## Amir Ben-Dor

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11718528/publications.pdf

Version: 2024-02-01

25 papers 6,402 citations

430874 18 h-index 642732 23 g-index

26 all docs

26 docs citations

26 times ranked

7055 citing authors

#	Article	IF	CITATIONS
1	Novel Rank-Based Statistical Methods Reveal MicroRNAs with Differential Expression in Multiple Cancer Types. PLoS ONE, 2009, 4, e8003.	2.5	150
2	High definition cytogenetics and oligonucleotide aCGH analyses of cisplatinâ€resistant ovarian cancer cells. Genes Chromosomes and Cancer, 2008, 47, 427-436.	2.8	15
3	The Fine-Scale and Complex Architecture of Human Copy-Number Variation. American Journal of Human Genetics, 2008, 82, 685-695.	6.2	315
4	Framework for Identifying Common Aberrations in DNA Copy Number Data., 2007, , 122-136.		8
5	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
6	Efficient Calculation of Interval Scores for DNA Copy Number Data Analysis. Journal of Computational Biology, 2006, 13, 215-228.	1.6	132
7	Molecular Signatures Determining Coronary Artery and Saphenous Vein Smooth Muscle Cell Phenotypes. Arteriosclerosis, Thrombosis, and Vascular Biology, 2006, 26, 1058-1065.	2.4	61
8	Differences in Vascular Bed Disease Susceptibility Reflect Differences in Gene Expression Response to Atherogenic Stimuli. Circulation Research, 2006, 98, 200-208.	4.5	71
9	ANALYSIS OF SNP-EXPRESSION ASSOCIATION MATRICES. Journal of Bioinformatics and Computational Biology, 2006, 04, 259-274.	0.8	4
10	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
11	Pathway analysis of coronary atherosclerosis. Physiological Genomics, 2005, 23, 103-118.	2.3	144
12	Exploratory Visualization of Array-Based Comparative Genomic Hybridization. Information Visualization, 2005, 4, 176-190.	1.9	6
13	Analysis of SNP-expression association matrices. , 2005, , 135-43.		2
14	Joint Analysis of DNA Copy Numbers and Gene Expression Levels. Lecture Notes in Computer Science, 2004, , 135-146.	1.3	20
15	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
16	Discovering Local Structure in Gene Expression Data: The Order-Preserving Submatrix Problem. Journal of Computational Biology, 2003, 10, 373-384.	1.6	391
17	Novel Role for the Potent Endogenous Inotrope Apelin in Human Cardiac Dysfunction. Circulation, 2003, 108, 1432-1439.	1.6	311
18	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

#	Article	IF	Citations
19	Identification of endothelial cell genes by combined database mining and microarray analysis. Physiological Genomics, 2003, 13, 249-262.	2.3	107
20	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
21	Gene-Expression Profiles in Hereditary Breast Cancer. New England Journal of Medicine, 2001, 344, 539-548.	27.0	1,669
22	Analysis of Expression Patterns: The Scope of the Problem, the Problem of Scope. Disease Markers, 2001, 17, 59-65.	1.3	8
23	Class discovery in gene expression data. , 2001, , .		73
24	Tissue Classification with Gene Expression Profiles. Journal of Computational Biology, 2000, 7, 559-583.	1.6	623
25	Clustering Gene Expression Patterns. Journal of Computational Biology, 1999, 6, 281-297.	1.6	959