

Roded Sharan

List of Publications by Year in descending order

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Version: 2024-02-01

73
papers

5,277
citations

218381

26
h-index

95083

68
g-index

76
all docs

76
docs citations

76
times ranked

6724
citing authors

#	ARTICLE	IF	CITATIONS
1	Network-based prediction of protein function. <i>Molecular Systems Biology</i> , 2007, 3, 88.	3.2	918
2	Associating Genes and Protein Complexes with Disease via Network Propagation. <i>PLoS Computational Biology</i> , 2010, 6, e1000641.	1.5	758
3	Network propagation: a universal amplifier of genetic associations. <i>Nature Reviews Genetics</i> , 2017, 18, 551-562.	7.7	514
4	Modeling cellular machinery through biological network comparison. <i>Nature Biotechnology</i> , 2006, 24, 427-433.	9.4	492
5	Using deep learning to model the hierarchical structure and function of a cell. <i>Nature Methods</i> , 2018, 15, 290-298.	9.0	292
6	Simultaneous Identification of Multiple Driver Pathways in Cancer. <i>PLoS Computational Biology</i> , 2013, 9, e1003054.	1.5	231
7	Identification of Protein Complexes by Comparative Analysis of Yeast and Bacterial Protein Interaction Data. <i>Journal of Computational Biology</i> , 2005, 12, 835-846.	0.8	161
8	Enhancing the Prioritization of Disease-Causing Genes through Tissue Specific Protein Interaction Networks. <i>PLoS Computational Biology</i> , 2012, 8, e1002690.	1.5	145
9	To Embed or Not: Network Embedding as a Paradigm in Computational Biology. <i>Frontiers in Genetics</i> , 2019, 10, 381.	1.1	123
10	Gene Essentiality Analyzed by <i>In Vivo</i> Transposon Mutagenesis and Machine Learning in a Stable Haploid Isolate of <i>Candida albicans</i> . <i>MBio</i> , 2018, 9, .	1.8	110
11	Few-shot learning creates predictive models of drug response that translate from high-throughput screens to individual patients. <i>Nature Cancer</i> , 2021, 2, 233-244.	5.7	92
12	ANAT: A Tool for Constructing and Analyzing Functional Protein Networks. <i>Science Signaling</i> , 2011, 4, p11.	1.6	78
13	Human protein interaction networks across tissues and diseases. <i>Frontiers in Genetics</i> , 2015, 6, 257.	1.1	76
14	Elucidation of Signaling Pathways from Large-Scale Phosphoproteomic Data Using Protein Interaction Networks. <i>Cell Systems</i> , 2016, 3, 585-593.e3.	2.9	72
15	Translation of Genotype to Phenotype by a Hierarchy of Cell Subsystems. <i>Cell Systems</i> , 2016, 2, 77-88.	2.9	72
16	Genome architecture and stability in the <i>Saccharomyces cerevisiae</i> knockout collection. <i>Nature</i> , 2019, 573, 416-420.	13.7	72
17	Interactome Mapping Provides a Network of Neurodegenerative Disease Proteins and Uncovers Widespread Protein Aggregation in Affected Brains. <i>Cell Reports</i> , 2020, 32, 108050.	2.9	64
18	Network-Based Integration of Disparate Omic Data To Identify "Silent Players" in Cancer. <i>PLoS Computational Biology</i> , 2015, 11, e1004595.	1.5	60

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19	Effect of SARS-CoV-2 proteins on vascular permeability. <i>ELife</i> , 2021, 10, .	2.8	53
20	A network-based analysis of colon cancer splicing changes reveals a tumorigenesis-favoring regulatory pathway emanating from ELK1. <i>Genome Research</i> , 2016, 26, 541-553.	2.4	45
21	An integer programming framework for inferring disease complexes from network data. <i>Bioinformatics</i> , 2016, 32, i271-i277.	1.8	44
22	Simultaneous Integration of Multi-omics Data Improves the Identification of Cancer Driver Modules. <i>Cell Systems</i> , 2019, 8, 456-466.e5.	2.9	43
23	PRINCIPLE: a tool for associating genes with diseases via network propagation. <i>Bioinformatics</i> , 2011, 27, 3325-3326.	1.8	42
24	Regulation of Sec16 levels and dynamics links proliferation and secretion. <i>Journal of Cell Science</i> , 2015, 128, 670-82.	1.2	39
25	A systematic approach to orient the human protein-protein interaction network. <i>Nature Communications</i> , 2019, 10, 3015.	5.8	39
26	BeWith: A Between-Within method to discover relationships between cancer modules via integrated analysis of mutual exclusivity, co-occurrence and functional interactions. <i>PLoS Computational Biology</i> , 2017, 13, e1005695.	1.5	38
27	Reconstructing Boolean Models of Signaling. <i>Journal of Computational Biology</i> , 2013, 20, 249-257.	0.8	34
28	A minimum-labeling approach for reconstructing protein networks across multiple conditions. <i>Algorithms for Molecular Biology</i> , 2014, 9, 1.	0.3	29
29	Proteomic Analysis of Dynein-Interacting Proteins in Amyotrophic Lateral Sclerosis Synaptosomes Reveals Alterations in the RNA-Binding Protein Staufen1. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 506-522.	2.5	27
30	Complexity and algorithms for copy-number evolution problems. <i>Algorithms for Molecular Biology</i> , 2017, 12, 13.	0.3	27
31	Identification of Essential Genes and Fluconazole Susceptibility Genes in <i>Candida glabrata</i> by Profiling Hermes Transposon Insertions. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3859-3870.	0.8	27
32	Gene architecture directs splicing outcome in separate nuclear spatial regions. <i>Molecular Cell</i> , 2022, 82, 1021-1034.e8.	4.5	26
33	Islands of Tractability for Parsimony Haplotyping. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2006, 3, 303-311.	1.9	24
34	The EXPANDER Integrated Platform for Transcriptome Analysis. <i>Journal of Molecular Biology</i> , 2019, 431, 2398-2406.	2.0	24
35	GLADIATOR: a global approach for elucidating disease modules. <i>Genome Medicine</i> , 2017, 9, 48.	3.6	23
36	Quantitative mass spectrometry analysis reveals a panel of nine proteins as diagnostic markers for colon adenocarcinomas. <i>Oncotarget</i> , 2018, 9, 13530-13544.	0.8	23

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37	Hidden Markov models lead to higher resolution maps of mutation signature activity in cancer. <i>Genome Medicine</i> , 2019, 11, 49.	3.6	22
38	The first enhancer in an enhancer chain safeguards subsequent enhancer-promoter contacts from a distance. <i>Genome Biology</i> , 2019, 20, 197.	3.8	21
39	Network-based approaches elucidate differences within APOBEC and clock-like signatures in breast cancer. <i>Genome Medicine</i> , 2020, 12, 52.	3.6	20
40	Systematic identification and correction of annotation errors in the genetic interaction map of <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2016, 44, e50-e50.	6.5	19
41	Mutational Signatures: From Methods to Mechanisms. <i>Annual Review of Biomedical Data Science</i> , 2021, 4, 189-206.	2.8	19
42	Network-Based Interpretation of Genomic Variation Data. <i>Journal of Molecular Biology</i> , 2013, 425, 3964-3969.	2.0	18
43	A Method for Predicting Protein-Protein Interaction Types. <i>PLoS ONE</i> , 2014, 9, e90904.	1.1	18
44	Comparative Analysis of Normalization Methods for Network Propagation. <i>Frontiers in Genetics</i> , 2019, 10, 4.	1.1	17
45	Modeling clinical and molecular covariates of mutational process activity in cancer. <i>Bioinformatics</i> , 2019, 35, i492-i500.	1.8	15
46	Modelling the Yeast Interactome. <i>Scientific Reports</i> , 2014, 4, 4273.	1.6	14
47	Quantifying deleterious effects of regulatory variants. <i>Nucleic Acids Research</i> , 2016, 45, gkw1263.	6.5	14
48	A motif-based framework for recognizing sequence families. <i>Bioinformatics</i> , 2005, 21, i387-i393.	1.8	13
49	Comparing the utility of in vivo transposon mutagenesis approaches in yeast species to infer gene essentiality. <i>Current Genetics</i> , 2020, 66, 1117-1134.	0.8	13
50	ANAT 2.0: reconstructing functional protein subnetworks. <i>BMC Bioinformatics</i> , 2017, 18, 495.	1.2	12
51	Network-Free Inference of Knockout Effects in Yeast. <i>PLoS Computational Biology</i> , 2010, 6, e1000635.	1.5	11
52	Experimental design schemes for learning Boolean network models. <i>Bioinformatics</i> , 2014, 30, i445-i452.	1.8	10
53	A network diffusion approach to inferring sample-specific function reveals functional changes associated with breast cancer. <i>PLoS Computational Biology</i> , 2017, 13, e1005793.	1.5	10
54	Multiplexing Schemes for Generic SNP Genotyping Assays. <i>Journal of Computational Biology</i> , 2005, 12, 514-533.	0.8	8

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55	INFERENCE OF PERSONALIZED DRUG TARGETS VIA NETWORK PROPAGATION. , 2016, , .		8
56	Long reads capture simultaneous enhancerâ€“promoter methylation status for cell-type deconvolution. <i>Bioinformatics</i> , 2021, 37, i327-i333.	1.8	8
57	A mixture model for signature discovery from sparse mutation data. <i>Genome Medicine</i> , 2021, 13, 173.	3.6	8
58	WebPropagate: A Web Server for Network Propagation. <i>Journal of Molecular Biology</i> , 2018, 430, 2231-2236.	2.0	7
59	A Sticky Multinomial Mixture Model of Strand-Coordinated Mutational Processes in Cancer. <i>IScience</i> , 2020, 23, 100900.	1.9	5
60	Prediction of cancer dependencies from expression data using deep learning. <i>Molecular Omics</i> , 2021, 17, 66-71.	1.4	5
61	Islands of tractability for parsimony haplotyping. , 2005, , 65-72.		4
62	Utilizing yeast chemogenomic profiles for the prediction of pharmacogenomic associations in humans. <i>Scientific Reports</i> , 2016, 6, 23703.	1.6	4
63	A Robustness Analysis of Dynamic Boolean Models of Cellular Circuits. <i>Journal of Computational Biology</i> , 2020, 27, 133-143.	0.8	4
64	Functional Alignment of Metabolic Networks. <i>Journal of Computational Biology</i> , 2016, 23, 390-399.	0.8	3
65	G2G: A web-server for the prediction of human synthetic lethal interactions. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1028-1031.	1.9	3
66	Toward a role model. <i>EMBO Reports</i> , 2013, 14, 948-948.	2.0	2
67	An optimization framework for network annotation. <i>Bioinformatics</i> , 2018, 34, i502-i508.	1.8	1
68	A data-driven approach for constructing mutation categories for mutational signature analysis. <i>PLoS Computational Biology</i> , 2021, 17, e1009542.	1.5	1
69	DNA Repair Footprint Uncovers Contribution of DNA Repair Mechanism to Mutational Signatures. , 2019, , .		1
70	<scp>ScalpelSig</scp> Designs Targeted Genomic Panels from Data to Detect Activity of Mutational Signatures. <i>Journal of Computational Biology</i> , 2022, 29, 56-73.	0.8	1
71	Deep Unfolding for Non-Negative Matrix Factorization with Application to Mutational Signature Analysis. <i>Journal of Computational Biology</i> , 2022, 29, 45-55.	0.8	1
72	Invited: From protein networks to disease mechanisms. , 2012, , .		0

#	ARTICLE	IF	CITATIONS
73	Session Introduction: Mutational Signatures: Etiology, Properties, and Role in Cancer. , 2019, , .		0