

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	GRAND: a database of gene regulatory network models across human conditions. <i>Nucleic Acids Research</i> , 2022, 50, D610-D621.	6.5	31
2	Looking back at the first twenty years of genomics. <i>Quantitative Biology</i> , 2022, 10, 6-16.	0.3	0
3	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
4	Predicting genotype-specific gene regulatory networks. <i>Genome Research</i> , 2022, 32, 524-533.	2.4	9
5	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
6	Connectivity in eQTL networks dictates reproducibility and genomic properties. <i>Cell Reports Methods</i> , 2022, 2, 100218.	1.4	3
7	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
8	BRCA1 and RNAi factors promote repair mediated by small RNAs and PALB2â€“RAD52. <i>Nature</i> , 2021, 591, 665-670.	13.7	30
9	Gene Targeting in Disease Networks. <i>Frontiers in Genetics</i> , 2021, 12, 649942.	1.1	11
10	Using graph convolutional neural networks to learn a representation for glycans. <i>Cell Reports</i> , 2021, 35, 109251.	2.9	25
11	Regulatory Network of PD1 Signaling Is Associated with Prognosis in Glioblastoma Multiforme. <i>Cancer Research</i> , 2021, 81, 5401-5412.	0.4	15
12	Environmental Influences Measured by Epigenetic Clock and Vulnerability Components at Birth Impact Clinical ASD Heterogeneity. <i>Genes</i> , 2021, 12, 1433.	1.0	3
13	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
14	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
15	Constructing gene regulatory networks using epigenetic data. <i>Npj Systems Biology and Applications</i> , 2021, 7, 45.	1.4	14
16	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
17	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
18	Nongenic cancer-risk SNPs affect oncogenes, tumour-suppressor genes, and immune function. <i>British Journal of Cancer</i> , 2020, 122, 569-577.	2.9	22

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19	<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
20	PUMA: PANDA Using MicroRNA Associations. <i>Bioinformatics</i> , 2020, 36, 4765-4773.	1.8	17
21	Transparency and reproducibility in artificial intelligence. <i>Nature</i> , 2020, 586, E14-E16.	13.7	233
22	Genome-Wide Sex and Gender Differences in Cancer. <i>Frontiers in Oncology</i> , 2020, 10, 597788.	1.3	64
23	Sex Differences in Gene Expression and Regulatory Networks across 29 Human Tissues. <i>Cell Reports</i> , 2020, 31, 107795.	2.9	207
24	MicroRNA-mRNA networks define translatable molecular outcome phenotypes in osteosarcoma. <i>Scientific Reports</i> , 2020, 10, 4409.	1.6	9
25	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
26	Data will Drive the Healthcare Revolution. , 2020, , .		0
27	Clustering Sparse Data With Feature Correlation With Application to Discover Subtypes in Cancer. <i>IEEE Access</i> , 2020, 8, 67775-67789.	2.6	1
28	Molecular networks in Network Medicine: Development and applications. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2020, 12, e1489.	6.6	128
29	A Novel Deep Learning Model by Stacking Conditional Restricted Boltzmann Machine and Deep Neural Network. , 2020, , .		2
30	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
31	Identification of differentially expressed gene sets using the Generalized Berkâ€“Jones statistic. <i>Bioinformatics</i> , 2019, 35, 4568-4576.	1.8	8
32	Estimating Sample-Specific Regulatory Networks. <i>IScience</i> , 2019, 14, 226-240.	1.9	120
33	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
34	lionessR: single sample network inference in R. <i>BMC Cancer</i> , 2019, 19, 1003.	1.1	26
35	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
36	Multisystem Analysis of <i>Mycobacterium tuberculosis</i> Reveals Kinase-Dependent Remodeling of the Pathogen-Environment Interface. <i>MBio</i> , 2018, 9, .	1.8	57

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37	Poly-ligand profiling differentiates trastuzumab-treated breast cancer patients according to their outcomes. <i>Nature Communications</i> , 2018, 9, 1219.	5.8	20
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	Detecting phenotype-driven transitions in regulatory network structure. <i>Npj Systems Biology and Applications</i> , 2018, 4, 16.	1.4	32
40	Data Analysis Strategies in Medical Imaging. <i>Clinical Cancer Research</i> , 2018, 24, 3492-3499.	3.2	115
41	Smooth quantile normalization. <i>Biostatistics</i> , 2018, 19, 185-198.	0.9	78
42	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
43	Gene Regulatory Network Analysis Identifies Sex-Linked Differences in Colon Cancer Drug Metabolism. <i>Cancer Research</i> , 2018, 78, 5538-5547.	0.4	81
44	Artificial intelligence in radiology. <i>Nature Reviews Cancer</i> , 2018, 18, 500-510.	12.8	1,953
45	Cancer subtype identification using somatic mutation data. <i>British Journal of Cancer</i> , 2018, 118, 1492-1501.	2.9	51
46	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
47	Histopathological Image QTL Discovery of Immune Infiltration Variants. <i>IScience</i> , 2018, 5, 80-89.	1.9	19
48	Plasma Exosome Profiling of Cancer Patients by a Next Generation Systems Biology Approach. <i>Scientific Reports</i> , 2017, 7, 42741.	1.6	38
49	Estimating gene regulatory networks with pandaR. <i>Bioinformatics</i> , 2017, 33, 2232-2234.	1.8	15
50	Biomarker correlation network in colorectal carcinoma by tumor anatomic location. <i>BMC Bioinformatics</i> , 2017, 18, 304.	1.2	18
51	Somatic Mutations Drive Distinct Imaging Phenotypes in Lung Cancer. <i>Cancer Research</i> , 2017, 77, 3922-3930.	0.4	307
52	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
53	Understanding Tissue-Specific Gene Regulation. <i>Cell Reports</i> , 2017, 21, 1077-1088.	2.9	314
54	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

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55	WebMeV: A Cloud Platform for Analyzing and Visualizing Cancer Genomic Data. <i>Cancer Research</i> , 2017, 77, e11-e14.	0.4	47
56	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
57	Challenges and emerging directions in single-cell analysis. <i>Genome Biology</i> , 2017, 18, 84.	3.8	258
58	Estimating drivers of cell state transitions using gene regulatory network models. <i>BMC Systems Biology</i> , 2017, 11, 139.	3.0	17
59	Regulatory network changes between cell lines and their tissues of origin. <i>BMC Genomics</i> , 2017, 18, 723.	1.2	51
60	Tissue-aware RNA-Seq processing and normalization for heterogeneous and sparse data. <i>BMC Bioinformatics</i> , 2017, 18, 437.	1.2	45
61	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
62	Exploratory Study to Identify Radiomics Classifiers for Lung Cancer Histology. <i>Frontiers in Oncology</i> , 2016, 6, 71.	1.3	306
63	Merkel Cell Polyomavirus Small T Antigen Promotes Pro-Glycolytic Metabolic Perturbations Required for Transformation. <i>PLoS Pathogens</i> , 2016, 12, e1006020.	2.1	60
64	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
65	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
66	DNA methylation profiling in human lung tissue identifies genes associated with COPD. <i>Epigenetics</i> , 2016, 11, 730-739.	1.3	73
67	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
68	BatchQC: interactive software for evaluating sample and batch effects in genomic data. <i>Bioinformatics</i> , 2016, 32, 3836-3838.	1.8	50
69	PyPanda: a Python package for gene regulatory network reconstruction. <i>Bioinformatics</i> , 2016, 32, 3363-3365.	1.8	15
70	Mitochondrial iron chelation ameliorates cigarette smoke-induced bronchitis and emphysema in mice. <i>Nature Medicine</i> , 2016, 22, 163-174.	15.2	206
71	Gender-Specific Molecular and Clinical Features Underlie Malignant Pleural Mesothelioma. <i>Cancer Research</i> , 2016, 76, 319-328.	0.4	73
72	Epigenetic remodeling regulates transcriptional changes between ovarian cancer and benign precursors. <i>JCI Insight</i> , 2016, 1, .	2.3	42

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73	Assessment of pharmacogenomic agreement. F1000Research, 2016, 5, 825.	0.8	34
74	Revisiting inconsistency in large pharmacogenomic studies. F1000Research, 2016, 5, 2333.	0.8	79
75	Bipartite Community Structure of eQTLs. PLoS Computational Biology, 2016, 12, e1005033.	1.5	50
76	Integrating transcriptional and protein interaction networks to prioritize condition-specific master regulators. BMC Systems Biology, 2015, 9, 80.	3.0	27
77	A network model for angiogenesis in ovarian cancer. BMC Bioinformatics, 2015, 16, 115.	1.2	60
78	High performance computing of gene regulatory networks using a message-passing model. , 2015, , .		8
79	Using shRNA experiments to validate gene regulatory networks. Genomics Data, 2015, 4, 123-126.	1.3	0
80	Haploinsufficiency of Hedgehog interacting protein causes increased emphysema induced by cigarette smoke through network rewiring. Genome Medicine, 2015, 7, 12.	3.6	61
81	Genetic control of gene expression at novel and established chronic obstructive pulmonary disease loci. Human Molecular Genetics, 2015, 24, 1200-1210.	1.4	43
82	Sexually-dimorphic targeting of functionally-related genes in COPD. BMC Systems Biology, 2014, 8, 118.	3.0	47
83	Relevance of different prior knowledge sources for inferring gene interaction networks. Frontiers in Genetics, 2014, 5, 177.	1.1	7
84	Analyzing networks of phenotypes in complex diseases: methodology and applications in COPD. BMC Systems Biology, 2014, 8, 78.	3.0	31
85	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.	0.8	18
86	Decoding tumour phenotype by noninvasive imaging using a quantitative radiomics approach. Nature Communications, 2014, 5, 4006.	5.8	3,355
87	Enhancing Reproducibility in Cancer Drug Screening: How Do We Move Forward?. Cancer Research, 2014, 74, 4016-4023.	0.4	90
88	Inference and validation of predictive gene networks from biomedical literature and gene expression data. Genomics, 2014, 103, 329-336.	1.3	40
89	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.	0.8	15
90	Comparative genome-wide transcriptional analysis of human left and right internal mammary arteries. Genomics, 2014, 104, 36-44.	1.3	13

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91	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
92	MicroRNA paraffin-based studies in osteosarcoma reveal reproducible independent prognostic profiles at 14q32. Genome Medicine, 2013, 5, 2.	3.6	96
93	Inconsistency in large pharmacogenomic studies. Nature, 2013, 504, 389-393.	13.7	467
94	Histone deacetylase mediated selective autophagy regulates COPD-associated cilia dysfunction. Journal of Clinical Investigation, 2013, 123, 5212-5230.	3.9	266
95	Passing Messages between Biological Networks to Refine Predicted Interactions. PLoS ONE, 2013, 8, e64832.	1.1	183
96	A Three-Gene Model to Robustly Identify Breast Cancer Molecular Subtypes. Journal of the National Cancer Institute, 2012, 104, 311-325.	3.0	272
97	GeneSigDB: a manually curated database and resource for analysis of gene expression signatures. Nucleic Acids Research, 2012, 40, D1060-D1066.	6.5	108
98	Angiogenic mRNA and microRNA Gene Expression Signature Predicts a Novel Subtype of Serous Ovarian Cancer. PLoS ONE, 2012, 7, e30269.	1.1	107
99	Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. Nature, 2012, 487, 491-495.	13.7	349
100	Genome-Wide Aberrant Splicing in Patients with Acute Myeloid Leukemia (AML) Identifies Potential Novel Targets. Blood, 2011, 118, 761-761.	0.6	0
101	AI Methods for Analyzing Microarray Data. , 2009, , 65-70.		0
102	Seeded Bayesian Networks: Constructing genetic networks from microarray data. BMC Systems Biology, 2008, 2, 57.	3.0	86
103	Extracting biology from high-dimensional biological data. Journal of Experimental Biology, 2007, 210, 1507-1517.	0.8	44
104	IEEE &sup>th</sup> BIBE Invited Plenary Keynote: Stochasticity and Networks in Genomic Data. , 2007, , .		0
105	Extracting meaning from functional genomics experiments. Toxicology and Applied Pharmacology, 2005, 207, 195-199.	1.3	90
106	Minimum information about a microarray experiment (MIAME) toward standards for microarray data. Nature Genetics, 2001, 29, 365-371.	9.4	3,750
107	Data, Analysis, and Standardization. , 0, , 215-229.		2
108	Variance due to Smooth Bias in Rat Liver and Kidney Baseline Gene Expression in a Large Multi-laboratory Data Set. , 0, , 87-99.		0

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109	Estimating Sample-Specific Regulatory Networks. SSRN Electronic Journal, 0, , .	0.4	3
110	AI Methods for Analyzing Microarray Data. , 0, , 877-884.		0