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List of Publications by Year in descending order

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Version: 2024-02-01

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	JASPAR 2022: the 9th release of the open-access database of transcription factor binding profiles. <i>Nucleic Acids Research</i> , 2022, 50, D165-D173.	14.5	902
2	Expressed prognostic biomarkers for primary prostate cancer independent of multifocality and transcriptome heterogeneity. <i>Cancer Gene Therapy</i> , 2022, 29, 1276-1284.	4.6	3
3	Pioneer transcription factors are associated with the modulation of DNA methylation patterns across cancers. <i>Epigenetics and Chromatin</i> , 2022, 15, 13.	3.9	13
4	Human MiniPromoters for ocular-rAAV expression in ON bipolar, cone, corneal, endothelial, Müller glial, and PAX6 cells. <i>Gene Therapy</i> , 2021, 28, 351-372.	4.5	18
5	Human White Adipose Tissue Displays Selective Insulin Resistance in the Obese State. <i>Diabetes</i> , 2021, 70, 1486-1497.	0.6	16
6	Crosstalk between microRNA expression and DNA methylation drives the hormone-dependent phenotype of breast cancer. <i>Genome Medicine</i> , 2021, 13, 72.	8.2	27
7	UniBind: maps of high-confidence direct TF-DNA interactions across nine species. <i>BMC Genomics</i> , 2021, 22, 482.	2.8	36
8	BiasAway: command-line and web server to generate nucleotide composition-matched DNA background sequences. <i>Bioinformatics</i> , 2021, 37, 1607-1609.	4.1	18
9	JASPAR 2020: update of the open-access database of transcription factor binding profiles. <i>Nucleic Acids Research</i> , 2020, 48, D87-D92.	14.5	1,039
10	Beware the Jaccard: the choice of similarity measure is important and non-trivial in genomic colocalisation analysis. <i>Briefings in Bioinformatics</i> , 2020, 21, 1523-1530.	6.5	24
11	MirGeneDB 2.0: the metazoan microRNA complement. <i>Nucleic Acids Research</i> , 2020, 48, D132-D141.	14.5	194
12	DNA copy number motifs are strong and independent predictors of survival in breast cancer. <i>Communications Biology</i> , 2020, 3, 153.	4.4	9
13	New MiniPromoter Ple345 (<i>NEFL</i>) Drives Strong and Specific Expression in Retinal Ganglion Cells of Mouse and Primate Retina. <i>Human Gene Therapy</i> , 2019, 30, 257-272.	2.7	21
14	Identification of novel cerebellar developmental transcriptional regulators with motif activity analysis. <i>BMC Genomics</i> , 2019, 20, 718.	2.8	11
15	High OGT activity is essential for MYC-driven proliferation of prostate cancer cells. <i>Theranostics</i> , 2019, 9, 2183-2197.	10.0	58
16	Twenty-Seven Tamoxifen-Inducible iCre-Driver Mouse Strains for Eye and Brain, Including Seventeen Carrying a New Inducible-First Constitutive-Ready Allele. <i>Genetics</i> , 2019, 211, 1155-1177.	2.9	17
17	A map of direct TF-DNA interactions in the human genome. <i>Nucleic Acids Research</i> , 2019, 47, e21-e21.	14.5	72
18	ReMap 2018: an updated atlas of regulatory regions from an integrative analysis of DNA-binding CHIP-seq experiments. <i>Nucleic Acids Research</i> , 2018, 46, D267-D275.	14.5	214

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19	Put science first and formatting later. EMBO Reports, 2018, 19, .	4.5	11
20	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
21	JASPAR RESTful API: accessing JASPAR data from any programming language. Bioinformatics, 2018, 34, 1612-1614.	4.1	13
22	Characterization of the human RFX transcription factor family by regulatory and target gene analysis. BMC Genomics, 2018, 19, 181.	2.8	73
23	Super-enhancers are transcriptionally more active and cell type-specific than stretch enhancers. Epigenetics, 2018, 13, 910-922.	2.7	37
24	Human Enhancers Harboring Specific Sequence Composition, Activity, and Genome Organization Are Linked to the Immune Response. Genetics, 2018, 209, 1055-1071.	2.9	16
25	Computational Analysis of Transcriptional Regulation Sites at the HTT Gene Locus. Journal of Huntington's Disease, 2018, 7, 223-237.	1.9	2
26	MANTA2, update of the Mongo database for the analysis of transcription factor binding site alterations. Scientific Data, 2018, 5, 180141.	5.3	11
27	An integrated expression atlas of miRNAs and their promoters in human and mouse. Nature Biotechnology, 2017, 35, 872-878.	17.5	456
28	DNA methylation at enhancers identifies distinct breast cancer lineages. Nature Communications, 2017, 8, 1379.	12.8	103
29	Intervene: a tool for intersection and visualization of multiple gene or genomic region sets. BMC Bioinformatics, 2017, 18, 287.	2.6	383
30	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
31	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
32	DNA Shape Features Improve Transcription Factor Binding Site Predictions In Vivo. Cell Systems, 2016, 3, 278-286.e4.	6.2	119
33	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
34	Evaluating the impact of single nucleotide variants on transcription factor binding. Nucleic Acids Research, 2016, 44, gkw691.	14.5	35
35	PAX6 MiniPromoters drive restricted expression from rAAV in the adult mouse retina. Molecular Therapy - Methods and Clinical Development, 2016, 3, 16051.	4.1	17
36	CAGED-oPOSSUM: motif enrichment analysis from CAGE-derived TSSs. Bioinformatics, 2016, 32, 2858-2860.	4.1	13

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37	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-D115.	14.5	968
38	DNA methylation profiling in human Huntington's disease brain. <i>Human Molecular Genetics</i> , 2016, 25, 2013-2030.	2.9	56
39	DeepCAGE Transcriptomics Reveal an Important Role of the Transcription Factor MAFB in the Lymphatic Endothelium. <i>Cell Reports</i> , 2015, 13, 1493-1504.	6.4	46
40	Cis-regulatory somatic mutations and gene-expression alteration in B-cell lymphomas. <i>Genome Biology</i> , 2015, 16, 84.	8.8	36
41	Identification of altered cis-regulatory elements in human disease. <i>Trends in Genetics</i> , 2015, 31, 67-76.	6.7	99
42	The Potential of MicroRNAs in Personalized Medicine against Cancers. <i>BioMed Research International</i> , 2014, 2014, 1-10.	1.9	26
43	TFBSshape: a motif database for DNA shape features of transcription factor binding sites. <i>Nucleic Acids Research</i> , 2014, 42, D148-D155.	14.5	111
44	JASPAR 2014: an extensively expanded and updated open-access database of transcription factor binding profiles. <i>Nucleic Acids Research</i> , 2014, 42, D142-D147.	14.5	915
45	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	27.8	1,838
46	Improving analysis of transcription factor binding sites within ChIP-Seq data based on topological motif enrichment. <i>BMC Genomics</i> , 2014, 15, 472.	2.8	47
47	Large scale chromosomal mapping of human microRNA structural clusters. <i>Nucleic Acids Research</i> , 2013, 41, 4392-4408.	14.5	48
48	The Next Generation of Transcription Factor Binding Site Prediction. <i>PLoS Computational Biology</i> , 2013, 9, e1003214.	3.2	160
49	Chromosomal periodicity and positional networks of genes in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2010, 6, 366.	7.2	34
50	MiReNA: finding microRNAs with high accuracy and no learning at genome scale and from deep sequencing data. <i>Bioinformatics</i> , 2010, 26, 2226-2234.	4.1	141