Harmen J Bussemaker

List of Publications by Year
in descending order

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	Transcription factor regulation of eQTL activity across individuals and tissues. PLoS Genetics, 2022, 18, e1009719.	3.5	14
2	Prediction of protein–ligand binding affinity from sequencing data with interpretable machine learning. Nature Biotechnology, 2022, 40, 1520-1527.	17.5	38
3	Transcription factor paralogs orchestrate alternative gene regulatory networks by context-dependent cooperation with multiple cofactors. Nature Communications, 2022, 13, .	12.8	20
4	Toward a Mechanistic Understanding of DNA Methylation Readout by Transcription Factors. Journal of Molecular Biology, 2020, 432, 1801-1815.	4.2	54
5	Context-Dependent Gene Regulation by Homeodomain Transcription Factor Complexes Revealed by Shape-Readout Deficient Proteins. Molecular Cell, 2020, 78, 152-167.e11.	9.7	26
6	Systematic in vitro profiling of off-target affinity, cleavage and efficiency for CRISPR enzymes. Nucleic Acids Research, 2020, 48, 5037-5053.	14.5	26
7	In vivo Hox binding specificity revealed by systematic changes to a single cis regulatory module. Nature Communications, 2019, 10, 3597.	12.8	27
8	Low-Affinity Binding Sites and the Transcription Factor Specificity Paradox in Eukaryotes. Annual Review of Cell and Developmental Biology, 2019, 35, 357-379.	9.4	144
9	High-throughput identification of human SNPs affecting regulatory element activity. Nature Genetics, 2019, 51, 1160-1169.	21.4	157
10	Accurate and sensitive quantification of protein-DNA binding affinity. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3692-E3701.	7.1	83
11	SelexGLM differentiates androgen and glucocorticoid receptor DNA-binding preference over an extended binding site. Genome Research, 2018, 28, 111-121.	5.5	32
12	A unified approach for quantifying and interpreting <scp>DNA</scp> shape readout by transcription factors. Molecular Systems Biology, 2018, 14, e7902.	7.2	35
13	Systematic prediction of DNA shape changes due to CpG methylation explains epigenetic effects on protein–DNA binding. Epigenetics and Chromatin, 2018, 11, 6.	3.9	65
14	Network-based approaches that exploit inferred transcription factor activity to analyze the impact of genetic variation on gene expression. Current Opinion in Systems Biology, 2017, 2, 98-102.	2.6	4
15	Quantitative Analysis of the DNA Methylation Sensitivity of Transcription Factor Complexes. Cell Reports, 2017, 19, 2383-2395.	6.4	100
16	Genome-wide mapping of autonomous promoter activity in human cells. Nature Biotechnology, 2017, 35, 145-153.	17.5	97
17	Identifying genetic modulators of the connectivity between transcription factors and their transcriptional targets. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1835-43.	7.1	9
18	DSSR: an integrated software tool for dissecting the spatial structure of RNA. Nucleic Acids Research, 2015, 43, gkv716.	14.5	204

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19	Quantitative modeling of transcription factor binding specificities using DNA shape. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 4654-4659.	7.1	218
20	Deconvolving the Recognition of DNA Shape from Sequence. Cell, 2015, 161, 307-318.	28.9	174
21	Recent progress in understanding transcription factor binding specificity. Briefings in Functional Genomics, 2015, 14, 1-2.	2.7	2
22	Evolving insights on how cytosine methylation affects protein-DNA binding. Briefings in Functional Genomics, 2015, 14, 61-73.	2.7	122
23	Building accurate sequence-to-affinity models from high-throughput in vitro protein-DNA binding data using FeatureREDUCE. ELife, 2015, 4, .	6.0	32
24	Harnessing Natural Sequence Variation to Dissect Posttranscriptional Regulatory Networks in Yeast. G3: Genes, Genomes, Genetics, 2014, 4, 1539-1553.	1.8	9
25	Identifying regulatory mechanisms underlying tumorigenesis using locus expression signature analysis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5747-5752.	7.1	7
26	ETO family protein Mtg16 regulates the balance of dendritic cell subsets by repressing Id2. Journal of Experimental Medicine, 2014, 211, 1623-1635.	8.5	49
27	In search of the determinants of enhancer–promoter interaction specificity. Trends in Cell Biology, 2014, 24, 695-702.	7.9	142
28	Characterizing a collective and dynamic component of chromatin immunoprecipitation enrichment profiles in yeast. BMC Genomics, 2014, 15, 494.	2.8	2
29	SELEX-seq: A Method for Characterizing the Complete Repertoire of Binding Site Preferences for Transcription Factor Complexes. Methods in Molecular Biology, 2014, 1196, 255-278.	0.9	68
30	DAF-16 and PQM-1: Partners in longevity. Aging, 2014, 6, 5-6.	3.1	6
31	PQM-1 Complements DAF-16 as a Key Transcriptional Regulator of DAF-2-Mediated Development and Longevity. Cell, 2013, 154, 676-690.	28.9	270
32	Evaluation of methods for modeling transcription factor sequence specificity. Nature Biotechnology, 2013, 31, 126-134.	17.5	341
33	Probing DNA shape and methylation state on a genomic scale with DNase I. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6376-6381.	7.1	151
34	Combinatorial control of diverse metabolic and physiological functions by transcriptional regulators of the yeast sulfur assimilation pathway. Molecular Biology of the Cell, 2012, 23, 3008-3024.	2.1	36
35	Perturbation-based analysis and modeling of combinatorial regulation in the yeast sulfur assimilation pathway. Molecular Biology of the Cell, 2012, 23, 2993-3007.	2.1	45
36	TLS/FUS (translocated in liposarcoma/fused in sarcoma) regulates target gene transcription via single-stranded DNA response elements. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6030-6035.	7.1	104

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37	Nuclear Pore Component Nup98 Is a Potential Tumor Suppressor and Regulates Posttranscriptional Expression of Select p53 Target Genes. Molecular Cell, 2012, 48, 799-810.	9.7	57
38	Cofactor Binding Evokes Latent Differences in DNA Binding Specificity between Hox Proteins. Cell, 2011, 147, 1270-1282.	28.9	454
39	Loss of Subcellular Lipid Transport Due to ARV1 Deficiency Disrupts Organelle Homeostasis and Activates the Unfolded Protein Response. Journal of Biological Chemistry, 2011, 286, 11951-11959.	3.4	34
40	Identifying the genetic determinants of transcription factor activity. Molecular Systems Biology, 2010, 6, 412.	7.2	31
41	Paired Hormone Response Elements Predict Caveolin-1 as a Glucocorticoid Target Gene. PLoS ONE, 2010, 5, e8839.	2.5	9
42	The RNA backbone plays a crucial role in mediating the intrinsic stability of the GpU dinucleotide platform and the GpUpA/GpA miniduplex. Nucleic Acids Research, 2010, 38, 4868-4876.	14.5	32
43	Systematic Protein Location Mapping Reveals Five Principal Chromatin Types in Drosophila Cells. Cell, 2010, 143, 212-224.	28.9	854
44	Global Chromatin Domain Organization of the Drosophila Genome. PLoS Genetics, 2008, 4, e1000045.	3.5	72
45	Predicting functional transcription factor binding through alignment-free and affinity-based analysis of orthologous promoter sequences. Bioinformatics, 2008, 24, i165-i171.	4.1	54
46	Inferring Condition-Specific Modulation of Transcription Factor Activity in Yeast through Regulon-Based Analysis of Genomewide Expression. PLoS ONE, 2008, 3, e3112.	2.5	35
47	TransfactomeDB: a resource for exploring the nucleotide sequence specificity and condition-specific regulatory activity of trans-acting factors. Nucleic Acids Research, 2007, 36, D125-D131.	14.5	24
48	Predictive Modeling of Genome-Wide mRNA Expression: From Modules to Molecules. Annual Review of Biophysics and Biomolecular Structure, 2007, 36, 329-347.	18.3	75
49	HP1 controls genomic targeting of four novel heterochromatin proteins in Drosophila. EMBO Journal, 2007, 26, 741-751.	7.8	48
50	Dissecting complex transcriptional responses using pathway-level scores based on prior information. BMC Bioinformatics, 2007, 8, S6.	2.6	19
51	Statistical mechanical modeling of genome-wide transcription factor occupancy data by MatrixREDUCE. Bioinformatics, 2006, 22, e141-e149.	4.1	259
52	Hotspots of transcription factor colocalization in the genome of Drosophila melanogaster. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 12027-12032.	7.1	182
53	Profiling condition-specific, genome-wide regulation of mRNA stability in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 17675-17680.	7.1	150
54	Comparative genome sequencing of Drosophila pseudoobscura: Chromosomal, gene, and cis-element evolution. Genome Research, 2005, 15, 1-18.	5.5	453

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55	T-profiler: scoring the activity of predefined groups of genes using gene expression data. Nucleic Acids Research, 2005, 33, W592-W595.	14.5	190
56	A Gene Expression Map for the Euchromatic Genome of Drosophila melanogaster. Science, 2004, 306, 655-660.	12.6	275
57	Defining transcriptional networks through integrative modeling of mRNA expression and transcription factor binding data. BMC Bioinformatics, 2004, 5, 31.	2.6	212
58	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. Nucleic Acids Research, 2003, 31, 2242-2251.	14.5	136
59	The Human Transcriptome Map Reveals Extremes in Gene Density, Intron Length, GC Content, and Repeat Pattern for Domains of Highly and Weakly Expressed Genes. Genome Research, 2003, 13, 1998-2004.	5.5	306
60	Genomewide analysis of Drosophila GAGA factor target genes reveals context-dependent DNA binding. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 2580-2585.	7.1	114
61	Genomic binding by the Drosophila Myc, Max, Mad/Mnt transcription factor network. Genes and Development, 2003, 17, 1101-1114.	5.9	352
62	Distinct HP1 and Su(var)3-9 complexes bind to sets of developmentally coexpressed genes depending on chromosomal location. Genes and Development, 2003, 17, 2825-2838.	5.9	153
63	REDUCE: an online tool for inferring cis-regulatory elements and transcriptional module activities from microarray data. Nucleic Acids Research, 2003, 31, 3487-3490.	14.5	49
64	Dissection of Transient Oxidative Stress Response inSaccharomyces cerevisiaeby Using DNA Microarrays. Molecular Biology of the Cell, 2002, 13, 2783-2794.	2.1	103
65	Hap4p overexpression in glucose-grown Saccharomyces cerevisiae induces cells to enter a novel metabolic state. Genome Biology, 2002, 4, R3.	9.6	90
66	Identification of genes expressed in C. elegans touch receptor neurons. Nature, 2002, 418, 331-335.	27.8	230
67	Regulatory element detection using correlation with expression. Nature Genetics, 2001, 27, 167-171.	21.4	648