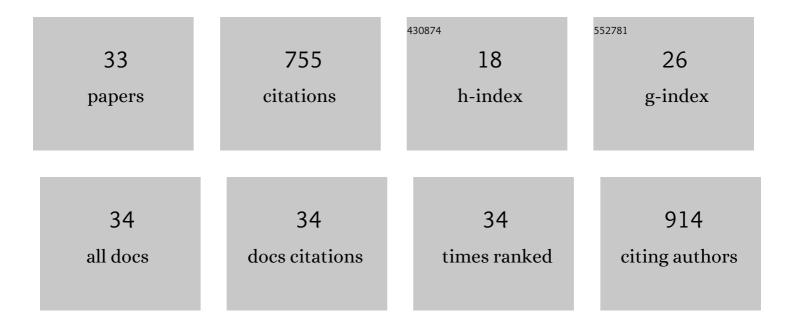
Junchao Xia

List of Publications by Year in descending order

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Ιυνισμλο Χιλ

#	Article	IF	CITATIONS
1	How Does Water Affect the Dynamics of the Room-Temperature Ionic Liquid 1-Hexyl-3-methylimidazolium Hexafluorophosphate and the Fluorescence Spectroscopy of Coumarin-153 When Dissolved in It?. Journal of Physical Chemistry B, 2008, 112, 1770-1776.	2.6	73
2	The cooling rate dependence of crystallization for liquid copper: A molecular dynamics study. Journal of Chemical Physics, 2001, 114, 7506-7512.	3.0	57
3	Simulating Replica Exchange: Markov State Models, Proposal Schemes, and the Infinite Swapping Limit. Journal of Physical Chemistry B, 2016, 120, 8289-8301.	2.6	42
4	Asynchronous replica exchange software for grid and heterogeneous computing. Computer Physics Communications, 2015, 196, 236-246.	7.5	35
5	Comparing alchemical and physical pathway methods for computing the absolute binding free energy of charged ligands. Physical Chemistry Chemical Physics, 2018, 20, 17081-17092.	2.8	34
6	Cooling rate dependence of structural properties of aluminium during rapid solidification. Journal of Physics Condensed Matter, 2001, 13, 1873-1890.	1.8	31
7	Sugar Folding:  A Novel Structural Prediction Tool for Oligosaccharides and Polysaccharides 2. Journal of Chemical Theory and Computation, 2007, 3, 1629-1643.	5.3	30
8	Simulation of the Burridge-Knopoff Model of Earthquakes with Variable Range Stress Transfer. Physical Review Letters, 2005, 95, 248501.	7.8	29
9	Sucrose in aqueous solution revisited, Part 1: Molecular dynamics simulations and direct and indirect dipolar coupling analysis. Biopolymers, 2012, 97, 276-288.	2.4	28
10	NMR Relaxation in Proteins with Fast Internal Motions and Slow Conformational Exchange: Model-Free Framework and Markov State Simulations. Journal of Physical Chemistry B, 2013, 117, 6625-6634.	2.6	28
11	When Sugars Get Wet. A Comprehensive Study of the Behavior of Water on the Surface of Oligosaccharides. Journal of Physical Chemistry B, 2009, 113, 11003-11015.	2.6	27
12	A Stochastic Solution to the Unbinned WHAM Equations. Journal of Physical Chemistry Letters, 2015, 6, 3834-3840.	4.6	27
13	Diffusion and Residence Time of Hydrogen Peroxide and Water in Crowded Protein Environments. Journal of Physical Chemistry B, 2007, 111, 13336-13344.	2.6	26
14	Near-mean-field behavior in the generalized Burridge-Knopoff earthquake model with variable-range stress transfer. Physical Review E, 2008, 77, 031132.	2.1	26
15	A tool for the prediction of structures of complex sugars. Journal of Biomolecular NMR, 2008, 42, 241-256.	2.8	23
16	Molecular Dynamics of the Proline Switch and Its Role in Crk Signaling. Journal of Physical Chemistry B, 2014, 118, 4535-4545.	2.6	21
17	Largeâ€scale asynchronous and distributed multidimensional replica exchange molecular simulations and efficiency analysis. Journal of Computational Chemistry, 2015, 36, 1772-1785.	3.3	19
18	Molecular dynamics simulation of the local inherent structure of liquid silicon at different temperatures. Physical Review B, 1999, 60, 3194-3199.	3.2	18

ЈИЛСНАО ХІА

#	Article	IF	CITATIONS
19	Searching and Optimizing Structure Ensembles for Complex Flexible Sugars. Journal of the American Chemical Society, 2011, 133, 15252-15255.	13.7	18
20	A combined treatment of hydration and dynamical effects for the modeling of host–guest binding thermodynamics: the SAMPL5 blinded challenge. Journal of Computer-Aided Molecular Design, 2017, 31, 29-44.	2.9	18
21	Sugar Folding:  A Novel Structural Prediction Tool for Oligosaccharides and Polysaccharides 1. Journal of Chemical Theory and Computation, 2007, 3, 1620-1628.	5.3	17
22	Large scale free energy calculations for blind predictions of protein–ligand binding: the D3R Grand Challenge 2015. Journal of Computer-Aided Molecular Design, 2016, 30, 743-751.	2.9	17
23	Locally weighted histogram analysis and stochastic solution for large-scale multi-state free energy estimation. Journal of Chemical Physics, 2016, 144, 034107.	3.0	16
24	Different Cooling Rate Dependences of Different Microstructure Units in Aluminium Glass by Molecular Dynamics Simulation. Chinese Physics Letters, 2000, 17, 34-36.	3.3	14
25	Sucrose in aqueous solution revisited, Part 2: Adaptively biased molecular dynamics simulations and computational analysis of NMR relaxation. Biopolymers, 2012, 97, 289-302.	2.4	14
26	Enhanced Sampling of Interdomain Motion Using Map-Restrained Langevin Dynamics and NMR: Application to Pin1. Journal of Molecular Biology, 2018, 430, 2164-2180.	4.2	12
27	Measuring the magnitude of internal motion in a complex hexasaccharide. Biopolymers, 2011, 95, 39-50.	2.4	11
28	Binding Energy Distribution Analysis Method: Hamiltonian Replica Exchange with Torsional Flattening for Binding Mode Prediction and Binding Free Energy Estimation. Journal of Chemical Theory and Computation, 2016, 12, 2459-2470.	5.3	11
29	Computational Study of the Conformational Structures of Saccharides in Solution Based on J Couplings and the "Fast Sugar Structure Prediction Software― Biomacromolecules, 2009, 10, 3081-3088.	5.4	9
30	Final Structures of Crystallization of Liquid Copper Studied by Molecular Dynamics Simulation. Chinese Physics Letters, 1999, 16, 850-852.	3.3	8
31	Improving Prediction Accuracy of Binding Free Energies and Poses of HIV Integrase Complexes Using the Binding Energy Distribution Analysis Method with Flattening Potentials. Journal of Chemical Information and Modeling, 2018, 58, 1356-1371.	5.4	7
32	Massive-Scale Binding Free Energy Simulations of HIV Integrase Complexes Using Asynchronous Replica Exchange Framework Implemented on the IBM WCG Distributed Network. Journal of Chemical Information and Modeling, 2019, 59, 1382-1397.	5.4	6
33	MODELS OF EARTHQUAKE FAULTS: ERGODICITY AND FORECASTING. International Journal of Modern Physics B, 2009, 23, 5553-5569.	2.0	2