Anthony Mathelier

List of Publications by Year
in descending order

50 papers	10,309 citations	186265 28 h-index	161849 54 g-index
70 all docs	70 docs citations	70 times ranked	22026 citing authors

#	Article	IF	Citations
1	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	27.8	1,838
2	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
3	JASPAR 2020: update of the open-access database of transcription factor binding profiles. Nucleic Acids Research, 2020, 48, D87-D92.	14.5	1,039
4	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
5	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
6	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
7	An integrated expression atlas of miRNAs and their promoters in human and mouse. Nature Biotechnology, 2017, 35, 872-878.	17.5	456
8	Intervene: a tool for intersection and visualization of multiple gene or genomic region sets. BMC Bioinformatics, 2017, 18, 287.	2.6	383
9	ReMap 2018: an updated atlas of regulatory regions from an integrative analysis of DNA-binding ChIP-seq experiments. Nucleic Acids Research, 2018, 46, D267-D275.	14.5	214
10	MirGeneDB 2.0: the metazoan microRNA complement. Nucleic Acids Research, 2020, 48, D132-D141.	14.5	194
11	The Next Generation of Transcription Factor Binding Site Prediction. PLoS Computational Biology, 2013, 9, e1003214.	3.2	160
12	MIReNA: finding microRNAs with high accuracy and no learning at genome scale and from deep sequencing data. Bioinformatics, 2010, 26, 2226-2234.	4.1	141
13	DNA Shape Features Improve Transcription Factor Binding Site Predictions InÂVivo. Cell Systems, 2016, 3, 278-286.e4.	6.2	119
14	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
15	TFBSshape: a motif database for DNA shape features of transcription factor binding sites. Nucleic Acids Research, 2014, 42, D148-D155.	14.5	111
16	DNA methylation at enhancers identifies distinct breast cancer lineages. Nature Communications, 2017, 8, 1379.	12.8	103
17	Identification of altered cis-regulatory elements in human disease. Trends in Genetics, 2015, 31, 67-76.	6.7	99
18	Characterization of the human RFX transcription factor family by regulatory and target gene analysis. BMC Genomics, 2018, 19, 181.	2.8	73

#	Article	IF	Citations
19	A map of direct TF–DNA interactions in the human genome. Nucleic Acids Research, 2019, 47, e21-e21.	14.5	72
20	High OGT activity is essential for MYC-driven proliferation of prostate cancer cells. Theranostics, 2019, 9, 2183-2197.	10.0	58
21	DNA methylation profiling in human Huntington's disease brain. Human Molecular Genetics, 2016, 25, 2013-2030.	2.9	56
22	Large scale chromosomal mapping of human microRNA structural clusters. Nucleic Acids Research, 2013, 41, 4392-4408.	14.5	48
23	Improving analysis of transcription factor binding sites within ChIP-Seq data based on topological motif enrichment. BMC Genomics, 2014, 15, 472.	2.8	47
24	DeepCAGE Transcriptomics Reveal an Important Role of the Transcription Factor MAFB in the Lymphatic Endothelium. Cell Reports, 2015, 13, 1493-1504.	6.4	46
25	Super-enhancers are transcriptionally more active and cell type-specific than stretch enhancers. Epigenetics, 2018, 13, 910-922.	2.7	37
26	Cis-regulatory somatic mutations and gene-expression alteration in B-cell lymphomas. Genome Biology, 2015, 16, 84.	8.8	36
27	UniBind: maps of high-confidence direct TF-DNA interactions across nine species. BMC Genomics, 2021, 22, 482.	2.8	36
28	Evaluating the impact of single nucleotide variants on transcription factor binding. Nucleic Acids Research, 2016, 44, gkw691.	14.5	35
29	Chromosomal periodicity and positional networks of genes in *Escherichia coli*. Molecular Systems Biology, 2010, 6, 366.	7.2	34
30	YY1 binding association with sex-biased transcription revealed through X-linked transcript levels and allelic binding analyses. Scientific Reports, 2016, 6, 37324.	3.3	32
31	Crosstalk between microRNA expression and DNA methylation drives the hormone-dependent phenotype of breast cancer. Genome Medicine, 2021, 13, 72.	8.2	27
32	The Potential of MicroRNAs in Personalized Medicine against Cancers. BioMed Research International, 2014, 2014, 1-10.	1.9	26
33	Beware the Jaccard: the choice of **similarity measure** is important and non-trivial in genomic colocalisation analysis. Briefings in Bioinformatics, 2020, 21, 1523-1530.	6.5	24
34	New MiniPromoter Ple345 (*NEFL*) Drives Strong and Specific Expression in Retinal Ganglion Cells of Mouse and Primate Retina. Human Gene Therapy, 2019, 30, 257-272.	2.7	21
35	Human MiniPromoters for ocular-rAAV expression in ON bipolar, cone, corneal, endothelial, Müller glial, and PAX6 cells. Gene Therapy, 2021, 28, 351-372.	4.5	18
36	BiasAway: command-line and web server to generate nucleotide composition-matched DNA background sequences. Bioinformatics, 2021, 37, 1607-1609.	4.1	18

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37	PAX6 MiniPromoters drive restricted expression from rAAV in the adult mouse retina. Molecular Therapy - Methods and Clinical Development, 2016, 3, 16051.	4.1	17
38	Twenty-Seven Tamoxifen-Inducible iCre-Driver Mouse Strains for Eye and Brain, Including Seventeen Carrying a New Inducible-First Constitutive-Ready Allele. Genetics, 2019, 211, 1155-1177.	2.9	17
39	Human Enhancers Harboring Specific Sequence Composition, Activity, and Genome Organization Are Linked to the Immune Response. Genetics, 2018, 209, 1055-1071.	2.9	16
40	Human White Adipose Tissue Displays Selective Insulin Resistance in the Obese State. Diabetes, 2021, 70, 1486-1497.	0.6	16
41	DeepCAGE transcriptomics identify HOXD10 as transcription factor regulating lymphatic endothelial responses to VEGF-C. Journal of Cell Science, 2016, 129, 2573-85.	2.0	15
42	CAGEd-oPOSSUM: motif enrichment analysis from CAGE-derived TSSs. Bioinformatics, 2016, 32, 2858-2860.	4.1	13
43	JASPAR RESTful API: accessing JASPAR data from any programming language. Bioinformatics, 2018, 34, 1612-1614.	4.1	13
44	Pioneer transcription factors are associated with the modulation of DNA methylation patterns across cancers. Epigenetics and Chromatin, 2022, 15, 13.	3.9	13
45	Put science first and formatting later. EMBO Reports, 2018, 19, .	4.5	11
46	Identification of novel cerebellar developmental transcriptional regulators with motif activity analysis. BMC Genomics, 2019, 20, 718.	2.8	11
47	MANTA2, update of the Mongo database for the analysis of transcription factor binding site alterations. Scientific Data, 2018, 5, 180141.	5.3	11
48	DNA copy number motifs are strong and independent predictors of survival in breast cancer. Communications Biology, 2020, 3, 153.	4.4	9
49	Expressed prognostic biomarkers for primary prostate cancer independent of multifocality and transcriptome heterogeneity. Cancer Gene Therapy, 2022, 29, 1276-1284.	4.6	3
50	Computational Analysis of Transcriptional Regulation Sites at the HTT Gene Locus. Journal of Huntington's Disease, 2018, 7, 223-237.	1.9	2