

# John Quackenbush

## List of Publications by Citations

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56  
papers

21,642  
citations

38  
h-index

66  
g-index

66  
ext. papers

24,278  
ext. citations

15.5  
avg, IF

6.59  
L-index

#	Paper	IF	Citations
56	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
55	The complete genome sequence of the gastric pathogen <i>Helicobacter pylori</i> . <i>Nature</i> , <b>1997</b> , 388, 539-47	50.4	3000
54	Decoding tumour phenotype by noninvasive imaging using a quantitative radiomics approach. <i>Nature Communications</i> , <b>2014</b> , 5, 4006	17.4	2330
53	Genomic sequence of a Lyme disease spirochaete, <i>Borrelia burgdorferi</i> . <i>Nature</i> , <b>1997</b> , 390, 580-6	50.4	1729
52	TM4 microarray software suite. <i>Methods in Enzymology</i> , <b>2006</b> , 411, 134-93	1.7	1525
51	Microarray data normalization and transformation. <i>Nature Genetics</i> , <b>2002</b> , 32 Suppl, 496-501	36.3	1466
50	The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon <i>Archaeoglobus fulgidus</i> . <i>Nature</i> , <b>1997</b> , 390, 364-70	50.4	1257
49	Computational analysis of microarray data. <i>Nature Reviews Genetics</i> , <b>2001</b> , 2, 418-27	30.1	1137
48	Artificial intelligence in radiology. <i>Nature Reviews Cancer</i> , <b>2018</b> , 18, 500-510	31.3	916
47	Multiple-laboratory comparison of microarray platforms. <i>Nature Methods</i> , <b>2005</b> , 2, 345-50	21.6	716
46	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 889-96	44.5	417
45	Independence and reproducibility across microarray platforms. <i>Nature Methods</i> , <b>2005</b> , 2, 337-44	21.6	368
44	RNA-Seq analysis in MeV. <i>Bioinformatics</i> , <b>2011</b> , 27, 3209-10	7.2	294
43	Global transcription profiling reveals comprehensive insights into hypoxic response in <i>Arabidopsis</i> . <i>Plant Physiology</i> , <b>2005</b> , 137, 1115-29	6.6	273
42	Comprehensive biostatistical analysis of CpG island methylator phenotype in colorectal cancer using a large population-based sample. <i>PLoS ONE</i> , <b>2008</b> , 3, e3698	3.7	245
41	Exploratory Study to Identify Radiomics Classifiers for Lung Cancer Histology. <i>Frontiers in Oncology</i> , <b>2016</b> , 6, 71	5.3	211
40	Somatic Mutations Drive Distinct Imaging Phenotypes in Lung Cancer. <i>Cancer Research</i> , <b>2017</b> , 77, 3922-3930	33.0	200

39	Open Source Software for the Analysis of Microarray Data. <i>BioTechniques</i> , <b>2003</b> , 34, S45-S51	2.5	172
38	Comparative analyses of potato expressed sequence tag libraries. <i>Plant Physiology</i> , <b>2003</b> , 131, 419-29	6.6	162
37	Genomics. Microarrays--guilt by association. <i>Science</i> , <b>2003</b> , 302, 240-1	33.3	141
36	Standards for microarray data. <i>Science</i> , <b>2002</b> , 298, 539	33.3	120
35	Assessing unmodified 70-mer oligonucleotide probe performance on glass-slide microarrays. <i>Genome Biology</i> , <b>2003</b> , 4, R5	18.3	108
34	Minimum information specification for in situ hybridization and immunohistochemistry experiments (MISFISHIE). <i>Nature Biotechnology</i> , <b>2008</b> , 26, 305-12	44.5	97
33	Variance of gene expression identifies altered network constraints in neurological disease. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002207	6	96
32	An optimized protocol for analysis of EST sequences. <i>Nucleic Acids Research</i> , <b>2000</b> , 28, 3657-65	20.1	96
31	Submission of microarray data to public repositories. <i>PLoS Biology</i> , <b>2004</b> , 2, E317	9.7	87
30	Extracting meaning from functional genomics experiments. <i>Toxicology and Applied Pharmacology</i> , <b>2005</b> , 207, 195-9	4.6	81
29	Seeded Bayesian Networks: constructing genetic networks from microarray data. <i>BMC Systems Biology</i> , <b>2008</b> , 2, 57	3.5	71
28	HPV16 E7 oncogene expression in normal human epithelial cells causes molecular changes indicative of an epithelial to mesenchymal transition. <i>Virology</i> , <b>2009</b> , 391, 57-63	3.6	69
27	Enhancing reproducibility in cancer drug screening: how do we move forward?. <i>Cancer Research</i> , <b>2014</b> , 74, 4016-23	10.1	64
26	Molecular processes during fat cell development revealed by gene expression profiling and functional annotation. <i>Genome Biology</i> , <b>2005</b> , 6, R108	18.3	58
25	Data standards for Omics data: the basis of data sharing and reuse. <i>Methods in Molecular Biology</i> , <b>2011</b> , 719, 31-69	1.4	52
24	Epstein-Barr virus nuclear antigen 3C regulated genes in lymphoblastoid cell lines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 337-42	11.5	47
23	Data standards for Omics science. <i>Nature Biotechnology</i> , <b>2004</b> , 22, 613-4	44.5	46
22	Functional classification analysis of somatically mutated genes in human breast and colorectal cancers. <i>Genomics</i> , <b>2008</b> , 91, 508-11	4.3	44

21	Extracting biology from high-dimensional biological data. <i>Journal of Experimental Biology</i> , <b>2007</b> , 210, 1507-17	3	38
20	Ovarian reserve status in young women is associated with altered gene expression in membrana granulosa cells. <i>Molecular Human Reproduction</i> , <b>2012</b> , 18, 362-71	4.4	37
19	Canonical NF-kappaB activation is essential for Epstein-Barr virus latent membrane protein 1 TES2/CTAR2 gene regulation. <i>Journal of Virology</i> , <b>2011</b> , 85, 6764-73	6.6	31
18	Data standards: a call to action. <i>OMICS A Journal of Integrative Biology</i> , <b>2006</b> , 10, 94-9	3.8	31
17	The limits of log-ratios. <i>BMC Biotechnology</i> , <b>2004</b> , 4, 3	3.5	27
16	Expression profiling of archival tumors for long-term health studies. <i>Clinical Cancer Research</i> , <b>2012</b> , 18, 6136-46	12.9	25
15	Sequential binary gene ratio tests define a novel molecular diagnostic strategy for malignant pleural mesothelioma. <i>Clinical Cancer Research</i> , <b>2013</b> , 19, 2493-502	12.9	21
14	Therapeutic implications of GIPC1 silencing in cancer. <i>PLoS ONE</i> , <b>2010</b> , 5, e15581	3.7	18
13	Development of the Minimum Information Specification for In Situ Hybridization and Immunohistochemistry Experiments (MISFISHIE). <i>OMICS A Journal of Integrative Biology</i> , <b>2006</b> , 10, 205-8	3.8	16
12	The quest for the mechanisms of life. <i>Biotechnology and Bioengineering</i> , <b>2003</b> , 84, 739-42	4.9	14
11	Standards for microarray data: an open letter. <i>Environmental Health Perspectives</i> , <b>2004</b> , 112, A666-7	8.4	13
10	Data reporting standards: making the things we use better. <i>Genome Medicine</i> , <b>2009</b> , 1, 111	14.4	12
9	Why is there a lack of consensus on molecular subgroups of glioblastoma? Understanding the nature of biological and statistical variability in glioblastoma expression data. <i>PLoS ONE</i> , <b>2011</b> , 6, e20826	3.7	12
8	Safikhani et al. reply. <i>Nature</i> , <b>2016</b> , 540, E6-E8	50.4	9
7	A guide to microarray experiments-an open letter to the scientific journals. <i>Lancet, The</i> , <b>2002</b> , 360, 1019-40	40	8
6	Plant database resources at The Institute for Genomic Research. <i>Methods in Molecular Biology</i> , <b>2007</b> , 406, 113-36	1.4	6
5	Response to Shields: WIAIME, we have a problem. <i>Trends in Genetics</i> , <b>2006</b> , 22, 471-2	8.5	6
4	nEASE: a method for gene ontology subclassification of high-throughput gene expression data. <i>Bioinformatics</i> , <b>2012</b> , 28, 726-8	7.2	5

- 3 High-Throughput Sequencing in Respiratory, Critical Care, and Sleep Medicine Research. An Official American Thoracic Society Workshop Report. *Annals of the American Thoracic Society*, **2019**, 16, 1-16 4-7 5
- 2 Minimum information about a functional genomics experiment: the state of microarray standards and their extension to other technologies. *Drug Discovery Today: TARGETS*, **2004**, 3, 159-164 4
- 1 DNA Microarray Technology and Applications [An Overview] 899-928