

Xiao-chen Bo

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

124 papers	2,825 citations	23 h-index	50 g-index
142 ext. papers	4,679 ext. citations	7.1 avg, IF	5.19 L-index

#	Paper	IF	Citations
124	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	6.8	
123	Assessment of two-pool multiplex long-amplicon nanopore sequencing of SARS-CoV-2. <i>Journal of Medical Virology</i> , 2022 , 94, 327-334	19.7	4
122	Dynamic Interplay between Structural Variations and 3D Genome Organization in Pancreatic Cancer.. <i>Advanced Science</i> , 2022 , e2200818	13.6	0
121	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	4
120	COMSUC: A web server for the identification of consensus molecular subtypes of cancer based on multiple methods and multi-omics data. <i>PLoS Computational Biology</i> , 2021 , 17, e1008769	5	1
119	Synthetic Lethal Interactions Prediction Based on Multiple Similarity Measures Fusion. <i>Journal of Computer Science and Technology</i> , 2021 , 36, 261-275	1.7	1
118	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	3.1	7
117	ggtreeExtra: Compact Visualization of Richly Annotated Phylogenetic Data. <i>Molecular Biology and Evolution</i> , 2021 , 38, 4039-4042	8.3	15
116	Computational methods for the prediction of chromatin interaction and organization using sequence and epigenomic profiles. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	2
115	A Metagraph-Based Model for Predicting Drug-Target Interaction on Heterogeneous Network. <i>Lecture Notes in Computer Science</i> , 2021 , 465-476	0.9	
114	Multi-dimensional data integration algorithm based on random walk with restart. <i>BMC Bioinformatics</i> , 2021 , 22, 97	3.6	3
113	Drug-Target Interaction Prediction Based on Adversarial Bayesian Personalized Ranking. <i>BioMed Research International</i> , 2021 , 2021, 6690154	3	2
112	clusterProfiler 4.0: A universal enrichment tool for interpreting omics data. <i>Innovation(China)</i> , 2021 , 2, 100141	17.8	238
111	Machine learning methods, databases and tools for drug combination prediction. <i>Briefings in Bioinformatics</i> , 2021 ,	13.4	5
110	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	6.8	2
109	LINCS dataset-based repositioning of rosiglitazone as a potential anti-human adenovirus drug. <i>Antiviral Research</i> , 2020 , 179, 104789	10.8	4
108	High-resolution annotation of the mouse preimplantation embryo transcriptome using long-read sequencing. <i>Nature Communications</i> , 2020 , 11, 2653	17.4	7

107	Comprehensive analysis of miRNA-gene regulatory network with clinical significance in human cancers. <i>Science China Life Sciences</i> , 2020 , 63, 1201-1212	8.5	5
106	Inhibition of Histone Deacetylation by MS-275 Alleviates Colitis by Activating the Vitamin D Receptor. <i>Journal of Crohns and Colitis</i> , 2020 , 14, 1103-1118	1.5	6
105	DeepHiC: A generative adversarial network for enhancing Hi-C data resolution. <i>PLoS Computational Biology</i> , 2020 , 16, e1007287	5	17
104	Domain-adversarial multi-task framework for novel therapeutic property prediction of compounds. <i>Bioinformatics</i> , 2020 , 36, 2848-2855	7.2	4
103	DTIGCCN: Prediction of drug-target interactions based on GCN and CNN 2020 ,		2
102	Exploring the classification of cancer cell lines from multiple omic views. <i>PeerJ</i> , 2020 , 8, e9440	3.1	2
101	PIMD: An Integrative Approach for Drug Repositioning Using Multiple Characterization Fusion. <i>Genomics, Proteomics and Bioinformatics</i> , 2020 , 18, 565-581	6.5	3
100	Genomic analyses reveal evolutionary and geologic context for the plateau fungus. <i>Chinese Medicine</i> , 2020 , 15, 107	4.7	0
99	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	13.4	20
98	Exploration of prognosis-related microRNA and transcription factor co-regulatory networks across cancer types. <i>RNA Biology</i> , 2019 , 16, 1010-1021	4.8	4
97	ARQ-197 enhances the antitumor effect of sorafenib in hepatocellular carcinoma cells via decelerating its intracellular clearance. <i>OncoTargets and Therapy</i> , 2019 , 12, 1629-1640	4.4	17
96	Stable H3K4me3 is associated with transcription initiation during early embryo development. <i>Bioinformatics</i> , 2019 , 35, 3931-3936	7.2	9
95	LIVE: a manually curated encyclopedia of experimentally validated interactions of lncRNAs. <i>Database: the Journal of Biological Databases and Curation</i> , 2019 , 2019,	5	8
94	A survey and evaluation of Web-based tools/databases for variant analysis of TCGA data. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1524-1541	13.4	23
93	Deep Learning and Its Applications in Biomedicine. <i>Genomics, Proteomics and Bioinformatics</i> , 2018 , 16, 17-32	6.5	239
92	A 472-SNP panel for pairwise kinship testing of second-degree relatives. <i>Forensic Science International: Genetics</i> , 2018 , 34, 178-185	4.3	23
91	Accurate identification of RNA editing sites from primitive sequence with deep neural networks. <i>Scientific Reports</i> , 2018 , 8, 6005	4.9	9
90	Lnc2Catlas: an atlas of long noncoding RNAs associated with risk of cancers. <i>Scientific Reports</i> , 2018 , 8, 1909	4.9	22

89	The landscape of the A-to-I RNA editome from 462 human genomes. <i>Scientific Reports</i> , 2018 , 8, 12069	4.9	8
88	CMTCN: a web tool for investigating cancer-specific microRNA and transcription factor co-regulatory networks. <i>PeerJ</i> , 2018 , 6, e5951	3.1	8
87	paraSNF: An Parallel Approach for Large-Scale Similarity Network Fusion. <i>Communications in Computer and Information Science</i> , 2018 , 155-167	0.3	
86	Prediction of DTIs for high-dimensional and class-imbalanced data based on CGAN 2018 ,		1
85	Deep learning-based transcriptome data classification for drug-target interaction prediction. <i>BMC Genomics</i> , 2018 , 19, 667	4.5	44
84	DTI-RCNN: New Efficient Hybrid Neural Network Model to Predict Drug-Target Interactions. <i>Lecture Notes in Computer Science</i> , 2018 , 104-114	0.9	6
83	Human enterovirus 71 protein interaction network prompts antiviral drug repositioning. <i>Scientific Reports</i> , 2017 , 7, 43143	4.9	8
82	Gut metagenomes of type 2 diabetic patients have characteristic single-nucleotide polymorphism distribution in <i>Bacteroides coprocola</i> . <i>Microbiome</i> , 2017 , 5, 15	16.6	18
81	Exploring spatially adjacent TFBS-clustered regions with Hi-C data. <i>Bioinformatics</i> , 2017 , 33, 2611-2614	7.2	1
80	Predicting potential gene ontology from cellular response data 2017 ,		1
79	BiRen: predicting enhancers with a deep-learning-based model using the DNA sequence alone. <i>Bioinformatics</i> , 2017 , 33, 1930-1936	7.2	70
78	NFP: An R Package for Characterizing and Comparing of Annotated Biological Networks. <i>BioMed Research International</i> , 2017 , 2017, 7457131	3	
77	Partners of patients with ulcerative colitis exhibit a biologically relevant dysbiosis in fecal microbial metacommunities. <i>World Journal of Gastroenterology</i> , 2017 , 23, 4624-4631	5.6	16
76	Discovery of novel therapeutic properties of drugs from transcriptional responses based on multi-label classification. <i>Scientific Reports</i> , 2017 , 7, 7136	4.9	11
75	Functional annotation of structural ncRNAs within enhancer RNAs in the human genome: implications for human disease. <i>Scientific Reports</i> , 2017 , 7, 15518	4.9	19
74	NFPscanner: a webtool for knowledge-based deciphering of biomedical networks. <i>BMC Bioinformatics</i> , 2017 , 18, 262	3.6	
73	3DSNP: a database for linking human noncoding SNPs to their three-dimensional interacting genes. <i>Nucleic Acids Research</i> , 2017 , 45, D643-D649	20.1	51
72	Drug-Target interaction prediction with a deep-learning-based model 2017 ,		6

71	paraGSEA: a scalable approach for large-scale gene expression profiling. <i>Nucleic Acids Research</i> , 2017 , 45, e155	20.1	6
70	Systematic Identification and Assessment of Therapeutic Targets for Breast Cancer Based on Genome-Wide RNA Interference Transcriptomes. <i>Genes</i> , 2017 , 8,	4.2	8
69	Genomics and Comparative Genomic Analyses Provide Insight into the Taxonomy and Pathogenic Potential of Novel Pathogens. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017 , 7, 105	5.9	4
68	Radiation protective effects of baclofen predicted by a computational drug repurposing strategy. <i>Pharmacological Research</i> , 2016 , 113, 475-483	10.2	5
67	Intra-host dynamics of Ebola virus during 2014. <i>Nature Microbiology</i> , 2016 , 1, 16151	26.6	54
66	Direct next-generation sequencing of virus-human mixed samples without pretreatment is favorable to recover virus genome. <i>Biology Direct</i> , 2016 , 11, 3	7.2	10
65	ICM: a web server for integrated clustering of multi-dimensional biomedical data. <i>Nucleic Acids Research</i> , 2016 , 44, W154-9	20.1	13
64	The relationships among host transcriptional responses reveal distinct signatures underlying viral infection-disease associations. <i>Molecular BioSystems</i> , 2016 , 12, 653-65		
63	Delhovo identification of replication-timing domains in the human genome by deep learning. <i>Bioinformatics</i> , 2016 , 32, 641-9	7.2	35
62	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	3.7	38
61	Neuroendocrine immunomodulation network dysfunction in SAMP8 mice and PrP-hAPPswe/PS1E9 mice: potential mechanism underlying cognitive impairment. <i>Oncotarget</i> , 2016 , 7, 22988-3005	3.3	15
60	iFORM: Incorporating Find Occurrence of Regulatory Motifs. <i>PLoS ONE</i> , 2016 , 11, e0168607	3.7	2
59	Genome-wide identification and characterisation of HOT regions in the human genome. <i>BMC Genomics</i> , 2016 , 17, 733	4.5	10
58	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	4.5	36
57	Genome Sequencing and Comparative Genomics Analysis Revealed Pathogenic Potential in as a Novel Fungal Pathogen Belonging to. <i>Frontiers in Microbiology</i> , 2016 , 7, 1541	5.7	7
56	RevEcoR: an R package for the reverse ecology analysis of microbiomes. <i>BMC Bioinformatics</i> , 2016 , 17, 294	3.6	16
55	PEDLA: predicting enhancers with a deep learning-based algorithmic framework. <i>Scientific Reports</i> , 2016 , 6, 28517	4.9	65
54	Exploring the efficacy of paternity and kinship testing based on single nucleotide polymorphisms. <i>Forensic Science International: Genetics</i> , 2016 , 22, 161-168	4.3	13

53	EHFPI: a database and analysis resource of essential host factors for pathogenic infection. <i>Nucleic Acids Research</i> , 2015 , 43, D946-55	20.1	13
52	An integrative analysis of TFBS-clustered regions reveals new transcriptional regulation models on the accessible chromatin landscape. <i>Scientific Reports</i> , 2015 , 5, 8465	4.9	27
51	Computational Prediction and Validation of BAHD1 as a Novel Molecule for Ulcerative Colitis. <i>Scientific Reports</i> , 2015 , 5, 12227	4.9	13
50	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, 225-38	3.1	6
49	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, 2511-9		5
48	Genetic diversity and evolutionary dynamics of Ebola virus in Sierra Leone. <i>Nature</i> , 2015 , 524, 93-6	50.4	121
47	Inferring Infection Patterns Based on a Connectivity Map of Host Transcriptional Responses. <i>Scientific Reports</i> , 2015 , 5, 15820	4.9	2
46	Functional annotation of HOT regions in the human genome: implications for human disease and cancer. <i>Scientific Reports</i> , 2015 , 5, 11633	4.9	20
45	Metagenomic sequencing of bile from gallstone patients to identify different microbial community patterns and novel biliary bacteria. <i>Scientific Reports</i> , 2015 , 5, 17450	4.9	43
44	Network fingerprint: a knowledge-based characterization of biomedical networks. <i>Scientific Reports</i> , 2015 , 5, 13286	4.9	9
43	Gene Ranking of RNA-Seq Data via Discriminant Non-Negative Matrix Factorization. <i>PLoS ONE</i> , 2015 , 10, e0137782	3.7	17
42	mmnet: An R Package for Metagenomics Systems Biology Analysis. <i>BioMed Research International</i> , 2015 , 2015, 167249	3	12
41	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, 870-85	3	11
40	Predicting drug side effects based on link prediction in bipartite network 2014 ,		7
39	ExpTreeDB: web-based query and visualization of manually annotated gene expression profiling experiments of human and mouse from GEO. <i>Bioinformatics</i> , 2014 , 30, 3379-86	7.2	5
38	GeneExpressionSignature: an R package for discovering functional connections using gene expression signatures. <i>OMICS A Journal of Integrative Biology</i> , 2013 , 17, 116-8	3.8	15
37	Proteomic analysis at the subcellular level for host targets against influenza A virus (H1N1). <i>Antiviral Research</i> , 2013 , 100, 673-87	10.8	12
36	Exploring the role of human miRNAs in virus-host interactions using systematic overlap analysis. <i>Bioinformatics</i> , 2013 , 29, 2375-9	7.2	8

35	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	5.3	33
34	Cellular microRNA let-7c 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, 2539-46	5.6	90
33	Targeting bacterial RNA polymerase σ 70 for development of broad-spectrum antisense antibacterials. <i>Recent Patents on Anti-infective Drug Discovery</i> , 2012 , 7, 213-22	1.6	
32	Comprehensive identification and annotation of cell type-specific and ubiquitous CTCF-binding sites in the human genome. <i>PLoS ONE</i> , 2012 , 7, e41374	3.7	89
31	Computational Approaches to Analyze the Strategies of Drug Repositioning*. <i>Progress in Biochemistry and Biophysics</i> , 2012 , 39, 1029-1036		1
30	A new method for measuring functional similarity of microRNAs. <i>Journal of Integrated OMICS</i> , 2011 , 1,	0.5	3
29	Characterization the regulation of herpesvirus miRNAs from the view of human protein interaction network. <i>BMC Systems Biology</i> , 2011 , 5, 93	3.5	4
28	Topology aware functional similarity of protein interaction networks based on gene ontology. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2011 , 2011, 6857-60	0.9	
27	Genome-wide analysis of the relationships between DNaseI HS, histone modifications and gene expression reveals distinct modes of chromatin domains. <i>Nucleic Acids Research</i> , 2011 , 39, 7428-43	20.1	46
26	GOSemSim: an R package for measuring semantic similarity among GO terms and gene products. <i>Bioinformatics</i> , 2010 , 26, 976-8	7.2	595
25	PerturbationAnalyzer: a tool for investigating the effects of concentration perturbation on protein interaction networks. <i>Bioinformatics</i> , 2010 , 26, 275-7	7.2	14
24	Analysis of synonymous codon usage bias in 09H1N1. <i>Virologica Sinica</i> , 2010 , 25, 329-40	6.4	10
23	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	9
22	ARDesigner: a web-based system for allosteric RNA design. <i>Journal of Biotechnology</i> , 2010 , 150, 466-73	3.7	9
21	Discovering Active Subnetwork in Protein Interaction Network*. <i>Progress in Biochemistry and Biophysics</i> , 2010 , 37, 208-217		1
20	EvoRSR: an integrated system for exploring evolution of RNA structural robustness. <i>BMC Bioinformatics</i> , 2009 , 10, 249	3.6	
19	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		
18	A novel representation of RNA secondary structure based on element-contact graphs. <i>BMC Bioinformatics</i> , 2008 , 9, 188	3.6	13

17	In silico genetic robustness analysis of secondary structural elements in the miRNA gene. <i>Journal of Molecular Evolution</i> , 2008 , 67, 560-9	3.1	8
16	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	15
15	Protocatechuic aldehyde inhibits hepatitis B virus replication both in vitro and in vivo. <i>Antiviral Research</i> , 2007 , 74, 59-64	10.8	76
14	RSRE: RNA structural robustness evaluator. <i>Nucleic Acids Research</i> , 2007 , 35, W314-9	20.1	8
13	Selection of antisense oligonucleotides based on multiple predicted target mRNA structures. <i>BMC Bioinformatics</i> , 2006 , 7, 122	3.6	10
12	RDMAS: a web server for RNA deleterious mutation analysis. <i>BMC Bioinformatics</i> , 2006 , 7, 404	3.6	25
11	AOBase: a database for antisense oligonucleotides selection and design. <i>Nucleic Acids Research</i> , 2006 , 34, D664-7	20.1	11
10	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, 757-64	3.4	11
9	Screening of specific antigens for SARS clinical diagnosis using a protein microarray. <i>Analyst, The</i> , 2005 , 130, 474-82	5	14
8	Selection and their antitumor activity of antisense oligonucleotides targeting messenger RNA of vascular endothelial growth factor receptor 2. <i>Chinese Journal of Cancer Research: Official Journal of China Anti-Cancer Association, Beijing Institute for Cancer Research</i> , 2005 , 17, 161-170	3.8	
7	TargetFinder: a software for antisense oligonucleotide target site selection based on MAST and secondary structures of target mRNA. <i>Bioinformatics</i> , 2005 , 21, 1401-2	7.2	53
6	HBVPathDB: a database of HBV infection-related molecular interaction network. <i>World Journal of Gastroenterology</i> , 2005 , 11, 1690-2	5.6	3
5	DeepHiC: A Generative Adversarial Network for Enhancing Hi-C Data Resolution		1
4	PEDLA: predicting enhancers with a deep learning-based algorithmic framework		2
3	Genome-wide identification and characterisation of HOT regions in the human genome		1
2	iFORM: incorporating Find Occurrence of Regulatory Motifs		2
1	Synthetic Lethal Interactions Prediction Based on Multiple Similarity Measures Fusion		1