

Zohar Yakhini

List of Publications by Year in descending order

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Version: 2024-02-01

123
papers

15,736
citations

53794

45
h-index

22166

113
g-index

141
all docs

141
docs citations

141
times ranked

23949
citing authors

#	ARTICLE	IF	CITATIONS
1	GORilla: a tool for discovery and visualization of enriched GO terms in ranked gene lists. BMC Bioinformatics, 2009, 10, 48.	2.6	3,032
2	Gene-Expression Profiles in Hereditary Breast Cancer. New England Journal of Medicine, 2001, 344, 539-548.	27.0	1,669
3	Polycomb-mediated methylation on Lys27 of histone H3 pre-marks genes for de novo methylation in cancer. Nature Genetics, 2007, 39, 232-236.	21.4	1,062
4	Clustering Gene Expression Patterns. Journal of Computational Biology, 1999, 6, 281-297.	1.6	959
5	Discovering Motifs in Ranked Lists of DNA Sequences. PLoS Computational Biology, 2007, 3, e39.	3.2	633
6	Tissue Classification with Gene Expression Profiles. Journal of Computational Biology, 2000, 7, 559-583.	1.6	623
7	Gene expression analysis reveals matrilysin as a key regulator of pulmonary fibrosis in mice and humans. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 6292-6297.	7.1	576
8	Inferring gene regulatory logic from high-throughput measurements of thousands of systematically designed promoters. Nature Biotechnology, 2012, 30, 521-530.	17.5	439
9	Discovering Local Structure in Gene Expression Data: The Order-Preserving Submatrix Problem. Journal of Computational Biology, 2003, 10, 373-384.	1.6	391
10	Developmental programming of CpG island methylation profiles in the human genome. Nature Structural and Molecular Biology, 2009, 16, 564-571.	8.2	345
11	Comparative genomic hybridization using oligonucleotide microarrays and total genomic DNA. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 17765-17770.	7.1	336
12	The Fine-Scale and Complex Architecture of Human Copy-Number Variation. American Journal of Human Genetics, 2008, 82, 685-695.	6.2	315
13	Novel Role for the Potent Endogenous Inotrope Apelin in Human Cardiac Dysfunction. Circulation, 2003, 108, 1432-1439.	1.6	311
14	miRNA-mRNA Integrated Analysis Reveals Roles for miRNAs in Primary Breast Tumors. PLoS ONE, 2011, 6, e16915.	2.5	278
15	Systematic discovery of cap-independent translation sequences in human and viral genomes. Science, 2016, 351, .	12.6	258
16	Array CGH analysis of copy number variation identifies 1284 new genes variant in healthy white males: implications for association studies of complex diseases. Human Molecular Genetics, 2007, 16, 2783-2794.	2.9	200
17	Molecular classification of familial non- <i>BRCA1/BRCA2</i> breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 2532-2537.	7.1	182
18	Global Methylation Patterns in Idiopathic Pulmonary Fibrosis. PLoS ONE, 2012, 7, e33770.	2.5	169

#	ARTICLE	IF	CITATIONS
19	Comparative Analysis of DNA Replication Timing Reveals Conserved Large-Scale Chromosomal Architecture. <i>PLoS Genetics</i> , 2010, 6, e1001011.	3.5	158
20	Novel Rank-Based Statistical Methods Reveal MicroRNAs with Differential Expression in Multiple Cancer Types. <i>PLoS ONE</i> , 2009, 4, e8003.	2.5	150
21	Global organization of replication time zones of the mouse genome. <i>Genome Research</i> , 2008, 18, 1562-1570.	5.5	148
22	Unraveling determinants of transcription factor binding outside the core binding site. <i>Genome Research</i> , 2015, 25, 1018-1029.	5.5	146
23	Pathway analysis of coronary atherosclerosis. <i>Physiological Genomics</i> , 2005, 23, 103-118.	2.3	144
24	Efficient Calculation of Interval Scores for DNA Copy Number Data Analysis. <i>Journal of Computational Biology</i> , 2006, 13, 215-228.	1.6	132
25	Association of N-Glycosylation with Breast Carcinoma and Systemic Features Using High-Resolution Quantitative UPLC. <i>Journal of Proteome Research</i> , 2014, 13, 2314-2327.	3.7	123
26	Deregulation of cancer-related miRNAs is a common event in both benign and malignant human breast tumors. <i>Carcinogenesis</i> , 2014, 35, 76-85.	2.8	119
27	Probing the effect of promoters on noise in gene expression using thousands of designed sequences. <i>Genome Research</i> , 2014, 24, 1698-1706.	5.5	118
28	Data storage in DNA with fewer synthesis cycles using composite DNA letters. <i>Nature Biotechnology</i> , 2019, 37, 1229-1236.	17.5	110
29	Identification of endothelial cell genes by combined database mining and microarray analysis. <i>Physiological Genomics</i> , 2003, 13, 249-262.	2.3	107
30	EGF Decreases the Abundance of MicroRNAs That Restrain Oncogenic Transcription Factors. <i>Science Signaling</i> , 2010, 3, ra43.	3.6	100
31	Marek's disease virus Meq transforms chicken cells via the v-Jun transcriptional cascade: A converging transforming pathway for avian oncoviruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 14831-14836.	7.1	92
32	Finding Approximate Tandem Repeats in Genomic Sequences. <i>Journal of Computational Biology</i> , 2005, 12, 928-942.	1.6	82
33	Spatial transcriptomics inferred from pathology whole-slide images links tumor heterogeneity to survival in breast and lung cancer. <i>Scientific Reports</i> , 2020, 10, 18802.	3.3	78
34	<scp>LIMT</scp> is a novel metastasis inhibiting lnc<scp>RNA</scp> suppressed by <scp>EGF</scp> and downregulated in aggressive breast cancer. <i>EMBO Molecular Medicine</i> , 2016, 8, 1052-1064.	6.9	77
35	Class discovery in gene expression data. , 2001, , .		73
36	Differences in Vascular Bed Disease Susceptibility Reflect Differences in Gene Expression Response to Atherogenic Stimuli. <i>Circulation Research</i> , 2006, 98, 200-208.	4.5	71

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37	Systematic Dissection of the Sequence Determinants of Gene 3â€™ End Mediated Expression Control. <i>PLoS Genetics</i> , 2015, 11, e1005147.	3.5	70
38	Clustering gene expression patterns. , 1999, , .		61
39	Molecular Signatures Determining Coronary Artery and Saphenous Vein Smooth Muscle Cell Phenotypes. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2006, 26, 1058-1065.	2.4	61
40	Molecular Rules Governing <i>De Novo</i> Methylation in Cancer. <i>Cancer Research</i> , 2014, 74, 1475-1483.	0.9	55
41	Identifying In-Trans Process Associated Genes in Breast Cancer by Integrated Analysis of Copy Number and Expression Data. <i>PLoS ONE</i> , 2013, 8, e53014.	2.5	54
42	DRIMust: a web server for discovering rank imbalanced motifs using suffix trees. <i>Nucleic Acids Research</i> , 2013, 41, W174-W179.	14.5	53
43	A Novel Translocation Breakpoint within the BPTF Gene Is Associated with a Pre-Malignant Phenotype. <i>PLoS ONE</i> , 2010, 5, e9657.	2.5	53
44	Universal DNA Tag Systems: A Combinatorial Design Scheme. <i>Journal of Computational Biology</i> , 2000, 7, 503-519.	1.6	52
45	Small Deletion Variants Have Stable Breakpoints Commonly Associated with Alu Elements. <i>PLoS ONE</i> , 2008, 3, e3104.	2.5	52
46	miRNA target enrichment analysis reveals directly active miRNAs in health and disease. <i>Nucleic Acids Research</i> , 2013, 41, e45-e45.	14.5	51
47	Spatial localization of co-regulated genes exceeds genomic gene clustering in the <i>Saccharomyces cerevisiae</i> genome. <i>Nucleic Acids Research</i> , 2013, 41, 2191-2201.	14.5	50
48	Proposed design of distributed macroalgal biorefineries: thermodynamics, bioconversion technology, and sustainability implications for developing economies. <i>Biofuels, Bioproducts and Biorefining</i> , 2014, 8, 67-82.	3.7	49
49	Systematic Investigation of Transcription Factor Activity in the Context of Chromatin Using Massively Parallel Binding and Expression Assays. <i>Molecular Cell</i> , 2017, 65, 604-617.e6.	9.7	48
50	Increasing CRISPR Efficiency and Measuring Its Specificity in HSPCs Using a Clinically Relevant System. <i>Molecular Therapy - Methods and Clinical Development</i> , 2020, 17, 1097-1107.	4.1	46
51	<i>GSTP1</i> Promoter Haplotypes Affect DNA Methylation Levels and Promoter Activity in Breast Carcinomas. <i>Cancer Research</i> , 2008, 68, 5562-5571.	0.9	44
52	Macroalgae Biorefinery from <i>Kappaphycus alvarezii</i> : Conversion Modeling and Performance Prediction for India and Philippines as Examples. <i>Bioenergy Research</i> , 2018, 11, 22-32.	3.9	42
53	Net primary productivity, biofuel production and CO ₂ emissions reduction potential of <i>Ulva</i> sp. (Chlorophyta) biomass in a coastal area of the Eastern Mediterranean. <i>Energy Conversion and Management</i> , 2017, 148, 1497-1507.	9.2	40
54	Serum N-glycan analysis in breast cancer patients â€“ Relation to tumour biology and clinical outcome. <i>Molecular Oncology</i> , 2016, 10, 59-72.	4.6	34

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55	Genetic variation in putative regulatory loci controlling gene expression in breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 7735-7740.	7.1	32
56	Gene expression and the concept of the phenotype. Studies in History and Philosophy of Science Part C: Studies in History and Philosophy of Biological and Biomedical Sciences, 2007, 38, 238-254.	1.3	32
57	Ischemia caused by time to freezing induces systematic microRNA and mRNA responses in cancer tissue. Molecular Oncology, 2011, 5, 564-576.	4.6	29
58	Divergent RNA binding specificity of yeast Puf2p. Rna, 2011, 17, 1479-1488.	3.5	25
59	Similarities and differences of gene expression in yeast stress conditions. Bioinformatics, 2007, 23, e184-e190.	4.1	24
60	A Synthetic Oligo Library and Sequencing Approach Reveals an Insulation Mechanism Encoded within Bacterial λ 54 Promoters. Cell Reports, 2017, 21, 845-858.	6.4	23
61	CRISPECTOR provides accurate estimation of genome editing translocation and off-target activity from comparative NGS data. Nature Communications, 2021, 12, 3042.	12.8	23
62	Efficient motif search in ranked lists and applications to variable gap motifs. Nucleic Acids Research, 2012, 40, 5832-5847.	14.5	22
63	Thermochemical hydrolysis of macroalgae Ulva for biorefinery: Taguchi robust design method. Scientific Reports, 2016, 6, 27761.	3.3	22
64	Joint Analysis of DNA Copy Numbers and Gene Expression Levels. Lecture Notes in Computer Science, 2004, , 135-146.	1.3	20
65	A supervised approach for identifying discriminating genotype patterns and its application to breast cancer data. Bioinformatics, 2007, 23, e91-e98.	4.1	20
66	A structural-based statistical approach suggests a cooperative activity of PUM1 and miR-410 in human 3'-untranslated regions. Silence: A Journal of RNA Regulation, 2010, 1, 17.	8.1	20
67	Finding approximate tandem repeats in genomic sequences. , 2004, , .		19
68	Reciprocal Reprogramming of Cancer Cells and Associated Mesenchymal Stem Cells in Gastric Cancer. Stem Cells, 2019, 37, 176-189.	3.2	18
69	IoT or NoT: Identifying IoT Devices in a Short Time Scale. , 2020, , .		18
70	Extending partial haplotypes to full genome haplotypes using chromosome conformation capture data. Bioinformatics, 2016, 32, i559-i566.	4.1	17
71	An <i>in Vivo</i> Binding Assay for RNA-Binding Proteins Based on Repression of a Reporter Gene. ACS Synthetic Biology, 2018, 7, 2765-2774.	3.8	16
72	A broad analysis of splicing regulation in yeast using a large library of synthetic introns. PLoS Genetics, 2021, 17, e1009805.	3.5	16

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73	Clinically driven semi-supervised class discovery in gene expression data. <i>Bioinformatics</i> , 2008, 24, i90-i97.	4.1	15
74	Peer group normalization and urine to blood context in steroid metabolomics: The case of CAH and obesity. <i>Steroids</i> , 2014, 88, 83-89.	1.8	15
75	SOLQC: Synthetic Oligo Library Quality Control tool. <i>Bioinformatics</i> , 2021, 37, 720-722.	4.1	14
76	Universal DNA tag systems. , 2000, , .		13
77	Optimization of probe coverage for high-resolution oligonucleotide aCGH. <i>Bioinformatics</i> , 2007, 23, e77-e83.	4.1	13
78	A combined sequence and structure based method for discovering enriched motifs in RNA from in vivo binding data. <i>Methods</i> , 2017, 118-119, 73-81.	3.8	13
79	Systematic Determination of Replication Activity Type Highlights Interconnections between Replication, Chromatin Structure and Nuclear Localization. <i>PLoS ONE</i> , 2012, 7, e48986.	2.5	13
80	ENViz: a Cytoscape App for integrated statistical analysis and visualization of sample-matched data with multiple data types. <i>Bioinformatics</i> , 2015, 31, 1683-1685.	4.1	12
81	A High-Throughput Approach for Associating MicroRNAs with Their Activity Conditions. <i>Journal of Computational Biology</i> , 2006, 13, 245-266.	1.6	11
82	An Efficient Minimum Free Energy Structure-Based Search Method for Riboswitch Identification Based on Inverse RNA Folding. <i>PLoS ONE</i> , 2015, 10, e0134262.	2.5	11
83	RNAPattMatch: a web server for RNA sequence/structure motif detection based on pattern matching with flexible gaps. <i>Nucleic Acids Research</i> , 2015, 43, W507-W512.	14.5	11
84	Synthetic 5' UTRs Can Either Up- or Downregulate Expression upon RNA-Binding Protein Binding. <i>Cell Systems</i> , 2019, 9, 93-106.e8.	6.2	11
85	BioLEGO " a web-based application for biorefinery design and evaluation of serial biomass fermentation. <i>Technology</i> , 2015, 03, 89-98.	1.4	10
86	Distributed flux balance analysis simulations of serial biomass fermentation by two organisms. <i>PLoS ONE</i> , 2020, 15, e0227363.	2.5	10
87	Using Expression Data to Discover RNA and DNA Regulatory Sequence Motifs. <i>Lecture Notes in Computer Science</i> , 2005, , 65-78.	1.3	9
88	Molecular harvesting with electroporation for tissue profiling. <i>Scientific Reports</i> , 2019, 9, 15750.	3.3	9
89	METHODS FOR ANALYSIS AND VISUALIZATION OF SNP GENOTYPE DATA FOR COMPLEX DISEASES. , 2002, , 548-61.		9
90	Analysis of Expression Patterns: The Scope of the Problem, the Problem of Scope. <i>Disease Markers</i> , 2001, 17, 59-65.	1.3	8

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91	Multiplexing Schemes for Generic SNP Genotyping Assays. <i>Journal of Computational Biology</i> , 2005, 12, 514-533.	1.6	8
92	Framework for Identifying Common Aberrations in DNA Copy Number Data. , 2007, , 122-136.		8
93	Overcoming the design, build, test bottleneck for synthesis of nonrepetitive protein-RNA cassettes. <i>Nature Communications</i> , 2021, 12, 1576.	12.8	8
94	SMARTIV: combined sequence and structure de-novo motif discovery for in-vivo RNA binding data. <i>Nucleic Acids Research</i> , 2018, 46, W221-W228.	14.5	7
95	Towards optimally multiplexed applications of universal DNA tag systems. , 2003, , .		7
96	Exploratory Visualization of Array-Based Comparative Genomic Hybridization. <i>Information Visualization</i> , 2005, 4, 176-190.	1.9	6
97	Mutual enrichment in ranked lists and the statistical assessment of position weight matrix motifs. <i>Algorithms for Molecular Biology</i> , 2014, 9, 11.	1.2	6
98	Prediction of Scar Size in Rats Six Months after Burns Based on Early Post-injury Polarization-Sensitive Optical Frequency Domain Imaging. <i>Frontiers in Physiology</i> , 2017, 8, 967.	2.8	6
99	Assessing heterogeneity in spatial data using the HTA index with applications to spatial transcriptomics and imaging. <i>Bioinformatics</i> , 2021, 37, 3796-3804.	4.1	6
100	Designing Optimally Multiplexed SNP Genotyping Assays. <i>Lecture Notes in Computer Science</i> , 2003, , 320-338.	1.3	5
101	Semi-supervised class discovery using quantitative phenotypes â€” CVD as a case study. <i>BMC Bioinformatics</i> , 2007, 8, S6.	2.6	5
102	Mutual enrichment in aggregated ranked lists with applications to gene expression regulation. <i>Bioinformatics</i> , 2016, 32, i464-i472.	4.1	5
103	Use of oligonucleotide microarrays to analyze gene expression patterns in pulmonary fibrosis reveals distinct patterns of gene expression in mice and humans. <i>Chest</i> , 2002, 121, 31S-32S.	0.8	5
104	Electroporation-based proteome sampling ex vivo enables the detection of brain melanoma protein signatures in a location proximate to visible tumor margins. <i>PLoS ONE</i> , 2022, 17, e0265866.	2.5	5
105	Towards Optimally Multiplexed Applications of Universal Arrays. <i>Journal of Computational Biology</i> , 2004, 11, 476-492.	1.6	4
106	ANALYSIS OF SNP-EXPRESSION ASSOCIATION MATRICES. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 259-274.	0.8	4
107	Predicting Methylation from Sequence and Gene Expression Using Deep Learning with Attention. <i>Lecture Notes in Computer Science</i> , 2019, , 179-190.	1.3	4
108	Sparse NIR optimization method (SNIRO) to quantify analyte composition with visible (VIS)/near infrared (NIR) spectroscopy (350â€”nm-2500â€”nm). <i>Analytica Chimica Acta</i> , 2019, 1051, 32-40.	5.4	4

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109	Sequence Reconstruction Under Stutter Noise in Enzymatic DNA Synthesis. , 2021, , .		4
110	Transcriptional Profiling of Non-small Cell Lung Cancer Using Oligonucleotide Microarrays. Chest, 2002, 121, 44S.	0.8	3
111	Genome-wide analysis of fitness data and its application to improve metabolic models. BMC Bioinformatics, 2018, 19, 368.	2.6	3
112	Analysis of SNP-expression association matrices. , 2005, , 135-43.		2
113	Dotted interval graphs. ACM Transactions on Algorithms, 2012, 8, 1-21.	1.0	2
114	Design and Analysis of Offshore Macroalgae Biorefineries. Methods in Molecular Biology, 2018, 1980, 9-33.	0.9	2
115	Efficient gene expression signature for a breast cancer immuno-subtype. PLoS ONE, 2021, 16, e0245215.	2.5	2
116	Designing optimally multiplexed SNP genotyping assays. Journal of Computer and System Sciences, 2005, 70, 399-417.	1.2	1
117	It Takes Two to Tango: Genotyping and Phenotyping in Genome-Wide Association Studies. Biological Theory, 2009, 4, 294-301.	1.5	1
118	miRNA normalization enables joint analysis of several datasets to increase sensitivity and to reveal novel miRNAs differentially expressed in breast cancer. PLoS Computational Biology, 2021, 17, e1008608.	3.2	1
119	Mutual Enrichment in Ranked Lists and the Statistical Assessment of Position Weight Matrix Motifs. Lecture Notes in Computer Science, 2013, , 273-286.	1.3	1
120	Optimizing analytical depth and cost efficiency of IEF-LC/MS proteomics. , 2014, , .		0
121	Mutual enrichment in aggregated ranked lists with applications to gene expression regulation. Bioinformatics, 2016, 33, btw727.	4.1	0
122	The Functional 3D Organization of Unicellular Genomes. Scientific Reports, 2019, 9, 12734.	3.3	0
123	On the stability of log-rank test under labeling errors. Bioinformatics, 2021, 37, 4451-4459.	4.1	0