Albin Sandelin

List of Publications by Year
in descending order

113 papers	36,625 citations	20815 60 h-index	20955 115 g-index
129 all docs	129 docs citations	129 times ranked	46502 citing authors

#	Article	IF	Citations
1	JASPAR 2022: the 9th release of the open-access database of transcription factor binding profiles. Nucleic Acids Research, 2022, 50, D165-D173.	14.5	902
2	Mesenchymal-epithelial crosstalk shapes intestinal regionalisation via Wnt and Shh signalling. Nature Communications, 2022, 13, 715.	12.8	15
3	Chromatin modifier HUSH co-operates with RNA decay factor NEXT to restrict transposable element expression. Molecular Cell, 2022, 82, 1691-1707.e8.	9.7	43
4	PAMP-triggered genetic reprogramming involves widespread alternative transcription initiation and an immediate transcription factor wave. Plant Cell, 2022, 34, 2615-2637.	6.6	12
5	TrancriptomeReconstructoR: data-driven annotation of complex transcriptomes. BMC Bioinformatics, 2021, 22, 290.	2.6	12
6	Genomic Stability and Phenotypic Characteristics of Industrially Produced Lacticaseibacillus rhamnosus GG in a Yogurt Matrix. Applied and Environmental Microbiology, 2021, 87, e0157521.	3.1	5
7	JASPAR 2020: update of the open-access database of transcription factor binding profiles. Nucleic Acids Research, 2020, 48, D87-D92.	14.5	1,039
8	Determinants of enhancer and promoter activities of regulatory elements. Nature Reviews Genetics, 2020, 21, 71-87.	16.3	464
9	Personalized B cell response to the Lactobacillus rhamnosus GG probiotic in healthy human subjects: a randomized trial. Gut Microbes, 2020, 12, 1854639.	9.8	5
10	Cancer Cell Acid Adaptation Gene Expression Response Is Correlated to Tumor-Specific Tissue Expression Profiles and Patient Survival. Cancers, 2020, 12, 2183.	3.7	19
11	The RNA exosome shapes the expression of key protein-coding genes. Nucleic Acids Research, 2020, 48, 8509-8528.	14.5	12
12	Functional annotation of human long noncoding RNAs via molecular phenotyping. Genome Research, 2020, 30, 1060-1072.	5.5	109
13	Characterization of Arabidopsis thaliana Promoter Bidirectionality and Antisense RNAs by Inactivation of Nuclear RNA Decay Pathways. Plant Cell, 2020, 32, 1845-1867.	6.6	50
14	A Two-Layered Targeting Mechanism Underlies Nuclear RNA Sorting by the Human Exosome. Cell Reports, 2020, 30, 2387-2401.e5.	6.4	44
15	Lactobacillus rhamnosus GG Genomic and Phenotypic Stability in an Industrial Production Process. Applied and Environmental Microbiology, 2020, 86, .	3.1	13
16	Organismal benefits of transcription speed control at gene boundaries. EMBO Reports, 2020, 21, e49315.	4.5	28
17	CAGEfightR: analysis of 5â€²-end data using R/Bioconductor. BMC Bioinformatics, 2019, 20, 487.	2.6	59
18	A Functional Link between Nuclear RNA Decay and Transcriptional Control Mediated by the Polycomb Repressive Complex 2. Cell Reports, 2019, 29, 1800-1811.e6.	6.4	32

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19	Comprehensive profiling of the fission yeast transcription start site activity during stress and media response. Nucleic Acids Research, 2019, 47, 1671-1691.	14.5	34
20	IsoformSwitchAnalyzeR: analysis of changes in genome-wide patterns of alternative splicing and its functional consequences. Bioinformatics, 2019, 35, 4469-4471.	4.1	189
21	PLZF targets developmental enhancers for activation during osteogenic differentiation of human mesenchymal stem cells. ELife, 2019, 8, .	6.0	32
22	A step-by-step guide to analyzing CAGE data using R/Bioconductor. F1000Research, 2019, 8, 886.	1.6	23
23	JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. Nucleic Acids Research, 2018, 46, D260-D266.	14.5	1,232
24	Characterization of the enhancer and promoter landscape of inflammatory bowel disease from human colon biopsies. Nature Communications, 2018, 9, 1661.	12.8	78
25	The RNA exosome contributes to gene expression regulation during stem cell differentiation. Nucleic Acids Research, 2018, 46, 11502-11513.	14.5	40
26	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease. PLoS Computational Biology, 2018, 14, e1005934.	3.2	17
27	Regulation of Laminin Î³2 Expression by CDX2 in Colonic Epithelial Cells Is Impaired During Active Inflammation. Journal of Cellular Biochemistry, 2017, 118, 298-307.	2.6	8
28	The Landscape of Isoform Switches in Human Cancers. Molecular Cancer Research, 2017, 15, 1206-1220.	3.4	208
29	Identification of Gene Transcription Start Sites and Enhancers Responding to Pulmonary Carbon Nanotube Exposure in Vivo. ACS Nano, 2017, 11, 3597-3613.	14.6	23
30	An integrated expression atlas of miRNAs and their promoters in human and mouse. Nature Biotechnology, 2017, 35, 872-878.	17.5	456
31	Relation between NOD2 genotype and changes in innate signaling in Crohnâ€™s disease on mRNA and miRNA levels. Npj Genomic Medicine, 2017, 2, 3.	3.8	7
32	Update of the FANTOM web resource: high resolution transcriptome of diverse cell types in mammals. Nucleic Acids Research, 2017, 45, D737-D743.	14.5	116
33	Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution. Diabetes, 2017, 66, 218-230.	0.6	27
34	On-the-fly selection of cell-specific enhancers, genes, miRNAs and proteins across the human body using SlideBase. Database: the Journal of Biological Databases and Curation, 2016, 2016, .	3.0	24
35	Regulating retrotransposon activity through the use of alternative transcription start sites. EMBO Reports, 2016, 17, 753-768.	4.5	21
36	The Adipose Transcriptional Response to Insulin Is Determined by Obesity, Not Insulin Sensitivity. Cell Reports, 2016, 16, 2317-2326.	6.4	35

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37	Principles for RNA metabolism and alternative transcription initiation within closely spaced promoters. Nature Genetics, 2016, 48, 984-994.	21.4	75
38	Identification of a Nuclear Exosome Decay Pathway for Processed Transcripts. Molecular Cell, 2016, 64, 520-533.	9.7	209
39	Transcriptome Analysis of Recurrently Deregulated Genes across Multiple Cancers Identifies New Pan-Cancer Biomarkers. Cancer Research, 2016, 76, 216-226.	0.9	80
40	JASPAR 2016: a major expansion and update of the open-access database of transcription factor binding profiles. Nucleic Acids Research, 2016, 44, D110-D115.	14.5	968
41	Abstract 2897: Recurrent transcriptome alterations across multiple cancer types. , 2016, , .		0
42	Remodeling of retrotransposon elements during epigenetic induction of adult visual cortical plasticityÂby HDAC inhibitors. Epigenetics and Chromatin, 2015, 8, 55.	3.9	32
43	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. Science, 2015, 347, 1010-1014.	12.6	517
44	Gateways to the FANTOM5 promoter level mammalian expression atlas. Genome Biology, 2015, 16, 22.	8.8	687
45	The frequent evolutionary birth and death of functional promoters in mouse and human. Genome Research, 2015, 25, 1546-1557.	5.5	55
46	A unified architecture of transcriptional regulatory elements. Trends in Genetics, 2015, 31, 426-433.	6.7	173
47	Human Gene Promoters Are Intrinsically Bidirectional. Molecular Cell, 2015, 60, 346-347.	9.7	55
48	Human nonsense-mediated RNA decay initiates widely by endonucleolysis and targets snoRNA host genes. Genes and Development, 2014, 28, 2498-2517.	5.9	163
49	Identification of TNF-Â-Responsive Promoters and Enhancers in the Intestinal Epithelial Cell Model Caco-2. DNA Research, 2014, 21, 569-583.	3.4	12
50	Genome-wide nucleosome map and cytosine methylation levels of an ancient human genome. Genome Research, 2014, 24, 454-466.	5.5	161
51	JASPAR 2014: an extensively expanded and updated open-access database of transcription factor binding profiles. Nucleic Acids Research, 2014, 42, D142-D147.	14.5	915
52	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	27.8	1,838
53	An atlas of active enhancers across human cell types and tissues. Nature, 2014, 507, 455-461.	27.8	2,269
54	Analysis of the DNA methylome and transcriptome in granulopoiesis reveals timed changes and dynamic enhancer methylation. Blood, 2014, 123, e79-e89.	1.4	72

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55	Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. Nature Genetics, 2014, 46, 558-566.	21.4	271
56	New histone supply regulates replication fork speed and PCNA unloading. Journal of Cell Biology, 2014, 204, 29-43.	5.2	132
57	Nuclear stability and transcriptional directionality separate functionally distinct RNA species. Nature Communications, 2014, 5, 5336.	12.8	165
58	spliceR: an R package for classification of alternative splicing and prediction of coding potential from RNA-seq data. BMC Bioinformatics, 2014, 15, 81.	2.6	100
59	Molecular Architecture of Transcription Factor Hotspots in Early Adipogenesis. Cell Reports, 2014, 7, 1434-1442.	6.4	58
60	Transcriptional profiling of the human fibrillin/LTBP gene family, key regulators of mesenchymal cell functions. Molecular Genetics and Metabolism, 2014, 112, 73-83.	1.1	39
61	CAGE-defined promoter regions of the genes implicated in Rett Syndrome. BMC Genomics, 2014, 15, 1177.	2.8	10
62	Polyadenylation siteâ€"induced decay of upstream transcripts enforces promoter directionality. Nature Structural and Molecular Biology, 2013, 20, 923-928.	8.2	258
63	Acute Genome-Wide Effects of Rosiglitazone on PPARÎ³ Transcriptional Networks in Adipocytes. Molecular Endocrinology, 2013, 27, 1536-1549.	3.7	51
64	Detection of Reverse Transcriptase Termination Sites Using cDNA Ligation and Massive Parallel Sequencing. Methods in Molecular Biology, 2013, 1038, 213-231.	0.9	11
65	GMD: measuring the distance between histograms with applications on high-throughput sequencing reads. Bioinformatics, 2012, 28, 1164-1165.	4.1	16
66	Cross-species ChIP-seq studies provide insights into regulatory strategies of PPARÎ³ in adipocytes. Transcription, 2012, 3, 19-24.	3.1	6
67	Interaction of Antidepressants with the Serotonin and Norepinephrine Transporters. Journal of Biological Chemistry, 2012, 287, 43694-43707.	3.4	73
68	Systematic identification of long noncoding RNAs expressed during zebrafish embryogenesis. Genome Research, 2012, 22, 577-591.	5.5	809
69	Metazoan promoters: emerging characteristics and insights into transcriptional regulation. Nature Reviews Genetics, 2012, 13, 233-245.	16.3	448
70	Biogenic mechanisms and utilization of small RNAs derived from human protein-coding genes. Nature Structural and Molecular Biology, 2011, 18, 1075-1082.	8.2	94
71	Systematic Clustering of Transcription Start Site Landscapes. PLoS ONE, 2011, 6, e23409.	2.5	59
72	Genomic and chromatin signals underlying transcription start-site selection. Trends in Genetics, 2011, 27, 475-485.	6.7	59

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73	Cross species comparison of C/EBPÎ± and PPARÎ³ profiles in mouse and human adipocytes reveals interdependent retention of binding sites. BMC Genomics, 2011, 12, 152.	2.8	88
74	Prediction of RNA Polymerase II recruitment, elongation and stalling from histone modification data. BMC Genomics, 2011, 12, 544.	2.8	31
75	PROMoter uPstream Transcripts share characteristics with mRNAs and are produced upstream of all three major types of mammalian promoters. Nucleic Acids Research, 2011, 39, 7179-7193.	14.5	139
76	Multivariate Hawkes process models of the occurrence of regulatory elements. BMC Bioinformatics, 2010, 11, 456.	2.6	40
77	Transcriptional regulation of gene expression clusters in motor neurons following spinal cord injury. BMC Genomics, 2010, 11, 365.	2.8	36
78	A conceptual framework for the identification of candidate drugs and drug targets in acute promyelocytic leukemia. Leukemia, 2010, 24, 1265-1275.	7.2	21
79	Gene expression analysis of the emergence of epileptiform activity after focal injection of kainic acid into mouse hippocampus. European Journal of Neuroscience, 2010, 32, 1364-1379.	2.6	25
80	3-Methylcholanthrene Induces Differential Recruitment of Aryl Hydrocarbon Receptor to Human Promoters. Toxicological Sciences, 2010, 117, 90-100.	3.1	31
81	JASPAR 2010: the greatly expanded open-access database of transcription factor binding profiles. Nucleic Acids Research, 2010, 38, D105-D110.	14.5	529
82	Genome-wide detection and analysis of hippocampus core promoters using DeepCAGE. Genome Research, 2009, 19, 255-265.	5.5	128
83	Discovery of Regulatory Elements is Improved by a Discriminatory Approach. PLoS Computational Biology, 2009, 5, e1000562.	3.2	27
84	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. Nature Genetics, 2009, 41, 553-562.	21.4	408
85	Dioxin Increases the Interaction Between Aryl Hydrocarbon Receptor and Estrogen Receptor Alpha at Human Promoters. Toxicological Sciences, 2009, 111, 254-266.	3.1	73
86	A code for transcription initiation in mammalian genomes. Genome Research, 2008, 18, 1-12.	5.5	237
87	Hidden layers of human small RNAs. BMC Genomics, 2008, 9, 157.	2.8	255
88	Prediction of Regulatory Elements. Methods in Molecular Biology, 2008, 453, 233-244.	0.9	7
89	Modeling promoter grammars with evolving hidden Markov models. Bioinformatics, 2008, 24, 1669-1675.	4.1	12
90	The genome landscape of ERÎ±- and ERÎ²-binding DNA regions. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2604-2609.	7.1	95

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91	Genome-Wide Identification of Estrogen Receptor Î±-Binding Sites in Mouse Liver. Molecular Endocrinology, 2008, 22, 10-22.	3.7	130
92	JASPAR, the open access database of transcription factor-binding profiles: new content and tools in the 2008 update. Nucleic Acids Research, 2007, 36, D102-D106.	14.5	603
93	Mammalian RNA polymerase II core promoters: insights from genome-wide studies. Nature Reviews Genetics, 2007, 8, 424-436.	16.3	435
94	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
95	Dynamic usage of transcription start sites within core promoters. Genome Biology, 2006, 7, R118.	9.6	75
96	Transcriptional and structural impact of TATA-initiation site spacing in mammalian core promoters. Genome Biology, 2006, 7, R78.	9.6	101
97	A new generation of JASPAR, the open-access repository for transcription factor binding site profiles. Nucleic Acids Research, 2006, 34, D95-D97.	14.5	200
98	Genome-wide analysis of mammalian promoter architecture and evolution. Nature Genetics, 2006, 38, 626-635.	21.4	1,201
99	The complexity of the mammalian transcriptome. Journal of Physiology, 2006, 575, 321-332.	2.9	91
100	A global genomic transcriptional code associated with CNS-expressed genes. Experimental Cell Research, 2006, 312, 3108-3119.	2.6	41
101	Evolutionary turnover of mammalian transcription start sites. Genome Research, 2006, 16, 713-722.	5.5	68
102	Antisense Transcription in the Mammalian Transcriptome. Science, 2005, 309, 1564-1566.	12.6	1,553
103	Exploring hepatic hormone actions using a compilation of gene expression profiles. BMC Physiology, 2005, 5, 8.	3.6	39
104	Prediction of Nuclear Hormone Receptor Response Elements. Molecular Endocrinology, 2005, 19, 595-606.	3.7	124
105	The Transcriptional Landscape of the Mammalian Genome. Science, 2005, 309, 1559-1563.	12.6	3,227
106	JASPAR: an open-access database for eukaryotic transcription factor binding profiles. Nucleic Acids Research, 2004, 32, 91D-94.	14.5	1,451
107	ConSite: web-based prediction of regulatory elements using cross-species comparison. Nucleic Acids Research, 2004, 32, W249-W252.	14.5	388
108	Applied bioinformatics for the identification of regulatory elements. Nature Reviews Genetics, 2004, 5, 276-287.	16.3	1,032

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109	Arrays of ultraconserved non-coding regions span the loci of key developmental genes in vertebrate genomes. BMC Genomics, 2004, 5, 99.	2.8	267
110	Constrained Binding Site Diversity within Families of Transcription Factors Enhances Pattern Discovery Bioinformatics. Journal of Molecular Biology, 2004, 338, 207-215.	4.2	157
111	Integrated analysis of yeast regulatory sequences for biologically linked clusters of genes. Functional and Integrative Genomics, 2003, 3, 125-134.	3.5	27
112	Identification of conserved regulatory elements by comparative genome analysis. Journal of Biology, 2003, 2, 13.	2.7	222
113	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. Nature, 2002, 420, 563-573.	27.8	1,548