

Thomas Manke

List of Publications by Year in Descending Order

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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.

66
papers

7,296
citations

35
h-index

71
g-index

71
ext. papers

10,852
ext. citations

12.9
avg, IF

5.86
L-index

#	Paper	IF	Citations
66	pyGenomeTracks: reproducible plots for multivariate genomic datasets. <i>Bioinformatics</i> , 2021 , 37, 422-423.2		50
65	Galaxy HiCExplorer 3: a web server for reproducible Hi-C, capture Hi-C and single-cell Hi-C data analysis, quality control and visualization. <i>Nucleic Acids Research</i> , 2020 , 48, W177-W184	20.1	40
64	DOT1L-mediated murine neuronal differentiation associates with H3K79me2 accumulation and preserves SOX2-enhancer accessibility. <i>Nature Communications</i> , 2020 , 11, 5200	17.4	4
63	CAPRI enables comparison of evolutionarily conserved RNA interacting regions. <i>Nature Communications</i> , 2019 , 10, 2682	17.4	20
62	snakePipes: facilitating flexible, scalable and integrative epigenomic analysis. <i>Bioinformatics</i> , 2019 , 35, 4757-4759	7.2	45
61	MAPCap allows high-resolution detection and differential expression analysis of transcription start sites. <i>Nature Communications</i> , 2019 , 10, 3219	17.4	12
60	CRUP: a comprehensive framework to predict condition-specific regulatory units. <i>Genome Biology</i> , 2019 , 20, 227	18.3	8
59	DOT1L promotes progenitor proliferation and primes neuronal layer identity in the developing cerebral cortex. <i>Nucleic Acids Research</i> , 2019 , 47, 168-183	20.1	19
58	Differential Methylation of H3K79 Reveals DOT1L Target Genes and Function in the Cerebellum In Vivo. <i>Molecular Neurobiology</i> , 2019 , 56, 4273-4287	6.2	8
57	High-resolution TADs reveal DNA sequences underlying genome organization in flies. <i>Nature Communications</i> , 2018 , 9, 189	17.4	292
56	Galaxy HiCExplorer: a web server for reproducible Hi-C data analysis, quality control and visualization. <i>Nucleic Acids Research</i> , 2018 , 46, W11-W16	20.1	76
55	RELACS nuclei barcoding enables high-throughput ChIP-seq. <i>Communications Biology</i> , 2018 , 1, 214	6.7	16
54	Integrative analysis of single-cell expression data reveals distinct regulatory states in bidirectional promoters. <i>Epigenetics and Chromatin</i> , 2018 , 11, 66	5.8	4
53	A comprehensive analysis of 195 DNA methylomes reveals shared and cell-specific features of partially methylated domains. <i>Genome Biology</i> , 2018 , 19, 150	18.3	41
52	Community-Driven Data Analysis Training for Biology. <i>Cell Systems</i> , 2018 , 6, 752-758.e1	10.6	62
51	Inactivation of Lsd1 triggers senescence in trophoblast stem cells by induction of Sirt4. <i>Cell Death and Disease</i> , 2017 , 8, e2631	9.8	22
50	DHX9 suppresses RNA processing defects originating from the Alu invasion of the human genome. <i>Nature</i> , 2017 , 544, 115-119	50.4	277

49	The histone code reader Spin1 controls skeletal muscle development. <i>Cell Death and Disease</i> , 2017 , 8, e3173	9.8	9
48	Epigenetic dynamics of monocyte-to-macrophage differentiation. <i>Epigenetics and Chromatin</i> , 2016 , 9, 33	5.8	54
47	Epigenomic Profiling of Human CD4 T Cells Supports a Linear Differentiation Model and Highlights Molecular Regulators of Memory Development. <i>Immunity</i> , 2016 , 45, 1148-1161	32.3	118
46	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016 , 167, 1145-1149	56.2	232
45	Nuclear Architecture Organized by Rif1 Underpins the Replication-Timing Program. <i>Molecular Cell</i> , 2016 , 61, 260-73	17.6	111
44	Standardizing chromatin research: a simple and universal method for ChIP-seq. <i>Nucleic Acids Research</i> , 2016 , 44, e67	20.1	56
43	Putative Prostate Cancer Risk SNP in an Androgen Receptor-Binding Site of the Melanophilin Gene Illustrates Enrichment of Risk SNPs in Androgen Receptor Target Sites. <i>Human Mutation</i> , 2016 , 37, 52-64	4.7	27
42	Functional interplay between MSL1 and CDK7 controls RNA polymerase II Ser5 phosphorylation. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 580-9	17.6	12
41	deepTools2: a next generation web server for deep-sequencing data analysis. <i>Nucleic Acids Research</i> , 2016 , 44, W160-5	20.1	2285
40	High-Affinity Sites Form an Interaction Network to Facilitate Spreading of the MSL Complex across the X Chromosome in Drosophila. <i>Molecular Cell</i> , 2015 , 60, 146-62	17.6	58
39	Suv39h-dependent H3K9me3 marks intact retrotransposons and silences LINE elements in mouse embryonic stem cells. <i>Molecular Cell</i> , 2014 , 55, 277-90	17.6	205
38	deepTools: a flexible platform for exploring deep-sequencing data. <i>Nucleic Acids Research</i> , 2014 , 42, W187-91	20.1	1212
37	MOF-associated complexes ensure stem cell identity and Xist repression. <i>ELife</i> , 2014 , 3, e02024	8.9	57
36	ChroMoS: an integrated web tool for SNP classification, prioritization and functional interpretation. <i>Bioinformatics</i> , 2013 , 29, 2197-8	7.2	22
35	Nontransformed, GM-CSF-dependent macrophage lines are a unique model to study tissue macrophage functions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, E2191-8	11.5	54
34	Anterior gradient 2 and 3—two prototype androgen-responsive genes transcriptionally upregulated by androgens and by oestrogens in prostate cancer cells. <i>FEBS Journal</i> , 2013 , 280, 1249-66	5.7	34
33	Validation of reported genetic risk factors for periodontitis in a large-scale replication study. <i>Journal of Clinical Periodontology</i> , 2013 , 40, 563-72	7.7	68
32	A transcription factor-based mechanism for mouse heterochromatin formation. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 1023-30	17.6	132

31	The NSL complex regulates housekeeping genes in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2012 , 8, e1002736	6	65
30	Heterochromatin boundaries are hotspots for de novo kinetochore formation. <i>Nature Cell Biology</i> , 2011 , 13, 799-808	23.4	100
29	MicroRNAs differentially expressed in postnatal aortic development downregulate elastin via 3' UTR and coding-sequence binding sites. <i>PLoS ONE</i> , 2011 , 6, e16250	3.7	84
28	Transcription factor binding predictions using TRAP for the analysis of ChIP-seq data and regulatory SNPs. <i>Nature Protocols</i> , 2011 , 6, 1860-9	18.8	149
27	The BTB and CNC homology 1 (BACH1) target genes are involved in the oxidative stress response and in control of the cell cycle. <i>Journal of Biological Chemistry</i> , 2011 , 286, 23521-32	5.4	107
26	Genome-wide expression profiling identifies an impairment of negative feedback signals in the Crohn's disease-associated NOD2 variant L1007fsinsC. <i>Journal of Immunology</i> , 2011 , 186, 4027-38	5.3	18
25	Mutational characterization of the bile acid receptor TGR5 in primary sclerosing cholangitis. <i>PLoS ONE</i> , 2010 , 5, e12403	3.7	90
24	Functional analysis and identification of cis-regulatory elements of human chromosome 21 gene promoters. <i>Nucleic Acids Research</i> , 2010 , 38, 6112-23	20.1	18
23	A genome-wide association study identifies GLT6D1 as a susceptibility locus for periodontitis. <i>Human Molecular Genetics</i> , 2010 , 19, 553-62	5.6	150
22	Screening of human gene promoter activities using transfected-cell arrays. <i>Gene</i> , 2010 , 450, 48-54	3.8	8
21	Quantifying the effect of sequence variation on regulatory interactions. <i>Human Mutation</i> , 2010 , 31, 477-83	4.7	48
20	PASTAA: identifying transcription factors associated with sets of co-regulated genes. <i>Bioinformatics</i> , 2009 , 25, 435-42	7.2	113
19	Paracrine control of oligodendrocyte differentiation by SRF-directed neuronal gene expression. <i>Nature Neuroscience</i> , 2009 , 12, 418-27	25.5	79
18	Promiscuous and depolarization-induced immediate-early response genes are induced by mechanical strain of osteoblasts. <i>Journal of Bone and Mineral Research</i> , 2009 , 24, 1247-62	6.3	24
17	Short ultraconserved promoter regions delineate a class of preferentially expressed alternatively spliced transcripts. <i>Genomics</i> , 2009 , 94, 308-16	4.3	8
16	Integrating sequence, evolution and functional genomics in regulatory genomics. <i>Genome Biology</i> , 2009 , 10, 202	18.3	17
15	Prioritization of gene regulatory interactions from large-scale modules in yeast. <i>BMC Bioinformatics</i> , 2008 , 9, 32	3.6	5
14	Statistical modeling of transcription factor binding affinities predicts regulatory interactions. <i>PLoS Computational Biology</i> , 2008 , 4, e1000039	5	42

13	Proteomic shifts in embryonic stem cells with gene dose modifications suggest the presence of balancer proteins in protein regulatory networks. <i>PLoS ONE</i> , 2007 , 2, e1218	3.7	21
12	Predicting transcription factor affinities to DNA from a biophysical model. <i>Bioinformatics</i> , 2007 , 23, 134-41	4.1	159
11	An entropic characterization of protein interaction networks and cellular robustness. <i>Journal of the Royal Society Interface</i> , 2006 , 3, 843-50	4.1	30
10	Control of replication initiation and heterochromatin formation in <i>Saccharomyces cerevisiae</i> by a regulator of meiotic gene expression. <i>Genes and Development</i> , 2005 , 19, 1811-22	12.6	44
9	Robustness and network evolution—An entropic principle. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2005 , 346, 682-696	3.3	112
8	Lethality and entropy of protein interaction networks. <i>Genome Informatics</i> , 2005 , 16, 159-63		7
7	Correlating protein-DNA and protein-protein interaction networks. <i>Journal of Molecular Biology</i> , 2003 , 333, 75-85	6.5	29
6	normR: Regime enrichment calling for ChIP-seq data		4
5	High-resolution TADs reveal DNA sequences underlying genome organization in flies		10
4	Community-driven data analysis training for biology		4
3	Partially methylated domains are hallmarks of a cell specific epigenome topology		4
2	snakePipes enable flexible, scalable and integrative epigenomic analysis		1
1	CRUP: A comprehensive framework to predict condition-specific regulatory units		1