

Xiao-chen Bo

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8096477/publications.pdf>

Version: 2024-02-01

130
papers

7,022
citations

172457

29
h-index

88630

70
g-index

142
all docs

142
docs citations

142
times ranked

8837
citing authors

#	ARTICLE	IF	CITATIONS
1	clusterProfiler 4.0: A universal enrichment tool for interpreting omics data. <i>Innovation(China)</i> , 2021, 2, 100141.	9.1	2,743
2	GOSemSim: an R package for measuring semantic similarity among GO terms and gene products. <i>Bioinformatics</i> , 2010, 26, 976-978.	4.1	978
3	Deep Learning and Its Applications in Biomedicine. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 17-32.	6.9	420
4	Genetic diversity and evolutionary dynamics of Ebola virus in Sierra Leone. <i>Nature</i> , 2015, 524, 93-96.	27.8	150
5	ggtreeExtra: Compact Visualization of Richly Annotated Phylogenetic Data. <i>Molecular Biology and Evolution</i> , 2021, 38, 4039-4042.	8.9	134
6	BiRen: predicting enhancers with a deep-learning-based model using the DNA sequence alone. <i>Bioinformatics</i> , 2017, 33, 1930-1936.	4.1	121
7	Comprehensive Identification and Annotation of Cell Type-Specific and Ubiquitous CTCF-Binding Sites in the Human Genome. <i>PLoS ONE</i> , 2012, 7, e41374.	2.5	119
8	Cellular microRNA inhibits M1 protein expression of the H1N1 influenza A virus in infected human lung epithelial cells. <i>Journal of Cellular and Molecular Medicine</i> , 2012, 16, 2539-2546.	3.6	110
9	TargetFinder: a software for antisense oligonucleotide target site selection based on MAST and secondary structures of target mRNA. <i>Bioinformatics</i> , 2005, 21, 1401-1402.	4.1	96
10	Protocatechuic aldehyde inhibits hepatitis B virus replication both in vitro and in vivo. <i>Antiviral Research</i> , 2007, 74, 59-64.	4.1	92
11	3DSNP: a database for linking human noncoding SNPs to their three-dimensional interacting genes. <i>Nucleic Acids Research</i> , 2017, 45, D643-D649.	14.5	90
12	PEDLA: predicting enhancers with a deep learning-based algorithmic framework. <i>Scientific Reports</i> , 2016, 6, 28517.	3.3	88
13	Metagenomic sequencing of bile from gallstone patients to identify different microbial community patterns and novel biliary bacteria. <i>Scientific Reports</i> , 2015, 5, 17450.	3.3	70
14	Intra-host dynamics of Ebola virus during 2014. <i>Nature Microbiology</i> , 2016, 1, 16151.	13.3	70
15	Influence of the Biliary System on Biliary Bacteria Revealed by Bacterial Communities of the Human Biliary and Upper Digestive Tracts. <i>PLoS ONE</i> , 2016, 11, e0150519.	2.5	70
16	Deep learning-based transcriptome data classification for drug-target interaction prediction. <i>BMC Genomics</i> , 2018, 19, 667.	2.8	66
17	Cogena, a novel tool for co-expressed gene-set enrichment analysis, applied to drug repositioning and drug mode of action discovery. <i>BMC Genomics</i> , 2016, 17, 414.	2.8	62
18	Nodes and biological processes identified on the basis of network analysis in the brain of the senescence accelerated mice as an Alzheimer's disease animal model. <i>Frontiers in Aging Neuroscience</i> , 2013, 5, 65.	3.4	57

#	ARTICLE	IF	CITATIONS
19	DeepHiC: A generative adversarial network for enhancing Hi-C data resolution. <i>PLoS Computational Biology</i> , 2020, 16, e1007287.	3.2	56
20	Genome-wide analysis of the relationships between DNase HS, histone modifications and gene expression reveals distinct modes of chromatin domains. <i>Nucleic Acids Research</i> , 2011, 39, 7428-7443.	14.5	52
21	New insights on human essential genes based on integrated analysis and the construction of the HEGIAP web-based platform. <i>Briefings in Bioinformatics</i> , 2020, 21, 1397-1410.	6.5	51
22	<i>DeÂnovo</i> identification of replication-timing domains in the human genome by deep learning. <i>Bioinformatics</i> , 2016, 32, 641-649.	4.1	48
23	A survey and evaluation of Web-based tools/databases for variant analysis of TCGA data. <i>Briefings in Bioinformatics</i> , 2019, 20, 1524-1541.	6.5	48
24	Machine learning methods, databases and tools for drug combination prediction. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	45
25	An integrative analysis of TFBS-clustered regions reveals new transcriptional regulation models on the accessible chromatin landscape. <i>Scientific Reports</i> , 2015, 5, 8465.	3.3	41
26	Gut metagenomes of type 2 diabetic patients have characteristic single-nucleotide polymorphism distribution in <i>Bacteroides coprocola</i> . <i>Microbiome</i> , 2017, 5, 15.	11.1	41
27	A 472-SNP panel for pairwise kinship testing of second-degree relatives. <i>Forensic Science International: Genetics</i> , 2018, 34, 178-185.	3.1	37
28	RevEcoR: an R package for the reverse ecology analysis of microbiomes. <i>BMC Bioinformatics</i> , 2016, 17, 294.	2.6	34
29	RDMAS: a web server for RNA deleterious mutation analysis. <i>BMC Bioinformatics</i> , 2006, 7, 404.	2.6	31
30	Functional annotation of structural ncRNAs within enhancer RNAs in the human genome: implications for human disease. <i>Scientific Reports</i> , 2017, 7, 15518.	3.3	26
31	Lnc2Catlas: an atlas of long noncoding RNAs associated with risk of cancers. <i>Scientific Reports</i> , 2018, 8, 1909.	3.3	26
32	Functional annotation of HOT regions in the human genome: implications for human disease and cancer. <i>Scientific Reports</i> , 2015, 5, 11633.	3.3	24
33	Partners of patients with ulcerative colitis exhibit a biologically relevant dysbiosis in fecal microbial metacommunities. <i>World Journal of Gastroenterology</i> , 2017, 23, 4624.	3.3	23
34	<p>ARQ-197 enhances the antitumor effect of sorafenib in hepatocellular carcinoma cells via decelerating its intracellular clearance</p>. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 1629-1640.	2.0	23
35	Stable H3K4me3 is associated with transcription initiation during early embryo development. <i>Bioinformatics</i> , 2019, 35, 3931-3936.	4.1	23
36	Gene Ranking of RNA-Seq Data via Discriminant Non-Negative Matrix Factorization. <i>PLoS ONE</i> , 2015, 10, e0137782.	2.5	22

#	ARTICLE	IF	CITATIONS
37	Exploring the efficacy of paternity and kinship testing based on single nucleotide polymorphisms. <i>Forensic Science International: Genetics</i> , 2016, 22, 161-168.	3.1	21
38	DTI-HETA: prediction of drug–target interactions based on GCN and GAT on heterogeneous graph. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	21
39	Forensic nanopore sequencing of STRs and SNPs using Verogen’s ForenSeq DNA Signature Prep Kit and MinION. <i>International Journal of Legal Medicine</i> , 2021, 135, 1685-1693.	2.2	20
40	In silico genetic robustness analysis of microRNA secondary structures: potential evidence of congruent evolution in microRNA. <i>BMC Evolutionary Biology</i> , 2007, 7, 223.	3.2	19
41	Direct next-generation sequencing of virus-human mixed samples without pretreatment is favorable to recover virus genome. <i>Biology Direct</i> , 2016, 11, 3.	4.6	19
42	Human enterovirus 71 protein interaction network prompts antiviral drug repositioning. <i>Scientific Reports</i> , 2017, 7, 43143.	3.3	19
43	GeneExpressionSignature: an R package for discovering functional connections using gene expression signatures. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 116-118.	2.0	18
44	Exploring the role of human miRNAs in virus–host interactions using systematic overlap analysis. <i>Bioinformatics</i> , 2013, 29, 2375-2379.	4.1	18
45	ICM: a web server for integrated clustering of multi-dimensional biomedical data. <i>Nucleic Acids Research</i> , 2016, 44, W154-W159.	14.5	18
46	High-resolution annotation of the mouse preimplantation embryo transcriptome using long-read sequencing. <i>Nature Communications</i> , 2020, 11, 2653.	12.8	17
47	Inhibition of Histone Deacetylation by MS-275 Alleviates Colitis by Activating the Vitamin D Receptor. <i>Journal of Crohn's and Colitis</i> , 2020, 14, 1103-1118.	1.3	17
48	Neuroendocrine immunomodulation network dysfunction in SAMP8 mice and PrP-hA ² PPswe/PS1 ^{E9} mice: potential mechanism underlying cognitive impairment. <i>Oncotarget</i> , 2016, 7, 22988-23005.	1.8	17
49	Computational Prediction and Validation of BAHD1 as a Novel Molecule for Ulcerative Colitis. <i>Scientific Reports</i> , 2015, 5, 12227.	3.3	16
50	Accurate identification of RNA editing sites from primitive sequence with deep neural networks. <i>Scientific Reports</i> , 2018, 8, 6005.	3.3	16
51	Computational methods for the prediction of chromatin interaction and organization using sequence and epigenomic profiles. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	16
52	Multi-dimensional data integration algorithm based on random walk with restart. <i>BMC Bioinformatics</i> , 2021, 22, 97.	2.6	16
53	Screening of specific antigens for SARS clinical diagnosis using a protein microarray. <i>Analyst</i> , The, 2005, 130, 474.	3.5	15
54	A novel representation of RNA secondary structure based on element-contact graphs. <i>BMC Bioinformatics</i> , 2008, 9, 188.	2.6	15

#	ARTICLE	IF	CITATIONS
55	PerturbationAnalyzer: a tool for investigating the effects of concentration perturbation on protein interaction networks. <i>Bioinformatics</i> , 2010, 26, 275-277.	4.1	15
56	Discovery of novel therapeutic properties of drugs from transcriptional responses based on multi-label classification. <i>Scientific Reports</i> , 2017, 7, 7136.	3.3	15
57	The landscape of the A-to-I RNA editome from 462 human genomes. <i>Scientific Reports</i> , 2018, 8, 12069.	3.3	15
58	Computational methods, databases and tools for synthetic lethality prediction. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	15
59	Proteomic analysis at the subcellular level for host targets against influenza A virus (H1N1). <i>Antiviral Research</i> , 2013, 100, 673-687.	4.1	13
60	EHFPI: a database and analysis resource of essential host factors for pathogenic infection. <i>Nucleic Acids Research</i> , 2015, 43, D946-D955.	14.5	13
61	DTI-RCNN: New Efficient Hybrid Neural Network Model to Predict Drug-Target Interactions. <i>Lecture Notes in Computer Science</i> , 2018, , 104-114.	1.3	13
62	A Co-Module Regulated by Therapeutic Drugs in a Molecular Subnetwork of Alzheimer's Disease Identified on the Basis of Traditional Chinese Medicine and SAMP8 Mice. <i>Current Alzheimer Research</i> , 2015, 12, 870-885.	1.4	13
63	Fibronectin is essential for hepatitis B virus propagation in vitro: May be a potential cellular target?. <i>Biochemical and Biophysical Research Communications</i> , 2006, 344, 757-764.	2.1	12
64	Selection of antisense oligonucleotides based on multiple predicted target mRNA structures. <i>BMC Bioinformatics</i> , 2006, 7, 122.	2.6	12
65	AOBase: a database for antisense oligonucleotides selection and design. <i>Nucleic Acids Research</i> , 2006, 34, D664-D667.	14.5	12
66	mmnet: An R Package for Metagenomics Systems Biology Analysis. <i>BioMed Research International</i> , 2015, 2015, 1-5.	1.9	12
67	Systematic Identification and Assessment of Therapeutic Targets for Breast Cancer Based on Genome-Wide RNA Interference Transcriptomes. <i>Genes</i> , 2017, 8, 86.	2.4	12
68	NegStacking: Drug-Target Interaction Prediction Based on Ensemble Learning and Logistic Regression. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2624-2634.	3.0	12
69	Assessment of two-pool multiplex long-read nanopore sequencing of SARS-CoV-2. <i>Journal of Medical Virology</i> , 2022, 94, 327-334.	5.0	12
70	Correlation between sequence conservation and structural thermodynamics of microRNA precursors from human, mouse, and chicken genomes. <i>BMC Evolutionary Biology</i> , 2010, 10, 329.	3.2	11
71	Predicting drug side effects based on link prediction in bipartite network. , 2014, , .		11
72	Network fingerprint: a knowledge-based characterization of biomedical networks. <i>Scientific Reports</i> , 2015, 5, 13286.	3.3	11

#	ARTICLE	IF	CITATIONS
73	Genome-wide identification and characterisation of HOT regions in the human genome. BMC Genomics, 2016, 17, 733.	2.8	11
74	Genome Sequencing and Comparative Genomics Analysis Revealed Pathogenic Potential in <i>Penicillium capsulatum</i> as a Novel Fungal Pathogen Belonging to Eurotiales. Frontiers in Microbiology, 2016, 7, 1541.	3.5	11
75	LINCS dataset-based repositioning of rosiglitazone as a potential anti-human adenovirus drug. Antiviral Research, 2020, 179, 104789.	4.1	11
76	Analysis of synonymous codon usage bias in 09H1N1. Virologica Sinica, 2010, 25, 329-340.	3.0	10
77	DTIGCCN: Prediction of drug-target interactions based on GCN and CNN. , 2020, , .		10
78	Dynamic Interplay between Structural Variations and 3D Genome Organization in Pancreatic Cancer. Advanced Science, 2022, 9, e2200818.	11.2	10
79	ARDesigner: A web-based system for allosteric RNA design. Journal of Biotechnology, 2010, 150, 466-473.	3.8	9
80	Drug-target interaction prediction with a deep-learning-based model. , 2017, , .		9
81	paraGSEA: a scalable approach for large-scale gene expression profiling. Nucleic Acids Research, 2017, 45, e155-e155.	14.5	9
82	PIMD: An Integrative Approach for Drug Repositioning Using Multiple Characterization Fusion. Genomics, Proteomics and Bioinformatics, 2020, 18, 565-581.	6.9	9
83	CMTCN: a web tool for investigating cancer-specific microRNA and transcription factor co-regulatory networks. PeerJ, 2018, 6, e5951.	2.0	9
84	RSRE: RNA structural robustness evaluator. Nucleic Acids Research, 2007, 35, W314-W319.	14.5	8
85	In Silico Genetic Robustness Analysis of Secondary Structural Elements in the miRNA Gene. Journal of Molecular Evolution, 2008, 67, 560-569.	1.8	8
86	A new method for measuring functional similarity of microRNAs. Journal of Integrated OMICS, 2011, 1, .	0.5	8
87	LIVE: a manually curated encyclopedia of experimentally validated interactions of lncRNAs. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	8
88	Genomic analyses reveal evolutionary and geologic context for the plateau fungus <i>Ophiocordyceps sinensis</i> . Chinese Medicine, 2020, 15, 107.	4.0	8
89	Comprehensive analysis of miRNA-gene regulatory network with clinical significance in human cancers. Science China Life Sciences, 2020, 63, 1201-1212.	4.9	8
90	Domain-adversarial multi-task framework for novel therapeutic property prediction of compounds. Bioinformatics, 2020, 36, 2848-2855.	4.1	8

#	ARTICLE	IF	CITATIONS
91	Drug-Target Interaction Prediction Based on Adversarial Bayesian Personalized Ranking. <i>BioMed Research International</i> , 2021, 2021, 1-16.	1.9	8
92	The hierarchical folding dynamics of topologically associating domains are closely related to transcriptional abnormalities in cancers. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1684-1693.	4.1	8
93	Effects of 5-h multimodal stress on the molecules and pathways involved in dendritic morphology and cognitive function. <i>Neurobiology of Learning and Memory</i> , 2015, 123, 225-238.	1.9	7
94	Exploring the associations of host genes for viral infection revealed by genome-wide RNAi and virus-host protein interactions. <i>Molecular BioSystems</i> , 2015, 11, 2511-2519.	2.9	7
95	Exploration of prognosis-related microRNA and transcription factor co-regulatory networks across cancer types. <i>RNA Biology</i> , 2019, 16, 1010-1021.	3.1	7
96	ExpTreeDB: Web-based query and visualization of manually annotated gene expression profiling experiments of human and mouse from GEO. <i>Bioinformatics</i> , 2014, 30, 3379-3386.	4.1	6
97	Radiation protective effects of baclofen predicted by a computational drug repurposing strategy. <i>Pharmacological Research</i> , 2016, 113, 475-483.	7.1	6
98	Genomics and Comparative Genomic Analyses Provide Insight into the Taxonomy and Pathogenic Potential of Novel <i>Emmonsia</i> Pathogens. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 105.	3.9	6
99	Exploring the classification of cancer cell lines from multiple omic views. <i>PeerJ</i> , 2020, 8, e9440.	2.0	6
100	ExpressVis: a biologist-oriented interactive web server for exploring multi-omics data. <i>Nucleic Acids Research</i> , 2022, 50, W312-W321.	14.5	6
101	Spatial density of open chromatin: an effective metric for the functional characterization of topologically associated domains. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	5
102	Synthetic Lethal Interactions Prediction Based on Multiple Similarity Measures Fusion. <i>Journal of Computer Science and Technology</i> , 2021, 36, 261-275.	1.5	5
103	HBVPathDB: A database of HBV infection-related molecular interaction network. <i>World Journal of Gastroenterology</i> , 2005, 11, 1690.	3.3	5
104	Characterization the regulation of herpesvirus miRNAs from the view of human protein interaction network. <i>BMC Systems Biology</i> , 2011, 5, 93.	3.0	4
105	Inferring Infection Patterns Based on a Connectivity Map of Host Transcriptional Responses. <i>Scientific Reports</i> , 2015, 5, 15820.	3.3	4
106	Regulatory patterns analysis of transcription factor binding site clustered regions and identification of key genes in endometrial cancer. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 812-823.	4.1	3
107	Systematic optimization of host-directed therapeutic targets and preclinical validation of repositioned antiviral drugs. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	3
108	Prediction of DTIs for high-dimensional and class-imbalanced data based on CGAN. , 2018, , .		2

#	ARTICLE	IF	CITATIONS
109	COMSUC: A web server for the identification of consensus molecular subtypes of cancer based on multiple methods and multi-omics data. PLoS Computational Biology, 2021, 17, e1008769.	3.2	2
110	Discovering Active Subnetwork in Protein Interaction Network*. Progress in Biochemistry and Biophysics, 2010, 37, 208-217.	0.3	2
111	iFORM: Incorporating Find Occurrence of Regulatory Motifs. PLoS ONE, 2016, 11, e0168607.	2.5	2
112	Dynamic Propagation Properties of Virus-Host Protein Interaction Network. , 2009, , .		1
113	Targeting Bacterial RNA Polymerase σ^{70} for Development of Broad-spectrum Antisense Antibacterials. Recent Patents on Anti-infective Drug Discovery, 2012, 7, 213-222.	0.8	1
114	Exploring spatially adjacent TFBS-clustered regions with Hi-C data. Bioinformatics, 2017, 33, 2611-2614.	4.1	1
115	Predicting potential gene ontology from cellular response data. , 2017, , .		1
116	Computational Approaches to Analyze the Strategies of Drug Repositioning*. Progress in Biochemistry and Biophysics, 2012, 39, 1029-1036.	0.3	1
117	Selection and their antitumor activity of antisense oligonucleotides targeting messenger RNA of vascular endothelial growth factor receptor 2. Chinese Journal of Cancer Research: Official Journal of China Anti-Cancer Association, Beijing Institute for Cancer Research, 2005, 17, 161-170.	2.2	0
118	Optimizing Reference Gene Set for Inter-Chip Normalization Using Genetic Algorithm. , 2009, , .		0
119	EvoRSR: an integrated system for exploring evolution of RNA structural robustness. BMC Bioinformatics, 2009, 10, 249.	2.6	0
120	Towards a Comprehensive HBV-Human Interaction Map. , 2009, , .		0
121	Topology aware functional similarity of protein interaction networks based on gene ontology. , 2011, 2011, 6857-60.		0
122	New insights into the landscape relationships of host response to bacterial pathogens. , 2015, , .		0
123	The relationships among host transcriptional responses reveal distinct signatures underlying viral infection-disease associations. Molecular BioSystems, 2016, 12, 653-665.	2.9	0
124	NFPscanner: a webtool for knowledge-based deciphering of biomedical networks. BMC Bioinformatics, 2017, 18, 262.	2.6	0
125	NFP: An R Package for Characterizing and Comparing of Annotated Biological Networks. BioMed Research International, 2017, 2017, 1-5.	1.9	0
126	A Metagraph-Based Model for Predicting Drug-Target Interaction on Heterogeneous Network. Lecture Notes in Computer Science, 2021, , 465-476.	1.3	0

#	ARTICLE	IF	CITATIONS
127	A Yeast BiFC-seq Method for Genome-wide Interactome Mapping. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 795-807.	6.9	0
128	Design of 16 S rRNA-based Oligonucleotide Array Using Group-specific Non-unique Probes in Large Scale Bacteria Detection*. <i>Progress in Biochemistry and Biophysics</i> , 2009, 36, 1025-1034.	0.3	0
129	Biomedical Applications Using Cloud Technologies. <i>Scientia Sinica Vitae</i> , 2013, 43, 569-578.	0.3	0
130	paraSNF: An Parallel Approach for Large-Scale Similarity Network Fusion. <i>Communications in Computer and Information Science</i> , 2018, , 155-167.	0.5	0