

# Hamid Hadi-Alijanvand

## List of Publications by Year in descending order

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Version: 2024-02-01

28  
papers

346  
citations

932766

10  
h-index

839053

18  
g-index

28  
all docs

28  
docs citations

28  
times ranked

653  
citing authors

#	ARTICLE	IF	CITATIONS
1	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> , 2020, 19, 4576-4586.	1.8	66
2	Inhibition study on insulin fibrillation and cytotoxicity by paclitaxel. <i>Journal of Biochemistry</i> , 2014, 155, 361-373.	0.9	42
3	Fibril formation of lysozyme upon interaction with sodium dodecyl sulfate at pH 9.2. <i>Colloids and Surfaces B: Biointerfaces</i> , 2007, 60, 55-61.	2.5	34
4	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> , 2011, 28, 919-928.	2.0	30
5	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> , 2014, 32, 1211-1230.	2.0	24
6	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> , 2020, 19, 4609-4623.	1.8	22
7	Potassium sorbate as an AGE activator for human serum albumin in the presence and absence of glucose. <i>International Journal of Biological Macromolecules</i> , 2013, 62, 146-154.	3.6	17
8	Thermal inactivation and conformational lock studies on horse liver alcohol dehydrogenase: Structural mechanism. <i>International Journal of Biological Macromolecules</i> , 2013, 58, 66-72.	3.6	15
9	Caseoperoxidase, mixed $\beta$ -casein-SDS-hemin-imidazole complex: a nano artificial enzyme. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 2619-2632.	2.0	15
10	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> , 2010, 399, 39-45.	1.1	14
11	Biophysical Insight into the SARS-CoV2 Spike-ACE2 Interaction and Its Modulation by Hepcidin through a Multifaceted Computational Approach. <i>ACS Omega</i> , 2022, 7, 17024-17042.	1.6	9
12	Kinetic stabilization of lysozyme upon interactions with $\beta$ -cyclodextrin through partial unfolding. <i>Journal of the Iranian Chemical Society</i> , 2011, 8, 553-561.	1.2	7
13	The inhibitory effect of ethylenediamine on mushroom tyrosinase. <i>International Journal of Biological Macromolecules</i> , 2012, 50, 573-577.	3.6	7
14	Implication of Disulfide Bridge Induced Thermal Reversibility, Structural and Functional Stability for Luciferase. <i>Protein and Peptide Letters</i> , 2014, 22, 23-30.	0.4	6
15	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> , 2011, 49, 487-492.	3.6	5
16	Inhibition of mushroom tyrosinase by a newly synthesized ligand: inhibition kinetics and computational simulations. <i>Journal of Biomolecular Structure and Dynamics</i> , 2012, 30, 448-459.	2.0	5
17	Partner-Specific Prediction of Protein-Dimer Stability from Unbound Structure of Monomer. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 733-745.	2.5	5
18	Soft regions of protein surface are potent for stable dimer formation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 3587-3598.	2.0	5

#	ARTICLE	IF	CITATIONS
19	Thermal Unfolding Pathway of PHD2 Catalytic Domain in Three Different PHD2 Species: Computational Approaches. PLoS ONE, 2012, 7, e47061.	1.1	4
20	Complex Stability is Encoded in Binding Patch Softness: a Monomer-Based Approach to Predict Inter-Subunit Affinity of Protein Dimers. Journal of Proteome Research, 2020, 19, 409-423.	1.8	4
21	Application of OmpF nanochannel forming protein in polynucleotide sequence recognition. Journal of Molecular Recognition, 2014, 27, 575-587.	1.1	3
22	A Folding Pathway-Dependent Score to Recognize Membrane Proteins. PLoS ONE, 2011, 6, e16778.	1.1	3
23	A hidden aggregation-prone structure in the heart of hypoxia inducible factor prolyl hydroxylase. Proteins: Structure, Function and Bioinformatics, 2016, 84, 611-623.	1.5	2
24	The Correlation of Cold Denaturation Temperature with Surface Stability Factor of Proteins. Protein Journal, 2007, 26, 395-402.	0.7	1
25	Effect of Lithium Drug on Binding Affinities of Glycogen Synthase Kinase-3 $\beta$ to Its Network Partners: A New Computational Approach. Journal of Chemical Information and Modeling, 2021, 61, 5280-5292.	2.5	1
26	HAMDAM-1 as a Sequence-Based Software for Studying the Physical Properties of Proteins. Biophysical Journal, 2010, 98, 197a.	0.2	0
27	Unfolding mechanism of PHD2 as a vital protein: all-atom simulation approach. Journal of the Iranian Chemical Society, 2013, 10, 907-914.	1.2	0
28	Journey of Poly-Nucleotides through OmpF Porin. Journal of Physical Chemistry B, 2015, 119, 6113-6128.	1.2	0