

Roded Sharan

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

89 papers	9,837 citations	43 h-index	91 g-index
91 ext. papers	11,430 ext. citations	7.3 avg, IF	6.27 L-index

#	Paper	IF	Citations
89	Effect of SARS-CoV-2 proteins on vascular permeability. <i>ELife</i> , 2021 , 10,	8.9	13
88	Interactome Mapping Provides a Network of Neurodegenerative Disease Proteins and Uncovers Widespread Protein Aggregation in Affected Brains. <i>Cell Reports</i> , 2020 , 32, 108050	10.6	20
87	A Robustness Analysis of Dynamic Boolean Models of Cellular Circuits. <i>Lecture Notes in Computer Science</i> , 2019 , 183-195	0.9	
86	To Embed or Not: Network Embedding as a Paradigm in Computational Biology. <i>Frontiers in Genetics</i> , 2019 , 10, 381	4.5	59
85	Comparative Analysis of Normalization Methods for Network Propagation. <i>Frontiers in Genetics</i> , 2019 , 10, 4	4.5	8
84	The EXPANDER Integrated Platform for Transcriptome Analysis. <i>Journal of Molecular Biology</i> , 2019 , 431, 2398-2406	6.5	13
83	A systematic approach to orient the human protein-protein interaction network. <i>Nature Communications</i> , 2019 , 10, 3015	17.4	12
82	WebPropagate: A Web Server for Network Propagation. <i>Journal of Molecular Biology</i> , 2018 , 430, 2231-2236	23.6	3
81	Quantitative mass spectrometry analysis reveals a panel of nine proteins as diagnostic markers for colon adenocarcinomas. <i>Oncotarget</i> , 2018 , 9, 13530-13544	3.3	12
80	Network propagation: a universal amplifier of genetic associations. <i>Nature Reviews Genetics</i> , 2017 , 18, 551-562	30.1	285
79	A network diffusion approach to inferring sample-specific function reveals functional changes associated with breast cancer. <i>PLoS Computational Biology</i> , 2017 , 13, e1005793	5	10
78	ANAT 2.0: reconstructing functional protein subnetworks. <i>BMC Bioinformatics</i> , 2017 , 18, 495	3.6	10
77	GLADIATOR: a global approach for elucidating disease modules. <i>Genome Medicine</i> , 2017 , 9, 48	14.4	10
76	An integer programming framework for inferring disease complexes from network data. <i>Bioinformatics</i> , 2016 , 32, i271-i277	7.2	37
75	Functional Alignment of Metabolic Networks. <i>Journal of Computational Biology</i> , 2016 , 23, 390-9	1.7	1
74	INFERENCE OF PERSONALIZED DRUG TARGETS VIA NETWORK PROPAGATION. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2016 , 21, 156-67	1.3	6
73	Functional Alignment of Metabolic Networks. <i>Lecture Notes in Computer Science</i> , 2015 , 243-255	0.9	

72	Network-Based Integration of Disparate Omic Data To Identify "Silent Players" in Cancer. <i>PLoS Computational Biology</i> , 2015 , 11, e1004595	5	50
71	Regulation of Sec16 levels and dynamics links proliferation and secretion. <i>Journal of Cell Science</i> , 2015 , 128, 670-82	5.3	22
70	Network orientation via shortest paths. <i>Bioinformatics</i> , 2014 , 30, 1449-55	7.2	18
69	A method for inferring medical diagnoses from patient similarities. <i>BMC Medicine</i> , 2013 , 11, 194	11.4	43
68	Network-based interpretation of genomic variation data. <i>Journal of Molecular Biology</i> , 2013 , 425, 3964-96.5		12
67	Pathway-based analysis of genomic variation data. <i>Current Opinion in Genetics and Development</i> , 2013 , 23, 622-6	4.9	12
66	Global alignment of protein-protein interaction networks. <i>Methods in Molecular Biology</i> , 2013 , 939, 21-34.4		6
65	Systematic identification of gene annotation errors in the widely used yeast mutation collections. <i>Nature Methods</i> , 2012 , 9, 373-8	21.6	58
64	Comparative analysis of protein networks. <i>Communications of the ACM</i> , 2012 , 55, 88-97	2.5	34
63	Enhancing the prioritization of disease-causing genes through tissue specific protein interaction networks. <i>PLoS Computational Biology</i> , 2012 , 8, e1002690	5	122
62	Large-scale elucidation of drug response pathways in humans. <i>Journal of Computational Biology</i> , 2012 , 19, 163-74	1.7	29
61	INDI: a computational framework for inferring drug interactions and their associated recommendations. <i>Molecular Systems Biology</i> , 2012 , 8, 592	12.2	131
60	PREDICT: a method for inferring novel drug indications with application to personalized medicine. <i>Molecular Systems Biology</i> , 2011 , 7, 496	12.2	466
59	An algorithmic framework for predicting side effects of drugs. <i>Journal of Computational Biology</i> , 2011 , 18, 207-18	1.7	103
58	Combining drug and gene similarity measures for drug-target elucidation. <i>Journal of Computational Biology</i> , 2011 , 18, 133-45	1.7	120
57	PRINCIPLE: a tool for associating genes with diseases via network propagation. <i>Bioinformatics</i> , 2011 , 27, 3325-6	7.2	31
56	Identification of protein complexes from co-immunoprecipitation data. <i>Bioinformatics</i> , 2011 , 27, 111-7	7.2	91
55	Processes of fungal proteome evolution and gain of function: gene duplication and domain rearrangement. <i>Physical Biology</i> , 2011 , 8, 035009	3	9

54	Expander: from expression microarrays to networks and functions. <i>Nature Protocols</i> , 2010 , 5, 303-22	18.8	165
53	The large-scale organization of the bacterial network of ecological co-occurrence interactions. <i>Nucleic Acids Research</i> , 2010 , 38, 3857-68	20.1	193
52	Associating genes and protein complexes with disease via network propagation. <i>PLoS Computational Biology</i> , 2010 , 6, e1000641	5	584
51	Transcriptional regulation by CHIP/LDB complexes. <i>PLoS Genetics</i> , 2010 , 6, e1001063	6	22
50	Topology-free querying of protein interaction networks. <i>Journal of Computational Biology</i> , 2010 , 17, 237-52	1.7	80
49	A novel HMM-based method for detecting enriched transcription factor binding sites reveals RUNX3 as a potential target in pancreatic cancer biology. <i>PLoS ONE</i> , 2010 , 5, e14423	3.7	2
48	Fast and accurate alignment of multiple protein networks. <i>Journal of Computational Biology</i> , 2009 , 16, 989-99	1.7	47
47	Toward accurate reconstruction of functional protein networks. <i>Molecular Systems Biology</i> , 2009 , 5, 248	12.2	80
46	A complex-centric view of protein network evolution. <i>Nucleic Acids Research</i> , 2009 , 37, e88	20.1	23
45	A network-based method for predicting disease-causing genes. <i>Journal of Computational Biology</i> , 2009 , 16, 181-9	1.7	74
44	Increased microRNA activity in human cancers. <i>PLoS ONE</i> , 2009 , 4, e6045	3.7	34
43	Topology-Free Querying of Protein Interaction Networks. <i>Lecture Notes in Computer Science</i> , 2009 , 74-89	0.9	13
42	Protein networks in disease. <i>Genome Research</i> , 2008 , 18, 644-52	9.7	589
41	A systems-level approach to mapping the telomere length maintenance gene circuitry. <i>Molecular Systems Biology</i> , 2008 , 4, 172	12.2	45
40	QNet: a tool for querying protein interaction networks. <i>Journal of Computational Biology</i> , 2008 , 15, 913-25	2.5	71
39	Improved network-based identification of protein orthologs. <i>Bioinformatics</i> , 2008 , 24, i200-6	7.2	16
38	NetworkBLAST: comparative analysis of protein networks. <i>Bioinformatics</i> , 2008 , 24, 594-6	7.2	86
37	Cross-Species Analysis of Protein-protein Interaction Networks. <i>Computational Biology</i> , 2008 , 163-185	0.7	1

36	Fast and Accurate Alignment of Multiple Protein Networks 2008 , 246-256		28
35	Network-based prediction of protein function. <i>Molecular Systems Biology</i> , 2007 , 3, 88	12.2	743
34	Comprehensive analysis of co-occurring domain sets in yeast proteins. <i>BMC Genomics</i> , 2007 , 8, 161	4.5	15
33	SPINE: a framework for signaling-regulatory pathway inference from cause-effect experiments. <i>Bioinformatics</i> , 2007 , 23, i359-66	7.2	85
32	Identification of conserved protein complexes based on a model of protein network evolution. <i>Bioinformatics</i> , 2007 , 23, e170-6	7.2	72
31	Transcriptional regulation of protein complexes within and across species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 1283-8	11.5	44
30	Gene loss rate: a probabilistic measure for the conservation of eukaryotic genes. <i>Nucleic Acids Research</i> , 2007 , 35, e7	20.1	21
29	Comparison of Protein-Protein Interaction Confidence Assignment Schemes. <i>Lecture Notes in Computer Science</i> , 2007 , 39-50	0.9	
28	QNet: A Tool for Querying Protein Interaction Networks. <i>Lecture Notes in Computer Science</i> , 2007 , 1-15	0.9	26
27	QPath: a method for querying pathways in a protein-protein interaction network. <i>BMC Bioinformatics</i> , 2006 , 7, 199	3.6	113
26	A direct comparison of protein interaction confidence assignment schemes. <i>BMC Bioinformatics</i> , 2006 , 7, 360	3.6	85
25	Analysis of SNP-expression association matrices. <i>Journal of Bioinformatics and Computational Biology</i> , 2006 , 4, 259-74	1	3
24	Genetic variation in putative regulatory loci controlling gene expression in breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 7735-40	11.5	26
23	Efficient algorithms for detecting signaling pathways in protein interaction networks. <i>Journal of Computational Biology</i> , 2006 , 13, 133-44	1.7	190
22	Systematic identification of functional orthologs based on protein network comparison. <i>Genome Research</i> , 2006 , 16, 428-35	9.7	142
21	Modeling cellular machinery through biological network comparison. <i>Nature Biotechnology</i> , 2006 , 24, 427-33	44.5	404
20	Analysis of SNP-expression association matrices 2005 , 135-43		2
19	Identification of protein complexes by comparative analysis of yeast and bacterial protein interaction data. <i>Journal of Computational Biology</i> , 2005 , 12, 835-46	1.7	120

18	Efficient Algorithms for Detecting Signaling Pathways in Protein Interaction Networks. <i>Lecture Notes in Computer Science</i> , 2005 , 1-13	0.9	11
17	EXPANDER--an integrative program suite for microarray data analysis. <i>BMC Bioinformatics</i> , 2005 , 6, 232	3.6	242
16	An initial blueprint for myogenic differentiation. <i>Genes and Development</i> , 2005 , 19, 553-69	12.6	335
15	Conserved patterns of protein interaction in multiple species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 1974-9	11.5	586
14	Identification of protein complexes by comparative analysis of yeast and bacterial protein interaction data 2004 ,		12
13	Revealing modularity and organization in the yeast molecular network by integrated analysis of highly heterogeneous genomewide data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 2981-6	11.5	298
12	PathBLAST: a tool for alignment of protein interaction networks. <i>Nucleic Acids Research</i> , 2004 , 32, W83-8	0.1	293
11	Cluster graph modification problems. <i>Discrete Applied Mathematics</i> , 2004 , 144, 173-182	1	200
10	CREME: Cis-Regulatory Module Explorer for the human genome. <i>Nucleic Acids Research</i> , 2004 , 32, W253-6	0.1	41
9	Genome-wide in silico identification of transcriptional regulators controlling the cell cycle in human cells. <i>Genome Research</i> , 2003 , 13, 773-80	9.7	242
8	CLICK and EXPANDER: a system for clustering and visualizing gene expression data. <i>Bioinformatics</i> , 2003 , 19, 1787-99	7.2	283
7	CREME: a framework for identifying cis-regulatory modules in human-mouse conserved segments. <i>Bioinformatics</i> , 2003 , 19 Suppl 1, i283-91	7.2	76
6	Conserved pathways within bacteria and yeast as revealed by global protein network alignment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 11394-9	11.5	394
5	Discovering statistically significant biclusters in gene expression data. <i>Bioinformatics</i> , 2002 , 18 Suppl 1, S136-44	7.2	576
4	Complexity classification of some edge modification problems. <i>Discrete Applied Mathematics</i> , 2001 , 113, 109-128	1	119
3	Complexity Classification of Some Edge Modification Problems. <i>Lecture Notes in Computer Science</i> , 1999 , 65-77	0.9	18
2	Open Community Challenge Reveals Molecular Network Modules with Key Roles in Diseases		10
1	Effect of SARS-CoV-2 proteins on vascular permeability		1

