Rajesh B Patil

List of Publications by Year
in descending order

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32	588	840119 11	642321 23
papers	citations	h-index	g-index

33	33	33	865
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Identification of bioactive compounds fromGlycyrrhiza glabraas possible inhibitor of SARS-CoV-2 spike glycoprotein and non-structural protein-15: a pharmacoinformatics study. Journal of Biomolecular Structure and Dynamics, 2021, 39, 4686-4700.	2.0	98
2	Sars-cov-2 host entry and replication inhibitors from Indian ginseng: an in-silico approach. Journal of Biomolecular Structure and Dynamics, 2021, 39, 4510-4521.	2.0	95
3	In-silicoinvestigation of phytochemicals fromAsparagus racemosusas plausible antiviral agent in COVID-19. Journal of Biomolecular Structure and Dynamics, 2021, 39, 5033-5047.	2.0	60
4	Computational and network pharmacology analysis of bioflavonoids as possible natural antiviral compounds in COVID-19. Informatics in Medicine Unlocked, 2021, 22, 100504.	1.9	36
5	Synthesis and biological activity of structurally diverse phthalazine derivatives: A systematic review. Bioorganic and Medicinal Chemistry, 2019, 27, 3979-3997.	1.4	32
6	Combination of system biology to probe the anti-viral activity of andrographolide and its derivative against COVID-19. RSC Advances, 2021, 11, 5065-5079.	1.7	28
7	Computational assessment of saikosaponins as adjuvant treatment for COVID-19: molecular docking, dynamics, and network pharmacology analysis. Molecular Diversity, 2021, 25, 1889-1904.	2.1	25
8	Synthesis, biological evaluation and docking study of some novel isoxazole clubbed 1,3,4-oxadiazoles derivatives. Medicinal Chemistry Research, 2018, 27, 1283-1291.	1.1	19
9	Exploring the therapeutic mechanisms of Cassia glauca in diabetes mellitus through network pharmacology, molecular docking and molecular dynamics. RSC Advances, 2021, 11, 39362-39375.	1.7	16
10	Computational assessment of select antiviral phytochemicals as potential SARS-Cov-2 main protease inhibitors: molecular dynamics guided ensemble docking and extended molecular dynamics. In Silico Pharmacology, 2021, 9, 44.	1.8	15
11	Pyrido[1,2â€a]pyrimidinâ€4â€ones: Ligandâ€based Design, Synthesis, and Evaluation as an Antiâ€inflammatory Agent. Journal of Heterocyclic Chemistry, 2017, 54, 3299-3313.	1.4	12
12	Computational and network pharmacology studies of Phyllanthus emblica to tackle SARS-CoV-2. Phytomedicine Plus, 2021, 1, 100095.	0.9	12
13	LQTA-R: A new 3D-QSAR methodology applied to a set of DGAT1 inhibitors. Computational Biology and Chemistry, 2018, 74, 123-131.	1.1	11
14	Synthesis, biological evaluations and computational studies of N-(3-(-2-(7-Chloroquinolin-2-yl)vinyl)) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 623-630.	1.0	11
15	Novel Î±-amylase and Î±-glucosidase inhibitors from selected Nigerian antidiabetic plants: anin silicoapproach. Journal of Biomolecular Structure and Dynamics, 2022, 40, 6340-6349.	2.0	11
16	Molecular Dynamics Guided Receptor Independent 4D QSAR Studies of Substituted Coumarins as Anticancer Agents. Current Computer-Aided Drug Design, 2015, 11, 39-50.	0.8	11
17	Preparation, characterization and in vitro evaluation of tablets containing microwave-assisted solid dispersions of apremilast. Polimery W Medycynie, 2019, 48, 17-24.	0.6	10
18	Benzene sulfonamide pyrazole thio-oxadiazole hybrid as potential antimicrobial and antitubercular agents. Research on Chemical Intermediates, 2018, 44, 4437-4453.	1.3	9

#	Article	IF	Citations
19	Molecular docking, pharmacophore based virtual screening and molecular dynamics studies towards the identification of potential leads for the management of H. pylori. RSC Advances, 2019, 9, 26176-26208.	1.7	9
20	4D-QSAR studies of coumarin derivatives as HIV-1 integrase 3â€²-processing inhibitors. Medicinal Chemistry Research, 2015, 24, 3062-3076.	1.1	8
21	Design, Synthesis and Biological Screening of Novel 1,3,4â€Oxadiazoles as Antitubercular Agents. ChemistrySelect, 2018, 3, 13304-13310.	0.7	8
22	Cocrystals of Apixaban with Improved Solubility and Permeability: Formulation, Physicochemical Characterization, Pharmacokinetic Evaluation, and Computational Studies. Assay and Drug Development Technologies, 2021, 19, 124-138.	0.6	8
23	Identification of Promising Biofilm Inhibitory and Cytotoxic Quinazolinâ€4â€one Derivatives: Synthesis, Evaluation, Molecular Docking and ADMET Studies. ChemistrySelect, 2019, 4, 3559-3566.	0.7	7
24	Patent landscape for discovery of promising acyltransferase DGAT and MGAT inhibitors. Expert Opinion on Therapeutic Patents, 2020, 30, 873-896.	2.4	7
25	Î±-Bisabolol Mitigates Colon Inflammation by Stimulating Colon PPAR-Î³ Transcription Factor: In Vivo and In Vitro Study. PPAR Research, 2022, 2022, 1-22.	1.1	7
26	Fungal biofilm inhibition by piperazineâ€sulphonamide linked Schiff bases: Design, synthesis, and biological evaluation. Archiv Der Pharmazie, 2018, 351, e1700354.	2.1	5
27	Structural insights of dipeptidyl peptidase-IV inhibitors through molecular dynamics-guided receptor-dependent 4D-QSAR studies. Molecular Diversity, 2018, 22, 575-583.	2.1	5
28	Comprehensive QSAR studies reveal structural insights into the NR2B subtype selective benzazepine derivatives as N-Methyl- -Aspartate receptor antagonists. Journal of Molecular Structure, 2019, 1197, 617-627.	1.8	5
29	Docking Simulations and Primary Assessment of Newly Synthesized Benzene Sulfonamide Pyrazole Oxadiazole Derivatives as Potential Antimicrobial and Antitubercular Agents. Polycyclic Aromatic Compounds, 2023, 43, 1799-1811.	1.4	4
30	Pharmacoinformatics approaches to identify potential hits against tetraacyldisaccharide 4â€²-kinase (LpxK) ofPseudomonas aeruginosa. RSC Advances, 2020, 10, 32856-32874.	1.7	3
31	Identification of dual site inhibitors of tankyrase through virtual screening of protein-ligand interaction fingerprint (PLIF)â€“derived pharmacophore models, molecular dynamics, and ADMET studies. Structural Chemistry, 2020, 31, 769-779.	1.0	1
32	Synthesis and Biological Evaluation of 3,4-Dihydro-2H-benzo[b][1,4]-oxazine-2-carboxylic Acid Derivatives as Antitubercular Agents. Asian Journal of Organic & Medicinal Chemistry, 2020, 5, 138-148.	0.1	0