

Dhiraj P Dhotre

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

1,126
citations

471509

17
h-index

414414

32
g-index

53
all docs

53
docs citations

53
times ranked

1830
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular analysis of gut microbiota in obesity among Indian individuals. <i>Journal of Biosciences</i> , 2012, 37, 647-657.	1.1	142
2	Molecular Characterization and Meta-Analysis of Gut Microbial Communities Illustrate Enrichment of Prevotella and Megasphaera in Indian Subjects. <i>Frontiers in Microbiology</i> , 2016, 7, 660.	3.5	110
3	Effective biotransformation and detoxification of anthraquinone dye reactive blue 4 by using aerobic bacterial granules. <i>Water Research</i> , 2017, 122, 603-613.	11.3	86
4	Characterization of bacterial community shift in human Ulcerative Colitis patients revealed by Illumina based 16S rRNA gene amplicon sequencing. <i>Gut Pathogens</i> , 2014, 6, 22.	3.4	84
5	Comparison of Small Gut and Whole Gut Microbiota of First-Degree Relatives With Adult Celiac Disease Patients and Controls. <i>Frontiers in Microbiology</i> , 2019, 10, 164.	3.5	68
6	The Gut Microbial Diversity of Newly Diagnosed Diabetics but Not of Prediabetics Is Significantly Different from That of Healthy Nondiabetics. <i>MSystems</i> , 2020, 5, .	3.8	64
7	Gut, oral and skin microbiome of Indian patrilineal families reveal perceptible association with age. <i>Scientific Reports</i> , 2020, 10, 5685.	3.3	50
8	Comparative genome analysis reveals key genetic factors associated with probiotic property in <i>Enterococcus faecium</i> strains. <i>BMC Genomics</i> , 2018, 19, 652.	2.8	45
9	Restoration of dysbiotic human gut microbiome for homeostasis. <i>Life Sciences</i> , 2021, 278, 119622.	4.3	41
10	World's Largest Mass Bathing Event Influences the Bacterial Communities of Godavari, a Holy River of India. <i>Microbial Ecology</i> , 2018, 76, 706-718.	2.8	39
11	A cross-sectional comparative study of gut bacterial community of Indian and Finnish children. <i>Scientific Reports</i> , 2017, 7, 10555.	3.3	37
12	Microbiome and imputed metagenome study of crude and refined petroleum-oil-contaminated soils: Potential for hydrocarbon degradation and plant-growth promotion. <i>Journal of Biosciences</i> , 2019, 44, 1.	1.1	34
13	Genomic and functional features of the biosurfactant producing <i>Bacillus</i> sp. AM13. <i>Functional and Integrative Genomics</i> , 2016, 16, 557-566.	3.5	27
14	Insights into Diversity and Imputed Metabolic Potential of Bacterial Communities in the Continental Shelf of Agatti Island. <i>PLoS ONE</i> , 2015, 10, e0129864.	2.5	26
15	Repeated mild traumatic brain injury affects microbial diversity in rat jejunum. <i>Journal of Biosciences</i> , 2019, 44, 1.	1.1	23
16	MicFunPred: A conserved approach to predict functional profiles from 16S rRNA gene sequence data. <i>Genomics</i> , 2021, 113, 3635-3643.	2.9	22
17	Draft Genome Sequences of Two Phytoplasma Strains Associated with Sugarcane Grassy Shoot (SCGS) and Bermuda Grass White Leaf (BGWL) Diseases. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 715-717.	2.6	20
18	Deep sequencing analysis of bacterial community structure of Soldhar hot spring, India. <i>Microbiology</i> , 2017, 86, 136-142.	1.2	19

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19	Draft genome of <i>Ochrobactrum intermedium</i> strain M86 isolated from non-ulcer dyspeptic individual from India. <i>Gut Pathogens</i> , 2013, 5, 7.	3.4	18
20	<i>Nitrincola alkalisediminis</i> sp. nov., an alkaliphilic bacterium isolated from an alkaline lake. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 1254-1259.	1.7	18
21	Mining the Core Gut Microbiome from a Sample Indian Population. <i>Indian Journal of Microbiology</i> , 2019, 59, 90-95.	2.7	15
22	<i>Nitrincola tapanii</i> sp. nov., a novel alkaliphilic bacterium from An Indian Soda Lake. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1106-1111.	1.7	14
23	Reclassification of <i>Phycicola gilvus</i> (Lee et al. 2008) and <i>Leifsonia pindariensis</i> (Reddy et al. 2008) as <i>Microterricola gilva</i> comb. nov. and <i>Microterricola pindariensis</i> comb. nov. and emended description of the genus <i>Microterricola</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 2766-2772.	1.7	12
24	Understanding the association between the human gut, oral and skin microbiome and the Ayurvedic concept of prakriti. <i>Journal of Biosciences</i> , 2019, 44, 1.	1.1	11
25	Draft Genome Sequences of <i>Yersinia pestis</i> Strains from the 1994 Plague Epidemic of Surat and 2002 Shimla Outbreak in India. <i>Indian Journal of Microbiology</i> , 2014, 54, 480-482.	2.7	10
26	Bacterial Communities Associated with the Biofilms Formed in High-Altitude Brackish Water PangongATso Located in the Himalayan Plateau. <i>Current Microbiology</i> , 2020, 77, 4072-4084.	2.2	10
27	Disruptions in oral and nasal microbiota in biomass and tobacco smoke associated chronic obstructive pulmonary disease. <i>Archives of Microbiology</i> , 2021, 203, 2087-2099.	2.2	9
28	Generation, annotation, and analysis of ESTs from midgut tissue of adult female <i>Anopheles stephensi</i> mosquitoes. <i>BMC Genomics</i> , 2009, 10, 386.	2.8	8
29	Contrasting Composition, Diversity and Predictive Metabolic Potential of the Rhizobacterial Microbiomes Associated with Native and Invasive <i>Prosopis</i> Congeners. <i>Current Microbiology</i> , 2021, 78, 2051-2060.	2.2	8
30	Treatment of industrial effluents and assessment of their impact on the structure and function of microbial diversity in a unique Anoxic-Aerobic sequential batch reactor (AnASBR). <i>Journal of Environmental Management</i> , 2020, 261, 110241.	7.8	7
31	Benchmarking of 16S rRNA gene databases using known strain sequences. <i>Bioinformatics</i> , 2021, 17, 377-391.	0.5	7
32	Microbiome and imputed metagenome study of crude and refined petroleum-oil-contaminated soils: Potential for hydrocarbon degradation and plant-growth promotion. <i>Journal of Biosciences</i> , 2019, 44, .	1.1	7
33	Genome Sequence of <i>Janibacter hoylei</i> MTCC8307, Isolated from the Stratospheric Air. <i>Journal of Bacteriology</i> , 2012, 194, 6629-6630.	2.2	6
34	Comparative genomics of whole-cell pertussis vaccine strains from India. <i>BMC Genomics</i> , 2020, 21, 345.	2.8	6
35	Potential of Health and Demographic Surveillance System in Asthma and Chronic Obstructive Pulmonary Disease Microbiome Research. <i>Frontiers in Public Health</i> , 2017, 5, 196.	2.7	5
36	A Microcosm Model for the Study of Microbial Community Shift and Carbon Emission from Landfills. <i>Indian Journal of Microbiology</i> , 2022, 62, 195-203.	2.7	5

#	ARTICLE	IF	CITATIONS
37	Role of Ectomycorrhizal Biotechnology in Pesticide Remediation. , 2020, , 315-330.		3
38	Transcriptome analysis of Anopheles stephensi embryo using expressed sequence tags. Journal of Biosciences, 2013, 38, 301-309.	1.1	2
39	Draft Genome Sequence of Methylophaga Ionarensis MPL ^T , a Haloalkaliphilic (Non-Methane-Utilizing) Methylophag. Genome Announcements, 2013, 1, .	0.8	2
40	Genome Sequence of Bordetella pertussis Vaccine Strain BP 165. Microbiology Resource Announcements, 2019, 8, .	0.6	2
41	Rectal administration of buttermilk processed with medicinal plants alters gut microbiome in obese individuals. Journal of Diabetes and Metabolic Disorders, 2021, 20, 1415-1427.	1.9	2
42	Probiotics: A Mainstream Therapy for the Disease Suppression. , 2022, , 257-257.		1
43	Human gut microbiome research in India: A retrospect and future opportunities. Proceedings of the Indian National Science Academy, 2019, , .	1.4	1
44	Sa1993 Constitutional and Functional Small Intestinal Microbiome of Patients With Celiac Disease, First Degree Relatives and Effect of Gluten Free Diet on Them. Gastroenterology, 2014, 146, S-349.	1.3	0
45	Integrated Genomic and Functional Characterization of the Anti-diabetic Potential of Arthrobacter sp. SW1. Current Microbiology, 2021, 78, 2577-2588.	2.2	0
46	Bioprospecting appraisal of Himalayan pindrow fir for pharmacological applications. , 2021, , 461-482.		0
47	Oral and nasal microbiota in healthy, tobacco smoke COPD (TSCOPD) and biomass smoke COPD (BMSCOPD) subjects from India. , 2016, , .		0
48	Induced sputum microbiome in smoker and non-smoker COPD subjects and its association with lung function in Indian subjects. , 2017, , .		0