

John C Matese

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

19
papers

40,027
citations

15
h-index

19
g-index

19
ext. papers

46,718
ext. citations

14.8
avg, IF

5.64
L-index

#	Paper	IF	Citations
19	Comprehensive single-cell transcriptome lineages of a proto-vertebrate. <i>Nature</i> , 2019 , 571, 349-354	50.4	81
18	The <i>Oxytricha trifallax</i> macronuclear genome: a complex eukaryotic genome with 16,000 tiny chromosomes. <i>PLoS Biology</i> , 2013 , 11, e1001473	9.7	145
17	Phylogenetic portrait of the <i>Saccharomyces cerevisiae</i> functional genome. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 1335-40	3.2	3
16	Coordination of growth rate, cell cycle, stress response, and metabolic activity in yeast. <i>Molecular Biology of the Cell</i> , 2008 , 19, 352-67	3.5	405
15	The Stanford Microarray Database: implementation of new analysis tools and open source release of software. <i>Nucleic Acids Research</i> , 2007 , 35, D766-70	20.1	130
14	The Stanford Microarray Database accommodates additional microarray platforms and data formats. <i>Nucleic Acids Research</i> , 2005 , 33, D580-2	20.1	151
13	Comparative genomic hybridizations of <i>Entamoeba</i> strains reveal unique genetic fingerprints that correlate with virulence. <i>Eukaryotic Cell</i> , 2005 , 4, 504-15		47
12	Standards for microarray data: an open letter. <i>Environmental Health Perspectives</i> , 2004 , 112, A666-7	8.4	13
11	Submission of microarray data to public repositories. <i>PLoS Biology</i> , 2004 , 2, E317	9.7	87
10	GeneXplorer: an interactive web application for microarray data visualization and analysis. <i>BMC Bioinformatics</i> , 2004 , 5, 141	3.6	15
9	The Stanford Microarray Database: data access and quality assessment tools. <i>Nucleic Acids Research</i> , 2003 , 31, 94-6	20.1	260
8	SOURCE: a unified genomic resource of functional annotations, ontologies, and gene expression data. <i>Nucleic Acids Research</i> , 2003 , 31, 219-23	20.1	325
7	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	3.5	1043
6	Minimum information about a microarray experiment (MIAME)-toward standards for microarray data. <i>Nature Genetics</i> , 2001 , 29, 365-71	36.3	3326
5	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, 10869-74	11.5	8341
4	Gene ontology: tool for the unification of biology. The Gene Ontology Consortium. <i>Nature Genetics</i> , 2000 , 25, 25-9	36.3	25593
3	Cortical granule exocytosis is triggered by different thresholds of calcium during fertilisation in sea urchin eggs. <i>Zygote</i> , 1998 , 6, 55-64, 65a	1.6	11

- 2 Regulated exocytosis and sequential construction of the extracellular matrix surrounding the sea urchin zygote. *Developmental Biology*, **1997**, 186, 16-26 3.1 51
- 1 Computational Methods and Bioinformatic Tools 769-904