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 | Gene-Expression Profiles in Hereditary Breast Cancer. New England Journal of Medicine, 2001, 344, 539-548. | 27.0 | 1,669 |
| 2 | Clustering Gene Expression Patterns. Journal of Computational Biology, 1999, 6, 281-297. | 1.6 | 959 |
| 3 | Tissue Classification with Gene Expression Profiles. Journal of Computational Biology, 2000, 7, 559-583. | 1.6 | 623 |
| 4 | 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 |
| 5 | Discovering Local Structure in Gene Expression Data: The Order-Preserving Submatrix Problem. Journal of Computational Biology, 2003, 10, 373-384. | 1.6 | 391 |
| 6 | 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 |
| 7 | The Fine-Scale and Complex Architecture of Human Copy-Number Variation. American Journal of Human Genetics, 2008, 82, 685-695. | 6.2 | 315 |
| 8 | Novel Role for the Potent Endogenous Inotrope Apelin in Human Cardiac Dysfunction. Circulation, 2003, 108, 1432-1439. | 1.6 | 311 |
| 9 | 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 |
| 10 | 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 |
| 11 | Novel Rank-Based Statistical Methods Reveal MicroRNAs with Differential Expression in Multiple Cancer Types. PLoS ONE, 2009, 4, e8003. | 2.5 | 150 |
| 12 | Pathway analysis of coronary atherosclerosis. Physiological Genomics, 2005, 23, 103-118. | 2.3 | 144 |
| 13 | Efficient Calculation of Interval Scores for DNA Copy Number Data Analysis. Journal of Computational Biology, 2006, 13, 215-228. | 1.6 | 132 |
| 14 | Identification of endothelial cell genes by combined database mining and microarray analysis. Physiological Genomics, 2003, 13, 249-262. | 2.3 | 107 |
| 15 | Class discovery in gene expression data. , 2001, , . | | 73 |
| 16 | Differences in Vascular Bed Disease Susceptibility Reflect Differences in Gene Expression Response to Atherogenic Stimuli. Circulation Research, 2006, 98, 200-208. | 4.5 | 71 |
| 17 | Molecular Signatures Determining Coronary Artery and Saphenous Vein Smooth Muscle Cell Phenotypes. Arteriosclerosis, Thrombosis, and Vascular Biology, 2006, 26, 1058-1065. | 2.4 | 61 |
| 18 | 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 |

| # | ARTICLE | IF | CITATION |
|----|---|-----|----------|
| 19 | Joint Analysis of DNA Copy Numbers and Gene Expression Levels. Lecture Notes in Computer Science, 2004, , 135-146. | 1.3 | 20 |
| 20 | High definition cytogenetics and oligonucleotide aCGH analyses of cisplatinâ€resistant ovarian cancer cells. Genes Chromosomes and Cancer, 2008, 47, 427-436. | 2.8 | 15 |
| 21 | Analysis of Expression Patterns: The Scope of the Problem, the Problem of Scope. Disease Markers, 2001, 17, 59-65. | 1.3 | 8 |
| 22 | Framework for Identifying Common Aberrations in DNA Copy Number Data., 2007, , 122-136. | | 8 |
| 23 | Exploratory Visualization of Array-Based Comparative Genomic Hybridization. Information Visualization, 2005, 4, 176-190. | 1.9 | 6 |
| 24 | ANALYSIS OF SNP-EXPRESSION ASSOCIATION MATRICES. Journal of Bioinformatics and Computational Biology, 2006, 04, 259-274. | 0.8 | 4 |
| 25 | Analysis of SNP-expression association matrices. , 2005, , 135-43. | | 2 |