

John C Matese

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6908903/publications.pdf>

Version: 2024-02-01

19
papers

51,460
citations

516710
16
h-index

839539
18
g-index

19
all docs

19
docs citations

19
times ranked

72910
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Comprehensive single-cell transcriptome lineages of a proto-vertebrate. <i>Nature</i> , 2019, 571, 349-354. | 27.8 | 162 |
| 2 | The <i>Oxytricha trifallax</i> Macronuclear Genome: A Complex Eukaryotic Genome with 16,000 Tiny Chromosomes. <i>PLoS Biology</i> , 2013, 11, e1001473. | 5.6 | 198 |
| 3 | Phylogenetic Portrait of the <i>Saccharomyces cerevisiae</i> Functional Genome. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1335-1340. | 1.8 | 4 |
| 4 | Coordination of Growth Rate, Cell Cycle, Stress Response, and Metabolic Activity in Yeast. <i>Molecular Biology of the Cell</i> , 2008, 19, 352-367. | 2.1 | 524 |
| 5 | The Stanford Microarray Database: implementation of new analysis tools and open source release of software. <i>Nucleic Acids Research</i> , 2007, 35, D766-D770. | 14.5 | 146 |
| 6 | Comparative Genomic Hybridizations of <i>Entamoeba</i> Strains Reveal Unique Genetic Fingerprints That Correlate with Virulence. <i>Eukaryotic Cell</i> , 2005, 4, 504-515. | 3.4 | 50 |
| 7 | Microarray Data Standards: An Open Letter. <i>Environmental Health Perspectives</i> , 2004, 112, A666-7. | 6.0 | 23 |
| 8 | Submission of Microarray Data to Public Repositories. <i>PLoS Biology</i> , 2004, 2, e317. | 5.6 | 102 |
| 9 | The Stanford Microarray Database accommodates additional microarray platforms and data formats. <i>Nucleic Acids Research</i> , 2004, 33, D580-D582. | 14.5 | 175 |
| 10 | GeneXplorer: an interactive web application for microarray data visualization and analysis. <i>BMC Bioinformatics</i> , 2004, 5, 141. | 2.6 | 18 |
| 11 | The Stanford Microarray Database: data access and quality assessment tools. <i>Nucleic Acids Research</i> , 2003, 31, 94-96. | 14.5 | 297 |
| 12 | SOURCE: a unified genomic resource of functional annotations, ontologies, and gene expression data. <i>Nucleic Acids Research</i> , 2003, 31, 219-223. | 14.5 | 376 |
| 13 | Identification of Genes Periodically Expressed in the Human Cell Cycle and Their Expression in Tumors. <i>Molecular Biology of the Cell</i> , 2002, 13, 1977-2000. | 2.1 | 1,352 |
| 14 | Gene expression patterns of breast carcinomas distinguish tumor subclasses with clinical implications. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 10869-10874. | 7.1 | 9,721 |
| 15 | Minimum information about a microarray experiment (MIAME) – toward standards for microarray data. <i>Nature Genetics</i> , 2001, 29, 365-371. | 21.4 | 3,750 |
| 16 | Gene Ontology: tool for the unification of biology. <i>Nature Genetics</i> , 2000, 25, 25-29. | 21.4 | 34,499 |
| 17 | Cortical granule exocytosis is triggered by different thresholds of calcium during fertilisation in sea urchin eggs. <i>Zygote</i> , 1998, 6, 55-63. | 1.1 | 11 |
| 18 | Regulated exocytosis and sequential construction of the extracellular matrix surrounding the sea urchin zygote. <i>Developmental Biology</i> , 1997, 186, 16-26. | 2.0 | 52 |

| # | ARTICLE | IF | CITATIONS |
|----|--|----|-----------|
| 19 | Computational Methods and Bioinformatic Tools. , 0, , 769-904. | | 0 |