

Tsjerk A Wassenaar

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

6,121
citations

279798

23
h-index

233421

45
g-index

50
all docs

50
docs citations

50
times ranked

6867
citing authors

#	ARTICLE	IF	CITATIONS
1	Martini 3: a general purpose force field for coarse-grained molecular dynamics. <i>Nature Methods</i> , 2021, 18, 382-388.	19.0	557
2	Asymmetric CorA Gating Mechanism as Observed by Molecular Dynamics Simulations. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 2407-2417.	5.4	10
3	General Protocol for Constructing Molecular Models of Nanodiscs. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 2869-2883.	5.4	11
4	Retinyl esters form lipid droplets independently of triacylglycerol and seipin. <i>Journal of Cell Biology</i> , 2021, 220, .	5.2	22
5	Competing Roles of Ca ²⁺ and Nonmuscle Myosin IIA on the Dynamics of the Metastasis-Associated Protein S100A4. <i>Journal of Physical Chemistry B</i> , 2021, 125, 10059-10071.	2.6	2
6	Sequential Voxel-Based Leaflet Segmentation of Complex Lipid Morphologies. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 7873-7885.	5.3	8
7	Structural characterization of supramolecular hollow nanotubes with atomistic simulations and SAXS. <i>Physical Chemistry Chemical Physics</i> , 2020, 22, 21083-21093.	2.8	14
8	Backmapping triangulated surfaces to coarse-grained membrane models. <i>Nature Communications</i> , 2020, 11, 2296.	12.8	86
9	Charge-dependent interactions of monomeric and filamentous actin with lipid bilayers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5861-5872.	7.1	35
10	Lipid-dependent conformational landscape of the ErbB2 growth factor receptor dimers. <i>Chemistry and Physics of Lipids</i> , 2020, 230, 104911.	3.2	7
11	LION/web: a web-based ontology enrichment tool for lipidomic data analysis. <i>GigaScience</i> , 2019, 8, .	6.4	128
12	Statistical efficiency of methods for computing free energy of hydration. <i>Journal of Chemical Physics</i> , 2018, 149, 144111.	3.0	16
13	Dopamine transporter oligomerization involves the scaffold domain, but spares the bundle domain. <i>PLoS Computational Biology</i> , 2018, 14, e1006229.	3.2	20
14	Lipid-Protein Interactions Are Unique Fingerprints for Membrane Proteins. <i>ACS Central Science</i> , 2018, 4, 709-717.	11.3	274
15	eTOX ALLIES: an automated pipeLine for linear interaction energy-based simulations. <i>Journal of Cheminformatics</i> , 2017, 9, 58.	6.1	7
16	A MoS ₂ -Based Capacitive Displacement Sensor for DNA Sequencing. <i>ACS Nano</i> , 2016, 10, 9009-9016.	14.6	40
17	Nucleobase-functionalized graphene nanoribbons for accurate high-speed DNA sequencing. <i>Nanoscale</i> , 2016, 8, 1861-1867.	5.6	52
18	Dynamic Cholesterol-Conditioned Dimerization of the G Protein Coupled Chemokine Receptor Type 4. <i>PLoS Computational Biology</i> , 2016, 12, e1005169.	3.2	75

#	ARTICLE	IF	CITATIONS
19	Molecular dynamics study of the effect of active site protonation on Helicobacter pylori 5â€²-methylthioadenosine/S-adenosylhomocysteine nucleosidase. European Biophysics Journal, 2015, 44, 685-696.	2.2	6
20	Probing Binding Sites and Mechanisms of Action of an I Ks Activator by Computations and Experiments. Biophysical Journal, 2015, 108, 62-75.	0.5	35
21	Spontaneous Adsorption of Coiled-Coil Model Peptides K and E to a Mixed Lipid Bilayer. Journal of Physical Chemistry B, 2015, 119, 4396-4408.	2.6	29
22	Characterization of thylakoid lipid membranes from cyanobacteria and higher plants by molecular dynamics simulations. Biochimica Et Biophysica Acta - Biomembranes, 2015, 1848, 1319-1330.	2.6	120
23	Computational Lipidomics with <i>insane</i> : A Versatile Tool for Generating Custom Membranes for Molecular Simulations. Journal of Chemical Theory and Computation, 2015, 11, 2144-2155.	5.3	847
24	Thermodynamic and kinetic characterization of transmembrane helix association. Physical Chemistry Chemical Physics, 2015, 17, 1390-1398.	2.8	25
25	Activation of the bacterial thermosensor DesK involves a serine zipper dimerization motif that is modulated by bilayer thickness. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6353-6358.	7.1	44
26	High-Throughput Simulations of Dimer and Trimer Assembly of Membrane Proteins. The DAFT Approach. Journal of Chemical Theory and Computation, 2015, 11, 2278-2291.	5.3	94
27	Synaptobrevin Transmembrane Domain Dimerization Studied by Multiscale Molecular Dynamics Simulations. Biophysical Journal, 2015, 109, 760-771.	0.5	22
28	The effect of triple glutamic mutations E9Q/E194Q/E204Q on the structural stability of bacteriorhodopsin. FEBS Journal, 2014, 281, 1181-1195.	4.7	4
29	Molecular dynamics investigation of Helicobacter pylori chemotactic protein CheY1 and two mutants. Journal of Molecular Modeling, 2014, 20, 2212.	1.8	3
30	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.	5.3	566
31	X-ray structure, thermodynamics, elastic properties and MD simulations of cardiolipin/dimyristoylphosphatidylcholine mixed membranes. Chemistry and Physics of Lipids, 2014, 178, 1-10.	3.2	42
32	Lipid Organization of the Plasma Membrane. Journal of the American Chemical Society, 2014, 136, 14554-14559.	13.7	734
33	Improved Parameters for the Martini Coarse-Grained Protein Force Field. Journal of Chemical Theory and Computation, 2013, 9, 687-697.	5.3	1,181
34	Mixing MARTINI: Electrostatic Coupling in Hybrid Atomisticâ€“Coarse-Grained Biomolecular Simulations. Journal of Physical Chemistry B, 2013, 117, 3516-3530.	2.6	145
35	Molecular Dynamics Simulations of Membrane Proteins. Methods in Molecular Biology, 2013, 1033, 85-101.	0.9	26
36	WeNMR: Structural Biology on the Grid. Journal of Grid Computing, 2012, 10, 743-767.	3.9	170

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37	SQUEEZE-E: The Optimal Solution for Molecular Simulations with Periodic Boundary Conditions. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 3618-3627.	5.3	6
38	A Flexible, Grid-Enabled Web Portal for GROMACS Molecular Dynamics Simulations. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 3463-3472.	5.3	32
39	The eNMR platform for structural biology. <i>Journal of Structural and Functional Genomics</i> , 2010, 11, 1-8.	1.2	18
40	Calcium binding to the purple membrane: A molecular dynamics study. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 669-681.	2.6	5
41	The conformation of the extracellular binding domain of Death Receptor 5 in the presence and absence of the activating ligand TRAIL: A molecular dynamics study. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 333-343.	2.6	15
42	How Sensitive Are Nanosecond Molecular Dynamics Simulations of Proteins to Changes in the Force Field?. <i>Journal of Physical Chemistry B</i> , 2007, 111, 6015-6025.	2.6	16
43	HADDOCK versus HADDOCK: New features and performance of HADDOCK2.0 on the CAPRI targets. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 726-733.	2.6	504
44	The effect of box shape on the dynamic properties of proteins simulated under periodic boundary conditions. <i>Journal of Computational Chemistry</i> , 2006, 27, 316-325.	3.3	33
45	A method to obtain a near-minimal-volume molecular simulation of a macromolecule, using periodic boundary conditions and rotational constraints. <i>Journal of Computational Chemistry</i> , 2004, 25, 1037-1046.	3.3	16