

Taehoon Kim

List of Publications by Year in descending order

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Version: 2024-02-01

10
papers

6,811
citations

932766

10
h-index

1372195

10
g-index

10
all docs

10
docs citations

10
times ranked

9168
citing authors

#	ARTICLE	IF	CITATIONS
1	Transmembrane Helix Assembly by Window Exchange Umbrella Sampling. <i>Physical Review Letters</i> , 2012, 108, 108102.	2.9	61
2	An ensemble dynamics approach to decipher solid-state NMR observables of membrane proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 252-262.	1.4	21
3	Improving the CHARMM Force Field for Polyunsaturated Fatty Acid Chains. <i>Journal of Physical Chemistry B</i> , 2012, 116, 9424-9431.	1.2	140
4	Influence of Hydrophobic Mismatch on Structures and Dynamics of Gramicidin A and Lipid Bilayers. <i>Biophysical Journal</i> , 2012, 102, 1551-1560.	0.2	92
5	Solid-State NMR Ensemble Dynamics as a Mediator between Experiment and Simulation. <i>Biophysical Journal</i> , 2011, 100, 2922-2928.	0.2	17
6	Revisiting Hydrophobic Mismatch with Free Energy Simulation Studies of Transmembrane Helix Tilt and Rotation. <i>Biophysical Journal</i> , 2010, 99, 175-183.	0.2	106
7	Novel free energy calculations to explore mechanisms and energetics of membrane protein structure and function. <i>Journal of Computational Chemistry</i> , 2009, 30, 1622-1633.	1.5	20
8	Molecular dynamics studies on structure and dynamics of phospholamban monomer and pentamer in membranes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 86-98.	1.5	22
9	CHARMM-GLUI: A web-based graphical user interface for CHARMM. <i>Journal of Computational Chemistry</i> , 2008, 29, 1859-1865.	1.5	5,402
10	Automated Builder and Database of Protein/Membrane Complexes for Molecular Dynamics Simulations. <i>PLoS ONE</i> , 2007, 2, e880.	1.1	930