Changjun Chen

List of Publications by Year
in descending order

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26	271	932766 10	940134 16
papers	citations	h-index	g-index

26	26	26	283
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Observation of multiple folding pathways of Î²-hairpin trpzip2 from independent continuous folding trajectories. Bioinformatics, 2008, 24, 659-665.	1.8	37
2	A Directed Essential Dynamics Simulation of Peptide Folding. Biophysical Journal, 2005, 88, 3276-3285.	0.2	28
3	Insights into Ligand Binding to PreQ1 Riboswitch Aptamer from Molecular Dynamics Simulations. PLoS ONE, 2014, 9, e92247.	1.1	26
4	Efficiently finding the minimum free energy path from steepest descent path. Journal of Chemical Physics, 2013, 138, 164122.	1.2	22
5	Molecular dynamics simulations of folding processes of a Î²-hairpin in an implicit solvent. Physical Biology, 2006, 3, 161-171.	0.8	18
6	Calculating the absolute binding free energy of the insulin dimer in an explicit solvent. RSC Advances, 2020, 10, 790-800.	1.7	17
7	Enhanced sampling of molecular dynamics simulation of peptides and proteins by double coupling to thermal bath. Journal of Biomolecular Structure and Dynamics, 2013, 31, 206-214.	2.0	14
8	Computational evidence that fast translation speed can increase the probability of cotranslational protein folding. Scientific Reports, 2015, 5, 15316.	1.6	14
9	Accurate free energy calculation along optimized paths. Journal of Computational Chemistry, 2010, 31, 1368-1375.	1.5	12
10	A fast tomographic method for searching the minimum free energy path. Journal of Chemical Physics, 2014, 141, 154109.	1.2	12
11	Simulation study of the role of the ribosomal exit tunnel on protein folding. Physical Review E, 2013, 87, 022701.	0.8	10
12	Free-energy calculations along a high-dimensional fragmented path with constrained dynamics. Physical Review E, 2012, 86, 031901.	0.8	9
13	All-atom contact potential approach to protein thermostability analysis. Biopolymers, 2007, 85, 28-37.	1.2	8
14	Binding free-energy calculation of an ion-peptide complex by constrained dynamics. Physical Review E, 2013, 87, 062705.	0.8	8
15	Identification of key residues in proteins by using their physical characters. Physical Review E, 2006, 73, 041926.	0.8	6
16	Improving the replica-exchange molecular-dynamics method for efficient sampling in the temperature space. Physical Review E, 2015, 91, 052708.	0.8	6
17	Combining the biased and unbiased sampling strategy into one convenient free energy calculation method. Journal of Computational Chemistry, 2019, 40, 1806-1815.	1.5	5
18	Walking freely in the energy and temperature space by the modified replica exchange molecular dynamics method. Journal of Computational Chemistry, 2016, 37, 1565-1575.	1.5	4

#	Article	IF	Citations
19	Calculation of the Local Free Energy Landscape in the Restricted Region by the Modified Tomographic Method. Journal of Physical Chemistry B, 2016, 120, 3061-3071.	1.2	4
20	FSATOOL: A useful tool to do the conformational sampling and trajectory analysis work for biomolecules. Journal of Computational Chemistry, 2020, 41, 156-164.	1.5	4
21	Fast exploration of an optimal path on the multidimensional free energy surface. PLoS ONE, 2017, 12, e0177740.	1.1	2
22	<scp>FSATOOL</scp> 2.0: An integrated molecular dynamics simulation and trajectory data analysis program. Journal of Computational Chemistry, 2022, 43, 215-224.	1.5	2
23	Constructing a multidimensional free energy surface like a spider weaving a web. Journal of Computational Chemistry, 2017, 38, 2298-2306.	1.5	1
24	Investigating the folding mechanism of the Nâ€terminal domain of ribosomal protein <scp>L9</scp>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 832-844.	1.5	1
25	Simulation Study of the Plasticity of k-Turn Motif inÂDifferent Environments. Biophysical Journal, 2020, 119, 1416-1426.	0.2	1
26	DYNAMIC MOVES IN LATTICE SIMULATION OF PROTEIN FOLDING. International Journal of Modern Physics C, 2004, 15, 885-892.	0.8	0