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List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Direct Observation of Cholesterol Dimers and Tetramers in Lipid Bilayers. Journal of Physical Chemistry B, 2021, 125, 1825-1837.	2.6	25
2	Finite-Size Effects and Optimal System Sizes in Simulations of Surfactant Micelle Self-Assembly. Journal of Physical Chemistry B, 2021, 125, 5068-5077.	2.6	11
3	Impact of Cholesterol Concentration and Lipid Phase on Structure and Fluctuation of Amyloid Precursor Protein. Journal of Physical Chemistry B, 2020, 124, 10173-10185.	2.6	9
4	Bicelles Rich in both Sphingolipids and Cholesterol and Their Use in Studies of Membrane Proteins. Journal of the American Chemical Society, 2020, 142, 12715-12729.	13.7	29
5	Exploring the impact of proteins on the line tension of a phase-separating ternary lipid mixture. Journal of Chemical Physics, 2019, 150, 204702.	3.0	18
6	Aerosol-OT Surfactant Forms Stable Reverse Micelles in Apolar Solvent in the Absence of Water. Journal of Physical Chemistry B, 2019, 123, 2546-2557.	2.6	23
7	Structure of APP-C991–99 and implications for role of extra-membrane domains in function and oligomerization. Biochimica Et Biophysica Acta - Biomembranes, 2018, 1860, 1698-1708.	2.6	38
8	Regimes of Complex Lipid Bilayer Phases Induced by Cholesterol Concentration in MD Simulation. Biophysical Journal, 2018, 115, 2167-2178.	0.5	37
9	Characterization of dynamics and mechanism in the self-assembly of AOT reverse micelles. Journal of Chemical Physics, 2018, 149, 144901.	3.0	6
10	Critical size dependence of domain formation observed in coarse-grained simulations of bilayers composed of ternary lipid mixtures. Journal of Chemical Physics, 2017, 147, 095101.	3.0	43
11	Bridging Microscopic and Macroscopic Mechanisms of p53-MDM2 Binding with Kinetic Network Models. Biophysical Journal, 2017, 113, 785-793.	0.5	77
12	Exploring the structure and stability of cholesterol dimer formation in multicomponent lipid bilayers. Journal of Computational Chemistry, 2017, 38, 1479-1488.	3.3	25
13	Specific Binding of Cholesterol to C99 Domain of Amyloid Precursor Protein Depends Critically on Charge State of Protein. Journal of Physical Chemistry Letters, 2016, 7, 3535-3541.	4.6	35
14	Markov models of the apo-MDM2 lid region reveal diffuse yet two-state binding dynamics and receptor poses for computational docking. Scientific Reports, 2016, 6, 31631.	3.3	17
15	On the use of mass scaling for stable and efficient simulated tempering with molecular dynamics. Journal of Computational Chemistry, 2016, 37, 2017-2028.	3.3	6
16	Microsecond simulations of mdm2 and its complex with p53 yield insight into force field accuracy and conformational dynamics. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1665-1676.	2.6	24