

Boris Lenhard

List of Publications by Citations

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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.

158
papers

24,873
citations

63
h-index

157
g-index

180
ext. papers

29,443
ext. citations

15
avg, IF

6.3
L-index

| # | Paper | IF | Citations |
|-----|---|------|-----------|
| 158 | The transcriptional landscape of the mammalian genome. <i>Science</i> , 2005 , 309, 1559-63 | 33.3 | 2807 |
| 157 | The accessible chromatin landscape of the human genome. <i>Nature</i> , 2012 , 489, 75-82 | 50.4 | 1900 |
| 156 | Antisense transcription in the mammalian transcriptome. <i>Science</i> , 2005 , 309, 1564-6 | 33.3 | 1354 |
| 155 | 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 |
| 154 | A promoter-level mammalian expression atlas. <i>Nature</i> , 2014 , 507, 462-70 | 50.4 | 1301 |
| 153 | JASPAR: an open-access database for eukaryotic transcription factor binding profiles. <i>Nucleic Acids Research</i> , 2004 , 32, D91-4 | 20.1 | 1197 |
| 152 | Genome-wide analysis of mammalian promoter architecture and evolution. <i>Nature Genetics</i> , 2006 , 38, 626-35 | 36.3 | 1021 |
| 151 | JASPAR 2014: an extensively expanded and updated open-access database of transcription factor binding profiles. <i>Nucleic Acids Research</i> , 2014 , 42, D142-7 | 20.1 | 795 |
| 150 | JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. <i>Nucleic Acids Research</i> , 2018 , 46, D260-D266 | 20.1 | 761 |
| 149 | JASPAR 2016: a major expansion and update of the open-access database of transcription factor binding profiles. <i>Nucleic Acids Research</i> , 2016 , 44, D110-5 | 20.1 | 738 |
| 148 | JASPAR 2020: update of the open-access database of transcription factor binding profiles. <i>Nucleic Acids Research</i> , 2020 , 48, D87-D92 | 20.1 | 569 |
| 147 | An atlas of combinatorial transcriptional regulation in mouse and man. <i>Cell</i> , 2010 , 140, 744-52 | 56.2 | 555 |
| 146 | JASPAR, the open access database of transcription factor-binding profiles: new content and tools in the 2008 update. <i>Nucleic Acids Research</i> , 2008 , 36, D102-6 | 20.1 | 541 |
| 145 | JASPAR 2010: the greatly expanded open-access database of transcription factor binding profiles. <i>Nucleic Acids Research</i> , 2010 , 38, D105-10 | 20.1 | 483 |
| 144 | Mammalian RNA polymerase II core promoters: insights from genome-wide studies. <i>Nature Reviews Genetics</i> , 2007 , 8, 424-36 | 30.1 | 394 |
| 143 | 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 |
| 142 | Metazoan promoters: emerging characteristics and insights into transcriptional regulation. <i>Nature Reviews Genetics</i> , 2012 , 13, 233-45 | 30.1 | 347 |

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| 141 | ConSite: web-based prediction of regulatory elements using cross-species comparison. <i>Nucleic Acids Research</i> , 2004 , 32, W249-52 | 20.1 | 341 |
| 140 | Genomic regulatory blocks encompass multiple neighboring genes and maintain conserved synteny in vertebrates. <i>Genome Research</i> , 2007 , 17, 545-55 | 9.7 | 264 |
| 139 | Integrative annotation of 21,037 human genes validated by full-length cDNA clones. <i>PLoS Biology</i> , 2004 , 2, e162 | 9.7 | 255 |
| 138 | Complex Loci in human and mouse genomes. <i>PLoS Genetics</i> , 2006 , 2, e47 | 6 | 246 |
| 137 | Cohesin-based chromatin interactions enable regulated gene expression within preexisting architectural compartments. <i>Genome Research</i> , 2013 , 23, 2066-77 | 9.7 | 232 |
| 136 | Arrays of ultraconserved non-coding regions span the loci of key developmental genes in vertebrate genomes. <i>BMC Genomics</i> , 2004 , 5, 99 | 4.5 | 229 |
| 135 | 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 |
| 134 | Plasticity of animal genome architecture unmasked by rapid evolution of a pelagic tunicate. <i>Science</i> , 2010 , 330, 1381-5 | 33.3 | 212 |
| 133 | Identification of conserved regulatory elements by comparative genome analysis. <i>Journal of Biology</i> , 2003 , 2, 13 | | 194 |
| 132 | Sox2 cooperates with Chd7 to regulate genes that are mutated in human syndromes. <i>Nature Genetics</i> , 2011 , 43, 607-11 | 36.3 | 187 |
| 131 | The genome-wide dynamics of the binding of Ldb1 complexes during erythroid differentiation. <i>Genes and Development</i> , 2010 , 24, 277-89 | 12.6 | 184 |
| 130 | A new generation of JASPAR, the open-access repository for transcription factor binding site profiles. <i>Nucleic Acids Research</i> , 2006 , 34, D95-7 | 20.1 | 173 |
| 129 | Long-range gene regulation links genomic type 2 diabetes and obesity risk regions to HHEX, SOX4, and IRX3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 775-80 | 11.5 | 159 |
| 128 | Patterns of regulatory activity across diverse human cell types predict tissue identity, transcription factor binding, and long-range interactions. <i>Genome Research</i> , 2013 , 23, 777-88 | 9.7 | 153 |
| 127 | Genomic regulatory blocks underlie extensive microsynteny conservation in insects. <i>Genome Research</i> , 2007 , 17, 1898-908 | 9.7 | 153 |
| 126 | TFBS: Computational framework for transcription factor binding site analysis. <i>Bioinformatics</i> , 2002 , 18, 1135-6 | 7.2 | 147 |
| 125 | Transcript annotation in FANTOM3: mouse gene catalog based on physical cDNAs. <i>PLoS Genetics</i> , 2006 , 2, e62 | 6 | 138 |
| 124 | TFBSTools: an R/bioconductor package for transcription factor binding site analysis. <i>Bioinformatics</i> , 2016 , 32, 1555-6 | 7.2 | 137 |

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|-----|---|------|-----|
| 123 | RNAdb 2.0--an expanded database of mammalian non-coding RNAs. <i>Nucleic Acids Research</i> , 2007 , 35, D178-82 | 20.1 | 134 |
| 122 | HBS1L-MYB intergenic variants modulate fetal hemoglobin via long-range MYB enhancers. <i>Journal of Clinical Investigation</i> , 2014 , 124, 1699-710 | 15.9 | 129 |
| 121 | Epigenetic reprogramming enables the transition from primordial germ cell to gonocyte. <i>Nature</i> , 2018 , 555, 392-396 | 50.4 | 127 |
| 120 | Two independent transcription initiation codes overlap on vertebrate core promoters. <i>Nature</i> , 2014 , 507, 381-385 | 50.4 | 121 |
| 119 | Amphioxus functional genomics and the origins of vertebrate gene regulation. <i>Nature</i> , 2018 , 564, 64-70 | 50.4 | 120 |
| 118 | CAGEr: precise TSS data retrieval and high-resolution promoterome mining for integrative analyses. <i>Nucleic Acids Research</i> , 2015 , 43, e51 | 20.1 | 117 |
| 117 | Zebrafish enhancer detection (ZED) vector: a new tool to facilitate transgenesis and the functional analysis of cis-regulatory regions in zebrafish. <i>Developmental Dynamics</i> , 2009 , 238, 2409-17 | 2.9 | 117 |
| 116 | RNAdb--a comprehensive mammalian noncoding RNA database. <i>Nucleic Acids Research</i> , 2005 , 33, D125-30 | 20.1 | 113 |
| 115 | Dynamic long-range chromatin interactions control Myb proto-oncogene transcription during erythroid development. <i>EMBO Journal</i> , 2012 , 31, 986-99 | 13 | 107 |
| 114 | Spatial enhancer clustering and regulation of enhancer-proximal genes by cohesin. <i>Genome Research</i> , 2015 , 25, 504-13 | 9.7 | 106 |
| 113 | Control of inducible gene expression links cohesin to hematopoietic progenitor self-renewal and differentiation. <i>Nature Immunology</i> , 2018 , 19, 932-941 | 19.1 | 103 |
| 112 | Topologically associating domains are ancient features that coincide with Metazoan clusters of extreme noncoding conservation. <i>Nature Communications</i> , 2017 , 8, 441 | 17.4 | 99 |
| 111 | In vivo live imaging of RNA polymerase II transcription factories in primary cells. <i>Genes and Development</i> , 2013 , 27, 767-77 | 12.6 | 99 |
| 110 | Targeting Aberrant Epigenetic Networks Mediated by PRMT1 and KDM4C in Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2016 , 29, 32-48 | 24.3 | 98 |
| 109 | Systematic human/zebrafish comparative identification of cis-regulatory activity around vertebrate developmental transcription factor genes. <i>Developmental Biology</i> , 2009 , 327, 526-40 | 3.1 | 94 |
| 108 | The DNA-binding protein CTCF limits proximal V(D)J recombination and restricts B enhancer interactions to the immunoglobulin light chain locus. <i>Immunity</i> , 2011 , 35, 501-13 | 32.3 | 92 |
| 107 | A cohesin-independent role for NIPBL at promoters provides insights in CdLS. <i>PLoS Genetics</i> , 2014 , 10, e1004153 | 6 | 87 |
| 106 | Chromatin and epigenetic features of long-range gene regulation. <i>Nucleic Acids Research</i> , 2013 , 41, 7185-99 | 20.1 | 87 |

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|-----|--|------|----|
| 105 | Transcriptional and structural impact of TATA-initiation site spacing in mammalian core promoters. <i>Genome Biology</i> , 2006 , 7, R78 | 18.3 | 85 |
| 104 | In silico detection of sequence variations modifying transcriptional regulation. <i>PLoS Computational Biology</i> , 2008 , 4, e5 | 5 | 81 |
| 103 | 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 |
| 102 | Transcriptional features of genomic regulatory blocks. <i>Genome Biology</i> , 2009 , 10, R38 | 18.3 | 77 |
| 101 | The aurora B kinase and the polycomb protein ring1B combine to regulate active promoters in quiescent lymphocytes. <i>Molecular Cell</i> , 2013 , 51, 647-61 | 17.6 | 75 |
| 100 | Ancora: a web resource for exploring highly conserved noncoding elements and their association with developmental regulatory genes. <i>Genome Biology</i> , 2008 , 9, R34 | 18.3 | 68 |
| 99 | r3Cseq: an R/Bioconductor package for the discovery of long-range genomic interactions from chromosome conformation capture and next-generation sequencing data. <i>Nucleic Acids Research</i> , 2013 , 41, e132 | 20.1 | 67 |
| 98 | The male germ cell gene regulator CTCFL is functionally different from CTCF and binds CTCF-like consensus sites in a nucleosome composition-dependent manner. <i>Epigenetics and Chromatin</i> , 2012 , 5, 8 | 5.8 | 66 |
| 97 | In vivo transcript profiling and phylogenetic analysis identifies suppressor of cytokine signaling 2 as a direct signal transducer and activator of transcription 5b target in liver. <i>Molecular Endocrinology</i> , 2007 , 21, 293-311 | | 65 |
| 96 | JASPAR 2022: the 9th release of the open-access database of transcription factor binding profiles. <i>Nucleic Acids Research</i> , 2021 , | 20.1 | 58 |
| 95 | Variants of CYP46A1 may interact with age and APOE to influence CSF Abeta42 levels in Alzheimer's disease. <i>Human Genetics</i> , 2004 , 114, 581-7 | 6.3 | 57 |
| 94 | tRNA recognition and evolution of determinants in seryl-tRNA synthesis. <i>Nucleic Acids Research</i> , 1999 , 27, 721-9 | 20.1 | 57 |
| 93 | DNA stretching induces Cas9 off-target activity. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 185-192 | 17.6 | 55 |
| 92 | The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts. <i>Nucleic Acids Research</i> , 2008 , 36, D793-9 | 20.1 | 52 |
| 91 | Regulog analysis: detection of conserved regulatory networks across bacteria: application to <i>Staphylococcus aureus</i> . <i>Genome Research</i> , 2004 , 14, 1362-73 | 9.7 | 51 |
| 90 | The mystery of extreme non-coding conservation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013 , 368, 20130021 | 5.8 | 50 |
| 89 | Genome-wide DNA methylation profiling of non-small cell lung carcinomas. <i>Epigenetics and Chromatin</i> , 2012 , 5, 9 | 5.8 | 49 |
| 88 | 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 |

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|----|---|------|----|
| 87 | Control of developmentally primed erythroid genes by combinatorial co-repressor actions. <i>Nature Communications</i> , 2015 , 6, 8893 | 17.4 | 47 |
| 86 | A cladistic model of ACE sequence variation with implications for myocardial infarction, Alzheimer disease and obesity. <i>Human Molecular Genetics</i> , 2004 , 13, 2647-57 | 5.6 | 47 |
| 85 | Conserved non-coding elements: developmental gene regulation meets genome organization. <i>Nucleic Acids Research</i> , 2017 , 45, 12611-12624 | 20.1 | 46 |
| 84 | Promoter architecture of mouse olfactory receptor genes. <i>Genome Research</i> , 2012 , 22, 486-97 | 9.7 | 46 |
| 83 | OikoBase: a genomics and developmental transcriptomics resource for the urochordate <i>Oikopleura dioica</i> . <i>Nucleic Acids Research</i> , 2013 , 41, D845-53 | 20.1 | 45 |
| 82 | GeneLynx: a gene-centric portal to the human genome. <i>Genome Research</i> , 2001 , 11, 2151-7 | 9.7 | 44 |
| 81 | Genome-wide, whole mount in situ analysis of transcriptional regulators in zebrafish embryos. <i>Developmental Biology</i> , 2013 , 380, 351-62 | 3.1 | 43 |
| 80 | Mammalian microRNA prediction through a support vector machine model of sequence and structure. <i>PLoS ONE</i> , 2007 , 2, e946 | 3.7 | 43 |
| 79 | Alternative promoter usage of the membrane glycoprotein CD36. <i>BMC Molecular Biology</i> , 2006 , 7, 8 | 4.5 | 43 |
| 78 | Identification of functional SNPs in the 5-prime flanking sequences of human genes. <i>BMC Genomics</i> , 2005 , 6, 18 | 4.5 | 41 |
| 77 | Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020 , 30, 1060-1072 | 9.7 | 41 |
| 76 | Exonic remnants of whole-genome duplication reveal cis-regulatory function of coding exons. <i>Nucleic Acids Research</i> , 2010 , 38, 1071-85 | 20.1 | 39 |
| 75 | A global genomic transcriptional code associated with CNS-expressed genes. <i>Experimental Cell Research</i> , 2006 , 312, 3108-19 | 4.2 | 39 |
| 74 | The random versus fragile breakage models of chromosome evolution: a matter of resolution. <i>Molecular Genetics and Genomics</i> , 2007 , 278, 487-91 | 3.1 | 38 |
| 73 | New technologies, new findings, and new concepts in the study of vertebrate cis-regulatory sequences. <i>Developmental Dynamics</i> , 2006 , 235, 870-85 | 2.9 | 37 |
| 72 | Exploring hepatic hormone actions using a compilation of gene expression profiles. <i>BMC Physiology</i> , 2005 , 5, 8 | 0 | 37 |
| 71 | Promoter architectures and developmental gene regulation. <i>Seminars in Cell and Developmental Biology</i> , 2016 , 57, 11-23 | 7.5 | 36 |
| 70 | BCL11B mutations in patients affected by a neurodevelopmental disorder with reduced type 2 innate lymphoid cells. <i>Brain</i> , 2018 , 141, 2299-2311 | 11.2 | 36 |

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|----|--|------|----|
| 69 | Retroviral enhancer detection insertions in zebrafish combined with comparative genomics reveal genomic regulatory blocks - a fundamental feature of vertebrate genomes. <i>Genome Biology</i> , 2007 , 8 Suppl 1, S4 | 18.3 | 36 |
| 68 | CpG-depleted promoters harbor tissue-specific transcription factor binding signals--implications for motif overrepresentation analyses. <i>Nucleic Acids Research</i> , 2009 , 37, 6305-15 | 20.1 | 33 |
| 67 | GenomicInteractions: An R/Bioconductor package for manipulating and investigating chromatin interaction data. <i>BMC Genomics</i> , 2015 , 16, 963 | 4.5 | 29 |
| 66 | A novel complex, RUNX1-MYEF2, represses hematopoietic genes in erythroid cells. <i>Molecular and Cellular Biology</i> , 2012 , 32, 3814-22 | 4.8 | 27 |
| 65 | Defining the active site of yeast seryl-tRNA synthetase. Mutations in motif 2 loop residues affect tRNA-dependent amino acid recognition. <i>Journal of Biological Chemistry</i> , 1997 , 272, 1136-41 | 5.4 | 27 |
| 64 | Genome-wide analysis shows that Ldb1 controls essential hematopoietic genes/pathways in mouse early development and reveals novel players in hematopoiesis. <i>Blood</i> , 2013 , 121, 2902-13 | 2.2 | 26 |
| 63 | Integrated analysis of yeast regulatory sequences for biologically linked clusters of genes. <i>Functional and Integrative Genomics</i> , 2003 , 3, 125-34 | 3.8 | 25 |
| 62 | The C-terminal extension of yeast seryl-tRNA synthetase affects stability of the enzyme and its substrate affinity. <i>Journal of Biological Chemistry</i> , 1996 , 271, 2455-61 | 5.4 | 25 |
| 61 | Transcriptional, post-transcriptional and chromatin-associated regulation of pri-miRNAs, pre-miRNAs and miRNAs. <i>Nucleic Acids Research</i> , 2016 , 44, 3070-81 | 20.1 | 25 |
| 60 | -----Widespread conservation and lineage-specific diversification of genome-wide DNA methylation patterns across arthropods. <i>PLoS Genetics</i> , 2020 , 16, e1008864 | 6 | 24 |
| 59 | Regulatory divergence of the duplicated chromosomal loci sox11a/b by subpartitioning and sequence evolution of enhancers in zebrafish. <i>Molecular Genetics and Genomics</i> , 2010 , 283, 171-84 | 3.1 | 24 |
| 58 | Synorth: exploring the evolution of synteny and long-range regulatory interactions in vertebrate genomes. <i>Genome Biology</i> , 2009 , 10, R86 | 18.3 | 21 |
| 57 | Long-range evolutionary constraints reveal cis-regulatory interactions on the human X chromosome. <i>Nature Communications</i> , 2015 , 6, 6904 | 17.4 | 20 |
| 56 | Genomewide DNA methylation analysis identifies novel methylated genes in non-small-cell lung carcinomas. <i>Journal of Thoracic Oncology</i> , 2013 , 8, 562-73 | 8.9 | 20 |
| 55 | Trans-splicing and operons in metazoans: translational control in maternally regulated development and recovery from growth arrest. <i>Molecular Biology and Evolution</i> , 2015 , 32, 585-99 | 8.3 | 19 |
| 54 | Dual-initiation promoters with intertwined canonical and TCT/TOP transcription start sites diversify transcript processing. <i>Nature Communications</i> , 2020 , 11, 168 | 17.4 | 17 |
| 53 | Conservative route to genome compaction in a miniature annelid. <i>Nature Ecology and Evolution</i> , 2021 , 5, 231-242 | 12.3 | 17 |
| 52 | SLIC-CAGE: high-resolution transcription start site mapping using nanogram-levels of total RNA. <i>Genome Research</i> , 2018 , 28, 1943-1956 | 9.7 | 17 |

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|----|--|------|----|
| 51 | Understanding the genetics of neuropsychiatric disorders: the potential role of genomic regulatory blocks. <i>Molecular Psychiatry</i> , 2020 , 25, 6-18 | 15.1 | 16 |
| 50 | Integrated analysis sheds light on evolutionary trajectories of young transcription start sites in the human genome. <i>Genome Research</i> , 2018 , 28, 676-688 | 9.7 | 15 |
| 49 | Transcriptional memory of cells of origin overrides E-catenin requirement of MLL cancer stem cells. <i>EMBO Journal</i> , 2017 , 36, 3139-3155 | 13 | 14 |
| 48 | Dissecting the transcriptional regulatory properties of human chromosome 16 highly conserved non-coding regions. <i>PLoS ONE</i> , 2011 , 6, e24824 | 3.7 | 13 |
| 47 | TBPL2/TFIIA complex establishes the maternal transcriptome through oocyte-specific promoter usage. <i>Nature Communications</i> , 2020 , 11, 6439 | 17.4 | 12 |
| 46 | Allele-specific analysis of cell fusion-mediated pluripotent reprogramming reveals distinct and predictive susceptibilities of human X-linked genes to reactivation. <i>Genome Biology</i> , 2017 , 18, 2 | 18.3 | 11 |
| 45 | 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 | 6.1 | 11 |
| 44 | GeneLynx mouse: integrated portal to the mouse genome. <i>Genome Research</i> , 2003 , 13, 1501-4 | 9.7 | 11 |
| 43 | C-terminal truncation of yeast SerRS is toxic for <i>Saccharomyces cerevisiae</i> due to altered mechanism of substrate recognition. <i>FEBS Letters</i> , 1998 , 439, 235-40 | 3.8 | 10 |
| 42 | Copy number variants in patients with intellectual disability affect the regulation of ARX transcription factor gene. <i>Human Genetics</i> , 2015 , 134, 1163-82 | 6.3 | 9 |
| 41 | A prioritization analysis of disease association by data-mining of functional annotation of human genes. <i>Genomics</i> , 2012 , 99, 1-9 | 4.3 | 9 |
| 40 | The order and logic of CD4 versus CD8 lineage choice and differentiation in mouse thymus. <i>Nature Communications</i> , 2021 , 12, 99 | 17.4 | 9 |
| 39 | RADICL-seq identifies general and cell type-specific principles of genome-wide RNA-chromatin interactions | | 8 |
| 38 | <i>Saccharomyces cerevisiae</i> displays a stable transcription start site landscape in multiple conditions. <i>FEMS Yeast Research</i> , 2019 , 19, | 3.1 | 8 |
| 37 | Gene characterization index: assessing the depth of gene annotation. <i>PLoS ONE</i> , 2008 , 3, e1440 | 3.7 | 7 |
| 36 | Neuronal genes deregulated in Cornelia de Lange Syndrome respond to removal and re-expression of cohesin. <i>Nature Communications</i> , 2021 , 12, 2919 | 17.4 | 7 |
| 35 | CNEr: A toolkit for exploring extreme noncoding conservation. <i>PLoS Computational Biology</i> , 2019 , 15, e1006940 | 5 | 6 |
| 34 | Distinct core promoter codes drive transcription initiation at key developmental transitions in a marine chordate. <i>BMC Genomics</i> , 2018 , 19, 164 | 4.5 | 6 |

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|----|---|------|---|
| 33 | Web-based tools and approaches to study long-range gene regulation in Metazoa. <i>Briefings in Functional Genomics & Proteomics</i> , 2009 , 8, 231-42 | | 6 |
| 32 | Integrator is recruited to promoter-proximally paused RNA Pol II to generate <i>Caenorhabditis elegans</i> piRNA precursors. <i>EMBO Journal</i> , 2021 , 40, e105564 | 13 | 6 |
| 31 | Functional Annotation of Human Long Non-Coding RNAs via Molecular Phenotyping | | 6 |
| 30 | Ancestrally Duplicated Conserved Noncoding Element Suggests Dual Regulatory Roles of HOTAIR in cis and trans. <i>IScience</i> , 2020 , 23, 101008 | 6.1 | 6 |
| 29 | Germ cell differentiation requires Tdrd7-dependent chromatin and transcriptome reprogramming marked by germ plasm relocalization. <i>Developmental Cell</i> , 2021 , 56, 641-656.e5 | 10.2 | 6 |
| 28 | Functional reconstruction of human AML reveals stem cell origin and vulnerability of treatment-resistant MLL-rearranged leukemia. <i>Science Translational Medicine</i> , 2021 , 13, | 17.5 | 6 |
| 27 | Computational characterization of modes of transcriptional regulation of nuclear receptor genes. <i>PLoS ONE</i> , 2014 , 9, e88880 | 3.7 | 5 |
| 26 | Naturally Occurring Isoleucyl-tRNA Synthetase without tRNA-dependent Pre-transfer Editing. <i>Journal of Biological Chemistry</i> , 2016 , 291, 8618-31 | 5.4 | 5 |
| 25 | Core promoters across the genome. <i>Nature Biotechnology</i> , 2017 , 35, 123-124 | 44.5 | 4 |
| 24 | Transcription Start Site Mapping Using Super-low Input Carrier-CAGE. <i>Journal of Visualized Experiments</i> , 2019 , | 1.6 | 4 |
| 23 | An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010 , 141, 369 | 56.2 | 3 |
| 22 | Widespread conservation and lineage-specific diversification of genome-wide DNA methylation patterns across arthropods | | 3 |
| 21 | Global regulatory transitions at core promoters demarcate the mammalian germline cycle | | 3 |
| 20 | Feedforward regulation of Myc coordinates lineage-specific with housekeeping gene expression during B cell progenitor cell differentiation. <i>PLoS Biology</i> , 2019 , 17, e2006506 | 9.7 | 2 |
| 19 | Exploring the foundation of genomics: a northern blot reference set for the comparative analysis of transcript profiling technologies. <i>Comparative and Functional Genomics</i> , 2004 , 5, 584-95 | | 2 |
| 18 | Integrated analysis sheds light on evolutionary trajectories of young transcription start sites in the human genome | | 2 |
| 17 | Embryonic tissue differentiation is characterized by transitions in cell cycle dynamic-associated core promoter regulation. <i>Nucleic Acids Research</i> , 2020 , 48, 8374-8392 | 20.1 | 1 |
| 16 | Making enhancers from spare parts of the genome. <i>Genome Biology</i> , 2011 , 12, 138 | 18.3 | 1 |

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|----|--|-----|---|
| 15 | GRID COMPUTING FOR THE ANALYSIS OF REGULATORY ELEMENTS IN CO-REGULATED SETS OF GENES. <i>Parallel Processing Letters</i> , 2004 , 14, 137-150 | 0.3 | 1 |
| 14 | Identification of downstream effectors of retinoic acid specifying the zebrafish pancreas by integrative genomics. <i>Scientific Reports</i> , 2021 , 11, 22717 | 4.9 | 1 |
| 13 | Topologically associated domains are ancient features that coincide with Metazoan clusters of extreme noncoding conservation | | 1 |
| 12 | Germ plasm localisation dynamics mark distinct phases of transcriptional and post-transcriptional regulation control in primordial germ cells | | 1 |
| 11 | Partial rescue of neuronal genes deregulated in Cornelia de Lange Syndrome by cohesin | | 1 |
| 10 | HBS1L-MYB intergenic Variants Modulate Fetal Hemoglobin Via Long-Range MYB Enhancers. <i>Blood</i> , 2013 , 122, 43-43 | 2.2 | 1 |
| 9 | A novel measure of non-coding genome conservation identifies genomic regulatory blocks within primates. <i>Bioinformatics</i> , 2019 , 35, 2354-2361 | 7.2 | 1 |
| 8 | Translog, a web browser for studying the expression divergence of homologous genes. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 1, S59 | 3.6 | |
| 7 | Reconstruction of Human AML Reveals Stem Cell Origin and Therapeutic Targets for Treatment Resistant CD34-/Lo MLL-Rearranged Leukemia. <i>Blood</i> , 2019 , 134, 3203-3203 | 2.2 | |
| 6 | ▣▣▣▣Widespread conservation and lineage-specific diversification of genome-wide DNA methylation patterns across arthropods 2020 , 16, e1008864 | | |
| 5 | ▣▣▣▣Widespread conservation and lineage-specific diversification of genome-wide DNA methylation patterns across arthropods 2020 , 16, e1008864 | | |
| 4 | ▣▣▣▣Widespread conservation and lineage-specific diversification of genome-wide DNA methylation patterns across arthropods 2020 , 16, e1008864 | | |
| 3 | ▣▣▣▣Widespread conservation and lineage-specific diversification of genome-wide DNA methylation patterns across arthropods 2020 , 16, e1008864 | | |
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| 1 | ▣▣▣▣Widespread conservation and lineage-specific diversification of genome-wide DNA methylation patterns across arthropods 2020 , 16, e1008864 | | |