John Quackenbush

List of Publications by Year
in descending order

110 papers	15,849 citations	76326 40 h-index	34986 98 g-index
134 all docs	134 docs citations	134 times ranked	26492 citing authors

#	Article	IF	Citations
1	Minimum information about a microarray experiment (MIAME)â€"toward standards for microarray data. Nature Genetics, 2001, 29, 365-371.	21.4	3,750
2	Decoding tumour phenotype by noninvasive imaging using a quantitative radiomics approach. Nature Communications, 2014, 5, 4006.	12.8	3,355
3	Artificial intelligence in radiology. Nature Reviews Cancer, 2018, 18, 500-510.	28.4	1,953
4	Inconsistency in large pharmacogenomic studies. Nature, 2013, 504, 389-393.	27.8	467
5	Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. Nature, 2012, 487, 491-495.	27.8	349
6	Understanding Tissue-Specific Gene Regulation. Cell Reports, 2017, 21, 1077-1088.	6.4	314
7	Somatic Mutations Drive Distinct Imaging Phenotypes in Lung Cancer. Cancer Research, 2017, 77, 3922-3930.	0.9	307
8	Exploratory Study to Identify Radiomics Classifiers for Lung Cancer Histology. Frontiers in Oncology, 2016, 6, 71.	2.8	306
9	A Three-Gene Model to Robustly Identify Breast Cancer Molecular Subtypes. Journal of the National Cancer Institute, 2012, 104, 311-325.	6.3	272
10	Histone deacetylase 6â€"mediated selective autophagy regulates COPD-associated cilia dysfunction. Journal of Clinical Investigation, 2013, 123, 5212-5230.	8.2	266
11	Challenges and emerging directions in single-cell analysis. Genome Biology, 2017, 18, 84.	8.8	258
12	Transparency and reproducibility in artificial intelligence. Nature, 2020, 586, E14-E16.	27.8	233
13	Sex Differences in Gene Expression and Regulatory Networks across 29 Human Tissues. Cell Reports, 2020, 31, 107795.	6.4	207
14	Mitochondrial iron chelation ameliorates cigarette smokeâ€"induced bronchitis and emphysema in mice. Nature Medicine, 2016, 22, 163-174.	30.7	206
15	Passing Messages between Biological Networks to Refine Predicted Interactions. PLoS ONE, 2013, 8, e64832.	2.5	183
16	Molecular networks in Network Medicine: Development and applications. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2020, 12, e1489.	6.6	128
17	Estimating Sample-Specific Regulatory Networks. IScience, 2019, 14, 226-240.	4.1	120
18	Data Analysis Strategies in Medical Imaging. Clinical Cancer Research, 2018, 24, 3492-3499.	7.0	115

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19	Integrated Genomics Reveals Convergent Transcriptomic Networks Underlying Chronic Obstructive Pulmonary Disease and Idiopathic Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 948-960.	5.6	110
20	GeneSigDB: a manually curated database and resource for analysis of gene expression signatures. Nucleic Acids Research, 2012, 40, D1060-D1066.	14.5	108
21	Angiogenic mRNA and microRNA Gene Expression Signature Predicts a Novel Subtype of Serous Ovarian Cancer. PLoS ONE, 2012, 7, e30269.	2.5	107
22	MicroRNA paraffin-based studies in osteosarcoma reveal reproducible independent prognostic profiles at 14q32. Genome Medicine, 2013, 5, 2.	8.2	96
23	Extracting meaning from functional genomics experiments. Toxicology and Applied Pharmacology, 2005, 207, 195-199.	2.8	90
24	Enhancing Reproducibility in Cancer Drug Screening: How Do We Move Forward?. Cancer Research, 2014, 74, 4016-4023.	0.9	90
25	Seeded Bayesian Networks: Constructing genetic networks from microarray data. BMC Systems Biology, 2008, 2, 57.	3.0	86
26	Exploring regulation in tissues with eQTL networks. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E7841-E7850.	7.1	82
27	Gene Regulatory Network Analysis Identifies Sex-Linked Differences in Colon Cancer Drug Metabolism. Cancer Research, 2018, 78, 5538-5547.	0.9	81
28	Revisiting inconsistency in large pharmacogenomic studies. F1000Research, 2016, 5, 2333.	1.6	79
29	Smooth quantile normalization. Biostatistics, 2018, 19, 185-198.	1.5	78
30	Functional interactors of three genome-wide association study genes are differentially expressed in severe chronic obstructive pulmonary disease lung tissue. Scientific Reports, 2017, 7, 44232.	3.3	76
31	DNA methylation profiling in human lung tissue identifies genes associated with COPD. Epigenetics, 2016, 11, 730-739.	2.7	73
32	Gender-Specific Molecular and Clinical Features Underlie Malignant Pleural Mesothelioma. Cancer Research, 2016, 76, 319-328.	0.9	73
33	Genome-Wide Sex and Gender Differences in Cancer. Frontiers in Oncology, 2020, 10, 597788.	2.8	64
34	Haploinsufficiency of Hedgehog interacting protein causes increased emphysema induced by cigarette smoke through network rewiring. Genome Medicine, 2015, 7, 12.	8.2	61
35	A network model for angiogenesis in ovarian cancer. BMC Bioinformatics, 2015, 16, 115.	2.6	60
36	Merkel Cell Polyomavirus Small T Antigen Promotes Pro-Glycolytic Metabolic Perturbations Required for Transformation. PLoS Pathogens, 2016, 12, e1006020.	4.7	60

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37	Multisystem Analysis of *Mycobacterium tuberculosis* Reveals Kinase-Dependent Remodeling of the Pathogen-Environment Interface. MBio, 2018, 9, .	4.1	57
38	Human Lung DNA Methylation Quantitative Trait Loci Colocalize with Chronic Obstructive Pulmonary Disease Genome-Wide Association Loci. American Journal of Respiratory and Critical Care Medicine, 2018, 197, 1275-1284.	5.6	56
39	Regulatory network changes between cell lines and their tissues of origin. BMC Genomics, 2017, 18, 723.	2.8	51
40	Cancer subtype identification using somatic mutation data. British Journal of Cancer, 2018, 118, 1492-1501.	6.4	51
41	BatchQC: interactive software for evaluating sample and batch effects in genomic data. Bioinformatics, 2016, 32, 3836-3838.	4.1	50
42	Bipartite Community Structure of eQTLs. PLoS Computational Biology, 2016, 12, e1005033.	3.2	50
43	Sexually-dimorphic targeting of functionally-related genes in COPD. BMC Systems Biology, 2014, 8, 118.	3.0	47
44	WebMeV: A Cloud Platform for Analyzing and Visualizing Cancer Genomic Data. Cancer Research, 2017, 77, e11-e14.	0.9	47
45	Tissue-aware RNA-Seq processing and normalization for heterogeneous and sparse data. BMC Bioinformatics, 2017, 18, 437.	2.6	45
46	Extracting biology from high-dimensional biological data. Journal of Experimental Biology, 2007, 210, 1507-1517.	1.7	44
47	Genetic control of gene expression at novel and established chronic obstructive pulmonary disease loci. Human Molecular Genetics, 2015, 24, 1200-1210.	2.9	43
48	Epigenetic remodeling regulates transcriptional changes between ovarian cancer and benign precursors. JCI Insight, 2016, 1, .	5.0	42
49	Inference and validation of predictive gene networks from biomedical literature and gene expression data. Genomics, 2014, 103, 329-336.	2.9	40
50	Gaussian and Mixed Graphical Models as (multi-)omics data analysis tools. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2020, 1863, 194418.	1.9	39
51	*Paenibacillus* infection with frequent viral coinfection contributes to postinfectious hydrocephalus in Ugandan infants. Science Translational Medicine, 2020, 12, .	12.4	39
52	Plasma Exosome Profiling of Cancer Patients by a Next Generation Systems Biology Approach. Scientific Reports, 2017, 7, 42741.	3.3	38
53	An imprinted non-coding genomic cluster at 14q32 defines clinically relevant molecular subtypes in osteosarcoma across multiple independent datasets. Journal of Hematology and Oncology, 2017, 10, 107.	17.0	38
54	Differential connectivity of gene regulatory networks distinguishes corticosteroid response in asthma. Journal of Allergy and Clinical Immunology, 2018, 141, 1250-1258.	2.9	35

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55	Ensemble genomic analysis in human lung tissue identifies novel genes for chronic obstructive pulmonary disease. Human Genomics, 2018, 12, 1.	2.9	35
56	The Impact of Stroma Admixture on Molecular Subtypes and Prognostic Gene Signatures in Serous Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 509-519.	2.5	34
57	Assessment of pharmacogenomic agreement. F1000Research, 2016, 5, 825.	1.6	34
58	Detecting phenotype-driven transitions in regulatory network structure. Npj Systems Biology and Applications, 2018, 4, 16.	3.0	32
59	Analyzing networks of phenotypes in complex diseases: methodology and applications in COPD. BMC Systems Biology, 2014, 8, 78.	3.0	31
60	GRAND: a database of gene regulatory network models across human conditions. Nucleic Acids Research, 2022, 50, D610-D621.	14.5	31
61	BRCA1 and RNAi factors promote repair mediated by small RNAs and PALB2â€"RAD52. Nature, 2021, 591, 665-670.	27.8	30
62	Nac1 Coordinates a Sub-network of Pluripotency Factors to Regulate Embryonic Stem Cell Differentiation. Cell Reports, 2016, 14, 1181-1194.	6.4	29
63	Integrating transcriptional and protein interaction networks to prioritize condition-specific master regulators. BMC Systems Biology, 2015, 9, 80.	3.0	27
64	lionessR: single sample network inference in R. BMC Cancer, 2019, 19, 1003.	2.6	26
65	Using graph convolutional neural networks to learn a representation for glycans. Cell Reports, 2021, 35, 109251.	6.4	25
66	Nongenic cancer-risk SNPs affect oncogenes, tumour-suppressor genes, and immune function. British Journal of Cancer, 2020, 122, 569-577.	6.4	22
67	Poly-ligand profiling differentiates trastuzumab-treated breast cancer patients according to their outcomes. Nature Communications, 2018, 9, 1219.	12.8	20
68	Histopathological Image QTL Discovery of Immune Infiltration Variants. IScience, 2018, 5, 80-89.	4.1	19
69	Differentiating progressive from nonprogressive T1 bladder cancer by gene expression profiling: Applying RNA-sequencing analysis on archived specimens. Urologic Oncology: Seminars and Original Investigations, 2014, 32, 327-336.	1.6	18
70	Biomarker correlation network in colorectal carcinoma by tumor anatomic location. BMC Bioinformatics, 2017, 18, 304.	2.6	18
71	Estimating drivers of cell state transitions using gene regulatory network models. BMC Systems Biology, 2017, 11, 139.	3.0	17
72	PUMA: PANDA Using MicroRNA Associations. Bioinformatics, 2020, 36, 4765-4773.	4.1	17

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73	Tumor associated seizures in glioblastomas are influenced by survival gene expression in a region-specific manner: A gene expression imaging study. Epilepsy Research, 2014, 108, 843-852.	1.6	15
74	PyPanda: a Python package for gene regulatory network reconstruction. Bioinformatics, 2016, 32, 3363-3365.	4.1	15
75	Estimating gene regulatory networks with pandaR. Bioinformatics, 2017, 33, 2232-2234.	4.1	15
76	DNA Methylation Is Predictive of Mortality in Current and Former Smokers. American Journal of Respiratory and Critical Care Medicine, 2020, 201, 1099-1109.	5.6	15
77	Regulatory Network of PD1 Signaling Is Associated with Prognosis in Glioblastoma Multiforme. Cancer Research, 2021, 81, 5401-5412.	0.9	15
78	Initial Validation of a Machine Learning-Derived Prognostic Test (KidneyIntelX) Integrating Biomarkers and Electronic Health Record Data To Predict Longitudinal Kidney Outcomes. Kidney360, 2020, 1, 731-739.	2.1	15
79	Constructing gene regulatory networks using epigenetic data. Npj Systems Biology and Applications, 2021, 7, 45.	3.0	14
80	Comparative genome-wide transcriptional analysis of human left and right internal mammary arteries. Genomics, 2014, 104, 36-44.	2.9	13
81	Diet-induced weight loss leads to a switch in gene regulatory network control in the rectal mucosa. Genomics, 2016, 108, 126-133.	2.9	13
82	Expression Quantitative Trait loci (QTL) in tumor adjacent normal breast tissue and breast tumor tissue. PLoS ONE, 2017, 12, e0170181.	2.5	12
83	Gene Targeting in Disease Networks. Frontiers in Genetics, 2021, 12, 649942.	2.3	11
84	Using a Single Daytime Performance Test to Identify Most Individuals at High-Risk for Performance Impairment during Extended Wake. Scientific Reports, 2019, 9, 16681.	3.3	9
85	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.	3.2	9
86	MicroRNA-mRNA networks define translatable molecular outcome phenotypes in osteosarcoma. Scientific Reports, 2020, 10, 4409.	3.3	9
87	Predicting genotype-specific gene regulatory networks. Genome Research, 2022, 32, 524-533.	5.5	9
88	High performance computing of gene regulatory networks using a message-passing model. , 2015, , .		8
89	Identification of differentially expressed gene sets using the Generalized Berkâ€"Jones statistic. Bioinformatics, 2019, 35, 4568-4576.	4.1	8
90	Relevance of different prior knowledge sources for inferring gene interaction networks. Frontiers in Genetics, 2014, 5, 177.	2.3	7

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91	An online notebook resource for reproducible inference, analysis and publication of gene regulatory networks. Nature Methods, 2022, 19, 511-513.	19.0	7
92	Environmental Influences Measured by Epigenetic Clock and Vulnerability Components at Birth Impact Clinical ASD Heterogeneity. Genes, 2021, 12, 1433.	2.4	3
93	Multi-omic regulatory networks capture downstream effects of kinase inhibition in Mycobacterium tuberculosis. Npj Systems Biology and Applications, 2021, 7, 8.	3.0	3
94	Estimating Sample-Specific Regulatory Networks. SSRN Electronic Journal, 0, , .	0.4	3
95	Gene regulatory network inference as relaxed graph matching. Proceedings of the AAAI Conference on Artificial Intelligence, 2021, 35, 10263-10272.	4.9	3
96	Connectivity in eQTL networks dictates reproducibility and genomic properties. Cell Reports Methods, 2022, 2, 100218.	2.9	3
97	Data, Analysis, and Standardization. , 0, , 215-229.		2
98	Analysis of morphological characteristics of IDH-mutant/wildtype brain tumors using whole-lesion phenotype analysis. Neuro-Oncology Advances, 2021, 3, vdab088.	0.7	2
99	A Novel Deep Learning Model by Stacking Conditional Restricted Boltzmann Machine and Deep Neural Network. , 2020, , .		2
100	Clustering Sparse Data With Feature Correlation With Application to Discover Subtypes in Cancer. IEEE Access, 2020, 8, 67775-67789.	4.2	1
101	gpuZoo: Cost-effective estimation of gene regulatory networks using the Graphics Processing Unit. NAR Genomics and Bioinformatics, 2022, 4, lqac002.	3.2	1
102	IEEE 7<sup>th</sup> BIBE Invited Plenary Keynote: Stochasticity and Networks in Genomic Data. , 2007, , .		0
103	Variance due to Smooth Bias in Rat Liver and Kidney Baseline Gene Expression in a Large Multi-laboratory Data Set. , 0, , 87-99.		0
104	Using shRNA experiments to validate gene regulatory networks. Genomics Data, 2015, 4, 123-126.	1.3	0
105	Data will Drive the Healthcare Revolution. , 2020, , .		0
106	AI Methods for Analyzing Microarray Data. , 2009, , 65-70.		0
107	Genome-Wide Aberrant Splicing in Patients with Acute Myeloid Leukemia (AML) Indetifies Potential Novel Targets. Blood, 2011, 118, 761-761.	1.4	0
108	Chapter 7: On the Integration of Prior Knowledge in the Inference of Regulatory Networks. Science, Engineering, and Biology Informatics, 2014, , 169-199.	0.1	0

#	ARTICLE	IF	CITATIONS
109	Looking back at the first twenty years of genomics. Quantitative Biology, 2022, 10, 6-16.	0.5	0
110	AI Methods for Analyzing Microarray Data. , 0, , 877-884.		0