

John Quackenbush

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/12068726/john-quackenbush-publications-by-year.pdf>

Version: 2024-04-26

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

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	High-Throughput Sequencing in Respiratory, Critical Care, and Sleep Medicine Research. An Official American Thoracic Society Workshop Report. <i>Annals of the American Thoracic Society</i> , 2019 , 16, 1-16	4.7	5
55	Artificial intelligence in radiology. <i>Nature Reviews Cancer</i> , 2018 , 18, 500-510	31.3	916
54	Somatic Mutations Drive Distinct Imaging Phenotypes in Lung Cancer. <i>Cancer Research</i> , 2017 , 77, 3922-3930	33.0	200
53	Exploratory Study to Identify Radiomics Classifiers for Lung Cancer Histology. <i>Frontiers in Oncology</i> , 2016 , 6, 71	5.3	211
52	Safikhani et al. reply. <i>Nature</i> , 2016 , 540, E6-E8	50.4	9
51	Decoding tumour phenotype by noninvasive imaging using a quantitative radiomics approach. <i>Nature Communications</i> , 2014 , 5, 4006	17.4	2330
50	Enhancing reproducibility in cancer drug screening: how do we move forward?. <i>Cancer Research</i> , 2014 , 74, 4016-23	10.1	64
49	Sequential binary gene ratio tests define a novel molecular diagnostic strategy for malignant pleural mesothelioma. <i>Clinical Cancer Research</i> , 2013 , 19, 2493-502	12.9	21
48	Expression profiling of archival tumors for long-term health studies. <i>Clinical Cancer Research</i> , 2012 , 18, 6136-46	12.9	25
47	Ovarian reserve status in young women is associated with altered gene expression in membrana granulosa cells. <i>Molecular Human Reproduction</i> , 2012 , 18, 362-71	4.4	37
46	nEASE: a method for gene ontology subclassification of high-throughput gene expression data. <i>Bioinformatics</i> , 2012 , 28, 726-8	7.2	5
45	Data standards for Omics data: the basis of data sharing and reuse. <i>Methods in Molecular Biology</i> , 2011 , 719, 31-69	1.4	52
44	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> , 2011 , 108, 337-42	11.5	47
43	Canonical NF-kappaB activation is essential for Epstein-Barr virus latent membrane protein 1 TES2/CTAR2 gene regulation. <i>Journal of Virology</i> , 2011 , 85, 6764-73	6.6	31
42	Variance of gene expression identifies altered network constraints in neurological disease. <i>PLoS Genetics</i> , 2011 , 7, e1002207	6	96
41	RNA-Seq analysis in MeV. <i>Bioinformatics</i> , 2011 , 27, 3209-10	7.2	294
40	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> , 2011 , 6, e20826	2.7	12

39	Therapeutic implications of GIPC1 silencing in cancer. <i>PLoS ONE</i> , 2010 , 5, e15581	3.7	18
38	HPV16 E7 oncogene expression in normal human epithelial cells causes molecular changes indicative of an epithelial to mesenchymal transition. <i>Virology</i> , 2009 , 391, 57-63	3.6	69
37	Data reporting standards: making the things we use better. <i>Genome Medicine</i> , 2009 , 1, 111	14.4	12
36	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008 , 26, 889-96	44.5	417
35	Minimum information specification for in situ hybridization and immunohistochemistry experiments (MISFISHIE). <i>Nature Biotechnology</i> , 2008 , 26, 305-12	44.5	97
34	Seeded Bayesian Networks: constructing genetic networks from microarray data. <i>BMC Systems Biology</i> , 2008 , 2, 57	3.5	71
33	Functional classification analysis of somatically mutated genes in human breast and colorectal cancers. <i>Genomics</i> , 2008 , 91, 508-11	4.3	44
32	Comprehensive biostatistical analysis of CpG island methylator phenotype in colorectal cancer using a large population-based sample. <i>PLoS ONE</i> , 2008 , 3, e3698	3.7	245
31	Plant database resources at The Institute for Genomic Research. <i>Methods in Molecular Biology</i> , 2007 , 406, 113-36	1.4	6
30	Extracting biology from high-dimensional biological data. <i>Journal of Experimental Biology</i> , 2007 , 210, 1507-17	3	38
29	Response to Shields: WIAME, we have a problemV <i>Trends in Genetics</i> , 2006 , 22, 471-2	8.5	6
28	Data standards: a call to action. <i>OMICS A Journal of Integrative Biology</i> , 2006 , 10, 94-9	3.8	31
27	Development of the Minimum Information Specification for In Situ Hybridization and Immunohistochemistry Experiments (MISFISHIE). <i>OMICS A Journal of Integrative Biology</i> , 2006 , 10, 205-8	3.8	16
26	TM4 microarray software suite. <i>Methods in Enzymology</i> , 2006 , 411, 134-93	1.7	1525
25	Molecular processes during fat cell development revealed by gene expression profiling and functional annotation. <i>Genome Biology</i> , 2005 , 6, R108	18.3	58
24	Multiple-laboratory comparison of microarray platforms. <i>Nature Methods</i> , 2005 , 2, 345-50	21.6	716
23	Independence and reproducibility across microarray platforms. <i>Nature Methods</i> , 2005 , 2, 337-44	21.6	368
22	Extracting meaning from functional genomics experiments. <i>Toxicology and Applied Pharmacology</i> , 2005 , 207, 195-9	4.6	81

21	Global transcription profiling reveals comprehensive insights into hypoxic response in Arabidopsis. <i>Plant Physiology</i> , 2005 , 137, 1115-29	6.6	273
20	Standards for microarray data: an open letter. <i>Environmental Health Perspectives</i> , 2004 , 112, A666-7	8.4	13
19	Submission of microarray data to public repositories. <i>PLoS Biology</i> , 2004 , 2, E317	9.7	87
18	Data standards for Omicscience. <i>Nature Biotechnology</i> , 2004 , 22, 613-4	44.5	46
17	The limits of log-ratios. <i>BMC Biotechnology</i> , 2004 , 4, 3	3.5	27
16	Minimum information about a functional genomics experiment: the state of microarray standards and their extension to other technologies. <i>Drug Discovery Today: TARGETS</i> , 2004 , 3, 159-164		4
15	Open Source Software for the Analysis of Microarray Data. <i>BioTechniques</i> , 2003 , 34, S45-S51	2.5	172
14	The quest for the mechanisms of life. <i>Biotechnology and Bioengineering</i> , 2003 , 84, 739-42	4.9	14
13	Genomics. Microarrays--guilt by association. <i>Science</i> , 2003 , 302, 240-1	33.3	141
12	Assessing unmodified 70-mer oligonucleotide probe performance on glass-slide microarrays. <i>Genome Biology</i> , 2003 , 4, R5	18.3	108
11	Comparative analyses of potato expressed sequence tag libraries. <i>Plant Physiology</i> , 2003 , 131, 419-29	6.6	162
10	Microarray data normalization and transformation. <i>Nature Genetics</i> , 2002 , 32 Suppl, 496-501	36.3	1466
9	Standards for microarray data. <i>Science</i> , 2002 , 298, 539	33.3	120
8	A guide to microarray experiments-an open letter to the scientific journals. <i>Lancet, The</i> , 2002 , 360, 1019-40		8
7	Minimum information about a microarray experiment (MIAME)-toward standards for microarray data. <i>Nature Genetics</i> , 2001 , 29, 365-71	36.3	3326
6	Computational analysis of microarray data. <i>Nature Reviews Genetics</i> , 2001 , 2, 418-27	30.1	1137
5	An optimized protocol for analysis of EST sequences. <i>Nucleic Acids Research</i> , 2000 , 28, 3657-65	20.1	96
4	The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon <i>Archaeoglobus fulgidus</i> . <i>Nature</i> , 1997 , 390, 364-70	50.4	1257

- 3 Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*. *Nature*, **1997**, 390, 580-6 50.4 1729
- 2 The complete genome sequence of the gastric pathogen *Helicobacter pylori*. *Nature*, **1997**, 388, 539-47 50.4 3000
- 1 DNA Microarray Technology and Applications [An Overview] 899-928