Xavier Periole

List of Publications by Year
in descending order

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44 papers	8,289 citations	147801 31 h-index	254184 43 g-index
47 all docs	47 docs citations	47 times ranked	7652 citing authors

#	Article	IF	Citations
1	The MARTINI Coarse-Grained Force Field: Extension to Proteins. Journal of Chemical Theory and Computation, 2008, 4, 819-834.	5.3	2,178
2	Improved Parameters for the Martini Coarse-Grained Protein Force Field. Journal of Chemical Theory and Computation, 2013, 9, 687-697.	5.3	1,181
3	Lipid Organization of the Plasma Membrane. Journal of the American Chemical Society, 2014, 136, 14554-14559.	13.7	734
4	Combining an Elastic Network With a Coarse-Grained Molecular Force Field: Structure, Dynamics, and Intermolecular Recognition. Journal of Chemical Theory and Computation, 2009, 5, 2531-2543.	5.3	571
5	Martini 3: a general purpose force field for coarse-grained molecular dynamics. Nature Methods, 2021, 18, 382-388.	19.0	557
6	The power of coarse graining in biomolecular simulations. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2014, 4, 225-248.	14.6	423
7	G Protein-Coupled Receptors Self-Assemble in Dynamics Simulations of Model Bilayers. Journal of the American Chemical Society, 2007, 129, 10126-10132.	13.7	298
8	Phytochemicals Perturb Membranes and Promiscuously Alter Protein Function. ACS Chemical Biology, 2014, 9, 1788-1798.	3.4	241
9	Dry Martini, a Coarse-Grained Force Field for Lipid Membrane Simulations with Implicit Solvent. Journal of Chemical Theory and Computation, 2015, 11, 260-275.	5.3	236
10	Structural Determinants of the Supramolecular Organization of G Protein-Coupled Receptors in Bilayers. Journal of the American Chemical Society, 2012, 134, 10959-10965.	13.7	199
11	Evidence for Cardiolipin Binding Sites on the Membrane-Exposed Surface of the Cytochrome bc₁. Journal of the American Chemical Society, 2013, 135, 3112-3120.	13.7	146
12	Computational â€˜microscopyâ€™ of cellular membranes. Journal of Cell Science, 2016, 129, 257-68.	2.0	119
13	Convergence and sampling efficiency in replica exchange simulations of peptide folding in explicit solvent. Journal of Chemical Physics, 2007, 126, 014903.	3.0	114
14	From light-harvesting to photoprotection: structural basis of the dynamic switch of the major antenna complex of plants (LHCII). Scientific Reports, 2015, 5, 15661.	3.3	108
15	The Martini Coarse-Grained Force Field. Methods in Molecular Biology, 2013, 924, 533-565.	0.9	107
16	A direct interaction of cholesterol with the dopamine transporter prevents its out-to-inward transition. PLoS Computational Biology, 2018, 14, e1005907.	3.2	81
17	Refining homology models by combining replicaâ€exchange molecular dynamics and statistical potentials. Proteins: Structure, Function and Bioinformatics, 2008, 72, 1171-1188.	2.6	75
18	Exchange pathways of plastoquinone and plastoquinol in the photosystem II complex. Nature Communications, 2017, 8, 15214.	12.8	71

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19	Improved Angle Potentials for Coarse-Grained Molecular Dynamics Simulations. Journal of Chemical Theory and Computation, 2013, 9, 3282-3292.	5.3	67
20	Comment on â€œOn using a too large integration time step in molecular dynamics simulations of coarse-grained molecular modelsâ€• by M. Winger, D. Trzesniak, R. Baron and W. F. van Gunsteren, Phys. Chem. Chem. Phys., 2009, 11, 1934. Physical Chemistry Chemical Physics, 2010, 12, 2254.	2.8	66
21	Rhodopsin Forms a Dimer with Cytoplasmic Helix 8 Contacts in Native Membranes. Biochemistry, 2012, 51, 1819-1821.	2.5	65
22	Factors That Affect the Degree of Twist in Î²-Sheet Structures: A Molecular Dynamics Simulation Study of a Cross-Î² Filament of the GNNQQNY Peptide. Journal of Physical Chemistry B, 2009, 113, 1728-1737.	2.6	59
23	Cholesterol binding to a conserved site modulates the conformation, pharmacology, and transport kinetics of the human serotonin transporter. Journal of Biological Chemistry, 2018, 293, 3510-3523.	3.4	55
24	Dimerization of Amino Acid Side Chains: Lessons from the Comparison of Different Force Fields. Journal of Chemical Theory and Computation, 2012, 8, 1003-1014.	5.3	54
25	Interplay of G Protein-Coupled Receptors with the Membrane: Insights from Supra-Atomic Coarse Grain Molecular Dynamics Simulations. Chemical Reviews, 2017, 117, 156-185.	47.7	50
26	Energetics Underlying Twist Polymorphisms in Amyloid Fibrils. Journal of Physical Chemistry B, 2018, 122, 1081-1091.	2.6	44
27	Molecular Dynamics Simulations of Transducin: Interdomain and Front to Back Communication in Activation and Nucleotide Exchange. Journal of Molecular Biology, 2004, 338, 469-481.	4.2	41
28	Atomistic and Coarse Grain Topologies for the Cofactors Associated with the Photosystem II Core Complex. Journal of Physical Chemistry B, 2015, 119, 7791-7803.	2.6	41
29	Protofibrillar Assembly Toward the Formation of Amyloid Fibrils. Journal of Physical Chemistry Letters, 2011, 2, 2385-2390.	4.6	39
30	In Silico Design of Robust Bolalipid Membranes. Biomacromolecules, 2012, 13, 196-205.	5.4	38
31	DNA-encircled lipid bilayers. Nanoscale, 2018, 10, 18463-18467.	5.6	35
32	Molecular Dynamics of Photosystem II Embedded in the Thylakoid Membrane. Journal of Physical Chemistry B, 2017, 121, 3237-3249.	2.6	34
33	Dimer Interface of the Human Serotonin Transporter and Effect of the Membrane Composition. Scientific Reports, 2018, 8, 5080.	3.3	32
34	An Amphotericin B Derivative Equally Potent to Amphotericin B and with Increased Safety. PLoS ONE, 2016, 11, e0162171.	2.5	29
35	Acidâ^'Base Equilibria in Rhodopsin:Â Dependence of the Protonation State of Glu134 on Its Environmentâ€. Biochemistry, 2004, 43, 6858-6864.	2.5	25
36	Insight into the molecular mechanism behind PEG-mediated stabilization of biofluid lipases. Scientific Reports, 2018, 8, 12293.	3.3	15

#	Article	IF	Citations
37	Mimicking the action of folding chaperones by Hamiltonian replicaâ€exchange molecular dynamics simulations: Application in the refinement of de novo models. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1744-1754.	2.6	14
38	Molecular Modeling Investigation of the Interaction between Humicola insolens Cutinase and SDS Surfactant Suggests a Mechanism for Enzyme Inactivation. Journal of Chemical Information and Modeling, 2019, 59, 1977-1987.	5.4	14
39	Molecular dynamics simulations from putative transition states of Î±â€spectrin SH3 domain. Proteins: Structure, Function and Bioinformatics, 2007, 69, 536-550.	2.6	13
40	Effect of palmitoylation on the dimer formation of the human dopamine transporter. Scientific Reports, 2021, 11, 4164.	3.3	8
41	Probing the free energy landscape of the FBP28WW domain using multiple techniques. Journal of Computational Chemistry, 2009, 30, 1059-1068.	3.3	6
42	The MARTINI Force Field. , 2008, , 5-19.		3
43	A Structurally Flexible Protein Backbone for the MARTINI Coarse Grained Force Field. Biophysical Journal, 2011, 100, 613a.	0.5	1
44	Probing Self-Assembly of G Protein-Coupled Receptor Oligomers in Membranes Using Molecular Dynamics Modeling and Experimental Approaches. , 2017, , 385-414.		1