Wenning Wang

List of Publications by Year
in descending order

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46 papers	922 citations	393982 19 h-index	500791 28 g-index
46 all docs	46 docs citations	46 times ranked	1292 citing authors

#	Article	IF	Citations
1	LGN/mInsc and LGN/NuMA Complex Structures Suggest Distinct Functions in Asymmetric Cell Division for the Par3/mInsc/LGN and GÎ±i/LGN/NuMA Pathways. Molecular Cell, 2011, 43, 418-431.	4.5	111
2	Artificial Aquaporin That Restores Wound Healing of Impaired Cells. Journal of the American Chemical Society, 2020, 142, 15638-15643.	6.6	54
3	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, 787-796.	6.6	53
4	Recent advances in atomic molecular dynamics simulation of intrinsically disordered proteins. Physical Chemistry Chemical Physics, 2021, 23, 777-784.	1.3	45
5	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.	1.1	42
6	Conformational Dynamics of apoâ€GlnBP Revealed by Experimental and Computational Analysis. Angewandte Chemie - International Edition, 2016, 55, 13990-13994.	7.2	41
7	Dynamic multivalent interactions of intrinsically disordered proteins. Current Opinion in Structural Biology, 2020, 62, 9-13.	2.6	41
8	The Dynamic Multisite Interactions between Two Intrinsically Disordered Proteins. Angewandte Chemie - International Edition, 2017, 56, 7515-7519.	7.2	39
9	Lipid-Induced Conformational Switch Controls Fusion Activity of Longin Domain SNARE Ykt6. Molecular Cell, 2010, 37, 383-395.	4.5	37
10	Insights into the Inhibitory Mechanism of D13-9001 to the Multidrug Transporter AcrB through Molecular Dynamics Simulations. Journal of Physical Chemistry B, 2016, 120, 2145-2154.	1.2	33
11	O/Ag(100) Surface:â€‰ A Density Functional Study with Slab Model. Journal of Physical Chemistry B, 2002, 106, 3662-3667.	1.2	30
12	The structural basis of Miranda-mediated Staufen localization during Drosophila neuroblast asymmetric division. Nature Communications, 2015, 6, 8381.	5.8	28
13	Formation and Characterization of the (Î·2-H2)CrO2, (Î·2-H2)2CrO2 and HCrO(OH) Molecules. Journal of Physical Chemistry A, 2001, 105, 10747-10752.	1.1	26
14	Phosphorylated Peptide Functionalization of Lanthanide Upconversion Nanoparticles for Tuning Nanomaterialâ€“Cell Interactions. ACS Applied Materials & Interfaces, 2016, 8, 6935-6943.	4.0	26
15	An Autoinhibited Conformation of LGN Reveals a Distinct Interaction Mode between GoLoco Motifs and TPR Motifs. Structure, 2013, 21, 1007-1017.	1.6	23
16	Gas-phase complexation of Î±-/Î²-cyclodextrin with amino acids studied by ion mobility-mass spectrometry and molecular dynamics simulations. Talanta, 2018, 186, 1-7.	2.9	23
17	Conformational stability and dynamics of the cancerâ€associated isoform Î”133p53Î² are modulated by p53 peptides and p53â€specific DNA. FASEB Journal, 2019, 33, 4225-4235.	0.2	22
18	Revealing Thermodynamics and Kinetics of Lipid Self-Assembly by Markov State Model Analysis. Journal of the American Chemical Society, 2020, 142, 21344-21352.	6.6	22

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19	Crystal Structures of the Scaffolding Protein LGN Reveal the General Mechanism by Which GoLoco Binding Motifs Inhibit the Release of GDP from Gî±i. Journal of Biological Chemistry, 2012, 287, 36766-36776.	1.6	21
20	Voltage-Driven Flipping of Zwitterionic Artificial Channels in Lipid Bilayers to Rectify Ion Transport. Journal of the American Chemical Society, 2021, 143, 11332-11336.	6.6	21
21	Extreme Fuzziness: Direct Interactions between Two IDPs. Biomolecules, 2019, 9, 81.	1.8	20
22	Molecular Dynamics Simulation of Membrane Proteins. Advances in Experimental Medicine and Biology, 2014, 805, 305-329.	0.8	16
23	Lipid Regulated Intramolecular Conformational Dynamics of SNARE-Protein Ykt6. Scientific Reports, 2016, 6, 30282.	1.6	15
24	Fast Discrimination of Sialylated N-Glycan Linkage Isomers with One-Step Derivatization by Microfluidic Capillary Electrophoresisâ€“Mass Spectrometry. Analytical Chemistry, 2022, 94, 4666-4676.	3.2	11
25	Glycerol transport through the aquaglyceroporin GlpF: bridging dynamics and kinetics with atomic simulation. Chemical Science, 2019, 10, 6957-6965.	3.7	10
26	Multiple conformational states and gate opening of outer membrane protein TolC revealed by molecular dynamics simulations. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2169-2179.	1.5	9
27	Conformational Dynamics and Proteinâ€“Substrate Interaction of ABC Transporter BtuCD at the Occluded State Revealed by Molecular Dynamics Simulations. Biochemistry, 2016, 55, 6897-6907.	1.2	9
28	Substrate binding accelerates the conformational transitions and substrate dissociation in multidrug efflux transporter AcrB. Frontiers in Microbiology, 2015, 6, 302.	1.5	8
29	Maltose-binding protein effectively stabilizes the partially closed conformation of the ATP-binding cassette transporter MalFGK₂. Physical Chemistry Chemical Physics, 2017, 19, 9366-9373.	1.3	8
30	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.	2.5	8
31	The importance of the compact disordered state in the fuzzy interactions between intrinsically disordered proteins. Chemical Science, 2022, 13, 2363-2377.	3.7	7
32	Theoretical study about adsorption of atomic oxygen on unmodified and I-modified Ag(100) surface. Journal of Chemical Physics, 2003, 118, 11210-11216.	1.2	6
33	Local Hybrid Divide-and-Conquer Method for the Computation of Medium and Large Molecules. Journal of Chemical Theory and Computation, 2008, 4, 2049-2056.	2.3	6
34	Dissecting the Conformational Dynamics-Modulated Enzyme Catalysis with Single-Molecule FRET. Journal of Physical Chemistry B, 2018, 122, 6179-6187.	1.2	6
35	An unconventional ligandâ€binding mechanism of substrateâ€binding proteins: MD simulation and Markov state model analysis of BtuF. Journal of Computational Chemistry, 2019, 40, 1440-1448.	1.5	6
36	Ligand-bound glutamine binding protein assumes multiple metastable binding sites with different binding affinities. Communications Biology, 2020, 3, 419.	2.0	6

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37	Unexpected Role of a Shortâ€Chain Dehydrogenase/Reductase Family Protein in Type II Polyketide Biosynthesis. Angewandte Chemie - International Edition, 2022, 61, .	7.2	6
38	Conformational Dynamics of apoâ€GlnBP Revealed by Experimental and Computational Analysis. Angewandte Chemie, 2016, 128, 14196-14200.	1.6	5
39	ATP Hydrolysis Induced Conformational Changes in the Vitamin B12 Transporter BtuCD Revealed by MD Simulations. PLoS ONE, 2016, 11, e0166980.	1.1	5
40	Crystal structure of the coiledâ€coil domain of Drosophila TRIM protein Brat. Proteins: Structure, Function and Bioinformatics, 2019, 87, 706-710.	1.5	4
41	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.	1.2	3
42	A Residue outside the Binding Site Determines the GÎ± Binding Specificity of GoLoco Motifs. Biochemistry, 2018, 57, 6562-6569.	1.2	3
43	The Dynamic Multisite Interactions between Two Intrinsically Disordered Proteins. Angewandte Chemie, 2017, 129, 7623-7627.	1.6	2
44	A revisit of the conformational dynamics of SNARE protein rYkt6. Biochemical and Biophysical Research Communications, 2018, 503, 2841-2847.	1.0	2
45	The Role of Calcium in Regulating the Conformational Dynamics of <scp>d</scp>-Galactose/<scp>d</scp>-Glucose-Binding Protein Revealed by Markov State Model Analysis. Journal of Chemical Information and Modeling, 2021, 61, 891-900.	2.5	2
46	Unexpected Role of a Shortâ€Chain Dehydrogenase/Reductase Family Protein in Type II Polyketide Biosynthesis. Angewandte Chemie, 0, , .	1.6	1