Sinosh Skariyachan

List of Publications by Year
in descending order

59 papers	1,255 citations	430442 18 h-index	377514 34 g-index
60 all docs	60 docs citations	60 times ranked	1701 citing authors

#	Article	IF	Citations
1	Enhanced polymer degradation of polyethylene and polypropylene by novel thermophilic consortia of Brevibacillus sps. and Aneurinibacillus sp. screened from waste management landfills and sewage treatment plants. Polymer Degradation and Stability, 2018, 149, 52-68.	2.7	195
2	Recent perspectives on the molecular basis of biofilm formation by Pseudomonas aeruginosa and approaches for treatment and biofilm dispersal. Folia Microbiologica, 2018, 63, 413-432.	1.1	96
3	Enhanced biodegradation of low and high-density polyethylene by novel bacterial consortia formulated from plastic-contaminated cow dung under thermophilic conditions. Environmental Science and Pollution Research, 2017, 24, 8443-8457.	2.7	85
4	Novel bacterial consortia isolated from plastic garbage processing areas demonstrated enhanced degradation for low density polyethylene. Environmental Science and Pollution Research, 2016, 23, 18307-18319.	2.7	81
5	Recent Aspects on the Pathogenesis Mechanism, Animal Models and Novel Therapeutic Interventions for Middle East Respiratory Syndrome Coronavirus Infections. Frontiers in Microbiology, 2019, 10, 569.	1.5	77
6	Novel consortia of Enterobacter and Pseudomonas formulated from cow dung exhibited enhanced biodegradation of polyethylene and polypropylene. Journal of Environmental Management, 2021, 284, 112030.	3.8	68
7	Environmental monitoring of bacterial contamination and antibiotic resistance patterns of the fecal coliforms isolated from Cauvery River, a major drinking water source in Karnataka, India. Environmental Monitoring and Assessment, 2015, 187, 279.	1.3	52
8	Recent advances in plastic degradation â€“ From microbial consortia-based methods to data sciences and computational biology driven approaches. Journal of Hazardous Materials, 2022, 426, 128086.	6.5	46
9	Selection and screening of microbial consortia for efficient and ecofriendly degradation of plastic garbage collected from urban and rural areas of Bangalore, India. Environmental Monitoring and Assessment, 2015, 187, 4174.	1.3	45
10	Herbal Lead as Ideal Bioactive Compounds Against Probable Drug Targets of Ebola Virus in Comparison with Known Chemical Analogue: A Computational Drug Discovery Perspective. Interdisciplinary Sciences, Computational Life Sciences, 2017, 9, 254-277.	2.2	42
11	Antimicrobial potential of metabolites extracted from bacterial symbionts associated with marine sponges in coastal area of Gulf of Mannar Biosphere, India. Letters in Applied Microbiology, 2014, 58, 231-241.	1.0	39
12	Screening of potential lead molecules against prioritised targets of multi-drug-resistant-Acinetobacter baumannii â€“ insights from molecular docking, molecular dynamic simulations and in vitro assays. Journal of Biomolecular Structure and Dynamics, 2019, 37, 1146-1169.	2.0	34
13	Structural and molecular basis of the interaction mechanism of selected drugs towards multiple targets of SARS-CoV-2 by molecular docking and dynamic simulation studies- deciphering the scope of repurposed drugs. Computers in Biology and Medicine, 2020, 126, 104054.	3.9	30
14	Nanoparticle Fullerene (C60) demonstrated stable binding with antibacterial potential towards probable targets of drug resistantSalmonella typhiâ€“ a computational perspective andin vitroinvestigation. Journal of Biomolecular Structure and Dynamics, 2017, 35, 3449-3468.	2.0	24
15	Recent perspectives on the virulent factors and treatment options for multidrug-resistant Acinetobacter baumannii. Critical Reviews in Microbiology, 2019, 45, 315-333.	2.7	24
16	Biopreservation potential of antimicrobial protein producing Pediococcus spp. towards selected food samples in comparison with chemical preservatives. International Journal of Food Microbiology, 2019, 291, 189-196.	2.1	24
17	Carbon fullerene and nanotube are probable binders to multiple targets of SARS-CoV-2: Insights from computational modeling and molecular dynamic simulation studies. Infection, Genetics and Evolution, 2021, 96, 105155.	1.0	21
18	Exploring inhibitory potential of Curcumin against various cancer targets by in silico virtual screening. Interdisciplinary Sciences, Computational Life Sciences, 2014, 6, 13-24.	2.2	20

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19	Recent Perspectives on Genome, Transmission, Clinical Manifestation, Diagnosis, Therapeutic Strategies, Vaccine Developments, and Challenges of Zika Virus Research. Frontiers in Microbiology, 2017, 8, 1761.	1.5	20
20	Structural insights on the interaction potential of natural leads against major protein targets of SARS-CoV-2: Molecular modelling, docking and dynamic simulation studies. Computers in Biology and Medicine, 2021, 132, 104325.	3.9	18
21	Natural epiestriol-16 act as potential lead molecule against prospective molecular targets of multidrug resistant Acinetobacter baumannii-Insight from in silico modelling and in vitro investigations. Infection, Genetics and Evolution, 2020, 82, 104314.	1.0	16
22	Computer aided screening and evaluation of herbal therapeutics against MRSA infections. Bioinformation, 2011, 7, 222-233.	0.2	16
23	Exploring insights for virulent gene inhibition of multidrug resistantSalmonella typhi,Vibrio cholerae, andStaphylococcus areusby potential phytoligands viain silicoscreening. Journal of Biomolecular Structure and Dynamics, 2014, 32, 1379-1395.	2.0	15
24	Environmental assessment of the degradation potential of mushroom fruit bodies of Pleurotus ostreatus (Jacq.: Fr.) P. Kumm. towards synthetic azo dyes and contaminating effluents collected from textile industries in Karnataka, India. Environmental Monitoring and Assessment, 2016, 188, 121.	1.3	14
25	Homology modelling of CB1 receptor and selection of potential inhibitor against Obesity. Bioinformation, 2012, 8, 523-528.	0.2	14
26	Response regulator GacA and transcriptional activator RhlR proteins involved in biofilm formation of Pseudomonas aeruginosa are prospective targets for natural lead molecules: Computational modelling, molecular docking and dynamic simulation studies. Infection, Genetics and Evolution, 2020, 85, 104448.	1.0	13
27	Secondary metabolites extracted from marine sponge associated Comamonas testosteroni and Citrobacter freundii as potential antimicrobials against MDR pathogens and hypothetical leads for VP40 matrix protein of Ebola virus: an in vitro and in silico investigation. Journal of Biomolecular Structure and Dynamics, 2016, 34, 1865-1883.	2.0	12
28	Prediction of binding potential of natural leads against the prioritized drug targets of chikungunya and dengue viruses by computational screening. 3 Biotech, 2018, 8, 274.	1.1	12
29	Mitogen activated protein kinase-1 and cell division control protein-42 are putative targets for the binding of novel natural lead molecules: a therapeutic intervention against Candida albicans. Journal of Biomolecular Structure and Dynamics, 2020, 38, 4584-4599.	2.0	10
30	A pilot study on water pollution and characterization of multidrug-resistant superbugs from Byramangala tank, Ramanagara district, Karnataka, India. Environmental Monitoring and Assessment, 2013, 185, 5483-5495.	1.3	9
31	Structure based virtual screening of novel inhibitors against multidrug resistant superbugs. Bioinformation, 2012, 8, 420-425.	0.2	8
32	Environmental monitoring and assessment of antibacterial metabolite producing actinobacteria screened from marine sediments in south coastal regions of Karnataka, India. Environmental Monitoring and Assessment, 2017, 189, 283.	1.3	7
33	Exploring the binding potential of carbon nanotubes and fullerene towards major drug targets of multidrug resistant bacterial pathogens and their utility as novel therapeutic agents. , 2018, , 1-29.		7
34	Investigating the therapeutic potential of herbal leads against drug resistantListeria monocytogenesby computational virtual screening andin vitroassays. Journal of Biomolecular Structure and Dynamics, 2015, 33, 2682-2694.	2.0	6
35	Understanding the Xylooligosaccharides Utilization Mechanism of Lactobacillus brevis and Bifidobacterium adolescentis: Proteins Involved and Their Conformational Stabilities for Effectual Binding. Molecular Biotechnology, 2022, 64, 75-89.	1.3	6
36	In silico exploration of novel phytoligands against probable drug target of Clostridium tetani. Interdisciplinary Sciences, Computational Life Sciences, 2012, 4, 273-281.	2.2	5

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37	Recent Perspectives on COVID-19 and Computer-Aided Virtual Screening of Natural Compounds for the Development of Therapeutic Agents Towards SARS-CoV-2. Methods in Pharmacology and Toxicology, 2020, , 433-471.	0.1	5
38	Deciphering effectual binding potential of xylo-substrates towards xylose isomerase and xylokinase through molecular docking and molecular dynamic simulation. Journal of Biomolecular Structure and Dynamics, 2021, 39, 3948-3957.	2.0	5
39	Mutational Variation Analysis of oprD Porin Gene in Multidrug-Resistant Clinical Isolates of Pseudomonas aeruginosa. Microbial Drug Resistance, 2020, 26, 869-879.	0.9	4
40	Cytotoxic effects of butyric acid derivatives through GPR109A receptor in Colorectal Carcinoma cells by in silico and in vitro methods. Journal of Molecular Structure, 2021, 1243, 130832.	1.8	4
41	Exploring the Medicinal Potential of the Fruit Bodies of Oyster Mushroom, Pleurotus ostreatus (Agaricomycetes), against Multidrug-Resistant Bacterial Isolates. International Journal of Medicinal Mushrooms, 2016, 18, 245-252.	0.9	3
42	Carbon fullerene acts as potential lead molecule against prospective molecular targets of biofilm-producing multidrug-resistant Acinetobacter baumanni and Pseudomonas aerugenosa: computational modeling and MD simulation studies. Journal of Biomolecular Structure and Dynamics, 2021, 39, 1121-1137.	2.0	3
43	Molecular Modeling on Streptolysin-O of Multidrug Resistant Streptococcus pyogenes and Computer Aided Screening and In Vitro Assay for Novel Herbal Inhibitors. Current Computer-Aided Drug Design, 2014, 10, 59-74.	0.8	3
44	Physicochemical and microbial pollution of a reservoir in South India and role of bacteriophage treatment to curtail drug-resistant bacterial pollution in water. Environmental Technology and Innovation, 2021, 24, 102012.	3.0	3
45	Selection of herbal therapeutics against deltatoxin mediated Clostridial infections. Bioinformation, 2011, 6, 375-379.	0.2	3
46	Application of Novel Microbial Consortia for Environmental Site Remediation and Hazardous Waste Management Toward Low- and High-Density Polyethylene and Prioritizing the Cost-Effective, Eco-friendly, and Sustainable Biotechnological Intervention. , 2018, , 1-48.		3
47	Computational Analysis of the Domain Architecture and Substrate-Gating Mechanism of Prolyl Oligopeptidases from Shewanella woodyi and Identification of Probable Lead Molecules. Interdisciplinary Sciences, Computational Life Sciences, 2016, 8, 284-293.	2.2	2
48	Novel Insight from Computational Virtual Screening Depict the Binding Potential of Selected Phytotherapeutics Against Probable Drug Targets of Clostridium difficile. Interdisciplinary Sciences, Computational Life Sciences, 2018, 10, 583-604.	2.2	2
49	Scope of computational biology and bioinformatics toward the discovery of potential therapeutic agents against viral diseases. Future Virology, 2022, 17, 257-260.	0.9	2
50	Exploring the Potential of Herbal Ligands Toward Multidrug-Resistant Bacterial Pathogens by Computational Drug Discovery. Translational Medicine Research, 2017, , 89-117.	0.0	1
51	Screening of Natural Lead Molecules Against Putative Molecular Targets of Drug-resistant Cryptococcus spp: An Insight from Computer-aided Molecular Design. Current Topics in Medicinal Chemistry, 2019, 18, 2681-2701.	1.0	1
52	Assessment of antibiotic resistance patterns of the fecal coliforms isolated from Cauvery River and screening of novel herbal lead molecules against probable drug targets of MDR pathogens by computational virtual screening. International Journal of Infectious Diseases, 2016, 45, 116.	1.5	0
53	Emergence of Multidrug-Resistant Bacteria in Freshwater Ecosystems (River) and Screening of Natural Therapeutics Against the Probable Drug Targets of Drug-Resistant Pathogens by Computational Biology Approaches. , 2017, , 109-132.		0
54	Application of Novel Microbial Consortia for Environmental Site Remediation and Hazardous Waste Management Toward Low- and High-Density Polyethylene and Prioritizing the Cost-Effective, Eco-friendly, and Sustainable Biotechnological Intervention. , 2019, , 431-478.		0

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55	Monitoring and assessment of the therapeutic impact of metabolites extracted from sponge-associated bacteria screened from Gulf of Mannar, southeast coast of India. Environmental Monitoring and Assessment, 2020, 192, 241.	1.3	0
56	Combinatorial Designing of Novel Lead Molecules Towards the Putative Drug Targets of Extreme Drug-Resistant Mycobacterium tuberculosis: A Future Insight for Molecular Medicine. , 2019, , 233-281.		0
57	Applications of computational intelligence and predictive analytics in screening potential lead molecules toward COVID-19: scope of repurposed drugs. , 2021, , 1-32.		0
58	C-demethylation and 1, 2-amino shift in (E)-2-(1-(3-aminophenyl) ethylidene)hydrazinecarboxamide to (E)-2-(2-aminobenzylidene)hydrazinecarboxamide and their applications. Scientific Reports, 2020, 10, 21913.	1.6	0
59	Computational analysis of the domain architecture and substrate-gating mechanism of prolyl oligopeptidases from Shewanella woodyi and identification probable lead molecules. Interdisciplinary Sciences, Computational Life Sciences, 2015, , .	2.2	0