Jonathan N Sachs

List of Publications by Year
in descending order

52 papers	2,938 citations	257450 24 h-index	175258 52 g-index
54 all docs	54 docs citations	54 times ranked	4394 citing authors

#	Article	IF	Citations
1	Potent inhibitors of toxic alpha-synuclein identified via cellular time-resolved FRET biosensors. Npj Parkinson's Disease, 2021, 7, 52.	5.3	22
2	Fluorescence-Based TNFR1 Biosensor for Monitoring Receptor Structural and Conformational Dynamics and Discovery of Small Molecule Modulators. Methods in Molecular Biology, 2021, 2248, 121-137.	0.9	11
3	How Do Ethanolamine Plasmalogens Contribute to Order and Structure of Neurological Membranes?. Journal of Physical Chemistry B, 2020, 124, 828-839.	2.6	23
4	Noncompetitive Allosteric Antagonism of Death Receptor 5 by a Synthetic Affibody Ligand. Biochemistry, 2020, 59, 3856-3868.	2.5	5
5	Discovery of Small Molecule Inhibitors of Huntingtin Exon 1 Aggregation by FRET-Based High-Throughput Screening in Living Cells. ACS Chemical Neuroscience, 2020, 11, 2286-2295.	3.5	20
6	Conformational states of TNFR1 as a molecular switch for receptor function. Protein Science, 2020, 29, 1401-1415.	7.6	18
7	The role of wild-type tau in Alzheimerâ€™s disease and related tauopathies. Journal of Life Sciences (Westlake Village, Calif), 2020, 2, 1-17.	1.8	3
8	Noncompetitive inhibitors of TNFR1 probe conformational activation states. Science Signaling, 2019, 12, .	3.6	40
9	Targeting the ensemble of heterogeneous tau oligomers in cells: A novel small molecule screening platform for tauopathies. Alzheimer's and Dementia, 2019, 15, 1489-1502.	0.8	53
10	Multiscale Computational Modeling of Tubulin-Tubulin Lateral Interaction. Biophysical Journal, 2019, 117, 1234-1249.	0.5	16
11	Chondroitin sulfate proteoglycan 4 enhanced melanoma motility and growth requires a cysteine in the core protein transmembrane domain. Melanoma Research, 2019, 29, 365-375.	1.2	10
12	Piecing it together: Unraveling the elusive structure-function relationship in single-pass membrane receptors. Biochimica Et Biophysica Acta - Biomembranes, 2017, 1859, 1398-1416.	2.6	18
13	Î±-Synucleinâ€™s Uniquely Long Amphipathic Helix Enhances its Membrane Binding and Remodeling Capacity. Journal of Membrane Biology, 2017, 250, 183-193.	2.1	27
14	An Innovative High-Throughput Screening Approach for Discovery of Small Molecules That Inhibit TNF Receptors. SLAS Discovery, 2017, 22, 950-961.	2.7	45
15	Soluble Extracellular Domain of Death Receptor 5 Inhibits TRAIL-Induced Apoptosis by Disrupting Receptorâ€“Receptor Interactions. Journal of Molecular Biology, 2017, 429, 2943-2953.	4.2	13
16	Death Receptor 5 Activation Is Energetically Coupled to Opening of the Transmembrane Domain Dimer. Biophysical Journal, 2017, 113, 381-392.	0.5	9
17	Minimal Nucleation State of Î±-Synuclein Is Stabilized by Dynamic Threonineâ€“Water Networks. ACS Chemical Neuroscience, 2017, 8, 1859-1864.	3.5	10
18	Polyunsaturated chains in asymmetric lipids disorder raft mixtures and preferentially associate with Î±-Synuclein. Biochimica Et Biophysica Acta - Biomembranes, 2017, 1859, 529-536.	2.6	12

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19	The IM30/Vipp1 C-terminus associates with the lipid bilayer and modulates membrane fusion. Biochimica Et Biophysica Acta - Bioenergetics, 2017, 1858, 126-136.	1.0	26
20	HuR Contributes to TRAIL Resistance by Restricting Death Receptor 4 Expression in Pancreatic Cancer Cells. Molecular Cancer Research, 2016, 14, 599-611.	3.4	45
21	Death Receptor 5 Networks Require Membrane Cholesterol for Proper Structure and Function. Journal of Molecular Biology, 2016, 428, 4843-4855.	4.2	15
22	Oxidation increases the strength of the methionine-aromatic interaction. Nature Chemical Biology, 2016, 12, 860-866.	8.0	53
23	From the New Editor-in-Chief. Applied Biochemistry and Biotechnology, 2016, 180, 1-2.	2.9	17
24	Membrane remodeling and mechanics: Experiments and simulations of Î±-Synuclein. Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 1594-1609.	2.6	43
25	Biophysics of Î±-synuclein induced membrane remodelling. Physical Chemistry Chemical Physics, 2015, 17, 15561-15568.	2.8	47
26	Î±-Synuclein Reduces Tension and Increases Undulations in Simulations of Small Unilamellar Vesicles. Biophysical Journal, 2015, 108, 1848-1851.	0.5	18
27	Open and Closed Conformations of the Isolated Transmembrane Domain of Death Receptor 5 Support a New Model of Activation. Biophysical Journal, 2014, 106, L21-L24.	0.5	16
28	Determining Structural and Mechanical Properties from Molecular Dynamics Simulations of Lipid Vesicles. Journal of Chemical Theory and Computation, 2014, 10, 4160-4168.	5.3	25
29	Î±-Synuclein-Induced Membrane Remodeling Is Driven by Binding Affinity, Partition Depth, and Interleaflet Order Asymmetry. Journal of the American Chemical Society, 2014, 136, 9962-9972.	13.7	90
30	TNFR1 Signaling Is Associated with Backbone Conformational Changes of Receptor Dimers Consistent with Overactivation in the R92Q TRAPS Mutant. Biochemistry, 2012, 51, 6545-6555.	2.5	37
31	The Nature of Membrane Curvature-Induction by Amphipathic Î±-Helices Relies upon Protein Length: Simulations of Î±-Synuclein and H0. Biophysical Journal, 2012, 102, 237a.	0.5	1
32	Î±-Synuclein Induces Both Positive Mean Curvature and Negative Gaussian Curvature in Membranes. Journal of the American Chemical Society, 2012, 134, 2613-2620.	13.7	108
33	The Methionine-aromatic Motif Plays a Unique Role in Stabilizing Protein Structure. Journal of Biological Chemistry, 2012, 287, 34979-34991.	3.4	261
34	Tumor Necrosis Factor-related Apoptosis-inducing Ligand (TRAIL) Induces Death Receptor 5 Networks That Are Highly Organized. Journal of Biological Chemistry, 2012, 287, 21265-21278.	3.4	70
35	Determination of Electron Density Profiles and Area from Simulations of Undulating Membranes. Biophysical Journal, 2011, 100, 2112-2120.	0.5	54
36	Interpretation of Fluctuation Spectra in Lipid Bilayer Simulations. Biophysical Journal, 2011, 100, 2104-2111.	0.5	117

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37	All-Atom and Coarse-Grained Molecular Dynamics Simulations of a Membrane Protein Stabilizing Polymer. Langmuir, 2011, 27, 10523-10537.	3.5	55
38	Interleaflet Interaction and Asymmetry in Phase Separated Lipid Bilayers: Molecular Dynamics Simulations. Journal of the American Chemical Society, 2011, 133, 6563-6577.	13.7	160
39	Extracting Experimental Measurables from Molecular Dynamics Simulations of Membranes. Annual Reports in Computational Chemistry, 2011, , 125-150.	1.7	5
40	NaCl Interactions with Phosphatidylcholine Bilayers Do Not Alter Membrane Structure but Induce Long-Range Ordering of Ions and Water. Journal of Membrane Biology, 2011, 244, 35-42.	2.1	38
41	Curvature Dynamics of Î±-Synuclein Familial Parkinson Disease Mutants. Journal of Biological Chemistry, 2009, 284, 7177-7189.	3.4	97
42	Inhibiting Lateral Domain Formation in Lipid Bilayers: Simulations of Alternative Steroid Headgroup Chemistries. Journal of the American Chemical Society, 2009, 131, 16362-16363.	13.7	20
43	Experimental verification of lipid bilayer structure through multi-scale modeling. Biochimica Et Biophysica Acta - Biomembranes, 2009, 1788, 2284-2290.	2.6	21
44	The Effect of Cholesterol on Short- and Long-Chain Monounsaturated Lipid Bilayers as Determined by Molecular Dynamics Simulations and X-Ray Scattering. Biophysical Journal, 2008, 95, 2792-2805.	0.5	148
45	Lipid Bilayer Structure Determined by the Simultaneous Analysis of Neutron and X-Ray Scattering Data. Biophysical Journal, 2008, 95, 2356-2367.	0.5	518
46	Curvature Effect on the Structure of Phospholipid Bilayers. Langmuir, 2007, 23, 1292-1299.	3.5	124
47	Environmental Effects on Glycophorin A Folding and Structure Examined through Molecular Simulations. Journal of Chemical Theory and Computation, 2005, 1, 375-388.	5.3	3
48	Changes in Phosphatidylcholine Headgroup Tilt and Water Order Induced by Monovalent Salts: Molecular Dynamics Simulations. Biophysical Journal, 2004, 86, 3772-3782.	0.5	130
49	Interpretation of small angle X-ray measurements guided by molecular dynamics simulations of lipid bilayers. Chemistry and Physics of Lipids, 2003, 126, 211-223.	3.2	52
50	Understanding the Hofmeister Effect in Interactions between Chaotropic Anions and Lipid Bilayers:Â Molecular Dynamics Simulations. Journal of the American Chemical Society, 2003, 125, 8742-8743.	13.7	132
51	Molecular dynamics simulations of ionic concentration gradients across model bilayers. Journal of Chemical Physics, 2003, 118, 1957-1969.	3.0	9
52	Dipole lattice membrane model for protein calculations. Proteins: Structure, Function and Bioinformatics, 2000, 41, 211-223.	2.6	25