Wenning Wang

List of Publications by Citations

43 papers	622 citations	15 h-index	23 g-index
46 ext. papers	780 ext. citations	7.2 avg, IF	4.46 L-index

#	Paper	IF	Citations
43	LGN/mInsc and LGN/NuMA complex structures suggest distinct functions in asymmetric cell division for the Par3/mInsc/LGN and G/LGN/NuMA pathways. *Molecular Cell*, **2011**, 43, 418-31	17.6	93
42	Creating conformational entropy by increasing interdomain mobility in ligand binding regulation: a revisit to N-terminal tandem PDZ domains of PSD-95. *Journal of the American Chemical Society*, **2009**, 131, 787-96	16.4	48
41	Reactions of Mn with H2O and MnO with H2. Matrix-Isolation FTIR and Quantum Chemical Studies. *Journal of Physical Chemistry A*, **2001**, 105, 5801-5807	2.8	36
40	The Dynamic Multisite Interactions between Two Intrinsically Disordered Proteins. *Angewandte Chemie - International Edition*, **2017**, 56, 7515-7519	16.4	31
39	Lipid-Induced conformational switch controls fusion activity of longin domain SNARE Ykt6. *Molecular Cell*, **2010**, 37, 383-95	17.6	30
38	O/Ag(100) Surface: A Density Functional Study with Slab Model. *Journal of Physical Chemistry B*, **2002**, 106, 3662-3667	3.4	26
37	Conformational Dynamics of apo-GlnBP Revealed by Experimental and Computational Analysis. *Angewandte Chemie - International Edition*, **2016**, 55, 13990-13994	16.4	26
36	The structural basis of Miranda-mediated Staufen localization during Drosophila neuroblast asymmetric division. *Nature Communications*, **2015**, 6, 8381	17.4	25
35	Insights into the Inhibitory Mechanism of D13-9001 to the Multidrug Transporter AcrB through Molecular Dynamics Simulations. *Journal of Physical Chemistry B*, **2016**, 120, 2145-54	3.4	24
34	Formation and Characterization of the (-H2)CrO2, (-H2)2CrO2 and HCrO(OH) Molecules. *Journal of Physical Chemistry A*, **2001**, 105, 10747-10752	2.8	23
33	Dynamic multivalent interactions of intrinsically disordered proteins. *Current Opinion in Structural Biology*, **2020**, 62, 9-13	8.1	23
32	Phosphorylated Peptide Functionalization of Lanthanide Upconversion Nanoparticles for Tuning Nanomaterial-Cell Interactions. *ACS Applied Materials & Interfaces*, **2016**, 8, 6935-43	9.5	21
31	An autoinhibited conformation of LGN reveals a distinct interaction mode between GoLoco motifs and TPR motifs. *Structure*, **2013**, 21, 1007-17	5.2	20
30	Artificial Aquaporin That Restores Wound Healing of Impaired Cells. *Journal of the American Chemical Society*, **2020**, 142, 15638-15643	16.4	19
29	Crystal structures of the scaffolding protein LGN reveal the general mechanism by which GoLoco binding motifs inhibit the release of GDP from G *Journal of Biological Chemistry*, **2012**, 287, 36766-76	5.4	18
28	Conformational stability and dynamics of the cancer-associated isoform 133p53are modulated by p53 peptides and p53-specific DNA. *FASEB Journal*, **2019**, 33, 4225-4235	0.9	14
27	Recent advances in atomic molecular dynamics simulation of intrinsically disordered proteins. *Physical Chemistry Chemical Physics*, **2021**, 23, 777-784	3.6	14

26	Lipid Regulated Intramolecular Conformational Dynamics of SNARE-Protein Ykt6. *Scientific Reports*, **2016**, 6, 30282	4.9	13
25	Extreme Fuzziness: Direct Interactions between Two IDPs. *Biomolecules*, **2019**, 9,	5.9	11
24	Gas-phase complexation of □/□-cyclodextrin with amino acids studied by ion mobility-mass spectrometry and molecular dynamics simulations. *Talanta*, **2018**, 186, 1-7	6.2	11
23	Molecular dynamics simulation of membrane proteins. *Advances in Experimental Medicine and Biology*, **2014**, 805, 305-29	3.6	10
22	Maltose-binding protein effectively stabilizes the partially closed conformation of the ATP-binding cassette transporter MalFGK. *Physical Chemistry Chemical Physics*, **2017**, 19, 9366-9373	3.6	7
21	Substrate binding accelerates the conformational transitions and substrate dissociation in multidrug efflux transporter AcrB. *Frontiers in Microbiology*, **2015**, 6, 302	5.7	7
20	Multiple conformational states and gate opening of outer membrane protein TolC revealed by molecular dynamics simulations. *Proteins: Structure, Function and Bioinformatics*, **2014**, 82, 2169-79	4.2	7
19	Voltage-Driven Flipping of Zwitterionic Artificial Channels in Lipid Bilayers to Rectify Ion Transport. *Journal of the American Chemical Society*, **2021**, 143, 11332-11336	16.4	7
18	Conformational Dynamics and Protein-Substrate Interaction of ABC Transporter BtuCD at the Occluded State Revealed by Molecular Dynamics Simulations. *Biochemistry*, **2016**, 55, 6897-6907	3.2	7
17	Local Hybrid Divide-and-Conquer Method for the Computation of Medium and Large Molecules. *Journal of Chemical Theory and Computation*, **2008**, 4, 2049-56	6.4	6
16	Dissecting the Conformational Dynamics-Modulated Enzyme Catalysis with Single-Molecule FRET. *Journal of Physical Chemistry B*, **2018**, 122, 6179-6187	3.4	6
15	Theoretical study about adsorption of atomic oxygen on unmodified and I-modified Ag(100) surface. *Journal of Chemical Physics*, **2003**, 118, 11210-11216	3.9	5
14	An unconventional ligand-binding mechanism of substrate-binding proteins: MD simulation and Markov state model analysis of BtuF. *Journal of Computational Chemistry*, **2019**, 40, 1440-1448	3.5	5
13	Glycerol transport through the aquaglyceroporin GlpF: bridging dynamics and kinetics with atomic simulation. *Chemical Science*, **2019**, 10, 6957-6965	9.4	3
12	Structural Features and Energetics of the Periplasmic Entrance Opening of the Outer Membrane Channel TolC Revealed by Molecular Dynamics Simulation and Markov State Model Analysis. *Journal of Chemical Information and Modeling*, **2019**, 59, 2359-2366	6.1	3
11	Revealing Thermodynamics and Kinetics of Lipid Self-Assembly by Markov State Model Analysis. *Journal of the American Chemical Society*, **2020**, 142, 21344-21352	16.4	3
10	Matrix isolation FTIR spectroscopic and density functional theoretical studies of the O2SiCO and O2Si(CO)2 molecules. *Journal of Chemical Physics*, **2002**, 116, 5643-5648	3.9	3
9	ATP Hydrolysis Induced Conformational Changes in the Vitamin B12 Transporter BtuCD Revealed by MD Simulations. *PLoS ONE*, **2016**, 11, e0166980	3.7	3

8	Conformational Dynamics of apo-GlnBP Revealed by Experimental and Computational Analysis. *Angewandte Chemie*, **2016**, 128, 14196-14200	3.6	3
7	A Residue outside the Binding Site Determines the G□Binding Specificity of GoLoco Motifs. *Biochemistry*, **2018**, 57, 6562-6569	3.2	3
6	The importance of the compact disordered state in the fuzzy interactions between intrinsically disordered proteins.. *Chemical Science*, **2022**, 13, 2363-2377	9.4	2
5	Ligand-bound glutamine binding protein assumes multiple metastable binding sites with different binding affinities. *Communications Biology*, **2020**, 3, 419	6.7	2
4	Crystal structure of the coiled-coil domain of Drosophila TRIM protein Brat. *Proteins: Structure, Function and Bioinformatics*, **2019**, 87, 706-710	4.2	1
3	A revisit of the conformational dynamics of SNARE protein rYkt6. *Biochemical and Biophysical Research Communications*, **2018**, 503, 2841-2847	3.4	1
2	The Role of Calcium in Regulating the Conformational Dynamics of d-Galactose/d-Glucose-Binding Protein Revealed by Markov State Model Analysis. *Journal of Chemical Information and Modeling*, **2021**, 61, 891-900	6.1	1
1	The Dynamic Multisite Interactions between Two Intrinsically Disordered Proteins. *Angewandte Chemie*, **2017**, 129, 7623-7627	3.6	0