Edward Lyman

List of Publications by Year
in descending order

43 papers	2,286 citations	257450 24 h-index	265206 42 g-index
45 all docs	45 docs citations	45 times ranked	2581 citing authors

#	Article	IF	Citations
1	Structural Basis of Membrane Bending by the N-BAR Protein Endophilin. Cell, 2012, 149, 137-145.	28.9	220
2	The Molecular Structure of the Liquid-Ordered Phase of Lipid Bilayers. Journal of the American Chemical Society, 2014, 136, 725-732.	13.7	217
3	Mechanism of Membrane Curvature Sensing by Amphipathic Helix Containing Proteins. Biophysical Journal, 2011, 100, 1271-1279.	0.5	184
4	Systematic Multiscale Parameterization of Heterogeneous Elastic Network Models of Proteins. Biophysical Journal, 2008, 95, 4183-4192.	0.5	148
5	Hexagonal Substructure and Hydrogen Bonding in Liquid-Ordered Phases Containing Palmitoyl Sphingomyelin. Biophysical Journal, 2015, 109, 948-955.	0.5	121
6	A Role for a Specific Cholesterol Interaction in Stabilizing the Apo Configuration of the Human A 2A Adenosine Receptor. Structure, 2009, 17, 1660-1668.	3.3	118
7	Ensemble-Based Convergence Analysis of Biomolecular Trajectories. Biophysical Journal, 2006, 91, 164-172.	0.5	106
8	Predictions for Cholesterol Interaction Sites on the A_{2A} Adenosine Receptor. Journal of the American Chemical Society, 2012, 134, 16512-16515.	13.7	98
9	Structure and Dynamics of the Actin Filament. Journal of Molecular Biology, 2010, 396, 252-263.	4.2	84
10	Understanding the Role of Amphipathic Helices in N-BAR Domain Driven Membrane Remodeling. Biophysical Journal, 2013, 104, 404-411.	0.5	81
11	Permeability of membranes in the liquid ordered and liquid disordered phases. Nature Communications, 2019, 10, 5616.	12.8	78
12	New Insights into BAR Domain-Induced Membrane Remodeling. Biophysical Journal, 2009, 97, 1616-1625.	0.5	74
13	Resolution Exchange Simulation with Incremental Coarsening. Journal of Chemical Theory and Computation, 2006, 2, 656-666.	5.3	69
14	Hierarchical coarse-graining strategy for protein-membrane systems to access mesoscopic scales. Faraday Discussions, 2010, 144, 347-357.	3.2	62
15	Identification of Two New Cholesterol Interaction Sites on the A2A Adenosine Receptor. Biophysical Journal, 2017, 113, 2415-2424.	0.5	61
16	Membrane Binding and Self-Association of the Epsin N-Terminal Homology Domain. Journal of Molecular Biology, 2012, 423, 800-817.	4.2	55
17	On the Structural Convergence of Biomolecular Simulations by Determination of the Effective Sample Size. Journal of Physical Chemistry B, 2007, 111, 12876-12882.	2.6	53
18	Neutron scattering in the biological sciences: progress and prospects. Acta Crystallographica Section D: Structural Biology, 2018, 74, 1129-1168.	2.3	47

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19	Nanoscale dynamics of cholesterol in the cell membrane. Journal of Biological Chemistry, 2019, 294, 12599-12609.	3.4	44
20	Membrane cholesterol depletion reduces downstream signaling activity of the adenosine A2A receptor. Biochimica Et Biophysica Acta - Biomembranes, 2019, 1861, 760-767.	2.6	44
21	Reconstructing atomistic detail for coarse-grained models with resolution exchange. Journal of Chemical Physics, 2008, 129, 114103.	3.0	36
22	Agonist Dynamics and Conformational Selection during Microsecond Simulations of the A2A Adenosine Receptor. Biophysical Journal, 2012, 102, 2114-2120.	0.5	36
23	Surface Shear Viscosity and Interleaflet Friction from Nonequilibrium Simulations of Lipid Bilayers. Journal of Chemical Theory and Computation, 2019, 15, 6471-6481.	5.3	27
24	Ligand-dependent cholesterol interactions with the human A2A adenosine receptor. Chemistry and Physics of Lipids, 2013, 169, 39-45.	3.2	26
25	Water under the BAR. Biophysical Journal, 2010, 99, 1783-1790.	0.5	25
26	From Dynamics to Membrane Organization: Experimental Breakthroughs Occasion a â€œModeling Manifestoâ€• Biophysical Journal, 2018, 115, 595-604.	0.5	25
27	Reconstructing protein remodeled membranes in molecular detail from mesoscopic models. Physical Chemistry Chemical Physics, 2011, 13, 10430.	2.8	23
28	Toward Hydrodynamics with Solvent Free Lipid Models: STRD Martini. Biophysical Journal, 2016, 111, 2689-2697.	0.5	19
29	Hysteresis and the Cholesterol Dependent Phase Transition in Binary Lipid Mixtures with the Martini Model. Journal of Physical Chemistry B, 2016, 120, 13086-13093.	2.6	14
30	Amphipathic Helicesâ€”Wedge? Or Nae Nae?. Biophysical Journal, 2016, 110, 1-2.	0.5	14
31	Ultrafast Formation of the Charge Transfer State of Prodan Reveals Unique Aspects of the Chromophore Environment. Journal of Physical Chemistry B, 2020, 124, 2643-2651.	2.6	11
32	Activation of G-protein-coupled receptors is thermodynamically linked to lipid solvation. Biophysical Journal, 2021, 120, 1777-1787.	0.5	10
33	Local Enrichment of Unsaturated Chains around the A_{2A} Adenosine Receptor. Biochemistry, 2019, 58, 4096-4105.	2.5	9
34	Full scale structural, mechanical and dynamical properties of HIV-1 liposomes. PLoS Computational Biology, 2022, 18, e1009781.	3.2	9
35	Resampling improves the efficiency of a â€œfast-switchâ€•equilibrium sampling protocol. Journal of Chemical Physics, 2009, 130, 081102.	3.0	8
36	Changes in pairwise correlations during running reshape global network state in the main olfactory bulb. Journal of Neurophysiology, 2021, 125, 1612-1623.	1.8	6

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37	Composition dependence of cholesterol flip-flop rates in physiological mixtures. Chemistry and Physics of Lipids, 2020, 232, 104967.	3.2	5
38	Curvature Energetics Determined by Alchemical Simulation on Four Topologically Distinct Lipid Phases. Journal of Physical Chemistry B, 2021, 125, 1815-1824.	2.6	5
39	Cholesterol Dependent Activity of the Adenosine A2A Receptor Is Modulated via the Cholesterol Consensus Motif. Molecules, 2022, 27, 3529.	3.8	5
40	Differential or Curvature Stress? Modus Vivendi. Biophysical Journal, 2020, 118, 535-537.	0.5	4
41	Laterally Resolved Small-Angle Scattering Intensity from Lipid Bilayer Simulations: An Exact and a Limited-Range Treatment. Journal of Chemical Theory and Computation, 2020, 16, 5287-5300.	5.3	4
42	Lipid-Lipid Interactions Determine the Membrane Spontaneous Curvature. Biophysical Journal, 2015, 108, 181a.	0.5	1
43	Retinal Flips the Script. Biophysical Journal, 2015, 108, 2754.	0.5	0