

Eric R May

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1833330/publications.pdf>

Version: 2024-02-01

39
papers

957
citations

471509

17
h-index

477307

29
g-index

45
all docs

45
docs citations

45
times ranked

1229
citing authors

#	ARTICLE	IF	CITATIONS
1	A favorable path to domain separation in the orange carotenoid protein. <i>Protein Science</i> , 2022, 31, 850-863.	7.6	3
2	Guanine Nucleotide-Dependent Conformational Selection Regulates Distinct Alternate Ribosome Bound States of the Translation Factor BipA. <i>FASEB Journal</i> , 2022, 36, .	0.5	0
3	Atomistic dynamics of a viral infection process: Release of membrane lytic peptides from a non-enveloped virus. <i>Science Advances</i> , 2021, 7, .	10.3	6
4	Molecular dynamics study of membrane permeabilization by wild-type and mutant lytic peptides from the non-enveloped Flock House virus. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183102.	2.6	8
5	Structural and dynamic asymmetry in icosahedrally symmetric virus capsids. <i>Current Opinion in Virology</i> , 2020, 45, 8-16.	5.4	10
6	Markov State Model of Lassa Virus Nucleoprotein Reveals Large Structural Changes during the Trimer to Monomer Transition. <i>Structure</i> , 2020, 28, 548-554.e3.	3.3	5
7	A Potent Host Defense Peptide Triggers DNA Damage and Is Active against Multidrug-Resistant Gram-Negative Pathogens. <i>ACS Infectious Diseases</i> , 2020, 6, 1250-1263.	3.8	13
8	The mitochondria-targeted peptide SS-31 binds lipid bilayers and modulates surface electrostatics as a key component of its mechanism of action. <i>Journal of Biological Chemistry</i> , 2020, 295, 7452-7469.	3.4	65
9	Computational Studies of Catalytic Loop Dynamics in <i>Yersinia</i> Protein Tyrosine Phosphatase Using Pathway Optimization Methods. <i>Journal of Physical Chemistry B</i> , 2019, 123, 7840-7851.	2.6	4
10	Structural Basis of Protein Kinase R Autophosphorylation. <i>Biochemistry</i> , 2019, 58, 2967-2977.	2.5	22
11	Molecular Dynamics Investigation into the Effect of Zinc(II) on the Structure and Membrane Interactions of the Antimicrobial Peptide Clavanin A. <i>Journal of Physical Chemistry B</i> , 2019, 123, 3163-3176.	2.6	18
12	Functional and structural basis of <i>E. coli</i> enolase inhibition by SF2312: a mimic of the carbanion intermediate. <i>Scientific Reports</i> , 2019, 9, 17106.	3.3	9
13	Catalytic Domains of Phosphodiesterase 5, 6, and 5/6 Chimera Display Differential Dynamics and Ligand Dissociation Energy Barriers. <i>Journal of Physical Chemistry B</i> , 2019, 123, 825-835.	2.6	5
14	Folding a viral peptide in different membrane environments: pathway and sampling analyses. <i>Journal of Biological Physics</i> , 2018, 44, 195-209.	1.5	6
15	BUMPy: A Model-Independent Tool for Constructing Lipid Bilayers of Varying Curvature and Composition. <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 6642-6652.	5.3	29
16	Understanding Conformational Dynamics of Complex Lipid Mixtures Relevant to Biology. <i>Journal of Membrane Biology</i> , 2018, 251, 609-631.	2.1	33
17	Molecular Dynamics Analysis of Cardiolipin and Monolysocardiolipin on Bilayer Properties. <i>Biophysical Journal</i> , 2018, 114, 2116-2127.	0.5	33
18	Evaluation of the hybrid resolution PACE model for the study of folding, insertion, and pore formation of membrane associated peptides. <i>Journal of Computational Chemistry</i> , 2017, 38, 1462-1471.	3.3	20

#	ARTICLE	IF	CITATIONS
19	Influence of membrane composition on the binding and folding of a membrane lytic peptide from the non-enveloped flock house virus. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2017, 1859, 1190-1199.	2.6	15
20	Buckling Under Pressure: Curvature-Based Lipid Segregation and Stability Modulation in Cardiolipin-Containing Bilayers. <i>Langmuir</i> , 2017, 33, 6937-6946.	3.5	68
21	Computational Investigation into the Solution Structure of Monomeric Lassa Virus Nucleoprotein and Insights into its RNA Binding Mechanism. <i>Biophysical Journal</i> , 2017, 112, 191a.	0.5	0
22	Lipid-Dependence of the Membrane Interactions of the Tim23 Channel Subunit of the Mitochondrial Protein Import Machinery. <i>Biophysical Journal</i> , 2017, 112, 84a-85a.	0.5	0
23	Cardiolipin mediates membrane and channel interactions of the mitochondrial TIM23 protein import complex receptor Tim50. <i>Science Advances</i> , 2017, 3, e1700532.	10.3	50
24	Influence of RNA Binding on the Structure and Dynamics of the Lassa Virus Nucleoprotein. <i>Biophysical Journal</i> , 2016, 110, 1246-1254.	0.5	5
25	Nonuniform elastic properties of macromolecules and effect of prestrain on their continuum nature. <i>Physical Review E</i> , 2016, 93, 012417.	2.1	11
26	Stability of Norwalk Virus Capsid Protein Interfaces Evaluated by in Silico Nanoindentation. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 103.	4.1	16
27	Recent developments in molecular simulation approaches to study spherical virus capsids. <i>Molecular Simulation</i> , 2014, 40, 878-888.	2.0	19
28	pH-Induced Stability Switching of the Bacteriophage HK97 Maturation Pathway. <i>Journal of the American Chemical Society</i> , 2014, 136, 3097-3107.	13.7	21
29	Integrin and Defensin Modulate the Mechanical Properties of Adenovirus. <i>Journal of Virology</i> , 2013, 87, 2756-2766.	3.4	76
30	Mechanics of bacteriophage maturation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2342-2347.	7.1	106
31	On the Morphology of Viral Capsids: Elastic Properties and Buckling Transitions. <i>Journal of Physical Chemistry B</i> , 2012, 116, 8604-8609.	2.6	38
32	Exploring the Symmetry and Mechanism of Virus Capsid Maturation Via an Ensemble of Pathways. <i>Biophysical Journal</i> , 2012, 102, 606-612.	0.5	37
33	Multiscale Modeling of Virus Structure, Assembly, and Dynamics. <i>Biological and Medical Physics Series</i> , 2012, , 167-189.	0.4	0
34	Viral Capsid Equilibrium Dynamics Reveals Nonuniform Elastic Properties. <i>Biophysical Journal</i> , 2011, 100, L59-L61.	0.5	33
35	Determination of Viral Capsid Elastic Properties from Equilibrium Thermal Fluctuations. <i>Physical Review Letters</i> , 2011, 106, 188101.	7.8	43
36	The flexible C-terminal arm of the Lassa arenavirus Z protein mediates interactions with multiple binding partners. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2251-2264.	2.6	11

#	ARTICLE	IF	CITATIONS
37	Coarse-Grained Molecular Dynamics Simulations of Phase Transitions in Mixed Lipid Systems Containing LPA, DOPA, and DOPE Lipids. <i>Biophysical Journal</i> , 2008, 94, 878-890.	0.5	27
38	Role of molecular tilt in thermal fluctuations of lipid membranes. <i>Physical Review E</i> , 2007, 76, 021913.	2.1	72
39	Molecular modeling of key elastic properties for inhomogeneous lipid bilayers. <i>Molecular Simulation</i> , 2007, 33, 787-797.	2.0	15