Sanbo Qin

List of Publications by Year
in descending order

46 papers	1,989 citations	257357 24 h-index	254106 43 g-index
47 all docs	47 docs citations	47 times ranked	2180 citing authors

#	Article	IF	Citations
1	Preferential Interactions of a Crowder Protein with the Specific Binding Site of a Native Protein Complex. Journal of Physical Chemistry Letters, 2022, 13, 792-800.	2.1	8
2	Characterizing protein kinase A (PKA) subunits as macromolecular regulators of PKA RIÎ± liquidâ€“liquid phase separation. Journal of Chemical Physics, 2021, 154, 221101.	1.2	6
3	Calculation of Second Virial Coefficients of Atomistic Proteins Using Fast Fourier Transform. Journal of Physical Chemistry B, 2019, 123, 8203-8215.	1.2	15
4	Transfer Free Energies of Test Proteins Into Crowded Protein Solutions Have Simple Dependence on Crowder Concentration. Frontiers in Molecular Biosciences, 2019, 6, 39.	1.6	8
5	Both Ligands and Macromolecular Crowders Preferentially Bind to Closed Conformations of Maltose Binding Protein. Biochemistry, 2019, 58, 2208-2217.	1.2	7
6	Why Do Disordered and Structured Proteins Behave Differently in Phase Separation?. Trends in Biochemical Sciences, 2018, 43, 499-516.	3.7	114
7	Intrinsically Disordered Protein Exhibits Both Compaction and Expansion under Macromolecular Crowding. Biophysical Journal, 2018, 114, 1067-1079.	0.2	67
8	Atomistic Modeling of Intrinsically Disordered Proteins Under Polyethylene Glycol Crowding: Quantitative Comparison with Experimental Data and Implication of Proteinâ€“Crowder Attraction. Journal of Physical Chemistry B, 2018, 122, 11262-11270.	1.2	13
9	Protein folding, binding, and droplet formation in cell-like conditions. Current Opinion in Structural Biology, 2017, 43, 28-37.	2.6	45
10	Prediction of homoprotein and heteroprotein complexes by protein docking and templateâ€based modeling: A CASPâ€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2016, 84, 323-348.	1.5	148
11	Fast Method for Computing Chemical Potentials and Liquidâ€“Liquid Phase Equilibria of Macromolecular Solutions. Journal of Physical Chemistry B, 2016, 120, 8164-8174.	1.2	41
12	Blind prediction of interfacial water positions in CAPRI. Proteins: Structure, Function and Bioinformatics, 2014, 82, 620-632.	1.5	50
13	Further Development of the FFT-based Method for Atomistic Modeling of Protein Folding and Binding under Crowding: Optimization of Accuracy and Speed. Journal of Chemical Theory and Computation, 2014, 10, 2824-2835.	2.3	27
14	Simulation and modeling of crowding effects on the thermodynamic and kinetic properties of proteins with atomic details. Biophysical Reviews, 2013, 5, 207-215.	1.5	26
15	FFT-Based Method for Modeling Protein Folding and Binding under Crowding: Benchmarking on Ellipsoidal and All-Atom Crowders. Journal of Chemical Theory and Computation, 2013, 9, 4633-4643.	2.3	30
16	Effects of Macromolecular Crowding on the Conformational Ensembles of Disordered Proteins. Journal of Physical Chemistry Letters, 2013, 4, 3429-3434.	2.1	50
17	PI2PE: a suite of web servers for predictions ranging from protein structure to binding kinetics. Biophysical Reviews, 2013, 5, 41-46.	1.5	2
18	Folding free energy surfaces of three small proteins under crowding: validation of the postprocessing method by direct simulation. Physical Biology, 2013, 10, 045001.	0.8	12

#	Article	IF	Citations
19	Using the concept of transient complex for affinity predictions in CAPRI rounds 20â€“27 and beyond. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2229-2236.	1.5	7
20	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1980-1987.	1.5	87
21	Prediction and Dissection of Widely-Varying Association Rate Constants of Actin-Binding Proteins. PLoS Computational Biology, 2012, 8, e1002696.	1.5	13
22	A method for computing association rate constants of atomistically represented proteins under macromolecular crowding. Physical Biology, 2012, 9, 066008.	0.8	26
23	Contrasting Factors on the Kinetic Path to Protein Complex Formation Diminish the Effects of Crowding Agents. Biophysical Journal, 2012, 103, 1011-1019.	0.2	39
24	Rationalizing 5000-Fold Differences in Receptor-Binding Rate Constants ofÂFour Cytokines. Biophysical Journal, 2011, 101, 1175-1183.	0.2	20
25	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	2.0	131
26	Structural Models of Protein-DNA Complexes Based on Interface Prediction and Docking. Current Protein and Peptide Science, 2011, 12, 531-539.	0.7	5
27	Automated Prediction of Protein Association Rate Constants. Structure, 2011, 19, 1744-1751.	1.6	111
28	Selection of nearâ€native poses in CAPRI rounds 13â€19. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3166-3173.	1.5	10
29	Effects of Macromolecular Crowding on Protein Conformational Changes. PLoS Computational Biology, 2010, 6, e1000833.	1.5	82
30	Method to Predict Crowding Effects by Postprocessing Molecular Dynamics Trajectories: Application to the Flap Dynamics of HIV-1 Protease. Journal of Physical Chemistry Letters, 2010, 1, 107-110.	2.1	39
31	Generalized fundamental measure theory for atomistic modeling of macromolecular crowding. Physical Review E, 2010, 81, 031919.	0.8	30
32	Dissection of the high rate constant for the binding of a ribotoxin to the ribosome. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 6974-6979.	3.3	28
33	Atomistic Modeling of Macromolecular Crowding Predicts Modest Increases in Protein Folding and Binding Stability. Biophysical Journal, 2009, 97, 12-19.	0.2	104
34	Effect of Macromolecular Crowding on Protein Binding Stability: Modest Stabilization and Significant Biological Consequences. Biophysical Journal, 2009, 97, 906-911.	0.2	101
35	A novel procedure for identification of the folding/unfolding patterns of dimeric proteins. Journal of Theoretical Biology, 2008, 250, 461-467.	0.8	0
36	Prediction of Salt and Mutational Effects on the Association Rate of U1A Protein and U1 Small Nuclear RNA Stem/Loop II. Journal of Physical Chemistry B, 2008, 112, 5955-5960.	1.2	24

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37	Modeling Proteinâ€“Protein and Proteinâ€“Nucleic Acid Interactions: Structure, Thermodynamics, and Kinetics. Annual Reports in Computational Chemistry, 2008, , 67-87.	0.9	3
38	meta-PPISP: a meta web server for protein-protein interaction site prediction. Bioinformatics, 2007, 23, 3386-3387.	1.8	162
39	PI2PE: protein interface/interior prediction engine. Nucleic Acids Research, 2007, 35, W357-W362.	6.5	32
40	Interaction-site prediction for protein complexes: a critical assessment. Bioinformatics, 2007, 23, 2203-2209.	1.8	161
41	Do electrostatic interactions destabilize proteinâ€“nucleic acid binding?. Biopolymers, 2007, 86, 112-118.	1.2	46
42	A holistic approach to protein docking. Proteins: Structure, Function and Bioinformatics, 2007, 69, 743-749.	1.5	20
43	Ca2+ Binding Effects on the C2 Domain Conformation of Human Cytosolic Phospholipase A2. Protein and Peptide Letters, 2006, 13, 91-94.	0.4	0
44	Mechanism of inhibition of Ca2+-transport activity of sarcoplasmic reticulum Ca2+-ATPase by anisodamine. Indian Journal of Biochemistry and Biophysics, 2006, 43, 351-9.	0.2	0
45	Predicting protein secondary structure and solvent accessibility with an improved multiple linear regression method. Proteins: Structure, Function and Bioinformatics, 2005, 61, 473-480.	1.5	18
46	Thermal and conformational stability of Ssh10b protein from archaeon Sulfolobus shibattae. Biochemical Journal, 2004, 382, 433-440.	1.7	21