

John Quackenbush

List of Publications by Year in Descending Order

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

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	gpuZoo: Cost-effective estimation of gene regulatory networks using the Graphics Processing Unit.. <i>NAR Genomics and Bioinformatics</i> , 2022 , 4, lqac002	3.7	0
115	Predicting genotype-specific gene regulatory networks.. <i>Genome Research</i> , 2022 , 32, 524-533	9.7	2
114	An online notebook resource for reproducible inference, analysis and publication of gene regulatory networks.. <i>Nature Methods</i> , 2022 ,	21.6	2
113	Connectivity in eQTL networks dictates reproducibility and genomic properties. <i>Cell Reports Methods</i> , 2022 , 2, 100218		0
112	Constructing gene regulatory networks using epigenetic data. <i>Npj Systems Biology and Applications</i> , 2021 , 7, 45	5	3
111	Gene regulatory network inference as relaxed graph matching. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2021 , 35, 10263-10272	5	1
110	Gene Targeting in Disease Networks. <i>Frontiers in Genetics</i> , 2021 , 12, 649942	4.5	3
109	Using graph convolutional neural networks to learn a representation for glycans. <i>Cell Reports</i> , 2021 , 35, 109251	10.6	7
108	Analysis of morphological characteristics of IDH-mutant/wildtype brain tumors using whole-lesion phenotype analysis. <i>Neuro-Oncology Advances</i> , 2021 , 3, vdab088	0.9	1
107	BRCA1 and RNAi factors promote repair mediated by small RNAs and PALB2-RAD52. <i>Nature</i> , 2021 , 591, 665-670	50.4	12
106	Regulatory Network of PD1 Signaling Is Associated with Prognosis in Glioblastoma Multiforme. <i>Cancer Research</i> , 2021 , 81, 5401-5412	10.1	3
105	GRAND: a database of gene regulatory network models across human conditions. <i>Nucleic Acids Research</i> , 2021 ,	20.1	7
104	Multi-omic regulatory networks capture downstream effects of kinase inhibition in Mycobacterium tuberculosis. <i>Npj Systems Biology and Applications</i> , 2021 , 7, 8	5	2
103	Sex Differences in Gene Expression and Regulatory Networks across 29 Human Tissues. <i>Cell Reports</i> , 2020 , 31, 107795	10.6	67
102	MicroRNA-mRNA networks define translatable molecular outcome phenotypes in osteosarcoma. <i>Scientific Reports</i> , 2020 , 10, 4409	4.9	6
101	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	10.2	6
100	Clustering Sparse Data With Feature Correlation With Application to Discover Subtypes in Cancer. <i>IEEE Access</i> , 2020 , 8, 67775-67789	3.5	1

99	A Novel Deep Learning Model by Stacking Conditional Restricted Boltzmann Machine and Deep Neural Network 2020 ,		1
98	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	1.8	7
97	Gaussian and Mixed Graphical Models as (multi-)omics data analysis tools. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020 , 1863, 194418	6	12
96	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	4	17
95	Nongenetic cancer-risk SNPs affect oncogenes, tumour-suppressor genes, and immune function. <i>British Journal of Cancer</i> , 2020 , 122, 569-577	8.7	13
94	infection with frequent viral coinfection contributes to postinfectious hydrocephalus in Ugandan infants. <i>Science Translational Medicine</i> , 2020 , 12,	17.5	13
93	PUMA: PANDA Using MicroRNA Associations. <i>Bioinformatics</i> , 2020 , 36, 4765-4773	7.2	8
92	Transparency and reproducibility in artificial intelligence. <i>Nature</i> , 2020 , 586, E14-E16	50.4	85
91	Genome-Wide Sex and Gender Differences in Cancer. <i>Frontiers in Oncology</i> , 2020 , 10, 597788	5.3	16
90	Molecular networks in Network Medicine: Development and applications. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2020 , 12, e1489	6.6	63
89	Identification of differentially expressed gene sets using the Generalized Berk-Jones statistic. <i>Bioinformatics</i> , 2019 , 35, 4568-4576	7.2	3
88	Estimating Sample-Specific Regulatory Networks. <i>IScience</i> , 2019 , 14, 226-240	6.1	48
87	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	4.9	7
86	lionessR: single sample network inference in R. <i>BMC Cancer</i> , 2019 , 19, 1003	4.8	10
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	4.7	5
84	Multisystem Analysis of Reveals Kinase-Dependent Remodeling of the Pathogen-Environment Interface. <i>MBio</i> , 2018 , 9,	7.8	38
83	Poly-ligand profiling differentiates trastuzumab-treated breast cancer patients according to their outcomes. <i>Nature Communications</i> , 2018 , 9, 1219	17.4	14
82	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	10.2	29

81	Detecting phenotype-driven transitions in regulatory network structure. <i>Npj Systems Biology and Applications</i> , 2018 , 4, 16	5	18
80	Data Analysis Strategies in Medical Imaging. <i>Clinical Cancer Research</i> , 2018 , 24, 3492-3499	12.9	66
79	Smooth quantile normalization. <i>Biostatistics</i> , 2018 , 19, 185-198	3.7	37
78	Ensemble genomic analysis in human lung tissue identifies novel genes for chronic obstructive pulmonary disease. <i>Human Genomics</i> , 2018 , 12, 1	6.8	20
77	Histopathological Image QTL Discovery of Immune Infiltration Variants. <i>IScience</i> , 2018 , 5, 80-89	6.1	8
76	Differential connectivity of gene regulatory networks distinguishes corticosteroid response in asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2018 , 141, 1250-1258	11.5	24
75	Gene Regulatory Network Analysis Identifies Sex-Linked Differences in Colon Cancer Drug Metabolism. <i>Cancer Research</i> , 2018 , 78, 5538-5547	10.1	41
74	Artificial intelligence in radiology. <i>Nature Reviews Cancer</i> , 2018 , 18, 500-510	31.3	916
73	Cancer subtype identification using somatic mutation data. <i>British Journal of Cancer</i> , 2018 , 118, 1492-1501	17	29
72	Plasma Exosome Profiling of Cancer Patients by a Next Generation Systems Biology Approach. <i>Scientific Reports</i> , 2017 , 7, 42741	4.9	32
71	Estimating gene regulatory networks with pandaR. <i>Bioinformatics</i> , 2017 , 33, 2232-2234	7.2	8
70	Biomarker correlation network in colorectal carcinoma by tumor anatomic location. <i>BMC Bioinformatics</i> , 2017 , 18, 304	3.6	13
69	Somatic Mutations Drive Distinct Imaging Phenotypes in Lung Cancer. <i>Cancer Research</i> , 2017 , 77, 3922-3930	20	200
68	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	4.9	57
67	Understanding Tissue-Specific Gene Regulation. <i>Cell Reports</i> , 2017 , 21, 1077-1088	10.6	175
66	Tissue-aware RNA-Seq processing and normalization for heterogeneous and sparse data. <i>BMC Bioinformatics</i> , 2017 , 18, 437	3.6	31
65	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	11.5	57
64	WebMeV: A Cloud Platform for Analyzing and Visualizing Cancer Genomic Data. <i>Cancer Research</i> , 2017 , 77, e11-e14	10.1	26

63	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	22.4	26
62	Challenges and emerging directions in single-cell analysis. <i>Genome Biology</i> , 2017 , 18, 84	18.3	166
61	Estimating drivers of cell state transitions using gene regulatory network models. <i>BMC Systems Biology</i> , 2017 , 11, 139	3.5	9
60	Regulatory network changes between cell lines and their tissues of origin. <i>BMC Genomics</i> , 2017 , 18, 723	4.5	28
59	Expression Quantitative Trait loci (QTL) in tumor adjacent normal breast tissue and breast tumor tissue. <i>PLoS ONE</i> , 2017 , 12, e0170181	3.7	9
58	DNA methylation profiling in human lung tissue identifies genes associated with COPD. <i>Epigenetics</i> , 2016 , 11, 730-739	5.7	48
57	Diet-induced weight loss leads to a switch in gene regulatory network control in the rectal mucosa. <i>Genomics</i> , 2016 , 108, 126-133	4.3	11
56	BatchQC: interactive software for evaluating sample and batch effects in genomic data. <i>Bioinformatics</i> , 2016 , 32, 3836-3838	7.2	31
55	PyPanda: a Python package for gene regulatory network reconstruction. <i>Bioinformatics</i> , 2016 , 32, 3363-3365	3.65	9
54	Mitochondrial iron chelation ameliorates cigarette smoke-induced bronchitis and emphysema in mice. <i>Nature Medicine</i> , 2016 , 22, 163-74	50.5	136
53	Gender-Specific Molecular and Clinical Features Underlie Malignant Pleural Mesothelioma. <i>Cancer Research</i> , 2016 , 76, 319-28	10.1	49
52	Epigenetic remodeling regulates transcriptional changes between ovarian cancer and benign precursors. <i>JCI Insight</i> , 2016 , 1,	9.9	28
51	Assessment of pharmacogenomic agreement. <i>F1000Research</i> , 2016 , 5, 825	3.6	25
50	Revisiting inconsistency in large pharmacogenomic studies. <i>F1000Research</i> , 2016 , 5, 2333	3.6	49
49	Bipartite Community Structure of eQTLs. <i>PLoS Computational Biology</i> , 2016 , 12, e1005033	5	28
48	Exploratory Study to Identify Radiomics Classifiers for Lung Cancer Histology. <i>Frontiers in Oncology</i> , 2016 , 6, 71	5.3	211
47	Merkel Cell Polyomavirus Small T Antigen Promotes Pro-Glycolytic Metabolic Perturbations Required for Transformation. <i>PLoS Pathogens</i> , 2016 , 12, e1006020	7.6	46
46	Nac1 Coordinates a Sub-network of Pluripotency Factors to Regulate Embryonic Stem Cell Differentiation. <i>Cell Reports</i> , 2016 , 14, 1181-1194	10.6	15

45	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	10.2	73
44	Using shRNA experiments to validate gene regulatory networks. <i>Genomics Data</i> , 2015 , 4, 123-6		
43	Haploinsufficiency of Hedgehog interacting protein causes increased emphysema induced by cigarette smoke through network rewiring. <i>Genome Medicine</i> , 2015 , 7, 12	14.4	45
42	Genetic control of gene expression at novel and established chronic obstructive pulmonary disease loci. <i>Human Molecular Genetics</i> , 2015 , 24, 1200-10	5.6	33
41	Integrating transcriptional and protein interaction networks to prioritize condition-specific master regulators. <i>BMC Systems Biology</i> , 2015 , 9, 80	3.5	18
40	A network model for angiogenesis in ovarian cancer. <i>BMC Bioinformatics</i> , 2015 , 16, 115	3.6	47
39	High performance computing of gene regulatory networks using a message-passing model 2015 ,		3
38	Decoding tumour phenotype by noninvasive imaging using a quantitative radiomics approach. <i>Nature Communications</i> , 2014 , 5, 4006	17.4	2330
37	Enhancing reproducibility in cancer drug screening: how do we move forward?. <i>Cancer Research</i> , 2014 , 74, 4016-23	10.1	64
36	Inference and validation of predictive gene networks from biomedical literature and gene expression data. <i>Genomics</i> , 2014 , 103, 329-36	4.3	28
35	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, 843-52	3	13
34	Comparative genome-wide transcriptional analysis of human left and right internal mammary arteries. <i>Genomics</i> , 2014 , 104, 36-44	4.3	9
33	Sexually-dimorphic targeting of functionally-related genes in COPD. <i>BMC Systems Biology</i> , 2014 , 8, 118	3.5	38
32	Relevance of different prior knowledge sources for inferring gene interaction networks. <i>Frontiers in Genetics</i> , 2014 , 5, 177	4.5	5
31	Analyzing networks of phenotypes in complex diseases: methodology and applications in COPD. <i>BMC Systems Biology</i> , 2014 , 8, 78	3.5	26
30	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, 327-36	2.8	15
29	Chapter 7: On the Integration of Prior Knowledge in the Inference of Regulatory Networks. <i>Science, Engineering, and Biology Informatics</i> , 2014 , 169-199		
28	MicroRNA paraffin-based studies in osteosarcoma reveal reproducible independent prognostic profiles at 14q32. <i>Genome Medicine</i> , 2013 , 5, 2	14.4	69

27	Inconsistency in large pharmacogenomic studies. <i>Nature</i> , 2013 , 504, 389-93	50.4	360
26	Histone deacetylase 6-mediated selective autophagy regulates COPD-associated cilia dysfunction. <i>Journal of Clinical Investigation</i> , 2013 , 123, 5212-30	15.9	210
25	Passing messages between biological networks to refine predicted interactions. <i>PLoS ONE</i> , 2013 , 8, e64832	9.7	108
24	Angiogenic mRNA and microRNA gene expression signature predicts a novel subtype of serous ovarian cancer. <i>PLoS ONE</i> , 2012 , 7, e30269	3.7	84
23	Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. <i>Nature</i> , 2012 , 487, 491-5	50.4	294
22	A three-gene model to robustly identify breast cancer molecular subtypes. <i>Journal of the National Cancer Institute</i> , 2012 , 104, 311-25	9.7	218
21	GeneSigDB: a manually curated database and resource for analysis of gene expression signatures. <i>Nucleic Acids Research</i> , 2012 , 40, D1060-6	20.1	89
20	Genome-Wide Aberrant Splicing in Patients with Acute Myeloid Leukemia (AML) Identifies Potential Novel Targets. <i>Blood</i> , 2011 , 118, 761-761	2.2	
19	AI Methods for Analyzing Microarray Data 2009 , 65-70		
18	Seeded Bayesian Networks: constructing genetic networks from microarray data. <i>BMC Systems Biology</i> , 2008 , 2, 57	3.5	71
17	Extracting biology from high-dimensional biological data. <i>Journal of Experimental Biology</i> , 2007 , 210, 1507-17	3	38
16	Extracting meaning from functional genomics experiments. <i>Toxicology and Applied Pharmacology</i> , 2005 , 207, 195-9	4.6	81
15	Minimum information about a microarray experiment (MIAME)-toward standards for microarray data. <i>Nature Genetics</i> , 2001 , 29, 365-71	36.3	3326
14	Data, Analysis, and Standardization215-229		1
13	Variance due to Smooth Bias in Rat Liver and Kidney Baseline Gene Expression in a Large Multi-laboratory Data Set87-99		
12	Estimating Sample-Specific Regulatory Networks. <i>SSRN Electronic Journal</i> ,	1	2
11	The impact of stroma on the discovery of molecular subtypes and prognostic gene signatures in serous ovarian cancer		1
10	Spectral clustering in regression-based biological networks		1

9	Tissue-aware RNA-Seq processing and normalization for heterogeneous and sparse data	6
8	Smooth Quantile Normalization	6
7	Understanding Tissue-specific Gene Regulation	1
6	Gene Regulatory Network Inference as Relaxed Graph Matching	2
5	Histopathological image QTL discovery of immune infiltration variants	1
4	GRAND: A database of gene regulatory network models across human conditions	2
3	Regulation of PD1 signaling is associated with prognosis in glioblastoma multiforme	3
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1	AI Methods for Analyzing Microarray Data877-884	