

Harmen J Bussemaker

List of Publications by Year in descending order

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67
papers

8,632
citations

71102

41
h-index

95266

68
g-index

75
all docs

75
docs citations

75
times ranked

10721
citing authors

#	ARTICLE	IF	CITATIONS
1	Systematic Protein Location Mapping Reveals Five Principal Chromatin Types in Drosophila Cells. <i>Cell</i> , 2010, 143, 212-224.	28.9	854
2	Regulatory element detection using correlation with expression. <i>Nature Genetics</i> , 2001, 27, 167-171.	21.4	648
3	Cofactor Binding Evokes Latent Differences in DNA Binding Specificity between Hox Proteins. <i>Cell</i> , 2011, 147, 1270-1282.	28.9	454
4	Comparative genome sequencing of <i>Drosophila pseudoobscura</i> : Chromosomal, gene, and cis-element evolution. <i>Genome Research</i> , 2005, 15, 1-18.	5.5	453
5	Genomic binding by the <i>Drosophila</i> Myc, Max, Mad/Mnt transcription factor network. <i>Genes and Development</i> , 2003, 17, 1101-1114.	5.9	352
6	Evaluation of methods for modeling transcription factor sequence specificity. <i>Nature Biotechnology</i> , 2013, 31, 126-134.	17.5	341
7	The Human Transcriptome Map Reveals Extremes in Gene Density, Intron Length, GC Content, and Repeat Pattern for Domains of Highly and Weakly Expressed Genes. <i>Genome Research</i> , 2003, 13, 1998-2004.	5.5	306
8	A Gene Expression Map for the Euchromatic Genome of <i>Drosophila melanogaster</i> . <i>Science</i> , 2004, 306, 655-660.	12.6	275
9	PQM-1 Complements DAF-16 as a Key Transcriptional Regulator of DAF-2-Mediated Development and Longevity. <i>Cell</i> , 2013, 154, 676-690.	28.9	270
10	Statistical mechanical modeling of genome-wide transcription factor occupancy data by MatrixREDUCE. <i>Bioinformatics</i> , 2006, 22, e141-e149.	4.1	259
11	Identification of genes expressed in <i>C. elegans</i> touch receptor neurons. <i>Nature</i> , 2002, 418, 331-335.	27.8	230
12	Quantitative modeling of transcription factor binding specificities using DNA shape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4654-4659.	7.1	218
13	Defining transcriptional networks through integrative modeling of mRNA expression and transcription factor binding data. <i>BMC Bioinformatics</i> , 2004, 5, 31.	2.6	212
14	DSSR: an integrated software tool for dissecting the spatial structure of RNA. <i>Nucleic Acids Research</i> , 2015, 43, gkv716.	14.5	204
15	T-profiler: scoring the activity of predefined groups of genes using gene expression data. <i>Nucleic Acids Research</i> , 2005, 33, W592-W595.	14.5	190
16	Hotspots of transcription factor colocalization in the genome of <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 12027-12032.	7.1	182
17	Deconvolving the Recognition of DNA Shape from Sequence. <i>Cell</i> , 2015, 161, 307-318.	28.9	174
18	High-throughput identification of human SNPs affecting regulatory element activity. <i>Nature Genetics</i> , 2019, 51, 1160-1169.	21.4	157

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19	Distinct HP1 and Su(var)3-9 complexes bind to sets of developmentally coexpressed genes depending on chromosomal location. <i>Genes and Development</i> , 2003, 17, 2825-2838.	5.9	153
20	Probing DNA shape and methylation state on a genomic scale with DNase I. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6376-6381.	7.1	151
21	Profiling condition-specific, genome-wide regulation of mRNA stability in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 17675-17680.	7.1	150
22	Low-Affinity Binding Sites and the Transcription Factor Specificity Paradox in Eukaryotes. <i>Annual Review of Cell and Developmental Biology</i> , 2019, 35, 357-379.	9.4	144
23	In search of the determinants of enhancer-promoter interaction specificity. <i>Trends in Cell Biology</i> , 2014, 24, 695-702.	7.9	142
24	Revisiting the codon adaptation index from a whole-genome perspective: analyzing the relationship between gene expression and codon occurrence in yeast using a variety of models. <i>Nucleic Acids Research</i> , 2003, 31, 2242-2251.	14.5	136
25	Evolving insights on how cytosine methylation affects protein-DNA binding. <i>Briefings in Functional Genomics</i> , 2015, 14, 61-73.	2.7	122
26	Genomewide analysis of Drosophila GAGA factor target genes reveals context-dependent DNA binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 2580-2585.	7.1	114
27	TLS/FUS (translocated in liposarcoma/fused in sarcoma) regulates target gene transcription via single-stranded DNA response elements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 6030-6035.	7.1	104
28	Dissection of Transient Oxidative Stress Response in <i>Saccharomyces cerevisiae</i> by Using DNA Microarrays. <i>Molecular Biology of the Cell</i> , 2002, 13, 2783-2794.	2.1	103
29	Quantitative Analysis of the DNA Methylation Sensitivity of Transcription Factor Complexes. <i>Cell Reports</i> , 2017, 19, 2383-2395.	6.4	100
30	Genome-wide mapping of autonomous promoter activity in human cells. <i>Nature Biotechnology</i> , 2017, 35, 145-153.	17.5	97
31	Hap4p overexpression in glucose-grown <i>Saccharomyces cerevisiae</i> induces cells to enter a novel metabolic state. <i>Genome Biology</i> , 2002, 4, R3.	9.6	90
32	Accurate and sensitive quantification of protein-DNA binding affinity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3692-E3701.	7.1	83
33	Predictive Modeling of Genome-Wide mRNA Expression: From Modules to Molecules. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2007, 36, 329-347.	18.3	75
34	Global Chromatin Domain Organization of the Drosophila Genome. <i>PLoS Genetics</i> , 2008, 4, e1000045.	3.5	72
35	SELEX-seq: A Method for Characterizing the Complete Repertoire of Binding Site Preferences for Transcription Factor Complexes. <i>Methods in Molecular Biology</i> , 2014, 1196, 255-278.	0.9	68
36	Systematic prediction of DNA shape changes due to CpG methylation explains epigenetic effects on protein-DNA binding. <i>Epigenetics and Chromatin</i> , 2018, 11, 6.	3.9	65

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37	Nuclear Pore Component Nup98 Is a Potential Tumor Suppressor and Regulates Posttranscriptional Expression of Select p53 Target Genes. <i>Molecular Cell</i> , 2012, 48, 799-810.	9.7	57
38	Predicting functional transcription factor binding through alignment-free and affinity-based analysis of orthologous promoter sequences. <i>Bioinformatics</i> , 2008, 24, i165-i171.	4.1	54
39	Toward A Mechanistic Understanding of DNA Methylation Readout by Transcription Factors. <i>Journal of Molecular Biology</i> , 2020, 432, 1801-1815.	4.2	54
40	REDUCE: an online tool for inferring cis-regulatory elements and transcriptional module activities from microarray data. <i>Nucleic Acids Research</i> , 2003, 31, 3487-3490.	14.5	49
41	ETO family protein Mtg16 regulates the balance of dendritic cell subsets by repressing Id2. <i>Journal of Experimental Medicine</i> , 2014, 211, 1623-1635.	8.5	49
42	HP1 controls genomic targeting of four novel heterochromatin proteins in <i>Drosophila</i> . <i>EMBO Journal</i> , 2007, 26, 741-751.	7.8	48
43	Perturbation-based analysis and modeling of combinatorial regulation in the yeast sulfur assimilation pathway. <i>Molecular Biology of the Cell</i> , 2012, 23, 2993-3007.	2.1	45
44	Prediction of protein-ligand binding affinity from sequencing data with interpretable machine learning. <i>Nature Biotechnology</i> , 2022, 40, 1520-1527.	17.5	38
45	Combinatorial control of diverse metabolic and physiological functions by transcriptional regulators of the yeast sulfur assimilation pathway. <i>Molecular Biology of the Cell</i> , 2012, 23, 3008-3024.	2.1	36
46	Inferring Condition-Specific Modulation of Transcription Factor Activity in Yeast through Regulon-Based Analysis of Genomewide Expression. <i>PLoS ONE</i> , 2008, 3, e3112.	2.5	35
47	A unified approach for quantifying and interpreting <sc>DNA</sc> shape readout by transcription factors. <i>Molecular Systems Biology</i> , 2018, 14, e7902.	7.2	35
48	Loss of Subcellular Lipid Transport Due to ARV1 Deficiency Disrupts Organelle Homeostasis and Activates the Unfolded Protein Response. <i>Journal of Biological Chemistry</i> , 2011, 286, 11951-11959.	3.4	34
49	The RNA backbone plays a crucial role in mediating the intrinsic stability of the GpU dinucleotide platform and the GpUpA/GpA miniduplex. <i>Nucleic Acids Research</i> , 2010, 38, 4868-4876.	14.5	32
50	SelexGLM differentiates androgen and glucocorticoid receptor DNA-binding preference over an extended binding site. <i>Genome Research</i> , 2018, 28, 111-121.	5.5	32
51	Building accurate sequence-to-affinity models from high-throughput in vitro protein-DNA binding data using FeatureREDUCE. <i>ELife</i> , 2015, 4, .	6.0	32
52	Identifying the genetic determinants of transcription factor activity. <i>Molecular Systems Biology</i> , 2010, 6, 412.	7.2	31
53	In vivo Hox binding specificity revealed by systematic changes to a single cis regulatory module. <i>Nature Communications</i> , 2019, 10, 3597.	12.8	27
54	Context-Dependent Gene Regulation by Homeodomain Transcription Factor Complexes Revealed by Shape-Readout Deficient Proteins. <i>Molecular Cell</i> , 2020, 78, 152-167.e11.	9.7	26

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55	Systematic in vitro profiling of off-target affinity, cleavage and efficiency for CRISPR enzymes. <i>Nucleic Acids Research</i> , 2020, 48, 5037-5053.	14.5	26
56	TransfactomeDB: a resource for exploring the nucleotide sequence specificity and condition-specific regulatory activity of trans-acting factors. <i>Nucleic Acids Research</i> , 2007, 36, D125-D131.	14.5	24
57	Transcription factor paralogs orchestrate alternative gene regulatory networks by context-dependent cooperation with multiple cofactors. <i>Nature Communications</i> , 2022, 13, .	12.8	20
58	Dissecting complex transcriptional responses using pathway-level scores based on prior information. <i>BMC Bioinformatics</i> , 2007, 8, S6.	2.6	19
59	Transcription factor regulation of eQTL activity across individuals and tissues. <i>PLoS Genetics</i> , 2022, 18, e1009719.	3.5	14
60	Paired Hormone Response Elements Predict Caveolin-1 as a Glucocorticoid Target Gene. <i>PLoS ONE</i> , 2010, 5, e8839.	2.5	9
61	Harnessing Natural Sequence Variation to Dissect Posttranscriptional Regulatory Networks in Yeast. <i>C3: Genes, Genomes, Genetics</i> , 2014, 4, 1539-1553.	1.8	9
62	Identifying genetic modulators of the connectivity between transcription factors and their transcriptional targets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1835-43.	7.1	9
63	Identifying regulatory mechanisms underlying tumorigenesis using locus expression signature analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5747-5752.	7.1	7
64	DAF-16 and PQM-1: Partners in longevity. <i>Aging</i> , 2014, 6, 5-6.	3.1	6
65	Network-based approaches that exploit inferred transcription factor activity to analyze the impact of genetic variation on gene expression. <i>Current Opinion in Systems Biology</i> , 2017, 2, 98-102.	2.6	4
66	Characterizing a collective and dynamic component of chromatin immunoprecipitation enrichment profiles in yeast. <i>BMC Genomics</i> , 2014, 15, 494.	2.8	2
67	Recent progress in understanding transcription factor binding specificity. <i>Briefings in Functional Genomics</i> , 2015, 14, 1-2.	2.7	2