

# Hideya Kawaji

## List of Publications by Year in Descending Order

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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.

140  
papers

14,979  
citations

47  
h-index

122  
g-index

154  
ext. papers

18,972  
ext. citations

11.7  
avg, IF

5.3  
L-index

| #   | Paper   | IF   | Citations |
|-----|---|------|-----------|
| 140 | is a multifunctional factor priming human embryonic genome activation.. <i>IScience</i> , <b>2022</b> , 25, 104137  | 6.1  | 1         |
| 139 | CREB3L1 overexpression as a potential diagnostic marker of Philadelphia chromosome-negative myeloproliferative neoplasms. <i>Cancer Science</i> , <b>2021</b> , 112, 884-892  | 6.9  | 5         |
| 138 | APOBEC3B is preferentially expressed at the G2/M phase of cell cycle. <i>Biochemical and Biophysical Research Communications</i> , <b>2021</b> , 546, 178-184   | 3.4  | 4         |
| 137 | Nanopore sequencing reveals TACC2 locus complexity and diversity of isoforms transcribed from an intronic promoter. <i>Scientific Reports</i> , <b>2021</b> , 11, 9355  | 4.9  | 0         |
| 136 | Dysregulation of post-transcriptional modification by copy number variable microRNAs in schizophrenia with enhanced glycation stress. <i>Translational Psychiatry</i> , <b>2021</b> , 11, 331                             | 8.6  | 2         |
| 135 | Chromosomal-scale de novo genome assemblies of Cynomolgus Macaque and Common Marmoset. <i>Scientific Data</i> , <b>2021</b> , 8, 159  | 8.2  | 1         |
| 134 | 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         |
| 133 | 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        |
| 132 | Significance of HMGA2 expression as independent poor prognostic marker in perihilar and distal cholangiocarcinoma resected with curative intent. <i>European Journal of Surgical Oncology</i> , <b>2021</b> , 47, 394-400 | 2.6  | 0         |
| 131 | CDK1 dependent phosphorylation of hTERT contributes to cancer progression. <i>Nature Communications</i> , <b>2020</b> , 11, 1557  | 17.4 | 12        |
| 130 | CREB3L1 Overexpression Can Reliably Discriminate Ph-MPNs from Reactive Cases. <i>Blood</i> , <b>2020</b> , 136, 41-41   | 2.2  |           |
| 129 | Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , <b>2020</b> , 30, 1060-1072  | 9.7  | 41        |
| 128 | Comparative transcriptomics of primary cells in vertebrates. <i>Genome Research</i> , <b>2020</b> , 30, 951-961   | 9.7  | 12        |
| 127 | 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         |
| 126 | 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        |
| 125 | Identification of novel cerebellar developmental transcriptional regulators with motif activity analysis. <i>BMC Genomics</i> , <b>2019</b> , 20, 718   | 4.5  | 3         |
| 124 | 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        |

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| 123 | CXCL4/PF4 is a predictive biomarker of cardiac differentiation potential of human induced pluripotent stem cells. <i>Scientific Reports</i> , <b>2019</b> , 9, 4638                                  | 4.9  | 3   |
| 122 | RNA sequencing analysis revealed the induction of CCL3 expression in human intracranial aneurysms. <i>Scientific Reports</i> , <b>2019</b> , 9, 10387  | 4.9  | 9   |
| 121 | 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  |
| 120 | Databases for CAGE Visualization and Analysis <b>2019</b> , 123-136  |      |     |
| 119 | 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  |
| 118 | Antisense Transcription in Loci Associated to Hereditary Neurodegenerative Diseases. <i>Molecular Neurobiology</i> , <b>2019</b> , 56, 5392-5415   | 6.2  | 15  |
| 117 | CD157 Marks Tissue-Resident Endothelial Stem Cells with Homeostatic and Regenerative Properties. <i>Cell Stem Cell</i> , <b>2018</b> , 22, 384-397.e6  | 18   | 92  |
| 116 | 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   |
| 115 | Transcriptional landscape of Mycobacterium tuberculosis infection in macrophages. <i>Scientific Reports</i> , <b>2018</b> , 8, 6758  | 4.9  | 41  |
| 114 | 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   |
| 113 | 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   |
| 112 | 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  |
| 111 | ChIP-Atlas: a data-mining suite powered by full integration of public ChIP-seq data. <i>EMBO Reports</i> , <b>2018</b> , 19,   | 6.5  | 238 |
| 110 | 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   |
| 109 | An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , <b>2017</b> , 543, 199-204   | 50.4 | 581 |
| 108 | Genome Annotation. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1525, 107-121   | 1.4  | 2   |
| 107 | High-resolution promoter map of human limbal epithelial cells cultured with keratinocyte growth factor and rho kinase inhibitor. <i>Scientific Reports</i> , <b>2017</b> , 7, 2845                   | 4.9  | 6   |
| 106 | Linking FANTOM5 CAGE peaks to annotations with CAGEscan. <i>Scientific Data</i> , <b>2017</b> , 4, 170147  | 8.2  | 10  |

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| 105 | Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. <i>EBioMedicine</i> , <b>2017</b> , 24, 257-266   | 8.8  | 13  |
| 104 | Hotspots of De Novo Point Mutations in Induced Pluripotent Stem Cells. <i>Cell Reports</i> , <b>2017</b> , 21, 308-315   | 10.6 | 33  |
| 103 | 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  |
| 102 | Correlation of EGFR or KRAS mutation status with 18F-FDG uptake on PET-CT scan in lung adenocarcinoma. <i>PLoS ONE</i> , <b>2017</b> , 12, e0175622  | 3.7  | 16  |
| 101 | Systematic analysis of transcription start sites in avian development. <i>PLoS Biology</i> , <b>2017</b> , 15, e2002887  | 9.7  | 22  |
| 100 | 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  |
| 99  | 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 |
| 98  | FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , <b>2017</b> , 4, 170112   | 8.2  | 88  |
| 97  | 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  |
| 96  | Promoter-level transcriptome in primary lesions of endometrial cancer identified biomarkers associated with lymph node metastasis. <i>Scientific Reports</i> , <b>2017</b> , 7, 14160  | 4.9  | 7   |
| 95  | Monitoring transcription initiation activities in rat and dog. <i>Scientific Data</i> , <b>2017</b> , 4, 170173  | 8.2  | 4   |
| 94  | Restricted Presence of POU6F2 in Human Corneal Endothelial Cells Uncovered by Extension of the Promoter-level Expression Atlas. <i>EBioMedicine</i> , <b>2017</b> , 25, 175-186  | 8.8  | 5   |
| 93  | 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  |
| 92  | 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  |
| 91  | 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  |
| 90  | 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   |
| 89  | Next-generation sequencing-based small RNA profiling of cerebrospinal fluid exosomes. <i>Neuroscience Letters</i> , <b>2017</b> , 636, 48-57   | 3.3  | 63  |
| 88  | Transcription start site profiling of 15 anatomical regions of the <i>Macaca mulatta</i> central nervous system. <i>Scientific Data</i> , <b>2017</b> , 4, 170163  | 8.2  | 2   |

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| 87 | 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  |
| 86 | 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  |
| 85 | CAGED-oPOSSUM: motif enrichment analysis from CAGE-derived TSSs. <i>Bioinformatics</i> , <b>2016</b> , 32, 2858-60   | 7.2  | 11  |
| 84 | Enhanced Identification of Transcriptional Enhancers Provides Mechanistic Insights into Diseases. <i>Trends in Genetics</i> , <b>2016</b> , 32, 76-88  | 8.5  | 59  |
| 83 | 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  |
| 82 | 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  |
| 81 | 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  |
| 80 | Novel biomarkers that assist in accurate discrimination of squamous cell carcinoma from adenocarcinoma of the lung. <i>BMC Cancer</i> , <b>2016</b> , 16, 760  | 4.8  | 30  |
| 79 | 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  |
| 78 | 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  |
| 77 | Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , <b>2015</b> , 16, 22  | 18.3 | 443 |
| 76 | 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  |
| 75 | A draft network of ligand-receptor-mediated multicellular signalling in human. <i>Nature Communications</i> , <b>2015</b> , 6, 7866  | 17.4 | 393 |
| 74 | 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  |
| 73 | 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  |
| 72 | 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  |
| 71 | Identification of chromatin marks at TERRA promoter and encoding region. <i>Biochemical and Biophysical Research Communications</i> , <b>2015</b> , 467, 1052-7  | 3.4  | 15  |
| 70 | 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  |

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| 69 | 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   |
| 68 | 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  |
| 67 | 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   |
| 66 | 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   |
| 65 | Discovery of molecular markers to discriminate corneal endothelial cells in the human body. <i>PLoS ONE</i> , <b>2015</b> , 10, e0117581   | 3.7  | 19   |
| 64 | 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    |
| 63 | The BioMart community portal: an innovative alternative to large, centralized data repositories. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, W589-98   | 20.1 | 468  |
| 62 | Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , <b>2015</b> , 347, 1010-4   | 33.3 | 384  |
| 61 | Association between the EGFR or KRAS mutation status and the FDG-PET findings in surgically resected lung adenocarcinoma.. <i>Journal of Clinical Oncology</i> , <b>2015</b> , 33, 7535-7535                   | 2.2  |      |
| 60 | Interactive visualization and analysis of large-scale sequencing datasets using ZENBU. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 217-9   | 44.5 | 124  |
| 59 | A promoter-level mammalian expression atlas. <i>Nature</i> , <b>2014</b> , 507, 462-70   | 50.4 | 1301 |
| 58 | An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , <b>2014</b> , 507, 455-461   | 50.4 | 1595 |
| 57 | CAGEExploreR: an R package for the analysis and visualization of promoter dynamics across multiple experiments. <i>Bioinformatics</i> , <b>2014</b> , 30, 1183-1184  | 7.2  | 5    |
| 56 | 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   |
| 55 | 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   |
| 54 | 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   |
| 53 | Transcription and enhancer profiling in human monocyte subsets. <i>Blood</i> , <b>2014</b> , 123, e90-9  | 2.2  | 101  |
| 52 | 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   |

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| 51 | Effects of cytosine methylation on transcription factor binding sites. <i>BMC Genomics</i> , <b>2014</b> , 15, 119   | 4.5  | 156 |
| 50 | Chromatin states reveal functional associations for globally defined transcription start sites in four human cell lines. <i>BMC Genomics</i> , <b>2014</b> , 15, 120   | 4.5  | 15  |
| 49 | High-throughput transcription profiling identifies putative epigenetic regulators of hematopoiesis. <i>Blood</i> , <b>2014</b> , 123, e46-57   | 2.2  | 19  |
| 48 | Transcriptional profiling of the human fibrillin/LTBP gene family, key regulators of mesenchymal cell functions. <i>Molecular Genetics and Metabolism</i> , <b>2014</b> , 112, 73-83   | 3.7  | 25  |
| 47 | CAGE-defined promoter regions of the genes implicated in Rett Syndrome. <i>BMC Genomics</i> , <b>2014</b> , 15, 1177   | 4.5  | 7   |
| 46 | Redefinition of the human mast cell transcriptome by deep-CAGE sequencing. <i>Blood</i> , <b>2014</b> , 123, e58-67  | 2.2  | 126 |
| 45 | Ceruloplasmin is a novel adipokine which is overexpressed in adipose tissue of obese subjects and in obesity-associated cancer cells. <i>PLoS ONE</i> , <b>2014</b> , 9, e80274  | 3.7  | 36  |
| 44 | 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> , <b>2014</b> , 111, 5289-94  | 11.5 | 85  |
| 43 | A transient disruption of fibroblastic transcriptional regulatory network facilitates trans-differentiation. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 8905-13   | 20.1 | 23  |
| 42 | The evolution of human cells in terms of protein innovation. <i>Molecular Biology and Evolution</i> , <b>2014</b> , 31, 1364-74  | 8.3  | 13  |
| 41 | The 3rd DBCLS BioHackathon: improving life science data integration with Semantic Web technologies. <i>Journal of Biomedical Semantics</i> , <b>2013</b> , 4, 6  | 2.2  | 22  |
| 40 | Capturing drug responses by quantitative promoter activity profiling. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , <b>2013</b> , 2, e77  | 4.5  | 1   |
| 39 | Automated workflow for preparation of cDNA for cap analysis of gene expression on a single molecule sequencer. <i>PLoS ONE</i> , <b>2012</b> , 7, e30809   | 3.7  | 18  |
| 38 | Novel small noncoding RNAs in mouse spermatozoa, zygotes and early embryos. <i>PLoS ONE</i> , <b>2012</b> , 7, e44542  | 3.7  | 89  |
| 37 | 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> , <b>2012</b> , 109, E944-53 | 11.5 | 212 |
| 36 | Unamplified cap analysis of gene expression on a single-molecule sequencer. <i>Genome Research</i> , <b>2011</b> , 21, 1150-9  | 9.7  | 143 |
| 35 | The RIKEN integrated database of mammals. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D861-70  | 20.1 | 18  |
| 34 | Update of the FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D856-60   | 20.1 | 45  |



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| 33 | Nuclear pore complex protein mediated nuclear localization of dicer protein in human cells. <i>PLoS ONE</i> , <b>2011</b> , 6, e23385  | 3.7  | 37  |
| 32 | Reduction of non-insert sequence reads by dimer eliminator LNA oligonucleotide for small RNA deep sequencing. <i>BioTechniques</i> , <b>2010</b> , 49, 751-5                 | 2.5  | 27  |
| 31 | Cross-mapping and the identification of editing sites in mature microRNAs in high-throughput sequencing libraries. <i>Genome Research</i> , <b>2010</b> , 20, 257-64         | 9.7  | 105 |
| 30 | An atlas of combinatorial transcriptional regulation in mouse and man. <i>Cell</i> , <b>2010</b> , 140, 744-52   | 56.2 | 555 |
| 29 | An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , <b>2010</b> , 141, 369  | 56.2 | 3   |
| 28 | SDRF2GRAPH: a visualization tool of a spreadsheet-based description of experimental processes. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 133                             | 3.6  | 3   |
| 27 | The Systems Biology Graphical Notation. <i>Nature Biotechnology</i> , <b>2009</b> , 27, 735-41   | 44.5 | 651 |
| 26 | The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , <b>2009</b> , 41, 553-62         | 36.3 | 356 |
| 25 | FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. <i>Genome Biology</i> , <b>2009</b> , 10, R39 | 18.3 | 56  |
| 24 | The FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. <i>Genome Biology</i> , <b>2009</b> , 10, R40                                   | 18.3 | 65  |
| 23 | Databases for CAGE Visualization and Analysis <b>2009</b> , 123-135  |      |     |
| 22 | Hidden layers of human small RNAs. <i>BMC Genomics</i> , <b>2008</b> , 9, 157  | 4.5  | 226 |
| 21 | Genome annotation. <i>Methods in Molecular Biology</i> , <b>2008</b> , 452, 125-39   | 1.4  | 6   |
| 20 | Exploration of small RNAs. <i>PLoS Genetics</i> , <b>2008</b> , 4, e22   | 6    | 71  |
| 19 | Pseudo-messenger RNA: phantoms of the transcriptome. <i>PLoS Genetics</i> , <b>2006</b> , 2, e23   | 6    | 51  |
| 18 | Dynamic usage of transcription start sites within core promoters. <i>Genome Biology</i> , <b>2006</b> , 7, R118  | 18.3 | 64  |
| 17 | Alternate transcription of the Toll-like receptor signaling cascade. <i>Genome Biology</i> , <b>2006</b> , 7, R10  | 18.3 | 63  |
| 16 | CAGE Basic/Analysis Databases: the CAGE resource for comprehensive promoter analysis. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D632-6                               | 20.1 | 69  |



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|----|--|------|------|
| 15 | Genome-wide analysis of mammalian promoter architecture and evolution. <i>Nature Genetics</i> , <b>2006</b> , 38, 626-35   | 36.3 | 1021 |
| 14 | Graph-based clustering for finding distant relationships in a large set of protein sequences. <i>Bioinformatics</i> , <b>2004</b> , 20, 243-52   | 7.2  | 31   |
| 13 | Construction of representative transcript and protein sets of human, mouse, and rat as a platform for their transcriptome and proteome analysis. <i>Genomics</i> , <b>2004</b> , 84, 913-21  | 4.3  | 22   |
| 12 | 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> , <b>2003</b> , 100, 15776-81 | 11.5 | 554  |
| 11 | Mouse proteome analysis. <i>Genome Research</i> , <b>2003</b> , 13, 1335-44  | 9.7  | 75   |
| 10 | Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , <b>2002</b> , 420, 563-73  | 50.4 | 1350 |
| 9  | Exploration of novel motifs derived from mouse cDNA sequences. <i>Genome Research</i> , <b>2002</b> , 12, 367-78   | 9.7  | 16   |
| 8  | Functional annotation of a full-length mouse cDNA collection. <i>Nature</i> , <b>2001</b> , 409, 685-90  | 50.4 | 560  |
| 7  | Predicting cell-type-specific non-coding RNA transcription from genome sequence  |      | 1    |
| 6  | BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. <i>F1000Research</i> , 8, 1677  | 3.6  |      |
| 5  | CAGEd-oPOSSUM: motif enrichment analysis from CAGE-derived TSSs  |      | 1    |
| 4  | Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease   |      | 2    |
| 3  | Integrative analysis of transcription factor occupancy at enhancers and disease risk loci in noncoding genomic regions   |      | 7    |
| 2  | Functional Annotation of Human Long Non-Coding RNAs via Molecular Phenotyping  |      | 6    |
| 1  | DUX4 regulates oocyte to embryo transition in human  |      | 2    |