

# Ying Xu

## List of Publications by Year in descending order

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Version: 2024-02-01

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	dbCAN2: a meta server for automated carbohydrate-active enzyme annotation. <i>Nucleic Acids Research</i> , 2018, 46, W95-W101.	14.5	1,641
2	A Bioinformatic Analysis of NAC Genes for Plant Cell Wall Development in Relation to Lignocellulosic Bioenergy Production. <i>Bioenergy Research</i> , 2009, 2, 217-232.	3.9	129
3	Structural and functional analyses of the mammalian TIN2-TPP1-TRF2 telomeric complex. <i>Cell Research</i> , 2017, 27, 1485-1502.	12.0	76
4	Carbohydrate and lignin are simultaneously solubilized from unpretreated switchgrass by microbial action at high temperature. <i>Energy and Environmental Science</i> , 2013, 6, 2186.	30.8	75
5	Single-cell RNA-sequencing atlas reveals an MDK-dependent immunosuppressive environment in ErbB pathway-mutated gallbladder cancer. <i>Journal of Hepatology</i> , 2021, 75, 1128-1141.	3.7	66
6	Deep-joint-learning analysis model of single cell transcriptome and open chromatin accessibility data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	58
7	Modern deep learning in bioinformatics. <i>Journal of Molecular Cell Biology</i> , 2021, 12, 823-827.	3.3	52
8	Transcriptome analysis reveals an important candidate gene involved in both nodal metastasis and prognosis in lung adenocarcinoma. <i>Cell and Bioscience</i> , 2019, 9, 92.	4.8	46
9	Metabolic Reprogramming in Cancer Is Induced to Increase Proton Production. <i>Cancer Research</i> , 2020, 80, 1143-1155.	0.9	43
10	Revisiting operons: an analysis of the landscape of transcriptional units in <i>E. coli</i> . <i>BMC Bioinformatics</i> , 2015, 16, 356.	2.6	39
11	Warburg Effects in Cancer and Normal Proliferating Cells: Two Tales of the Same Name. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 273-286.	6.9	39
12	Fenton reactions drive nucleotide and ATP syntheses in cancer. <i>Journal of Molecular Cell Biology</i> , 2018, 10, 448-459.	3.3	38
13	Classifying Breast Cancer Subtypes Using Multiple Kernel Learning Based on Omics Data. <i>Genes</i> , 2019, 10, 200.	2.4	34
14	Deep cross-omics cycle attention model for joint analysis of single-cell multi-omics data. <i>Bioinformatics</i> , 2021, 37, 4091-4099.	4.1	31
15	DMINDA: an integrated web server for DNA motif identification and analyses. <i>Nucleic Acids Research</i> , 2014, 42, W12-W19.	14.5	30
16	Revealing the transcriptomic complexity of switchgrass by PacBio long-read sequencing. <i>Biotechnology for Biofuels</i> , 2018, 11, 170.	6.2	30
17	Identification of a novel melatonin-binding nuclear receptor: Vitamin D receptor. <i>Journal of Pineal Research</i> , 2020, 68, e12618.	7.4	30
18	Identification of Gene-Expression Signatures and Protein Markers for Breast Cancer Grading and Staging. <i>PLoS ONE</i> , 2015, 10, e0138213.	2.5	30

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19	Analysis of strand-specific RNA-seq data using machine learning reveals the structures of transcription units in <i>Clostridium thermocellum</i> . <i>Nucleic Acids Research</i> , 2015, 43, e67-e67.	14.5	24
20	Systematic analyses of glutamine and glutamate metabolisms across different cancer types. <i>Chinese Journal of Cancer</i> , 2017, 36, 88.	4.9	24
21	Global O-GlcNAc Levels Modulate Transcription of the Adipocyte Secretome during Chronic Insulin Resistance. <i>Frontiers in Endocrinology</i> , 2014, 5, 223.	3.5	20
22	New Insights into Clostridia Through Comparative Analyses of Their 40 Genomes. <i>Bioenergy Research</i> , 2014, 7, 1481-1492.	3.9	16
23	The internal interaction in RBBP5 regulates assembly and activity of MLL1 methyltransferase complex. <i>Nucleic Acids Research</i> , 2019, 47, 10426-10438.	14.5	16
24	Structural insights into chromosome attachment to the nuclear envelope by an inner nuclear membrane protein Bqt4 in fission yeast. <i>Nucleic Acids Research</i> , 2019, 47, 1573-1584.	14.5	16
25	Elucidation of Functional Roles of Sialic Acids in Cancer Migration. <i>Frontiers in Oncology</i> , 2020, 10, 401.	2.8	16
26	Downregulation of ATP6V1A Involved in Alzheimer's Disease via Synaptic Vesicle Cycle, Phagosome, and Oxidative Phosphorylation. <i>Oxidative Medicine and Cellular Longevity</i> , 2021, 2021, 1-15.	4.0	16
27	Identification of Essential Proteins Based on Ranking Edge-Weights in Protein-Protein Interaction Networks. <i>PLoS ONE</i> , 2014, 9, e108716.	2.5	15
28	pDAWG: An Integrated Database for Plant Cell Wall Genes. <i>Bioenergy Research</i> , 2009, 2, 209-216.	3.9	13
29	SeqTU: A Web Server for Identification of Bacterial Transcription Units. <i>Scientific Reports</i> , 2017, 7, 43925.	3.3	13
30	Transcriptomic analysis identifies organ-specific metastasis genes and pathways across different primary sites. <i>Journal of Translational Medicine</i> , 2021, 19, 31.	4.4	13
31	An Interpretable Computer-Aided Diagnosis Method for Periodontitis From Panoramic Radiographs. <i>Frontiers in Physiology</i> , 2021, 12, 655556.	2.8	13
32	Competition between DNA Methylation, Nucleotide Synthesis, and Antioxidation in Cancer versus Normal Tissues. <i>Cancer Research</i> , 2017, 77, 4185-4195.	0.9	12
33	Genome-Scale Identification of Cell-Wall-Related Genes in Switchgrass through Comparative Genomics and Computational Analyses of Transcriptomic Data. <i>Bioenergy Research</i> , 2016, 9, 172-180.	3.9	10
34	Neural Functions Play Different Roles in Triple Negative Breast Cancer (TNBC) and non-TNBC. <i>Scientific Reports</i> , 2020, 10, 3065.	3.3	10
35	Detection of Alzheimer's disease using features of brain region-of-interest-based individual network constructed with the sMRI image. <i>Computerized Medical Imaging and Graphics</i> , 2022, 98, 102057.	5.8	9
36	Down-Regulation of Insulin Like Growth Factor 1 Involved in Alzheimer's Disease via MAPK, Ras, and FoxO Signaling Pathways. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-15.	4.0	9

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37	Elucidation of drivers of high-level production of lactates throughout a cancer development. <i>Journal of Molecular Cell Biology</i> , 2015, 7, 267-279.	3.3	8
38	The Inner Nuclear Membrane Protein Bqt4 in Fission Yeast Contains a DNA-Binding Domain Essential for Telomere Association with the Nuclear Envelope. <i>Structure</i> , 2019, 27, 335-343.e3.	3.3	8
39	Co-expression based cancer staging and application. <i>Scientific Reports</i> , 2020, 10, 10624.	3.3	8
40	TRANSCRIPTIONAL PROFILING OF DEFINITIVE ENDODERM DERIVED FROM HUMAN EMBRYONIC STEM CELLS. , 2007, , .		8
41	Proteomic biomarkers for lung cancer progression. <i>Biomarkers in Medicine</i> , 2018, 12, 205-215.	1.4	7
42	Elucidation and analyses of the regulatory networks of upland and lowland ecotypes of switchgrass in response to drought and salt stresses. <i>PLoS ONE</i> , 2018, 13, e0204426.	2.5	7
43	A POINT-PROCESS MODEL FOR RAPID IDENTIFICATION OF POST-TRANSLATIONAL MODIFICATIONS. , 2005, , .		6
44	PRIME: A Mass Spectrum Data Mining Tool for De Nova Sequencing and PTMs Identification. <i>Journal of Computer Science and Technology</i> , 2005, 20, 483-490.	1.5	6
45	Somatic mutations may not be the primary drivers of cancer formation. <i>International Journal of Cancer</i> , 2015, 137, 2762-2765.	5.1	6
46	Structural and functional analyses of microbial metabolic networks reveal novel insights into genome-scale metabolic fluxes. <i>Briefings in Bioinformatics</i> , 2019, 20, 1590-1603.	6.5	6
47	Integrative Functional Genomic Analysis of Molecular Signatures and Mechanistic Pathways in the Cell Cycle Underlying Alzheimer's Disease. <i>Oxidative Medicine and Cellular Longevity</i> , 2021, 2021, 1-11.	4.0	6
48	PROTEIN STRUCTURE-STRUCTURE ALIGNMENT WITH DISCRETE FREQUENT DISTANCE. , 2007, , .		6
49	Operon Prediction in Microbial Genomes Using Decision Tree Approach. , 2007, , .		5
50	Physical properties of DNA may direct the binding of nucleoid-associated proteins along the E. coli genome. <i>Mathematical Biosciences</i> , 2018, 301, 50-58.	1.9	5
51	CaMeRe: A Novel Tool for Inference of Cancer Metabolic Reprogramming. <i>Frontiers in Oncology</i> , 2020, 10, 207.	2.8	5
52	Downregulation of PIK3CB Involved in Alzheimer's Disease via Apoptosis, Axon Guidance, and FoxO Signaling Pathway. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-15.	4.0	5
53	Molecular Signatures of Mitochondrial Complexes Involved in Alzheimer's Disease via Oxidative Phosphorylation and Retrograde Endocannabinoid Signaling Pathways. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-12.	4.0	5
54	On Connected $[g, f + 1]$ -Factors in Graphs. <i>Combinatorica</i> , 2005, 25, 393-405.	1.2	4

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55	Gender specificity improves the early-stage detection of clear cell renal cell carcinoma based on methylomic biomarkers. <i>Biomarkers in Medicine</i> , 2018, 12, 607-618.	1.4	4
56	A novel matched-pairs feature selection method considering with tumor purity for differential gene expression analyses. <i>Mathematical Biosciences</i> , 2019, 311, 39-48.	1.9	4
57	Clear Cell Meningioma in the Central Nervous System: Analysis of Surveillance, Epidemiology, and End Results Database. <i>Frontiers in Oncology</i> , 2020, 10, 592800.	2.8	4
58	Cross-Talking Pathways of Forkhead Box O1 (FOXO1) Are Involved in the Pathogenesis of Alzheimer's Disease and Huntington's Disease. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-14.	4.0	4
59	Investigations on control algorithm of steady-state cornering and control strategy for dynamical correction in a steer-by-wire system. <i>Journal of Zhejiang University: Science A</i> , 2009, 10, 900-908.	2.4	3
60	DTA-SiST: de novo transcriptome assembly by using simplified suffix trees. <i>BMC Bioinformatics</i> , 2019, 20, 698.	2.6	3
61	Quantitative estimation of intracellular oxidative stress in human tissues. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	3
62	Multi-Classification of Cancer Samples Based on Co-Expression Analyses. , 2019, , .		2
63	Integrative genomic analysis of PPP3R1 in Alzheimer's disease: a potential biomarker for predictive, preventive, and personalized medical approach. <i>EPMA Journal</i> , 2021, 12, 647-658.	6.1	2
64	PROMOCO: a New Program for Prediction of cis Regulatory Elements: From High-Information Content Analysis to Clique Identification. , 0, , .		1
65	Structural genomics analysis of alternative splicing and its application in modeling structures of alternatively spliced variants. , 0, , .		1
66	COMPUTATIONAL ELUCIDATION OF OPERONS AND UBER-OPERONS. <i>Series on Advances in Bioinformatics and Computational Biology</i> , 2008, , 233-257.	0.2	1
67	MICROBIAL PATHWAY MODELS. <i>Series on Advances in Bioinformatics and Computational Biology</i> , 2008, , 315-344.	0.2	1
68	Gene Expression Profiling of Paired Pre- and Post-Prednisolone (PRED) BM Samples from Childhood ALL Identifies Robust Signatures for PRED Response and Eventual Outcome.. <i>Blood</i> , 2006, 108, 222-222.	1.4	1
69	AST: An Automated Sequence-Sampling Method for Improving the Taxonomic Diversity of Gene Phylogenetic Trees. <i>PLoS ONE</i> , 2014, 9, e98844.	2.5	1
70	SORTING GENOMES BY TRANSLOCATIONS AND DELETIONS. , 2006, , .		1
71	Identification of Cancer Development Related Pathways Based on Co-Expression Analyses. , 2020, , .		1
72	Mathematical model and computational scheme for multi-phase modeling of cellular population and microenvironmental dynamics in soft tissue. <i>PLoS ONE</i> , 2021, 16, e0260108.	2.5	1

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73	Structural analysis of FGFR1 kinase activation through molecular dynamics simulation. , 0, , .		0
74	A knowledge base for computational pathway reconstruction. , 0, , .		0
75	Molecular modeling of full-length OxyR from shewanella oneidensis MR-1 and molecular dynamics studies of the activation domain. , 0, , .		0
76	CUBIC: search for binding sites. , 0, , .		0
77	Pathway mapping with operon information: an integer-programming method. , 0, , .		0
78	Computational inference of transcription regulation and response networks in <i>Synechococcus</i> sp. WH8102. , 0, , .		0
79	An Approximate Bayesian Detection Scheme with Applications to Tandem Mass Spectrometry Data Analysis. , 2006, , .		0
80	Patient Survival Prediction from Gene Expression Data. , 0, , 89-111.		0
81	Detect the Different Isoforms Using GeneChip Human Exon 1.0 ST Arrays. , 2009, , .		0
82	COMPUTATIONAL RECONSTRUCTION OF THE CARBON FIXATION PATHWAY IN <i>SYNECHOCOCCUS</i> SP. WH 8102. , 2005, , .		0
83	PREDICTION OF BIOLOGICAL PATHWAYS THROUGH DATA MINING AND INFORMATION FUSION. Series on Advances in Bioinformatics and Computational Biology, 2008, , 281-314.	0.2	0
84	PREDICTION OF REGULONS THROUGH COMPARATIVE GENOME ANALYSES. Series on Advances in Bioinformatics and Computational Biology, 2008, , 259-279.	0.2	0
85	Understanding metabolic reprogramming in tumor microenvironment. Medical Review, 2021, 1, 111-113.	1.2	0