

Boris Lenhard

List of Publications by Year in Descending Order

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Version: 2024-04-20

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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	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
157	Identification of downstream effectors of retinoic acid specifying the zebrafish pancreas by integrative genomics. <i>Scientific Reports</i> , 2021 , 11, 22717	4.9	1
156	JASPAR 2022: the 9th release of the open-access database of transcription factor binding profiles. <i>Nucleic Acids Research</i> , 2021 ,	20.1	58
155	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
154	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
153	Conservative route to genome compaction in a miniature annelid. <i>Nature Ecology and Evolution</i> , 2021 , 5, 231-242	12.3	17
152	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
151	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
150	TBPL2/TFIIA complex establishes the maternal transcriptome through oocyte-specific promoter usage. <i>Nature Communications</i> , 2020 , 11, 6439	17.4	12
149	-----Widespread conservation and lineage-specific diversification of genome-wide DNA methylation patterns across arthropods. <i>PLoS Genetics</i> , 2020 , 16, e1008864	6	24
148	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
147	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
146	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
145	Ancestrally Duplicated Conserved Noncoding Element Suggests Dual Regulatory Roles of HOTAIR in cis and trans. <i>IScience</i> , 2020 , 23, 101008	6.1	6
144	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020 , 30, 1060-1072	9.7	41
143	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
142	Understanding the genetics of neuropsychiatric disorders: the potential role of genomic regulatory blocks. <i>Molecular Psychiatry</i> , 2020 , 25, 6-18	15.1	16

141	Widespread conservation and lineage-specific diversification of genome-wide DNA methylation patterns across arthropods 2020 , 16, e1008864		
140	Widespread conservation and lineage-specific diversification of genome-wide DNA methylation patterns across arthropods 2020 , 16, e1008864		
139	Widespread conservation and lineage-specific diversification of genome-wide DNA methylation patterns across arthropods 2020 , 16, e1008864		
138	Widespread conservation and lineage-specific diversification of genome-wide DNA methylation patterns across arthropods 2020 , 16, e1008864		
137	Widespread conservation and lineage-specific diversification of genome-wide DNA methylation patterns across arthropods 2020 , 16, e1008864		
136	Widespread conservation and lineage-specific diversification of genome-wide DNA methylation patterns across arthropods 2020 , 16, e1008864		
135	CNEr: A toolkit for exploring extreme noncoding conservation. <i>PLoS Computational Biology</i> , 2019 , 15, e1006940	5	6
134	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
133	DNA stretching induces Cas9 off-target activity. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 185-192.6	2.6	55
132	Transcription Start Site Mapping Using Super-low Input Carrier-CAGE. <i>Journal of Visualized Experiments</i> , 2019 ,	1.6	4
131	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	
130	A novel measure of non-coding genome conservation identifies genomic regulatory blocks within primates. <i>Bioinformatics</i> , 2019 , 35, 2354-2361	7.2	1
129	<i>Saccharomyces cerevisiae</i> displays a stable transcription start site landscape in multiple conditions. <i>FEMS Yeast Research</i> , 2019 , 19,	3.1	8
128	Epigenetic reprogramming enables the transition from primordial germ cell to gonocyte. <i>Nature</i> , 2018 , 555, 392-396	50.4	127
127	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
126	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
125	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
124	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

123	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
122	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
121	Amphioxus functional genomics and the origins of vertebrate gene regulation. <i>Nature</i> , 2018 , 564, 64-70	50.4	120
120	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
119	Core promoters across the genome. <i>Nature Biotechnology</i> , 2017 , 35, 123-124	44.5	4
118	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
117	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
116	Conserved non-coding elements: developmental gene regulation meets genome organization. <i>Nucleic Acids Research</i> , 2017 , 45, 12611-12624	20.1	46
115	Targeting Aberrant Epigenetic Networks Mediated by PRMT1 and KDM4C in Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2016 , 29, 32-48	24.3	98
114	Promoter architectures and developmental gene regulation. <i>Seminars in Cell and Developmental Biology</i> , 2016 , 57, 11-23	7.5	36
113	TFBSTools: an R/bioconductor package for transcription factor binding site analysis. <i>Bioinformatics</i> , 2016 , 32, 1555-6	7.2	137
112	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
111	Naturally Occurring Isoleucyl-tRNA Synthetase without tRNA-dependent Pre-transfer Editing. <i>Journal of Biological Chemistry</i> , 2016 , 291, 8618-31	5.4	5
110	Transcriptional, post-transcriptional and chromatin-associated regulation of pri-miRNAs, pre-miRNAs and moRNAs. <i>Nucleic Acids Research</i> , 2016 , 44, 3070-81	20.1	25
109	CAGEr: precise TSS data retrieval and high-resolution promoterome mining for integrative analyses. <i>Nucleic Acids Research</i> , 2015 , 43, e51	20.1	117
108	Long-range evolutionary constraints reveal cis-regulatory interactions on the human X chromosome. <i>Nature Communications</i> , 2015 , 6, 6904	17.4	20
107	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
106	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

105	GenomicInteractions: An R/Bioconductor package for manipulating and investigating chromatin interaction data. <i>BMC Genomics</i> , 2015 , 16, 963	4.5	29
104	Control of developmentally primed erythroid genes by combinatorial co-repressor actions. <i>Nature Communications</i> , 2015 , 6, 8893	17.4	47
103	Spatial enhancer clustering and regulation of enhancer-proximal genes by cohesin. <i>Genome Research</i> , 2015 , 25, 504-13	9.7	106
102	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014 , 507, 462-70	50.4	1301
101	Two independent transcription initiation codes overlap on vertebrate core promoters. <i>Nature</i> , 2014 , 507, 381-385	50.4	121
100	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
99	Computational characterization of modes of transcriptional regulation of nuclear receptor genes. <i>PLoS ONE</i> , 2014 , 9, e88880	3.7	5
98	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
97	A cohesin-independent role for NIPBL at promoters provides insights in CdLS. <i>PLoS Genetics</i> , 2014 , 10, e1004153	6	87
96	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
95	Cohesin-based chromatin interactions enable regulated gene expression within preexisting architectural compartments. <i>Genome Research</i> , 2013 , 23, 2066-77	9.7	232
94	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
93	Genome-wide, whole mount in situ analysis of transcriptional regulators in zebrafish embryos. <i>Developmental Biology</i> , 2013 , 380, 351-62	3.1	43
92	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
91	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
90	Chromatin and epigenetic features of long-range gene regulation. <i>Nucleic Acids Research</i> , 2013 , 41, 7185-91	20.1	87
89	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
88	The mystery of extreme non-coding conservation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013 , 368, 20130021	5.8	50

87	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
86	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
85	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
84	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
83	HBS1L-MYB intergenic Variants Modulate Fetal Hemoglobin Via Long-Range MYB Enhancers. <i>Blood</i> , 2013 , 122, 43-43	2.2	1
82	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
81	A novel complex, RUNX1-MYEF2, represses hematopoietic genes in erythroid cells. <i>Molecular and Cellular Biology</i> , 2012 , 32, 3814-22	4.8	27
80	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
79	Genome-wide DNA methylation profiling of non-small cell lung carcinomas. <i>Epigenetics and Chromatin</i> , 2012 , 5, 9	5.8	49
78	Metazoan promoters: emerging characteristics and insights into transcriptional regulation. <i>Nature Reviews Genetics</i> , 2012 , 13, 233-45	30.1	347
77	The accessible chromatin landscape of the human genome. <i>Nature</i> , 2012 , 489, 75-82	50.4	1900
76	Dynamic long-range chromatin interactions control Myb proto-oncogene transcription during erythroid development. <i>EMBO Journal</i> , 2012 , 31, 986-99	13	107
75	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
74	Promoter architecture of mouse olfactory receptor genes. <i>Genome Research</i> , 2012 , 22, 486-97	9.7	46
73	The DNA-binding protein CTCF limits proximal V(D)J recombination and restricts enhancer interactions to the immunoglobulin light chain locus. <i>Immunity</i> , 2011 , 35, 501-13	32.3	92
72	Dissecting the transcriptional regulatory properties of human chromosome 16 highly conserved non-coding regions. <i>PLoS ONE</i> , 2011 , 6, e24824	3.7	13
71	Sox2 cooperates with Chd7 to regulate genes that are mutated in human syndromes. <i>Nature Genetics</i> , 2011 , 43, 607-11	36.3	187
70	Making enhancers from spare parts of the genome. <i>Genome Biology</i> , 2011 , 12, 138	18.3	1

69	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
68	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
67	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
66	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
65	Plasticity of animal genome architecture unmasked by rapid evolution of a pelagic tunicate. <i>Science</i> , 2010 , 330, 1381-5	33.3	212
64	An atlas of combinatorial transcriptional regulation in mouse and man. <i>Cell</i> , 2010 , 140, 744-52	56.2	555
63	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010 , 141, 369	56.2	3
62	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
61	Translog, a web browser for studying the expression divergence of homologous genes. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 1, S59	3.6	
60	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
59	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
58	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
57	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
56	Synorth: exploring the evolution of synteny and long-range regulatory interactions in vertebrate genomes. <i>Genome Biology</i> , 2009 , 10, R86	18.3	21
55	Transcriptional features of genomic regulatory blocks. <i>Genome Biology</i> , 2009 , 10, R38	18.3	77
54	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
53	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
52	In silico detection of sequence variations modifying transcriptional regulation. <i>PLoS Computational Biology</i> , 2008 , 4, e5	5	81

51	Gene characterization index: assessing the depth of gene annotation. <i>PLoS ONE</i> , 2008 , 3, e1440	3.7	7
50	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
49	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
48	Mammalian microRNA prediction through a support vector machine model of sequence and structure. <i>PLoS ONE</i> , 2007 , 2, e946	3.7	43
47	Mammalian RNA polymerase II core promoters: insights from genome-wide studies. <i>Nature Reviews Genetics</i> , 2007 , 8, 424-36	30.1	394
46	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
45	RNAdb 2.0--an expanded database of mammalian non-coding RNAs. <i>Nucleic Acids Research</i> , 2007 , 35, D178-82	20.1	134
44	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
43	Genomic regulatory blocks underlie extensive microsynteny conservation in insects. <i>Genome Research</i> , 2007 , 17, 1898-908	9.7	153
42	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
41	Genomic regulatory blocks encompass multiple neighboring genes and maintain conserved synteny in vertebrates. <i>Genome Research</i> , 2007 , 17, 545-55	9.7	264
40	A global genomic transcriptional code associated with CNS-expressed genes. <i>Experimental Cell Research</i> , 2006 , 312, 3108-19	4.2	39
39	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
38	Complex Loci in human and mouse genomes. <i>PLoS Genetics</i> , 2006 , 2, e47	6	246
37	Transcript annotation in FANTOM3: mouse gene catalog based on physical cDNAs. <i>PLoS Genetics</i> , 2006 , 2, e62	6	138
36	Transcriptional and structural impact of TATA-initiation site spacing in mammalian core promoters. <i>Genome Biology</i> , 2006 , 7, R78	18.3	85
35	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
34	Alternative promoter usage of the membrane glycoprotein CD36. <i>BMC Molecular Biology</i> , 2006 , 7, 8	4.5	43

33	Genome-wide analysis of mammalian promoter architecture and evolution. <i>Nature Genetics</i> , 2006 , 38, 626-35	36.3	1021
32	The transcriptional landscape of the mammalian genome. <i>Science</i> , 2005 , 309, 1559-63	33.3	2807
31	RNAdb--a comprehensive mammalian noncoding RNA database. <i>Nucleic Acids Research</i> , 2005 , 33, D125-30.1	30.1	113
30	Antisense transcription in the mammalian transcriptome. <i>Science</i> , 2005 , 309, 1564-6	33.3	1354
29	Identification of functional SNPs in the 5-prime flanking sequences of human genes. <i>BMC Genomics</i> , 2005 , 6, 18	4.5	41
28	Exploring hepatic hormone actions using a compilation of gene expression profiles. <i>BMC Physiology</i> , 2005 , 5, 8	0	37
27	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
26	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
25	JASPAR: an open-access database for eukaryotic transcription factor binding profiles. <i>Nucleic Acids Research</i> , 2004 , 32, D91-4	20.1	1197
24	ConSite: web-based prediction of regulatory elements using cross-species comparison. <i>Nucleic Acids Research</i> , 2004 , 32, W249-52	20.1	341
23	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
22	Integrative annotation of 21,037 human genes validated by full-length cDNA clones. <i>PLoS Biology</i> , 2004 , 2, e162	9.7	255
21	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
20	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
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 of yeast regulatory sequences for biologically linked clusters of genes. <i>Functional and Integrative Genomics</i> , 2003 , 3, 125-34	3.8	25
17	Identification of conserved regulatory elements by comparative genome analysis. <i>Journal of Biology</i> , 2003 , 2, 13		194
16	GeneLynx mouse: integrated portal to the mouse genome. <i>Genome Research</i> , 2003 , 13, 1501-4	9.7	11

15	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
14	TFBS: Computational framework for transcription factor binding site analysis. <i>Bioinformatics</i> , 2002 , 18, 1135-6	7.2	147
13	GeneLynx: a gene-centric portal to the human genome. <i>Genome Research</i> , 2001 , 11, 2151-7	9.7	44
12	tRNA recognition and evolution of determinants in seryl-tRNA synthesis. <i>Nucleic Acids Research</i> , 1999 , 27, 721-9	20.1	57
11	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
10	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
9	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
8	Widespread conservation and lineage-specific diversification of genome-wide DNA methylation patterns across arthropods		3
7	Topologically associated domains are ancient features that coincide with Metazoan clusters of extreme noncoding conservation		1
6	Integrated analysis sheds light on evolutionary trajectories of young transcription start sites in the human genome		2
5	Germ plasm localisation dynamics mark distinct phases of transcriptional and post-transcriptional regulation control in primordial germ cells		1
4	Partial rescue of neuronal genes deregulated in Cornelia de Lange Syndrome by cohesin		1
3	Global regulatory transitions at core promoters demarcate the mammalian germline cycle		3
2	RADICL-seq identifies general and cell type-specific principles of genome-wide RNA-chromatin interactions		8
1	Functional Annotation of Human Long Non-Coding RNAs via Molecular Phenotyping		6