

# Nir Friedman

## List of Publications by Year in descending order

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104  
papers

51,235  
citations

34493

54  
h-index

35168

102  
g-index

127  
all docs

127  
docs citations

127  
times ranked

69865  
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.	6.5	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.	9.4	81
3	NovoSpaRc: flexible spatial reconstruction of single-cell gene expression with optimal transport. <i>Nature Protocols</i> , 2021, 16, 4177-4200.	5.5	55
4	Early sample tagging and pooling enables simultaneous SARS-CoV-2 detection and variant sequencing. <i>Science Translational Medicine</i> , 2021, 13, eabj2266.	5.8	9
5	Deciphering eukaryotic gene-regulatory logic with 100 million random promoters. <i>Nature Biotechnology</i> , 2020, 38, 56-65.	9.4	188
6	Selective flexible packaging pathways of the segmented genome of influenza A virus. <i>Nature Communications</i> , 2020, 11, 4355.	5.8	26
7	Gene expression cartography. <i>Nature</i> , 2019, 576, 132-137.	13.7	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.	2.9	76
9	Genetic screen of the yeast environmental stress response dynamics uncovers distinct regulatory phases. <i>Molecular Systems Biology</i> , 2019, 15, e8939.	3.2	20
10	Fine-Resolution Mapping of TF Binding and Chromatin Interactions. <i>Cell Reports</i> , 2018, 22, 2797-2807.	2.9	46
11	Temporal profiling of redox-dependent heterogeneity in single cells. <i>ELife</i> , 2018, 7, .	2.8	27
12	A synthetic biology approach to probing nucleosome symmetry. <i>ELife</i> , 2017, 6, .	2.8	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.	13.5	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.	3.9	45
15	Elucidating Combinatorial Chromatin States at Single-Nucleosome Resolution. <i>Molecular Cell</i> , 2016, 63, 1080-1088.	4.5	29
16	Mapping the Landscape of a Eukaryotic Degronome. <i>Molecular Cell</i> , 2016, 63, 1055-1065.	4.5	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.	3.2	46
18	Mapping Nucleosome Resolution Chromosome Folding in Yeast by Micro-C. <i>Cell</i> , 2015, 162, 108-119.	13.5	540

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19	Clk post-transcriptional control denoises circadian transcription both temporally and spatially. <i>Nature Communications</i> , 2015, 6, 7056.	5.8	41
20	High-Resolution Chromatin Dynamics during a Yeast Stress Response. <i>Molecular Cell</i> , 2015, 58, 371-386.	4.5	183
21	Epigenomics and the structure of the living genome. <i>Genome Research</i> , 2015, 25, 1482-1490.	2.4	48
22	Chromatin Dynamics and the RNA Exosome Function in Concert to Regulate Transcriptional Homeostasis. <i>Cell Reports</i> , 2015, 13, 1610-1622.	2.9	34
23	High-Resolution Sequencing and Modeling Identifies Distinct Dynamic RNA Regulatory Strategies. <i>Cell</i> , 2014, 159, 1698-1710.	13.5	196
24	Chromatin state dynamics during blood formation. <i>Science</i> , 2014, 345, 943-949.	6.0	699
25	Single-cell RNA-seq reveals dynamic paracrine control of cellular variation. <i>Nature</i> , 2014, 510, 363-369.	13.7	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.	5.5	7,054
27	Comprehensive Mapping of DNA Damage: From Static Genetic Maps to Condition-Specific Maps. <i>Molecular Cell</i> , 2013, 49, 234-236.	4.5	0
28	Systematic Dissection of Roles for Chromatin Regulators in a Yeast Stress Response. <i>PLoS Biology</i> , 2012, 10, e1001369.	2.6	162
29	A High-Throughput Chromatin Immunoprecipitation Approach Reveals Principles of Dynamic Gene Regulation in Mammals. <i>Molecular Cell</i> , 2012, 47, 810-822.	4.5	375
30	High-Resolution View of the Yeast Meiotic Program Revealed by Ribosome Profiling. <i>Science</i> , 2012, 335, 552-557.	6.0	496
31	A functional selection model explains evolutionary robustness despite plasticity in regulatory networks. <i>Molecular Systems Biology</i> , 2012, 8, 619.	3.2	54
32	Running to stand still. <i>Nature</i> , 2012, 484, 171-172.	13.7	3
33	Comparative Functional Genomics of the Fission Yeasts. <i>Science</i> , 2011, 332, 930-936.	6.0	458
34	Densely Interconnected Transcriptional Circuits Control Cell States in Human Hematopoiesis. <i>Cell</i> , 2011, 144, 296-309.	13.5	843
35	High Throughput Determination of TGF $\beta$ 1/SMAD3 Targets in A549 Lung Epithelial Cells. <i>PLoS ONE</i> , 2011, 6, e20319.	1.1	57
36	Dynamics of Sir3 spreading in budding yeast: secondary recruitment sites and euchromatic localization. <i>EMBO Journal</i> , 2011, 30, 1012-1026.	3.5	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.	9.4	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.	9.4	524
39	From large-scale assays to mechanistic insights: computational analysis of interactions. <i>Current Opinion in Biotechnology</i> , 2011, 22, 87-93.	3.3	5
40	Patterns and Mechanisms of Ancestral Histone Protein Inheritance in Budding Yeast. <i>PLoS Biology</i> , 2011, 9, e1001075.	2.6	136
41	Physical Module Networks: an integrative approach for reconstructing transcription regulation. <i>Bioinformatics</i> , 2011, 27, i177-i185.	1.8	37
42	An integrative clustering and modeling algorithm for dynamical gene expression data. <i>Bioinformatics</i> , 2011, 27, i392-i400.	1.8	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.	3.3	46
44	Substantial Histone Reduction Modulates Genomewide Nucleosomal Occupancy and Global Transcriptional Output. <i>PLoS Biology</i> , 2011, 9, e1001086.	2.6	193
45	The DNA Damage Road Map. <i>Science</i> , 2010, 330, 1327-1328.	6.0	1
46	Blood mononuclear cell gene expression signature of postpartum depression. <i>Molecular Psychiatry</i> , 2010, 15, 93-100.	4.1	73
47	Comprehensive comparative analysis of strand-specific RNA sequencing methods. <i>Nature Methods</i> , 2010, 7, 709-715.	9.0	662
48	Modularity and directionality in genetic interaction maps. <i>Bioinformatics</i> , 2010, 26, i228-i236.	1.8	27
49	Replication and Active Demethylation Represent Partially Overlapping Mechanisms for Erasure of H3K4me3 in Budding Yeast. <i>PLoS Genetics</i> , 2010, 6, e1000837.	1.5	39
50	High-resolution nucleosome mapping reveals transcription-dependent promoter packaging. <i>Genome Research</i> , 2010, 20, 90-100.	2.4	332
51	Paternally Induced Transgenerational Environmental Reprogramming of Metabolic Gene Expression in Mammals. <i>Cell</i> , 2010, 143, 1084-1096.	13.5	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.	13.9	122
53	RNA polymerase mapping during stress responses reveals widespread nonproductive transcription in yeast. <i>Genome Biology</i> , 2010, 11, R75.	13.9	52
54	Development and evaluation of RNA-seq methods. <i>Genome Biology</i> , 2010, 11, P26.	13.9	5

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55	Ab initio construction of a eukaryotic transcriptome by massively parallel mRNA sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3264-3269.	3.3	201
56	Identifying novel constrained elements by exploiting biased substitution patterns. <i>Bioinformatics</i> , 2009, 25, i54-i62.	1.8	296
57	Structure and function of a transcriptional network activated by the MAPK Hog1. <i>Nature Genetics</i> , 2008, 40, 1300-1306.	9.4	197
58	Physiological and molecular evidence of heat acclimation memory: a lesson from thermal responses and ischemic cross-tolerance in the heart. <i>Physiological Genomics</i> , 2008, 34, 78-87.	1.0	51
59	Cell Cycle and Chaperone-Mediated Regulation of H3K56ac Incorporation in Yeast. <i>PLoS Genetics</i> , 2008, 4, e1000270.	1.5	133
60	Nucleosome positioning from tiling microarray data. <i>Bioinformatics</i> , 2008, 24, i139-i146.	1.8	19
61	A Novel Bayesian DNA Motif Comparison Method for Clustering and Retrieval. <i>PLoS Computational Biology</i> , 2008, 4, e1000010.	1.5	40
62	Mitochondrial processes are impaired in hereditary inclusion body myopathy. <i>Human Molecular Genetics</i> , 2008, 17, 3663-3674.	1.4	49
63	A Functional and Regulatory Map of Asthma. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2008, 38, 324-336.	1.4	50
64	Phylogeny reconstruction: increasing the accuracy of pairwise distance estimation using Bayesian inference of evolutionary rates. <i>Bioinformatics</i> , 2007, 23, e136-e141.	1.8	8
65	Automatic genome-wide reconstruction of phylogenetic gene trees. <i>Bioinformatics</i> , 2007, 23, i549-i558.	1.8	129
66	Dynamics of Replication-Independent Histone Turnover in Budding Yeast. <i>Science</i> , 2007, 315, 1405-1408.	6.0	501
67	Natural history and evolutionary principles of gene duplication in fungi. <i>Nature</i> , 2007, 449, 54-61.	13.7	611
68	Towards an Integrated Protein-Protein Interaction Network: A Relational Markov Network Approach. <i>Journal of Computational Biology</i> , 2006, 13, 145-164.	0.8	39
69	Multivariate Information Bottleneck. <i>Neural Computation</i> , 2006, 18, 1739-1789.	1.3	56
70	Predicting Transcription Factor Binding Sites Using Structural Knowledge. <i>Lecture Notes in Computer Science</i> , 2005, , 522-537.	1.0	2
71	From signatures to models: understanding cancer using microarrays. <i>Nature Genetics</i> , 2005, 37, S38-S45.	9.4	331
72	Peripheral blood mononuclear cell gene expression profiles identify emergent post-traumatic stress disorder among trauma survivors. <i>Molecular Psychiatry</i> , 2005, 10, 500-513.	4.1	257

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73	Ab Initio Prediction of Transcription Factor Targets Using Structural Knowledge. PLoS Computational Biology, 2005, 1, e1.	1.5	100
74	Single-Nucleosome Mapping of Histone Modifications in <i>S. cerevisiae</i> . PLoS Biology, 2005, 3, e328.	2.6	451
75	CIS: compound importance sampling method for protein-DNA binding site p-value estimation. Bioinformatics, 2005, 21, 596-600.	1.8	23
76	A Gamma mixture model better accounts for among site rate heterogeneity. Bioinformatics, 2005, 21, ii151-ii158.	1.8	129
77	Towards an Integrated Protein-Protein Interaction Network. Lecture Notes in Computer Science, 2005, , 14-30.	1.0	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.	1.2	73
79	Inferring quantitative models of regulatory networks from expression data. Bioinformatics, 2004, 20, i248-i256.	1.8	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.	3.3	335
81	Blood transcriptional signatures of multiple sclerosis: Unique gene expression of disease activity. Annals of Neurology, 2004, 55, 410-417.	2.8	139
82	Inferring Cellular Networks Using Probabilistic Graphical Models. Science, 2004, 303, 799-805.	6.0	1,003
83	Comparative analysis of algorithms for signal quantitation from oligonucleotide microarrays. Bioinformatics, 2004, 20, 839-846.	1.8	83
84	A module map showing conditional activity of expression modules in cancer. Nature Genetics, 2004, 36, 1090-1098.	9.4	622
85	Title is missing!. Machine Learning, 2003, 50, 95-125.	3.4	516
86	Module networks: identifying regulatory modules and their condition-specific regulators from gene expression data. Nature Genetics, 2003, 34, 166-176.	9.4	1,543
87	Human and porcine early kidney precursors as a new source for transplantation. Nature Medicine, 2003, 9, 53-60.	15.2	267
88	Modeling dependencies in protein-DNA binding sites. , 2003, , .		106
89	Context-Specific Bayesian Clustering for Gene Expression Data. Journal of Computational Biology, 2002, 9, 169-191.	0.8	72
90	A Structural EM Algorithm for Phylogenetic Inference. Journal of Computational Biology, 2002, 9, 331-353.	0.8	95

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91	Practical Approaches to Analyzing Results of Microarray Experiments. American Journal of Respiratory Cell and Molecular Biology, 2002, 27, 125-132.	1.4	82
92	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.	1.8	102
93	Transcriptional Profiling of Non-small Cell Lung Cancer Using Oligonucleotide Microarrays. Chest, 2002, 121, 44S.	0.4	3
94	On decision-theoretic foundations for defaults. Artificial Intelligence, 2001, 133, 1-33.	3.9	8
95	Plausibility measures and default reasoning. Journal of the ACM, 2001, 48, 648-685.	1.8	86
96	Class discovery in gene expression data. , 2001, , .		73
97	Learning Probabilistic Relational Models. , 2001, , 307-335.		288
98	First-order conditional logic for default reasoning revisited. ACM Transactions on Computational Logic, 2000, 1, 175-207.	0.7	21
99	Tissue Classification with Gene Expression Profiles. Journal of Computational Biology, 2000, 7, 559-583.	0.8	623
100	Using Bayesian Networks to Analyze Expression Data. Journal of Computational Biology, 2000, 7, 601-620.	0.8	2,653
101	10.1162/jmlr.2003.3.4-5.679. Applied Physics Letters, 2000, 1, .	1.5	19
102	Belief Revision: A Critique. Journal of Logic, Language and Information, 1999, 8, 401-420.	0.4	33
103	Bayesian Network Classifiers. Machine Learning, 1997, 29, 131-163.	3.4	3,662
104	Modeling belief in dynamic systems, part I: Foundations. Artificial Intelligence, 1997, 95, 257-316.	3.9	43