

Zhe Zhang

List of Publications by Year in descending order

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15
papers

1,450
citations

566801

15
h-index

996533

15
g-index

15
all docs

15
docs citations

15
times ranked

2196
citing authors

#	ARTICLE	IF	CITATIONS
1	Rational Design of Small-Molecule Stabilizers of Spermine Synthase Dimer by Virtual Screening and Free Energy-Based Approach. PLoS ONE, 2014, 9, e110884.	1.1	20
2	A Y328C missense mutation in spermine synthase causes a mild form of Snyder-Robinson syndrome. Human Molecular Genetics, 2013, 22, 3789-3797.	1.4	31
3	On the Dielectric Constant of Proteins: Smooth Dielectric Function for Macromolecular Modeling and Its Implementation in DelPhi. Journal of Chemical Theory and Computation, 2013, 9, 2126-2136.	2.3	446
4	A rational free energy-based approach to understanding and targeting disease-causing missense mutations. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 643-651.	2.2	18
5	Enhancing Human Spermine Synthase Activity by Engineered Mutations. PLoS Computational Biology, 2013, 9, e1002924.	1.5	19
6	In Silico Investigation of pH-Dependence of Prolactin and Human Growth Hormone Binding to Human Prolactin Receptor. Communications in Computational Physics, 2013, 13, 207-222.	0.7	20
7	Using DelPhi Capabilities to Mimic Protein's Conformational Reorganization with Amino Acid Specific Dielectric Constants. Communications in Computational Physics, 2013, 13, 13-30.	0.7	23
8	Analyzing Effects of Naturally Occurring Missense Mutations. Computational and Mathematical Methods in Medicine, 2012, 2012, 1-15.	0.7	111
9	DelPhi: a comprehensive suite for DelPhi software and associated resources. BMC Biophysics, 2012, 5, 9.	4.4	315
10	Predicting folding free energy changes upon single point mutations. Bioinformatics, 2012, 28, 664-671.	1.8	85
11	On the role of electrostatics in protein-protein interactions. Physical Biology, 2011, 8, 035001.	0.8	139
12	In Silico and In Vitro Investigations of the Mutability of Disease-Causing Missense Mutation Sites in Spermine Synthase. PLoS ONE, 2011, 6, e20373.	1.1	53
13	In silico modeling of pH optimum of protein-protein binding. Proteins: Structure, Function and Bioinformatics, 2011, 79, 925-936.	1.5	49
14	Developing hybrid approaches to predict pK _a values of ionizable groups. Proteins: Structure, Function and Bioinformatics, 2011, 79, 3389-3399.	1.5	36
15	Computational analysis of missense mutations causing Snyder-Robinson syndrome. Human Mutation, 2010, 31, 1043-1049.	1.1	85