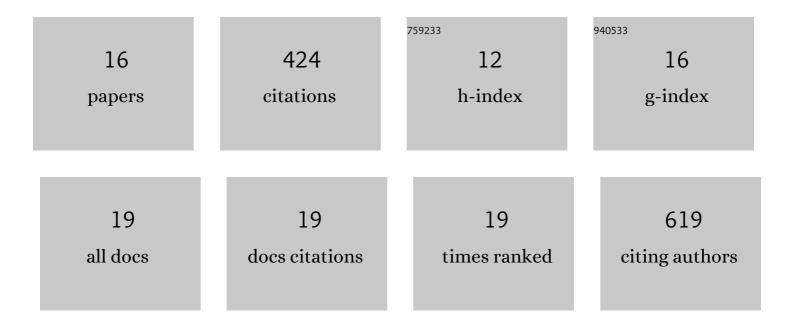
George A Pantelopulos

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Bridging Microscopic and Macroscopic Mechanisms of p53-MDM2 Binding with Kinetic Network Models. Biophysical Journal, 2017, 113, 785-793.	0.5	77
2	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
3	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
4	Regimes of Complex Lipid Bilayer Phases Induced by Cholesterol Concentration in MD Simulation. Biophysical Journal, 2018, 115, 2167-2178.	0.5	37
5	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
6	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
7	Exploring the structure and stability of cholesterol dimer formation in multicomponent lipid bilayers. Journal of Computational Chemistry, 2017, 38, 1479-1488.	3.3	25
8	Direct Observation of Cholesterol Dimers and Tetramers in Lipid Bilayers. Journal of Physical Chemistry B, 2021, 125, 1825-1837.	2.6	25
9	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
10	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
11	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
12	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
13	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
14	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
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	Characterization of dynamics and mechanism in the self-assembly of AOT reverse micelles. Journal of Chemical Physics, 2018, 149, 144901.	3.0	6