

# Shuanghong Huo

## List of Publications by Year in descending order

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34  
papers

5,439  
citations

430442

18  
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395343

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g-index

36  
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36  
docs citations

36  
times ranked

6546  
citing authors

#	ARTICLE	IF	CITATIONS
1	Interplay between human islet amyloid polypeptide aggregates and micro-heterogeneous membranes. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2021, 1863, 183691.	1.4	3
2	Approximating dynamic proximity with a hybrid geometry energy-based kernel for diffusion maps. <i>Journal of Chemical Physics</i> , 2019, 151, 105101.	1.2	1
3	Observations on AMBER Force Field Performance under the Conditions of Low pH and High Salt Concentrations. <i>Journal of Physical Chemistry B</i> , 2017, 121, 9838-9847.	1.2	4
4	Inherent structure versus geometric metric for state space discretization. <i>Journal of Computational Chemistry</i> , 2016, 37, 1251-1258.	1.5	2
5	Long-Range Reactivity Modulations in Geranyl Chloride Derivatives. <i>Journal of Organic Chemistry</i> , 2016, 81, 10964-10974.	1.7	3
6	Network representation of conformational transitions between hidden intermediates of Rd-apocytochrome b562. <i>Journal of Chemical Physics</i> , 2015, 143, 135101.	1.2	6
7	Euclidean sections of protein conformation space and their implications in dimensionality reduction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2585-2596.	1.5	5
8	Evaluation of Dimensionality-Reduction Methods from Peptide Foldingâ€“Unfolding Simulations. <i>Journal of Chemical Theory and Computation</i> , 2013, 9, 2490-2497.	2.3	34
9	Graph representation of protein free energy landscape. <i>Journal of Chemical Physics</i> , 2013, 139, 185101.	1.2	8
10	Effects of Two Solvent Conditions on the Free Energy Landscape of the BBL Peripheral Subunit Binding Domain. <i>Journal of Physical Chemistry B</i> , 2012, 116, 646-652.	1.2	4
11	Conformations of Islet Amyloid Polypeptide Monomers in a Membrane Environment: Implications for Fibril Formation. <i>PLoS ONE</i> , 2012, 7, e47150.	1.1	30
12	Observation of Two Families of Folding Pathways of BBL. <i>Biophysical Journal</i> , 2011, 100, 2457-2465.	0.2	9
13	Quantum mechanical studies on model $\beta$ -pleated sheets. <i>Journal of Computational Chemistry</i> , 2010, 31, 1216-1223.	1.5	10
14	A Novel Mutant Cardiac Troponin C Disrupts Molecular Motions Critical for Calcium Binding Affinity and Cardiomyocyte Contractility. <i>Biophysical Journal</i> , 2008, 94, 3577-3589.	0.2	62
15	Predicting the Folding Pathway of Engrailed Homeodomain with a Probabilistic Roadmap Enhanced Reaction-Path Algorithm. <i>Biophysical Journal</i> , 2008, 94, 1622-1629.	0.2	11
16	Formation and Growth of Oligomers: A Monte Carlo Study of an Amyloid Tau Fragment. <i>PLoS Computational Biology</i> , 2008, 4, e1000238.	1.5	104
17	Structural and Pathway Complexity of $\beta^2$ -Strand Reorganization within Aggregates of Human Transthyretin(105~115) Peptide. <i>Journal of Physical Chemistry B</i> , 2007, 111, 5425-5433.	1.2	21
18	Temperature-Dependent Probabilistic Roadmap Algorithm for Calculating Variationally Optimized Conformational Transition Pathways. <i>Journal of Chemical Theory and Computation</i> , 2007, 3, 17-25.	2.3	14

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19	Evaluation of Configurational Entropy Methods from Peptide Folding~Unfolding Simulation. Journal of Physical Chemistry B, 2007, 111, 13807-13813.	1.2	25
20	The Sequence-Dependent Unfolding Pathway Plays a Critical Role in the Amyloidogenicity of Transthyretin. Biochemistry, 2006, 45, 11992-12002.	1.2	28
21	Peptide Plane Can Flip in Two Opposite Directions:~ Implication in Amyloid Formation of Transthyretin. Journal of Physical Chemistry B, 2006, 110, 5829-5833.	1.2	18
22	Potential influence of Asp in the Ca <sup>2+</sup> coordination position 5 of parvalbumin on the calcium-binding affinity: A computational study. Journal of Inorganic Biochemistry, 2006, 100, 1879-1887.	1.5	5
23	Initial Conformational Changes of Human Transthyretin under Partially Denaturing Conditions. Biophysical Journal, 2005, 89, 433-443.	0.2	26
24	Intrinsic versus mutation dependent instability/flexibility: a comparative analysis of the structure and dynamics of wild-type transthyretin and its pathogenic variants. Journal of Structural Biology, 2004, 148, 153-168.	1.3	20
25	Why is Leu55~Pro55 transthyretin variant the most amyloidogenic: Insights from molecular dynamics simulations of transthyretin monomers. Protein Science, 2003, 12, 1222-1231.	3.1	43
26	Long Time Dynamic Simulations:~ Exploring the Folding Pathways of an Alzheimer's Amyloid A $\beta$ -Peptide. Accounts of Chemical Research, 2002, 35, 473-481.	7.6	59
27	Molecular Dynamics and Free Energy Analyses of Cathepsin D~Inhibitor Interactions:~ Insight into Structure-Based Ligand Design. Journal of Medicinal Chemistry, 2002, 45, 1412-1419.	2.9	168
28	Computational alanine scanning of the 1:1 human growth hormone-receptor complex. Journal of Computational Chemistry, 2002, 23, 15-27.	1.5	288
29	Solvation Model Based on Weighted Solvent Accessible Surface Area. Journal of Physical Chemistry B, 2001, 105, 5055-5067.	1.2	107
30	Calculating Structures and Free Energies of Complex Molecules:~ Combining Molecular Mechanics and Continuum Models. Accounts of Chemical Research, 2000, 33, 889-897.	7.6	4,098
31	Direct computation of long time processes in peptides and proteins: Reaction path study of the coil-to-helix transition in polyalanine. Proteins: Structure, Function and Bioinformatics, 1999, 36, 249-261.	1.5	47
32	Direct computation of long time processes in peptides and proteins: Reaction path study of the coil-to-helix transition in polyalanine. , 1999, 36, 249.		3
33	Molecular Dynamics Simulation Study of the B-States of Solvated Carbon Monoxymyoglobin. Journal of the American Chemical Society, 1997, 119, 2541-2551.	6.6	51
34	The MaxFlux algorithm for calculating variationally optimized reaction paths for conformational transitions in many body systems at finite temperature. Journal of Chemical Physics, 1997, 107, 5000-5006.	1.2	122