Dong Xu

List of Publications by Year
in descending order

157	5,419	117625	102487
papers	citations	34	66
		h-index	g-index

159	159	159	7652
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Routine Microsecond Molecular Dynamics Simulations with AMBER on GPUs. 1. Generalized Born. Journal of Chemical Theory and Computation, 2012, 8, 1542-1555.	5.3	1,633
2	Soybean (Glycine max) SWEET gene family: insights through comparative genomics, transcriptome profiling and whole genome re-sequence analysis. BMC Genomics, 2015, 16, 520.	2.8	173
3	scGNN is a novel graph neural network framework for single-cell RNA-Seq analyses. Nature Communications, 2021, 12, 1882.	12.8	139
4	MUFOLDâ€ŠS: New deep inceptionâ€insideâ€inception networks for protein secondary structure prediction. Proteins: Structure, Function and Bioinformatics, 2018, 86, 592-598.	2.6	134
5	Identification and Comparative Analysis of Differential Gene Expression in Soybean Leaf Tissue under Drought and Flooding Stress Revealed by RNA-Seq. Frontiers in Plant Science, 2016, 7, 1044.	3.6	116
6	Human Gait Recognition With Matrix Representation. IEEE Transactions on Circuits and Systems for Video Technology, 2006, 16, 896-903.	8.3	114
7	Genome-wide transcriptome analysis of soybean primary root under varying water-deficit conditions. BMC Genomics, 2016, 17, 57.	2.8	99
8	DM3Loc: multi-label mRNA subcellular localization prediction and analysis based on multi-head self-attention mechanism. Nucleic Acids Research, 2021, 49, e46-e46.	14.5	95
9	iPhosâ€PseEvo: Identifying Human Phosphorylated Proteins by Incorporating Evolutionary Information into General PseAAC via Grey System Theory. Molecular Informatics, 2017, 36, 1600010.	2.5	94
10	Imbalanced multi-label learning for identifying antimicrobial peptides and their functional types. Bioinformatics, 2016, 32, 3745-3752.	4.1	92
11	Capsule network for protein post-translational modification site prediction. Bioinformatics, 2019, 35, 2386-2394.	4.1	92
12	Overcoming Wntâ€Î²-catenin dependent anticancer therapy resistance in leukaemia stem cells. Nature Cell Biology, 2020, 22, 689-700.	10.3	89
13	Major Soybean Maturity Gene Haplotypes Revealed by SNPViz Analysis of 72 Sequenced Soybean Genomes. PLoS ONE, 2014, 9, e94150.	2.5	89
14	The human epilepsy mutation GABRG2(Q390X) causes chronic subunit accumulation and neurodegeneration. Nature Neuroscience, 2015, 18, 988-996.	14.8	82
15	Predicting DNA Methylation State of CpG Dinucleotide Using Genome Topological Features and Deep Networks. Scientific Reports, 2016, 6, 19598.	3.3	75
16	A self-attention based message passing neural network for predicting molecular lipophilicity and aqueous solubility. Journal of Cheminformatics, 2020, 12, 15.	6.1	73
17	Automated Tongue Feature Extraction for ZHENG Classification in Traditional Chinese Medicine. Evidence-based Complementary and Alternative Medicine, 2012, 2012, 1-14.	1.2	64
18	Transcriptional responses of Arabidopsis thaliana to chewing and sucking insect herbivores. Frontiers in Plant Science, 2014, 5, 565.	3.6	61

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19	Strategies for Inhibition of MDR1 Gene Expression. Molecular Pharmacology, 2004, 66, 268-275.	2.3	56
20	Fuzzified Image Enhancement for Deep Learning in Iris Recognition. IEEE Transactions on Fuzzy Systems, 2020, 28, 92-99.	9.8	55
21	RNALocate v2.0: an updated resource for RNA subcellular localization with increased coverage and annotation. Nucleic Acids Research, 2022, 50, D333-D339.	14.5	54
22	Comparative analysis of the drought-responsive transcriptome in soybean lines contrasting for canopy wilting. Plant Science, 2015, 240, 65-78.	3.6	53
23	Selective Inhibition of P-glycoprotein Expression in Multidrug-Resistant Tumor Cells by a Designed Transcriptional Regulator. Journal of Pharmacology and Experimental Therapeutics, 2002, 302, 963-971.	2.5	51
24	Diverse and divergent protein post-translational modifications in two growth stages of a natural microbial community. Nature Communications, 2014, 5, 4405.	12.8	51
25	xMDFF: molecular dynamics flexible fitting of low-resolution X-ray structures. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2344-2355.	2.5	50
26	ezCADD: A Rapid 2D/3D Visualization-Enabled Web Modeling Environment for Democratizing Computer-Aided Drug Design. Journal of Chemical Information and Modeling, 2019, 59, 18-24.	5.4	47
27	Identification of new loci for salt tolerance in soybean by high-resolution genome-wide association mapping. BMC Genomics, 2019, 20, 318.	2.8	46
28	Rank-One Projections With Adaptive Margins for Face Recognition. IEEE Transactions on Systems, Man, and Cybernetics, 2007, 37, 1226-1236.	5.0	44
29	Plant-derived phosphocholine facilitates cellular uptake of anti-pulmonary fibrotic HJT-sRNA-m7. Science China Life Sciences, 2019, 62, 309-320.	4.9	43
30	AI-Aided Design of Novel Targeted Covalent Inhibitors against SARS-CoV-2. Biomolecules, 2022, 12, 746.	4.0	43
31	Mapping and confirmation of loci for salt tolerance in a novel soybean germplasm, Fiskeby III. Theoretical and Applied Genetics, 2018, 131, 513-524.	3.6	42
32	Deep learning shapes single-cell data analysis. Nature Reviews Molecular Cell Biology, 2022, 23, 303-304.	37.0	40
33	Studies of the Mechanism of Phenol Hydroxylase:Â Mutants Tyr289Phe, Asp54Asn, and Arg281Metâ€. Biochemistry, 2001, 40, 12369-12378.	2.5	39
34	Effect of lipo-chitooligosaccharide on early growth of C_4 grass seedlings. Journal of Experimental Botany, 2015, 66, 5727-5738.	4.8	39
35	DL-PRO: A novel deep learning method for protein model quality assessment. , 2014, 2014, 2071-2078.		38
36	Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing. Scientific Data, 2021, 8, 50.	5.3	38

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37	Neural relational inference to learn long-range allosteric interactions in proteins from molecular dynamics simulations. Nature Communications, 2022, 13, 1661.	12.8	38
38	A missense mutation in SLC6A1 associated with Lennox-Gastaut syndrome impairs GABA transporter 1 protein trafficking and function. Experimental Neurology, 2019, 320, 112973.	4.1	37
39	Identification of quantitative trait loci underlying resistance to southern root-knot and reniform nematodes in soybean accession PI 567516C. Molecular Breeding, 2015, 35, 131.	2.1	34
40	FALCON@home: a high-throughput protein structure prediction server based on remote homologue recognition. Bioinformatics, 2016, 32, 462-464.	4.1	34
41	Visual Event Recognition in News Video using Kernel Methods with Multi-Level Temporal Alignment. , 2007, , .		33
42	Inductive inference of gene regulatory network using supervised and semi-supervised graph neural networks. Computational and Structural Biotechnology Journal, 2020, 18, 3335-3343.	4.1	31
43	Endoplasmic reticulum retention and degradation of a mutation in SLC6A1 associated with epilepsy and autism. Molecular Brain, 2020, 13, 76.	2.6	30
44	Large-scale prediction of protein ubiquitination sites using a multimodal deep architecture. BMC Systems Biology, 2018, 12, 109.	3.0	29
45	Characterization of Select Wild Soybean Accessions in the USDA Germplasm Collection for Seed Composition and Agronomic Traits. Crop Science, 2019, 59, 233-251.	1.8	29
46	Flowerâ€visiting insects and their potential impact on transgene flow in rice. Journal of Applied Ecology, 2014, 51, 1357-1365.	4.0	27
47	Single-Cell Techniques and Deep Learning in Predicting Drug Response. Trends in Pharmacological Sciences, 2020, 41, 1050-1065.	8.7	27
48	The Evolution of Soybean Knowledge Base (SoyKB). Methods in Molecular Biology, 2017, 1533, 149-159.	0.9	25
49	Molecular insights into the improved clinical performance of PEGylated interferon therapeutics: a molecular dynamics perspective. RSC Advances, 2018, 8, 2315-2322.	3.6	23
50	In-Situ Metabolomic Analysis of <i>Setaria viridis</i> Roots Colonized by Beneficial Endophytic Bacteria. Molecular Plant-Microbe Interactions, 2020, 33, 272-283.	2.6	23
51	DeePaN: deep patient graph convolutional network integrating clinico-genomic evidence to stratify lung cancers for immunotherapy. Npj Digital Medicine, 2021, 4, 14.	10.9	23
52	Understanding the differences of the ligand binding/unbinding pathways between phosphorylated and non-phosphorylated ARH1 using molecular dynamics simulations. Scientific Reports, 2017, 7, 12439.	3.3	21
53	Assessing and predicting drug-induced anticholinergic risks: an integrated computational approach. Therapeutic Advances in Drug Safety, 2017, 8, 361-370.	2.4	21
54	Improving Protein Gamma-Turn Prediction Using Inception Capsule Networks. Scientific Reports, 2018, 8, 15741.	3.3	21

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55	Disrupting KATP channels diminishes the estrogen-mediated protection in female mutant mice during ischemia-reperfusion. Clinical Proteomics, 2014, 11, 19.	2.1	19
56	Tongue Images Classification Based on Constrained High Dispersal Network. Evidence-based Complementary and Alternative Medicine, 2017, 2017, 1-12.	1.2	19
57	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. Scientific Reports, 2018, 8, 9939.	3.3	19
58	Genetic mosaicism, intrafamilial phenotypic heterogeneity, and molecular defects of a novel missense SLC6A1 mutation associated with epilepsy and ADHD. Experimental Neurology, 2021, 342, 113723.	4.1	19
59	Computational Analysis of the Ligand Binding Site of the Extracellular ATP Receptor, DORN1. PLoS ONE, 2016, 11, e0161894.	2.5	18
60	Leveraging Systematic Functional Analysis to Benchmark an <i>In Silico</i> Framework Distinguishes Driver from Passenger MEK Mutants in Cancer. Cancer Research, 2020, 80, 4233-4243.	0.9	18
61	Soybean transcription factor ORFeome associated with drought resistance: a valuable resource to accelerate research on abiotic stress resistance. BMC Genomics, 2015, 16, 596.	2.8	17
62	Tongue Image Analysis and Its Mobile App Development for Health Diagnosis. Advances in Experimental Medicine and Biology, 2017, 1005, 99-121.	1.6	17
63	Element Rearrangement for Tensor-Based Subspace Learning. , 2007, , .		16
64	CORRELATION BETWEEN POSTTRANSLATIONAL MODIFICATION AND INTRINSIC DISORDER IN PROTEIN. , 2011, , .		16
65	Protein Loop Modeling Using Deep Generative Adversarial Network. , 2017, , .		16
66	Deep learning analysis and age prediction from shoeprints. Forensic Science International, 2021, 327, 110987.	2.2	16
67	Trends in Alzheimer's Disease Research Based upon Machine Learning Analysis of PubMed Abstracts. International Journal of Biological Sciences, 2019, 15, 2065-2074.	6.4	15
68	Differentiating enteric Escherichia coli from environmental bacteria through the putative glucosyltransferase gene (ycjM). Water Research, 2014, 61, 224-231.	11.3	14
69	Diagnosis of thyroid neoplasm using support vector machine algorithms based on platelet RNA-seq. Endocrine, 2021, 72, 758-783.	2.3	14
70	Impact of frailty on inpatient outcomes in thyroid cancer surgery: 10-year results from the U.S. national inpatient sample. Journal of Otolaryngology - Head and Neck Surgery, 2020, 49, 51.	1.9	13
71	Differential protein structural disturbances and suppression of assembly partners produced by nonsense GABRG2 epilepsy mutations: implications for disease phenotypic heterogeneity. Scientific Reports, 2016, 6, 35294.	3.3	12
72	Understanding the Phosphorylation Mechanism by Using Quantum Chemical Calculations and Molecular Dynamics Simulations. Journal of Physical Chemistry B, 2017, 121, 3565-3573.	2.6	12

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73	Implications of Off‑Target Serotoninergic Drug Activity: An Analysis of Serotonin Syndrome Reports Using a Systematic Bioinformatics Approach. Pharmacotherapy, 2018, 38, 888-898.	2.6	12
74	PSICA: a fast and accurate web service for protein model quality analysis. Nucleic Acids Research, 2019, 47, W443-W450.	14.5	12
75	G2PDeep: a web-based deep-learning framework for quantitative phenotype prediction and discovery of genomic markers. Nucleic Acids Research, 2021, 49, W228-W236.	14.5	12
76	Bioinformatics Analysis of Protein Phosphorylation in Plant Systems Biology Using P3DB. Methods in Molecular Biology, 2017, 1558, 127-138.	0.9	12
77	PROFILES AND FUZZY K-NEAREST NEIGHBOR ALGORITHM FOR PROTEIN SECONDARY STRUCTURE PREDICTION. , 2005, , .		12
78	Computational methods for protein localization prediction. Computational and Structural Biotechnology Journal, 2021, 19, 5834-5844.	4.1	12
79	An efficient branch-and-bound algorithm for the assignment of protein backbone NMR peaks. , 0, , .		11
80	Intrinsic Terminator Prediction and Its Application in Synechococcus sp. WH8102. Journal of Computer Science and Technology, 2005, 20, 465-482.	1.5	11
81	Protein Databases on the Internet. Current Protocols in Protein Science, 2012, 70, Unit2.6.	2.8	11
82	Genotypic variation of gene expression during the soybean innate immunity response. Plant Genetic Resources: Characterisation and Utilisation, 2014, 12, S27-S30.	0.8	11
83	New genotypes of Helicobacter Pylori VacA d-region identified from global strains. BMC Molecular and Cell Biology, 2021, 22, 4.	2.0	11
84	BridgeDb app: unifying identifier mapping services for Cytoscape. F1000Research, 2014, 3, 148.	1.6	11
85	Digital tongue image analyses for health assessment. Medical Review, 2021, 1, 172-198.	1.2	11
86	BFDCA: A Comprehensive Tool of Using Bayes Factor for Differential Co-Expression Analysis. Journal of Molecular Biology, 2017, 429, 446-453.	4.2	10
87	G2S: a web-service for annotating genomic variants on 3D protein structures. Bioinformatics, 2018, 34, 1949-1950.	4.1	10
88	Proteomic and Bioinformatic Profiling of Transporters in Higher Plant Mitochondria. Biomolecules, 2020, 10, 1190.	4.0	10
89	Survey sequencing of soybean elucidates the genome structure, composition and identifies novel repeats. Functional Plant Biology, 2006, 33, 765.	2.1	10
90	Zinc is a master-regulator of sperm function associated with binding, motility, and metabolic modulation during porcine sperm capacitation. Communications Biology, 2022, 5, .	4.4	10

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91	Computational Challenges in Characterization of Bacteria and Bacteria-Host Interactions Based on Genomic Data. Journal of Computer Science and Technology, 2012, 27, 225-239.	1.5	9
92	A multimodal deep architecture for large-scale protein ubiquitylation site prediction. , 2017, , .		9
93	Domain-specific Topic Model for Knowledge Discovery through Conversational Agents in Data Intensive Scientific Communities. , 2018, , .		9
94	Why Is a High Temperature Needed by Thermus thermophilus Argonaute During mRNA Silencing: A Theoretical Study. Frontiers in Chemistry, 2018, 6, 223.	3.6	9
95	IMPRes-Pro: A high dimensional multiomics integration method for in silico hypothesis generation. Methods, 2020, 173, 16-23.	3.8	9
96	A deep dense inception network for protein betaâ€turn prediction. Proteins: Structure, Function and Bioinformatics, 2020, 88, 143-151.	2.6	9
97	Assessing deep learning methods in <i>cis</i>-regulatory motif finding based on genomic sequencing data. Briefings in Bioinformatics, 2022, 23, .	6.5	9
98	GENOME-SCALE PROTEIN FUNCTION PREDICTION IN YEAST SACCHAROMYCES CEREVISIAE THROUGH INTEGRATING MULTIPLE SOURCES OF HIGH-THROUGHPUT DATA. , 2004, , .		9
99	Features for automated tongue image shape classification. , 2012, , .		8
100	BioJava-ModFinder: identification of protein modifications in 3D structures from the Protein Data Bank. Bioinformatics, 2017, 33, 2047-2049.	4.1	8
101	DeepDom: Predicting protein domain boundary from sequence alone using stacked bidirectional LSTM. , 2018, , .		8
102	ZHENG classification in Traditional Chinese Medicine based on modified specular-free tongue images. , 2012, , .		7
103	Improving degree-based variable ordering heuristics for solving constraint satisfaction problems. Journal of Heuristics, 2016, 22, 125-145.	1.4	7
104	MSBIS: A Multi-Step Biomedical Informatics Screening Approach for Identifying Medications that Mitigate the Risks of Metoclopramide-Induced Tardive Dyskinesia. EBioMedicine, 2017, 26, 132-137.	6.1	7
105	How oncogenic mutations activate human MAP kinase 1 (MEK1): a molecular dynamics simulation study. Journal of Biomolecular Structure and Dynamics, 2020, 38, 3942-3958.	3.5	7
106	Artificial Intelligence-Driven Structurization of Diagnostic Information in Free-Text Pathology Reports. Journal of Pathology Informatics, 2020, 11, 4.	1.7	7
107	Protein structural model selection based on protein-dependent scoring function. Statistics and Its Interface, 2012, 5, 109-115.	0.3	7
108	Bioinformatics and Fuzzy Logic. , 2006, , .		6

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109	Protein Databases on the Internet. Current Protocols in Molecular Biology, 2012, 97, Unit 19.4..	2.9	6
110	Polymorphism of the glucosyltransferase gene (ycjM) in Escherichia coli and its use for tracking human fecal pollution in water. Science of the Total Environment, 2015, 537, 260-267.	8.0	6
111	OMPcontact: An Outer Membrane Protein Inter-Barrel Residue Contact Prediction Method. Journal of Computational Biology, 2017, 24, 217-228.	1.6	6
112	A Fast Projection-Based Algorithm for Clustering Big Data. Interdisciplinary Sciences, Computational Life Sciences, 2019, 11, 360-366.	3.6	6
113	Domain-specific Topic Model for Knowledge Discovery in Computational and Data-Intensive Scientific Communities. IEEE Transactions on Knowledge and Data Engineering, 2021, , 1-1.	5.7	5
114	COMBINING SEQUENCE AND STRUCTURAL PROFILES FOR PROTEIN SOLVENT ACCESSIBILITY PREDICTION. , 2008, , .		5
115	Overlapping Community Detection Based on Membership Degree Propagation. Entropy, 2021, 23, 15.	2.2	5
116	Evolutionary Dynamics of Indels in SARS-CoV-2 Spike Glycoprotein. Evolutionary Bioinformatics, 2021, 17, 117693432110646.	1.2	5
117	A new clustering-based method for protein structure selection. , 2008, , .		4
118	A new Hidden Markov Model for protein Quality Assessment using compatibility between protein sequence and structure. Tsinghua Science and Technology, 2014, 19, 559-567.	6.1	4
119	Exploring Human Diseases and Biological Mechanisms by Protein Structure Prediction and Modeling. Advances in Experimental Medicine and Biology, 2016, 939, 39-61.	1.6	4
120	Experimental identification and computational characterization of a novel extracellular metalloproteinase produced by Clostridium sordellii. RSC Advances, 2017, 7, 13928-13938.	3.6	4
121	An aggressive car-following model in the view of driving style. Canadian Journal of Civil Engineering, 2017, 44, 775-782.	1.3	4
122	Comparative Effectiveness of High-Dose Versus Standard-Dose Influenza Vaccines in Preventing Postinfluenza Deaths. Journal of Infectious Diseases, 2018, 218, 336-337.	4.0	4
123	A rectified factor network based biclustering method for detecting cancer-related coding genes and miRNAs, and their interactions. Methods, 2019, 166, 22-30.	3.8	4
124	IDENTIFICATION OF REGULATORY BINDING SITES USING MINIMUM SPANNING TREES. , 2002, , .		4
125	Coxiella burnetii Virulent Phase I and Avirulent Phase II Variants Differentially Manipulate Autophagy Pathway in Neutrophils. Infection and Immunity, 2022, 90, IAI0053421.	2.2	4
126	High-Resolution Translatome Analysis Reveals Cortical Cell Programs During Early Soybean Nodulation. Frontiers in Plant Science, 2022, 13, 820348.	3.6	4

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127	P53-Dependent Cell-Killing by Selective Repression of Thymidine Kinase and Reduced Prodrug Activation. Molecular Pharmacology, 2003, 64, 289-297.	2.3	3
128	NEW MDS AND CLUSTERING BASED ALGORITHMS FOR PROTEIN MODEL QUALITY ASSESSMENT AND SELECTION. International Journal on Artificial Intelligence Tools, 2013, 22, 1360006.	1.0	3
129	Selective refinement and selection of near-native models in protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1823-1835.	2.6	3
130	Variation in Gene Expression between Two Sorghum bicolor Lines Differing in Innate Immunity Response. Plants, 2021, 10, 1536.	3.5	3
131	Characterization of Protein Structure and Function at Genome Scale with a Computational Prediction Pipeline. , 2003, 25, 269-293.		3
132	GUV-Net for high fidelity shoeprint generation. Complex & Intelligent Systems, 0, , 1.	6.5	3
133	MUfoldQA_G: High-accuracy protein model QA via retraining and transformation. Computational and Structural Biotechnology Journal, 2021, 19, 6282-6290.	4.1	3
134	Rank-one Projections with Adaptive Margins for Face Recognition. , 0, , .		2
135	An automatic tongue detection and segmentation framework for computer-aided tongue image analysis. , 2011, , .		2
136	PRIMEGENSw3: A Web-Based Tool for High-Throughput Primer and Probe Design. , 2011, , .		2
137	Human encoded miRNAs that regulate the inflenenza virus genome. , 2012, , .		2
138	Classification of tongue images based on doublet and color space dictionary. , 2016, , .		2
139	Use of a Bioinformaticsâ€Based Toxicity Scoring System to Assess Serotonin Burden and Predict Populationâ€Level Adverse Drug Events from Concomitant Serotonergic Drug Therapy. Pharmacotherapy, 2019, 39, 171-181.	2.6	2
140	Detecting Cancer Survival Related Gene Markers Based on Rectified Factor Network. Frontiers in Bioengineering and Biotechnology, 2020, 8, 349.	4.1	2
141	Protein threading using PROSPECT: Design and evaluation. Proteins: Structure, Function and Bioinformatics, 2000, 40, 343-354.	2.6	2
142	A Multi-Level Iterative Bi-Clustering Method for Discovering miRNA Co-regulation Network of Abiotic Stress Tolerance in Soybeans. Frontiers in Plant Science, 2022, 13, 860791.	3.6	2
143	The essential tryptophan residues of pig kidney aminoacylase. IUBMB Life, 1997, 43, 1277-1283.	3.4	1
144	FACE RECOGNITION â€" A GENERALIZED MARGINAL FISHER ANALYSIS APPROACH. International Journal of Image and Graphics, 2007, 07, 583-591.	1.5	1

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145	Integrating Gene Expression Data and Pathway Knowledge for In Silico Hypothesis Generation with IMPRes. , 2018, , .		1
146	Extracting Molecular Entities and Their Interactions from Pathway Figures Based on Deep Learning. , 2019, , .		1
147	A Fast Algorithm for Low-Resolution Protein Structure Prediction. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2006, , .	0.5	1
148	Large-Scale Integrative Analysis of Soybean Transcriptome Using an Unsupervised Autoencoder Model. Frontiers in Plant Science, 2022, 13, 831204.	3.6	1
149	Discovering trends and hotspots of biosafety and biosecurity research via machine learning. Briefings in Bioinformatics, 2022, 23, .	6.5	1
150	Mapping Genes to Pathways Using Ontological Fuzzy Rule Systems. IEEE International Conference on Fuzzy Systems, 2007, , .	0.0	0
151	Bioinformatics Analyses ofArabidopsis thaliana Tiling Array Expression Data. , 0, , 57-70.		0
152	Predicting Functional Modules Using Microarray and Protein Interaction Data. , 0, , 307-329.		0
153	A Hybrid Consensus and Clustering Method for Protein Structure Selection. , 2011, , .		0
154	Editorial: Computational Resources for Understanding Biomacromolecular Covalent Modifications. Frontiers in Cell and Developmental Biology, 2021, 9, 728127.	3.7	0
155	Comparison of different parathyroid autograft project after total parathyroidectomy in patients with secondary hyperparathyroidism. American Journal of Otolaryngology - Head and Neck Medicine and Surgery, 2021, 42, 103085.	1.3	0
156	Acupuncture and Tuina Knowledge Graph for Ancient Literature of Traditional Chinese Medicine. , 2021, , .		0
157	Design and Implementation of Probability-Based Scoring Function for Peptide Mass Fingerprinting Protein Identification. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2006, , .	0.5	0