

Dong Xu

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.

25
papers

2,318
citations

15
h-index

28
g-index

28
ext. papers

2,778
ext. citations

4.9
avg, IF

5.52
L-index

#	Paper	IF	Citations
25	DeepDom: Predicting protein domain boundary from sequence alone using stacked bidirectional LSTM. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2019 , 24, 66-75	1.3	4
24	Exploring Human Diseases and Biological Mechanisms by Protein Structure Prediction and Modeling. <i>Advances in Experimental Medicine and Biology</i> , 2016 , 939, 39-61	3.6	2
23	AIDA: ab initio domain assembly for automated multi-domain protein structure prediction and domain-domain interaction prediction. <i>Bioinformatics</i> , 2015 , 31, 2098-105	7.2	34
22	Exploring the speed and performance of molecular replacement with AMPLE using QUARK ab initio protein models. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 338-43		21
21	FFAS-3D: improving fold recognition by including optimized structural features and template re-ranking. <i>Bioinformatics</i> , 2014 , 30, 660-7	7.2	83
20	AIDA: ab initio domain assembly server. <i>Nucleic Acids Research</i> , 2014 , 42, W308-13	20.1	35
19	Multi-Dimensional Scaling and MODELLER-Based Evolutionary Algorithms for Protein Model Refinement 2014 , 2014, 1038-1045		4
18	A comparative assessment and analysis of 20 representative sequence alignment methods for protein structure prediction. <i>Scientific Reports</i> , 2013 , 3, 2619	4.9	128
17	Protein depth calculation and the use for improving accuracy of protein fold recognition. <i>Journal of Computational Biology</i> , 2013 , 20, 805-16	1.7	13
16	Toward optimal fragment generations for ab initio protein structure assembly. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013 , 81, 229-39	4.2	156
15	Ab Initio structure prediction for Escherichia coli: towards genome-wide protein structure modeling and fold assignment. <i>Scientific Reports</i> , 2013 , 3, 1895	4.9	34
14	ThreaDom: extracting protein domain boundary information from multiple threading alignments. <i>Bioinformatics</i> , 2013 , 29, i247-56	7.2	56
13	Fast and Accurate Calculation of Protein Depth by Euclidean Distance Transform. <i>Lecture Notes in Computer Science</i> , 2013 , 7821, 304-316	0.9	4
12	Ab initio protein structure assembly using continuous structure fragments and optimized knowledge-based force field. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012 , 80, 1715-35	4.2	607
11	Structure and location of the regulatory β subunits in the β phosphorylase kinase complex. <i>Journal of Biological Chemistry</i> , 2012 , 287, 36651-61	5.4	13
10	Improving the physical realism and structural accuracy of protein models by a two-step atomic-level energy minimization. <i>Biophysical Journal</i> , 2011 , 101, 2525-34	2.9	600
9	Automated protein structure modeling in CASP9 by I-TASSER pipeline combined with QUARK-based ab initio folding and FG-MD-based structure refinement. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79 Suppl 10, 147-60	4.2	111

8	MUFOLD: A new solution for protein 3D structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 1137-52	4.2	60
7	Generating triangulated macromolecular surfaces by Euclidean Distance Transform. <i>PLoS ONE</i> , 2009 , 4, e8140	3.7	82
6	Homogeneous Description for Heterogeneous Cross-Media Resources 2008 ,		1
5	Geometric moment invariants. <i>Pattern Recognition</i> , 2008 , 41, 240-249	7.7	105
4	Shape Representation and Invariant Description of Protein Tertiary Structure in Applications to Shape Retrieval and Classification 2008 , 556-562		1
3	2006 ,		3
2	3-D Curve Moment Invariants for Curve Recognition 2006 , 572-577		4
1	Protein threading using PROSPECT: Design and evaluation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000 , 40, 343-354	4.2	157