Lymphatic Endothelium. <i>Cell Reports</i> , 2015, 13, 1493-1504. | 6.2 | 47 |
| 124 | Remodeling of retrotransposon elements during epigenetic induction of adult visual cortical plasticity by HDAC inhibitors. <i>Epigenetics and Chromatin</i> , 2015, 8, 55. | 3.8 | 32 |
| 125 | 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. | 2.3 | 13 |
| 126 | Expression analysis of the long non-coding RNA antisense to Uchl1 (AS Uchl1) during dopaminergic cells' differentiation in vitro and in neurochemical models of Parkinson's disease. <i>Frontiers in Cellular Neuroscience</i> , 2015, 9, 114. | 3.8 | 116 |

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|-----|---|------|-----------|
| 127 | SINEUPs are modular antisense long non-coding RNAs that increase synthesis of target proteins in cells. <i>Frontiers in Cellular Neuroscience</i> , 2015, 9, 174. | 3.8 | 81 |
| 128 | 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. | 2.5 | 9 |
| 129 | The Constrained Maximal Expression Level Owing to Haploidy Shapes Gene Content on the Mammalian X Chromosome. <i>PLoS Biology</i> , 2015, 13, e1002315. | 5.3 | 33 |
| 130 | Application of Gene Expression Trajectories Initiated from ErbB Receptor Activation Highlights the Dynamics of Divergent Promoter Usage. <i>PLoS ONE</i> , 2015, 10, e0144176. | 2.5 | 1 |
| 131 | Engineering mammalian cell factories with SINEUP noncoding RNAs to improve translation of secreted proteins. <i>Gene</i> , 2015, 569, 287-293. | 2.3 | 35 |
| 132 | Biased Allelic Expression in Human Primary Fibroblast Single Cells. <i>American Journal of Human Genetics</i> , 2015, 96, 70-80. | 6.0 | 120 |
| 133 | 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. | 2.7 | 14 |
| 134 | Characterization of Novel Transcripts of Human Papillomavirus Type 16 Using Cap Analysis Gene Expression Technology. <i>Journal of Virology</i> , 2015, 89, 2448-2452. | 3.4 | 6 |
| 135 | Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015, 16, 22. | 8.5 | 713 |
| 136 | Krimper Enforces an Antisense Bias on piRNA Pools by Binding AGO3 in the Drosophila Germline. <i>Molecular Cell</i> , 2015, 59, 553-563. | 9.4 | 65 |
| 137 | The frequent evolutionary birth and death of functional promoters in mouse and human. <i>Genome Research</i> , 2015, 25, 1546-1557. | 5.5 | 56 |
| 138 | Telomerase Reverse Transcriptase Regulates microRNAs. <i>International Journal of Molecular Sciences</i> , 2015, 16, 1192-1208. | 4.1 | 23 |
| 139 | A draft network of ligand-receptor-mediated multicellular signalling in human. <i>Nature Communications</i> , 2015, 6, 7866. | 12.8 | 701 |
| 140 | Intrinsically disordered proteins drive membrane curvature. <i>Nature Communications</i> , 2015, 6, 7875. | 12.8 | 232 |
| 141 | Transcriptional Dynamics Reveal Critical Roles for Non-coding RNAs in the Immediate-Early Response. <i>PLoS Computational Biology</i> , 2015, 11, e1004217. | 3.0 | 23 |
| 142 | CAGEr: precise TSS data retrieval and high-resolution promoterome mining for integrative analyses. <i>Nucleic Acids Research</i> , 2015, 43, e51-e51. | 13.8 | 206 |
| 143 | Technical Advance: Transcription factor, promoter, and enhancer utilization in human myeloid cells. <i>Journal of Leukocyte Biology</i> , 2015, 97, 985-995. | 3.2 | 23 |
| 144 | Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics. <i>Nucleic Acids Research</i> , 2015, 43, 6969-6982. | 13.8 | 58 |

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|-----|--|------|-----------|
| 145 | STAP cells are derived from ES cells. <i>Nature</i> , 2015, 525, E4-E5. | 35.3 | 8 |
| 146 | SINEUPs: A new class of natural and synthetic antisense long non-coding RNAs that activate translation. <i>RNA Biology</i> , 2015, 12, 771-779. | 3.3 | 85 |
| 147 | Complementing tissue characterization by integrating transcriptome profiling from the Human Protein Atlas and from the FANTOM5 consortium. <i>Nucleic Acids Research</i> , 2015, 43, 6787-6798. | 13.8 | 106 |
| 148 | Expression Specificity of Disease-Associated lncRNAs: Toward Personalized Medicine. <i>Current Topics in Microbiology and Immunology</i> , 2015, 394, 237-258. | 0.0 | 34 |
| 149 | Complexity of Mammalian Transcriptome Analyzed by RNA Deep Sequencing. , 2015, , 3-22. | | 2 |
| 150 | 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. | 5.5 | 52 |
| 151 | Paradigm shifts in genomics through the FANTOM projects. <i>Mammalian Genome</i> , 2015, 26, 391-402. | 2.2 | 98 |
| 152 | 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. | 3.8 | 11 |
| 153 | Differential roles of epigenetic changes and Foxp3 expression in regulatory T cell-specific transcriptional regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5289-5294. | 7.4 | 114 |
| 154 | Digital expression profiling of the compartmentalized transcriptome of Purkinje neurons. <i>Genome Research</i> , 2014, 24, 1396-1410. | 5.5 | 52 |
| 155 | PAPD5-mediated 3' adenylation and subsequent degradation of miR-21 is disrupted in proliferative disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11467-11472. | 7.4 | 133 |
| 156 | Analytical Modeling and Analysis of a Constrained Layer Damped Plate to Examine the Impact of the Transverse Compressional Damping Component. <i>Mechanics of Advanced Materials and Structures</i> , 2014, 21, 669-679. | 2.5 | 5 |
| 157 | Recombinant hyaluronidase. <i>Clinical and Experimental Ophthalmology</i> , 2014, 42, 298-298. | 2.8 | 4 |
| 158 | Mesencephalic dopaminergic neurons express a repertoire of olfactory receptors and respond to odorant-like molecules. <i>BMC Genomics</i> , 2014, 15, 729. | 2.9 | 50 |
| 159 | Diversity and dynamics of the <i>Drosophila</i> transcriptome. <i>Nature</i> , 2014, 512, 393-399. | 35.3 | 682 |
| 160 | Two independent transcription initiation codes overlap on vertebrate core promoters. <i>Nature</i> , 2014, 507, 381-385. | 35.3 | 183 |
| 161 | An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014, 507, 455-461. | 35.3 | 2,342 |
| 162 | The enhancer and promoter landscape of human regulatory and conventional T-cell subpopulations. <i>Blood</i> , 2014, 123, e68-e78. | 1.4 | 78 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 163 | 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. | 2.2 | 16 |
| 164 | Analysis of the DNA methylome and transcriptome in granulopoiesis reveals timed changes and dynamic enhancer methylation. <i>Blood</i> , 2014, 123, e79-e89. | 1.4 | 74 |
| 165 | Comparison of CAGE and RNA-seq transcriptome profiling using clonally amplified and single-molecule next-generation sequencing. <i>Genome Research</i> , 2014, 24, 708-717. | 5.5 | 104 |
| 166 | Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. <i>Nature Genetics</i> , 2014, 46, 558-566. | 20.1 | 275 |
| 167 | Neuroendocrine tumours: the role of imaging for diagnosis and therapy. <i>Nature Reviews Endocrinology</i> , 2014, 10, 102-114. | 9.4 | 125 |
| 168 | Transcription and enhancer profiling in human monocyte subsets. <i>Blood</i> , 2014, 123, e90-e99. | 1.4 | 166 |
| 169 | Mice in the ENCODE spotlight. <i>Nature</i> , 2014, 515, 346-347. | 35.3 | 11 |
| 170 | Specific Mesothelial Signature Marks the Heterogeneity of Mesenchymal Stem Cells From High-Grade Serous Ovarian Cancer. <i>Stem Cells</i> , 2014, 32, 2998-3011. | 3.5 | 16 |
| 171 | Widespread genome transcription: New possibilities for RNA therapies. <i>Biochemical and Biophysical Research Communications</i> , 2014, 452, 294-301. | 2.2 | 38 |
| 172 | The Exploding Genetic Code. <i>ChemBioChem</i> , 2014, 15, 1691-1694. | 2.7 | 45 |
| 173 | Sulfenome mining in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11545-11550. | 7.4 | 168 |
| 174 | Comparative validation of the <i>D. melanogaster</i> modENCODE transcriptome annotation. <i>Genome Research</i> , 2014, 24, 1209-1223. | 5.5 | 160 |
| 175 | The devil in the details of RNA-seq. <i>Nature Biotechnology</i> , 2014, 32, 882-884. | 20.4 | 35 |
| 176 | MOIRAI: a compact workflow system for CAGE analysis. <i>BMC Bioinformatics</i> , 2014, 15, 144. | 2.6 | 67 |
| 177 | Chromatin states reveal functional associations for globally defined transcription start sites in four human cell lines. <i>BMC Genomics</i> , 2014, 15, 120. | 2.9 | 19 |
| 178 | RECLU: a pipeline to discover reproducible transcriptional start sites and their alternative regulation using capped analysis of gene expression (CAGE). <i>BMC Genomics</i> , 2014, 15, 269. | 2.9 | 62 |
| 179 | CAGE-defined promoter regions of the genes implicated in Rett Syndrome. <i>BMC Genomics</i> , 2014, 15, 1177. | 2.9 | 10 |
| 180 | Redefinition of the human mast cell transcriptome by deep-CAGE sequencing. <i>Blood</i> , 2014, 123, e58-e67. | 1.4 | 180 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 181 | Detecting Expressed Genes Using CAGE. <i>Methods in Molecular Biology</i> , 2014, 1164, 67-85. | 0.7 | 177 |
| 182 | Thoracic Rat Spinal Cord Contusion Injury Induces Remote Spinal Gliogenesis but Not Neurogenesis or Gliogenesis in the Brain. <i>PLoS ONE</i> , 2014, 9, e102896. | 2.5 | 17 |
| 183 | Dynamic regulation of the transcription initiation landscape at single nucleotide resolution during vertebrate embryogenesis. <i>Genome Research</i> , 2013, 23, 1938-1950. | 5.5 | 122 |
| 184 | Comparison of RNA- or LNA-hybrid oligonucleotides in template-switching reactions for high-speed sequencing library preparation. <i>BMC Genomics</i> , 2013, 14, 665. | 2.9 | 23 |
| 185 | Population transcriptomics with single-cell resolution: A new field made possible by microfluidics. <i>BioEssays</i> , 2013, 35, 131-140. | 2.5 | 20 |
| 186 | Chromatin signatures and retrotransposon profiling in mouse embryos reveal regulation of LINE-1 by RNA. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 332-338. | 7.8 | 203 |
| 187 | High-fidelity promoter profiling reveals widespread alternative promoter usage and transposon-driven developmental gene expression. <i>Genome Research</i> , 2013, 23, 169-180. | 5.5 | 183 |
| 188 | Regional differences in gene expression and promoter usage in aged human brains. <i>Neurobiology of Aging</i> , 2013, 34, 1825-1836. | 3.1 | 31 |
| 189 | Endogenous Retrotransposition Activates Oncogenic Pathways in Hepatocellular Carcinoma. <i>Cell</i> , 2013, 153, 101-111. | 27.3 | 359 |
| 190 | Noncoding RNA: The Major Output of Gene Expression. , 2013, , 181-213. | | 0 |
| 191 | Suppression of artifacts and barcode bias in high-throughput transcriptome analyses utilizing template switching. <i>Nucleic Acids Research</i> , 2013, 41, e44-e44. | 13.8 | 67 |
| 192 | Temporal dynamics and transcriptional control using single-cell gene expression analysis. <i>Genome Biology</i> , 2013, 14, R118. | 9.1 | 43 |
| 193 | A comprehensive promoter landscape identifies a novel promoter for CD133 in restricted tissues, cancers, and stem cells. <i>Frontiers in Genetics</i> , 2013, 4, 209. | 2.3 | 12 |
| 194 | Promoter architecture of mouse olfactory receptor genes. <i>Genome Research</i> , 2012, 22, 486-497. | 5.5 | 54 |
| 195 | NMDA Receptor Regulation Prevents Regression of Visual Cortical Function in the Absence of Mecp2. <i>Neuron</i> , 2012, 76, 1078-1090. | 7.9 | 169 |
| 196 | The GENCODE v7 catalog of human long noncoding RNAs: Analysis of their gene structure, evolution, and expression. <i>Genome Research</i> , 2012, 22, 1775-1789. | 5.5 | 4,551 |
| 197 | Long non-coding antisense RNA controls Uchl1 translation through an embedded SINEB2 repeat. <i>Nature</i> , 2012, 491, 454-457. | 35.3 | 908 |
| 198 | Metazoan promoters: emerging characteristics and insights into transcriptional regulation. <i>Nature Reviews Genetics</i> , 2012, 13, 233-245. | 16.4 | 462 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 199 | CAGE (Cap Analysis of Gene Expression): A Protocol for the Detection of Promoter and Transcriptional Networks. <i>Methods in Molecular Biology</i> , 2012, 786, 181-200. | 0.7 | 98 |
| 200 | Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012, 22, 1658-1667. | 5.5 | 167 |
| 201 | Landscape of transcription in human cells. <i>Nature</i> , 2012, 489, 101-108. | 35.3 | 4,661 |
| 202 | Structure by Sequencing: Discovery of Hidden Messages in the Noncoding RNA Fraction. <i>Molecular Cell</i> , 2012, 48, 153-155. | 9.4 | 4 |
| 203 | Automated Workflow for Preparation of cDNA for Cap Analysis of Gene Expression on a Single Molecule Sequencer. <i>PLoS ONE</i> , 2012, 7, e30809. | 2.5 | 24 |
| 204 | piRNAs Warrant Investigation in Rett Syndrome: An Omics Perspective. <i>Disease Markers</i> , 2012, 33, 261-275. | 1.3 | 23 |
| 205 | Trehalose-Enhanced Isolation of Neuronal Sub-Types from Adult Mouse Brain. <i>BioTechniques</i> , 2012, 52, 381-385. | 1.7 | 90 |
| 206 | Site-specific DICER and DROSHA RNA products control the DNA-damage response. <i>Nature</i> , 2012, 488, 231-235. | 35.3 | 471 |
| 207 | Conservation and divergence in Toll-like receptor 4-regulated gene expression in primary human versus mouse macrophages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E944-53. | 7.4 | 336 |
| 208 | Activation of Wnt Signaling by Chemically Induced Dimerization of LRP5 Disrupts Cellular Homeostasis. <i>PLoS ONE</i> , 2012, 7, e30814. | 2.5 | 15 |
| 209 | FXVD6, a Na,K-ATPase Regulator, Is Expressed in Type II Taste Cells. <i>Bioscience, Biotechnology and Biochemistry</i> , 2011, 75, 1061-1066. | 1.3 | 11 |
| 210 | Unamplified cap analysis of gene expression on a single-molecule sequencer. <i>Genome Research</i> , 2011, 21, 1150-1159. | 5.5 | 176 |
| 211 | Chromatin-associated RNA interference components contribute to transcriptional regulation in <i>Drosophila</i> . <i>Nature</i> , 2011, 480, 391-395. | 35.3 | 206 |
| 212 | Somatic retrotransposition alters the genetic landscape of the human brain. <i>Nature</i> , 2011, 479, 534-537. | 35.3 | 637 |
| 213 | Direct generation of functional dopaminergic neurons from mouse and human fibroblasts. <i>Nature</i> , 2011, 476, 224-227. | 35.3 | 953 |
| 214 | Profiling transcription initiation in human aged brain using deep-CAGE. <i>BMC Bioinformatics</i> , 2011, 12, . | 2.6 | 3 |
| 215 | Whole transcriptome analysis: what are we still missing?. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2011, 3, 527-543. | 6.8 | 22 |
| 216 | Long non-coding RNA modifies chromatin. <i>BioEssays</i> , 2011, 33, 830-839. | 2.5 | 183 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 217 | NanoCAGE: A High-Resolution Technique to Discover and Interrogate Cell Transcriptomes. Cold Spring Harbor Protocols, 2011, 2011, pdb.prot5559-pdb.prot5559. | 0.3 | 61 |
| 218 | Update of the FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. Nucleic Acids Research, 2011, 39, D856-D860. | 13.8 | 49 |
| 219 | The Reality of Pervasive Transcription. PLoS Biology, 2011, 9, e1000625. | 5.3 | 389 |
| 220 | Genome-wide analysis of promoter architecture in <i>Drosophila melanogaster</i> . Genome Research, 2011, 21, 182-192. | 5.5 | 220 |
| 221 | DeepCAGE: Genome-Wide Mapping of Transcription Start Sites. , 2011, , 23-46. | | 1 |
| 222 | Definition of Promotome-Transcriptome Architecture Using CAGEscan. , 2011, , 47-61. | | 0 |
| 223 | The Short Non-Coding Transcriptome of the Protozoan Parasite <i>Trypanosoma cruzi</i> . PLoS Neglected Tropical Diseases, 2011, 5, e1283. | 2.4 | 35 |
| 224 | Nuclear Pore Complex Protein Mediated Nuclear Localization of Dicer Protein in Human Cells. PLoS ONE, 2011, 6, e23385. | 2.5 | 40 |
| 225 | Core promoter structure and genomic context reflect histone 3 lysine 9 acetylation patterns. BMC Genomics, 2010, 11, 257. | 2.9 | 34 |
| 226 | Linking promoters to functional transcripts in small samples with nanoCAGE and CAGEscan. Nature Methods, 2010, 7, 528-534. | 19.2 | 155 |
| 227 | Reduction of Non-Insert Sequence Reads by Dimer Eliminator LNA Oligonucleotide for Small RNA Deep Sequencing. BioTechniques, 2010, 49, 751-755. | 1.7 | 32 |
| 228 | High Sensitivity TSS Prediction: Estimates of Locations Where TSS Cannot Occur. PLoS ONE, 2010, 5, e13934. | 2.5 | 8 |
| 229 | RNA Dust: Where are the Genes?. DNA Research, 2010, 17, 209-209. | 3.4 | 0 |
| 230 | Building promoter aware transcriptional regulatory networks using siRNA perturbation and deepCAGE. Nucleic Acids Research, 2010, 38, 8141-8148. | 13.8 | 17 |
| 231 | RNA Dust: Where are the Genes?. DNA Research, 2010, 17, 51-59. | 3.4 | 58 |
| 232 | The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. Genome Research, 2010, 20, 791-803. | 5.5 | 84 |
| 233 | Cross-mapping and the identification of editing sites in mature microRNAs in high-throughput sequencing libraries. Genome Research, 2010, 20, 257-264. | 5.5 | 127 |
| 234 | Molecular mechanisms of pituitary organogenesis: In search of novel regulatory genes. Molecular and Cellular Endocrinology, 2010, 323, 4-19. | 3.2 | 142 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 235 | An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 140, 744-752. | 27.3 | 671 |
| 236 | An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 141, 369. | 27.3 | 4 |
| 237 | From identification to validation to gene count. <i>Genome Biology</i> , 2010, 11, . | 9.1 | 1 |
| 238 | Beyond the FANTOM4. <i>Genome Biology</i> , 2010, 11, O11. | 9.1 | 0 |
| 239 | Genome-wide detection and analysis of hippocampus core promoters using DeepCAGE. <i>Genome Research</i> , 2009, 19, 255-265. | 5.5 | 129 |
| 240 | High-Throughput Verification of Transcriptional Starting Sites by Deep-Race. <i>BioTechniques</i> , 2009, 46, 130-132. | 1.7 | 33 |
| 241 | Tunable fractionation of nucleic acids. <i>BioTechniques</i> , 2009, 47, 1041-1043. | 1.7 | 4 |
| 242 | Whole genome transcriptome analysis. <i>RNA Biology</i> , 2009, 6, 107-112. | 3.3 | 44 |
| 243 | Annotating non-coding transcription using functional genomics strategies. <i>Briefings in Functional Genomics</i> , 2009, 8, 437-443. | 2.9 | 5 |
| 244 | The long and short of RNAs. <i>Nature</i> , 2009, 457, 974-975. | 35.3 | 47 |
| 245 | Tiny RNAs associated with transcription start sites in animals. <i>Nature Genetics</i> , 2009, 41, 572-578. | 20.1 | 328 |
| 246 | The regulated retrotransposon transcriptome of mammalian cells. <i>Nature Genetics</i> , 2009, 41, 563-571. | 20.1 | 746 |
| 247 | The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562. | 20.1 | 408 |
| 248 | Is sequencing enlightenment ending the dark age of the transcriptome?. <i>Nature Methods</i> , 2009, 6, 711-713. | 19.2 | 28 |
| 249 | Unexpected expression of $\hat{1}\pm$ - and $\hat{1}2$ -globin in mesencephalic dopaminergic neurons and glial cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15454-15459. | 7.4 | 245 |
| 250 | Discovery of transcriptional regulators and signaling pathways in the developing pituitary gland by bioinformatic and genomic approaches. <i>Genomics</i> , 2009, 93, 449-460. | 2.9 | 61 |
| 251 | Small RNAs derived from snoRNAs. <i>Rna</i> , 2009, 15, 1233-1240. | 3.5 | 389 |
| 252 | Generation of Full-Length cDNA Libraries: Focus on Plants. <i>Methods in Molecular Biology</i> , 2009, 533, 49-68. | 0.7 | 2 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 253 | Methods for analyzing deep sequencing expression data: constructing the human and mouse promoterome with deepCAGE data. <i>Genome Biology</i> , 2009, 10, R79. | 9.1 | 132 |
| 254 | FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. <i>Genome Biology</i> , 2009, 10, R39. | 9.1 | 67 |
| 255 | The FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. <i>Genome Biology</i> , 2009, 10, R40. | 9.1 | 73 |
| 256 | A code for transcription initiation in mammalian genomes. <i>Genome Research</i> , 2008, 18, 1-12. | 5.5 | 246 |
| 257 | Non-coding RNA transcription: turning on neighbours. <i>Nature Cell Biology</i> , 2008, 10, 1023-1024. | 9.9 | 32 |
| 258 | Rapidly evolving human promoter regions. <i>Nature Genetics</i> , 2008, 40, 1262-1263. | 20.1 | 18 |
| 259 | Hunting hidden transcripts. <i>Nature Methods</i> , 2008, 5, 587-589. | 19.2 | 8 |
| 260 | Hidden layers of human small RNAs. <i>BMC Genomics</i> , 2008, 9, 157. | 2.9 | 258 |
| 261 | Multifaceted mammalian transcriptome. <i>Current Opinion in Cell Biology</i> , 2008, 20, 274-280. | 5.4 | 77 |
| 262 | From CAGE to DeepCAGE: High-Throughput Transcription Start Site and Promoter Identification for Gene Network Analysis. , 2008, , 55-75. | | 0 |
| 263 | A rescue strategy for multimapping short sequence tags refines surveys of transcriptional activity by CAGE. <i>Genomics</i> , 2008, 91, 281-288. | 2.9 | 93 |
| 264 | Placental expression profiling in preeclampsia: local overproduction of hemoglobin may drive pathological changes. <i>Fertility and Sterility</i> , 2008, 90, 1834-1843. | 0.9 | 74 |
| 265 | Glutamate 14 is a candidate mediator of sweet/umami signal transduction in the posterior region of the mouse tongue. <i>Biochemical and Biophysical Research Communications</i> , 2008, 376, 504-508. | 2.2 | 39 |
| 266 | Genome-wide analysis of cancer/testis gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20422-20427. | 7.4 | 301 |
| 267 | A Resource for Transcriptomic Analysis in the Mouse Brain. <i>PLoS ONE</i> , 2008, 3, e3012. | 2.5 | 12 |
| 268 | Development of a DNA Barcode Tagging Method for Monitoring Dynamic Changes in Gene Expression by using an Ultra High-Throughput Sequencer. <i>BioTechniques</i> , 2008, 45, 95-97. | 1.7 | 30 |
| 269 | Transcriptomics resources for functional genomics. <i>Briefings in Functional Genomics & Proteomics</i> , 2007, 6, 171-179. | 3.5 | 0 |
| 270 | Constructing the landscape of the mammalian transcriptome. <i>Journal of Experimental Biology</i> , 2007, 210, 1497-1506. | 1.7 | 40 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 271 | Genomic organization of transcriptomes in mammals: Coregulation and cofunctionality. <i>Genomics</i> , 2007, 89, 580-587. | 2.9 | 56 |
| 272 | Noncoding RNA transcription beyond annotated genes. <i>Current Opinion in Genetics and Development</i> , 2007, 17, 139-144. | 3.3 | 125 |
| 273 | Diversity of Ca ²⁺ -activated K ⁺ channel transcripts in inner ear hair cells. <i>Gene</i> , 2007, 386, 11-23. | 2.3 | 28 |
| 274 | Splicing bypasses 3' end formation signals to allow complex gene architectures. <i>Gene</i> , 2007, 403, 188-193. | 2.3 | 8 |
| 275 | Simplified ontologies allowing comparison of developmental mammalian gene expression. <i>Genome Biology</i> , 2007, 8, R229. | 9.1 | 12 |
| 276 | CAGE-TSSchip: promoter-based expression profiling using the 5'-leading label of capped transcripts. <i>Genome Biology</i> , 2007, 8, R42. | 9.1 | 3 |
| 277 | Gene Organization in Rice Revealed by Full-Length cDNA Mapping and Gene Expression Analysis through Microarray. <i>PLoS ONE</i> , 2007, 2, e1235. | 2.5 | 52 |
| 278 | Mammalian RNA polymerase II core promoters: insights from genome-wide studies. <i>Nature Reviews Genetics</i> , 2007, 8, 424-436. | 16.4 | 443 |
| 279 | Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816. | 35.3 | 4,757 |
| 280 | Informatic and genomic analysis of melanocyte cDNA libraries as a resource for the study of melanocyte development and function. <i>Pigment Cell & Melanoma Research</i> , 2007, 20, 201-209. | 3.3 | 3 |
| 281 | Large-scale clustering of CAGE tag expression data. <i>BMC Bioinformatics</i> , 2007, 8, 161. | 2.6 | 8 |
| 282 | Dynamic usage of transcription start sites within core promoters. <i>Genome Biology</i> , 2006, 7, R118. | 9.1 | 75 |
| 283 | Transcriptional and structural impact of TATA-initiation site spacing in mammalian core promoters. <i>Genome Biology</i> , 2006, 7, R78. | 9.1 | 104 |
| 284 | Alternate transcription of the Toll-like receptor signaling cascade. <i>Genome Biology</i> , 2006, 7, R10. | 9.1 | 67 |
| 285 | Genome-wide review of transcriptional complexity in mouse protein kinases and phosphatases. <i>Genome Biology</i> , 2006, 7, R5. | 9.1 | 48 |
| 286 | CAGE Basic/Analysis Databases: the CAGE resource for comprehensive promoter analysis. <i>Nucleic Acids Research</i> , 2006, 34, D632-D636. | 13.8 | 80 |
| 287 | Transcriptional network dynamics in macrophage activation. <i>Genomics</i> , 2006, 88, 133-142. | 2.9 | 125 |
| 288 | Constructing ORFeome resources with removable termination codons. <i>BioTechniques</i> , 2006, 41, 44-50. | 1.7 | 31 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 289 | Genome-wide analysis of mammalian promoter architecture and evolution. <i>Nature Genetics</i> , 2006, 38, 626-635. | 20.1 | 1,227 |
| 290 | The complexity of the mammalian transcriptome. <i>Journal of Physiology</i> , 2006, 575, 321-332. | 2.8 | 92 |
| 291 | Tagging mammalian transcription complexity. <i>Trends in Genetics</i> , 2006, 22, 501-510. | 6.7 | 85 |
| 292 | Computational promoter analysis of mouse, rat and human antimicrobial peptide-coding genes. <i>BMC Bioinformatics</i> , 2006, 7, S8. | 2.6 | 26 |
| 293 | LOCATE: a mouse protein subcellular localization database. <i>Nucleic Acids Research</i> , 2006, 34, D213-D217. | 13.8 | 72 |
| 294 | Evolutionary turnover of mammalian transcription start sites. <i>Genome Research</i> , 2006, 16, 713-722. | 5.5 | 70 |
| 295 | Mice and Men: Their Promoter Properties. <i>PLoS Genetics</i> , 2006, 2, e54. | 3.3 | 95 |
| 296 | Clusters of Internally Primed Transcripts Reveal Novel Long Noncoding RNAs. <i>PLoS Genetics</i> , 2006, 2, e37. | 3.3 | 149 |
| 297 | Pseudo-“Messenger RNA: Phantoms of the Transcriptome. <i>PLoS Genetics</i> , 2006, 2, e23. | 3.3 | 58 |
| 298 | The Abundance of Short Proteins in the Mammalian Proteome. <i>PLoS Genetics</i> , 2006, 2, e52. | 3.3 | 194 |
| 299 | Genome Network and FANTOM3: Assessing the Complexity of the Transcriptome. <i>PLoS Genetics</i> , 2006, 2, e63. | 3.3 | 26 |
| 300 | Complex Loci in Human and Mouse Genomes. <i>PLoS Genetics</i> , 2006, 2, e47. | 3.3 | 293 |
| 301 | Heterotachy in Mammalian Promoter Evolution. <i>PLoS Genetics</i> , 2006, 2, e30. | 3.3 | 103 |
| 302 | A Method for Similarity Search of Genomic Positional Expression Using CAGE. <i>PLoS Genetics</i> , 2006, 2, e44. | 3.3 | 4 |
| 303 | Differential Use of Signal Peptides and Membrane Domains Is a Common Occurrence in the Protein Output of Transcriptional Units. <i>PLoS Genetics</i> , 2006, 2, e46. | 3.3 | 37 |
| 304 | A Simple Physical Model Predicts Small Exon Length Variations. <i>PLoS Genetics</i> , 2006, 2, e45. | 3.3 | 69 |
| 305 | Transcript Annotation in FANTOM3: Mouse Gene Catalog Based on Physical cDNAs. <i>PLoS Genetics</i> , 2006, 2, e62. | 3.3 | 166 |
| 306 | Discrimination of Non-Protein-Coding Transcripts from Protein-Coding mRNA. <i>RNA Biology</i> , 2006, 3, 40-48. | 3.3 | 120 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 307 | A molecular neuroethological approach for identifying and characterizing a cascade of behaviorally regulated genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15212-15217. | 7.4 | 178 |
| 308 | Antisense Transcription in the Mammalian Transcriptome. <i>Science</i> , 2005, 309, 1564-1566. | 19.6 | 1,574 |
| 309 | Tag-based approaches for transcriptome research and genome annotation. <i>Nature Methods</i> , 2005, 2, 495-502. | 19.2 | 165 |
| 310 | Differential Expression of Genes within the Cochlea as Defined by a Custom Mouse Inner Ear Microarray. <i>JARO - Journal of the Association for Research in Otolaryngology</i> , 2005, 6, 75-89. | 1.9 | 38 |
| 311 | Cytoskeletal Rearrangements in Synovial Fibroblasts as a Novel Pathophysiological Determinant of Modeled Rheumatoid Arthritis. <i>PLoS Genetics</i> , 2005, 1, e48. | 3.3 | 49 |
| 312 | Computational analysis suggests that alternative first exons are involved in tissue-specific transcription in rice (<i>Oryza sativa</i>). <i>Bioinformatics</i> , 2005, 21, 1758-1763. | 4.2 | 26 |
| 313 | Transcriptome analysis of the aphid bacteriocyte, the symbiotic host cell that harbors an endocellular mutualistic bacterium, <i>Buchnera</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5477-5482. | 7.4 | 220 |
| 314 | The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563. | 19.6 | 3,268 |
| 315 | Protein-protein interactions of the hyperthermophilic archaeon <i>Pyrococcus horikoshii</i> OT3. <i>Genome Biology</i> , 2005, 6, R98. | 9.1 | 12 |
| 316 | Transcriptional profiling of genes responsive to abscisic acid and gibberellin in rice: phenotyping and comparative analysis between rice and <i>Arabidopsis</i> . <i>Physiological Genomics</i> , 2004, 17, 87-100. | 2.2 | 78 |
| 317 | Solution Structure of the SEA Domain from the Murine Homologue of Ovarian Cancer Antigen CA125 (MUC16). <i>Journal of Biological Chemistry</i> , 2004, 279, 13174-13182. | 3.4 | 75 |
| 318 | 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, 5069-5074. | 7.4 | 70 |
| 319 | Comparative Analysis of Plant and Animal Calcium Signal Transduction Element Using Plant Full-Length cDNA Data. <i>Molecular Biology and Evolution</i> , 2004, 21, 1855-1870. | 9.0 | 69 |
| 320 | FREP: a database of functional repeats in mouse cDNAs. <i>Nucleic Acids Research</i> , 2004, 32, 471D-475. | 13.8 | 6 |
| 321 | The Status, Quality, and Expansion of the NIH Full-Length cDNA Project: The Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2004, 14, 2121-2127. | 5.5 | 491 |
| 322 | Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162. | 5.3 | 290 |
| 323 | CTAB-Urea Method Purifies RNA from Melanin for cDNA Microarray Analysis. <i>Pigment Cell & Melanoma Research</i> , 2004, 17, 312-315. | 3.3 | 27 |
| 324 | Libraries enriched for alternatively spliced exons reveal splicing patterns in melanocytes and melanomas. <i>Nature Methods</i> , 2004, 1, 233-239. | 19.2 | 47 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 325 | Solution structure of the RWD domain of the mouse GCN2 protein. <i>Protein Science</i> , 2004, 13, 2089-2100. | 7.7 | 68 |
| 326 | Full-length cDNAs from chicken bursal lymphocytes to facilitate gene function analysis. <i>Genome Biology</i> , 2004, 6, R6. | 9.1 | 105 |
| 327 | Identification of unique transcripts from a mouse full-length, subtracted inner ear cDNA library. <i>Genomics</i> , 2004, 83, 1012-1023. | 2.9 | 23 |
| 328 | Solution structure of a Bola-like protein from <i>Mus musculus</i> . <i>Protein Science</i> , 2004, 13, 545-548. | 7.7 | 49 |
| 329 | Construction of a full-length cDNA library from young spikelets of hexaploid wheat and its characterization by large-scale sequencing of expressed sequence tags. <i>Genes and Genetic Systems</i> , 2004, 79, 227-232. | 0.6 | 48 |
| 330 | Genetic control of the innate immune response. <i>BMC Immunology</i> , 2003, 4, 5. | 2.2 | 120 |
| 331 | Comprehensive Analysis of NAC Family Genes in <i>Oryza sativa</i> and <i>Arabidopsis thaliana</i> . <i>DNA Research</i> , 2003, 10, 239-247. | 3.4 | 950 |
| 332 | Cap analysis gene expression for high-throughput analysis of transcriptional starting point and identification of promoter usage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15776-15781. | 7.4 | 681 |
| 333 | Comparative genomics of <i>Physcomitrella patens</i> gametophytic transcriptome and <i>Arabidopsis thaliana</i> : Implication for land plant evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 8007-8012. | 7.4 | 341 |
| 334 | Multiple tissue-specific promoters control expression of the murine tartrate-resistant acid phosphatase gene. <i>Gene</i> , 2003, 307, 111-123. | 2.3 | 54 |
| 335 | Antisense transcripts with rice full-length cDNAs. <i>Genome Biology</i> , 2003, 5, R5. | 9.1 | 113 |
| 336 | Targeting a Complex Transcriptome: The Construction of the Mouse Full-Length cDNA Encyclopedia. <i>Genome Research</i> , 2003, 13, 1273-1289. | 5.5 | 154 |
| 337 | Genomics Approach to Abscisic Acid- and Gibberellin-responsive Genes in Rice. <i>DNA Research</i> , 2003, 10, 249-261. | 3.4 | 58 |
| 338 | Analysis of the Mouse Transcriptome for Genes Involved in the Function of the Nervous System. <i>Genome Research</i> , 2003, 13, 1395-1401. | 5.5 | 31 |
| 339 | Continued Discovery of Transcriptional Units Expressed in Cells of the Mouse Mononuclear Phagocyte Lineage. <i>Genome Research</i> , 2003, 13, 1360-1365. | 5.5 | 41 |
| 340 | Phosphoregulators: Protein Kinases and Protein Phosphatases of Mouse. <i>Genome Research</i> , 2003, 13, 1443-1454. | 5.5 | 43 |
| 341 | Collection, Mapping, and Annotation of Over 28,000 cDNA Clones from japonica Rice. <i>Science</i> , 2003, 301, 376-379. | 19.6 | 837 |
| 342 | Exploration of the Cell-Cycle Genes Found Within the RIKEN FANTOM2 Data Set. <i>Genome Research</i> , 2003, 13, 1366-1375. | 5.5 | 16 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 343 | Subtraction of cap-trapped full-length cDNA libraries to select rare transcripts. <i>BioTechniques</i> , 2003, 35, 510-518. | 1.7 | 12 |
| 344 | A Computer-Based Method of Selecting Clones for a Full-Length cDNA Project: Simultaneous Collection of Negligibly Redundant and Variant cDNAs. <i>Genome Research</i> , 2002, 12, 1127-1134. | 5.5 | 28 |
| 345 | The <i>Drosophila</i> Gene Collection: Identification of Putative Full-Length cDNAs for 70% of <i>D. melanogaster</i> Genes. <i>Genome Research</i> , 2002, 12, 1294-1300. | 5.5 | 181 |
| 346 | Inferring Alternative Splicing Patterns in Mouse from a Full-Length cDNA Library and Microarray Data. <i>Genome Research</i> , 2002, 12, 1286-1293. | 5.5 | 21 |
| 347 | Functional Annotation of a Full-Length <i>Arabidopsis</i> cDNA Collection. <i>Science</i> , 2002, 296, 141-145. | 19.6 | 634 |
| 348 | Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16899-16903. | 7.4 | 1,628 |
| 349 | On biased distribution of introns in various eukaryotes. <i>Gene</i> , 2002, 300, 89-95. | 2.3 | 61 |
| 350 | Comprehensive sequence analysis of translation termination sites in various eukaryotes. <i>Gene</i> , 2002, 300, 79-87. | 2.3 | 15 |
| 351 | Extra-Long First-Strand cDNA Synthesis. <i>BioTechniques</i> , 2002, 32, 984-985. | 1.7 | 29 |
| 352 | Cytoplasmic RNA Extraction from Fresh and Frozen Mammalian Tissues. <i>BioTechniques</i> , 2002, 33, 306-309. | 1.7 | 12 |
| 353 | A framework for integrating the songbird brain. <i>Journal of Comparative Physiology A: Neuroethology, Sensory, Neural, and Behavioral Physiology</i> , 2002, 188, 961-980. | 1.7 | 31 |
| 354 | Monitoring the expression pattern of around 7,000 <i>Arabidopsis</i> genes under ABA treatments using a full-length cDNA microarray. <i>Functional and Integrative Genomics</i> , 2002, 2, 282-291. | 3.4 | 402 |
| 355 | Monitoring the expression profiles of 7000 <i>Arabidopsis</i> genes under drought, cold and high-salinity stresses using a full-length cDNA microarray. <i>Plant Journal</i> , 2002, 31, 279-292. | 5.8 | 1,712 |
| 356 | Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562. | 35.3 | 6,401 |
| 357 | Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002, 420, 563-573. | 35.3 | 1,563 |
| 358 | Mapping of 19032 mouse cDNAs on mouse chromosomes. <i>Journal of Structural and Functional Genomics</i> , 2002, 2, 23-28. | 1.1 | 2 |
| 359 | Functional annotation of a full-length mouse cDNA collection. <i>Nature</i> , 2001, 409, 685-690. | 35.3 | 655 |
| 360 | Balanced-Size and Long-Size Cloning of Full-Length, Cap-Trapped cDNAs into Vectors of the Novel $\hat{\text{I}}$ -FLC Family Allows Enhanced Gene Discovery Rate and Functional Analysis. <i>Genomics</i> , 2001, 77, 79-90. | 2.9 | 74 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 361 | Comparative evaluation of 5' end-sequence quality of clones in CAP trapper and other full-length-cDNA libraries. <i>Gene</i> , 2001, 263, 93-102. | 2.3 | 37 |
| 362 | Correlation between sequence conservation of the 5' untranslated region and codon usage bias in <i>Mus musculus</i> genes. <i>Gene</i> , 2001, 276, 101-105. | 2.3 | 34 |
| 363 | Removal of PolyA Tails from Full-Length cDNA Libraries for High-Efficiency Sequencing. <i>BioTechniques</i> , 2001, 31, 1042-1049. | 1.7 | 13 |
| 364 | Cloning Full-Length, Cap-Trapper-Selected cDNAs by Using the Single-Strand Linker Ligation Method. <i>BioTechniques</i> , 2001, 30, 1250-1254. | 1.7 | 50 |
| 365 | Meeting Report: 14th International Mouse Genome Conference. <i>Mammalian Genome</i> , 2001, 12, 401-405. | 2.2 | 0 |
| 366 | Arabidopsis encyclopedia using full-length cDNAs and its application. <i>Plant Physiology and Biochemistry</i> , 2001, 39, 211-220. | 5.9 | 34 |
| 367 | Delineating developmental and metabolic pathways in vivo by expression profiling using the RIKEN set of 18,816 full-length enriched mouse cDNA arrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 2199-2204. | 7.4 | 197 |
| 368 | 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. | 6.6 | 19 |
| 369 | Monitoring the Expression Pattern of 1300 Arabidopsis Genes under Drought and Cold Stresses by Using a Full-Length cDNA Microarray. <i>Plant Cell</i> , 2001, 13, 61-72. | 6.6 | 992 |
| 370 | Computer-Based Methods for the Mouse Full-Length cDNA Encyclopedia: Real-Time Sequence Clustering for Construction of a Nonredundant cDNA Library. <i>Genome Research</i> , 2001, 11, 281-289. | 5.5 | 25 |
| 371 | Computer-Based Methods for the Mouse Full-Length cDNA Encyclopedia: Real-Time Sequence Clustering for Construction of a Nonredundant cDNA Library. <i>Genome Research</i> , 2001, 11, 281-289. | 5.5 | 19 |
| 372 | RIKEN Integrated Sequence Analysis (RISA) System--384-Format Sequencing Pipeline with 384 Multicapillary Sequencer. <i>Genome Research</i> , 2000, 10, 1757-1771. | 5.5 | 52 |
| 373 | Normalization and Subtraction of Cap-Trapper-Selected cDNAs to Prepare Full-Length cDNA Libraries for Rapid Discovery of New Genes. <i>Genome Research</i> , 2000, 10, 1617-1630. | 5.5 | 264 |
| 374 | Increased specificity of reverse transcription priming by trehalose and oligo-blockers allows high-efficiency window separation of mRNA display. <i>Nucleic Acids Research</i> , 1999, 27, 1345-1349. | 13.8 | 39 |
| 375 | [2] High-efficiency full-length cDNA cloning. <i>Methods in Enzymology</i> , 1999, 303, 19-44. | 1.7 | 170 |
| 376 | Automated Filtration-Based High-Throughput Plasmid Preparation System. <i>Genome Research</i> , 1999, 9, 463-470. | 5.5 | 28 |
| 377 | High-efficiency cloning of Arabidopsis full-length cDNA by biotinylated CAP trapper. <i>Plant Journal</i> , 1998, 15, 707-720. | 5.8 | 220 |
| 378 | Characterization of Gene Expression in Mouse Blastocyst Using Single-Pass Sequencing of 3995 Clones. <i>Genomics</i> , 1998, 49, 167-179. | 2.9 | 47 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 379 | 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. | 7.4 | 232 |
| 380 | 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. | 7.4 | 38 |
| 381 | High Efficiency Selection of Full-length cDNA by Improved Biotinylated Cap Trapper. DNA Research, 1997, 4, 61-66. | 3.4 | 90 |
| 382 | Simple and rapid preparation of plasmid template by a filtration method using microtiter filter plates. Nucleic Acids Research, 1997, 25, 1315-1316. | 13.8 | 29 |
| 383 | A Novel Control System for Polymerase Chain Reaction Using a RIKEN GS384 Thermalcycler. DNA Research, 1997, 4, 387-391. | 3.4 | 6 |
| 384 | High-Efficiency Full-Length cDNA Cloning by Biotinylated CAP Trapper. Genomics, 1996, 37, 327-336. | 2.9 | 303 |
| 385 | A discontinuous buffer system increasing resolution and reproducibility in DNA sequencing on high voltage horizontal ultrathin-layer electrophoresis. Electrophoresis, 1995, 16, 1836-1845. | 2.8 | 13 |
| 386 | A simple discontinuous buffer system for increased resolution and speed in gel electrophoretic analysis of DNA sequence. Nucleic Acids Research, 1990, 18, 204-204. | 13.8 | 15 |
| 387 | Wavelet profiles: their application in Oryza sativa DNA sequence analysis. , 0, , . | | 4 |
| 388 | Single-Cell Convert-Seq Decodes Regulatory Factors Driving Neuronal Diversity. SSRN Electronic Journal, 0, , . | 0.3 | 1 |
| 389 | The 1% Gift to humanity: The Human Genome Project II. Cell Research, 0, , . | 12.0 | 0 |