Seyed Shahriar Arab

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3707067/publications.pdf

Version: 2024-02-01

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	NETAL: a new graph-based method for global alignment of proteinâ€“protein interaction networks. Bioinformatics, 2013, 29, 1654-1662.	1.8	151
2	Prediction of protein surface accessibility with information theory. Proteins: Structure, Function and Bioinformatics, 2001, 42, 452-459.	1.5	120
3	CentiServer: A Comprehensive Resource, Web-Based Application and R Package for Centrality Analysis. PLoS ONE, 2015, 10, e0143111.	1.1	85
4	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
5	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
6	Phytochemicals, withaferin A and carnosol, overcome pancreatic cancer stem cells as c-Met inhibitors. Biomedicine and Pharmacotherapy, 2018, 106, 1527-1536.	2.5	46
7	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
8	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
9	A pairwise residue contact area-based mean force potential for discrimination of native protein structure. BMC Bioinformatics, 2010, 11, 16.	1.2	26
10	Inhibition of guinea pig aldehyde oxidase activity by different flavonoid compounds: An in vitro study. Bioorganic Chemistry, 2016, 64, 74-84.	2.0	25
11	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
12	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
13	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
14	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
15	The inhibitory effects of biomimetically designed peptides on Î±-synuclein aggregation. Archives of Biochemistry and Biophysics, 2017, 634, 96-106.	1.4	19
16	A tale of two symmetrical tails: Structural and functional characteristics of palindromes in proteins. BMC Bioinformatics, 2008, 9, 274.	1.2	18
17	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
18	How Hepatitis C Virus Leads to Hepatocellular Carcinoma: A Network-Based Study. Hepatitis Monthly, 2016, 16, e36005.	0.1	17

#	Article	IF	Citations
19	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
20	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
21	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
22	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
23	Catalytic efficiency and thermostability improvement of Suc2 invertase through rational site-directed mutagenesis. Enzyme and Microbial Technology, 2017, 96, 14-22.	1.6	13
24	RepCOOL: computational drug repositioning via integrating heterogeneous biological networks. Journal of Translational Medicine, 2020, 18, 375.	1.8	13
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	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
27	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
28	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
29	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
30	The hot sites of Î±-synuclein in amyloid fibril formation. Scientific Reports, 2020, 10, 12175.	1.6	10
31	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
32	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
33	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
34	Loop modelling 1.0. Journal of Molecular Graphics and Modelling, 2018, 84, 64-68.	1.3	7
35	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
36	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

#	Article	IF	Citations
37	Protein structure prediction using bio-inspired algorithm: A review. , 2012, , .		5
38	Synthesis and investigation of new Hesperadin analogues antitumor effects on HeLa cells. Journal of Chemical Biology, 2014, 7, 85-91.	2.2	5
39	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
40	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
41	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
42	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
43	Evaluating the accuracy of protein design using native secondary sub-structures. BMC Bioinformatics, 2016, 17, 353.	1.2	4
44	Application of a novel pH-responsive gemini surfactant for delivery of curcumin molecules. Materials Research Express, 2020, 7, 065403.	0.8	4
45	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
46	A method for protein accessibility prediction based on residue types and conformational states. Computational Biology and Chemistry, 2007, 31, 384-388.	1.1	3
47	STON: A novel method for protein three-dimensional structure comparison. Computers in Biology and Medicine, 2009, 39, 166-172.	3.9	3
48	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
49	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
50	Overcoming drug resistance by co-targeting. , 2010, , .		2
51	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
52	Bayesian alignment of proteins via Delaunay tetrahedralization. Journal of Applied Statistics, 2015, 42, 1064-1079.	0.6	1
53	Computational Analysis of Nanoparticle Features on Protein Corona Composition in Biological Nanoparticle-Protein Interactions. , 2019, , .		1
54	Finding protein active sites using approximate sub-graph isomorphism. , 2011, , .		0

#	Article	IF	Citations
55	OligoCOOL: A mobile application for nucleotide sequence analysis. Biochemistry and Molecular Biology Education, 2019, 47, 201-206.	0.5	0
56	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
57	Abstract B2-44: Structure-based design of inhibitory peptides for LRP6. , 2015, , .		0
58	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
59	Estimating Bifurcating Consensus Phylogenetic Trees Using Evolutionary Imperialist Competitive Algorithm. Current Bioinformatics, 2019, 14, 728-739.	0.7	0
60	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
61	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
62	Reconstruction of Intercellular Signaling Network by Cytokine-Receptor Interactions. Iranian Journal of Biotechnology, 2021, 19, e2560.	0.3	0
63	Filtering of the Gene Signature as the Predictors of Cisplatin-Resistance in Ovarian Cancer. Iranian Journal of Biotechnology, 2021, 19, e2643.	0.3	0