Min-Yi Shen

List of Publications by Year
in descending order

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	Comparative Protein Structure Modeling Using Modeller. Current Protocols in Bioinformatics, 2006, 15, Unit-5.6.	25.8	2,858
2	Statistical potential for assessment and prediction of protein structures. Protein Science, 2006, 15, 2507-2524.	7.6	2,104
3	Protein Structure Modeling with MODELLER. Methods in Molecular Biology, 2008, 426, 145-159.	0.9	1,187
4	Comparative Protein Structure Modeling Using MODELLER. Current Protocols in Protein Science, 2007, 50, Unit 2.9.	2.8	1,056
5	MODBASE: a database of annotated comparative protein structure models and associated resources. Nucleic Acids Research, 2006, 34, D291-D295.	14.5	265
6	A composite score for predicting errors in protein structure models. Protein Science, 2006, 15, 1653-1666.	7.6	160
7	How well can the accuracy of comparative protein structure models be predicted?. Protein Science, 2008, 17, 1881-1893.	7.6	138
8	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
9	Long Time Dynamics of Met-Enkephalin: Comparison of Explicit and Implicit Solvent Models. Biophysical Journal, 2002, 82, 1791-1808.	0.5	108
10	All-atom fast protein folding simulations: The villin headpiece. Proteins: Structure, Function and Bioinformatics, 2002, 49, 439-445.	2.6	97
11	Extended ab initio studies of the vinylideneâ€“acetylene rearrangement. Journal of Chemical Physics, 1997, 106, 3237-3242.	3.0	88
12	Large-Scale Context in Protein Folding:Â Villin Headpieceâ€. Biochemistry, 2003, 42, 664-671.	2.5	56
13	Protein complex compositions predicted by structural similarity. Nucleic Acids Research, 2006, 34, 2943-2952.	14.5	56
14	The optimal size of a globular protein domain: A simple sphere-packing model. Chemical Physics Letters, 2005, 405, 224-228.	2.6	51
15	Minimalist Representations and the Importance of Nearest Neighbor Effects in Protein Folding Simulations. Journal of Molecular Biology, 2006, 363, 835-857.	4.2	40
16	Structural Modeling of Protein Interactions by Analogy: Application to PSD-95. PLoS Computational Biology, 2006, 2, e153.	3.2	39
17	Computer Simulation of Met-Enkephalin Using Explicit Atom and United Atom Potentials:â€‰ Similarities, Differences, and Suggestions for Improvement. Journal of Physical Chemistry B, 2003, 107, 1685-1691.	2.6	27
18	A MNDO study of carbon clusters with specifically fitted parameters. Theoretica Chimica Acta, 1995, 92, 269-280.	0.8	19

#	Article	IF	Citations
19	A simple method for faster nonbonded force evaluations. Journal of Computational Chemistry, 2005, 26, 691-698.	3.3	16
20	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
21	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
22	Hydration structure of met-enkephalin: A molecular dynamics study. Journal of Chemical Physics, 2003, 118, 1989-1995.	3.0	10
23	Modeling Protein Structure from its Sequence. Current Protocols in Bioinformatics, 2003, 3, 5.1.1.	25.8	6