

# Abdallah Sayyed-Ahmad

## List of Publications by Year in descending order

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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	Amyloid- $\beta$ peptide dimers undergo a random coil to $\beta$ -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
2	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
3	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
4	Role of Oxidized Gly25, Gly29, and Gly33 Residues on the Interactions of A $\beta$ 42 with Lipid Membranes. ACS Chemical Neuroscience, 2020, 11, 535-548.	3.5	9
5	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
6	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
7	Computational and biochemical characterization of two partially overlapping interfaces and multiple weak-affinity K-Ras dimers. Scientific Reports, 2017, 7, 40109.	3.3	85
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	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
10	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
11	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
12	pMD-Membrane: A Tool to Determine Allosteric Binding Pockets in Membrane-Bound Biomolecules. Biophysical Journal, 2016, 110, 254a.	0.5	0
13	pMD-Membrane: A Method for Ligand Binding Site Identification in Membrane-Bound Proteins. PLoS Computational Biology, 2015, 11, e1004469.	3.2	31
14	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
15	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
16	Design of an optical water pollution sensor using a single-layer guided-mode resonance filter. Photonic Sensors, 2013, 3, 224-230.	5.0	6
17	The Role of Conserved Waters in Conformational Transitions of Q61H K-ras. PLoS Computational Biology, 2012, 8, e1002394.	3.2	48
18	Aggregation behavior of ibuprofen, cholic acid and dodecylphosphocholine micelles. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 3040-3047.	2.6	23

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19	Structure and Dynamics of Cholic Acid and Dodecylphosphocholine <sup>+</sup> Cholic Acid Aggregates. <i>Langmuir</i> , 2010, 26, 13407-13414.	3.5	28
20	Relative free energy of binding between antimicrobial peptides and SDS or DPC micelles. <i>Molecular Simulation</i> , 2009, 35, 986-997.	2.0	23
21	Poisson-Nernst-Planck Models of Nonequilibrium Ion Electrodifffusion through a Protegrin Transmembrane Pore. <i>PLoS Computational Biology</i> , 2009, 5, e1000277.	3.2	46
22	Determining the Orientation of Protegrin-1 in DLPC Bilayers Using an Implicit Solvent-Membrane Model. <i>PLoS ONE</i> , 2009, 4, e4799.	2.5	16
23	On the Nature of Antimicrobial Activity: A Model for Protegrin-1 Pores. <i>Journal of the American Chemical Society</i> , 2008, 130, 4338-4346.	13.7	56
24	Basin model inversion using information theory and seismic data. <i>Geophysics</i> , 2007, 72, R99-R108.	2.6	1
25	Transcriptional regulatory network refinement and quantification through kinetic modeling, gene expression microarray data and information theory. <i>BMC Bioinformatics</i> , 2007, 8, 20.	2.6	27
26	Efficient solution technique for solving the Poisson-Boltzmann equation. <i>Journal of Computational Chemistry</i> , 2004, 25, 1068-1074.	3.3	23
27	Toward Automated Cell Model Development through Information Theory. <i>Journal of Physical Chemistry A</i> , 2003, 107, 10554-10565.	2.5	12
28	The Karyote <sup>+</sup> Physico-Chemical Genomic, Proteomic, Metabolic Cell Modeling System. <i>OMICS A Journal of Integrative Biology</i> , 2003, 7, 269-283.	2.0	10