

# Weixin Xu

## List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	pH-Dependent Conformational Ensemble and Polymorphism of Amyloid- $\beta$ Core Fragment. Journal of Physical Chemistry B, 2013, 117, 8392-8399.	1.2	13
2	Acidic pH retards the fibrillization of human islet amyloid polypeptide due to electrostatic repulsion of histidines. Journal of Chemical Physics, 2013, 139, 055102.	1.2	38
3	Effect of Self-Assembly of Fullerene Nano-Particles on Lipid Membrane. PLoS ONE, 2013, 8, e77436.	1.1	21
4	Dynamical Stability and Assembly Cooperativity of $\beta$ -Sheet Amyloid Oligomers – Effect of Polarization. Journal of Physical Chemistry B, 2012, 116, 13368-13373.	1.2	19
5	Configuration-Dependent Diffusion Dynamics of Downhill and Two-State Protein Folding. Journal of Physical Chemistry B, 2012, 116, 5152-5159.	1.2	23
6	Molecular Dynamics Simulation Study on the Molecular Structures of the Amylin Fibril Models. Journal of Physical Chemistry B, 2012, 116, 13991-13999.	1.2	19
7	Intrinsic Determinants of A $\beta$ 24 pH-Dependent Self-Assembly Revealed by Combined Computational and Experimental Studies. PLoS ONE, 2011, 6, e24329.	1.1	26
8	Effects of cholesterol on pore formation in lipid bilayers induced by human islet amyloid polypeptide fragments: A coarse-grained molecular dynamics study. Physical Review E, 2011, 84, 051922.	0.8	27
9	The Molecular Basis of Distinct Aggregation Pathways of Islet Amyloid Polypeptide. Journal of Biological Chemistry, 2011, 286, 6291-6300.	1.6	104
10	Amyloidogenesis Abolished by Proline Substitutions but Enhanced by Lipid Binding. PLoS Computational Biology, 2009, 5, e1000357.	1.5	39
11	Assembly dynamics of two- $\beta$ sheets revealed by molecular dynamics simulations. Journal of Chemical Physics, 2009, 130, 164709.	1.2	28
12	Conformation Preorganization: Effects of S20G Mutation on the Structure of Human Islet Amyloid Polypeptide Segment. Journal of Physical Chemistry B, 2009, 113, 7308-7314.	1.2	30
13	Ab initio folding simulation of Trpcage by replica exchange with hybrid Hamiltonian. Biophysical Chemistry, 2008, 137, 116-125.	1.5	24
14	A GLOBAL OPTIMIZATION SCHEME: KERNEL REPLICA EXCHANGE SIMULATION METHOD FOR PROTEIN FOLDING. Journal of Theoretical and Computational Chemistry, 2008, 07, 177-187.	1.8	2
15	Global optimisation by replica exchange with scaled hybrid Hamiltonians. Molecular Simulation, 2008, 34, 575-590.	0.9	7
16	Reversible folding simulation by hybrid Hamiltonian replica exchange. Journal of Chemical Physics, 2008, 128, 175105.	1.2	25
17	Hybrid Hamiltonian replica exchange molecular dynamics simulation method employing the Poisson-Boltzmann model. Journal of Chemical Physics, 2007, 127, 084119.	1.2	19