Dongbo Bu

List of Publications by Year in descending order

42 papers	2,164 citations	471509 17 h-index	302126 39 g-index
46 all docs	46 docs citations	46 times ranked	3036 citing authors

#	Article	IF	Citations
1	The Genomes of Oryza sativa: A History of Duplications. PLoS Biology, 2005, 3, e38.	5.6	808
2	Topological structure analysis of the protein-protein interaction network in budding yeast. Nucleic Acids Research, 2003, 31, 2443-2450.	14.5	614
3	Organization of the Caenorhabditis elegans small non-coding transcriptome: Genomic features, biogenesis, and expression. Genome Research, 2005, 16, 20-29.	5.5	104
4	Protein threading using residue co-variation and deep learning. Bioinformatics, 2018, 34, i263-i273.	4.1	66
5	FragmentâEHMM: A new approach to protein structure prediction. Protein Science, 2008, 17, 1925-1934.	7.6	57
6	Improving protein fold recognition by extracting fold-specific features from predicted residueâ€“residue contacts. Bioinformatics, 2017, 33, 3749-3757.	4.1	47
7	Resilience of human gut microbial communities for the long stay with multiple dietary shifts. Gut, 2019, 68, 2254-2255.	12.1	45
8	CopulaNet: Learning residue co-evolution directly from multiple sequence alignment for protein structure prediction. Nature Communications, 2021, 12, 2535.	12.8	44
9	The interactome as a tree--an attempt to visualize the protein-protein interaction network in yeast. Nucleic Acids Research, 2004, 32, 4804-4811.	14.5	43
10	MicroRNA regulation of messenger-like noncoding RNAs: a network of mutual microRNA control. Trends in Genetics, 2008, 24, 323-327.	6.7	36
11	FALCON@home: a high-throughput protein structure prediction server based on remote homologue recognition. Bioinformatics, 2016, 32, 462-464.	4.1	34
12	DIFFUSE: predicting isoform functions from sequences and expression profiles via deep learning. Bioinformatics, 2019, 35, i284-i294.	4.1	28
13	MS-Simulator: Predicting Y-Ion Intensities for Peptides with Two Charges Based on the Intensity Ratio of Neighboring Ions. Journal of Proteome Research, 2012, 11, 4509-4516.	3.7	25
14	Deriving the Probabilities of Water Loss and Ammonia Loss for Amino Acids from Tandem Mass Spectra. Journal of Proteome Research, 2008, 7, 202-208.	3.7	24
15	Toward Automated Identification of Glycan Branching Patterns Using Multistage Mass Spectrometry with Intelligent Precursor Selection. Analytical Chemistry, 2018, 90, 14412-14422.	6.5	23
16	Faster and more accurate global protein function assignment from protein interaction networks using the MFGO algorithm. FEBS Letters, 2006, 580, 1891-1896.	2.8	20
17	The effect of N-glycosylation of SARS-CoV-2 spike protein on the virus interaction with the host cell ACE2 receptor. IScience, 2021, 24, 103272.	4.1	20
18	Improving residueâ€“residue contact prediction via low-rank and sparse decomposition of residue correlation matrix. Biochemical and Biophysical Research Communications, 2016, 472, 217-222.	2.1	19

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19	OpenMS-Simulator: an open-source software for theoretical tandem mass spectrum prediction. BMC Bioinformatics, 2015, 16, 110.	2.6	14
20	Multilevel structural characteristics for the natural substrate proteins of bacterial small heat shock proteins. Protein Science, 2014, 23, 229-237.	7.6	9
21	Finding Nearly Optimal GDT Scores. Journal of Computational Biology, 2011, 18, 693-704.	1.6	8
22	ISSEC: inferring contacts among protein secondary structure elements using deep object detection. BMC Bioinformatics, 2020, 21, 503.	2.6	8
23	AN ITERATIVE ALGORITHM TO QUANTIFY FACTORS INFLUENCING PEPTIDE FRAGMENTATION DURING TANDEM MASS SPECTROMETRY. Journal of Bioinformatics and Computational Biology, 2007, 05, 297-311.	0.8	6
24	Improving prediction of burial state of residues by exploiting correlation among residues. BMC Bioinformatics, 2017, 18, 70.	2.6	6
25	De novo glycan structural identification from mass spectra using tree merging strategy. Computational Biology and Chemistry, 2019, 80, 217-224.	2.3	6
26	Predicting protein inter-residue contacts using composite likelihood maximization and deep learning. BMC Bioinformatics, 2019, 20, 537.	2.6	6
27	Multistage mass spectrometry with intelligent precursor selection for N-glycan branching pattern analysis. Carbohydrate Polymers, 2020, 237, 116122.	10.2	6
28	FragQA: predicting local fragment quality of a sequence-structure alignment. Genome Informatics, 2007, 19, 27-39.	0.4	6
29	A Fragmentation Event Model for Peptide Identification by Mass Spectrometry. Lecture Notes in Computer Science, 2008, , 154-166.	1.3	5
30	Genome-wide analysis of mammalian DNA segment fusion/fission. Journal of Theoretical Biology, 2006, 240, 200-208.	1.7	4
31	FINER: enhancing the prediction of tissue-specific functions of isoforms by refining isoform interaction networks. NAR Genomics and Bioinformatics, 2021, 3, lqab057.	3.2	3
32	Microbiome Resilience and Health Implications for People in Half-Year Travel. Frontiers in Immunology, 2022, 13, 848994.	4.8	2
33	Mainstream encodingâ€“decoding methods of DNA data storage. CCF Transactions on High Performance Computing, 2022, 4, 23-33.	1.7	2
34	LEX-SVM: EXPLORING THE POTENTIAL OF EXON EXPRESSION PROFILING FOR DISEASE CLASSIFICATION. Journal of Bioinformatics and Computational Biology, 2011, 09, 299-316.	0.8	1
35	Predicting human contacts through alternating direction method of multipliers. International Journal of Modern Physics C, 2019, 30, 1940014.	1.7	1
36	Constructing effective energy functions for protein structure prediction through broadening attraction-basin and reverse Monte Carlo sampling. BMC Bioinformatics, 2019, 20, 135.	2.6	1

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37	HepParser: An Intelligent Software Program for Deciphering Low-Molecular-Weight Heparin Based on Mass Spectrometry. Frontiers in Chemistry, 2021, 9, 723149.	3.6	1
38	ProALIGN: Directly Learning Alignments for Protein Structure Prediction via Exploiting Context-Specific Alignment Motifs. Journal of Computational Biology, 2022, 29, 92-105.	1.6	1
39	FALCON2: a web server for high-quality prediction of protein tertiary structures. BMC Bioinformatics, 2021, 22, 439.	2.6	0
40	TagDict: Prediction of Theoretical Spectra of Peptides Based on A Tag Dictionary. Current Bioinformatics, 2018, 13, 444-449.	1.5	0
41	Filling gaps of genome scaffolds via probabilistic searching optical maps against assembly graph. BMC Bioinformatics, 2021, 22, 533.	2.6	0
42	SASA-Net: A spatial-aware self-attention mechanism for building protein 3D structure directly from inter-residue distances. , 2021, , .		0