Guanghua Xiao

List of Publications by Year
in descending order

84 papers	3,833 citations	126907 33 h-index	144013 57 g-index
97 all docs	97 docs citations	97 times ranked	8964 citing authors

#	Article	IF	Citations
1	A community computational challenge to predict the activity of pairs of compounds. Nature Biotechnology, 2014, 32, 1213-1222.	17.5	264
2	Pathology Image Analysis Using Segmentation Deep Learning Algorithms. American Journal of Pathology, 2019, 189, 1686-1698.	3.8	232
3	A 12-Gene Set Predicts Survival Benefits from Adjuvant Chemotherapy in Non–Small Cell Lung Cancer Patients. Clinical Cancer Research, 2013, 19, 1577-1586.	7.0	226
4	Comparing Statistical Methods for Constructing Large Scale Gene Networks. PLoS ONE, 2012, 7, e29348.	2.5	156
5	Artificial Intelligence in Lung Cancer Pathology Image Analysis. Cancers, 2019, 11, 1673.	3.7	152
6	Comprehensive Computational Pathological Image Analysis Predicts Lung Cancer Prognosis. Journal of Thoracic Oncology, 2017, 12, 501-509.	1.1	138
7	Development and Validation of a Nomogram Prognostic Model for SCLC Patients. Journal of Thoracic Oncology, 2018, 13, 1338-1348.	1.1	138
8	Beclin 2 Functions in Autophagy, Degradation of G Protein-Coupled Receptors, and Metabolism. Cell, 2013, 154, 1085-1099.	28.9	130
9	Increased autophagy blocks HER2-mediated breast tumorigenesis. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4176-4181.	7.1	106
10	Decreased BECN1 mRNA Expression in Human Breast Cancer is Associated With Estrogen Receptor-Negative Subtypes and Poor Prognosis. EBioMedicine, 2015, 2, 255-263.	6.1	95
11	Prediction of human population responses to toxic compounds by a collaborative competition. Nature Biotechnology, 2015, 33, 933-940.	17.5	88
12	Computational Staining of Pathology Images to Study the Tumor Microenvironment in Lung Cancer. Cancer Research, 2020, 80, 2056-2066.	0.9	88
13	Review of Biological Network Data and Its Applications. Genomics and Informatics, 2013, 11, 200.	0.8	79
14	LCE: an open web portal to explore gene expression and clinical associations in lung cancer. Oncogene, 2019, 38, 2551-2564.	5.9	78
15	Comprehensive analysis of lung cancer pathology images to discover tumor shape and boundary features that predict survival outcome. Scientific Reports, 2018, 8, 10393.	3.3	77
16	Validation of a Serum Screen for Alzheimer's Disease Across Assay Platforms, Species, and Tissues. Journal of Alzheimer's Disease, 2014, 42, 1325-1335.	2.6	73
17	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. Nature Communications, 2016, 7, 12460.	12.8	73
18	eIF5B drives integrated stress response-dependent translation of PD-L1 in lung cancer. Nature Cancer, 2020, 1, 533-545.	13.2	73

#	Article	IF	Citations
19	Enhanced construction of gene regulatory networks using hub gene information. BMC Bioinformatics, 2017, 18, 186.	2.6	71
20	KDM4/JMJD2 Histone Demethylase Inhibitors Block Prostate Tumor Growth by Suppressing the Expression of AR and BMYB-Regulated Genes. Chemistry and Biology, 2015, 22, 1185-1196.	6.0	66
21	ConvPath: A software tool for lung adenocarcinoma digital pathological image analysis aided by a convolutional neural network. EBioMedicine, 2019, 50, 103-110.	6.1	66
22	Design and bioinformatics analysis of genome-wide CLIP experiments. Nucleic Acids Research, 2015, 43, 5263-5274.	14.5	65
23	Evaluation of the 7th and 8th editions of the AJCC/UICC TNM staging systems for lung cancer in a large North American cohort. Oncotarget, 2017, 8, 66784-66795.	1.8	63
24	Sorting nexin 5 mediates virus-induced autophagy and immunity. Nature, 2021, 589, 456-461.	27.8	61
25	A comparative study of rank aggregation methods for partial and top ranked lists in genomic applications. Briefings in Bioinformatics, 2019, 20, 178-189.	6.5	56
26	Mice With Increased Numbers of Polyploid Hepatocytes Maintain Regenerative Capacity But Develop Fewer Hepatocellular Carcinomas Following Chronic Liver Injury. Gastroenterology, 2020, 158, 1698-1712.e14.	1.3	55
27	Autophagy is required for G1/G0quiescence in response to nitrogen starvation inSaccharomyces cerevisiae. Autophagy, 2014, 10, 1702-1711.	9.1	54
28	VAMPr: VAriant Mapping and Prediction of antibiotic resistance via explainable features and machine learning. PLoS Computational Biology, 2020, 16, e1007511.	3.2	50
29	Tumor-suppressor function of Beclin 1 in breast cancer cells requires E-cadherin. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	50
30	TLR9 and beclinÂ1 crosstalk regulates muscle AMPK activation in exercise. Nature, 2020, 578, 605-609.	27.8	46
31	Cell-autonomous immune gene expression is repressed in pulmonary neuroendocrine cells and small cell lung cancer. Communications Biology, 2021, 4, 314.	4.4	44
32	SHOX2 is a Potent Independent Biomarker to Predict Survival of WHO Grade IIâ€"III Diffuse Gliomas. EBioMedicine, 2016, 13, 80-89.	6.1	43
33	Multisite evaluations of a T 2 â€relaxationâ€underâ€spinâ€tagging (TRUST) MRI technique to measure brain oxygenation. Magnetic Resonance in Medicine, 2016, 75, 680-687.	3.0	42
34	Interaction between the autophagy protein Beclin 1 and Na+,K+-ATPase during starvation, exercise, and ischemia. JCI Insight, 2020, 5, .	5.0	37
35	The role of homeostatic regulation between tumor suppressor DAB2IP and oncogenic Skp2 in prostate cancer growth. Oncotarget, 2014, 5, 6425-6436.	1.8	35
36	Genetic and Epigenetic Features of Rapidly Progressing IDH-Mutant Astrocytomas. Journal of Neuropathology and Experimental Neurology, 2018, 77, 542-548.	1.7	34

#	Article	IF	Citations
37	Automatic extraction of cell nuclei from H&E-stained histopathological images. Journal of Medical Imaging, 2017, 4, 027502.	1.5	32
38	Microvessel prediction in H&E Stained Pathology Images using fully convolutional neural networks. BMC Bioinformatics, 2018, 19, 64.	2.6	32
39	Histone lysine demethylase KDM4B regulates the alternative splicing of the androgen receptor in response to androgen deprivation. Nucleic Acids Research, 2019, 47, 11623-11636.	14.5	30
40	GeNeCK: a web server for gene network construction and visualization. BMC Bioinformatics, 2019, 20, 12.	2.6	29
41	A permutation-based non-parametric analysis of CRISPR screen data. BMC Genomics, 2017, 18, 545.	2.8	26
42	Dysfunctional adaptive immune response in adolescents and young adults with suicide behavior. Psychoneuroendocrinology, 2020, 111, 104487.	2.7	26
43	Ensemble-Based Network Aggregation Improves the Accuracy of Gene Network Reconstruction. PLoS ONE, 2014, 9, e106319.	2.5	26
44	A deep learning-based model for screening and staging pneumoconiosis. Scientific Reports, 2021, 11, 2201.	3.3	24
45	A Model-Based Approach to Identify Binding Sites in CLIP-Seq Data. PLoS ONE, 2014, 9, e93248.	2.5	22
46	STING controls energy stress-induced autophagy and energy metabolism via STX17. Journal of Cell Biology, 2022, 221, .	5.2	21
47	Modeling Three-Dimensional Chromosome Structures Using Gene Expression Data. Journal of the American Statistical Association, 2011, 106, 61-72.	3.1	20
48	Identifying CDKN3 Gene Expression as a Prognostic Biomarker in Lung Adenocarcinoma via Meta-analysis. Cancer Informatics, 2015, 14s2, CIN.S17287.	1.9	19
49	A Community Challenge for Inferring Genetic Predictors of Gene Essentialities through Analysis of a Functional Screen of Cancer Cell Lines. Cell Systems, 2017, 5, 485-497.e3.	6.2	19
50	Type and case volume of health care facility influences survival and surgery selection in cases with early‐stage non–small cell lung cancer. Cancer, 2019, 125, 4252-4259.	4.1	19
51	Modeling Three-Dimensional Chromosome Structures Using Gene Expression Data. Journal of the American Statistical Association, 2011, 106, 61-72.	3.1	19
52	A Bayesian hidden Potts mixture model for analyzing lung cancer pathology images. Biostatistics, 2019, 20, 565-581.	1.5	17
53	A Bayesian zero-inflated negative binomial regression model for the integrative analysis of microbiome data. Biostatistics, 2021, 22, 522-540.	1.5	17
54	Large-Scale Profiling of RBP-circRNA Interactions from Public CLIP-Seq Datasets. Genes, 2020, 11, 54.	2.4	17

#	Article	IF	Citations
55	Main bronchus location is a predictor for metastasis and prognosis in lung adenocarcinoma: A large cohort analysis. Lung Cancer, 2018, 120, 22-26.	2.0	16
56	Adaptive Prediction Model in Prospective Molecular Signature–Based Clinical Studies. Clinical Cancer Research, 2014, 20, 531-539.	7.0	15
57	MB-GAN: Microbiome Simulation via Generative Adversarial Network. GigaScience, 2021, 10, .	6.4	14
58	Systematic Analysis of Gene Expression in Lung Adenocarcinoma and Squamous Cell Carcinoma with a Case Study of FAM83A and FAM83B. Cancers, 2019, 11, 886.	3.7	13
59	Validation of the 12-gene Predictive Signature for Adjuvant Chemotherapy Response in Lung Cancer. Clinical Cancer Research, 2019, 25, 150-157.	7.0	13
60	HARMONIES: A Hybrid Approach for Microbiome Networks Inference via Exploiting Sparsity. Frontiers in Genetics, 2020, 11, 445.	2.3	12
61	Statistical completion of a partially identified graph with applications for the estimation of gene regulatory networks. Biostatistics, 2015, 16, 670-685.	1.5	11
62	Lung Cancer Pathological Image Analysis Using a Hidden Potts Model. Cancer Informatics, 2017, 16, 117693511771191.	1.9	10
63	Development and Validation of a Nomogram Prognostic Model for Patients With Advanced Non-Small-Cell Lung Cancer. Cancer Informatics, 2019, 18, 117693511983754.	1.9	10
64	Deep Learning of Rhabdomyosarcoma Pathology Images for Classification and Survival Outcome Prediction. American Journal of Pathology, 2022, 192, 917-925.	3.8	10
65	DIGREM: an integrated web-based platform for detecting effective multi-drug combinations. Bioinformatics, 2019, 35, 1792-1794.	4.1	8
66	Development and Validation of a Pathology Image Analysis-based Predictive Model for Lung Adenocarcinoma Prognosis - A Multi-cohort Study. Scientific Reports, 2019, 9, 6886.	3.3	8
67	Bayesian multiple instance regression for modeling immunogenic neoantigens. Statistical Methods in Medical Research, 2020, 29, 3032-3047.	1.5	8
68	Evaluating short-term forecasting of COVID-19 cases among different epidemiological models under a Bayesian framework. GigaScience, 2021, 10, .	6.4	8
69	A Bayesian mark interaction model for analysis of tumor pathology images. Annals of Applied Statistics, 2019, 13, 1708-1732.	1.1	8
70	iScreen: Image-Based High-Content RNAi Screening Analysis Tools. Journal of Biomolecular Screening, 2015, 20, 998-1002.	2.6	6
71	A two-stage approach of gene network analysis for high-dimensional heterogeneous data. Biostatistics, 2018, 19, 216-232.	1.5	6
72	Development of a Data Model and Data Commons for Germ Cell Tumors. JCO Clinical Cancer Informatics, 2020, 4, 555-566.	2.1	6

#	Article	IF	Citations
73	Usefulness of a Simple Algorithm to Identify Hypertensive Patients Who Benefit from Intensive Blood Pressure Lowering. American Journal of Cardiology, 2018, 122, 248-254.	1.6	5
74	Molecular Markers of Carcinogenesis for Risk Stratification of Individuals with Colorectal Polyps: A Case–Control Study. Cancer Prevention Research, 2014, 7, 1023-1034.	1.5	4
75	Assessing consistency across functional screening datasets in cancer cells. Bioinformatics, 2021, 37, 4540-4547.	4.1	4
76	Fused lasso regression for identifying differential correlations in brain connectome graphs. Statistical Analysis and Data Mining, 2018, 11, 203-226.	2.8	3
77	Molecular differences across invasive lung adenocarcinoma morphological subgroups. Translational Lung Cancer Research, 2020, 9, 1029-1040.	2.8	3
78	Bayesian Joint Analysis of Gene Expression Data and Gene Functional Annotations. Statistics in Biosciences, 2012, 4, 300-318.	1.2	2
79	SCT Promoter Methylation Is a Highly Discriminative Biomarker for Lung and Many Other Cancers. IEEE Life Sciences Letters, 2015, 1, 30-33.	1.2	2
80	Integrating germline and somatic genetics to identify genes associated with lung cancer. Genetic Epidemiology, 2020, 44, 233-247.	1.3	2
81	Integrative Analysis of Gene Networks and Their Application to Lung Adenocarcinoma Studies. Cancer Informatics, 2017, 16, 117693511769077.	1.9	1
82	MetaPrism: A versatile toolkit for joint taxa/gene analysis of metagenomic sequencing data. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	1
83	Lung Cancer Computational Biology and Resources. Cold Spring Harbor Perspectives in Medicine, 2022, 12, a038273.	6.2	1
84	RCRdiff: A fully integrated Bayesian method for differential expression analysis using raw NanoString nCounter data. Statistics in Medicine, 2022, 41, 665-680.	1.6	1