Viviana Monje-Galvan

List of Publications by Year
in descending order

27 papers	2,483 citations	759190 12 h-index	794568 19 g-index
30 all docs	30 docs citations	30 times ranked	3873 citing authors

#	Article	IF	Citations
1	Interaction of Cyanine-D112 with Binary Lipid Mixtures: Molecular Dynamics Simulation and Differential Scanning Calorimetry Study. ACS Omega, 2022, 7, 9765-9774.	3.5	1
2	A multiscale coarse-grained model of the SARS-CoV-2 virion. Biophysical Journal, 2021, 120, 1097-1104.	0.5	139
3	Molecular interactions of theÂM and E integral membrane proteins of SARS-CoV-2. Faraday Discussions, 2021, 232, 49-67.	3.2	19
4	Modeling Protein-Lipid Interactions during Viral Assembly of SARS-CoV-2. Biophysical Journal, 2021, 120, 49a.	0.5	0
5	Protein acylation by saturated very long chain fatty acids and endocytosis are involved in necroptosis. Cell Chemical Biology, 2021, 28, 1298-1309.e7.	5.2	21
6	Interfacial properties of aqueous solutions of butanol isomers and cyclohexane. Fluid Phase Equilibria, 2020, 513, 112551.	2.5	4
7	Binding mechanism of the matrix domain of HIV-1 gag on lipid membranes. ELife, 2020, 9, .	6.0	21
8	Lipid-Lipid and Lipid-Protein Interactions of the Matrix Domain of HIV-Gag at the Viral Assembly Site. Biophysical Journal, 2019, 116, 518a.	0.5	0
9	Setting Up All-Atom Molecular Dynamics Simulations to Study the Interactions of Peripheral Membrane Proteins with Model Lipid Bilayers. Methods in Molecular Biology, 2019, 1949, 325-339.	0.9	8
10	Developing and Testing of Lipid Force Fields with Applications to Modeling Cellular Membranes. Chemical Reviews, 2019, 119, 6227-6269.	47.7	72
11	Modeling Lipid Membranes. , 2019, , 741-759.		0
12	Effect of Membrane Lipid Packing on Stable Binding of the ALPS Peptide. Journal of Chemical Theory and Computation, 2019, 15, 1418-1429.	5.3	33
13	Molecular Interactions of the Matrix Domain of HIV-1 Gag Protein at the Membrane Interface. Biophysical Journal, 2018, 114, 33a.	0.5	1
14	Preferred Binding Mechanism of Osh4â€™s Amphipathic Lipid-Packing Sensor Motif, Insights from Molecular Dynamics. Journal of Physical Chemistry B, 2018, 122, 9713-9723.	2.6	18
15	Asymmetric Membrane Models for the PM And TGN of Yeast, An All-Atom Molecular Dynamics Study. Biophysical Journal, 2017, 112, 137a.	0.5	0
16	Two sterols, two bilayers: insights on membrane structure from molecular dynamics. Molecular Simulation, 2017, 43, 1179-1188.	2.0	10
17	Dual Action of Hydrotropes at the Water/Oil Interface. Journal of Physical Chemistry C, 2017, 121, 16423-16431.	3.1	24
18	Influence of Cholesterol on Phospholipid Bilayer Structure and Dynamics. Journal of Physical Chemistry B, 2016, 120, 11761-11772.	2.6	47

#	Article	IF	Citations
19	Lo/Ld Phase Coexistence and Interaction in Model Membranes with IPCÂLipids. Biophysical Journal, 2016, 110, 86a.	0.5	0
20	Peripheral membrane proteins: Tying the knot between experiment and computation. Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 1584-1593.	2.6	48
21	Modeling Lipid Membranes. , 2016, , 1-19.		0
22	Membrane Binding of the Osh4 Curvature-Sensing Peptide. Biophysical Journal, 2015, 108, 466a.	0.5	0
23	Modeling Yeast Organelle Membranes and How Lipid Diversity Influences Bilayer Properties. Biochemistry, 2015, 54, 6852-6861.	2.5	58
24	STâ€analyzer: A webâ€based user interface for simulation trajectory analysis. Journal of Computational Chemistry, 2014, 35, 957-963.	3.3	12
25	CHARMM-GUIMembrane Buildertoward realistic biological membrane simulations. Journal of Computational Chemistry, 2014, 35, 1997-2004.	3.3	1,802
26	Molecular Dynamic Studies on Organelle-Specific Yeast Membrane Models and Amphipathic Lipid Packing Sensor Motif Binding Mechanism. Biophysical Journal, 2014, 106, 710a.	0.5	0
27	Improving the CHARMM Force Field for Polyunsaturated Fatty Acid Chains. Journal of Physical Chemistry B, 2012, 116, 9424-9431.	2.6	140