

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	Full-length transcriptome assembly from RNA-Seq data without a reference genome. <i>Nature Biotechnology</i> , 2011, 29, 644-652.	17.5	17,264
2	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
3	Bayesian Network Classifiers. <i>Machine Learning</i> , 1997, 29, 131-163.	5.4	3,662
4	Using Bayesian Networks to Analyze Expression Data. <i>Journal of Computational Biology</i> , 2000, 7, 601-620.	1.6	2,653
5	Module networks: identifying regulatory modules and their condition-specific regulators from gene expression data. <i>Nature Genetics</i> , 2003, 34, 166-176.	21.4	1,543
6	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
7	Inferring Cellular Networks Using Probabilistic Graphical Models. <i>Science</i> , 2004, 303, 799-805.	12.6	1,003
8	Paternally Induced Transgenerational Environmental Reprogramming of Metabolic Gene Expression in Mammals. <i>Cell</i> , 2010, 143, 1084-1096.	28.9	990
9	Single-cell RNA-seq reveals dynamic paracrine control of cellular variation. <i>Nature</i> , 2014, 510, 363-369.	27.8	872
10	Densely Interconnected Transcriptional Circuits Control Cell States in Human Hematopoiesis. <i>Cell</i> , 2011, 144, 296-309.	28.9	843
11	Chromatin state dynamics during blood formation. <i>Science</i> , 2014, 345, 943-949.	12.6	699
12	Comprehensive comparative analysis of strand-specific RNA sequencing methods. <i>Nature Methods</i> , 2010, 7, 709-715.	19.0	662
13	Tissue Classification with Gene Expression Profiles. <i>Journal of Computational Biology</i> , 2000, 7, 559-583.	1.6	623
14	A module map showing conditional activity of expression modules in cancer. <i>Nature Genetics</i> , 2004, 36, 1090-1098.	21.4	622
15	Natural history and evolutionary principles of gene duplication in fungi. <i>Nature</i> , 2007, 449, 54-61.	27.8	611
16	Mapping Nucleosome Resolution Chromosome Folding in Yeast by Micro-C. <i>Cell</i> , 2015, 162, 108-119.	28.9	540
17	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
18	Title is missing!. <i>Machine Learning</i> , 2003, 50, 95-125.	5.4	516

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19	Dynamics of Replication-Independent Histone Turnover in Budding Yeast. <i>Science</i> , 2007, 315, 1405-1408.	12.6	501
20	High-Resolution View of the Yeast Meiotic Program Revealed by Ribosome Profiling. <i>Science</i> , 2012, 335, 552-557.	12.6	496
21	Comparative Functional Genomics of the Fission Yeasts. <i>Science</i> , 2011, 332, 930-936.	12.6	458
22	Single-Nucleosome Mapping of Histone Modifications in <i>S. cerevisiae</i> . <i>PLoS Biology</i> , 2005, 3, e328.	5.6	451
23	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
24	Sfp1 is a stress- and nutrient-sensitive regulator of ribosomal protein gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 14315-14322.	7.1	335
25	High-resolution nucleosome mapping reveals transcription-dependent promoter packaging. <i>Genome Research</i> , 2010, 20, 90-100.	5.5	332
26	From signatures to models: understanding cancer using microarrays. <i>Nature Genetics</i> , 2005, 37, S38-S45.	21.4	331
27	Identifying novel constrained elements by exploiting biased substitution patterns. <i>Bioinformatics</i> , 2009, 25, i54-i62.	4.1	296
28	Learning Probabilistic Relational Models. , 2001, , 307-335.		288
29	Human and porcine early kidney precursors as a new source for transplantation. <i>Nature Medicine</i> , 2003, 9, 53-60.	30.7	267
30	Peripheral blood mononuclear cell gene expression profiles identify emergent post-traumatic stress disorder among trauma survivors. <i>Molecular Psychiatry</i> , 2005, 10, 500-513.	7.9	257
31	Gene expression cartography. <i>Nature</i> , 2019, 576, 132-137.	27.8	216
32	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.	7.1	201
33	Structure and function of a transcriptional network activated by the MAPK Hog1. <i>Nature Genetics</i> , 2008, 40, 1300-1306.	21.4	197
34	High-Resolution Sequencing and Modeling Identifies Distinct Dynamic RNA Regulatory Strategies. <i>Cell</i> , 2014, 159, 1698-1710.	28.9	196
35	Substantial Histone Reduction Modulates Genomewide Nucleosomal Occupancy and Global Transcriptional Output. <i>PLoS Biology</i> , 2011, 9, e1001086.	5.6	193
36	Deciphering eukaryotic gene-regulatory logic with 100 million random promoters. <i>Nature Biotechnology</i> , 2020, 38, 56-65.	17.5	188

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37	High-Resolution Chromatin Dynamics during a Yeast Stress Response. <i>Molecular Cell</i> , 2015, 58, 371-386.	9.7	183
38	Inferring quantitative models of regulatory networks from expression data. <i>Bioinformatics</i> , 2004, 20, i248-i256.	4.1	162
39	Systematic Dissection of Roles for Chromatin Regulators in a Yeast Stress Response. <i>PLoS Biology</i> , 2012, 10, e1001369.	5.6	162
40	Blood transcriptional signatures of multiple sclerosis: Unique gene expression of disease activity. <i>Annals of Neurology</i> , 2004, 55, 410-417.	5.3	139
41	Patterns and Mechanisms of Ancestral Histone Protein Inheritance in Budding Yeast. <i>PLoS Biology</i> , 2011, 9, e1001075.	5.6	136
42	Cell Cycle and Chaperone-Mediated Regulation of H3K56ac Incorporation in Yeast. <i>PLoS Genetics</i> , 2008, 4, e1000270.	3.5	133
43	A Gamma mixture model better accounts for among site rate heterogeneity. <i>Bioinformatics</i> , 2005, 21, ii151-ii158.	4.1	129
44	Automatic genome-wide reconstruction of phylogenetic gene trees. <i>Bioinformatics</i> , 2007, 23, i549-i558.	4.1	129
45	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
46	Modeling dependencies in protein-DNA binding sites. , 2003, , .		106
47	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. <i>Bioinformatics</i> , 2002, 18, 1116-1123.	4.1	102
48	Ab Initio Prediction of Transcription Factor Targets Using Structural Knowledge. <i>PLoS Computational Biology</i> , 2005, 1, e1.	3.2	100
49	A Structural EM Algorithm for Phylogenetic Inference. <i>Journal of Computational Biology</i> , 2002, 9, 331-353.	1.6	95
50	Plausibility measures and default reasoning. <i>Journal of the ACM</i> , 2001, 48, 648-685.	2.2	86
51	Comparative analysis of algorithms for signal quantitation from oligonucleotide microarrays. <i>Bioinformatics</i> , 2004, 20, 839-846.	4.1	83
52	Practical Approaches to Analyzing Results of Microarray Experiments. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2002, 27, 125-132.	2.9	82
53	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
54	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

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55	Class discovery in gene expression data. , 2001, , .		73
56	Stress-related genomic responses during the course of heat acclimation and its association with ischemic-reperfusion cross-tolerance. <i>Journal of Applied Physiology</i> , 2004, 97, 1496-1507.	2.5	73
57	Blood mononuclear cell gene expression signature of postpartum depression. <i>Molecular Psychiatry</i> , 2010, 15, 93-100.	7.9	73
58	Context-Specific Bayesian Clustering for Gene Expression Data. <i>Journal of Computational Biology</i> , 2002, 9, 169-191.	1.6	72
59	Dynamics of Sir3 spreading in budding yeast: secondary recruitment sites and euchromatic localization. <i>EMBO Journal</i> , 2011, 30, 1012-1026.	7.8	58
60	High Throughput Determination of TGF β 1/SMAD3 Targets in A549 Lung Epithelial Cells. <i>PLoS ONE</i> , 2011, 6, e20319.	2.5	57
61	Multivariate Information Bottleneck. <i>Neural Computation</i> , 2006, 18, 1739-1789.	2.2	56
62	NovoSpaRc: flexible spatial reconstruction of single-cell gene expression with optimal transport. <i>Nature Protocols</i> , 2021, 16, 4177-4200.	12.0	55
63	A functional selection model explains evolutionary robustness despite plasticity in regulatory networks. <i>Molecular Systems Biology</i> , 2012, 8, 619.	7.2	54
64	RNA polymerase mapping during stress responses reveals widespread nonproductive transcription in yeast. <i>Genome Biology</i> , 2010, 11, R75.	9.6	52
65	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.	2.3	51
66	Mapping the Landscape of a Eukaryotic Degronome. <i>Molecular Cell</i> , 2016, 63, 1055-1065.	9.7	51
67	A Functional and Regulatory Map of Asthma. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2008, 38, 324-336.	2.9	50
68	Mitochondrial processes are impaired in hereditary inclusion body myopathy. <i>Human Molecular Genetics</i> , 2008, 17, 3663-3674.	2.9	49
69	Epigenomics and the structure of the living genome. <i>Genome Research</i> , 2015, 25, 1482-1490.	5.5	48
70	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
71	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
72	Fine-Resolution Mapping of TF Binding and Chromatin Interactions. <i>Cell Reports</i> , 2018, 22, 2797-2807.	6.4	46

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73	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
74	Modeling belief in dynamic systems, part I: Foundations. <i>Artificial Intelligence</i> , 1997, 95, 257-316.	5.8	43
75	Clk post-transcriptional control denoises circadian transcription both temporally and spatially. <i>Nature Communications</i> , 2015, 6, 7056.	12.8	41
76	A Novel Bayesian DNA Motif Comparison Method for Clustering and Retrieval. <i>PLoS Computational Biology</i> , 2008, 4, e1000010.	3.2	40
77	Towards an Integrated Protein-Protein Interaction Network: A Relational Markov Network Approach. <i>Journal of Computational Biology</i> , 2006, 13, 145-164.	1.6	39
78	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
79	Physical Module Networks: an integrative approach for reconstructing transcription regulation. <i>Bioinformatics</i> , 2011, 27, i177-i185.	4.1	37
80	Chromatin Dynamics and the RNA Exosome Function in Concert to Regulate Transcriptional Homeostasis. <i>Cell Reports</i> , 2015, 13, 1610-1622.	6.4	34
81	Belief Revision: A Critique. <i>Journal of Logic, Language and Information</i> , 1999, 8, 401-420.	0.6	33
82	Elucidating Combinatorial Chromatin States at Single-Nucleosome Resolution. <i>Molecular Cell</i> , 2016, 63, 1080-1088.	9.7	29
83	Modularity and directionality in genetic interaction maps. <i>Bioinformatics</i> , 2010, 26, i228-i236.	4.1	27
84	Temporal profiling of redox-dependent heterogeneity in single cells. <i>ELife</i> , 2018, 7, .	6.0	27
85	An integrative clustering and modeling algorithm for dynamical gene expression data. <i>Bioinformatics</i> , 2011, 27, i392-i400.	4.1	26
86	Selective flexible packaging pathways of the segmented genome of influenza A virus. <i>Nature Communications</i> , 2020, 11, 4355.	12.8	26
87	CIS: compound importance sampling method for protein-DNA binding site p-value estimation. <i>Bioinformatics</i> , 2005, 21, 596-600.	4.1	23
88	First-order conditional logic for default reasoning revisited. <i>ACM Transactions on Computational Logic</i> , 2000, 1, 175-207.	0.9	21
89	Genetic screen of the yeast environmental stress response dynamics uncovers distinct regulatory phases. <i>Molecular Systems Biology</i> , 2019, 15, e8939.	7.2	20
90	Nucleosome positioning from tiling microarray data. <i>Bioinformatics</i> , 2008, 24, i139-i146.	4.1	19

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91	10.1162/jmlr.2003.3.4-5.679. Applied Physics Letters, 2000, 1, .	3.3	19
92	A synthetic biology approach to probing nucleosome symmetry. ELife, 2017, 6, .	6.0	16
93	Early sample tagging and pooling enables simultaneous SARS-CoV-2 detection and variant sequencing. Science Translational Medicine, 2021, 13, eabj2266.	12.4	9
94	On decision-theoretic foundations for defaults. Artificial Intelligence, 2001, 133, 1-33.	5.8	8
95	Phylogeny reconstruction: increasing the accuracy of pairwise distance estimation using Bayesian inference of evolutionary rates. Bioinformatics, 2007, 23, e136-e141.	4.1	8
96	Transcription feedback dynamics in the wake of cytoplasmic mRNA degradation shutdown. Nucleic Acids Research, 2022, 50, 5864-5880.	14.5	8
97	Development and evaluation of RNA-seq methods. Genome Biology, 2010, 11, P26.	9.6	5
98	From large-scale assays to mechanistic insights: computational analysis of interactions. Current Opinion in Biotechnology, 2011, 22, 87-93.	6.6	5
99	Transcriptional Profiling of Non-small Cell Lung Cancer Using Oligonucleotide Microarrays. Chest, 2002, 121, 44S.	0.8	3
100	Running to stand still. Nature, 2012, 484, 171-172.	27.8	3
101	Towards an Integrated Protein-Protein Interaction Network. Lecture Notes in Computer Science, 2005, , 14-30.	1.3	3
102	Predicting Transcription Factor Binding Sites Using Structural Knowledge. Lecture Notes in Computer Science, 2005, , 522-537.	1.3	2
103	The DNA Damage Road Map. Science, 2010, 330, 1327-1328.	12.6	1
104	Efficient Exact <l>p</l>-Value Computation for Small Sample, Sparse, and Surprising Categorical Data. Journal of Computational Biology, 2004, 11, 867-886.	1.6	1
105	Comprehensive Mapping of DNA Damage: From Static Genetic Maps to Condition-Specific Maps. Molecular Cell, 2013, 49, 234-236.	9.7	0