

# Nir Friedman

## List of Publications by Year in descending order

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105  
papers

51,235  
citations

30070

54  
h-index

30087

103  
g-index

127  
all docs

127  
docs citations

127  
times ranked

62627  
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcription feedback dynamics in the wake of cytoplasmic mRNA degradation shutdown. <i>Nucleic Acids Research</i> , 2022, 50, 5864-5880.	14.5	8
2	ChIP-seq of plasma cell-free nucleosomes identifies gene expression programs of the cells of origin. <i>Nature Biotechnology</i> , 2021, 39, 586-598.	17.5	81
3	NovoSpaRc: flexible spatial reconstruction of single-cell gene expression with optimal transport. <i>Nature Protocols</i> , 2021, 16, 4177-4200.	12.0	55
4	Early sample tagging and pooling enables simultaneous SARS-CoV-2 detection and variant sequencing. <i>Science Translational Medicine</i> , 2021, 13, eabj2266.	12.4	9
5	Deciphering eukaryotic gene-regulatory logic with 100 million random promoters. <i>Nature Biotechnology</i> , 2020, 38, 56-65.	17.5	188
6	Selective flexible packaging pathways of the segmented genome of influenza A virus. <i>Nature Communications</i> , 2020, 11, 4355.	12.8	26
7	Gene expression cartography. <i>Nature</i> , 2019, 576, 132-137.	27.8	216
8	Dynamics of Chromatin and Transcription during Transient Depletion of the RSC Chromatin Remodeling Complex. <i>Cell Reports</i> , 2019, 26, 279-292.e5.	6.4	76
9	Genetic screen of the yeast environmental stress response dynamics uncovers distinct regulatory phases. <i>Molecular Systems Biology</i> , 2019, 15, e8939.	7.2	20
10	Fine-Resolution Mapping of TF Binding and Chromatin Interactions. <i>Cell Reports</i> , 2018, 22, 2797-2807.	6.4	46
11	Temporal profiling of redox-dependent heterogeneity in single cells. <i>ELife</i> , 2018, 7, .	6.0	27
12	A synthetic biology approach to probing nucleosome symmetry. <i>ELife</i> , 2017, 6, .	6.0	16
13	Perturb-Seq: Dissecting Molecular Circuits with Scalable Single-Cell RNA Profiling of Pooled Genetic Screens. <i>Cell</i> , 2016, 167, 1853-1866.e17.	28.9	1,144
14	Nuclear receptors control pro-viral and antiviral metabolic responses to hepatitis C virus infection. <i>Nature Chemical Biology</i> , 2016, 12, 1037-1045.	8.0	45
15	Elucidating Combinatorial Chromatin States at Single-Nucleosome Resolution. <i>Molecular Cell</i> , 2016, 63, 1080-1088.	9.7	29
16	Mapping the Landscape of a Eukaryotic Degronome. <i>Molecular Cell</i> , 2016, 63, 1055-1065.	9.7	51
17	Condition-specific genetic interaction maps reveal crosstalk between the cAMP and PKA and the HOG MAPK pathways in the activation of the general stress response. <i>Molecular Systems Biology</i> , 2015, 11, 829.	7.2	46
18	Mapping Nucleosome Resolution Chromosome Folding in Yeast by Micro-C. <i>Cell</i> , 2015, 162, 108-119.	28.9	540

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19	Clk post-transcriptional control denoises circadian transcription both temporally and spatially. <i>Nature Communications</i> , 2015, 6, 7056.	12.8	41
20	High-Resolution Chromatin Dynamics during a Yeast Stress Response. <i>Molecular Cell</i> , 2015, 58, 371-386.	9.7	183
21	Epigenomics and the structure of the living genome. <i>Genome Research</i> , 2015, 25, 1482-1490.	5.5	48
22	Chromatin Dynamics and the RNA Exosome Function in Concert to Regulate Transcriptional Homeostasis. <i>Cell Reports</i> , 2015, 13, 1610-1622.	6.4	34
23	High-Resolution Sequencing and Modeling Identifies Distinct Dynamic RNA Regulatory Strategies. <i>Cell</i> , 2014, 159, 1698-1710.	28.9	196
24	Chromatin state dynamics during blood formation. <i>Science</i> , 2014, 345, 943-949.	12.6	699
25	Single-cell RNA-seq reveals dynamic paracrine control of cellular variation. <i>Nature</i> , 2014, 510, 363-369.	27.8	872
26	De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis. <i>Nature Protocols</i> , 2013, 8, 1494-1512.	12.0	7,054
27	Comprehensive Mapping of DNA Damage: From Static Genetic Maps to Condition-Specific Maps. <i>Molecular Cell</i> , 2013, 49, 234-236.	9.7	0
28	Systematic Dissection of Roles for Chromatin Regulators in a Yeast Stress Response. <i>PLoS Biology</i> , 2012, 10, e1001369.	5.6	162
29	A High-Throughput Chromatin Immunoprecipitation Approach Reveals Principles of Dynamic Gene Regulation in Mammals. <i>Molecular Cell</i> , 2012, 47, 810-822.	9.7	375
30	High-Resolution View of the Yeast Meiotic Program Revealed by Ribosome Profiling. <i>Science</i> , 2012, 335, 552-557.	12.6	496
31	A functional selection model explains evolutionary robustness despite plasticity in regulatory networks. <i>Molecular Systems Biology</i> , 2012, 8, 619.	7.2	54
32	Running to stand still. <i>Nature</i> , 2012, 484, 171-172.	27.8	3
33	Comparative Functional Genomics of the Fission Yeasts. <i>Science</i> , 2011, 332, 930-936.	12.6	458
34	Densely Interconnected Transcriptional Circuits Control Cell States in Human Hematopoiesis. <i>Cell</i> , 2011, 144, 296-309.	28.9	843
35	High Throughput Determination of TGF $\beta$ 1/SMAD3 Targets in A549 Lung Epithelial Cells. <i>PLoS ONE</i> , 2011, 6, e20319.	2.5	57
36	Dynamics of Sir3 spreading in budding yeast: secondary recruitment sites and euchromatic localization. <i>EMBO Journal</i> , 2011, 30, 1012-1026.	7.8	58

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37	Full-length transcriptome assembly from RNA-Seq data without a reference genome. <i>Nature Biotechnology</i> , 2011, 29, 644-652.	17.5	17,264
38	Metabolic labeling of RNA uncovers principles of RNA production and degradation dynamics in mammalian cells. <i>Nature Biotechnology</i> , 2011, 29, 436-442.	17.5	524
39	From large-scale assays to mechanistic insights: computational analysis of interactions. <i>Current Opinion in Biotechnology</i> , 2011, 22, 87-93.	6.6	5
40	Patterns and Mechanisms of Ancestral Histone Protein Inheritance in Budding Yeast. <i>PLoS Biology</i> , 2011, 9, e1001075.	5.6	136
41	Physical Module Networks: an integrative approach for reconstructing transcription regulation. <i>Bioinformatics</i> , 2011, 27, i177-i185.	4.1	37
42	An integrative clustering and modeling algorithm for dynamical gene expression data. <i>Bioinformatics</i> , 2011, 27, i392-i400.	4.1	26
43	Exploring transcription regulation through cell-to-cell variability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6329-6334.	7.1	46
44	Substantial Histone Reduction Modulates Genomewide Nucleosomal Occupancy and Global Transcriptional Output. <i>PLoS Biology</i> , 2011, 9, e1001086.	5.6	193
45	The DNA Damage Road Map. <i>Science</i> , 2010, 330, 1327-1328.	12.6	1
46	Blood mononuclear cell gene expression signature of postpartum depression. <i>Molecular Psychiatry</i> , 2010, 15, 93-100.	7.9	73
47	Comprehensive comparative analysis of strand-specific RNA sequencing methods. <i>Nature Methods</i> , 2010, 7, 709-715.	19.0	662
48	Modularity and directionality in genetic interaction maps. <i>Bioinformatics</i> , 2010, 26, i228-i236.	4.1	27
49	Replication and Active Demethylation Represent Partially Overlapping Mechanisms for Erasure of H3K4me3 in Budding Yeast. <i>PLoS Genetics</i> , 2010, 6, e1000837.	3.5	39
50	High-resolution nucleosome mapping reveals transcription-dependent promoter packaging. <i>Genome Research</i> , 2010, 20, 90-100.	5.5	332
51	Paternally Induced Transgenerational Environmental Reprogramming of Metabolic Gene Expression in Mammals. <i>Cell</i> , 2010, 143, 1084-1096.	28.9	990
52	Strand-specific RNA sequencing reveals extensive regulated long antisense transcripts that are conserved across yeast species. <i>Genome Biology</i> , 2010, 11, R87.	9.6	122
53	RNA polymerase mapping during stress responses reveals widespread nonproductive transcription in yeast. <i>Genome Biology</i> , 2010, 11, R75.	9.6	52
54	Development and evaluation of RNA-seq methods. <i>Genome Biology</i> , 2010, 11, P26.	9.6	5

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55	Ab initio construction of a eukaryotic transcriptome by massively parallel mRNA sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3264-3269.	7.1	201
56	Identifying novel constrained elements by exploiting biased substitution patterns. Bioinformatics, 2009, 25, i54-i62.	4.1	296
57	Structure and function of a transcriptional network activated by the MAPK Hog1. Nature Genetics, 2008, 40, 1300-1306.	21.4	197
58	Physiological and molecular evidence of heat acclimation memory: a lesson from thermal responses and ischemic cross-tolerance in the heart. Physiological Genomics, 2008, 34, 78-87.	2.3	51
59	Cell Cycle and Chaperone-Mediated Regulation of H3K56ac Incorporation in Yeast. PLoS Genetics, 2008, 4, e1000270.	3.5	133
60	Nucleosome positioning from tiling microarray data. Bioinformatics, 2008, 24, i139-i146.	4.1	19
61	A Novel Bayesian DNA Motif Comparison Method for Clustering and Retrieval. PLoS Computational Biology, 2008, 4, e1000010.	3.2	40
62	Mitochondrial processes are impaired in hereditary inclusion body myopathy. Human Molecular Genetics, 2008, 17, 3663-3674.	2.9	49
63	A Functional and Regulatory Map of Asthma. American Journal of Respiratory Cell and Molecular Biology, 2008, 38, 324-336.	2.9	50
64	Phylogeny reconstruction: increasing the accuracy of pairwise distance estimation using Bayesian inference of evolutionary rates. Bioinformatics, 2007, 23, e136-e141.	4.1	8
65	Automatic genome-wide reconstruction of phylogenetic gene trees. Bioinformatics, 2007, 23, i549-i558.	4.1	129
66	Dynamics of Replication-Independent Histone Turnover in Budding Yeast. Science, 2007, 315, 1405-1408.	12.6	501
67	Natural history and evolutionary principles of gene duplication in fungi. Nature, 2007, 449, 54-61.	27.8	611
68	Towards an Integrated Protein-Protein Interaction Network: A Relational Markov Network Approach. Journal of Computational Biology, 2006, 13, 145-164.	1.6	39
69	Multivariate Information Bottleneck. Neural Computation, 2006, 18, 1739-1789.	2.2	56
70	Predicting Transcription Factor Binding Sites Using Structural Knowledge. Lecture Notes in Computer Science, 2005, , 522-537.	1.3	2
71	From signatures to models: understanding cancer using microarrays. Nature Genetics, 2005, 37, S38-S45.	21.4	331
72	Peripheral blood mononuclear cell gene expression profiles identify emergent post-traumatic stress disorder among trauma survivors. Molecular Psychiatry, 2005, 10, 500-513.	7.9	257

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73	Ab Initio Prediction of Transcription Factor Targets Using Structural Knowledge. PLoS Computational Biology, 2005, 1, e1.	3.2	100
74	Single-Nucleosome Mapping of Histone Modifications in <i>S. cerevisiae</i> . PLoS Biology, 2005, 3, e328.	5.6	451
75	CIS: compound importance sampling method for protein-DNA binding site p-value estimation. Bioinformatics, 2005, 21, 596-600.	4.1	23
76	A Gamma mixture model better accounts for among site rate heterogeneity. Bioinformatics, 2005, 21, ii151-ii158.	4.1	129
77	Towards an Integrated Protein-Protein Interaction Network. Lecture Notes in Computer Science, 2005, , 14-30.	1.3	3
78	Stress-related genomic responses during the course of heat acclimation and its association with ischemic-reperfusion cross-tolerance. Journal of Applied Physiology, 2004, 97, 1496-1507.	2.5	73
79	Inferring quantitative models of regulatory networks from expression data. Bioinformatics, 2004, 20, i248-i256.	4.1	162
80	Sfp1 is a stress- and nutrient-sensitive regulator of ribosomal protein gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 14315-14322.	7.1	335
81	Blood transcriptional signatures of multiple sclerosis: Unique gene expression of disease activity. Annals of Neurology, 2004, 55, 410-417.	5.3	139
82	Inferring Cellular Networks Using Probabilistic Graphical Models. Science, 2004, 303, 799-805.	12.6	1,003
83	Comparative analysis of algorithms for signal quantitation from oligonucleotide microarrays. Bioinformatics, 2004, 20, 839-846.	4.1	83
84	A module map showing conditional activity of expression modules in cancer. Nature Genetics, 2004, 36, 1090-1098.	21.4	622
85	Efficient Exact &lt;p>&lt;/p>-Value Computation for Small Sample, Sparse, and Surprising Categorical Data. Journal of Computational Biology, 2004, 11, 867-886.	1.6	1
86	Title is missing!. Machine Learning, 2003, 50, 95-125.	5.4	516
87	Module networks: identifying regulatory modules and their condition-specific regulators from gene expression data. Nature Genetics, 2003, 34, 166-176.	21.4	1,543
88	Human and porcine early kidney precursors as a new source for transplantation. Nature Medicine, 2003, 9, 53-60.	30.7	267
89	Modeling dependencies in protein-DNA binding sites. , 2003, , .		106
90	Context-Specific Bayesian Clustering for Gene Expression Data. Journal of Computational Biology, 2002, 9, 169-191.	1.6	72

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91	A Structural EM Algorithm for Phylogenetic Inference. Journal of Computational Biology, 2002, 9, 331-353.	1.6	95
92	Practical Approaches to Analyzing Results of Microarray Experiments. American Journal of Respiratory Cell and Molecular Biology, 2002, 27, 125-132.	2.9	82
93	A branch-and-bound algorithm for the inference of ancestral amino-acid sequences when the replacement rate varies among sites: Application to the evolution of five gene families. Bioinformatics, 2002, 18, 1116-1123.	4.1	102
94	Transcriptional Profiling of Non-small Cell Lung Cancer Using Oligonucleotide Microarrays. Chest, 2002, 121, 44S.	0.8	3
95	On decision-theoretic foundations for defaults. Artificial Intelligence, 2001, 133, 1-33.	5.8	8
96	Plausibility measures and default reasoning. Journal of the ACM, 2001, 48, 648-685.	2.2	86
97	Class discovery in gene expression data. , 2001, , .		73
98	Learning Probabilistic Relational Models. , 2001, , 307-335.		288
99	First-order conditional logic for default reasoning revisited. ACM Transactions on Computational Logic, 2000, 1, 175-207.	0.9	21
100	Tissue Classification with Gene Expression Profiles. Journal of Computational Biology, 2000, 7, 559-583.	1.6	623
101	Using Bayesian Networks to Analyze Expression Data. Journal of Computational Biology, 2000, 7, 601-620.	1.6	2,653
102	10.1162/jmlr.2003.3.4-5.679. Applied Physics Letters, 2000, 1, .	3.3	19
103	Belief Revision: A Critique. Journal of Logic, Language and Information, 1999, 8, 401-420.	0.6	33
104	Bayesian Network Classifiers. Machine Learning, 1997, 29, 131-163.	5.4	3,662
105	Modeling belief in dynamic systems, part I: Foundations. Artificial Intelligence, 1997, 95, 257-316.	5.8	43