

Sinosh Skariyachan

List of Publications by Year in descending order

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Version: 2024-02-01

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	Understanding the Xylooligosaccharides Utilization Mechanism of <i>Lactobacillus brevis</i> and <i>Bifidobacterium adolescentis</i> : Proteins Involved and Their Conformational Stabilities for Effectual Binding. <i>Molecular Biotechnology</i> , 2022, 64, 75-89.	1.3	6
2	Recent advances in plastic degradation – From microbial consortia-based methods to data sciences and computational biology driven approaches. <i>Journal of Hazardous Materials</i> , 2022, 426, 128086.	6.5	46
3	Scope of computational biology and bioinformatics toward the discovery of potential therapeutic agents against viral diseases. <i>Future Virology</i> , 2022, 17, 257-260.	0.9	2
4	Deciphering effectual binding potential of xylo-substrates towards xylose isomerase and xylokinase through molecular docking and molecular dynamic simulation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 3948-3957.	2.0	5
5	Carbon fullerene acts as potential lead molecule against prospective molecular targets of biofilm-producing multidrug-resistant <i>Acinetobacter baumannii</i> and <i>Pseudomonas aeruginosa</i> : computational modeling and MD simulation studies. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 1121-1137.	2.0	3
6	Novel consortia of <i>Enterobacter</i> and <i>Pseudomonas</i> formulated from cow dung exhibited enhanced biodegradation of polyethylene and polypropylene. <i>Journal of Environmental Management</i> , 2021, 284, 112030.	3.8	68
7	Structural insights on the interaction potential of natural leads against major protein targets of SARS-CoV-2: Molecular modelling, docking and dynamic simulation studies. <i>Computers in Biology and Medicine</i> , 2021, 132, 104325.	3.9	18
8	Cytotoxic effects of butyric acid derivatives through GPR109A receptor in Colorectal Carcinoma cells by in silico and in vitro methods. <i>Journal of Molecular Structure</i> , 2021, 1243, 130832.	1.8	4
9	Physicochemical and microbial pollution of a reservoir in South India and role of bacteriophage treatment to curtail drug-resistant bacterial pollution in water. <i>Environmental Technology and Innovation</i> , 2021, 24, 102012.	3.0	3
10	Applications of computational intelligence and predictive analytics in screening potential lead molecules toward COVID-19: scope of repurposed drugs. , 2021, , 1-32.		0
11	Carbon fullerene and nanotube are probable binders to multiple targets of SARS-CoV-2: Insights from computational modeling and molecular dynamic simulation studies. <i>Infection, Genetics and Evolution</i> , 2021, 96, 105155.	1.0	21
12	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 <i>Candida albicans</i> . <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 4584-4599.	2.0	10
13	Recent Perspectives on COVID-19 and Computer-Aided Virtual Screening of Natural Compounds for the Development of Therapeutic Agents Towards SARS-CoV-2. <i>Methods in Pharmacology and Toxicology</i> , 2020, , 433-471.	0.1	5
14	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. <i>Computers in Biology and Medicine</i> , 2020, 126, 104054.	3.9	30
15	Monitoring and assessment of the therapeutic impact of metabolites extracted from sponge-associated bacteria screened from Gulf of Mannar, southeast coast of India. <i>Environmental Monitoring and Assessment</i> , 2020, 192, 241.	1.3	0
16	Response regulator GacA and transcriptional activator RhIR proteins involved in biofilm formation of <i>Pseudomonas aeruginosa</i> are prospective targets for natural lead molecules: Computational modelling, molecular docking and dynamic simulation studies. <i>Infection, Genetics and Evolution</i> , 2020, 85, 104448.	1.0	13
17	Mutational Variation Analysis of <i>oprD</i> Porin Gene in Multidrug-Resistant Clinical Isolates of <i>Pseudomonas aeruginosa</i> . <i>Microbial Drug Resistance</i> , 2020, 26, 869-879.	0.9	4
18	Natural epiestriol-16 act as potential lead molecule against prospective molecular targets of multidrug resistant <i>Acinetobacter baumannii</i> -Insight from in silico modelling and in vitro investigations. <i>Infection, Genetics and Evolution</i> , 2020, 82, 104314.	1.0	16

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19	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
20	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
21	Recent perspectives on the virulent factors and treatment options for multidrug-resistant <i>Acinetobacter baumannii</i> . Critical Reviews in Microbiology, 2019, 45, 315-333.	2.7	24
22	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
23	Biopreservation potential of antimicrobial protein producing <i>Pediococcus</i> spp. towards selected food samples in comparison with chemical preservatives. International Journal of Food Microbiology, 2019, 291, 189-196.	2.1	24
24	Screening of potential lead molecules against prioritised targets of multi-drug-resistant <i>Acinetobacter baumannii</i> – insights from molecular docking, molecular dynamic simulations and <i>in vitro</i> assays. Journal of Biomolecular Structure and Dynamics, 2019, 37, 1146-1169.	2.0	34
25	Combinatorial Designing of Novel Lead Molecules Towards the Putative Drug Targets of Extreme Drug-Resistant <i>Mycobacterium tuberculosis</i> : A Future Insight for Molecular Medicine. , 2019, , 233-281.		0
26	Screening of Natural Lead Molecules Against Putative Molecular Targets of Drug-resistant <i>Cryptococcus</i> spp: An Insight from Computer-aided Molecular Design. Current Topics in Medicinal Chemistry, 2019, 18, 2681-2701.	1.0	1
27	Enhanced polymer degradation of polyethylene and polypropylene by novel thermophilic consortia of <i>Brevibacillus</i> spp. and <i>Aneurinibacillus</i> sp. screened from waste management landfills and sewage treatment plants. Polymer Degradation and Stability, 2018, 149, 52-68.	2.7	195
28	Recent perspectives on the molecular basis of biofilm formation by <i>Pseudomonas aeruginosa</i> and approaches for treatment and biofilm dispersal. Folia Microbiologica, 2018, 63, 413-432.	1.1	96
29	Novel Insight from Computational Virtual Screening Depict the Binding Potential of Selected Phytotherapeutics Against Probable Drug Targets of <i>Clostridium difficile</i> . Interdisciplinary Sciences, Computational Life Sciences, 2018, 10, 583-604.	2.2	2
30	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
31	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
32	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
33	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
34	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
35	Exploring the Potential of Herbal Ligands Toward Multidrug-Resistant Bacterial Pathogens by Computational Drug Discovery. Translational Medicine Research, 2017, , 89-117.	0.0	1
36	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

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37	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
38	Nanoparticle Fullerene (C60) demonstrated stable binding with antibacterial potential towards probable targets of drug resistant <i>Salmonella typhi</i> – a computational perspective and <i>in vitro</i> investigation. Journal of Biomolecular Structure and Dynamics, 2017, 35, 3449-3468.	2.0	24
39	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
40	Exploring the Medicinal Potential of the Fruit Bodies of Oyster Mushroom, <i>Pleurotus ostreatus</i> (Agaricomycetes), against Multidrug-Resistant Bacterial Isolates. International Journal of Medicinal Mushrooms, 2016, 18, 245-252.	0.9	3
41	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
42	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
43	Secondary metabolites extracted from marine sponge associated <i>Comamonas testosteroni</i> and <i>Citrobacter freundii</i> as potential antimicrobials against MDR pathogens and hypothetical leads for VP40 matrix protein of Ebola virus: an <i>in vitro</i> and <i>in silico</i> investigation. Journal of Biomolecular Structure and Dynamics, 2016, 34, 1865-1883.	2.0	12
44	Environmental assessment of the degradation potential of mushroom fruit bodies of <i>Pleurotus ostreatus</i> (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
45	Computational Analysis of the Domain Architecture and Substrate-Gating Mechanism of Prolyl Oligopeptidases from <i>Shewanella woodyi</i> and Identification of Probable Lead Molecules. Interdisciplinary Sciences, Computational Life Sciences, 2016, 8, 284-293.	2.2	2
46	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
47	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
48	Investigating the therapeutic potential of herbal leads against drug resistant <i>Listeria monocytogenes</i> by computational virtual screening and <i>in vitro</i> assays. Journal of Biomolecular Structure and Dynamics, 2015, 33, 2682-2694.	2.0	6
49	Computational analysis of the domain architecture and substrate-gating mechanism of prolyl oligopeptidases from <i>Shewanella woodyi</i> and identification probable lead molecules. Interdisciplinary Sciences, Computational Life Sciences, 2015, , .	2.2	0
50	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
51	Exploring insights for virulent gene inhibition of multidrug resistant <i>Salmonella typhi</i> , <i>Vibrio cholerae</i> , and <i>Staphylococcus aureus</i> by potential phytoligands via <i>in silico</i> screening. Journal of Biomolecular Structure and Dynamics, 2014, 32, 1379-1395.	2.0	15
52	Exploring inhibitory potential of Curcumin against various cancer targets by <i>in silico</i> virtual screening. Interdisciplinary Sciences, Computational Life Sciences, 2014, 6, 13-24.	2.2	20
53	Molecular Modeling on Streptolysin-O of Multidrug Resistant <i>Streptococcus pyogenes</i> and Computer Aided Screening and <i>In Vitro</i> Assay for Novel Herbal Inhibitors. Current Computer-Aided Drug Design, 2014, 10, 59-74.	0.8	3
54	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

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55	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
56	Structure based virtual screening of novel inhibitors against multidrug resistant superbugs. Bioinformation, 2012, 8, 420-425.	0.2	8
57	Homology modelling of CB1 receptor and selection of potential inhibitor against Obesity. Bioinformation, 2012, 8, 523-528.	0.2	14
58	Computer aided screening and evaluation of herbal therapeutics against MRSA infections. Bioinformation, 2011, 7, 222-233.	0.2	16
59	Selection of herbal therapeutics against deltatotoxin mediated Clostridial infections. Bioinformation, 2011, 6, 375-379.	0.2	3