Arun Bahadur Gurung

List of Publications by Year in descending order

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Version: 2024-02-01

43 papers

645 citations

758635 12 h-index 24 g-index

43 all docs 43 docs citations

43 times ranked

967 citing authors

#	Article	IF	Citations
1	Unravelling lead antiviral phytochemicals for the inhibition of SARS-CoV-2 Mpro enzyme through in silico approach. Life Sciences, 2020, 255, 117831.	2.0	132
2	An Updated Review of Computer-Aided Drug Design and Its Application to COVID-19. BioMed Research International, 2021, 2021, 1-18.	0.9	95
3	In silico structure modelling of SARS-CoV-2 Nsp13 helicase and Nsp14 and repurposing of FDA approved antiviral drugs as dual inhibitors. Gene Reports, 2020, 21, 100860.	0.4	55
4	Exploring the physicochemical profile and the binding patterns of selected novel anticancer Himalayan plant derived active compounds with macromolecular targets. Informatics in Medicine Unlocked, 2016, 5, 1-14.	1.9	40
5	Molecular docking and dynamics simulation study of bioactive compounds from Ficus carica L. with important anticancer drug targets. PLoS ONE, 2021, 16, e0254035.	1.1	32
6	Structure-based virtual screening of phytochemicals and repurposing of FDA approved antiviral drugs unravels lead molecules as potential inhibitors of coronavirus 3C-like protease enzyme. Journal of King Saud University - Science, 2020, 32, 2845-2853.	1.6	30
7	Binding of small molecules at interface of protein–protein complex – A newer approach to rational drug design. Saudi Journal of Biological Sciences, 2017, 24, 379-388.	1.8	19
8	In silico screening of FDA approved drugs reveals ergotamine and dihydroergotamine as potential coronavirus main protease enzyme inhibitors. Saudi Journal of Biological Sciences, 2020, 27, 2674-2682.	1.8	18
9	Human serum albumin reduces the potency of acetylcholinesterase inhibitor based drugs for Alzheimer's disease. Chemico-Biological Interactions, 2016, 249, 1-9.	1.7	15
10	Identification of molecular descriptors for design of novel Isoalloxazine derivatives as potential Acetylcholinesterase inhibitors against Alzheimer's disease. Journal of Biomolecular Structure and Dynamics, 2017, 35, 1729-1742.	2.0	15
11	In silico analyses of major active constituents of fingerroot (Boesenbergia rotunda) unveils inhibitory activities against SARS-CoV-2 main protease enzyme. Saudi Journal of Biological Sciences, 2022, 29, 65-74.	1.8	14
12	Discovery of novel drug candidates for inhibition of soluble epoxide hydrolase of arachidonic acid cascade pathway implicated in atherosclerosis. Computational Biology and Chemistry, 2018, 74, 1-11.	1.1	13
13	Identification of SARS-CoV-2 inhibitors from extracts of Houttuynia cordata Thunb Saudi Journal of Biological Sciences, 2021, 28, 7517-7527.	1.8	13
14	The potential of Paritaprevir and Emetine as inhibitors of SARS-CoV-2 RdRp. Saudi Journal of Biological Sciences, 2021, 28, 1426-1432.	1.8	11
15	Identification of potential SARS-CoV-2 entry inhibitors by targeting the interface region between the spike RBD and human ACE2. Journal of Infection and Public Health, 2021, 14, 227-237.	1.9	11
16	An in silico approach unveils the potential of antiviral compounds in preclinical and clinical trials as SARS-CoV-2 omicron inhibitors. Saudi Journal of Biological Sciences, 2022, 29, 103297.	1.8	11
17	Serum albumin interaction with xanthine drugs at nano-bio interfaces: A combined multi-spectroscopic and molecular modelling approach. Journal of Molecular Liquids, 2017, 242, 919-927.	2.3	10
18	Molecular modelling studies unveil potential binding sites on human serum albumin for selected experimental and in silico COVID-19 drug candidate molecules. Saudi Journal of Biological Sciences, 2022, 29, 53-64.	1.8	10

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19	Structural and functional insights into the major mutations of SARS-CoV-2 Spike RBD and its interaction with human ACE2 receptor. Journal of King Saud University - Science, 2022, 34, 101773.	1.6	9
20	Impact of tyrosine nitration at positions Tyr307 and Tyr335 on structural dynamics of Lipoprotein-associated phospholipase A2–A therapeutically important cardiovascular biomarker for atherosclerosis. International Journal of Biological Macromolecules, 2018, 107, 1956-1964.	3.6	8
21	Correlation of cholinergic drug induced quenching of acetylcholinesterase bound thioflavin-T fluorescence with their inhibition activity. Spectrochimica Acta - Part A: Molecular and Biomolecular Spectroscopy, 2018, 189, 250-257.	2.0	8
22	Artesunate induces substantial topological alterations in the SARS-CoV-2 Nsp1 protein structure. Journal of King Saud University - Science, 2022, 34, 101810.	1.6	8
23	An <i>in silico</i> approach to understand the structureâ€"function properties of a serine protease (Bacifrinase) from <i>Bacillus cereus</i> and experimental evidence to support the interaction of Bacifrinase with fibrinogen and thrombin. Journal of Biomolecular Structure and Dynamics, 2017, 35, 622-644.	2.0	7
24	Interactome analysis and design of inhibitors against selected protein targets of Ser/Thr protein kinase (STPK) signaling pathways in Mycobacterium tuberculosis H37Rv. Genetics and Molecular Research, 2015, 14, 10390-10403.	0.3	6
25	Molecular docking elucidates the plausible mechanisms underlying the anticancer properties of acetyldigitoxigenin from Adenium obesum. Saudi Journal of Biological Sciences, 2020, 27, 1907-1911.	1.8	6
26	Met117 oxidation leads to enhanced flexibility of cardiovascular biomarker-lipoprotein-associated phospholipase A2 and reduced substrate binding affinity with platelet-activating factor. International Journal of Biological Macromolecules, 2018, 112, 831-840.	3.6	5
27	Plastome of Saraca asoca (Detarioideae, Fabaceae): Annotation, comparison among subfamily and molecular typing. Saudi Journal of Biological Sciences, 2021, 28, 1487-1493.	1.8	5
28	Impact of a nonâ€synonymous Q281R polymorphism on structure of human Lipoproteinâ€Associated Phospholipase A ₂ (Lpâ€PLA ₂). Journal of Cellular Biochemistry, 2018, 119, 7009-7021.	1.2	4
29	Bioprospection of antiâ€inflammatory phytochemicals suggests rutaecarpine and quinine as promising 15â€ipoxygenase inhibitors. Journal of Cellular Biochemistry, 2019, 120, 13598-13613.	1.2	4
30	Analysis of the Bioactive Metabolites of the Endangered Mexican Lost Fungi ⟨i⟩Campanophyllum⟨ i⟩ – A Report from India. Mycobiology, 2020, 48, 58-69.	0.6	4
31	The cp genome characterization of Adenium obesum: Gene content, repeat organization and phylogeny. Saudi Journal of Biological Sciences, 2021, 28, 3768-3775.	1.8	4
32	RNA-Seq analysis reveals the role of MYB12, MYB111 and MBW complex repressors in regulation of flavonoid biosynthesis in stigmas of saffron (Crocus sativus L.) flowers. Acta Physiologiae Plantarum, 2022, 44, 1.	1.0	4
33	Disruption of redox catalytic functions of peroxiredoxin-thioredoxin complex in Mycobacterium tuberculosis H37Rv using small interface binding molecules. Computational Biology and Chemistry, 2017, 67, 69-83.	1.1	3
34	Structure based virtual screening identifies Pranlukast as a potential inhibitor against Plasmodium falciparum Adenosine Deaminase enzyme. Gene Reports, 2017, 6, 54-66.	0.4	3
35	In silico molecular modelling, structural dynamics simulation and characterization of antifungal nature of \hat{l}^2 -glucosidase enzyme from Sechium edule. Journal of Biomolecular Structure and Dynamics, 2020, 39, 1-9.	2.0	3
36	Dissecting molecular evolutionary relationship of Krameriaceae inferred from phylotranscriptomic analysis. Bangladesh Journal of Plant Taxonomy, 2020, 27, 427-433.	0.1	3

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37	Potential of antiviral peptide-based SARS-CoV-2 inactivators to combat COVID-19. PLoS ONE, 2022, 17, e0268919.	1.1	2
38	Data-mining technique identifies potential target proteins playing a dual role in inflammation and oxidative stress pathways in relation to atherosclerosis plaque development. Informatics in Medicine Unlocked, 2020, 18, 100278.	1.9	1
39	Identification of potential drug-like molecules for inhibition of the inflammatory activity of cyclooxygenase-2. Journal of Biomolecular Structure and Dynamics, 2020, 38, 5293-5306.	2.0	1
40	High-throughput virtual screening of novel potent inhibitor(s) for Human Vanin-1 enzyme. Journal of Biomolecular Structure and Dynamics, 2020, , 1-16.	2.0	1
41	Identification of novel drug candidates for the inhibition of catalytic cleavage activity of coronavirus 3CL-like protease enzyme. Current Pharmaceutical Biotechnology, 2021, 22, .	0.9	1
42	Transcriptome characterization of Larrea tridentata and identification of genes associated with phenylpropanoid metabolic pathways. PLoS ONE, 2022, 17, e0265231.	1.1	1
43	Insights into plastome of Fagonia indica Burm.f. (Zygophyllaceae): organization, annotation and phylogeny. Saudi Journal of Biological Sciences, 2022, 29, 1313-1321.	1.8	0