Ying Xu

List of Publications by Year
in descending order

85 papers	2,901 citations	361413 20 h-index	197818 49 g-index
86 all docs	86 docs citations	86 times ranked	4386 citing authors

#	Article	IF	Citations
1	Downregulation of PIK3CB Involved in Alzheimer's Disease via Apoptosis, Axon Guidance, and FoxO Signaling Pathway. Oxidative Medicine and Cellular Longevity, 2022, 2022, 1-15.	4.0	5
2	Cross-Talking Pathways of Forkhead Box O1 (FOXO1) Are Involved in the Pathogenesis of Alzheimer's Disease and Huntington's Disease. Oxidative Medicine and Cellular Longevity, 2022, 2022, 1-14.	4.0	4
3	Detection of Alzheimer's disease using features of brain region-of-interest-based individual network constructed with the sMRI image. Computerized Medical Imaging and Graphics, 2022, 98, 102057.	5.8	9
4	Molecular Signatures of Mitochondrial Complexes Involved in Alzheimer's Disease via Oxidative Phosphorylation and Retrograde Endocannabinoid Signaling Pathways. Oxidative Medicine and Cellular Longevity, 2022, 2022, 1-12.	4.0	5
5	Quantitative estimation of intracellular oxidative stress in human tissues. Briefings in Bioinformatics, 2022, 23, .	6.5	3
6	Down-Regulation of Insulin Like Growth Factor 1 Involved in Alzheimer's Disease via MAPK, Ras, and FoxO Signaling Pathways. Oxidative Medicine and Cellular Longevity, 2022, 2022, 1-15.	4.0	9
7	Deep-joint-learning analysis model of single cell transcriptome and open chromatin accessibility data. Briefings in Bioinformatics, 2021, 22, .	6.5	58
8	Modern deep learning in bioinformatics. Journal of Molecular Cell Biology, 2021, 12, 823-827.	3.3	52
9	Transcriptomic analysis identifies organ-specific metastasis genes and pathways across different primary sites. Journal of Translational Medicine, 2021, 19, 31.	4.4	13
10	Downregulation of ATP6V1A Involved in Alzheimer's Disease via Synaptic Vesicle Cycle, Phagosome, and Oxidative Phosphorylation. Oxidative Medicine and Cellular Longevity, 2021, 2021, 1-15.	4.0	16
11	Deep cross-omics cycle attention model for joint analysis of single-cell multi-omics data. Bioinformatics, 2021, 37, 4091-4099.	4.1	31
12	An Interpretable Computer-Aided Diagnosis Method for Periodontitis From Panoramic Radiographs. Frontiers in Physiology, 2021, 12, 655556.	2.8	13
13	Single-cell RNA-sequencing atlas reveals an MDK-dependent immunosuppressive environment in ErbB pathway-mutated gallbladder cancer. Journal of Hepatology, 2021, 75, 1128-1141.	3.7	66
14	Integrative Functional Genomic Analysis of Molecular Signatures and Mechanistic Pathways in the Cell Cycle Underlying Alzheimer's Disease. Oxidative Medicine and Cellular Longevity, 2021, 2021, 1-11.	4.0	6
15	Mathematical model and computational scheme for multi-phase modeling of cellular population and microenvironmental dynamics in soft tissue. PLoS ONE, 2021, 16, e0260108.	2.5	1
16	Integrative genomic analysis of PPP3R1 in Alzheimer's disease: a potential biomarker for predictive, preventive, and personalized medical approach. EPMA Journal, 2021, 12, 647-658.	6.1	2
17	Understanding metabolic reprogramming in tumor microenvironment. Medical Review, 2021, 1, 111-113.	1.2	0
18	Identification of a novel melatonin-binding nuclear receptor: Vitamin D receptor. Journal of Pineal Research, 2020, 68, e12618.	7.4	30

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19	CaMeRe: A Novel Tool for Inference of Cancer Metabolic Reprogramming. Frontiers in Oncology, 2020, 10, 207.	2.8	5
20	Co-expression based cancer staging and application. Scientific Reports, 2020, 10, 10624.	3.3	8
21	Neural Functions Play Different Roles in Triple Negative Breast Cancer (TNBC) and non-TNBC. Scientific Reports, 2020, 10, 3065.	3.3	10
22	Elucidation of Functional Roles of Sialic Acids in Cancer Migration. Frontiers in Oncology, 2020, 10, 401.	2.8	16
23	Metabolic Reprogramming in Cancer Is Induced to Increase Proton Production. Cancer Research, 2020, 80, 1143-1155.	0.9	43
24	Clear Cell Meningioma in the Central Nervous System: Analysis of Surveillance, Epidemiology, and End Results Database. Frontiers in Oncology, 2020, 10, 592800.	2.8	4
25	Identification of Cancer Development Related Pathways Based on Co-Expression Analyses. , 2020, , .		1
26	The internal interaction in RBBP5 regulates assembly and activity of MLL1 methyltransferase complex. Nucleic Acids Research, 2019, 47, 10426-10438.	14.5	16
27	Warburg Effects in Cancer and Normal Proliferating Cells: Two Tales of the Same Name. Genomics, Proteomics and Bioinformatics, 2019, 17, 273-286.	6.9	39
28	A novel matched-pairs feature selection method considering with tumor purity for differential gene expression analyses. Mathematical Biosciences, 2019, 311, 39-48.	1.9	4
29	Classifying Breast Cancer Subtypes Using Multiple Kernel Learning Based on Omics Data. Genes, 2019, 10, 200.	2.4	34
30	Multi-Classification of Cancer Samples Based on Co-Expression Analyses. , 2019, , .		2
31	DTA-SiST: de novo transcriptome assembly by using simplified suffix trees. BMC Bioinformatics, 2019, 20, 698.	2.6	3
32	Transcriptome analysis reveals an important candidate gene involved in both nodal metastasis and prognosis in lung adenocarcinoma. Cell and Bioscience, 2019, 9, 92.	4.8	46
33	Structural insights into chromosome attachment to the nuclear envelope by an inner nuclear membrane protein Bqt4 in fission yeast. Nucleic Acids Research, 2019, 47, 1573-1584.	14.5	16
34	The Inner Nuclear Membrane Protein Bqt4 in Fission Yeast Contains a DNA-Binding Domain Essential for Telomere Association with the Nuclear Envelope. Structure, 2019, 27, 335-343.e3.	3.3	8
35	Structural and functional analyses of microbial metabolic networks reveal novel insights into genome-scale metabolic fluxes. Briefings in Bioinformatics, 2019, 20, 1590-1603.	6.5	6
36	Proteomic biomarkers for lung cancer progression. Biomarkers in Medicine, 2018, 12, 205-215.	1.4	7

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37	Physical properties of DNA may direct the binding of nucleoid-associated proteins along the E. coli genome. Mathematical Biosciences, 2018, 301, 50-58.	1.9	5
38	Gender specificity improves the early-stage detection of clear cell renal cell carcinoma based on methylomic biomarkers. Biomarkers in Medicine, 2018, 12, 607-618.	1.4	4
39	Elucidation and analyses of the regulatory networks of upland and lowland ecotypes of switchgrass in response to drought and salt stresses. PLoS ONE, 2018, 13, e0204426.	2.5	7
40	dbCAN2: a meta server for automated carbohydrate-active enzyme annotation. Nucleic Acids Research, 2018, 46, W95-W101.	14.5	1,641
41	Revealing the transcriptomic complexity of switchgrass by PacBio long-read sequencing. Biotechnology for Biofuels, 2018, 11, 170.	6.2	30
42	Fenton reactions drive nucleotide and ATP syntheses in cancer. Journal of Molecular Cell Biology, 2018, 10, 448-459.	3.3	38
43	SeqTU: A Web Server for Identification of Bacterial Transcription Units. Scientific Reports, 2017, 7, 43925.	3.3	13
44	Competition between DNA Methylation, Nucleotide Synthesis, and Antioxidation in Cancer versus Normal Tissues. Cancer Research, 2017, 77, 4185-4195.	0.9	12
45	Structural and functional analyses of the mammalian TIN2-TPP1-TRF2 telomeric complex. Cell Research, 2017, 27, 1485-1502.	12.0	76
46	Systematic analyses of glutamine and glutamate metabolisms across different cancer types. Chinese Journal of Cancer, 2017, 36, 88.	4.9	24
47	Genome-Scale Identification of Cell-Wall-Related Genes in Switchgrass through Comparative Genomics and Computational Analyses of Transcriptomic Data. Bioenergy Research, 2016, 9, 172-180.	3.9	10
48	Revisiting operons: an analysis of the landscape of transcriptional units in E. coli. BMC Bioinformatics, 2015, 16, 356.	2.6	39
49	Somatic mutations may not be the primary drivers of cancer formation. International Journal of Cancer, 2015, 137, 2762-2765.	5.1	6
50	Elucidation of drivers of high-level production of lactates throughout a cancer development. Journal of Molecular Cell Biology, 2015, 7, 267-279.	3.3	8
51	Analysis of strand-specific RNA-seq data using machine learning reveals the structures of transcription units in Clostridium thermocellum. Nucleic Acids Research, 2015, 43, e67-e67.	14.5	24
52	Identification of Gene-Expression Signatures and Protein Markers for Breast Cancer Grading and Staging. PLoS ONE, 2015, 10, e0138213.	2.5	30
53	Identification of Essential Proteins Based on Ranking Edge-Weights in Protein-Protein Interaction Networks. PLoS ONE, 2014, 9, e108716.	2.5	15
54	DMINDA: an integrated web server for DNA motif identification and analyses. Nucleic Acids Research, 2014, 42, W12-W19.	14.5	30

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55	New Insights into Clostridia Through Comparative Analyses of Their 40 Genomes. Bioenergy Research, 2014, 7, 1481-1492.	3.9	16
56	Global O-GlcNAc Levels Modulate Transcription of the Adipocyte Secretome during Chronic Insulin Resistance. Frontiers in Endocrinology, 2014, 5, 223.	3.5	20
57	AST: An Automated Sequence-Sampling Method for Improving the Taxonomic Diversity of Gene Phylogenetic Trees. PLoS ONE, 2014, 9, e98844.	2.5	1
58	Carbohydrate and lignin are simultaneously solubilized from unpretreated switchgrass by microbial action at high temperature. Energy and Environmental Science, 2013, 6, 2186.	30.8	75
59	Detect the Different Isoforms Using GeneChip Human Exon 1.0 ST Arrays. , 2009, , .		0
60	A Bioinformatic Analysis of NAC Genes for Plant Cell Wall Development in Relation to Lignocellulosic Bioenergy Production. Bioenergy Research, 2009, 2, 217-232.	3.9	129
61	pDAWG: An Integrated Database for Plant Cell Wall Genes. Bioenergy Research, 2009, 2, 209-216.	3.9	13
62	Investigations on control algorithm of steady-state cornering and control strategy for dynamical correction in a steer-by-wire system. Journal of Zhejiang University: Science A, 2009, 10, 900-908.	2.4	3
63	COMPUTATIONAL ELUCIDATION OF OPERONS AND UBER-OPERONS. Series on Advances in Bioinformatics and Computational Biology, 2008, , 233-257.	0.2	1
64	MICROBIAL PATHWAY MODELS. Series on Advances in Bioinformatics and Computational Biology, 2008, , 315-344.	0.2	1
65	PREDICTION OF BIOLOGICAL PATHWAYS THROUGH DATA MINING AND INFORMATION FUSION. Series on Advances in Bioinformatics and Computational Biology, 2008, , 281-314.	0.2	0
66	PREDICTION OF REGULONS THROUGH COMPARATIVE GENOME ANALYSES. Series on Advances in Bioinformatics and Computational Biology, 2008, , 259-279.	0.2	0
67	Operon Prediction in Microbial Genomes Using Decision Tree Approach. , 2007, , .		5
68	TRANSCRIPTIONAL PROFILING OF DEFINITIVE ENDODERM DERIVED FROM HUMAN EMBRYONIC STEM CELLS. , 2007, , .		8
69	PROTEIN STRUCTURE-STRUCTURE ALIGNMENT WITH DISCRETE FRÃ‰CHET DISTANCE. , 2007, , .		6
70	An Approximate Bayesian Detection Scheme with Applications to Tandem Mass Spectrometry Data Analysis. , 2006, , .		0
71	Gene Expression Profiling of Paired Pre- and Post-Prednisolone (PRED) BM Samples from Childhood ALL Identifies Robust Signatures for PRED Response and Eventual Outcome.. Blood, 2006, 108, 222-222.	1.4	1
72	SORTING GENOMES BY TRANSLOCATIONS AND DELETIONS. , 2006, , .		1

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73	A POINT-PROCESS MODEL FOR RAPID IDENTIFICATION OF POST-TRANSLATIONAL MODIFICATIONS. , 2005, , .		6
74	On Connected [g,f +1]-Factors in Graphs. Combinatorica, 2005, 25, 393-405.	1.2	4
75	PRIME: A Mass Spectrum Data Mining Tool for De Nova Sequencing and PTMs Identification. Journal of Computer Science and Technology, 2005, 20, 483-490.	1.5	6
76	COMPUTATIONAL RECONSTRUCTION OF THE CARBON FIXATION PATHWAY IN <i>SYNECHOCOCCUS SP. WH 8102</i>. , 2005, , .		0
77	Structural analysis of FGFR1 kinase activation through molecular dynamics simulation. , 0, , .		0
78	A knowledge base for computational pathway reconstruction. , 0, , .		0
79	Molecular modeling of full-lengh OxyR from shewanella oneidensis MR-1 and molecular dynamics studies of the activation domain. , 0, , .		0
80	CUBIC: search for binding sites. , 0, , .		0
81	Pathway mapping with operon information: an integer-programming method. , 0, , .		0
82	Computational inference of transcription regulation and response networks in Synechococcus sp. WH8102. , 0, , .		0
83	PROMOCO: a New Program for Prediction of cis Regulatory Elements: From High-Information Content Analysis to Clique Identification. , 0, , .		1
84	Structural genomics analysis of alternative splicing and its application in modeling structures of alternatively spliced variants. , 0, , .		1
85	Patient Survival Prediction from Gene Expression Data. , 0, , 89-111.		0