Dong Xu

List of Publications by Citations

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	Ab initio protein structure assembly using continuous structure fragments and optimized knowledge-based force field. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 1715-35	4.2	607
24	Improving the physical realism and structural accuracy of protein models by a two-step atomic-level energy minimization. *Biophysical Journal*, **2011**, 101, 2525-34	2.9	600
23	Protein threading using PROSPECT: Design and evaluation. *Proteins: Structure, Function and Bioinformatics*, **2000**, 40, 343-354	4.2	157
22	Toward optimal fragment generations for ab initio protein structure assembly. *Proteins: Structure, Function and Bioinformatics*, **2013**, 81, 229-39	4.2	156
21	A comparative assessment and analysis of 20 representative sequence alignment methods for protein structure prediction. *Scientific Reports*, **2013**, 3, 2619	4.9	128
20	Automated protein structure modeling in CASP9 by I-TASSER pipeline combined with QUARK-based ab initio folding and FG-MD-based structure refinement. *Proteins: Structure, Function and Bioinformatics*, **2011**, 79 Suppl 10, 147-60	4.2	111
19	Geometric moment invariants. *Pattern Recognition*, **2008**, 41, 240-249	7.7	105
18	FFAS-3D: improving fold recognition by including optimized structural features and template re-ranking. *Bioinformatics*, **2014**, 30, 660-7	7.2	83
17	Generating triangulated macromolecular surfaces by Euclidean Distance Transform. *PLoS ONE*, **2009**, 4, e8140	3.7	82
16	MUFOLD: A new solution for protein 3D structure prediction. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 1137-52	4.2	60
15	ThreaDom: extracting protein domain boundary information from multiple threading alignments. *Bioinformatics*, **2013**, 29, i247-56	7.2	56
14	AIDA: ab initio domain assembly server. *Nucleic Acids Research*, **2014**, 42, W308-13	20.1	35
13	AIDA: ab initio domain assembly for automated multi-domain protein structure prediction and domain-domain interaction prediction. *Bioinformatics*, **2015**, 31, 2098-105	7.2	34
12	Ab Initio structure prediction for Escherichia coli: towards genome-wide protein structure modeling and fold assignment. *Scientific Reports*, **2013**, 3, 1895	4.9	34
11	Exploring the speed and performance of molecular replacement with AMPLE using QUARK ab initio protein models. *Acta Crystallographica Section D: Biological Crystallography*, **2015**, 71, 338-43		21
10	Protein depth calculation and the use for improving accuracy of protein fold recognition. *Journal of Computational Biology*, **2013**, 20, 805-16	1.7	13
9	Structure and location of the regulatory □subunits in the (β)4 phosphorylase kinase complex. *Journal of Biological Chemistry*, **2012**, 287, 36651-61	5.4	13

List of Publications

8	Multi-Dimensional Scaling and MODELLER-Based Evolutionary Algorithms for Protein Model Refinement **2014**, 2014, 1038-1045		4
7	DeepDom: Predicting protein domain boundary from sequence alone using stacked bidirectional LSTM. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2019**, 24, 66-75	1.3	4
6	3-D Curve Moment Invariants for Curve Recognition **2006**, 572-577		4
5	Fast and Accurate Calculation of Protein Depth by Euclidean Distance Transform. *Lecture Notes in Computer Science*, **2013**, 7821, 304-316	0.9	4
4	**2006**,		3
3	Exploring Human Diseases and Biological Mechanisms by Protein Structure Prediction and Modeling. *Advances in Experimental Medicine and Biology*, **2016**, 939, 39-61	3.6	2
2	Homogeneous Description for Heterogeneous Cross-Media Resources **2008**,		1
1	Shape Representation and Invariant Description of Protein Tertiary Structure in Applications to Shape Retrieval and Classification **2008**, 556-562		1