Eric Jakobsson

List of Publications by Year
in descending order

67	3,866	172207	123241
papers	citations	29 h-index	61 g-index

71	71	71	4029
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Anomalously Immobilized Water:â€‰ A New Water Phase Induced by Confinement in Nanotubes. Nano Letters, 2003, 3, 589-592.	4.5	411
2	An Improved United Atom Force Field for Simulation of Mixed Lipid Bilayers. Journal of Physical Chemistry B, 2009, 113, 2748-2763.	1.2	267
3	Cholesterol-Induced Modifications in Lipid Bilayers: A Simulation Study. Biophysical Journal, 2002, 83, 1842-1853.	0.2	225
4	Identification of the prokaryotic ligand-gated ion channels and their implications for the mechanisms and origins of animal Cys-loop ion channels. Genome Biology, 2004, 6, R4.	13.9	218
5	Electrolytic Transport in Modified Carbon Nanotubes. Nano Letters, 2003, 3, 1399-1403.	4.5	188
6	The theory of ion transport through membrane channels. Progress in Biophysics and Molecular Biology, 1985, 46, 51-96.	1.4	171
7	Simulation of the Early Stages of Nano-Domain Formation in Mixed Bilayers of Sphingomyelin, Cholesterol, and Dioleylphosphatidylcholine. Biophysical Journal, 2004, 87, 3312-3322.	0.2	164
8	Sphingomyelin-Cholesterol Domains in Phospholipid Membranes: Atomistic Simulation. Biophysical Journal, 2004, 87, 1092-1100.	0.2	161
9	Structure of Sphingomyelin Bilayers: A Simulation Study. Biophysical Journal, 2003, 85, 3624-3635.	0.2	134
10	Molecular Simulation of Dioleoylphosphatidylcholine Lipid Bilayers at Differing Levels of Hydration. Biophysical Journal, 2001, 81, 3005-3015.	0.2	128
11	Combined Monte Carlo and Molecular Dynamics Simulation of Fully Hydrated Dioleyl and Palmitoyl-oleyl Phosphatidylcholine Lipid Bilayers. Biophysical Journal, 1999, 77, 2462-2469.	0.2	126
12	Sequence-Function Analysis of the K+-Selective Family of Ion Channels Using a Comprehensive Alignment and the KcsA Channel Structure. Biophysical Journal, 2003, 84, 2929-2942.	0.2	112
13	Simulation Study of a Gramicidin/Lipid Bilayer System in Excess Water and Lipid. I. Structure of the Molecular Complex. Biophysical Journal, 1999, 76, 1929-1938.	0.2	108
14	Towards a Unified Understanding of Lithium Action in Basic Biology and its Significance for Applied Biology. Journal of Membrane Biology, 2017, 250, 587-604.	1.0	103
15	Cholesterol Packing around Lipids with Saturated and Unsaturated Chains: A Simulation Study. Langmuir, 2008, 24, 6858-6865.	1.6	97
16	Distinct mechanisms regulating mechanical force-induced Ca2+ signals at the plasma membrane and the ER in human MSCs. ELife, 2015, 4, e04876.	2.8	90
17	Hierarchical Approach to Predicting Permeation in Ion Channels. Biophysical Journal, 2001, 81, 2473-2483.	0.2	79
18	A Coarse-Grained Model Based on Morse Potential for Water and n-Alkanes. Journal of Chemical Theory and Computation, 2010, 6, 851-863.	2.3	75

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19	Simulation Study of a Gramicidin/Lipid Bilayer System in Excess Water and Lipid. II. Rates and Mechanisms of Water Transport. Biophysical Journal, 1999, 76, 1939-1950.	0.2	71
20	Cholesterol Surrogates: A Comparison of Cholesterol and 16:0 Ceramide in POPC Bilayers. Biophysical Journal, 2007, 92, 920-927.	0.2	71
21	Combined Monte Carlo and Molecular Dynamics Simulation of Hydrated Lipid-Cholesterol Lipid Bilayers at Low Cholesterol Concentration. Biophysical Journal, 2001, 80, 1104-1114.	0.2	70
22	The Influence of Amino Acid Protonation States on Molecular Dynamics Simulations of the Bacterial Porin OmpF. Biophysical Journal, 2006, 90, 112-123.	0.2	67
23	Optimization of Hydrocarbon Chain Interaction Parameters:â€‰ Application to the Simulation of Fluid Phase Lipid Bilayers. Journal of Physical Chemistry B, 1999, 103, 6323-6327.	1.2	59
24	Collective motion artifacts arising in long-duration molecular dynamics simulations. Journal of Computational Chemistry, 2000, 21, 121-131.	1.5	59
25	Combined Monte Carlo and molecular dynamics simulation of hydrated dipalmitoylâ€“phosphatidylcholineâ€“cholesterol lipid bilayers. Journal of Chemical Physics, 2001, 114, 5435-5443.	1.2	55
26	Lateral Organization in Lipid-Cholesterol Mixed Bilayers. Biophysical Journal, 2007, 92, 440-447.	0.2	49
27	Application of combined Monte Carlo and molecular dynamics method to simulation of dipalmitoyl phosphatidylcholine lipid bilayer. Journal of Computational Chemistry, 1999, 20, 1153-1164.	1.5	47
28	Ionization States of Residues in OmpF and Mutants: Effects of Dielectric Constant and Interactions between Residues. Biophysical Journal, 2004, 86, 690-704.	0.2	47
29	Backbone Statistical Potential from Local Sequence-Structure Interactions in Protein Loops. Journal of Physical Chemistry B, 2010, 114, 1859-1869.	1.2	33
30	Domain-Based Identification and Analysis of Glutamate Receptor Ion Channels and Their Relatives in Prokaryotes. PLoS ONE, 2010, 5, e12827.	1.1	20
31	An assessment of true and false positive detection rates of stepwise epistatic model selection as a function of sample size and number of markers. Heredity, 2019, 122, 660-671.	1.2	18
32	A Biophysical Model for Integration of Electrical, Osmotic, and pH Regulation in the Human Bronchial Epithelium. Biophysical Journal, 2010, 98, 1476-1485.	0.2	17
33	Sampling Multiple Scoring Functions Can Improve Protein Loop Structure Prediction Accuracy. Journal of Chemical Information and Modeling, 2011, 51, 1656-1666.	2.5	17
34	Automated Optimization of Waterâ€“Water Interaction Parameters for a Coarse-Grained Model. Journal of Physical Chemistry B, 2014, 118, 1603-1611.	1.2	17
35	Three-Dimensional Encapsulation of Saccharomyces cerevisiae in Silicate Matrices Creates Distinct Metabolic States as Revealed by Gene Chip Analysis. ACS Nano, 2017, 11, 3560-3575.	7.3	17
36	Nanoporous Silica-Based Protocells at Multiple Scales for Designs of Life and Nanomedicine. Life, 2015, 5, 214-229.	1.1	16

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37	Systems Biology Understanding of the Effects of Lithium on Cancer. Frontiers in Oncology, 2019, 9, 296.	1.3	16
38	The Physical Interpretation of Mathematical Models for Sodium Permeability Changes in Excitable Membranes. Biophysical Journal, 1973, 13, 1200-1211.	0.2	15
39	Effects of Lithium and Other Monovalent Ions on Palmitoyl Oleoyl Phosphatidylcholine Bilayer. Langmuir, 2017, 33, 1105-1115.	1.6	14
40	Conservation in Mammals of Genes Associated with Aggression-Related Behavioral Phenotypes in Honey Bees. PLoS Computational Biology, 2016, 12, e1004921.	1.5	14
41	A fully coupled transient excited state model for the sodium channel. Journal of Mathematical Biology, 1978, 5, 121-142.	0.8	13
42	Functional significance of the A-current. Biological Cybernetics, 1993, 70, 109-114.	0.6	13
43	Simulations of lipid membranes with atomic resolution. Computers in Physics, 1998, 12, 328.	0.6	13
44	Building a Knowledge-Based Statistical Potential by Capturing High-Order Inter-residue Interactions and its Applications in Protein Secondary Structure Assessment. Journal of Chemical Information and Modeling, 2013, 53, 500-508.	2.5	11
45	Systems Biology Understanding of the Effects of Lithium on Affective and Neurodegenerative Disorders. Frontiers in Neuroscience, 2018, 12, 933.	1.4	11
46	Transferable interactions of Li+ and Mg2+ ions in polarizable models. Journal of Chemical Physics, 2020, 153, 104113.	1.2	11
47	Transforming Chemistry Education through Computational Science. Computing in Science and Engineering, 2008, 10, 34-39.	1.2	10
48	Conjugated double bonds in lipid bilayers: A molecular dynamics simulation study. Chemistry and Physics of Lipids, 2011, 164, 251-257.	1.5	10
49	Interactions of Monovalent and Divalent Cations at Palmitoyl-Oleoyl-Phosphatidylcholine Interface. Langmuir, 2019, 35, 10522-10532.	1.6	10
50	Digital biology: an emerging and promising discipline. Trends in Biotechnology, 2005, 23, 113-117.	4.9	9
51	Molecular dynamic simulation study of cholesterol and conjugated double bonds in lipid bilayers. Chemistry and Physics of Lipids, 2011, 164, 811-818.	1.5	8
52	Rationally designing antisense therapy to keep up with evolving bacterial resistance. PLoS ONE, 2019, 14, e0209894.	1.1	8
53	Predicting Protein-Protein Interaction by the Mirrortree Method: Possibilities and Limitations. PLoS ONE, 2013, 8, e81100.	1.1	8
54	The cPLA2 C2Î± Domain in Solution: Structure and Dynamics of Its Ca2+-activated and Cation-Free States. Biophysical Journal, 2007, 92, 966-976.	0.2	7

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55	Identifying bacterial and archaeal homologs of pentameric ligand-gated ion channel (pLGIC) family using domain-based and alignment-based approaches. Channels, 2011, 5, 325-344.	1.5	7
56	Simulation of charge transport in ion channels andÂnanopores withÂanisotropicÂpermittivity. Journal of Computational Electronics, 2009, 8, 98-109.	1.3	6
57	Integrating multiple scoring functions to improve protein loop structure conformation space sampling. , 2010, , .		5
58	High-Dimensional Parameter Search Method to Determine Force Field Mixing Terms in Molecular Simulations. Langmuir, 2022, 38, 2840-2851.	1.6	5
59	MotifNetwork: A Grid-enabled Workflow for High-throughput Domain Analysis of Biological Sequences: Implications for annotation and study of phylogeny, protein interactions, and intraspecies variation. , 2007, , .		4
60	MotifNetwork: Genome-Wide Domain Analysis using Grid-enabled Workflows. , 2007, , .		4
61	Using Optimal F-Measure and Random Resampling in Gene Ontology Enrichment Calculations. Frontiers in Applied Mathematics and Statistics, 2019, 5, .	0.7	3
62	The biology student workbench project. Biochemistry and Molecular Biology Education, 2001, 29, 165-166.	0.5	2
63	The biology student workbench project. Biochemistry and Molecular Biology Education, 2001, 29, 165-166.	0.5	1
64	Evolutionary coupling in the KV1.2-β2complex. Channels, 2010, 4, 355-374.	1.5	1
65	Motion and meaning. Nature, 2001, 414, 394-394.	13.7	0
66	Entropic boundary conditions towards safe artificial superintelligence. Journal of Experimental and Theoretical Artificial Intelligence, 2023, 35, 1-33.	1.8	0
67	ResidueFinder: extracting individual residue mentions from protein literature. Journal of Biomedical Semantics, 2021, 12, 14.	0.9	0