

Dong Xu

List of Publications by Year in descending order

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157
papers

5,419
citations

117625

34
h-index

102487

66
g-index

159
all docs

159
docs citations

159
times ranked

7652
citing authors

#	ARTICLE	IF	CITATIONS
1	Assessing deep learning methods in <i>cis</i> -regulatory motif finding based on genomic sequencing data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	9
2	RNAlocate v2.0: an updated resource for RNA subcellular localization with increased coverage and annotation. <i>Nucleic Acids Research</i> , 2022, 50, D333-D339.	14.5	54
3	<i>Coxiella burnetii</i> Virulent Phase I and Avirulent Phase II Variants Differentially Manipulate Autophagy Pathway in Neutrophils. <i>Infection and Immunity</i> , 2022, 90, IA10053421.	2.2	4
4	Deep learning shapes single-cell data analysis. <i>Nature Reviews Molecular Cell Biology</i> , 2022, 23, 303-304.	37.0	40
5	Large-Scale Integrative Analysis of Soybean Transcriptome Using an Unsupervised Autoencoder Model. <i>Frontiers in Plant Science</i> , 2022, 13, 831204.	3.6	1
6	Neural relational inference to learn long-range allosteric interactions in proteins from molecular dynamics simulations. <i>Nature Communications</i> , 2022, 13, 1661.	12.8	38
7	A Multi-Level Iterative Bi-Clustering Method for Discovering miRNA Co-regulation Network of Abiotic Stress Tolerance in Soybeans. <i>Frontiers in Plant Science</i> , 2022, 13, 860791.	3.6	2
8	High-Resolution Translatome Analysis Reveals Cortical Cell Programs During Early Soybean Nodulation. <i>Frontiers in Plant Science</i> , 2022, 13, 820348.	3.6	4
9	Discovering trends and hotspots of biosafety and biosecurity research via machine learning. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	1
10	AI-Aided Design of Novel Targeted Covalent Inhibitors against SARS-CoV-2. <i>Biomolecules</i> , 2022, 12, 746.	4.0	43
11	Zinc is a master-regulator of sperm function associated with binding, motility, and metabolic modulation during porcine sperm capacitation. <i>Communications Biology</i> , 2022, 5, .	4.4	10
12	Diagnosis of thyroid neoplasm using support vector machine algorithms based on platelet RNA-seq. <i>Endocrine</i> , 2021, 72, 758-783.	2.3	14
13	DM3Loc: multi-label mRNA subcellular localization prediction and analysis based on multi-head self-attention mechanism. <i>Nucleic Acids Research</i> , 2021, 49, e46-e46.	14.5	95
14	New genotypes of <i>Helicobacter Pylori</i> VacA d-region identified from global strains. <i>BMC Molecular and Cell Biology</i> , 2021, 22, 4.	2.0	11
15	Domain-specific Topic Model for Knowledge Discovery in Computational and Data-Intensive Scientific Communities. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2021, , 1-1.	5.7	5
16	DeePaN: deep patient graph convolutional network integrating clinico-genomic evidence to stratify lung cancers for immunotherapy. <i>Npj Digital Medicine</i> , 2021, 4, 14.	10.9	23
17	Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing. <i>Scientific Data</i> , 2021, 8, 50.	5.3	38
18	scGNN is a novel graph neural network framework for single-cell RNA-Seq analyses. <i>Nature Communications</i> , 2021, 12, 1882.	12.8	139

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19	G2PDeep: a web-based deep-learning framework for quantitative phenotype prediction and discovery of genomic markers. <i>Nucleic Acids Research</i> , 2021, 49, W228-W236.	14.5	12
20	Variation in Gene Expression between Two Sorghum bicolor Lines Differing in Innate Immunity Response. <i>Plants</i> , 2021, 10, 1536.	3.5	3
21	Editorial: Computational Resources for Understanding Biomacromolecular Covalent Modifications. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 728127.	3.7	0
22	Genetic mosaicism, intrafamilial phenotypic heterogeneity, and molecular defects of a novel missense SLC6A1 mutation associated with epilepsy and ADHD. <i>Experimental Neurology</i> , 2021, 342, 113723.	4.1	19
23	Deep learning analysis and age prediction from shoeprints. <i>Forensic Science International</i> , 2021, 327, 110987.	2.2	16
24	Comparison of different parathyroid autograft project after total parathyroidectomy in patients with secondary hyperparathyroidism. <i>American Journal of Otolaryngology - Head and Neck Medicine and Surgery</i> , 2021, 42, 103085.	1.3	0
25	Computational methods for protein localization prediction. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5834-5844.	4.1	12
26	Overlapping Community Detection Based on Membership Degree Propagation. <i>Entropy</i> , 2021, 23, 15.	2.2	5
27	Evolutionary Dynamics of Indels in SARS-CoV-2 Spike Glycoprotein. <i>Evolutionary Bioinformatics</i> , 2021, 17, 117693432110646.	1.2	5
28	MUFoldQA_G: High-accuracy protein model QA via retraining and transformation. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 6282-6290.	4.1	3
29	Digital tongue image analyses for health assessment. <i>Medical Review</i> , 2021, 1, 172-198.	1.2	11
30	Acupuncture and Tuina Knowledge Graph for Ancient Literature of Traditional Chinese Medicine. , 2021, , .		0
31	IMPRes-Pro: A high dimensional multiomics integration method for in silico hypothesis generation. <i>Methods</i> , 2020, 173, 16-23.	3.8	9
32	In-Situ Metabolomic Analysis of <i>Setaria viridis</i> Roots Colonized by Beneficial Endophytic Bacteria. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 272-283.	2.6	23
33	A deep dense inception network for protein beta-turn prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 143-151.	2.6	9
34	Fuzzified Image Enhancement for Deep Learning in Iris Recognition. <i>IEEE Transactions on Fuzzy Systems</i> , 2020, 28, 92-99.	9.8	55
35	How oncogenic mutations activate human MAP kinase 1 (MEK1): a molecular dynamics simulation study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 3942-3958.	3.5	7
36	Inductive inference of gene regulatory network using supervised and semi-supervised graph neural networks. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3335-3343.	4.1	31

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37	Impact of frailty on inpatient outcomes in thyroid cancer surgery: 10-year results from the U.S. national inpatient sample. <i>Journal of Otolaryngology - Head and Neck Surgery</i> , 2020, 49, 51.	1.9	13
38	Proteomic and Bioinformatic Profiling of Transporters in Higher Plant Mitochondria. <i>Biomolecules</i> , 2020, 10, 1190.	4.0	10
39	Single-Cell Techniques and Deep Learning in Predicting Drug Response. <i>Trends in Pharmacological Sciences</i> , 2020, 41, 1050-1065.	8.7	27
40	Endoplasmic reticulum retention and degradation of a mutation in SLC6A1 associated with epilepsy and autism. <i>Molecular Brain</i> , 2020, 13, 76.	2.6	30
41	Detecting Cancer Survival Related Gene Markers Based on Rectified Factor Network. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 349.	4.1	2
42	A self-attention based message passing neural network for predicting molecular lipophilicity and aqueous solubility. <i>Journal of Cheminformatics</i> , 2020, 12, 15.	6.1	73
43	Leveraging Systematic Functional Analysis to Benchmark an <i>In Silico</i> Framework Distinguishes Driver from Passenger MEK Mutants in Cancer. <i>Cancer Research</i> , 2020, 80, 4233-4243.	0.9	18
44	Overcoming Wnt β -catenin dependent anticancer therapy resistance in leukaemia stem cells. <i>Nature Cell Biology</i> , 2020, 22, 689-700.	10.3	89
45	Artificial Intelligence-Driven Structurization of Diagnostic Information in Free-Text Pathology Reports. <i>Journal of Pathology Informatics</i> , 2020, 11, 4.	1.7	7
46	A Fast Projection-Based Algorithm for Clustering Big Data. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019, 11, 360-366.	3.6	6
47	PSICA: a fast and accurate web service for protein model quality analysis. <i>Nucleic Acids Research</i> , 2019, 47, W443-W450.	14.5	12
48	A rectified factor network based biclustering method for detecting cancer-related coding genes and miRNAs, and their interactions. <i>Methods</i> , 2019, 166, 22-30.	3.8	4
49	A missense mutation in SLC6A1 associated with Lennox-Gastaut syndrome impairs GABA transporter 1 protein trafficking and function. <i>Experimental Neurology</i> , 2019, 320, 112973.	4.1	37
50	Identification of new loci for salt tolerance in soybean by high-resolution genome-wide association mapping. <i>BMC Genomics</i> , 2019, 20, 318.	2.8	46
51	Extracting Molecular Entities and Their Interactions from Pathway Figures Based on Deep Learning. , 2019, , .		1
52	Trends in Alzheimer's Disease Research Based upon Machine Learning Analysis of PubMed Abstracts. <i>International Journal of Biological Sciences</i> , 2019, 15, 2065-2074.	6.4	15
53	ezCADD: A Rapid 2D/3D Visualization-Enabled Web Modeling Environment for Democratizing Computer-Aided Drug Design. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 18-24.	5.4	47
54	Use of a Bioinformatics-Based Toxicity Scoring System to Assess Serotonin Burden and Predict Population-Level Adverse Drug Events from Concomitant Serotonergic Drug Therapy. <i>Pharmacotherapy</i> , 2019, 39, 171-181.	2.6	2

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55	Characterization of Select Wild Soybean Accessions in the USDA Germplasm Collection for Seed Composition and Agronomic Traits. <i>Crop Science</i> , 2019, 59, 233-251.	1.8	29
56	Capsule network for protein post-translational modification site prediction. <i>Bioinformatics</i> , 2019, 35, 2386-2394.	4.1	92
57	Plant-derived phosphocholine facilitates cellular uptake of anti-pulmonary fibrotic HJT-sRNA-m7. <i>Science China Life Sciences</i> , 2019, 62, 309-320.	4.9	43
58	MUFOLDaESS: New deep inception-inside inception networks for protein secondary structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 592-598.	2.6	134
59	G2S: a web-service for annotating genomic variants on 3D protein structures. <i>Bioinformatics</i> , 2018, 34, 1949-1950.	4.1	10
60	Molecular insights into the improved clinical performance of PEGylated interferon therapeutics: a molecular dynamics perspective. <i>RSC Advances</i> , 2018, 8, 2315-2322.	3.6	23
61	Comparative Effectiveness of High-Dose Versus Standard-Dose Influenza Vaccines in Preventing Postinfluenza Deaths. <i>Journal of Infectious Diseases</i> , 2018, 218, 336-337.	4.0	4
62	Mapping and confirmation of loci for salt tolerance in a novel soybean germplasm, Fiskeby III. <i>Theoretical and Applied Genetics</i> , 2018, 131, 513-524.	3.6	42
63	Domain-specific Topic Model for Knowledge Discovery through Conversational Agents in Data Intensive Scientific Communities. , 2018, , .		9
64	Integrating Gene Expression Data and Pathway Knowledge for In Silico Hypothesis Generation with IMPRes. , 2018, , .		1
65	Large-scale prediction of protein ubiquitination sites using a multimodal deep architecture. <i>BMC Systems Biology</i> , 2018, 12, 109.	3.0	29
66	Improving Protein Gamma-Turn Prediction Using Inception Capsule Networks. <i>Scientific Reports</i> , 2018, 8, 15741.	3.3	21
67	Implications of Off-Target Serotonergic Drug Activity: An Analysis of Serotonin Syndrome Reports Using a Systematic Bioinformatics Approach. <i>Pharmacotherapy</i> , 2018, 38, 888-898.	2.6	12
68	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. <i>Scientific Reports</i> , 2018, 8, 9939.	3.3	19
69	Why Is a High Temperature Needed by <i>Thermus thermophilus</i> Argonaute During mRNA Silencing: A Theoretical Study. <i>Frontiers in Chemistry</i> , 2018, 6, 223.	3.6	9
70	DeepDom: Predicting protein domain boundary from sequence alone using stacked bidirectional LSTM. , 2018, , .		8
71	iPhosPseEvo: Identifying Human Phosphorylated Proteins by Incorporating Evolutionary Information into General PseAAC via Grey System Theory. <i>Molecular Informatics</i> , 2017, 36, 1600010.	2.5	94
72	Experimental identification and computational characterization of a novel extracellular metalloproteinase produced by <i>Clostridium sordellii</i> . <i>RSC Advances</i> , 2017, 7, 13928-13938.	3.6	4

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73	Understanding the Phosphorylation Mechanism by Using Quantum Chemical Calculations and Molecular Dynamics Simulations. <i>Journal of Physical Chemistry B</i> , 2017, 121, 3565-3573.	2.6	12
74	The Evolution of Soybean Knowledge Base (SoyKB). <i>Methods in Molecular Biology</i> , 2017, 1533, 149-159.	0.9	25
75	BFDC: A Comprehensive Tool of Using Bayes Factor for Differential Co-Expression Analysis. <i>Journal of Molecular Biology</i> , 2017, 429, 446-453.	4.2	10
76	Understanding the differences of the ligand binding/unbinding pathways between phosphorylated and non-phosphorylated ARH1 using molecular dynamics simulations. <i>Scientific Reports</i> , 2017, 7, 12439.	3.3	21
77	Assessing and predicting drug-induced anticholinergic risks: an integrated computational approach. <i>Therapeutic Advances in Drug Safety</i> , 2017, 8, 361-370.	2.4	21
78	Tongue Image Analysis and Its Mobile App Development for Health Diagnosis. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1005, 99-121.	1.6	17
79	MSBIS: A Multi-Step Biomedical Informatics Screening Approach for Identifying Medications that Mitigate the Risks of Metoclopramide-Induced Tardive Dyskinesia. <i>EBioMedicine</i> , 2017, 26, 132-137.	6.1	7
80	An aggressive car-following model in the view of driving style. <i>Canadian Journal of Civil Engineering</i> , 2017, 44, 775-782.	1.3	4
81	OMPcontact: An Outer Membrane Protein Inter-Barrel Residue Contact Prediction Method. <i>Journal of Computational Biology</i> , 2017, 24, 217-228.	1.6	6
82	A multimodal deep architecture for large-scale protein ubiquitylation site prediction. , 2017, , .		9
83	Tongue Images Classification Based on Constrained High Dispersal Network. <i>Evidence-based Complementary and Alternative Medicine</i> , 2017, 2017, 1-12.	1.2	19
84	BioJava-ModFinder: identification of protein modifications in 3D structures from the Protein Data Bank. <i>Bioinformatics</i> , 2017, 33, 2047-2049.	4.1	8
85	Protein Loop Modeling Using Deep Generative Adversarial Network. , 2017, , .		16
86	Bioinformatics Analysis of Protein Phosphorylation in Plant Systems Biology Using P3DB. <i>Methods in Molecular Biology</i> , 2017, 1558, 127-138.	0.9	12
87	Computational Analysis of the Ligand Binding Site of the Extracellular ATP Receptor, DORN1. <i>PLoS ONE</i> , 2016, 11, e0161894.	2.5	18
88	Identification and Comparative Analysis of Differential Gene Expression in Soybean Leaf Tissue under Drought and Flooding Stress Revealed by RNA-Seq. <i>Frontiers in Plant Science</i> , 2016, 7, 1044.	3.6	116
89	Classification of tongue images based on doublet and color space dictionary. , 2016, , .		2
90	Genome-wide transcriptome analysis of soybean primary root under varying water-deficit conditions. <i>BMC Genomics</i> , 2016, 17, 57.	2.8	99

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91	Improving degree-based variable ordering heuristics for solving constraint satisfaction problems. <i>Journal of Heuristics</i> , 2016, 22, 125-145.	1.4	7
92	Imbalanced multi-label learning for identifying antimicrobial peptides and their functional types. <i>Bioinformatics</i> , 2016, 32, 3745-3752.	4.1	92
93	Differential protein structural disturbances and suppression of assembly partners produced by nonsense GABRG2 epilepsy mutations: implications for disease phenotypic heterogeneity. <i>Scientific Reports</i> , 2016, 6, 35294.	3.3	12
94	Predicting DNA Methylation State of CpG Dinucleotide Using Genome Topological Features and Deep Networks. <i>Scientific Reports</i> , 2016, 6, 19598.	3.3	75
95	Exploring Human Diseases and Biological Mechanisms by Protein Structure Prediction and Modeling. <i>Advances in Experimental Medicine and Biology</i> , 2016, 939, 39-61.	1.6	4
96	FALCON@home: a high-throughput protein structure prediction server based on remote homologue recognition. <i>Bioinformatics</i> , 2016, 32, 462-464.	4.1	34
97	Selective refinement and selection of near-native models in protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1823-1835.	2.6	3
98	The human epilepsy mutation GABRG2(Q390X) causes chronic subunit accumulation and neurodegeneration. <i>Nature Neuroscience</i> , 2015, 18, 988-996.	14.8	82
99	Soybean (<i>Glycine max</i>) SWEET gene family: insights through comparative genomics, transcriptome profiling and whole genome re-sequencing analysis. <i>BMC Genomics</i> , 2015, 16, 520.	2.8	173
100	Identification of quantitative trait loci underlying resistance to southern root-knot and reniform nematodes in soybean accession PI 567516C. <i>Molecular Breeding</i> , 2015, 35, 131.	2.1	34
101	Soybean transcription factor ORFeome associated with drought resistance: a valuable resource to accelerate research on abiotic stress resistance. <i>BMC Genomics</i> , 2015, 16, 596.	2.8	17
102	Effect of lipo-chitooligosaccharide on early growth of <i>C₄</i> grass seedlings. <i>Journal of Experimental Botany</i> , 2015, 66, 5727-5738.	4.8	39
103	Polymorphism of the glucosyltransferase gene (<i>ycjM</i>) in <i>Escherichia coli</i> and its use for tracking human fecal pollution in water. <i>Science of the Total Environment</i> , 2015, 537, 260-267.	8.0	6
104	Comparative analysis of the drought-responsive transcriptome in soybean lines contrasting for canopy wilting. <i>Plant Science</i> , 2015, 240, 65-78.	3.6	53
105	Transcriptional responses of <i>Arabidopsis thaliana</i> to chewing and sucking insect herbivores. <i>Frontiers in Plant Science</i> , 2014, 5, 565.	3.6	61
106	A new Hidden Markov Model for protein Quality Assessment using compatibility between protein sequence and structure. <i>Tsinghua Science and Technology</i> , 2014, 19, 559-567.	6.1	4
107	Diverse and divergent protein post-translational modifications in two growth stages of a natural microbial community. <i>Nature Communications</i> , 2014, 5, 4405.	12.8	51
108	DL-PRO: A novel deep learning method for protein model quality assessment. , 2014, 2014, 2071-2078.		38

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109	Genotypic variation of gene expression during the soybean innate immunity response. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, S27-S30.	0.8	11
110	Disrupting KATP channels diminishes the estrogen-mediated protection in female mutant mice during ischemia-reperfusion. <i>Clinical Proteomics</i> , 2014, 11, 19.	2.1	19
111	xMDFF: molecular dynamics flexible fitting of low-resolution X-ray structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2344-2355.	2.5	50
112	Flower-visiting insects and their potential impact on transgene flow in rice. <i>Journal of Applied Ecology</i> , 2014, 51, 1357-1365.	4.0	27
113	Differentiating enteric <i>Escherichia coli</i> from environmental bacteria through the putative glucosyltransferase gene (<i>ycjM</i>). <i>Water Research</i> , 2014, 61, 224-231.	11.3	14
114	BridgeDb app: unifying identifier mapping services for Cytoscape. <i>F1000Research</i> , 2014, 3, 148.	1.6	11
115	Major Soybean Maturity Gene Haplotypes Revealed by SNPviz Analysis of 72 Sequenced Soybean Genomes. <i>PLoS ONE</i> , 2014, 9, e94150.	2.5	89
116	NEW MDS AND CLUSTERING BASED ALGORITHMS FOR PROTEIN MODEL QUALITY ASSESSMENT AND SELECTION. <i>International Journal on Artificial Intelligence Tools</i> , 2013, 22, 1360006.	1.0	3
117	Automated Tongue Feature Extraction for ZHENG Classification in Traditional Chinese Medicine. <i>Evidence-based Complementary and Alternative Medicine</i> , 2012, 2012, 1-14.	1.2	64
118	Protein Databases on the Internet. <i>Current Protocols in Molecular Biology</i> , 2012, 97, Unit 19.4..	2.9	6
119	Human encoded miRNAs that regulate the influenza virus genome. , 2012, , .		2
120	ZHENG classification in Traditional Chinese Medicine based on modified specular-free tongue images. , 2012, , .		7
121	Protein Databases on the Internet. <i>Current Protocols in Protein Science</i> , 2012, 70, Unit2.6.	2.8	11
122	Features for automated tongue image shape classification. , 2012, , .		8
123	Computational Challenges in Characterization of Bacteria and Bacteria-Host Interactions Based on Genomic Data. <i>Journal of Computer Science and Technology</i> , 2012, 27, 225-239.	1.5	9
124	Routine Microsecond Molecular Dynamics Simulations with AMBER on GPUs. 1. Generalized Born. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 1542-1555.	5.3	1,633
125	Protein structural model selection based on protein-dependent scoring function. <i>Statistics and Its Interface</i> , 2012, 5, 109-115.	0.3	7
126	An automatic tongue detection and segmentation framework for computer-aided tongue image analysis. , 2011, , .		2

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127	PRIMEGENSw3: A Web-Based Tool for High-Throughput Primer and Probe Design. , 2011, , .		2
128	A Hybrid Consensus and Clustering Method for Protein Structure Selection. , 2011, , .		0
129	CORRELATION BETWEEN POSTTRANSLATIONAL MODIFICATION AND INTRINSIC DISORDER IN PROTEIN. , 2011, , .		16
130	A new clustering-based method for protein structure selection. , 2008, , .		4
131	COMBINING SEQUENCE AND STRUCTURAL PROFILES FOR PROTEIN SOLVENT ACCESSIBILITY PREDICTION. , 2008, , .		5
132	Visual Event Recognition in News Video using Kernel Methods with Multi-Level Temporal Alignment. , 2007, , .		33
133	FACE RECOGNITION "A GENERALIZED MARGINAL FISHER ANALYSIS APPROACH. International Journal of Image and Graphics, 2007, 07, 583-591.	1.5	1
134	Mapping Genes to Pathways Using Ontological Fuzzy Rule Systems. IEEE International Conference on Fuzzy Systems, 2007, , .	0.0	0
135	Rank-One Projections With Adaptive Margins for Face Recognition. IEEE Transactions on Systems, Man, and Cybernetics, 2007, 37, 1226-1236.	5.0	44
136	Element Rearrangement for Tensor-Based Subspace Learning. , 2007, , .		16
137	Human Gait Recognition With Matrix Representation. IEEE Transactions on Circuits and Systems for Video Technology, 2006, 16, 896-903.	8.3	114
138	Bioinformatics and Fuzzy Logic. , 2006, , .		6
139	Survey sequencing of soybean elucidates the genome structure, composition and identifies novel repeats. Functional Plant Biology, 2006, 33, 765.	2.1	10
140	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
141	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
142	Intrinsic Terminator Prediction and Its Application in Synechococcus sp. WH8102. Journal of Computer Science and Technology, 2005, 20, 465-482.	1.5	11
143	PROFILES AND FUZZY K-NEAREST NEIGHBOR ALGORITHM FOR PROTEIN SECONDARY STRUCTURE PREDICTION. , 2005, , .		12
144	Strategies for Inhibition of MDR1 Gene Expression. Molecular Pharmacology, 2004, 66, 268-275.	2.3	56

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145	GENOME-SCALE PROTEIN FUNCTION PREDICTION IN YEAST SACCHAROMYCES CEREVISIAE THROUGH INTEGRATING MULTIPLE SOURCES OF HIGH-THROUGHPUT DATA. , 2004, , .		9
146	P53-Dependent Cell-Killing by Selective Repression of Thymidine Kinase and Reduced Prodrug Activation. Molecular Pharmacology, 2003, 64, 289-297.	2.3	3
147	Characterization of Protein Structure and Function at Genome Scale with a Computational Prediction Pipeline. , 2003, 25, 269-293.		3
148	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
149	IDENTIFICATION OF REGULATORY BINDING SITES USING MINIMUM SPANNING TREES. , 2002, , .		4
150	Studies of the Mechanism of Phenol Hydroxylase: Mutants Tyr289Phe, Asp54Asn, and Arg281Met. Biochemistry, 2001, 40, 12369-12378.	2.5	39
151	Protein threading using PROSPECT: Design and evaluation. Proteins: Structure, Function and Bioinformatics, 2000, 40, 343-354.	2.6	2
152	The essential tryptophan residues of pig kidney aminoacylase. IUBMB Life, 1997, 43, 1277-1283.	3.4	1
153	An efficient branch-and-bound algorithm for the assignment of protein backbone NMR peaks. , 0, , .		11
154	Rank-one Projections with Adaptive Margins for Face Recognition. , 0, , .		2
155	Bioinformatics Analyses of Arabidopsis thaliana Tiling Array Expression Data. , 0, , 57-70.		0
156	Predicting Functional Modules Using Microarray and Protein Interaction Data. , 0, , 307-329.		0
157	GUV-Net for high fidelity shoeprint generation. Complex & Intelligent Systems, 0, , 1.	6.5	3