Vivek Dhar Dwivedi

List of Publications by Year
in descending order

41 papers	786 citations	567144 15 h-index	552653 26 g-index
45 all docs	45 docs citations	45 times ranked	912 citing authors

#	Article	IF	Citations
1	SARS-CoV-2 M^{pro}inhibitors: identification of anti-SARS-CoV-2 M^{pro}compounds from FDA approved drugs. Journal of Biomolecular Structure and Dynamics, 2022, 40, 2769-2784.	2.0	41
2	Understanding on the possible routes for SARS CoV-2 invasion via ACE2 in the host linked with multiple organs damage. Infection, Genetics and Evolution, 2022, 99, 105254.	1.0	21
3	Discovery of Bispecific Lead Compounds from Azadirachta indica against ZIKA NS2B-NS3 Protease and NS5 RNA Dependent RNA Polymerase Using Molecular Simulations. Molecules, 2022, 27, 2562.	1.7	12
4	Computational assessment of Withania somnifera phytomolecules as putative inhibitors of Mycobacterium tuberculosis CTP synthase PyrG. Journal of Biomolecular Structure and Dynamics, 2022, , 1-14.	2.0	1
5	Molecular pathogenesis of Japanese encephalitis and possible therapeutic strategies. Archives of Virology, 2022, 167, 1739-1762.	0.9	20
6	Discovery of Small Molecules from Echinacea angustifolia Targeting RNA-Dependent RNA Polymerase of Japanese Encephalitis Virus. Life, 2022, 12, 952.	1.1	11
7	Structure-based screening and validation of bioactive compounds as Zika virus methyltransferase (MTase) inhibitors through first-principle density functional theory, classical molecular simulation and QM/MM affinity estimation. Journal of Biomolecular Structure and Dynamics, 2021, 39, 2338-2351.	2.0	30
8	DenvInD: dengue virus inhibitors database for clinical and molecular research. Briefings in Bioinformatics, 2021, 22, .	3.2	13
9	Anti-dengue infectivity evaluation of bioflavonoid from Azadirachta indica by dengue virus serine protease inhibition. Journal of Biomolecular Structure and Dynamics, 2021, 39, 1417-1430.	2.0	38
10	Exploration of natural compounds with anti-SARS-CoV-2 activityviainhibition of SARS-CoV-2 Mpro. Briefings in Bioinformatics, 2021, 22, 1361-1377.	3.2	108
11	Structure-Based Identification of Natural Products as SARS-CoV-2 Mpro Antagonist from Echinacea angustifolia Using Computational Approaches. Viruses, 2021, 13, 305.	1.5	25
12	Cannabinoid Type-2 Receptor Agonist, JWH133 May Be a Possible Candidate for Targeting Infection, Inflammation, and Immunity in COVID-19. Immuno, 2021, 1, 285-304.	0.6	1
13	Mechanistic insights into the Japanese encephalitis virus RNA dependent RNA polymerase protein inhibition by bioflavonoids from Azadirachta indica. Scientific Reports, 2021, 11, 18125.	1.6	20
14	Promising Antiviral Activities of Natural Flavonoids against SARS-CoV-2 Targets: Systematic Review. International Journal of Molecular Sciences, 2021, 22, 11069.	1.8	54
15	Computational and In Vitro Experimental Investigations Reveal Anti-Viral Activity of Licorice and Glycyrrhizin against Severe Acute Respiratory Syndrome Coronavirus 2. Pharmaceuticals, 2021, 14, 1216.	1.7	13
16	Integration of biometric ID for the effective collection and epidemiological evaluation of antibiotic prescription in tuberculosis and other diseases: A medical hypothesis. Journal of Global Antimicrobial Resistance, 2020, 21, 439-444.	0.9	2
17	Î±-Bisabolol, a Dietary Bioactive Phytochemical Attenuates Dopaminergic Neurodegeneration through Modulation of Oxidative Stress, Neuroinflammation and Apoptosis in Rotenone-Induced Rat Model of Parkinsonâ€™s Disease. Biomolecules, 2020, 10, 1421.	1.8	37
18	Synergistic effect of vitamin D and remdesivir can fight COVID-19. Journal of Biomolecular Structure and Dynamics, 2020, 39, 1-2.	2.0	23

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19	A multi-target approach for discovery of antiviral compounds against dengue virus from green tea. Network Modeling Analysis in Health Informatics and Bioinformatics, 2020, 9, 1.	1.2	2
20	Computational insights into tetracyclines as inhibitors against SARS-CoV-2 Mpro via combinatorial molecular simulation calculations. Life Sciences, 2020, 257, 118080.	2.0	64
21	Density functional theory and molecular dynamics simulation support Ganoderma lucidum triterpenoids as broad range antagonist of matrix metalloproteinases. Journal of Molecular Liquids, 2020, 311, 113322.	2.3	13
22	Microbial Proteomics: Development in Technologies and Applications. Journal of Bio-agriculture, 2020, , .	0.0	0
23	Computational investigation of phytomolecules as resuscitation-promoting factor B (RpfB) inhibitors for clinical suppression of Mycobacterium tuberculosis dormancy reactivation. Infection, Genetics and Evolution, 2020, 83, 104356.	1.0	8
24	Computational aided mechanistic understanding of Camellia sinensis bioactive compounds against coâ€chaperone p23 as potential anticancer agent. Journal of Cellular Biochemistry, 2019, 120, 19064-19075.	1.2	15
25	Discovery of Ganoderma lucidum triterpenoids as potential inhibitors against Dengue virus NS2B-NS3 protease. Scientific Reports, 2019, 9, 19059.	1.6	75
26	Application of Whole Genome Sequencing (WGS) Approach Against Identification of Foodborne Bacteria. , 2019, , 131-148.		1
27	Ribonucleotide reductase as a drug target against drug resistance Mycobacterium leprae : A molecular docking study. Infection, Genetics and Evolution, 2018, 60, 58-65.	1.0	7
28	Co-chaperon p23 inhibitors: Identification of anticancer compounds from traditional Chinese medicine database. Gene Reports, 2018, 10, 135-140.	0.4	2
29	Biological Data Analysis Program (BDAP): a multitasking biological sequence analysis program. Neural Computing and Applications, 2018, 30, 1493-1501.	3.2	2
30	First report of Fusarium solani causing wilt of Melia dubia. Forest Pathology, 2018, 48, e12398.	0.5	5
31	Deciphering the Biochemical Pathway and Pharmacokinetic Study of Amyloid Î²eta-42 with Superparamagnetic Iron Oxide Nanoparticles (SPIONs) Using Systems Biology Approach. Molecular Neurobiology, 2018, 55, 3224-3236.	1.9	18
32	Genomics, proteomics and evolution of dengue virus. Briefings in Functional Genomics, 2017, 16, elw040.	1.3	31
33	Internal transcribed spacer sequence database of plant fungal pathogens: PFP-ITSS database. Informatics in Medicine Unlocked, 2017, 7, 34-38.	1.9	4
34	Identification of new potent inhibitors of dengue virus NS3 protease from traditional Chinese medicine database. VirusDisease, 2016, 27, 220-225.	1.0	18
35	In silico evaluation of inhibitory potential of triterpenoids from Azadirachta indica against therapeutic target of dengue virus, NS2B-NS3 protease. Journal of Vector Borne Diseases, 2016, 53, 156-61.	0.1	20
36	In Silico Analysis of Sequenceâ€"Structureâ€"Function Relationship of the Escherichia coli Methionine Synthase. Interdisciplinary Sciences, Computational Life Sciences, 2015, 7, 382-390.	2.2	4

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37	In silico analysis of L-asparaginase from different source organisms. Interdisciplinary Sciences, Computational Life Sciences, 2014, 6, 93-99.	2.2	10
38	Computational analysis of physico-chemical properties and homology modeling of carbonic anhydrase from Cordyceps militaris. Network Modeling Analysis in Health Informatics and Bioinformatics, 2013, 2, 209-212.	1.2	6
39	Comparative modeling and docking studies of Î²-galactosidase from Aspergillus niger. Network Modeling Analysis in Health Informatics and Bioinformatics, 2013, 2, 297-302.	1.2	2
40	Computational analysis of xanthine dehydrogenase enzyme from different source organisms. Network Modeling Analysis in Health Informatics and Bioinformatics, 2013, 2, 185-189.	1.2	6
41	Amino acid sequence based in silico analysis of Î²- galactosidases. International Journal on Bioinformatics & Biosciences, 2013, 3, 37-44.	0.2	2