Seyed Shahriar Arab

List of Publications by Year
in descending order

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63 papers	1,026 citations	471061 17 h-index	454577 30 g-index
65 all docs	65 docs citations	65 times ranked	1654 citing authors

#	Article	IF	Citations
1	Computational assessment of pigment epithelium-derived factor as an anti-cancer protein during its interaction with the receptors. Journal of Biomolecular Structure and Dynamics, 2023, 41, 4575-4591.	2.0	2
2	Insight into molecular characteristics of SARS-CoV-2 spike protein following D614G point mutation, a molecular dynamics study. Journal of Biomolecular Structure and Dynamics, 2022, 40, 5634-5642.	2.0	24
3	PSSMCOOL: a comprehensive R package for generating evolutionary-based descriptors of protein sequences from PSSM profiles. Biology Methods and Protocols, 2022, 7, bpac008.	1.0	12
4	Evaluation of pH change effects on the HSA folding and its drug binding characteristics, a computational biology investigation. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1908-1925.	1.5	3
5	Efficacy assessment of a triple anthrax chimeric antigen as a vaccine candidate in guinea pigs: challenge test with Bacillus anthracis 17 JB strain spores. Immunopharmacology and Immunotoxicology, 2021, 43, 495-502.	1.1	0
6	Exome sequencing reveals novel rare variants in Iranian familial multiple sclerosis: The importance of POLD2 in the disease pathogenesis. Genomics, 2021, 113, 2645-2655.	1.3	5
7	Prediction of chemoresistance trait of cancer cell lines using machine learning algorithms and systems biology analysis. Journal of Big Data, 2021, 8, .	6.9	4
8	Topological Analysis of Regulatory Networks Reveals Functionally Key Genes and miRNAs Involved in the Differentiation of Mesenchymal Stem Cells. Iranian Journal of Biotechnology, 2021, 19, e2565.	0.3	0
9	Reconstruction of Intercellular Signaling Network by Cytokine-Receptor Interactions. Iranian Journal of Biotechnology, 2021, 19, e2560.	0.3	0
10	Filtering of the Gene Signature as the Predictors of Cisplatin-Resistance in Ovarian Cancer. Iranian Journal of Biotechnology, 2021, 19, e2643.	0.3	0
11	RepCOOL: computational drug repositioning via integrating heterogeneous biological networks. Journal of Translational Medicine, 2020, 18, 375.	1.8	13
12	177Lu-labeled cyclic RGD peptide as an imaging and targeted radionuclide therapeutic agent in non-small cell lung cancer: Biological evaluation and preclinical study. Bioorganic Chemistry, 2020, 102, 104100.	2.0	14
13	The hot sites of Î±-synuclein in amyloid fibril formation. Scientific Reports, 2020, 10, 12175.	1.6	10
14	Application of a novel pH-responsive gemini surfactant for delivery of curcumin molecules. Materials Research Express, 2020, 7, 065403.	0.8	4
15	Multifunctional Acidocin 4356 Combats Pseudomonas aeruginosa through Membrane Perturbation and Virulence Attenuation: Experimental Results Confirm Molecular Dynamics Simulation. Applied and Environmental Microbiology, 2020, 86, .	1.4	5
16	Radiosynthesis, Biological Evaluation, and Preclinical Study of a ⁶⁸Ga-Labeled Cyclic RGD Peptide as an Early Diagnostic Agent for Overexpressed Î±_vÎ²₃ Integrin Receptors in Non-Small-Cell Lung Cancer. Contrast Media and Molecular Imaging, 2020, 2020, 1-11.	0.4	11
17	Effects of Linker Flexibility and Conformational Changes of IP3 Receptor on Split Luciferase Complementation Assay. Iranian Journal of Biotechnology, 2020, 18, e2423.	0.3	0
18	Computational simulations assessment of mutations impact on streptokinase (SK) from a group G streptococci with enhanced activity â€“ insights into the functional roles of structural dynamics flexibility of SK and stabilization of SKâ€“Ï¼plasmin catalytic complex. Journal of Biomolecular Structure and Dynamics, 2019, 37, 1944-1955.	2.0	6

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19	Computational Analysis of Nanoparticle Features on Protein Corona Composition in Biological Nanoparticle-Protein Interactions. , 2019, , .		1
20	OligoCOOL: A mobile application for nucleotide sequence analysis. Biochemistry and Molecular Biology Education, 2019, 47, 201-206.	0.5	0
21	Production and characterization of virus-like particles of grapevine fanleaf virus presenting L2 epitope of human papillomavirus minor capsid protein. BMC Biotechnology, 2019, 19, 81.	1.7	15
22	Estimating Bifurcating Consensus Phylogenetic Trees Using Evolutionary Imperialist Competitive Algorithm. Current Bioinformatics, 2019, 14, 728-739.	0.7	0
23	Computationally Design of Inhibitory Peptides Against Wnt Signaling Pathway: In Silico Insight on Complex of DKK1 and LRP6. International Journal of Peptide Research and Therapeutics, 2018, 24, 49-60.	0.9	10
24	Identification of Phytochemicals Targeting c-Met Kinase Domain using Consensus Docking and Molecular Dynamics Simulation Studies. Cell Biochemistry and Biophysics, 2018, 76, 135-145.	0.9	31
25	Can any â€œnon-specific charge modification within microtubule binding domains of Tauâ€•be a prerequisite of the protein amyloid aggregation? An in vitro study on the 1N4R isoform. International Journal of Biological Macromolecules, 2018, 109, 188-204.	3.6	12
26	Immunomodulatory effects of a rationally designed peptide mimetic of human IFNÎ² in EAE model of multiple sclerosis. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2018, 82, 49-61.	2.5	8
27	Phytochemicals, withaferin A and carnosol, overcome pancreatic cancer stem cells as c-Met inhibitors. Biomedicine and Pharmacotherapy, 2018, 106, 1527-1536.	2.5	46
28	Improving the thermal stability of azoreductase from Halomonas elongata by introducing a disulfide bond via siteâ€directed mutagenesis. Biotechnology and Applied Biochemistry, 2018, 65, 883-891.	1.4	5
29	Loop modelling 1.0. Journal of Molecular Graphics and Modelling, 2018, 84, 64-68.	1.3	7
30	Are Pro8/Pro18 really critical for functional dynamic behavior of human endostatin N-terminal peptide? A comparative molecular dynamics study. Journal of the Iranian Chemical Society, 2017, 14, 2023-2039.	1.2	6
31	The inhibitory effects of biomimetically designed peptides on Î±-synuclein aggregation. Archives of Biochemistry and Biophysics, 2017, 634, 96-106.	1.4	19
32	Increase of Bacillus badius Phenylalanine dehydrogenase specificity towards phenylalanine substrate by site-directed mutagenesis. Archives of Biochemistry and Biophysics, 2017, 635, 44-51.	1.4	11
33	Engineering disulfide bonds in Selenomonas ruminantium Î²-xylosidase by experimental and computational methods. International Journal of Biological Macromolecules, 2017, 95, 248-255.	3.6	14
34	A novel enzyme based SPR-biosensor to detect bromocriptine as an ergoline derivative drug. Sensors and Actuators B: Chemical, 2017, 240, 519-527.	4.0	46
35	Catalytic efficiency and thermostability improvement of Suc2 invertase through rational site-directed mutagenesis. Enzyme and Microbial Technology, 2017, 96, 14-22.	1.6	13
36	HOXB7 and Hsa-miR-222 as the Potential Therapeutic Candidates for Metastatic Colorectal Cancer. Recent Patents on Anti-Cancer Drug Discovery, 2016, 11, 434-443.	0.8	13

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37	How Hepatitis C Virus Leads to Hepatocellular Carcinoma: A Network-Based Study. Hepatitis Monthly, 2016, 16, e36005.	0.1	17
38	Evaluating the accuracy of protein design using native secondary sub-structures. BMC Bioinformatics, 2016, 17, 353.	1.2	4
39	Appraisal of role of the polyanionic inducer length on amyloid formation by 412-residue 1N4R Tau protein: A comparative study. Archives of Biochemistry and Biophysics, 2016, 609, 1-19.	1.4	24
40	PDB2Graph: A toolbox for identifying critical amino acids map in proteins based on graph theory. Computers in Biology and Medicine, 2016, 72, 151-159.	3.9	5
41	Î±-Cyperone of Cyperus rotundus is an effective candidate for reduction of inflammation by destabilization of microtubule fibers in brain. Journal of Ethnopharmacology, 2016, 194, 219-227.	2.0	30
42	Inhibition of guinea pig aldehyde oxidase activity by different flavonoid compounds: An in vitro study. Bioorganic Chemistry, 2016, 64, 74-84.	2.0	25
43	Mitochondrial membrane disruption by aggregation products of ALS-causing superoxide dismutase-1 mutants. International Journal of Biological Macromolecules, 2015, 75, 290-297.	3.6	23
44	Bayesian alignment of proteins via Delaunay tetrahedralization. Journal of Applied Statistics, 2015, 42, 1064-1079.	0.6	1
45	Enhancement of Thermostability and Kinetic Efficiency of Aspergillus niger PhyA Phytase by Site-Directed Mutagenesis. Applied Biochemistry and Biotechnology, 2015, 175, 2528-2541.	1.4	19
46	CentiServer: A Comprehensive Resource, Web-Based Application and R Package for Centrality Analysis. PLoS ONE, 2015, 10, e0143111.	1.1	85
47	Abstract B2-44: Structure-based design of inhibitory peptides for LRP6. , 2015, , .		0
48	MemBuilder: a web-based graphical interface to build heterogeneously mixed membrane bilayers for the GROMACS biomolecular simulation program. Bioinformatics, 2014, 30, 439-441.	1.8	54
49	Development of a highlyâ€potent antiâ€angiogenic <scp>VEGF</scp>_{8â€“109} heterodimer by directed blocking of its VEGFRâ€2 binding site. FEBS Journal, 2014, 281, 4479-4494.	2.2	18
50	Synthesis and investigation of new Hesperadin analogues antitumor effects on HeLa cells. Journal of Chemical Biology, 2014, 7, 85-91.	2.2	5
51	The design of a new truncated and engineered alpha1-antitrypsin based on theoretical studies: an antiprotease therapeutics for pulmonary diseases. Theoretical Biology and Medical Modelling, 2013, 10, 36.	2.1	8
52	NETAL: a new graph-based method for global alignment of proteinâ€“protein interaction networks. Bioinformatics, 2013, 29, 1654-1662.	1.8	151
53	PUTRACER: A NOVEL METHOD FOR IDENTIFICATION OF CONTINUOUS-DOMAINS IN MULTI-DOMAIN PROTEINS. Journal of Bioinformatics and Computational Biology, 2013, 11, 1340012.	0.3	3
54	Protein structure prediction using bio-inspired algorithm: A review. , 2012, , .		5

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55	Finding protein active sites using approximate sub-graph isomorphism. , 2011, , .		0
56	A pairwise residue contact area-based mean force potential for discrimination of native protein structure. BMC Bioinformatics, 2010, 11, 16.	1.2	26
57	Overcoming drug resistance by co-targeting. , 2010, , .		2
58	STON: A novel method for protein three-dimensional structure comparison. Computers in Biology and Medicine, 2009, 39, 166-172.	3.9	3
59	A tale of two symmetrical tails: Structural and functional characteristics of palindromes in proteins. BMC Bioinformatics, 2008, 9, 274.	1.2	18
60	A method for protein accessibility prediction based on residue types and conformational states. Computational Biology and Chemistry, 2007, 31, 384-388.	1.1	3
61	Prediction of protein secondary structure based on residue pair types and conformational states using dynamic programming algorithm. FEBS Letters, 2005, 579, 3397-3400.	1.3	7
62	Prediction of protein surface accessibility with information theory. Proteins: Structure, Function and Bioinformatics, 2001, 42, 452-459.	1.5	120
63	Applying In Silico Approaches for Designing a Chimeric InaV/N-DFPase Protein and Evaluating its Binding with Diisopropyl-Fluorophosphate. International Letters of Natural Sciences, 0, 75, 41-51.	1.0	0