

Min-Yi Shen

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

8,522
citations

471509

17
h-index

642732

23
g-index

23
all docs

23
docs citations

23
times ranked

16862
citing authors

#	ARTICLE	IF	CITATIONS
1	How well can the accuracy of comparative protein structure models be predicted?. Protein Science, 2008, 17, 1881-1893.	7.6	138
2	Protein Structure Modeling with MODELLER. Methods in Molecular Biology, 2008, 426, 145-159.	0.9	1,187
3	Comparative Protein Structure Modeling Using MODELLER. Current Protocols in Protein Science, 2007, 50, Unit 2.9.	2.8	1,056
4	Comparative Protein Structure Modeling Using Modeller. Current Protocols in Bioinformatics, 2006, 15, Unit-5.6.	25.8	2,858
5	Minimalist Representations and the Importance of Nearest Neighbor Effects in Protein Folding Simulations. Journal of Molecular Biology, 2006, 363, 835-857.	4.2	40
6	A composite score for predicting errors in protein structure models. Protein Science, 2006, 15, 1653-1666.	7.6	160
7	Statistical potential for assessment and prediction of protein structures. Protein Science, 2006, 15, 2507-2524.	7.6	2,104
8	Protein complex compositions predicted by structural similarity. Nucleic Acids Research, 2006, 34, 2943-2952.	14.5	56
9	Structural Modeling of Protein Interactions by Analogy: Application to PSD-95. PLoS Computational Biology, 2006, 2, e153.	3.2	39
10	MODBASE: a database of annotated comparative protein structure models and associated resources. Nucleic Acids Research, 2006, 34, D291-D295.	14.5	265
11	The optimal size of a globular protein domain: A simple sphere-packing model. Chemical Physics Letters, 2005, 405, 224-228.	2.6	51
12	A simple method for faster nonbonded force evaluations. Journal of Computational Chemistry, 2005, 26, 691-698.	3.3	16
13	Modeling Protein Structure from its Sequence. Current Protocols in Bioinformatics, 2003, 3, 5.1.1.	25.8	6
14	Large-Scale Context in Protein Folding: A Villin Headpiece. Biochemistry, 2003, 42, 664-671.	2.5	56
15	Computer Simulation of Met-Enkephalin Using Explicit Atom and United Atom Potentials: Similarities, Differences, and Suggestions for Improvement. Journal of Physical Chemistry B, 2003, 107, 1685-1691.	2.6	27
16	Investigations into Sequence and Conformational Dependence of Backbone Entropy, Inter-basin Dynamics and the Flory Isolated-pair Hypothesis for Peptides. Journal of Molecular Biology, 2003, 331, 693-711.	4.2	118
17	Folding and misfolding of the papillomavirus E6 interacting peptide E6ap. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 7087-7092.	7.1	11
18	Long time dynamics of Met-enkephalin: Tests of mode-coupling theory and implicit solvent models. Journal of Chemical Physics, 2003, 118, 5143-5156.	3.0	12

#	ARTICLE	IF	CITATIONS
19	Hydration structure of met-enkephalin: A molecular dynamics study. <i>Journal of Chemical Physics</i> , 2003, 118, 1989-1995.	3.0	10
20	Long Time Dynamics of Met-Enkephalin: Comparison of Explicit and Implicit Solvent Models. <i>Biophysical Journal</i> , 2002, 82, 1791-1808.	0.5	108
21	All-atom fast protein folding simulations: The villin headpiece. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 49, 439-445.	2.6	97
22	Extended ab initio studies of the vinylidene \rightarrow acetylene rearrangement. <i>Journal of Chemical Physics</i> , 1997, 106, 3237-3242.	3.0	88
23	A MNDO study of carbon clusters with specifically fitted parameters. <i>Theoretica Chimica Acta</i> , 1995, 92, 269-280.	0.8	19