

# John C Matese

## List of Publications by Citations

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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	Gene ontology: tool for the unification of biology. The Gene Ontology Consortium. <i>Nature Genetics</i> , <b>2000</b> , 25, 25-9	36.3	25593
18	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> , <b>2001</b> , 98, 10869-74	11.5	8341
17	Minimum information about a microarray experiment (MIAME)-toward standards for microarray data. <i>Nature Genetics</i> , <b>2001</b> , 29, 365-71	36.3	3326
16	Identification of genes periodically expressed in the human cell cycle and their expression in tumors. <i>Molecular Biology of the Cell</i> , <b>2002</b> , 13, 1977-2000	3.5	1043
15	Coordination of growth rate, cell cycle, stress response, and metabolic activity in yeast. <i>Molecular Biology of the Cell</i> , <b>2008</b> , 19, 352-67	3.5	405
14	SOURCE: a unified genomic resource of functional annotations, ontologies, and gene expression data. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 219-23	20.1	325
13	The Stanford Microarray Database: data access and quality assessment tools. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 94-6	20.1	260
12	The Stanford Microarray Database accommodates additional microarray platforms and data formats. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D580-2	20.1	151
11	The <i>Oxytricha trifallax</i> macronuclear genome: a complex eukaryotic genome with 16,000 tiny chromosomes. <i>PLoS Biology</i> , <b>2013</b> , 11, e1001473	9.7	145
10	The Stanford Microarray Database: implementation of new analysis tools and open source release of software. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D766-70	20.1	130
9	Submission of microarray data to public repositories. <i>PLoS Biology</i> , <b>2004</b> , 2, E317	9.7	87
8	Comprehensive single-cell transcriptome lineages of a proto-vertebrate. <i>Nature</i> , <b>2019</b> , 571, 349-354	50.4	81
7	Regulated exocytosis and sequential construction of the extracellular matrix surrounding the sea urchin zygote. <i>Developmental Biology</i> , <b>1997</b> , 186, 16-26	3.1	51
6	Comparative genomic hybridizations of <i>Entamoeba</i> strains reveal unique genetic fingerprints that correlate with virulence. <i>Eukaryotic Cell</i> , <b>2005</b> , 4, 504-15		47
5	GeneXplorer: an interactive web application for microarray data visualization and analysis. <i>BMC Bioinformatics</i> , <b>2004</b> , 5, 141	3.6	15
4	Standards for microarray data: an open letter. <i>Environmental Health Perspectives</i> , <b>2004</b> , 112, A666-7	8.4	13
3	Cortical granule exocytosis is triggered by different thresholds of calcium during fertilisation in sea urchin eggs. <i>Zygote</i> , <b>1998</b> , 6, 55-64, 65a	1.6	11

- 2 Phylogenetic portrait of the *Saccharomyces cerevisiae* functional genome. *G3: Genes, Genomes, Genetics*, **2013**, 3, 1335-40 3.2 3
- 1 Computational Methods and Bioinformatic Tools 769-904