Kristyna Pluhackova

List of Publications by Year
in descending order

36	2,694	304602	360920
papers	citations	22 h-index	35 g-index

37	37	37	3902
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Gasdermin-A3 pore formation propagates along variable pathways. Nature Communications, 2022, 13, 2609.	5.8	25
2	A cholesterol analog stabilizes the human Î² ₂ -adrenergic receptor nonlinearly with temperature. Science Signaling, 2022, 15, .	1.6	8
3	The Hidden Intricacies of Aquaporins: Remarkable Details in a Common Structural Scaffold. Small, 2022, 18, .	5.2	8
4	Native-like membrane models of E. coli polar lipid extract shed light on the importance of lipid composition complexity. BMC Biology, 2021, 19, 4.	1.7	33
5	Monitoring the binding and insertion of a single transmembrane protein by an insertase. Nature Communications, 2021, 12, 7082.	5.8	16
6	Lipids and Phosphorylation Conjointly Modulate Complex Formation of Î²2-Adrenergic Receptor and Î²-arrestin2. Frontiers in Cell and Developmental Biology, 2021, 9, 807913.	1.8	13
7	Lipid Dynamics in Membranes Slowed Down by Transmembrane Proteins. Frontiers in Cell and Developmental Biology, 2020, 8, 579388.	1.8	16
8	Structural Model of the mIgM B-Cell Receptor Transmembrane Domain From Self-Association Molecular Dynamics Simulations. Frontiers in Immunology, 2018, 9, 2947.	2.2	17
9	Closely related, yet unique: Distinct homo- and heterodimerization patterns of G protein coupled chemokine receptors and their fine-tuning by cholesterol. PLoS Computational Biology, 2018, 14, e1006062.	1.5	33
10	Dynamic processes in biological membrane mimics revealed by quasielastic neutron scattering. Chemistry and Physics of Lipids, 2017, 206, 28-42.	1.5	16
11	Critical Comparison of Biomembrane Force Fields: Proteinâ€“Lipid Interactions at the Membrane Interface. Journal of Chemical Theory and Computation, 2017, 13, 2310-2321.	2.3	62
12	The Multifaceted Role of SNARE Proteins in Membrane Fusion. Frontiers in Physiology, 2017, 8, 5.	1.3	226
13	A Critical Comparison of Biomembrane Force Fields: Structure and Dynamics of Model DMPC, POPC, and POPE Bilayers. Journal of Physical Chemistry B, 2016, 120, 3888-3903.	1.2	138
14	Exploring the Formation and the Structure of Synaptobrevin Oligomers in a Model Membrane. Biophysical Journal, 2016, 110, 2004-2015.	0.2	13
15	Binding Characteristics of Sphingosine-1-Phosphate to ApoM hints to Assisted Release Mechanism via the ApoM Calyx-Opening. Scientific Reports, 2016, 6, 30655.	1.6	21
16	A Coiled-Coil Peptide Shaping Lipid Bilayers upon Fusion. Biophysical Journal, 2016, 111, 2162-2175.	0.2	36
17	Synaptobrevin transmembrane domain determines the structure and dynamics of the SNARE motif and the linker region. Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 855-865.	1.4	31
18	Dynamic Cholesterol-Conditioned Dimerization of the G Protein Coupled Chemokine Receptor Type 4. PLoS Computational Biology, 2016, 12, e1005169.	1.5	75

#	Article	IF	Citations
19	Biomembranes in atomistic and coarse-grained simulations. Journal of Physics Condensed Matter, 2015, 27, 323103.	0.7	61
20	Spontaneous Adsorption of Coiled-Coil Model Peptides K and E to a Mixed Lipid Bilayer. Journal of Physical Chemistry B, 2015, 119, 4396-4408.	1.2	29
21	High-Throughput Simulations of Dimer and Trimer Assembly of Membrane Proteins. The DAFT Approach. Journal of Chemical Theory and Computation, 2015, 11, 2278-2291.	2.3	94
22	Extension of the LOPLS-AA Force Field for Alcohols, Esters, and Monoolein Bilayers and its Validation by Neutron Scattering Experiments. Journal of Physical Chemistry B, 2015, 119, 15287-15299.	1.2	42
23	Synaptobrevin Transmembrane Domain Dimerization Studied by Multiscale Molecular Dynamics Simulations. Biophysical Journal, 2015, 109, 760-771.	0.2	22
24	Going Backward: An Efficient Multiscale Approach using Reverse Transformation. Biophysical Journal, 2014, 106, 640a.	0.2	2
25	Going Backward: A Flexible Geometric Approach to Reverse Transformation from Coarse Grained to Atomistic Models. Journal of Chemical Theory and Computation, 2014, 10, 676-690.	2.3	566
26	Molecular Dynamics Simulations of Membrane Proteins. Methods in Molecular Biology, 2013, 1033, 85-101.	0.4	26
27	Optimization of the OPLS-AA Force Field for Long Hydrocarbons. Journal of Chemical Theory and Computation, 2012, 8, 1459-1470.	2.3	474
28	Guanineâ€“aspartic acid interactions probed with IRâ€“UV resonance spectroscopy. Physical Chemistry Chemical Physics, 2010, 12, 3597.	1.3	14
29	Phenylalanyl-Glycyl-Phenylalanine Tripeptide: A Model System for Aromaticâ^'Aromatic Side Chain Interactions in Proteins. Journal of Chemical Theory and Computation, 2009, 5, 2248-2256.	2.3	23
30	Benchmark database on isolated small peptides containing an aromatic side chain: comparison between wave function and density functional theory methods and empirical force field. Physical Chemistry Chemical Physics, 2008, 10, 2747.	1.3	146
31	On the Importance of Electron Correlation Effects for the Intramolecular Stacking Geometry of a Bis-Thiophene Derivative. Journal of Physical Chemistry A, 2008, 112, 12469-12474.	1.1	23
32	Quantum Chemical Benchmark Energy and Geometry Database for Molecular Clusters and Complex Molecular Systems (www.begdb.com): A Users Manual and Examples. Collection of Czechoslovak Chemical Communications, 2008, 73, 1261-1270.	1.0	144
33	Vicinal Amino Alcohols as Organocatalysts in Asymmetric Cross-Aldol Reaction of Ketones:â€‰ Application in the Synthesis of Convolutamydine A. Organic Letters, 2007, 9, 5473-5476.	2.4	178
34	Stabilisation energy of C6H6â‹¯C6X6(X = F, Cl, Br, I, CN) complexes: complete basis set limit calculations at MP2 and CCSD(T) levels. Physical Chemistry Chemical Physics, 2007, 9, 755-760.	1.3	37
35	Theoretical Investigation of the Unexpected Red Shift in the Halothane[ellipsis (horizontal)]Acetone Complex. AIP Conference Proceedings, 2007, , .	0.3	0
36	On the Nature of the Surprisingly Small (Red) Shift in the Halothaneâ‹…â‹…â‹…Acetone Complex. ChemPhysChem, 2007, 8, 1352-1356.	1.0	26