

# Hamid Hadi-Alijanvand

## List of Publications by Citations

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26  
papers

248  
citations

10  
h-index

15  
g-index

28  
ext. papers

301  
ext. citations

4.3  
avg, IF

3.52  
L-index

#	Paper	IF	Citations
26	The Discovery of a Putative Allosteric Site in the SARS-CoV-2 Spike Protein Using an Integrated Structural/Dynamic Approach. <i>Journal of Proteome Research</i> , <b>2020</b> , 19, 4576-4586	5.6	36
25	Inhibition study on insulin fibrillation and cytotoxicity by paclitaxel. <i>Journal of Biochemistry</i> , <b>2014</b> , 155, 361-73	3.1	32
24	Fibril formation of lysozyme upon interaction with sodium dodecyl sulfate at pH 9.2. <i>Colloids and Surfaces B: Biointerfaces</i> , <b>2007</b> , 60, 55-61	6	31
23	Structure and stability analysis of cytotoxic complex of camel $\beta$ lactalbumin and unsaturated fatty acids produced at high temperature. <i>Journal of Biomolecular Structure and Dynamics</i> , <b>2011</b> , 28, 919-28	3.6	23
22	Interaction of 2-APB, dantrolene, and TDMT with IP3R and RyR modulates ER stress-induced programmed cell death I and II in neuron-like PC12 cells: an experimental and computational investigation. <i>Journal of Biomolecular Structure and Dynamics</i> , <b>2014</b> , 32, 1211-30	3.6	19
21	Caseoperoxidase, mixed $\beta$ casein-SDS-hemin-imidazole complex: a nano artificial enzyme. <i>Journal of Biomolecular Structure and Dynamics</i> , <b>2015</b> , 33, 2619-32	3.6	13
20	Potassium sorbate as an AGE activator for human serum albumin in the presence and absence of glucose. <i>International Journal of Biological Macromolecules</i> , <b>2013</b> , 62, 146-54	7.9	12
19	Studying the Effects of ACE2 Mutations on the Stability, Dynamics, and Dissociation Process of SARS-CoV-2 S1/hACE2 Complexes. <i>Journal of Proteome Research</i> , <b>2020</b> , 19, 4609-4623	5.6	12
18	Targeting enteroviral 2A protease by a 16-mer synthetic peptide: inhibition of 2Apro-induced apoptosis in a stable Tet-on HeLa cell line. <i>Virology</i> , <b>2010</b> , 399, 39-45	3.6	11
17	Thermal inactivation and conformational lock studies on horse liver alcohol dehydrogenase: structural mechanism. <i>International Journal of Biological Macromolecules</i> , <b>2013</b> , 58, 66-72	7.9	10
16	Kinetic stabilization of lysozyme upon interactions with $\beta$ cyclodextrin through partial unfolding. <i>Journal of the Iranian Chemical Society</i> , <b>2011</b> , 8, 553-561	2	7
15	Implication of disulfide bridge induced thermal reversibility, structural and functional stability for luciferase. <i>Protein and Peptide Letters</i> , <b>2015</b> , 22, 23-30	1.9	6
14	The inhibitory effect of ethylenediamine on mushroom tyrosinase. <i>International Journal of Biological Macromolecules</i> , <b>2012</b> , 50, 573-7	7.9	6
13	Thermal unfolding pathway of PHD2 catalytic domain in three different PHD2 species: computational approaches. <i>PLoS ONE</i> , <b>2012</b> , 7, e47061	3.7	4
12	Homology modeling, docking, molecular dynamics simulation, and structural analyses of coxsakievirus B3 2A protease: an enzyme involved in the pathogenesis of inflammatory myocarditis. <i>International Journal of Biological Macromolecules</i> , <b>2011</b> , 49, 487-92	7.9	4
11	Soft regions of protein surface are potent for stable dimer formation. <i>Journal of Biomolecular Structure and Dynamics</i> , <b>2020</b> , 38, 3587-3598	3.6	4
10	Partner-Specific Prediction of Protein-Dimer Stability from Unbound Structure of Monomer. <i>Journal of Chemical Information and Modeling</i> , <b>2018</b> , 58, 733-745	6.1	3

9	Inhibition of mushroom tyrosinase by a newly synthesized ligand: inhibition kinetics and computational simulations. <i>Journal of Biomolecular Structure and Dynamics</i> , <b>2012</b> , 30, 448-59	3.6	3
8	Complex Stability is Encoded in Binding Patch Softness: a Monomer-Based Approach to Predict Inter-Subunit Affinity of Protein Dimers. <i>Journal of Proteome Research</i> , <b>2020</b> , 19, 409-423	5.6	3
7	A hidden aggregation-prone structure in the heart of hypoxia inducible factor prolyl hydroxylase. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2016</b> , 84, 611-23	4.2	2
6	Application of OmpF nanochannel forming protein in polynucleotide sequence recognition. <i>Journal of Molecular Recognition</i> , <b>2014</b> , 27, 575-87	2.6	2
5	A folding pathway-dependent score to recognize membrane proteins. <i>PLoS ONE</i> , <b>2011</b> , 6, e16778	3.7	2
4	The correlation of cold denaturation temperature with surface stability factor of proteins. <i>Protein Journal</i> , <b>2007</b> , 26, 395-402	3.9	1
3	Effect of Lithium Drug on Binding Affinities of Glycogen Synthase Kinase-3 $\beta$ to Its Network Partners: A New Computational Approach. <i>Journal of Chemical Information and Modeling</i> , <b>2021</b> , 61, 5280-5292	6.1	1
2	Journey of poly-nucleotides through OmpF porin. <i>Journal of Physical Chemistry B</i> , <b>2015</b> , 119, 6113-28	3.4	
1	Unfolding mechanism of PHD2 as a vital protein: all-atom simulation approach. <i>Journal of the Iranian Chemical Society</i> , <b>2013</b> , 10, 907-914	2	