Dong Xu

List of Publications by Year
in descending order

28 papers	3,037 citations	567144 15 h-index	752573 20 g-index
28 all docs	28 docs citations	28 times ranked	4740 citing authors

#	Article	IF	Citations
1	Improving the Physical Realism and Structural Accuracy of Protein Models by a Two-Step Atomic-Level Energy Minimization. Biophysical Journal, 2011, 101, 2525-2534.	0.2	871
2	*Ab initio* protein structure assembly using continuous structure fragments and optimized knowledgeâ€based force field. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1715-1735.	1.5	744
3	Toward optimal fragment generations for *ab initio* protein structure assembly. Proteins: Structure, Function and Bioinformatics, 2013, 81, 229-239.	1.5	191
4	Protein threading using PROSPECT: Design and evaluation. Proteins: Structure, Function and Bioinformatics, 2000, 40, 343-354.	1.5	182
5	A comparative assessment and analysis of 20 representative sequence alignment methods for protein structure prediction. Scientific Reports, 2013, 3, 2619.	1.6	171
6	Automated protein structure modeling in CASP9 by Iâ€TASSER pipeline combined with QUARKâ€based *ab initio* folding and FGâ€MDâ€based structure refinement. Proteins: Structure, Function and Bioinformatics, 2011, 79, 147-160.	1.5	139
7	Geometric moment invariants. Pattern Recognition, 2008, 41, 240-249.	5.1	138
8	Generating Triangulated Macromolecular Surfaces by Euclidean Distance Transform. PLoS ONE, 2009, 4, e8140.	1.1	113
9	FFAS-3D: improving fold recognition by including optimized structural features and template re-ranking. Bioinformatics, 2014, 30, 660-667.	1.8	97
10	ThreaDom: extracting protein domain boundary information from multiple threading alignments. Bioinformatics, 2013, 29, i247-i256.	1.8	79
11	MUFOLD: A new solution for protein 3D structure prediction. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1137-1152.	1.5	67
12	AIDA: *ab initio* domain assembly for automated multi-domain protein structure prediction and domainâ€"domain interaction prediction. Bioinformatics, 2015, 31, 2098-2105.	1.8	59
13	AIDA: ab initio domain assembly server. Nucleic Acids Research, 2014, 42, W308-W313.	6.5	47
14	Ab Initio structure prediction for Escherichia coli: towards genome-wide protein structure modeling and fold assignment. Scientific Reports, 2013, 3, 1895.	1.6	43
15	Exploring the speed and performance of molecular replacement with *AMPLE* using *QUARK ab initio* protein models. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 338-343.	2.5	25
16	Protein Depth Calculation and the Use for Improving Accuracy of Protein Fold Recognition. Journal of Computational Biology, 2013, 20, 805-816.	0.8	19
17	Structure and Location of the Regulatory Î² Subunits in the (αβγδ)4 Phosphorylase Kinase Complex. Journal of Biological Chemistry, 2012, 287, 36651-36661.	1.6	16
18	3-D Curve Moment Invariants for Curve Recognition. , 2006, , 572-577.		8

#	Article	IF	Citations
19	Multi-dimensional scaling and MODELLER-based evolutionary algorithms for protein model refinement. , 2014, 2014, 1038-1045.		6
20	Content-based 3-D Shape Retrieval for Pervasive Computing. , 2006, , .		5
21	Fast and Accurate Calculation of Protein Depth by Euclidean Distance Transform. Lecture Notes in Computer Science, 2013, 7821, 304-316.	1.0	5
22	Exploring Human Diseases and Biological Mechanisms by Protein Structure Prediction and Modeling. Advances in Experimental Medicine and Biology, 2016, 939, 39-61.	0.8	4
23	DeepDom: Predicting protein domain boundary from sequence alone using stacked bidirectional LSTM. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2019, 24, 66-75.	0.7	4
24	Shape Representation and Invariant Description of Protein Tertiary Structure in Applications to Shape Retrieval and Classification. , 2008, , 556-562.		2
25	SHREC’08 entry: 3D face recognition using moment invariants. , 2008, , .		1
26	Homogeneous Description for Heterogeneous Cross-Media Resources. , 2008, , .		1
27	Common Substructure Extraction of Proteins by Geometric Invariants. , 2007, , .		0
28	SHREC’08 entry: Invariant features for robust shape retrieval. , 2008, , .		0