Erik van Nimwegen

List of Publications by Year
in descending order

110 papers	15,690 citations	44069 48 h-index	30922 102 g-index
136 all docs	136 docs citations	136 times ranked	26146 citing authors

#	Article	IF	Citations
1	Multiomic atlas with functional stratification and developmental dynamics of zebrafish cis-regulatory elements. Nature Genetics, 2022, 54, 1037-1050.	21.4	26
2	Whole genome phylogenies reflect the distributions of recombination rates for many bacterial species. ELife, 2021, 10, .	6.0	42
3	Bayesian inference of gene expression states from single-cell RNA-seq data. Nature Biotechnology, 2021, 39, 1008-1016.	17.5	50
4	Investigate the origins of COVID-19. Science, 2021, 372, 694-694.	12.6	92
5	Genome-wide gene expression noise in Escherichia coli is condition-dependent and determined by propagation of noise through the regulatory network. PLoS Biology, 2021, 19, e3001491.	5.6	29
6	Using fluorescence flow cytometry data for single-cell gene expression analysis in bacteria. PLoS ONE, 2020, 15, e0240233.	2.5	14
7	Tead transcription factors differentially regulate cortical development. Scientific Reports, 2020, 10, 4625.	3.3	38
8	Subpopulations of sensorless bacteria drive fitness in fluctuating environments. PLoS Biology, 2020, 18, e3000952.	5.6	13
9	Subpopulations of sensorless bacteria drive fitness in fluctuating environments. , 2020, 18, e3000952.		0
10	Subpopulations of sensorless bacteria drive fitness in fluctuating environments. , 2020, 18, e3000952.		0
11	Subpopulations of sensorless bacteria drive fitness in fluctuating environments. , 2020, 18, e3000952.		0
12	Subpopulations of sensorless bacteria drive fitness in fluctuating environments. , 2020, 18, e3000952.		0
13	Subpopulations of sensorless bacteria drive fitness in fluctuating environments. , 2020, 18, e3000952.		0
14	Subpopulations of sensorless bacteria drive fitness in fluctuating environments. , 2020, 18, e3000952.		0
15	Using fluorescence flow cytometry data for single-cell gene expression analysis in bacteria. , 2020, 15, e0240233.		0
16	Using fluorescence flow cytometry data for single-cell gene expression analysis in bacteria. , 2020, 15, e0240233.		0
17	Using fluorescence flow cytometry data for single-cell gene expression analysis in bacteria. , 2020, 15, e0240233.		0
18	Using fluorescence flow cytometry data for single-cell gene expression analysis in bacteria. , 2020, 15, e0240233.		0

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19	Using fluorescence flow cytometry data for single-cell gene expression analysis in bacteria. , 2020, 15, e0240233.		0
20	Crunch: integrated processing and modeling of ChIP-seq data in terms of regulatory motifs. Genome Research, 2019, 29, 1164-1177.	5.5	7
21	Initiation of chromosome replication controls both division and replication cycles in E. coli through a double-adder mechanism. ELife, 2019, 8, .	6.0	50
22	Monitoring single-cell gene regulation under dynamically controllable conditions with integrated microfluidics and software. Nature Communications, 2018, 9, 212.	12.8	105
23	Single-cell <scp>mRNA</scp> profiling reveals the hierarchical response of mi <scp>RNA</scp> targets to mi <scp>RNA</scp> induction. Molecular Systems Biology, 2018, 14, e8266.	7.2	24
24	Discovery of physiological and cancer-related regulators of 3′ UTR processing with KAPAC. Genome Biology, 2018, 19, 44.	8.8	54
25	Automated incorporation of pairwise dependency in transcription factor binding site prediction using dinucleotide weight tensors. PLoS Computational Biology, 2017, 13, e1005176.	3.2	10
26	The Genomic Context and Corecruitment of SP1 Affect ERRα Coactivation by PGC-1α in Muscle Cells. Molecular Endocrinology, 2016, 30, 809-825.	3.7	20
27	The SIB Swiss Institute of Bioinformatics′ resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37.	14.5	64
28	The ISMARA client. F1000Research, 2016, 5, 2851.	1.6	4
29	Inferring Contacting Residues within and between Proteins: What Do the Probabilities Mean?. PLoS Computational Biology, 2016, 12, e1004726.	3.2	16
30	A large-scale, in vivo transcription factor screen defines bivalent chromatin as a key property of regulatory factors mediating <i>Drosophila</i> wing development. Genome Research, 2015, 25, 514-523.	5.5	45
31	ARMADA: Using motif activity dynamics to infer gene regulatory networks from gene expression data. Methods, 2015, 85, 62-74.	3.8	5
32	Quantifying the strength of miRNA–target interactions. Methods, 2015, 85, 90-99.	3.8	21
33	Expression noise facilitates the evolution of gene regulation. ELife, 2015, 4, .	6.0	88
34	Tead2 expression levels control Yap/Taz subcellular distribution, zyxin expression, and epithelial-mesenchymal transition. Journal of Cell Science, 2014, 127, 1523-36.	2.0	113
35	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. Nucleic Acids Research, 2014, 42, W436-W441.	14.5	13
36	Embryonic stem cell-specific microRNAs contribute to pluripotency by inhibiting regulators of multiple differentiation pathways. Nucleic Acids Research, 2014, 42, 9313-9326.	14.5	32

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37	Automated Reconstruction of Whole-Genome Phylogenies from Short-Sequence Reads. Molecular Biology and Evolution, 2014, 31, 1077-1088.	8.9	399
38	Computational modeling identifies key gene regulatory interactions underlying phenobarbital-mediated tumor promotion. Nucleic Acids Research, 2014, 42, 4180-4195.	14.5	17
39	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	27.8	1,838
40	An epigenetic profile of early Tâ€cell development from multipotent progenitors to committed Tâ€cell descendants. European Journal of Immunology, 2014, 44, 1181-1193.	2.9	21
41	ISMARA: automated modeling of genomic signals as a democracy of regulatory motifs. Genome Research, 2014, 24, 869-884.	5.5	278
42	Global 3â€² UTR shortening has a limited effect on protein abundance in proliferating T cells. Nature Communications, 2014, 5, 5465.	12.8	164
43	Transcriptional Network Analysis in Muscle Reveals AP-1 as a Partner of PGC-1Î± in the Regulation of the Hypoxic Gene Program. Molecular and Cellular Biology, 2014, 34, 2996-3012.	2.3	32
44	Optimal Joint Segmentation and Tracking of Escherichia Coli in the Mother Machine. Lecture Notes in Computer Science, 2014, , 25-36.	1.3	20
45	Pegylated IFN-Î± regulates hepatic gene expression through transient Jak/STAT activation. Journal of Clinical Investigation, 2014, 124, 1568-1581.	8.2	43
46	Parity induces differentiation and reduces Wnt/Notch signaling ratio and proliferation potential of basal stem/progenitor cells isolated from mouse mammary epithelium. Breast Cancer Research, 2013, 15, R36.	5.0	82
47	Quantitative analysis of persister fractions suggests different mechanisms of formation among environmental isolates of E. coli. BMC Microbiology, 2013, 13, 25.	3.3	65
48	A biophysical miRNA-mRNA interaction model infers canonical and noncanonical targets. Nature Methods, 2013, 10, 253-255.	19.0	129
49	Sox4 Is a Master Regulator of Epithelial-Mesenchymal Transition by Controlling Ezh2 Expression and Epigenetic Reprogramming. Cancer Cell, 2013, 23, 768-783.	16.8	415
50	Modeling of epigenome dynamics identifies transcription factors that mediate Polycomb targeting. Genome Research, 2013, 23, 60-73.	5.5	108
51	Nucleosome Free Regions in Yeast Promoters Result from Competitive Binding of Transcription Factors That Interact with Chromatin Modifiers. PLoS Computational Biology, 2013, 9, e1003181.	3.2	28
52	Timescales and bottlenecks in miRNAâ€dependent gene regulation. Molecular Systems Biology, 2013, 9, 711.	7.2	54
53	Klf4 Is a Transcriptional Regulator of Genes Critical for EMT, Including Jnk1 (Mapk8). PLoS ONE, 2013, 8, e57329.	2.5	130
54	SwissRegulon, a database of genome-wide annotations of regulatory sites: recent updates. Nucleic Acids Research, 2012, 41, D214-D220.	14.5	137

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55	The Corepressor NCoR1 Antagonizes PGC-1α and Estrogen-Related Receptor α in the Regulation of Skeletal Muscle Function and Oxidative Metabolism. Molecular and Cellular Biology, 2012, 32, 4913-4924.	2.3	74
56	MotEvo: integrated Bayesian probabilistic methods for inferring regulatory sites and motifs on multiple alignments of DNA sequences. Bioinformatics, 2012, 28, 487-494.	4.1	114
57	Chromatin measurements reveal contributions of synthesis and decay to steady€state mRNA levels. Molecular Systems Biology, 2012, 8, 593.	7.2	48
58	Adipose Tissue MicroRNAs as Regulators of CCL2 Production in Human Obesity. Diabetes, 2012, 61, 1986-1993.	0.6	263
59	Tyrosine phosphatase SHP2 promotes breast cancer progression and maintains tumor-initiating cells via activation of key transcription factors and a positive feedback signaling loop. Nature Medicine, 2012, 18, 529-537.	30.7	224
60	DNA-binding factors shape the mouse methylome at distal regulatory regions. Nature, 2011, 480, 490-495.	27.8	1,203
61	Update of the FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. Nucleic Acids Research, 2011, 39, D856-D860.	14.5	49
62	Transcription Factor Binding Site Positioning in Yeast: Proximal Promoter Motifs Characterize TATA-Less Promoters. PLoS ONE, 2011, 6, e24279.	2.5	30
63	Correlating Gene Expression Variation with cis-Regulatory Polymorphism in Saccharomyces cerevisiae. Genome Biology and Evolution, 2010, 2, 697-707.	2.5	31
64	Co-expression of FBN1 with mesenchyme-specific genes in mouse cell lines: implications for phenotypic variability in Marfan syndrome. European Journal of Human Genetics, 2010, 18, 1209-1215.	2.8	39
65	Disentangling Direct from Indirect Co-Evolution of Residues in Protein Alignments. PLoS Computational Biology, 2010, 6, e1000633.	3.2	171
66	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. Cell, 2010, 140, 744-752.	28.9	667
67	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. Cell, 2010, 141, 369.	28.9	4
68	MicroRNA-221â€"222 Regulate the Cell Cycle in Mast Cells. Journal of Immunology, 2009, 182, 433-445.	0.8	95
69	The functional importance of telomere clustering: Global changes in gene expression result from SIR factor dispersion. Genome Research, 2009, 19, 611-625.	5.5	110
70	Scaling laws in functional genome content across prokaryotic clades and lifestyles. Trends in Genetics, 2009, 25, 243-247.	6.7	52
71	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. Nature Genetics, 2009, 41, 553-562.	21.4	408
72	Methods for analyzing deep sequencing expression data: constructing the human and mouse promoterome with deepCAGE data. Genome Biology, 2009, 10, R79.	9.6	131

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73	FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. Genome Biology, 2009, 10, R39.	9.6	67
74	Universal patterns of purifying selection at noncoding positions in bacteria. Genome Research, 2008, 18, 148-160.	5.5	55
75	The evolution of domain-content in bacterial genomes. Biology Direct, 2008, 3, 51.	4.6	26
76	Computational analysis of small RNA cloning data. Methods, 2008, 44, 13-21.	3.8	61
77	Computational Analysis of Full-length cDNAs Reveals Frequent Coupling Between Transcriptional and Splicing Programs. DNA Research, 2008, 15, 63-72.	3.4	3
78	Genome-wide Expression Profiling, In Vivo DNA Binding Analysis, and Probabilistic Motif Prediction Reveal Novel Abf1 Target Genes during Fermentation, Respiration, and Sporulation in Yeast. Molecular Biology of the Cell, 2008, 19, 2193-2207.	2.1	29
79	Accurate prediction of protein–protein interactions from sequence alignments using a Bayesian method. Molecular Systems Biology, 2008, 4, 165.	7.2	173
80	SwissRegulon: a database of genome-wide annotations of regulatory sites. Nucleic Acids Research, 2007, 35, D127-D131.	14.5	123
81	Inference of miRNA targets using evolutionary conservation and pathway analysis. BMC Bioinformatics, 2007, 8, 69.	2.6	282
82	Finding regulatory elements and regulatory motifs: a general probabilistic framework. BMC Bioinformatics, 2007, 8, S4.	2.6	42
83	Detecting Regulatory Sites Using PhyloGibbs. Methods in Molecular Biology, 2007, 395, 381-402.	0.9	11
84	Scaling Laws in the Functional Content of Genomes. , 2006, , 236-253.		14
85	The types and prevalence of alternative splice forms. Current Opinion in Structural Biology, 2006, 16, 362-367.	5.7	29
86	SPA: A Probabilistic Algorithm for Spliced Alignment. PLoS Genetics, 2006, 2, e24.	3.5	21
87	A Simple Physical Model Predicts Small Exon Length Variations. PLoS Genetics, 2006, 2, e45.	3.5	69
88	Influenza Escapes Immunity Along Neutral Networks. Science, 2006, 314, 1884-1886.	12.6	54
89	A Bayesian Algorithm for Reconstructing Two-Component Signaling Networks. Lecture Notes in Computer Science, 2006, , 44-55.	1.3	0
90	Identification of clustered microRNAs using an ab initio prediction method. BMC Bioinformatics, 2005, 6, 267.	2.6	219

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91	PhyloGibbs: A Gibbs Sampler Incorporating Phylogenetic Information. Lecture Notes in Computer Science, 2005, , 30-41.	1.3	5
92	PhyloGibbs: A Gibbs Sampling Motif Finder That Incorporates Phylogeny. PLoS Computational Biology, 2005, 1, e67.	3.2	236
93	Analysis of Human Immunodeficiency Virus Cytopathicity by Using a New Method for Quantitating Viral Dynamics in Cell Culture. Journal of Virology, 2005, 79, 4025-4032.	3.4	18
94	The Transcriptional Landscape of the Mammalian Genome. Science, 2005, 309, 1559-1563.	12.6	3,227
95	Transformation fingerprint: induced STAT3-C, v-Src and Ha-Ras cause small initial changes but similar established profiles in mRNA. Oncogene, 2004, 23, 8455-8463.	5.9	23
96	Scaling laws in the functional content of genomes. Trends in Genetics, 2003, 19, 479-484.	6.7	267
97	A probabilistic method to detect regulatory modules. Bioinformatics, 2003, 19, i292-i301.	4.1	172
98	Decay Rates of Human mRNAs: Correlation With Functional Characteristics and Sequence Attributes. Genome Research, 2003, 13, 1863-1872.	5.5	467
99	Splice Variation in Mouse Full-Length cDNAs Identified by Mapping to the Mouse Genome. Genome Research, 2002, 12, 1377-1385.	5.5	60
100	The Evolutionary Unfolding of Complexity. Natural Computing Series, 2002, , 67-94.	2.2	20
101	Probabilistic clustering of sequences: Inferring new bacterial regulons by comparative genomics. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 7323-7328.	7.1	57
102	Optimizing Epochal Evolutionary Search: Population-Size Dependent Theory. Machine Learning, 2001, 45, 77-114.	5.4	35
103	Dynamics of One-pass Germinal Center Models: Implications for Affinity Maturation. Bulletin of Mathematical Biology, 2000, 62, 121-153.	1.9	35
104	Metastable Evolutionary Dynamics: Crossing Fitness Barriers or Escaping via Neutral Paths?. Bulletin of Mathematical Biology, 2000, 62, 799-848.	1.9	99
105	Optimizing epochal evolutionary search: population-size independent theory. Computer Methods in Applied Mechanics and Engineering, 2000, 186, 171-194.	6.6	30
106	Neutral evolution of mutational robustness. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 9716-9720.	7.1	510
107	Statistical Dynamics of the Royal Road Genetic Algorithm. Theoretical Computer Science, 1999, 229, 41-102.	0.9	98
108	The frequency distribution of gene family sizes in complete genomes. Molecular Biology and Evolution, 1998, 15, 583-589.	8.9	201

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109	Finite populations induce metastability in evolutionary search. Physics Letters, Section A: General, Atomic and Solid State Physics, 1997, 229, 144-150.	2.1	85
110	Detecting Regulatory Sites Using PhyloGibbs. , 0, , 381-402.		0