Xiao-chen Bo

List of Publications by Year
in descending order

130	7,022	172457	88630
papers	citations	29	70
		h-index	g-index

142	142	142	8837
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A Yeast BiFC-seq Method for Genome-wide Interactome Mapping. Genomics, Proteomics and Bioinformatics, 2022, 20, 795-807.	6.9	0
2	Machine learning methods, databases and tools for drug combination prediction. Briefings in Bioinformatics, 2022, 23, .	6.5	45
3	Assessment of twoâ€pool multiplex longâ€amplicon nanopore sequencing of SARSâ€CoVâ€2. Journal of Medical Virology, 2022, 94, 327-334.	5.0	12
4	Regulatory patterns analysis of transcription factor binding site clustered regions and identification of key genes in endometrial cancer. Computational and Structural Biotechnology Journal, 2022, 20, 812-823.	4.1	3
5	Computational methods, databases and tools for synthetic lethality prediction. Briefings in Bioinformatics, 2022, 23, .	6.5	15
6	Systematic optimization of host-directed therapeutic targets and preclinical validation of repositioned antiviral drugs. Briefings in Bioinformatics, 2022, 23, .	6.5	3
7	DTI-HETA: prediction of drugâ€"target interactions based on GCN and GAT on heterogeneous graph. Briefings in Bioinformatics, 2022, 23, .	6.5	21
8	ExpressVis: a biologist-oriented interactive web server for exploring multi-omics data. Nucleic Acids Research, 2022, 50, W312-W321.	14.5	6
9	Dynamic Interplay between Structural Variations and 3D Genome Organization in Pancreatic Cancer. Advanced Science, 2022, 9, e2200818.	11.2	10
10	NegStacking: Drugˆ'Target Interaction Prediction Based on Ensemble Learning and Logistic Regression. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2624-2634.	3.0	12
11	Spatial density of open chromatin: an effective metric for the functional characterization of topologically associated domains. Briefings in Bioinformatics, 2021, 22, .	6.5	5
12	Computational methods for the prediction of chromatin interaction and organization using sequence and epigenomic profiles. Briefings in Bioinformatics, 2021, 22, .	6.5	16
13	A Metagraph-Based Model for Predicting Drug-Target Interaction on Heterogeneous Network. Lecture Notes in Computer Science, 2021, , 465-476.	1.3	0
14	Multi-dimensional data integration algorithm based on random walk with restart. BMC Bioinformatics, 2021, 22, 97.	2.6	16
15	Drug-Target Interaction Prediction Based on Adversarial Bayesian Personalized Ranking. BioMed Research International, 2021, 2021, 1-16.	1.9	8
16	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
17	Synthetic Lethal Interactions Prediction Based on Multiple Similarity Measures Fusion. Journal of Computer Science and Technology, 2021, 36, 261-275.	1.5	5
18	Forensic nanopore sequencing of STRs and SNPs using Verogenâ€™s ForenSeq DNA Signature Prep Kit and MinION. International Journal of Legal Medicine, 2021, 135, 1685-1693.	2.2	20

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19	ggtreeExtra: Compact Visualization of Richly Annotated Phylogenetic Data. Molecular Biology and Evolution, 2021, 38, 4039-4042.	8.9	134
20	clusterProfiler 4.0: A universal enrichment tool for interpreting omics data. Innovation(China), 2021, 2, 100141.	9.1	2,743
21	The hierarchical folding dynamics of topologically associating domains are closely related to transcriptional abnormalities in cancers. Computational and Structural Biotechnology Journal, 2021, 19, 1684-1693.	4.1	8
22	New insights on human essential genes based on integrated analysis and the construction of the HEGIAP web-based platform. Briefings in Bioinformatics, 2020, 21, 1397-1410.	6.5	51
23	PIMD: An Integrative Approach for Drug Repositioning Using Multiple Characterization Fusion. Genomics, Proteomics and Bioinformatics, 2020, 18, 565-581.	6.9	9
24	Genomic analyses reveal evolutionary and geologic context for the plateau fungus Ophiocordyceps sinensis. Chinese Medicine, 2020, 15, 107.	4.0	8
25	LINCS dataset-based repositioning of rosiglitazone as a potential anti-human adenovirus drug. Antiviral Research, 2020, 179, 104789.	4.1	11
26	High-resolution annotation of the mouse preimplantation embryo transcriptome using long-read sequencing. Nature Communications, 2020, 11, 2653.	12.8	17
27	Comprehensive analysis of miRNA-gene regulatory network with clinical significance in human cancers. Science China Life Sciences, 2020, 63, 1201-1212.	4.9	8
28	Inhibition of Histone Deacetylation by MS-275 Alleviates Colitis by Activating the Vitamin D Receptor. Journal of Crohn's and Colitis, 2020, 14, 1103-1118.	1.3	17
29	DeepHiC: A generative adversarial network for enhancing Hi-C data resolution. PLoS Computational Biology, 2020, 16, e1007287.	3.2	56
30	Domain-adversarial multi-task framework for novel therapeutic property prediction of compounds. Bioinformatics, 2020, 36, 2848-2855.	4.1	8
31	DTIGCCN: Prediction of drug-target interactions based on GCN and CNN. , 2020, , .		10
32	Exploring the classification of cancer cell lines from multiple omic views. PeerJ, 2020, 8, e9440.	2.0	6
33	Exploration of prognosis-related microRNA and transcription factor co-regulatory networks across cancer types. RNA Biology, 2019, 16, 1010-1021.	3.1	7
34	<p>ARQ-197 enhances the antitumor effect of sorafenib in hepatocellular carcinoma cells via decelerating its intracellular clearance</p>. OncoTargets and Therapy, 2019, Volume 12, 1629-1640.	2.0	23
35	Stable H3K4me3 is associated with transcription initiation during early embryo development. Bioinformatics, 2019, 35, 3931-3936.	4.1	23
36	LIVE: a manually curated encyclopedia of experimentally validated interactions of lncRNAs. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	8

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37	A survey and evaluation of Web-based tools/databases for variant analysis of TCGA data. Briefings in Bioinformatics, 2019, 20, 1524-1541.	6.5	48
38	Deep Learning and Its Applications in Biomedicine. Genomics, Proteomics and Bioinformatics, 2018, 16, 17-32.	6.9	420
39	A 472-SNP panel for pairwise kinship testing of second-degree relatives. Forensic Science International: Genetics, 2018, 34, 178-185.	3.1	37
40	Accurate identification of RNA editing sites from primitive sequence with deep neural networks. Scientific Reports, 2018, 8, 6005.	3.3	16
41	Lnc2Catlas: an atlas of long noncoding RNAs associated with risk of cancers. Scientific Reports, 2018, 8, 1909.	3.3	26
42	Prediction of DTIs for high-dimensional and class-imbalanced data based on CGAN. , 2018, , .		2
43	Deep learning-based transcriptome data classification for drug-target interaction prediction. BMC Genomics, 2018, 19, 667.	2.8	66
44	DTI-RCNN: New Efficient Hybrid Neural Network Model to Predict Drug–Target Interactions. Lecture Notes in Computer Science, 2018, , 104-114.	1.3	13
45	The landscape of the A-to-I RNA editome from 462 human genomes. Scientific Reports, 2018, 8, 12069.	3.3	15
46	CMTCN: a web tool for investigating cancer-specific microRNA and transcription factor co-regulatory networks. PeerJ, 2018, 6, e5951.	2.0	9
47	paraSNF: An Parallel Approach for Large-Scale Similarity Network Fusion. Communications in Computer and Information Science, 2018, , 155-167.	0.5	0
48	Human enterovirus 71 protein interaction network prompts antiviral drug repositioning. Scientific Reports, 2017, 7, 43143.	3.3	19
49	Gut metagenomes of type 2 diabetic patients have characteristic single-nucleotide polymorphism distribution in Bacteroides coprocola. Microbiome, 2017, 5, 15.	11.1	41
50	Exploring spatially adjacent TFBS-clustered regions with Hi-C data. Bioinformatics, 2017, 33, 2611-2614.	4.1	1
51	Predicting potential gene ontology from cellular response data. , 2017, , .		1
52	BiRen: predicting enhancers with a deep-learning-based model using the DNA sequence alone. Bioinformatics, 2017, 33, 1930-1936.	4.1	121
53	Discovery of novel therapeutic properties of drugs from transcriptional responses based on multi-label classification. Scientific Reports, 2017, 7, 7136.	3.3	15
54	Functional annotation of structural ncRNAs within enhancer RNAs in the human genome: implications for human disease. Scientific Reports, 2017, 7, 15518.	3.3	26

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55	NFPscanner: a webtool for knowledge-based deciphering of biomedical networks. BMC Bioinformatics, 2017, 18, 262.	2.6	0
56	3DSNP: a database for linking human noncoding SNPs to their three-dimensional interacting genes. Nucleic Acids Research, 2017, 45, D643-D649.	14.5	90
57	Drug–target interaction prediction with a deep-learning-based model. , 2017, , .		9
58	paraGSEA: a scalable approach for large-scale gene expression profiling. Nucleic Acids Research, 2017, 45, e155-e155.	14.5	9
59	Systematic Identification and Assessment of Therapeutic Targets for Breast Cancer Based on Genome-Wide RNA Interference Transcriptomes. Genes, 2017, 8, 86.	2.4	12
60	Genomics and Comparative Genomic Analyses Provide Insight into the Taxonomy and Pathogenic Potential of Novel Emmonsia Pathogens. Frontiers in Cellular and Infection Microbiology, 2017, 7, 105.	3.9	6
61	NFP: An R Package for Characterizing and Comparing of Annotated Biological Networks. BioMed Research International, 2017, 2017, 1-5.	1.9	0
62	Partners of patients with ulcerative colitis exhibit a biologically relevant dysbiosis in fecal microbial metacommunities. World Journal of Gastroenterology, 2017, 23, 4624.	3.3	23
63	Genome-wide identification and characterisation of HOT regions in the human genome. BMC Genomics, 2016, 17, 733.	2.8	11
64	Cogena, a novel tool for co-expressed gene-set enrichment analysis, applied to drug repositioning and drug mode of action discovery. BMC Genomics, 2016, 17, 414.	2.8	62
65	Genome Sequencing and Comparative Genomics Analysis Revealed Pathogenic Potential in Penicillium capsulatum as a Novel Fungal Pathogen Belonging to Eurotiales. Frontiers in Microbiology, 2016, 7, 1541.	3.5	11
66	RevEcoR: an R package for the reverse ecology analysis of microbiomes. BMC Bioinformatics, 2016, 17, 294.	2.6	34
67	PEDLA: predicting enhancers with a deep learning-based algorithmic framework. Scientific Reports, 2016, 6, 28517.	3.3	88
68	Exploring the efficacy of paternity and kinship testing based on single nucleotide polymorphisms. Forensic Science International: Genetics, 2016, 22, 161-168.	3.1	21
69	Radiation protective effects of baclofen predicted by a computational drug repurposing strategy. Pharmacological Research, 2016, 113, 475-483.	7.1	6
70	Intra-host dynamics of Ebola virus during 2014. Nature Microbiology, 2016, 1, 16151.	13.3	70
71	Direct next-generation sequencing of virus-human mixed samples without pretreatment is favorable to recover virus genome. Biology Direct, 2016, 11, 3.	4.6	19
72	ICM: a web server for integrated clustering of multi-dimensional biomedical data. Nucleic Acids Research, 2016, 44, W154-W159.	14.5	18

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73	The relationships among host transcriptional responses reveal distinct signatures underlying viral infection-disease associations. Molecular BioSystems, 2016, 12, 653-665.	2.9	0
74	*De novo* identification of replication-timing domains in the human genome by deep learning. Bioinformatics, 2016, 32, 641-649.	4.1	48
75	Influence of the Biliary System on Biliary Bacteria Revealed by Bacterial Communities of the Human Biliary and Upper Digestive Tracts. PLoS ONE, 2016, 11, e0150519.	2.5	70
76	Neuroendocrine immunomodulation network dysfunction in SAMP8 mice and PrP-hAβPPswe/PS1ΔE9 mice: potential mechanism underlying cognitive impairment. Oncotarget, 2016, 7, 22988-23005.	1.8	17
77	iFORM: Incorporating Find Occurrence of Regulatory Motifs. PLoS ONE, 2016, 11, e0168607.	2.5	2
78	Inferring Infection Patterns Based on a Connectivity Map of Host Transcriptional Responses. Scientific Reports, 2015, 5, 15820.	3.3	4
79	Functional annotation of HOT regions in the human genome: implications for human disease and cancer. Scientific Reports, 2015, 5, 11633.	3.3	24
80	Metagenomic sequencing of bile from gallstone patients to identify different microbial community patterns and novel biliary bacteria. Scientific Reports, 2015, 5, 17450.	3.3	70
81	Network fingerprint: a knowledge-based characterization of biomedical networks. Scientific Reports, 2015, 5, 13286.	3.3	11
82	Gene Ranking of RNA-Seq Data via Discriminant Non-Negative Matrix Factorization. PLoS ONE, 2015, 10, e0137782.	2.5	22
83	mmnet: An R Package for Metagenomics Systems Biology Analysis. BioMed Research International, 2015, 2015, 1-5.	1.9	12
84	EHFPI: a database and analysis resource of essential host factors for pathogenic infection. Nucleic Acids Research, 2015, 43, D946-D955.	14.5	13
85	An integrative analysis of TFBS-clustered regions reveals new transcriptional regulation models on the accessible chromatin landscape. Scientific Reports, 2015, 5, 8465.	3.3	41
86	Computational Prediction and Validation of BAHD1 as a Novel Molecule for UlcerativeColitis. Scientific Reports, 2015, 5, 12227.	3.3	16
87	Effects of 5-h multimodal stress on the molecules and pathways involved in dendritic morphology and cognitive function. Neurobiology of Learning and Memory, 2015, 123, 225-238.	1.9	7
88	Exploring the associations of host genes for viral infection revealed by genome-wide RNAi and virus–host protein interactions. Molecular BioSystems, 2015, 11, 2511-2519.	2.9	7
89	Genetic diversity and evolutionary dynamics of Ebola virus in Sierra Leone. Nature, 2015, 524, 93-96.	27.8	150
90	New insights into the landscape relationships of host response to bacterial pathogens. , 2015, , .		0

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91	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. Current Alzheimer Research, 2015, 12, 870-885.	1.4	13
92	Predicting drug side effects based on link prediction in bipartite network. , 2014, , .		11
93	ExpTreeDB: Web-based query and visualization of manually annotated gene expression profiling experiments of human and mouse from GEO. Bioinformatics, 2014, 30, 3379-3386.	4.1	6
94	GeneExpressionSignature: an R package for discovering functional connections using gene expression signatures. OMICS A Journal of Integrative Biology, 2013, 17, 116-118.	2.0	18
95	Proteomic analysis at the subcellular level for host targets against influenza A virus (H1N1). Antiviral Research, 2013, 100, 673-687.	4.1	13
96	Exploring the role of human miRNAs in virus–host interactions using systematic overlap analysis. Bioinformatics, 2013, 29, 2375-2379.	4.1	18
97	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. Frontiers in Aging Neuroscience, 2013, 5, 65.	3.4	57
98	Biomedical Applications Using Cloud Technologies. Scientia Sinica Vitae, 2013, 43, 569-578.	0.3	0
99	Targeting Bacterial RNA Polymerase σ70 for Development of Broadspectrum Antisense Antibacterials. Recent Patents on Anti-infective Drug Discovery, 2012, 7, 213-222.	0.8	1
100	Cellular micro<scp>RNA</scp> let–7c inhibits M1 protein expression of the H1N1 influenza <scp>A</scp> virus in infected human lung epithelial cells. Journal of Cellular and Molecular Medicine, 2012, 16, 2539-2546.	3.6	110
101	Comprehensive Identification and Annotation of Cell Type-Specific and Ubiquitous CTCF-Binding Sites in the Human Genome. PLoS ONE, 2012, 7, e41374.	2.5	119
102	Computational Approaches to Analyze the Strategies of Drug Repositioning*. Progress in Biochemistry and Biophysics, 2012, 39, 1029-1036.	0.3	1
103	A new method for measuring functional similarity of microRNAs. Journal of Integrated OMICS, 2011, 1, .	0.5	8
104	Characterization the regulation of herpesvirus miRNAs from the view of human protein interaction network. BMC Systems Biology, 2011, 5, 93.	3.0	4
105	Topology aware functional similarity of protein interaction networks based on gene ontology. , 2011, 2011, 6857-60.		0
106	Genome-wide analysis of the relationships between DNaseI HS, histone modifications and gene expression reveals distinct modes of chromatin domains. Nucleic Acids Research, 2011, 39, 7428-7443.	14.5	52
107	Analysis of synonymous codon usage bias in 09H1N1. Virologica Sinica, 2010, 25, 329-340.	3.0	10
108	Correlation between sequence conservation and structural thermodynamics of microRNA precursors from human, mouse, and chicken genomes. BMC Evolutionary Biology, 2010, 10, 329.	3.2	11

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109	ARDesigner: A web-based system for allosteric RNA design. Journal of Biotechnology, 2010, 150, 466-473.	3.8	9
110	GOSemSim: an R package for measuring semantic similarity among GO terms and gene products. Bioinformatics, 2010, 26, 976-978.	4.1	978
111	PerturbationAnalyzer: a tool for investigating the effects of concentration perturbation on protein interaction networks. Bioinformatics, 2010, 26, 275-277.	4.1	15
112	Discovering Active Subnetwork in Protein Interaction Network*. Progress in Biochemistry and Biophysics, 2010, 37, 208-217.	0.3	2
113	Optimizing Reference Gene Set for Inter-Chip Normalization Using Genetic Algorithm. , 2009, , .		0
114	Dynamic Propagation Properties of Virus-Host Protein Interaction Network. , 2009, , .		1
115	EvoRSR: an integrated system for exploring evolution of RNA structural robustness. BMC Bioinformatics, 2009, 10, 249.	2.6	0
116	Towards a Comprehensive HBV-Human Interaction Map. , 2009, , .		0
117	Design of 16 S rRNA-based Oligonucleotide Array Using Group-specific Non-unique Probes in Large Scale Bacteria Detection*. Progress in Biochemistry and Biophysics, 2009, 36, 1025-1034.	0.3	0
118	In Silico Genetic Robustness Analysis of Secondary Structural Elements in the miRNA Gene. Journal of Molecular Evolution, 2008, 67, 560-569.	1.8	8
119	A novel representation of RNA secondary structure based on element-contact graphs. BMC Bioinformatics, 2008, 9, 188.	2.6	15
120	RSRE: RNA structural robustness evaluator. Nucleic Acids Research, 2007, 35, W314-W319.	14.5	8
121	In silico genetic robustness analysis of microRNA secondary structures: potential evidence of congruent evolution in microRNA. BMC Evolutionary Biology, 2007, 7, 223.	3.2	19
122	Protocatechuic aldehyde inhibits hepatitis B virus replication both in vitro and in vivo. Antiviral Research, 2007, 74, 59-64.	4.1	92
123	Fibronectin is essential for hepatitis B virus propagation in vitro: May be a potential cellular target?. Biochemical and Biophysical Research Communications, 2006, 344, 757-764.	2.1	12
124	Selection of antisense oligonucleotides based on multiple predicted target mRNA structures. BMC Bioinformatics, 2006, 7, 122.	2.6	12
125	RDMAS: a web server for RNA deleterious mutation analysis. BMC Bioinformatics, 2006, 7, 404.	2.6	31
126	AOBase: a database for antisense oligonucleotides selection and design. Nucleic Acids Research, 2006, 34, D664-D667.	14.5	12

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127	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
128	TargetFinder: a software for antisense oligonucleotide target site selection based on MAST and secondary structures of target mRNA. Bioinformatics, 2005, 21, 1401-1402.	4.1	96
129	Screening of specific antigens for SARS clinical diagnosis using a protein microarray. Analyst, The, 2005, 130, 474.	3.5	15
130	HBVPathDB: A database of HBV infection-related molecular interaction network. World Journal of Gastroenterology, 2005, 11, 1690.	3.3	5