Kai Zhu

List of Publications by Year
in descending order

15	1,960	623188 14	996533 15
papers	citations	h-index	g-index

15	15	15	3282
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The VSGB 2.0 model: A next generation energy model for high resolution protein structure modeling. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2794-2812.	1.5	773
2	Docking Covalent Inhibitors: A Parameter Free Approach To Pose Prediction and Scoring. Journal of Chemical Information and Modeling, 2014, 54, 1932-1940.	2.5	326
3	Antibody structure determination using a combination of homology modeling, energyâ€based refinement, and loop prediction. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1646-1655.	1.5	167
4	Structure-Based Virtual Screening Approach for Discovery of Covalently Bound Ligands. Journal of Chemical Information and Modeling, 2014, 54, 1941-1950.	2.5	117
5	Long loop prediction using the protein local optimization program. Proteins: Structure, Function and Bioinformatics, 2006, 65, 438-452.	1.5	110
6	Improved Methods for Side Chain and Loop Predictions via the Protein Local Optimization Program:â€‰Variable Dielectric Model for Implicitly Improving the Treatment of Polarization Effects. Journal of Chemical Theory and Computation, 2007, 3, 2108-2119.	2.3	104
7	Toward better refinement of comparative models: Predicting loops in inexact environments. Proteins: Structure, Function and Bioinformatics, 2008, 72, 959-971.	1.5	80
8	Successful prediction of the intra- and extracellular loops of four G-protein-coupled receptors. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 8275-8280.	3.3	61
9	Selection of Nanobodies that Block the Enzymatic and Cytotoxic Activities of the Binary Clostridium Difficile Toxin CDT. Scientific Reports, 2015, 5, 7850.	1.6	55
10	Assignment of polar states for protein amino acid residues using an interaction cluster decomposition algorithm and its application to high resolution protein structure modeling. Proteins: Structure, Function and Bioinformatics, 2006, 66, 824-837.	1.5	40
11	Progress in super long loop prediction. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2920-2935.	1.5	40
12	Multiscale Optimization of a Truncated Newton Minimization Algorithm and Application to Proteins and Proteinâ^'Ligand Complexes. Journal of Chemical Theory and Computation, 2007, 3, 640-648.	2.3	29
13	Ab initio structure prediction of the antibody hypervariable H3 loop. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1081-1089.	1.5	28
14	Loop prediction for a GPCR homology model: Algorithms and results. Proteins: Structure, Function and Bioinformatics, 2013, 81, 214-228.	1.5	21
15	Prediction of Long Loops with Embedded Secondary Structure Using the Protein Local Optimization Program. Journal of Chemical Theory and Computation, 2013, 9, 1846-1864.	2.3	9