

John Quackenbush

List of Publications by Year in descending order

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Version: 2024-02-01

110
papers

15,849
citations

76196

40
h-index

34900

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. <i>Nature Genetics</i> , 2001, 29, 365-371.	9.4	3,750
2	Decoding tumour phenotype by noninvasive imaging using a quantitative radiomics approach. <i>Nature Communications</i> , 2014, 5, 4006.	5.8	3,355
3	Artificial intelligence in radiology. <i>Nature Reviews Cancer</i> , 2018, 18, 500-510.	12.8	1,953
4	Inconsistency in large pharmacogenomic studies. <i>Nature</i> , 2013, 504, 389-393.	13.7	467
5	Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. <i>Nature</i> , 2012, 487, 491-495.	13.7	349
6	Understanding Tissue-Specific Gene Regulation. <i>Cell Reports</i> , 2017, 21, 1077-1088.	2.9	314
7	Somatic Mutations Drive Distinct Imaging Phenotypes in Lung Cancer. <i>Cancer Research</i> , 2017, 77, 3922-3930.	0.4	307
8	Exploratory Study to Identify Radiomics Classifiers for Lung Cancer Histology. <i>Frontiers in Oncology</i> , 2016, 6, 71.	1.3	306
9	A Three-Gene Model to Robustly Identify Breast Cancer Molecular Subtypes. <i>Journal of the National Cancer Institute</i> , 2012, 104, 311-325.	3.0	272
10	Histone deacetylase mediated selective autophagy regulates COPD-associated cilia dysfunction. <i>Journal of Clinical Investigation</i> , 2013, 123, 5212-5230.	3.9	266
11	Challenges and emerging directions in single-cell analysis. <i>Genome Biology</i> , 2017, 18, 84.	3.8	258
12	Transparency and reproducibility in artificial intelligence. <i>Nature</i> , 2020, 586, E14-E16.	13.7	233
13	Sex Differences in Gene Expression and Regulatory Networks across 29 Human Tissues. <i>Cell Reports</i> , 2020, 31, 107795.	2.9	207
14	Mitochondrial iron chelation ameliorates cigarette smokeâ€”induced bronchitis and emphysema in mice. <i>Nature Medicine</i> , 2016, 22, 163-174.	15.2	206
15	Passing Messages between Biological Networks to Refine Predicted Interactions. <i>PLoS ONE</i> , 2013, 8, e64832.	1.1	183
16	Molecular networks in Network Medicine: Development and applications. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2020, 12, e1489.	6.6	128
17	Estimating Sample-Specific Regulatory Networks. <i>IScience</i> , 2019, 14, 226-240.	1.9	120
18	Data Analysis Strategies in Medical Imaging. <i>Clinical Cancer Research</i> , 2018, 24, 3492-3499.	3.2	115

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19	Integrated Genomics Reveals Convergent Transcriptomic Networks Underlying Chronic Obstructive Pulmonary Disease and Idiopathic Pulmonary Fibrosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 194, 948-960.	2.5	110
20	GeneSigDB: a manually curated database and resource for analysis of gene expression signatures. <i>Nucleic Acids Research</i> , 2012, 40, D1060-D1066.	6.5	108
21	Angiogenic mRNA and microRNA Gene Expression Signature Predicts a Novel Subtype of Serous Ovarian Cancer. <i>PLoS ONE</i> , 2012, 7, e30269.	1.1	107
22	MicroRNA paraffin-based studies in osteosarcoma reveal reproducible independent prognostic profiles at 14q32. <i>Genome Medicine</i> , 2013, 5, 2.	3.6	96
23	Extracting meaning from functional genomics experiments. <i>Toxicology and Applied Pharmacology</i> , 2005, 207, 195-199.	1.3	90
24	Enhancing Reproducibility in Cancer Drug Screening: How Do We Move Forward?. <i>Cancer Research</i> , 2014, 74, 4016-4023.	0.4	90
25	Seeded Bayesian Networks: Constructing genetic networks from microarray data. <i>BMC Systems Biology</i> , 2008, 2, 57.	3.0	86
26	Exploring regulation in tissues with eQTL networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7841-E7850.	3.3	82
27	Gene Regulatory Network Analysis Identifies Sex-Linked Differences in Colon Cancer Drug Metabolism. <i>Cancer Research</i> , 2018, 78, 5538-5547.	0.4	81
28	Revisiting inconsistency in large pharmacogenomic studies. <i>F1000Research</i> , 2016, 5, 2333.	0.8	79
29	Smooth quantile normalization. <i>Biostatistics</i> , 2018, 19, 185-198.	0.9	78
30	Functional interactors of three genome-wide association study genes are differentially expressed in severe chronic obstructive pulmonary disease lung tissue. <i>Scientific Reports</i> , 2017, 7, 44232.	1.6	76
31	DNA methylation profiling in human lung tissue identifies genes associated with COPD. <i>Epigenetics</i> , 2016, 11, 730-739.	1.3	73
32	Gender-Specific Molecular and Clinical Features Underlie Malignant Pleural Mesothelioma. <i>Cancer Research</i> , 2016, 76, 319-328.	0.4	73
33	Genome-Wide Sex and Gender Differences in Cancer. <i>Frontiers in Oncology</i> , 2020, 10, 597788.	1.3	64
34	Haploinsufficiency of Hedgehog interacting protein causes increased emphysema induced by cigarette smoke through network rewiring. <i>Genome Medicine</i> , 2015, 7, 12.	3.6	61
35	A network model for angiogenesis in ovarian cancer. <i>BMC Bioinformatics</i> , 2015, 16, 115.	1.2	60
36	Merkel Cell Polyomavirus Small T Antigen Promotes Pro-Glycolytic Metabolic Perturbations Required for Transformation. <i>PLoS Pathogens</i> , 2016, 12, e1006020.	2.1	60

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37	Multisystem Analysis of <i>Mycobacterium tuberculosis</i> Reveals Kinase-Dependent Remodeling of the Pathogen-Environment Interface. <i>MBio</i> , 2018, 9, .	1.8	57
38	Human Lung DNA Methylation Quantitative Trait Loci Colocalize with Chronic Obstructive Pulmonary Disease Genome-Wide Association Loci. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 197, 1275-1284.	2.5	56
39	Regulatory network changes between cell lines and their tissues of origin. <i>BMC Genomics</i> , 2017, 18, 723.	1.2	51
40	Cancer subtype identification using somatic mutation data. <i>British Journal of Cancer</i> , 2018, 118, 1492-1501.	2.9	51
41	BatchQC: interactive software for evaluating sample and batch effects in genomic data. <i>Bioinformatics</i> , 2016, 32, 3836-3838.	1.8	50
42	Bipartite Community Structure of eQTLs. <i>PLoS Computational Biology</i> , 2016, 12, e1005033.	1.5	50
43	Sexually-dimorphic targeting of functionally-related genes in COPD. <i>BMC Systems Biology</i> , 2014, 8, 118.	3.0	47
44	WebMeV: A Cloud Platform for Analyzing and Visualizing Cancer Genomic Data. <i>Cancer Research</i> , 2017, 77, e11-e14.	0.4	47
45	Tissue-aware RNA-Seq processing and normalization for heterogeneous and sparse data. <i>BMC Bioinformatics</i> , 2017, 18, 437.	1.2	45
46	Extracting biology from high-dimensional biological data. <i>Journal of Experimental Biology</i> , 2007, 210, 1507-1517.	0.8	44
47	Genetic control of gene expression at novel and established chronic obstructive pulmonary disease loci. <i>Human Molecular Genetics</i> , 2015, 24, 1200-1210.	1.4	43
48	Epigenetic remodeling regulates transcriptional changes between ovarian cancer and benign precursors. <i>JCI Insight</i> , 2016, 1, .	2.3	42
49	Inference and validation of predictive gene networks from biomedical literature and gene expression data. <i>Genomics</i> , 2014, 103, 329-336.	1.3	40
50	Gaussian and Mixed Graphical Models as (multi-)omics data analysis tools. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194418.	0.9	39
51	<i>Paenibacillus</i> infection with frequent viral coinfection contributes to postinfectious hydrocephalus in Ugandan infants. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	39
52	Plasma Exosome Profiling of Cancer Patients by a Next Generation Systems Biology Approach. <i>Scientific Reports</i> , 2017, 7, 42741.	1.6	38
53	An imprinted non-coding genomic cluster at 14q32 defines clinically relevant molecular subtypes in osteosarcoma across multiple independent datasets. <i>Journal of Hematology and Oncology</i> , 2017, 10, 107.	6.9	38
54	Differential connectivity of gene regulatory networks distinguishes corticosteroid response in asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 1250-1258.	1.5	35

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55	Ensemble genomic analysis in human lung tissue identifies novel genes for chronic obstructive pulmonary disease. <i>Human Genomics</i> , 2018, 12, 1.	1.4	35
56	The Impact of Stroma Admixture on Molecular Subtypes and Prognostic Gene Signatures in Serous Ovarian Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 509-519.	1.1	34
57	Assessment of pharmacogenomic agreement. <i>F1000Research</i> , 2016, 5, 825.	0.8	34
58	Detecting phenotype-driven transitions in regulatory network structure. <i>Npj Systems Biology and Applications</i> , 2018, 4, 16.	1.4	32
59	Analyzing networks of phenotypes in complex diseases: methodology and applications in COPD. <i>BMC Systems Biology</i> , 2014, 8, 78.	3.0	31
60	GRAND: a database of gene regulatory network models across human conditions. <i>Nucleic Acids Research</i> , 2022, 50, D610-D621.	6.5	31
61	BRCA1 and RNAi factors promote repair mediated by small RNAs and PALB2â€“RAD52. <i>Nature</i> , 2021, 591, 665-670.	13.7	30
62	Nac1 Coordinates a Sub-network of Pluripotency Factors to Regulate Embryonic Stem Cell Differentiation. <i>Cell Reports</i> , 2016, 14, 1181-1194.	2.9	29
63	Integrating transcriptional and protein interaction networks to prioritize condition-specific master regulators. <i>BMC Systems Biology</i> , 2015, 9, 80.	3.0	27
64	lionessR: single sample network inference in R. <i>BMC Cancer</i> , 2019, 19, 1003.	1.1	26
65	Using graph convolutional neural networks to learn a representation for glycans. <i>Cell Reports</i> , 2021, 35, 109251.	2.9	25
66	Nongenetic cancer-risk SNPs affect oncogenes, tumour-suppressor genes, and immune function. <i>British Journal of Cancer</i> , 2020, 122, 569-577.	2.9	22
67	Poly-ligand profiling differentiates trastuzumab-treated breast cancer patients according to their outcomes. <i>Nature Communications</i> , 2018, 9, 1219.	5.8	20
68	Histopathological Image QTL Discovery of Immune Infiltration Variants. <i>IScience</i> , 2018, 5, 80-89.	1.9	19
69	Differentiating progressive from nonprogressive T1 bladder cancer by gene expression profiling: Applying RNA-sequencing analysis on archived specimens. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2014, 32, 327-336.	0.8	18
70	Biomarker correlation network in colorectal carcinoma by tumor anatomic location. <i>BMC Bioinformatics</i> , 2017, 18, 304.	1.2	18
71	Estimating drivers of cell state transitions using gene regulatory network models. <i>BMC Systems Biology</i> , 2017, 11, 139.	3.0	17
72	PUMA: PANDA Using MicroRNA Associations. <i>Bioinformatics</i> , 2020, 36, 4765-4773.	1.8	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. <i>Epilepsy Research</i> , 2014, 108, 843-852.	0.8	15
74	PyPanda: a Python package for gene regulatory network reconstruction. <i>Bioinformatics</i> , 2016, 32, 3363-3365.	1.8	15
75	Estimating gene regulatory networks with pandaR. <i>Bioinformatics</i> , 2017, 33, 2232-2234.	1.8	15
76	DNA Methylation Is Predictive of Mortality in Current and Former Smokers. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 201, 1099-1109.	2.5	15
77	Regulatory Network of PD1 Signaling Is Associated with Prognosis in Glioblastoma Multiforme. <i>Cancer Research</i> , 2021, 81, 5401-5412.	0.4	15
78	Initial Validation of a Machine Learning-Derived Prognostic Test (KidneyIntelX) Integrating Biomarkers and Electronic Health Record Data To Predict Longitudinal Kidney Outcomes. <i>Kidney360</i> , 2020, 1, 731-739.	0.9	15
79	Constructing gene regulatory networks using epigenetic data. <i>Npj Systems Biology and Applications</i> , 2021, 7, 45.	1.4	14
80	Comparative genome-wide transcriptional analysis of human left and right internal mammary arteries. <i>Genomics</i> , 2014, 104, 36-44.	1.3	13
81	Diet-induced weight loss leads to a switch in gene regulatory network control in the rectal mucosa. <i>Genomics</i> , 2016, 108, 126-133.	1.3	13
82	Expression Quantitative Trait loci (QTL) in tumor adjacent normal breast tissue and breast tumor tissue. <i>PLoS ONE</i> , 2017, 12, e0170181.	1.1	12
83	Gene Targeting in Disease Networks. <i>Frontiers in Genetics</i> , 2021, 12, 649942.	1.1	11
84	Using a Single Daytime Performance Test to Identify Most Individuals at High-Risk for Performance Impairment during Extended Wake. <i>Scientific Reports</i> , 2019, 9, 16681.	1.6	9
85	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.	1.5	9
86	MicroRNA-mRNA networks define translatable molecular outcome phenotypes in osteosarcoma. <i>Scientific Reports</i> , 2020, 10, 4409.	1.6	9
87	Predicting genotype-specific gene regulatory networks. <i>Genome Research</i> , 2022, 32, 524-533.	2.4	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. <i>Bioinformatics</i> , 2019, 35, 4568-4576.	1.8	8
90	Relevance of different prior knowledge sources for inferring gene interaction networks. <i>Frontiers in Genetics</i> , 2014, 5, 177.	1.1	7

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91	An online notebook resource for reproducible inference, analysis and publication of gene regulatory networks. <i>Nature Methods</i> , 2022, 19, 511-513.	9.0	7
92	Environmental Influences Measured by Epigenetic Clock and Vulnerability Components at Birth Impact Clinical ASD Heterogeneity. <i>Genes</i> , 2021, 12, 1433.	1.0	3
93	Multi-omic regulatory networks capture downstream effects of kinase inhibition in <i>Mycobacterium tuberculosis</i> . <i>Npj Systems Biology and Applications</i> , 2021, 7, 8.	1.4	3
94	Estimating Sample-Specific Regulatory Networks. <i>SSRN Electronic Journal</i> , 0, , .	0.4	3
95	Gene regulatory network inference as relaxed graph matching. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2021, 35, 10263-10272.	3.6	3
96	Connectivity in eQTL networks dictates reproducibility and genomic properties. <i>Cell Reports Methods</i> , 2022, 2, 100218.	1.4	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. <i>Neuro-Oncology Advances</i> , 2021, 3, vdab088.	0.4	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. <i>IEEE Access</i> , 2020, 8, 67775-67789.	2.6	1
101	gpuZoo: Cost-effective estimation of gene regulatory networks using the Graphics Processing Unit. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac002.	1.5	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. <i>Genomics Data</i> , 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) Identifies Potential Novel Targets. <i>Blood</i> , 2011, 118, 761-761.	0.6	0
108	Chapter 7: On the Integration of Prior Knowledge in the Inference of Regulatory Networks. <i>Science, Engineering, and Biology Informatics</i> , 2014, , 169-199.	0.1	0

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109	Looking back at the first twenty years of genomics. <i>Quantitative Biology</i> , 2022, 10, 6-16.	0.3	0
110	AI Methods for Analyzing Microarray Data. , 0, , 877-884.		0