

Erik van Nimwegen

List of Publications by Year in descending order

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Version: 2024-02-01

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 | The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563. | 12.6 | 3,227 |
| 2 | A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470. | 27.8 | 1,838 |
| 3 | DNA-binding factors shape the mouse methylome at distal regulatory regions. <i>Nature</i> , 2011, 480, 490-495. | 27.8 | 1,203 |
| 4 | An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 140, 744-752. | 28.9 | 667 |
| 5 | Neutral evolution of mutational robustness. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 9716-9720. | 7.1 | 510 |
| 6 | Decay Rates of Human mRNAs: Correlation With Functional Characteristics and Sequence Attributes. <i>Genome Research</i> , 2003, 13, 1863-1872. | 5.5 | 467 |
| 7 | Sox4 Is a Master Regulator of Epithelial-Mesenchymal Transition by Controlling Ezh2 Expression and Epigenetic Reprogramming. <i>Cancer Cell</i> , 2013, 23, 768-783. | 16.8 | 415 |
| 8 | The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562. | 21.4 | 408 |
| 9 | Automated Reconstruction of Whole-Genome Phylogenies from Short-Sequence Reads. <i>Molecular Biology and Evolution</i> , 2014, 31, 1077-1088. | 8.9 | 399 |
| 10 | Inference of miRNA targets using evolutionary conservation and pathway analysis. <i>BMC Bioinformatics</i> , 2007, 8, 69. | 2.6 | 282 |
| 11 | ISMARA: automated modeling of genomic signals as a democracy of regulatory motifs. <i>Genome Research</i> , 2014, 24, 869-884. | 5.5 | 278 |
| 12 | Scaling laws in the functional content of genomes. <i>Trends in Genetics</i> , 2003, 19, 479-484. | 6.7 | 267 |
| 13 | Adipose Tissue MicroRNAs as Regulators of CCL2 Production in Human Obesity. <i>Diabetes</i> , 2012, 61, 1986-1993. | 0.6 | 263 |
| 14 | PhyloGibbs: A Gibbs Sampling Motif Finder That Incorporates Phylogeny. <i>PLoS Computational Biology</i> , 2005, 1, e67. | 3.2 | 236 |
| 15 | Tyrosine phosphatase SHP2 promotes breast cancer progression and maintains tumor-initiating cells via activation of key transcription factors and a positive feedback signaling loop. <i>Nature Medicine</i> , 2012, 18, 529-537. | 30.7 | 224 |
| 16 | Identification of clustered microRNAs using an ab initio prediction method. <i>BMC Bioinformatics</i> , 2005, 6, 267. | 2.6 | 219 |
| 17 | The frequency distribution of gene family sizes in complete genomes. <i>Molecular Biology and Evolution</i> , 1998, 15, 583-589. | 8.9 | 201 |
| 18 | Accurate prediction of protein-protein interactions from sequence alignments using a Bayesian method. <i>Molecular Systems Biology</i> , 2008, 4, 165. | 7.2 | 173 |

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|----|---|------|-----------|
| 19 | A probabilistic method to detect regulatory modules. <i>Bioinformatics</i> , 2003, 19, i292-i301. | 4.1 | 172 |
| 20 | Disentangling Direct from Indirect Co-Evolution of Residues in Protein Alignments. <i>PLoS Computational Biology</i> , 2010, 6, e1000633. | 3.2 | 171 |
| 21 | Global 3' UTR shortening has a limited effect on protein abundance in proliferating T cells. <i>Nature Communications</i> , 2014, 5, 5465. | 12.8 | 164 |
| 22 | SwissRegulon, a database of genome-wide annotations of regulatory sites: recent updates. <i>Nucleic Acids Research</i> , 2012, 41, D214-D220. | 14.5 | 137 |
| 23 | Methods for analyzing deep sequencing expression data: constructing the human and mouse promoterome with deepCAGE data. <i>Genome Biology</i> , 2009, 10, R79. | 9.6 | 131 |
| 24 | Klf4 Is a Transcriptional Regulator of Genes Critical for EMT, Including Jnk1 (Mapk8). <i>PLoS ONE</i> , 2013, 8, e57329. | 2.5 | 130 |
| 25 | A biophysical miRNA-mRNA interaction model infers canonical and noncanonical targets. <i>Nature Methods</i> , 2013, 10, 253-255. | 19.0 | 129 |
| 26 | SwissRegulon: a database of genome-wide annotations of regulatory sites. <i>Nucleic Acids Research</i> , 2007, 35, D127-D131. | 14.5 | 123 |
| 27 | MotEvo: integrated Bayesian probabilistic methods for inferring regulatory sites and motifs on multiple alignments of DNA sequences. <i>Bioinformatics</i> , 2012, 28, 487-494. | 4.1 | 114 |
| 28 | Tead2 expression levels control Yap/Taz subcellular distribution, zyxin expression, and epithelial-mesenchymal transition. <i>Journal of Cell Science</i> , 2014, 127, 1523-36. | 2.0 | 113 |
| 29 | The functional importance of telomere clustering: Global changes in gene expression result from SIR factor dispersion. <i>Genome Research</i> , 2009, 19, 611-625. | 5.5 | 110 |
| 30 | Modeling of epigenome dynamics identifies transcription factors that mediate Polycomb targeting. <i>Genome Research</i> , 2013, 23, 60-73. | 5.5 | 108 |
| 31 | Monitoring single-cell gene regulation under dynamically controllable conditions with integrated microfluidics and software. <i>Nature Communications</i> , 2018, 9, 212. | 12.8 | 105 |
| 32 | Metastable Evolutionary Dynamics: Crossing Fitness Barriers or Escaping via Neutral Paths?. <i>Bulletin of Mathematical Biology</i> , 2000, 62, 799-848. | 1.9 | 99 |
| 33 | Statistical Dynamics of the Royal Road Genetic Algorithm. <i>Theoretical Computer Science</i> , 1999, 229, 41-102. | 0.9 | 98 |
| 34 | MicroRNA-221/222 Regulate the Cell Cycle in Mast Cells. <i>Journal of Immunology</i> , 2009, 182, 433-445. | 0.8 | 95 |
| 35 | Investigate the origins of COVID-19. <i>Science</i> , 2021, 372, 694-694. | 12.6 | 92 |
| 36 | Expression noise facilitates the evolution of gene regulation. <i>ELife</i> , 2015, 4, . | 6.0 | 88 |

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|----|---|------|-----------|
| 37 | Finite populations induce metastability in evolutionary search. <i>Physics Letters, Section A: General, Atomic and Solid State Physics</i> , 1997, 229, 144-150. | 2.1 | 85 |
| 38 | Parity induces differentiation and reduces Wnt/Notch signaling ratio and proliferation potential of basal stem/progenitor cells isolated from mouse mammary epithelium. <i>Breast Cancer Research</i> , 2013, 15, R36. | 5.0 | 82 |
| 39 | The Corepressor NCoR1 Antagonizes PGC-1 β and Estrogen-Related Receptor α in the Regulation of Skeletal Muscle Function and Oxidative Metabolism. <i>Molecular and Cellular Biology</i> , 2012, 32, 4913-4924. | 2.3 | 74 |
| 40 | A Simple Physical Model Predicts Small Exon Length Variations. <i>PLoS Genetics</i> , 2006, 2, e45. | 3.5 | 69 |
| 41 | FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. <i>Genome Biology</i> , 2009, 10, R39. | 9.6 | 67 |
| 42 | Quantitative analysis of persister fractions suggests different mechanisms of formation among environmental isolates of <i>E. coli</i> . <i>BMC Microbiology</i> , 2013, 13, 25. | 3.3 | 65 |
| 43 | The SIB Swiss Institute of Bioinformatics'™ resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016, 44, D27-D37. | 14.5 | 64 |
| 44 | Computational analysis of small RNA cloning data. <i>Methods</i> , 2008, 44, 13-21. | 3.8 | 61 |
| 45 | Splice Variation in Mouse Full-Length cDNAs Identified by Mapping to the Mouse Genome. <i>Genome Research</i> , 2002, 12, 1377-1385. | 5.5 | 60 |
| 46 | Probabilistic clustering of sequences: Inferring new bacterial regulons by comparative genomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 7323-7328. | 7.1 | 57 |
| 47 | Universal patterns of purifying selection at noncoding positions in bacteria. <i>Genome Research</i> , 2008, 18, 148-160. | 5.5 | 55 |
| 48 | Influenza Escapes Immunity Along Neutral Networks. <i>Science</i> , 2006, 314, 1884-1886. | 12.6 | 54 |
| 49 | Timescales and bottlenecks in miRNA-dependent gene regulation. <i>Molecular Systems Biology</i> , 2013, 9, 711. | 7.2 | 54 |
| 50 | Discovery of physiological and cancer-related regulators of 3' UTR processing with KAPAC. <i>Genome Biology</i> , 2018, 19, 44. | 8.8 | 54 |
| 51 | Scaling laws in functional genome content across prokaryotic clades and lifestyles. <i>Trends in Genetics</i> , 2009, 25, 243-247. | 6.7 | 52 |
| 52 | Bayesian inference of gene expression states from single-cell RNA-seq data. <i>Nature Biotechnology</i> , 2021, 39, 1008-1016. | 17.5 | 50 |
| 53 | Initiation of chromosome replication controls both division and replication cycles in <i>E. coli</i> through a double-adder mechanism. <i>ELife</i> , 2019, 8, . | 6.0 | 50 |
| 54 | Update of the FANTOM web resource: from mammalian transcriptional landscape to its dynamic regulation. <i>Nucleic Acids Research</i> , 2011, 39, D856-D860. | 14.5 | 49 |

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|----|---|------|-----------|
| 55 | Chromatin measurements reveal contributions of synthesis and decay to steady-state mRNA levels. <i>Molecular Systems Biology</i> , 2012, 8, 593. | 7.2 | 48 |
| 56 | A large-scale, in vivo transcription factor screen defines bivalent chromatin as a key property of regulatory factors mediating <i>Drosophila</i> wing development. <i>Genome Research</i> , 2015, 25, 514-523. | 5.5 | 45 |
| 57 | Pegylated IFN- β regulates hepatic gene expression through transient Jak/STAT activation. <i>Journal of Clinical Investigation</i> , 2014, 124, 1568-1581. | 8.2 | 43 |
| 58 | Finding regulatory elements and regulatory motifs: a general probabilistic framework. <i>BMC Bioinformatics</i> , 2007, 8, S4. | 2.6 | 42 |
| 59 | Whole genome phylogenies reflect the distributions of recombination rates for many bacterial species. <i>ELife</i> , 2021, 10, . | 6.0 | 42 |
| 60 | Co-expression of FBN1 with mesenchyme-specific genes in mouse cell lines: implications for phenotypic variability in Marfan syndrome. <i>European Journal of Human Genetics</i> , 2010, 18, 1209-1215. | 2.8 | 39 |
| 61 | Tead transcription factors differentially regulate cortical development. <i>Scientific Reports</i> , 2020, 10, 4625. | 3.3 | 38 |
| 62 | Dynamics of One-pass Germinal Center Models: Implications for Affinity Maturation. <i>Bulletin of Mathematical Biology</i> , 2000, 62, 121-153. | 1.9 | 35 |
| 63 | Optimizing Epochal Evolutionary Search: Population-Size Dependent Theory. <i>Machine Learning</i> , 2001, 45, 77-114. | 5.4 | 35 |
| 64 | Embryonic stem cell-specific microRNAs contribute to pluripotency by inhibiting regulators of multiple differentiation pathways. <i>Nucleic Acids Research</i> , 2014, 42, 9313-9326. | 14.5 | 32 |
| 65 | Transcriptional Network Analysis in Muscle Reveals AP-1 as a Partner of PGC-1 β in the Regulation of the Hypoxic Gene Program. <i>Molecular and Cellular Biology</i> , 2014, 34, 2996-3012. | 2.3 | 32 |
| 66 | Correlating Gene Expression Variation with cis-Regulatory Polymorphism in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology and Evolution</i> , 2010, 2, 697-707. | 2.5 | 31 |
| 67 | Optimizing epochal evolutionary search: population-size independent theory. <i>Computer Methods in Applied Mechanics and Engineering</i> , 2000, 186, 171-194. | 6.6 | 30 |
| 68 | Transcription Factor Binding Site Positioning in Yeast: Proximal Promoter Motifs Characterize TATA-Less Promoters. <i>PLoS ONE</i> , 2011, 6, e24279. | 2.5 | 30 |
| 69 | The types and prevalence of alternative splice forms. <i>Current Opinion in Structural Biology</i> , 2006, 16, 362-367. | 5.7 | 29 |
| 70 | 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. <i>Molecular Biology of the Cell</i> , 2008, 19, 2193-2207. | 2.1 | 29 |
| 71 | Genome-wide gene expression noise in <i>Escherichia coli</i> is condition-dependent and determined by propagation of noise through the regulatory network. <i>PLoS Biology</i> , 2021, 19, e3001491. | 5.6 | 29 |
| 72 | Nucleosome Free Regions in Yeast Promoters Result from Competitive Binding of Transcription Factors That Interact with Chromatin Modifiers. <i>PLoS Computational Biology</i> , 2013, 9, e1003181. | 3.2 | 28 |

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|----|---|------|-----------|
| 73 | The evolution of domain-content in bacterial genomes. <i>Biology Direct</i> , 2008, 3, 51. | 4.6 | 26 |
| 74 | Multiomic atlas with functional stratification and developmental dynamics of zebrafish cis-regulatory elements. <i>Nature Genetics</i> , 2022, 54, 1037-1050. | 21.4 | 26 |
| 75 | Single-cell mRNA profiling reveals the hierarchical response of miRNA targets to miRNA induction. <i>Molecular Systems Biology</i> , 2018, 14, e8266. | 7.2 | 24 |
| 76 | Transformation fingerprint: induced STAT3-C, v-Src and Ha-Ras cause small initial changes but similar established profiles in mRNA. <i>Oncogene</i> , 2004, 23, 8455-8463. | 5.9 | 23 |
| 77 | SPA: A Probabilistic Algorithm for Spliced Alignment. <i>PLoS Genetics</i> , 2006, 2, e24. | 3.5 | 21 |
| 78 | An epigenetic profile of early T-cell development from multipotent progenitors to committed T-cell descendants. <i>European Journal of Immunology</i> , 2014, 44, 1181-1193. | 2.9 | 21 |
| 79 | Quantifying the strength of miRNA-target interactions. <i>Methods</i> , 2015, 85, 90-99. | 3.8 | 21 |
| 80 | The Evolutionary Unfolding of Complexity. <i>Natural Computing Series</i> , 2002, , 67-94. | 2.2 | 20 |
| 81 | The Genomic Context and Corecruitment of SP1 Affect ERR α Coactivation by PGC-1 α in Muscle Cells. <i>Molecular Endocrinology</i> , 2016, 30, 809-825. | 3.7 | 20 |
| 82 | Optimal Joint Segmentation and Tracking of Escherichia Coli in the Mother Machine. <i>Lecture Notes in Computer Science</i> , 2014, , 25-36. | 1.3 | 20 |
| 83 | Analysis of Human Immunodeficiency Virus Cytopathicity by Using a New Method for Quantitating Viral Dynamics in Cell Culture. <i>Journal of Virology</i> , 2005, 79, 4025-4032. | 3.4 | 18 |
| 84 | Computational modeling identifies key gene regulatory interactions underlying phenobarbital-mediated tumor promotion. <i>Nucleic Acids Research</i> , 2014, 42, 4180-4195. | 14.5 | 17 |
| 85 | Inferring Contacting Residues within and between Proteins: What Do the Probabilities Mean?. <i>PLoS Computational Biology</i> , 2016, 12, e1004726. | 3.2 | 16 |
| 86 | Scaling Laws in the Functional Content of Genomes. , 2006, , 236-253. | | 14 |
| 87 | Using fluorescence flow cytometry data for single-cell gene expression analysis in bacteria. <i>PLoS ONE</i> , 2020, 15, e0240233. | 2.5 | 14 |
| 88 | Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. <i>Nucleic Acids Research</i> , 2014, 42, W436-W441. | 14.5 | 13 |
| 89 | Subpopulations of sensorless bacteria drive fitness in fluctuating environments. <i>PLoS Biology</i> , 2020, 18, e3000952. | 5.6 | 13 |
| 90 | Detecting Regulatory Sites Using PhyloGibbs. <i>Methods in Molecular Biology</i> , 2007, 395, 381-402. | 0.9 | 11 |

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|-----|---|------|-----------|
| 91 | Automated incorporation of pairwise dependency in transcription factor binding site prediction using dinucleotide weight tensors. <i>PLoS Computational Biology</i> , 2017, 13, e1005176. | 3.2 | 10 |
| 92 | Crunch: integrated processing and modeling of ChIP-seq data in terms of regulatory motifs. <i>Genome Research</i> , 2019, 29, 1164-1177. | 5.5 | 7 |
| 93 | PhyloGibbs: A Gibbs Sampler Incorporating Phylogenetic Information. <i>Lecture Notes in Computer Science</i> , 2005, , 30-41. | 1.3 | 5 |
| 94 | ARMADA: Using motif activity dynamics to infer gene regulatory networks from gene expression data. <i>Methods</i> , 2015, 85, 62-74. | 3.8 | 5 |
| 95 | An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 141, 369. | 28.9 | 4 |
| 96 | The ISMARA client. <i>F1000Research</i> , 2016, 5, 2851. | 1.6 | 4 |
| 97 | Computational Analysis of Full-length cDNAs Reveals Frequent Coupling Between Transcriptional and Splicing Programs. <i>DNA Research</i> , 2008, 15, 63-72. | 3.4 | 3 |
| 98 | A Bayesian Algorithm for Reconstructing Two-Component Signaling Networks. <i>Lecture Notes in Computer Science</i> , 2006, , 44-55. | 1.3 | 0 |
| 99 | Subpopulations of sensorless bacteria drive fitness in fluctuating environments. , 2020, 18, e3000952. | | 0 |
| 100 | Subpopulations of sensorless bacteria drive fitness in fluctuating environments. , 2020, 18, e3000952. | | 0 |
| 101 | Subpopulations of sensorless bacteria drive fitness in fluctuating environments. , 2020, 18, e3000952. | | 0 |
| 102 | Subpopulations of sensorless bacteria drive fitness in fluctuating environments. , 2020, 18, e3000952. | | 0 |
| 103 | Subpopulations of sensorless bacteria drive fitness in fluctuating environments. , 2020, 18, e3000952. | | 0 |
| 104 | Subpopulations of sensorless bacteria drive fitness in fluctuating environments. , 2020, 18, e3000952. | | 0 |
| 105 | Using fluorescence flow cytometry data for single-cell gene expression analysis in bacteria. , 2020, 15, e0240233. | | 0 |
| 106 | Using fluorescence flow cytometry data for single-cell gene expression analysis in bacteria. , 2020, 15, e0240233. | | 0 |
| 107 | Using fluorescence flow cytometry data for single-cell gene expression analysis in bacteria. , 2020, 15, e0240233. | | 0 |
| 108 | Using fluorescence flow cytometry data for single-cell gene expression analysis in bacteria. , 2020, 15, e0240233. | | 0 |

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| 109 | Using fluorescence flow cytometry data for single-cell gene expression analysis in bacteria. , 2020, 15, e0240233. | | 0 |
| 110 | Detecting Regulatory Sites Using PhyloGibbs. , 0, , 381-402. | | 0 |