Xing Qiu

List of Publications by Year
in descending order

100 papers	2,531 citations	201674 27 h-index	223800 46 g-index
116 all docs	116 docs citations	116 times ranked	4141 citing authors

#	Article	IF	Citations
1	Genomic Analysis of *Clostridioides difficile* in 2 Regions of the United States Reveals a Diversity of Strains and Limited Transmission. Journal of Infectious Diseases, 2022, 225, 121-129.	4.0	2
2	Identifiability analysis of linear ordinary differential equation systems with a single trajectory. Applied Mathematics and Computation, 2022, 430, 127260.	2.2	0
3	Airway Gene Expression Correlates of Respiratory Syncytial Virus Disease Severity and Microbiome Composition in Infants. Journal of Infectious Diseases, 2021, 223, 1639-1649.	4.0	17
4	Whole‐brain computational modeling reveals disruption of microscale brain dynamics in HIV infected individuals. Human Brain Mapping, 2021, 42, 95-109.	3.6	5
5	Increased risk for cerebral small vessel disease is associated with quantitative susceptibility mapping in HIV infected and uninfected individuals. NeuroImage: Clinical, 2021, 32, 102786.	2.7	8
6	Mitochondrial toxicity before and after combination antiretroviral therapy, a Magnetic Resonance Spectroscopy study. NeuroImage: Clinical, 2021, 31, 102693.	2.7	1
7	Airway gene-expression classifiers for respiratory syncytial virus (RSV) disease severity in infants. BMC Medical Genomics, 2021, 14, 57.	1.5	5
8	Super-delta2: an enhanced differential expression analysis procedure for multi-group comparisons of RNA-seq data. Bioinformatics, 2021, 37, 2627-2636.	4.1	5
9	Functional MRI Correlates of Sleep Quality in HIV. Nature and Science of Sleep, 2021, Volume 13, 291-301.	2.7	5
10	A longitudinal analysis of brain extracellular free water in HIV infected individuals. Scientific Reports, 2021, 11, 8273.	3.3	7
11	CX3CR1 Engagement by Respiratory Syncytial Virus Leads to Induction of Nucleolin and Dysregulation of Cilium-Related Genes. Journal of Virology, 2021, 95, .	3.4	14
12	Fixel-Based Analysis and Free Water Corrected DTI Evaluation of HIV-Associated Neurocognitive Disorders. Frontiers in Neurology, 2021, 12, 725059.	2.4	7
13	Biological Network Inference With GRASP: A Bayesian Network Structure Learning Method Using Adaptive Sequential Monte Carlo. Frontiers in Genetics, 2021, 12, 764020.	2.3	1
14	A systems genomics approach uncovers molecular associates of RSV severity. PLoS Computational Biology, 2021, 17, e1009617.	3.2	3
15	MatchMixeR: a cross-platform normalization method for gene expression data integration. Bioinformatics, 2020, 36, 2486-2491.	4.1	10
16	Spatial regression analysis of MR diffusion reveals subject-specific white matter changes associated with repetitive head impacts in contact sports. Scientific Reports, 2020, 10, 13606.	3.3	6
17	Unbiased analysis of peripheral blood mononuclear cells reveals CD4 T cell response to RSV matrix protein. Vaccine: X, 2020, 5, 100065.	2.1	0
18	Pathomechanisms of HIV-Associated Cerebral Small Vessel Disease: A Comprehensive Clinical and Neuroimaging Protocol and Analysis Pipeline. Frontiers in Neurology, 2020, 11, 595463.	2.4	6

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19	Correlation Between the True and False Discoveries in a Positively Dependent Multiple Comparison Problem. , 2020, , 63-79.		0
20	Abstract TP477: Vessel Diameter, Brain Perfusion and Small Vessel Disease Burden in HIV+ Population and Controls. Stroke, 2020, 51, .	2.0	0
21	Genomic analysis of Clostridioides difficile in two regions reveals a diversity of strains and limited transmission. Infection Control and Hospital Epidemiology, 2020, 41, s237-s238.	1.8	0
22	1409. Genomic Variation Among Respiratory Syncytial Viruses. Open Forum Infectious Diseases, 2020, 7, S712-S712.	0.9	0
23	133. validation of a Global Respiratory Severity Score in Infants with Primary RSV Infection. Open Forum Infectious Diseases, 2020, 7, S196-S197.	0.9	0
24	Measuring the Severity of Respiratory Illness in the First 2 Years of Life in Preterm and Term Infants. Journal of Pediatrics, 2019, 214, 12-19.e3.	1.8	3
25	Microbiome-Transcriptome Interactions Related to Severity of Respiratory Syncytial Virus Infection. Scientific Reports, 2019, 9, 13824.	3.3	30
26	Skeletal muscle mitoflashes, pH, and the role of uncoupling protein-3. Archives of Biochemistry and Biophysics, 2019, 663, 239-248.	3.0	10
27	Differences in the influenza-specific CD4 T cell immunodominance hierarchy and functional potential between children and young adults. Scientific Reports, 2019, 9, 791.	3.3	12
28	Highly efficient hypothesis testing methods for regression-type tests with correlated observations and heterogeneous variance structure. BMC Bioinformatics, 2019, 20, 185.	2.6	3
29	Restructured GEO: restructuring Gene Expression Omnibus metadata for genome dynamics analysis. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	17
30	415. Airway Gene-Expression Classifiers for Respiratory Syncytial Virus (RSV) Disease Severity in Infants. Open Forum Infectious Diseases, 2019, 6, S210-S210.	0.9	0
31	Comparison of the Michigan Hand Outcomes Questionnaire, Boston Carpal Tunnel Questionnaire, and PROMIS Instruments in Carpal Tunnel Syndrome. Journal of Hand Surgery, 2019, 44, 366-373.	1.6	17
32	Senescent Phenotype Induced by p90RSK-NRF2 Signaling Sensitizes Monocytes and Macrophages to Oxidative Stress in HIV-Positive Individuals. Circulation, 2019, 139, 1199-1216.	1.6	45
33	Parameter Estimation and Variable Selection for Big Systems of Linear Ordinary Differential Equations: A Matrix-Based Approach. Journal of the American Statistical Association, 2019, 114, 657-667.	3.1	11
34	Aims, Study Design, and Enrollment Results From the Assessing Predictors of Infant Respiratory Syncytial Virus Effects and Severity Study. JMIR Research Protocols, 2019, 8, e12907.	1.0	9
35	Alteration of brain network topology in HIV-associated neurocognitive disorder: A novel functional connectivity perspective. NeuroImage: Clinical, 2018, 17, 768-777.	2.7	37
36	Virus-Specific Antibody, Viral Load, and Disease Severity in Respiratory Syncytial Virus Infection. Journal of Infectious Diseases, 2018, 218, 208-217.	4.0	34

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37	Neonatal gut and respiratory microbiota: coordinated development through time and space. Microbiome, 2018, 6, 193.	11.1	68
38	Some equivalence relationships of regularized regressions. Mathematics for Applications, 2018, 7, 3-10.	0.3	2
39	Development of a Global Respiratory Severity Score (GRSS) for Respiratory Syncytial Virus Infection in Infants. Journal of Infectious Diseases, 2017, 215, jiw624.	4.0	32
40	FUNNEL-GSEA: FUNctioNal ELastic-net regression in time-course gene set enrichment analysis. Bioinformatics, 2017, 33, 1944-1952.	4.1	27
41	Association of Dynamic Changes in the CD4 T-Cell Transcriptome With Disease Severity During Primary Respiratory Syncytial Virus Infection in Young Infants. Journal of Infectious Diseases, 2017, 216, 1027-1037.	4.0	17
42	The preliminary radiogenomics association between MR perfusion imaging parameters and genomic biomarkers, and their predictive performance of overall survival in patients with glioblastoma. Journal of Neuro-Oncology, 2017, 135, 553-560.	2.9	24
43	Comparison of the Michigan Hand Outcomes Questionnaire, Boston Carpal Tunnel Questionnaire, and PROMIS Instruments in Carpal Tunnel Syndrome. Journal of Hand Surgery, 2017, 42, S2.	1.6	0
44	Combination antiretroviral therapy improves cognitive performance and functional connectivity in treatment-naïve HIV-infected individuals. Journal of NeuroVirology, 2017, 23, 704-712.	2.1	44
45	Frontline Science: c-Myc regulates P-selectin glycoprotein ligand-1 expression in monocytes during HIV-1 infection. Journal of Leukocyte Biology, 2017, 102, 953-964.	3.3	8
46	The Uniform Pattern of Growth and Skeletal Maturation during the Human Adolescent Growth Spurt. Scientific Reports, 2017, 7, 16705.	3.3	97
47	Impact of prematurity and nutrition on the developing gut microbiome and preterm infant growth. Microbiome, 2017, 5, 158.	11.1	115
48	Super-delta: a new differential gene expression analysis procedure with robust data normalization. BMC Bioinformatics, 2017, 18, 582.	2.6	10
49	Selective pre-priming of HA-specific CD4 T cells restores immunological reactivity to HA on heterosubtypic influenza infection. PLoS ONE, 2017, 12, e0176407.	2.5	7
50	High-dimensional linear state space models for dynamic microbial interaction networks. PLoS ONE, 2017, 12, e0187822.	2.5	9
51	Moments of Distance from a Vertex to a Uniformly Distributed Random Point within Arbitrary Triangles. Mathematical Problems in Engineering, 2016, 2016, 1-10.	1.1	3
52	Improved spatial regression analysis of diffusion tensor imaging for lesion detection during longitudinal progression of multiple sclerosis in individual subjects. Physics in Medicine and Biology, 2016, 61, 2497-2513.	3.0	4
53	Total Hip Arthroplasty for Femoral Neck Fractures: Improved Outcomes With Higher Hospital Volumes. Journal of Orthopaedic Trauma, 2016, 30, 597-604.	1.4	31
54	Controllability and stability analysis of large transcriptomic dynamic systems for host response to influenza infection in human. Infectious Disease Modelling, 2016, 1, 52-70.	1.9	9

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55	The Healthy Infant Nasal Transcriptome: A Benchmark Study. Scientific Reports, 2016, 6, 33994.	3.3	25
56	Spatial regression analysis of serial DTI for subject-specific longitudinal changes of neurodegenerative disease. NeuroImage: Clinical, 2016, 11, 291-301.	2.7	4
57	Ion-Current-Based Temporal Proteomic Profiling of Influenza-A-Virus-Infected Mouse Lungs Revealed Underlying Mechanisms of Altered Integrity of the Lung Microvascular Barrier. Journal of Proteome Research, 2016, 15, 540-553.	3.7	11
58	Diversity in Compartmental Dynamics of Gene Regulatory Networks: The Immune Response in Primary Influenza A Infection in Mice. PLoS ONE, 2015, 10, e0138110.	2.5	8
59	Reducing Prenatal Phthalate Exposure Through Maternal Dietary Changes: Results from a Pilot Study. Maternal and Child Health Journal, 2015, 19, 1936-1942.	1.5	19
60	Platelet Activation in Human Immunodeficiency Virus Type-1 Patients Is Not Altered with Cocaine Abuse. PLoS ONE, 2015, 10, e0130061.	2.5	7
61	A New Information Criterion Based on Langevin Mixture Distribution for Clustering Circular Data with Application to Time Course Genomic Data. Statistica Sinica, 2015, , .	0.3	2
62	Modeling Genome-Wide Dynamic Regulatory Network in Mouse Lungs with Influenza Infection Using High-Dimensional Ordinary Differential Equations. PLoS ONE, 2014, 9, e95276.	2.5	16
63	Evaluation of Bias-Variance Trade-Off for Commonly Used Post-Summarizing Normalization Procedures in Large-Scale Gene Expression Studies. PLoS ONE, 2014, 9, e99380.	2.5	14
64	Using the Health Belief Model to Illustrate Factors That Influence Risk Assessment during Pregnancy and Implications for Prenatal Education about Endocrine Disruptors. Policy Futures in Education, 2014, 12, 961-974.	1.8	14
65	ERK5 Activation in Macrophages Promotes Efferocytosis and Inhibits Atherosclerosis. Circulation, 2014, 130, 180-191.	1.6	61
66	Intima modifier locus 2 controls endothelial cell activation and vascular permeability. Physiological Genomics, 2014, 46, 624-633.	2.3	4
67	The impact of quantile and rank normalization procedures on the testing power of gene differential expression analysis. BMC Bioinformatics, 2013, 14, 124.	2.6	64
68	SPatial REgression Analysis of Diffusion tensor imaging (SPREAD) for longitudinal progression of neurodegenerative disease in individual subjects. Magnetic Resonance Imaging, 2013, 31, 1657-1667.	1.8	10
69	Gene Selection with the Î´-Sequence Method. Methods in Molecular Biology, 2013, 972, 57-71.	0.9	1
70	High-Resolution Temporal Response Patterns to Influenza Vaccine Reveal a Distinct Human Plasma Cell Gene Signature. Scientific Reports, 2013, 3, 2327.	3.3	70
71	High-Dimensional Ordinary Differential Equation Models for Reconstructing Genome-Wide Dynamic Regulatory Networks. Springer Proceedings in Mathematics and Statistics, 2013, , 173-190.	0.2	2
72	Ribosomal Protein L17, RpL17, is an Inhibitor of Vascular Smooth Muscle Growth and Carotid Intima Formation. Circulation, 2012, 126, 2418-2427.	1.6	50

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73	Identical De Novo Mutation in the Type 1 Ryanodine Receptor Gene Associated With Fatal, Stress-Induced Malignant Hyperthermia in Two Unrelated Families. Survey of Anesthesiology, 2012, 56, 156-157.	0.1	1
74	Functionally Distinct Subpopulations of CpG-Activated Memory B Cells. Scientific Reports, 2012, 2, 345.	3.3	21
75	Hyperintensity on diffusion weighted image along ipsilateral cortical spinal tract after cerebral ischemic stroke: A diffusion tensor analysis. European Journal of Radiology, 2012, 81, 292-297.	2.6	20
76	Correlation Analysis of Quantitative Diffusion Parameters in Ipsilateral Cerebral Peduncle during Wallerian Degeneration with Motor Function Outcome after Cerebral Ischemic Stroke. Journal of Neuroimaging, 2012, 22, 255-260.	2.0	17
77	Quantification of accuracy and precision of multi-center DTI measurements: A diffusion phantom and human brain study. NeuroImage, 2011, 56, 1398-1411.	4.2	130
78	Identical de novoÂ Mutation in the Type 1 Ryanodine Receptor Gene Associated with Fatal, Stress-induced Malignant Hyperthermia in Two Unrelated Families. Anesthesiology, 2011, 115, 938-945.	2.5	83
79	Hierarchical Parallelization of Gene Differential Association Analysis. BMC Bioinformatics, 2011, 12, 374.	2.6	2
80	HER2 amplification, overexpression and score criteria in esophageal adenocarcinoma. Modern Pathology, 2011, 24, 899-907.	5.5	72
81	MR diffusion tensor and perfusion-weighted imaging in preoperative grading of supratentorial nonenhancing gliomas. Neuro-Oncology, 2011, 13, 447-455.	1.2	87
82	Comparison of the Paley Method Using Chronological Age with Use of Skeletal Maturity for Predicting Mature Limb Length in Children. Journal of Bone and Joint Surgery - Series A, 2011, 93, 1051-1056.	3.0	37
83	Are Endoscopic Therapies Appropriate for Superficial Submucosal Esophageal Adenocarcinoma? An Analysis of Esophagectomy Specimens. Journal of the American College of Surgeons, 2010, 210, 418-427.	0.5	172
84	A new gene selection procedure based on the covariance distance. Bioinformatics, 2010, 26, 348-354.	4.1	20
85	Genomic Responses from the Estrogen-responsive Element-dependent Signaling Pathway Mediated by Estrogen Receptor Î± Are Required to Elicit Cellular Alterations. Journal of Biological Chemistry, 2009, 284, 15277-15288.	3.4	21
86	Detecting intergene correlation changes in microarray analysis: a new approach to gene selection. BMC Bioinformatics, 2009, 10, 20.	2.6	66
87	Does the Value of PET-CT Extend Beyond Pretreatment Staging? An Analysis of Survival in Surgical Patients with Esophageal Cancer. Journal of Gastrointestinal Surgery, 2009, 13, 2121-2127.	1.7	19
88	Cobb Angle Progression in Adolescent Scoliosis Begins at the Intervertebral Disc. Spine, 2009, 34, 2782-2786.	2.0	63
89	TESTING DIFFERENTIAL EXPRESSION IN NONOVERLAPPING GENE PAIRS: A NEW PERSPECTIVE FOR THE EMPIRICAL BAYES METHOD. Journal of Bioinformatics and Computational Biology, 2008, 06, 301-316.	0.8	7
90	Gene expression profiling reveals that the regulation of estrogen-responsive element-independent genes by 17Î²-estradiol-estrogen receptor Î² is uncoupled from the induction of phenotypic changes in cell models. Journal of Molecular Endocrinology, 2008, 40, 211-229.	2.5	10

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91	Discussion of: Treeletsâ€"An adaptive multi-scale basis for sparse unordered data. Annals of Applied Statistics, 2008, 2, .	1.1	0
92	COMMENTS ON PROBABILISTIC MODELS BEHIND THE CONCEPT OF FALSE DISCOVERY RATE. Journal of Bioinformatics and Computational Biology, 2007, 05, 963-975.	0.8	4
93	Control of the mean number of false discoveries, Bonferroni and stability of multiple testing. Annals of Applied Statistics, 2007, 1, .	1.1	115
94	Statistical methods and microarray data. Nature Biotechnology, 2007, 25, 25-26.	17.5	43
95	SOME COMMENTS ON INSTABILITY OF FALSE DISCOVERY RATE ESTIMATION. Journal of Bioinformatics and Computational Biology, 2006, 04, 1057-1068.	0.8	33
96	Utility of correlation measures in analysis of gene expression. NeuroRx, 2006, 3, 384-395.	6.0	32
97	Assessing stability of gene selection in microarray data analysis. BMC Bioinformatics, 2006, 7, 50.	2.6	66
98	Utility of correlation measures in analysis of gene expression. Neurotherapeutics, 2006, 3, 384-395.	4.4	0
99	The effects of normalization on the correlation structure of microarray data. BMC Bioinformatics, 2005, 6, 120.	2.6	89
100	Correlation Between Gene Expression Levels and Limitations of the Empirical Bayes Methodology for Finding Differentially Expressed Genes. Statistical Applications in Genetics and Molecular Biology, 2005, 4, Article34.	0.6	75