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	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
2	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
3	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
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	Loop prediction for a GPCR homology model: Algorithms and results. Proteins: Structure, Function and Bioinformatics, 2013, 81, 214-228.	1.5	21
6	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
7	Ab initio structure prediction of the antibody hypervariable H3 loop. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1081-1089.	1.5	28
8	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
9	Progress in super long loop prediction. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2920-2935.	1.5	40
10	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
11	Toward better refinement of comparative models: Predicting loops in inexact environments. Proteins: Structure, Function and Bioinformatics, 2008, 72, 959-971.	1.5	80
12	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
13	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
14	Long loop prediction using the protein local optimization program. Proteins: Structure, Function and Bioinformatics, 2006, 65, 438-452.	1.5	110
15	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