Abdallah Sayyed-Ahmad

List of Publications by Year
in descending order

28 papers	758 citations	516710 16 h-index	526287 27 g-index
29 all docs	29 docs citations	29 times ranked	903 citing authors

#	Article	IF	Citations
1	Computational and biochemical characterization of two partially overlapping interfaces and multiple weak-affinity K-Ras dimers. Scientific Reports, 2017, 7, 40109.	3.3	85
2	Spatiotemporal Analysis of K-Ras Plasma Membrane Interactions Reveals Multiple High Order Homo-oligomeric Complexes. Journal of the American Chemical Society, 2017, 139, 13466-13475.	13.7	73
3	Amyloid-Î² peptide dimers undergo a random coil to Î²-sheet transition in the aqueous phase but not at the neuronal membrane. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	60
4	On the Nature of Antimicrobial Activity:â€‰ A Model for Protegrin-1 Pores. Journal of the American Chemical Society, 2008, 130, 4338-4346.	13.7	56
5	The Role of Conserved Waters in Conformational Transitions of Q61H K-ras. PLoS Computational Biology, 2012, 8, e1002394.	3.2	48
6	Poisson-Nernst-Planck Models of Nonequilibrium Ion Electrodiffusion through a Protegrin Transmembrane Pore. PLoS Computational Biology, 2009, 5, e1000277.	3.2	46
7	Computational Equilibrium Thermodynamic and Kinetic Analysis of K-Ras Dimerization through an Effector Binding Surface Suggests Limited Functional Role. Journal of Physical Chemistry B, 2016, 120, 8547-8556.	2.6	45
8	Distinct dynamics and interaction patterns in H- and K-Ras oncogenic P-loop mutants. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1618-1632.	2.6	44
9	Conformational and Dynamical Effects of Tyr32 Phosphorylation in K-Ras: Molecular Dynamics Simulation and Markov State Models Analysis. Journal of Physical Chemistry B, 2019, 123, 7667-7675.	2.6	35
10	pMD-Membrane: A Method for Ligand Binding Site Identification in Membrane-Bound Proteins. PLoS Computational Biology, 2015, 11, e1004469.	3.2	31
11	Structure and Dynamics of Cholic Acid and Dodecylphosphocholineâ^'Cholic Acid Aggregates. Langmuir, 2010, 26, 13407-13414.	3.5	28
12	Transcriptional regulatory network refinement and quantification through kinetic modeling, gene expression microarray data and information theory. BMC Bioinformatics, 2007, 8, 20.	2.6	27
13	Efficient solution technique for solving the Poisson-Boltzmann equation. Journal of Computational Chemistry, 2004, 25, 1068-1074.	3.3	23
14	Relative free energy of binding between antimicrobial peptides and SDS or DPC micelles. Molecular Simulation, 2009, 35, 986-997.	2.0	23
15	Aggregation behavior of ibuprofen, cholic acid and dodecylphosphocholine micelles. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 3040-3047.	2.6	23
16	Mixed-Probe Simulation and Probe-Derived Surface Topography Map Analysis for Ligand Binding Site Identification. Journal of Chemical Theory and Computation, 2017, 13, 1851-1861.	5.3	23
17	Determining the Orientation of Protegrin-1 in DLPC Bilayers Using an Implicit Solvent-Membrane Model. PLoS ONE, 2009, 4, e4799.	2.5	16
18	Toward Automated Cell Model Development through Information Theoryâ€. Journal of Physical Chemistry A, 2003, 107, 10554-10565.	2.5	12

#	Article	IF	Citations
19	The KaryoteÂ® Physico-Chemical Genomic, Proteomic, Metabolic Cell Modeling System. OMICS A Journal of Integrative Biology, 2003, 7, 269-283.	2.0	10
20	Intracellular crowding effects on the self-association of the bacterial cell division protein FtsZ. Archives of Biochemistry and Biophysics, 2014, 564, 12-19.	3.0	9
21	Role of Oxidized Gly25, Gly29, and Gly33 Residues on the Interactions of AÎ²‹sub›1â€“42‹/sub› with Lipid Membranes. ACS Chemical Neuroscience, 2020, 11, 535-548.	3.5	9
22	Molecular simulations of IDPs: From ensemble generation to IDP interactions leading to disorder-to-order transitions. Progress in Molecular Biology and Translational Science, 2021, 183, 135-185.	1.7	9
23	Design of an optical water pollution sensor using a single-layer guided-mode resonance filter. Photonic Sensors, 2013, 3, 224-230.	5.0	6
24	Investigation of Changes in Tetracycline Repressor Binding upon Mutations in the Tetracycline Operator. Journal of Chemical & Engineering Data, 2014, 59, 3167-3176.	1.9	6
25	Hotspot Identification on Protein Surfaces Using Probe-Based MD Simulations: Successes and Challenges. Current Topics in Medicinal Chemistry, 2019, 18, 2278-2283.	2.1	6
26	How to make an undruggable enzyme druggable: lessons from ras proteins. Advances in Protein Chemistry and Structural Biology, 2020, 122, 181-202.	2.3	3
27	Basin model inversion using information theory and seismic data. Geophysics, 2007, 72, R99-R108.	2.6	1
28	pMD-Membrane: A Tool to Determine Allosteric Binding Pockets in Membrane-Bound Biomolecules. Biophysical Journal, 2016, 110, 254a.	0.5	0