John Quackenbush

List of Publications by Citations

116 papers	10,935 citations	37 h-index	104 g-index
134 ext. papers	13,723 ext. citations	9.7 avg, IF	6.06 L-index

#	Paper	IF	Citations
116	Minimum information about a microarray experiment (MIAME)-toward standards for microarray data. *Nature Genetics*, **2001**, 29, 365-71	36.3	3326
115	Decoding tumour phenotype by noninvasive imaging using a quantitative radiomics approach. *Nature Communications*, **2014**, 5, 4006	17.4	2330
114	Artificial intelligence in radiology. *Nature Reviews Cancer*, **2018**, 18, 500-510	31.3	916
113	Inconsistency in large pharmacogenomic studies. *Nature*, **2013**, 504, 389-93	50.4	360
112	Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. *Nature*, **2012**, 487, 491-5	50.4	294
111	A three-gene model to robustly identify breast cancer molecular subtypes. *Journal of the National Cancer Institute*, **2012**, 104, 311-25	9.7	218
110	Exploratory Study to Identify Radiomics Classifiers for Lung Cancer Histology. *Frontiers in Oncology*, **2016**, 6, 71	5.3	211
109	Histone deacetylase 6-mediated selective autophagy regulates COPD-associated cilia dysfunction. *Journal of Clinical Investigation*, **2013**, 123, 5212-30	15.9	210
108	Somatic Mutations Drive Distinct Imaging Phenotypes in Lung Cancer. *Cancer Research*, **2017**, 77, 3922-3930	9.1	200
107	Understanding Tissue-Specific Gene Regulation. *Cell Reports*, **2017**, 21, 1077-1088	10.6	175
106	Challenges and emerging directions in single-cell analysis. *Genome Biology*, **2017**, 18, 84	18.3	166
105	Mitochondrial iron chelation ameliorates cigarette smoke-induced bronchitis and emphysema in mice. *Nature Medicine*, **2016**, 22, 163-74	50.5	136
104	Passing messages between biological networks to refine predicted interactions. *PLoS ONE*, **2013**, 8, e64832	3.7	108
103	GeneSigDB: a manually curated database and resource for analysis of gene expression signatures. *Nucleic Acids Research*, **2012**, 40, D1060-6	20.1	89
102	Transparency and reproducibility in artificial intelligence. *Nature*, **2020**, 586, E14-E16	50.4	85
101	Angiogenic mRNA and microRNA gene expression signature predicts a novel subtype of serous ovarian cancer. *PLoS ONE*, **2012**, 7, e30269	3.7	84
100	Extracting meaning from functional genomics experiments. *Toxicology and Applied Pharmacology*, **2005**, 207, 195-9	4.6	81

99	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	10.2	73
98	Seeded Bayesian Networks: constructing genetic networks from microarray data. *BMC Systems Biology*, **2008**, 2, 57	3.5	71
97	MicroRNA paraffin-based studies in osteosarcoma reveal reproducible independent prognostic profiles at 14q32. *Genome Medicine*, **2013**, 5, 2	14.4	69
96	Sex Differences in Gene Expression and Regulatory Networks across 29 Human Tissues. *Cell Reports* , **2020**, 31, 107795	10.6	67
95	Data Analysis Strategies in Medical Imaging. *Clinical Cancer Research*, **2018**, 24, 3492-3499	12.9	66
94	Enhancing reproducibility in cancer drug screening: how do we move forward?. *Cancer Research*, **2014**, 74, 4016-23	10.1	64
93	Molecular networks in Network Medicine: Development and applications. *Wiley Interdisciplinary Reviews: Systems Biology and Medicine*, **2020**, 12, e1489	6.6	63
92	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	4.9	57
91	Exploring regulation in tissues with eQTL networks. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, E7841-E7850	11.5	57
90	Gender-Specific Molecular and Clinical Features Underlie Malignant Pleural Mesothelioma. *Cancer Research*, **2016**, 76, 319-28	10.1	49
89	Revisiting inconsistency in large pharmacogenomic studies. *F1000Research*, **2016**, 5, 2333	3.6	49
88	Estimating Sample-Specific Regulatory Networks. *IScience*, **2019**, 14, 226-240	6.1	48
87	DNA methylation profiling in human lung tissue identifies genes associated with COPD. *Epigenetics*, **2016**, 11, 730-739	5.7	48
86	A network model for angiogenesis in ovarian cancer. *BMC Bioinformatics*, **2015**, 16, 115	3.6	47
85	Merkel Cell Polyomavirus Small T Antigen Promotes Pro-Glycolytic Metabolic Perturbations Required for Transformation. *PLoS Pathogens*, **2016**, 12, e1006020	7.6	46
84	Haploinsufficiency of Hedgehog interacting protein causes increased emphysema induced by cigarette smoke through network rewiring. *Genome Medicine*, **2015**, 7, 12	14.4	45
83	Gene Regulatory Network Analysis Identifies Sex-Linked Differences in Colon Cancer Drug Metabolism. *Cancer Research*, **2018**, 78, 5538-5547	10.1	41
82	Multisystem Analysis of Reveals Kinase-Dependent Remodeling of the Pathogen-Environment Interface. *MBio*, **2018**, 9,	7.8	38

81	Sexually-dimorphic targeting of functionally-related genes in COPD. *BMC Systems Biology*, **2014**, 8, 118	3.5	38
80	Extracting biology from high-dimensional biological data. *Journal of Experimental Biology*, **2007**, 210, 1507-17	3	38
79	Smooth quantile normalization. *Biostatistics*, **2018**, 19, 185-198	3.7	37
78	Genetic control of gene expression at novel and established chronic obstructive pulmonary disease loci. *Human Molecular Genetics*, **2015**, 24, 1200-10	5.6	33
77	Plasma Exosome Profiling of Cancer Patients by a Next Generation Systems Biology Approach. *Scientific Reports*, **2017**, 7, 42741	4.9	32
76	Tissue-aware RNA-Seq processing and normalization for heterogeneous and sparse data. *BMC Bioinformatics*, **2017**, 18, 437	3.6	31
75	BatchQC: interactive software for evaluating sample and batch effects in genomic data. *Bioinformatics*, **2016**, 32, 3836-3838	7.2	31
74	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	10.2	29
73	Cancer subtype identification using somatic mutation data. *British Journal of Cancer*, **2018**, 118, 1492-1501	8.7	29
72	Inference and validation of predictive gene networks from biomedical literature and gene expression data. *Genomics*, **2014**, 103, 329-36	4.3	28
71	Regulatory network changes between cell lines and their tissues of origin. *BMC Genomics*, **2017**, 18, 723	4.5	28
70	Epigenetic remodeling regulates transcriptional changes between ovarian cancer and benign precursors. *JCI Insight*, **2016**, 1,	9.9	28
69	Bipartite Community Structure of eQTLs. *PLoS Computational Biology*, **2016**, 12, e1005033	5	28
68	WebMeV: A Cloud Platform for Analyzing and Visualizing Cancer Genomic Data. *Cancer Research*, **2017**, 77, e11-e14	10.1	26
67	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	22.4	26
66	Analyzing networks of phenotypes in complex diseases: methodology and applications in COPD. *BMC Systems Biology*, **2014**, 8, 78	3.5	26
65	Assessment of pharmacogenomic agreement. *F1000Research*, **2016**, 5, 825	3.6	25
64	Differential connectivity of gene regulatory networks distinguishes corticosteroid response in asthma. *Journal of Allergy and Clinical Immunology*, **2018**, 141, 1250-1258	11.5	24

63	Ensemble genomic analysis in human lung tissue identifies novel genes for chronic obstructive pulmonary disease. *Human Genomics*, **2018**, 12, 1	6.8	20
62	Detecting phenotype-driven transitions in regulatory network structure. *Npj Systems Biology and Applications*, **2018**, 4, 16	5	18
61	Integrating transcriptional and protein interaction networks to prioritize condition-specific master regulators. *BMC Systems Biology*, **2015**, 9, 80	3.5	18
60	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	4	17
59	Genome-Wide Sex and Gender Differences in Cancer. *Frontiers in Oncology*, **2020**, 10, 597788	5.3	16
58	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, 327-36	2.8	15
57	Nac1 Coordinates a Sub-network of Pluripotency Factors to Regulate Embryonic Stem Cell Differentiation. *Cell Reports*, **2016**, 14, 1181-1194	10.6	15
56	Poly-ligand profiling differentiates trastuzumab-treated breast cancer patients according to their outcomes. *Nature Communications*, **2018**, 9, 1219	17.4	14
55	Biomarker correlation network in colorectal carcinoma by tumor anatomic location. *BMC Bioinformatics*, **2017**, 18, 304	3.6	13
54	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, 843-52	3	13
53	Nongenic cancer-risk SNPs affect oncogenes, tumour-suppressor genes, and immune function. *British Journal of Cancer*, **2020**, 122, 569-577	8.7	13
52	infection with frequent viral coinfection contributes to postinfectious hydrocephalus in Ugandan infants. *Science Translational Medicine*, **2020**, 12,	17.5	13
51	Gaussian and Mixed Graphical Models as (multi-)omics data analysis tools. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2020**, 1863, 194418	6	12
50	BRCA1 and RNAi factors promote repair mediated by small RNAs and PALB2-RAD52. *Nature*, **2021**, 591, 665-670	50.4	12
49	Diet-induced weight loss leads to a switch in gene regulatory network control in the rectal mucosa. *Genomics*, **2016**, 108, 126-133	4.3	11
48	lionessR: single sample network inference in R. *BMC Cancer*, **2019**, 19, 1003	4.8	10
47	PyPanda: a Python package for gene regulatory network reconstruction. *Bioinformatics*, **2016**, 32, 3363-3365	7.3	9
46	Comparative genome-wide transcriptional analysis of human left and right internal mammary arteries. *Genomics*, **2014**, 104, 36-44	4.3	9

45	Estimating drivers of cell state transitions using gene regulatory network models. *BMC Systems Biology*, **2017**, 11, 139	3.5	9
44	Expression Quantitative Trait loci (QTL) in tumor adjacent normal breast tissue and breast tumor tissue. *PLoS ONE*, **2017**, 12, e0170181	3.7	9
43	Estimating gene regulatory networks with pandaR. *Bioinformatics*, **2017**, 33, 2232-2234	7.2	8
42	Histopathological Image QTL Discovery of Immune Infiltration Variants. *IScience*, **2018**, 5, 80-89	6.1	8
41	PUMA: PANDA Using MicroRNA Associations. *Bioinformatics*, **2020**, 36, 4765-4773	7.2	8
40	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	1.8	7
39	Using graph convolutional neural networks to learn a representation for glycans. *Cell Reports*, **2021**, 35, 109251	10.6	7
38	Using a Single Daytime Performance Test to Identify Most Individuals at High-Risk for Performance Impairment during Extended Wake. *Scientific Reports*, **2019**, 9, 16681	4.9	7
37	GRAND: a database of gene regulatory network models across human conditions. *Nucleic Acids Research*, **2021**,	20.1	7
36	MicroRNA-mRNA networks define translatable molecular outcome phenotypes in osteosarcoma. *Scientific Reports*, **2020**, 10, 4409	4.9	6
35	DNA Methylation Is Predictive of Mortality in Current and Former Smokers. *American Journal of Respiratory and Critical Care Medicine*, **2020**, 201, 1099-1109	10.2	6
34	Tissue-aware RNA-Seq processing and normalization for heterogeneous and sparse data		6
33	Smooth Quantile Normalization		6
32	Relevance of different prior knowledge sources for inferring gene interaction networks. *Frontiers in Genetics*, **2014**, 5, 177	4.5	5
31	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
30	Identification of differentially expressed gene sets using the Generalized Berk-Jones statistic. *Bioinformatics*, **2019**, 35, 4568-4576	7.2	3
29	High performance computing of gene regulatory networks using a message-passing model **2015**,		3
28	Constructing gene regulatory networks using epigenetic data. *Npj Systems Biology and Applications*, **2021**, 7, 45	5	3

27	Gene Targeting in Disease Networks. *Frontiers in Genetics*, **2021**, 12, 649942	4.5	3
26	Regulation of PD1 signaling is associated with prognosis in glioblastoma multiforme		3
25	Regulatory Network of PD1 Signaling Is Associated with Prognosis in Glioblastoma Multiforme. *Cancer Research*, **2021**, 81, 5401-5412	10.1	3
24	Estimating Sample-Specific Regulatory Networks. *SSRN Electronic Journal*,	1	2
23	Gene Regulatory Network Inference as Relaxed Graph Matching		2
22	GRAND: A database of gene regulatory network models across human conditions		2
21	Multi-omic regulatory networks capture downstream effects of kinase inhibition in Mycobacterium tuberculosis. *Npj Systems Biology and Applications*, **2021**, 7, 8	5	2
20	Predicting genotype-specific gene regulatory networks.. *Genome Research*, **2022**, 32, 524-533	9.7	2
19	An online notebook resource for reproducible inference, analysis and publication of gene regulatory networks.. *Nature Methods*, **2022**,	21.6	2
18	Clustering Sparse Data With Feature Correlation With Application to Discover Subtypes in Cancer. *IEEE Access*, **2020**, 8, 67775-67789	3.5	1
17	Data, Analysis, and Standardization215-229		1
16	A Novel Deep Learning Model by Stacking Conditional Restricted Boltzmann Machine and Deep Neural Network **2020**,		1
15	Gene regulatory network inference as relaxed graph matching. *Proceedings of the AAAI Conference on Artificial Intelligence*, **2021**, 35, 10263-10272	5	1
14	The impact of stroma on the discovery of molecular subtypes and prognostic gene signatures in serous ovarian cancer		1
13	Spectral clustering in regression-based biological networks		1
12	Understanding Tissue-specific Gene Regulation		1
11	Histopathological image QTL discovery of immune infiltration variants		1
10	Analysis of morphological characteristics of IDH-mutant/wildtype brain tumors using whole-lesion phenotype analysis. *Neuro-Oncology Advances*, **2021**, 3, vdab088	0.9	1

9   gpuZoo: Cost-effective estimation of gene regulatory networks using the Graphics Processing Unit   1

8   gpuZoo: Cost-effective estimation of gene regulatory networks using the Graphics Processing Unit.. *NAR Genomics and Bioinformatics*, **2022**, 4, lqac002   3.7   0

7   Connectivity in eQTL networks dictates reproducibility and genomic properties. *Cell Reports Methods*, **2022**, 2, 100218   0

6   Using shRNA experiments to validate gene regulatory networks. *Genomics Data*, **2015**, 4, 123-6

5   Variance due to Smooth Bias in Rat Liver and Kidney Baseline Gene Expression in a Large Multi-laboratory Data Set87-99

4   AI Methods for Analyzing Microarray Data **2009**, 65-70

3   Genome-Wide Aberrant Splicing in Patients with Acute Myeloid Leukemia (AML) Indetifies Potential Novel Targets. *Blood*, **2011**, 118, 761-761   2.2

2   Chapter 7: On the Integration of Prior Knowledge in the Inference of Regulatory Networks. *Science, Engineering, and Biology Informatics*, **2014**, 169-199

1   AI Methods for Analyzing Microarray Data877-884