

Subhash Chandra

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

49
papers

422
citations

12
h-index

18
g-index

56
ext. papers

595
ext. citations

3
avg, IF

4.43
L-index

#	Paper	IF	Citations
49	In silico screening of natural compounds against COVID-19 by targeting Mpro and ACE2 using molecular docking. <i>European Review for Medical and Pharmacological Sciences</i> , 2020 , 24, 4529-4536	2.9	71
48	Structure-based screening of novel lichen compounds against SARS Coronavirus main protease (Mpro) as potentials inhibitors of COVID-19. <i>Molecular Diversity</i> , 2021 , 25, 1665-1677	3.1	27
47	A plant based protective antigen [PA(dIV)] vaccine expressed in chloroplasts demonstrates protective immunity in mice against anthrax. <i>Vaccine</i> , 2011 , 29, 4521-33	4.1	26
46	Identification and characterization of immunodominant B-cell epitope of the C-terminus of protective antigen of Bacillus anthracis. <i>Molecular Immunology</i> , 2009 , 46, 2107-15	4.3	25
45	Molecular docking and molecular dynamics simulation approach to screen natural compounds for inhibition of by targeting peptide deformylase. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 39, 823-840	3.6	22
44	Enolase of Mycobacterium tuberculosis is a surface exposed plasminogen binding protein. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017 , 1861, 3355-3364	4	19
43	3D QSAR, pharmacophore and molecular docking studies of known inhibitors and designing of novel inhibitors for M18 aspartyl aminopeptidase of Plasmodium falciparum. <i>BMC Structural Biology</i> , 2016 , 16, 12	2.7	18
42	screening of anti-inflammatory compounds from Lichen by targeting cyclooxygenase-2. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020 , 38, 3544-3562	3.6	17
41	In silico screening of potential antidiabetic phytochemicals from Phyllanthus emblica against therapeutic targets of type 2 diabetes. <i>Journal of Ethnopharmacology</i> , 2020 , 248, 112268	5	17
40	Predictive modeling by deep learning, virtual screening and molecular dynamics study of natural compounds against SARS-CoV-2 main protease. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 39, 6728-6746	3.6	16
39	Virtual screening of anti-HIV1 compounds against SARS-CoV-2: machine learning modeling, chemoinformatics and molecular dynamics simulation based analysis. <i>Scientific Reports</i> , 2020 , 10, 20397	4.9	15
38	Foliar application of organic and inorganic iron formulation induces differential detoxification response to improve growth and biofortification in soybean. <i>Plant Physiology Reports</i> , 2019 , 24, 119-128	1.4	12
37	Identification of natural inhibitors against Mpro of SARS-CoV-2 by molecular docking, molecular dynamics simulation, and MM/PBSA methods. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020 , 1-12	3.6	11
36	Identification of potential Mycolyltransferase Ag85C inhibitors of Mycobacterium tuberculosis H37Rv via Virtual High Throughput Screening and Binding free energy studies. <i>Journal of Molecular Graphics and Modelling</i> , 2020 , 98, 107584	2.8	10
35	A dynamic simulation study of FDA drug from zinc database against COVID-19 main protease receptor. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020 , 1-17	3.6	10
34	Immune response and protective efficacy of live attenuated Salmonella vaccine expressing antigens of Mycobacterium avium subsp. paratuberculosis against challenge in mice. <i>Vaccine</i> , 2012 , 31, 242-51	4.1	9
33	Molecular dynamics simulation for screening phytochemicals as α -amylase inhibitors from medicinal plants. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 39, 6524-6538	3.6	8

32	Virtual screening of natural compounds as inhibitors of EGFR 696-1022 T790M associated with non-small cell lung cancer. <i>Bioinformation</i> , 2016 , 12, 311-317	1.1	8
31	Foliar Application of Iron Fortified Bacteriosiderophore Improves Growth and Grain Fe Concentration in Wheat and Soybean. <i>Indian Journal of Microbiology</i> , 2019 , 59, 344-350	3.7	7
30	Evaluation of the ability of N-terminal fragment of lethal factor of Bacillus anthracis for delivery of Mycobacterium T cell antigen ESAT-6 into cytosol of antigen presenting cells to elicit effective cytotoxic T lymphocyte response. <i>Biochemical and Biophysical Research Communications</i> , 2006 , 351, 702-7	3.4	6
29	High Throughput Virtual Screening to Identify Novel natural product Inhibitors for MethionyltRNA-Synthetase of Brucella melitensis. <i>Bioinformation</i> , 2017 , 13, 8-16	1.1	5
28	identification of natural fungicide from against isocitrate lyase of. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 39, 4816-4834	3.6	4
27	Identification of Berbamine, Oxyacanthine and Rutin from Berberis asiatica as anti-SARS-CoV-2 compounds: An in silico study. <i>Journal of Molecular Graphics and Modelling</i> , 2021 , 109, 108028	2.8	4
26	Using Chou's 5-steps rule to study pharmacophore-based virtual screening of SARS-CoV-2 Mpro inhibitors. <i>Molecular Diversity</i> , 2021 , 25, 1731-1744	3.1	4
25	Screening of potential bio-molecules from against SARS-CoV-2 main protease using computational approaches. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 1-12	3.6	4
24	Molecular basis for the repurposing of histamine H2-receptor antagonist to treat COVID-19. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 1-18	3.6	4
23	Molecular docking and molecular dynamics simulation approaches for evaluation of laccase-mediated biodegradation of various industrial dyes. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 1-11	3.6	4
22	Identification of luteolin -7-glucoside and epicatechin gallate from , as novel EGFR L858R kinase inhibitors against lung cancer: Docking and simulation-based study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 39, 5048-5057	3.6	3
21	Evaluation of predictive models based on random forest, decision tree and support vector machine classifiers and virtual screening of anti-mycobacterial compounds. <i>International Journal of Computational Biology and Drug Design</i> , 2017 , 10, 248	0.4	3
20	In silico prediction of anti-malarial hit molecules based on machine learning methods. <i>International Journal of Computational Biology and Drug Design</i> , 2015 , 8, 40-53	0.4	3
19	Computational investigation of drug bank compounds against 3C-like protease (3CL) of SARS-CoV-2 using deep learning and molecular dynamics simulation. <i>Molecular Diversity</i> , 2021 , 1	3.1	3
18	Comparative analysis of machine learning based QSAR models and molecular docking studies to screen potential anti-tubercular inhibitors against InhA of mycobacterium tuberculosis. <i>International Journal of Computational Biology and Drug Design</i> , 2018 , 11, 209	0.4	3
17	Identification of Putative Elicitors From Plant Root Exudates Responsible for PsoR Activation in Plant-Beneficial spp. by Docking and Molecular Dynamics Simulation Approaches to Decipher Plant-Microbe Interaction.. <i>Frontiers in Plant Science</i> , 2022 , 13, 875494	6.2	3
16	Induction of cytotoxic T lymphocyte response against Mycobacterial antigen using domain I of anthrax edema factor as antigen delivery system. <i>Biochemical and Biophysical Research Communications</i> , 2007 , 357, 50-5	3.4	2
15	Molecular Docking Study of drug molecules from Drug Bank database against COVID-19 Mpro protein		2

14	Repurposing of FDA approved drugs against serovar Typhi by targeting dihydrofolate reductase: an study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020 , 1-14	3.6	2
13	Deep-learning based repurposing of FDA-approved drugs against dihydrofolate reductase and molecular dynamics study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 1-17	3.6	2
12	Antimicrobial activity of methanolic extracts of Vernonia cinerea against Xanthomonas oryzae and identification of their compounds using in silico techniques. <i>PLoS ONE</i> , 2021 , 16, e0252759	3.7	2
11	identification of antidiabetic target for phytochemicals of and mechanistic insights by molecular dynamics simulations. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 1-18	3.6	2
10	Identification of potent Antigen 85C inhibitors of Mycobacterium tuberculosis via in-house lichen library and binding free energy studies Part-II. <i>Journal of Molecular Graphics and Modelling</i> , 2021 , 103, 107822	2.8	2
9	QSAR modeling and pharmacoinformatics of SARS coronavirus 3C-like protease inhibitors. <i>Computers in Biology and Medicine</i> , 2021 , 134, 104483	7	2
8	A spotlight on the recent advances in bacterial plant diseases and their footprint on crop production 2020 , 37-69		1
7	Assessment of activity of chalcone compounds as inhibitors of 3-chymotrypsin like protease (3CL) of SARS-CoV-2: in silico study.. <i>Structural Chemistry</i> , 2022 , 1-17	1.8	1
6	screening of natural compounds to inhibit interaction of human ACE2 receptor and spike protein of SARS-CoV-2 for the prevention of COVID-19. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 1-13	3.6	1
5	Recent advances on computational approach towards potential drug discovery against leishmaniasis 2021 , 63-84		1
4	In silico prediction and evaluation of interaction between protein arginine N-methyltransferase 5 cancer target and curcumin derivatives by molecular docking and simulation. <i>International Journal of Computational Biology and Drug Design</i> , 2017 , 10, 79	0.4	
3	Identification of SARS-CoV-2 RNA dependent RNA polymerase inhibitors using pharmacophore modelling, molecular docking and molecular dynamics simulation approaches. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 1-12	3.6	
2	IN SILICO IDENTIFICATION OF NOVEL EGFR TYROSINE KINASE INHIBITORS ASSOCIATED WITH NON-SMALL CELL LUNG CANCER FROM PHYTOCHEMICAL LIBRARY. <i>International Research Journal of Pharmacy</i> , 2016 , 7, 22-25	0.2	
1	Identification of Zinc-Binding Inhibitors of Matrix Metalloproteinase-9 to Prevent Cancer Through Deep Learning and Molecular Dynamics Simulation Approach.. <i>Frontiers in Molecular Biosciences</i> , 2022 , 9, 857430	5.6	