Yogesh S Shouche

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4815949/publications.pdf

Version: 2024-02-01

38720 64755 9,278 258 50 79 citations g-index h-index papers 261 261 261 12259 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Extracellular Synthesis of Crystalline Silver Nanoparticles and Molecular Evidence of Silver Resistance from $\langle i \rangle$ Morganella $\langle i \rangle$ sp.: Towards Understanding Biochemical Synthesis Mechanism. ChemBioChem, 2008, 9, 1415-1422.	1.3	261
2	Genomic characterization and epidemiology of an emerging SARS-CoV-2 variant in Delhi, India. Science, 2021, 374, 995-999.	6.0	230
3	Bacterial Aerobic Synthesis of Nanocrystalline Magnetite. Journal of the American Chemical Society, 2005, 127, 9326-9327.	6.6	190
4	Bacteria-Mediated Precursor-Dependent Biosynthesis of Superparamagnetic Iron Oxide and Iron Sulfide Nanoparticles. Langmuir, 2008, 24, 5787-5794.	1.6	184
5	STUDIES ON CULTURED AND UNCULTURED MICROBIOTA OF WILD CULEX QUINQUEFASCIATUS MOSQUITO MIDGUT BASED ON 16S RIBOSOMAL RNA GENE ANALYSIS. American Journal of Tropical Medicine and Hygiene, 2004, 70, 597-603.	0.6	169
6	Isolation and Functional Characterization of Siderophore-Producing Lead- and Cadmium-Resistant Pseudomonas putida KNP9. Current Microbiology, 2005, 50, 233-237.	1.0	167
7	Fluoroquinolones and <i>qnr</i> Genes in Sediment, Water, Soil, and Human Fecal Flora in an Environment Polluted by Manufacturing Discharges. Environmental Science & Environm	4.6	158
8	Phylogenetic characterization of bacteria in the gut of house flies (Musca domestica L.). FEMS Microbiology Ecology, 2012, 79, 581-593.	1.3	144
9	Molecular analysis of gut microbiota in obesity among Indian individuals. Journal of Biosciences, 2012, 37, 647-657.	0.5	142
10	Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass-Spectrometry (MALDI-TOF MS) Based Microbial Identifications: Challenges and Scopes for Microbial Ecologists. Frontiers in Microbiology, 2016, 7, 1359.	1.5	142
11	The miR-30 family microRNAs confer epithelial phenotype to human pancreatic cells. Islets, 2009, 1, 137-147.	0.9	136
12	Antimicrobial activity of marine bacteria associated with sponges from the waters off the coast of South East India. Microbiological Research, 2006, 161, 252-262.	2.5	131
13	Bacterial Synthesis of Copper/Copper Oxide Nanoparticles. Journal of Nanoscience and Nanotechnology, 2008, 8, 3191-3196.	0.9	124
14	Microbiology of Lonar Lake and other soda lakes. ISME Journal, 2013, 7, 468-476.	4.4	124
15	Practice and prospects of microbial preservation. FEMS Microbiology Letters, 2013, 339, 1-9.	0.7	122
16	Tracking the influence of long-term chromium pollution on soil bacterial community structures by comparative analyses of 16S rRNA gene phylotypes. Research in Microbiology, 2009, 160, 1-9.	1.0	120
17	Comparative Genome Analysis of Megasphaera sp. Reveals Niche Specialization and Its Potential Role in the Human Gut. PLoS ONE, 2013, 8, e79353.	1.1	120
18	Phylogenetic diversity of culturable fungi from the deep-sea sediments of the Central Indian Basin and their growth characteristics. Fungal Diversity, 2010, 40, 89-102.	4.7	116

#	Article	IF	Citations
19	Cultivable Bacterial Diversity of Alkaline Lonar Lake, India. Microbial Ecology, 2008, 55, 163-172.	1.4	111
20	Molecular Characterization and Meta-Analysis of Gut Microbial Communities Illustrate Enrichment of Prevotella and Megasphaera in Indian Subjects. Frontiers in Microbiology, 2016, 7, 660.	1.5	110
21	Microbial diversity and soil physiochemical characteristic of higher altitude. PLoS ONE, 2019, 14, e0213844.	1.1	104
22	Exploration of Microbial Diversity and Community Structure of Lonar Lake: The Only Hypersaline Meteorite Crater Lake within Basalt Rock. Frontiers in Microbiology, 2015, 6, 1553.	1.5	100
23	Fungal Community Analysis in the Deep-Sea Sediments of the Central Indian Basin by Culture-Independent Approach. Microbial Ecology, 2011, 61, 507-517.	1.4	90
24	A Treatment Plant Receiving Waste Water from Multiple Bulk Drug Manufacturers Is a Reservoir for Highly Multi-Drug Resistant Integron-Bearing Bacteria. PLoS ONE, 2013, 8, e77310.	1.1	90
25	Molecular analyses of microbial diversity associated with the Lonar soda lake in India: An impact crater in a basalt area. Research in Microbiology, 2006, 157, 928-937.	1.0	88
26	Decolourization of naphthalene-containing sulfonated azo dyes by Kerstersia sp. strain VKY1. Enzyme and Microbial Technology, 2007, 40, 204-211.	1.6	88
27	Studies on cultured and uncultured microbiota of wild culex quinquefasciatus mosquito midgut based on 16s ribosomal RNA gene analysis. American Journal of Tropical Medicine and Hygiene, 2004, 70, 597-603.	0.6	88
28	Microbial cultivation and the role of microbial resource centers in the omics era. Applied Microbiology and Biotechnology, 2013, 97, 51-62.	1.7	85
29	Characterization of bacterial community shift in human Ulcerative Colitis patients revealed by Illumina based 16S rRNA gene amplicon sequencing. Gut Pathogens, 2014, 6, 22.	1.6	84
30	Hyperoxaluria leads to dysbiosis and drives selective enrichment of oxalate metabolizing bacterial species in recurrent kidney stone endures. Scientific Reports, 2016, 6, 34712.	1.6	84
31	Aeromonas culicicola sp. nov., from the midgut of Culex quinquefasciatus International Journal of Systematic and Evolutionary Microbiology, 2002, 52, 1723-1728.	0.8	84
32	Isolation and Characterization of Nonrhizobial Plant Growth Promoting Bacteria from Nodules of Kudzu (Pueraria thunbergiana) and Their Effect on Wheat Seedling Growth. Current Microbiology, 2008, 56, 134-139.	1.0	81
33	Gut Microbial Diversity Assessment of Indian Type-2-Diabetics Reveals Alterations in Eubacteria, Archaea, and Eukaryotes. Frontiers in Microbiology, 2017, 8, 214.	1.5	81
34	Factors influencing the gut microbiome in children: from infancy to childhood. Journal of Biosciences, 2019, 44, 1.	0.5	81
35	The cag Pathogenicity Island of Helicobacter pylori Is Disrupted in the Majority of Patient Isolates from Different Human Populations. Journal of Clinical Microbiology, 2004, 42, 5302-5308.	1.8	80
36	Species identification and authentication of tissues of animal origin using mitochondrial and nuclear markers. Meat Science, 2007, 76, 666-674.	2.7	80

#	Article	IF	Citations
37	Phyllosphere microbiome: Diversity and functions. Microbiological Research, 2022, 254, 126888.	2.5	77
38	Fungal diversity in deep-sea sediments revealed by culture-dependent and culture-independent approaches. Fungal Ecology, 2012, 5, 543-553.	0.7	76
39	Investigation of methanogen population structure in biogas reactor by molecular characterization of methyl-coenzyme M reductase A (mcrA) genes. Bioresource Technology, 2008, 99, 5317-5326.	4.8	71
40	Four marine-derived fungi for bioremediation of raw textile mill effluents. Biodegradation, 2010, 21, 217-233.	1.5	70
41	Genus-Wide Physicochemical Evidence of Extracellular Crystalline Silver Nanoparticles Biosynthesis by Morganella spp. PLoS ONE, 2011, 6, e21401.	1.1	69
42	Comparison of Small Gut and Whole Gut Microbiota of First-Degree Relatives With Adult Celiac Disease Patients and Controls. Frontiers in Microbiology, 2019, 10, 164.	1.5	68
43	Natural yeast flora of different varieties of grapes used for wine making in India. Food Microbiology, 2009, 26, 801-808.	2.1	67
44	Microbiome analysis reveals the abundance of bacterial pathogens in Rousettus leschenaultii guano. Scientific Reports, 2016, 6, 36948.	1.6	65
45	The Gut Microbial Diversity of Newly Diagnosed Diabetics but Not of Prediabetics Is Significantly Different from That of Healthy Nondiabetics. MSystems, 2020, 5, .	1.7	64
46	Green synthesis of gold and silver nanoparticles by an actinomycete Gordonia amicalis HS-11: Mechanistic aspects and biological application. Process Biochemistry, 2016, 51, 374-383.	1.8	63
47	Active methylotrophs in the sediments of Lonar Lake, a saline and alkaline ecosystem formed by meteor impact. ISME Journal, 2010, 4, 1470-1480.	4.4	59
48	Comparative analysis of fecal microflora of healthy full-term Indian infants born with different methods of delivery (vaginal vs cesarean): Acinetobacter sp. prevalence in vaginally born infants. Journal of Biosciences, 2012, 37, 989-998.	0.5	57
49	Molecular diversity of methanogens and identification of Methanolobus sp. as active methylotrophic Archaea in Lonar crater lake sediments. FEMS Microbiology Ecology, 2012, 81, 43-51.	1.3	56
50	The microbiome in urogenital schistosomiasis and induced bladder pathologies. PLoS Neglected Tropical Diseases, 2017, 11, e0005826.	1.3	56
51	Midgut Microbial Community of Culex quinquefasciatus Mosquito Populations from India. PLoS ONE, 2013, 8, e80453.	1.1	53
52	Prevalence and subtype analysis of Blastocystis in healthy Indian individuals. Infection, Genetics and Evolution, 2015, 31, 296-299.	1.0	53
53	Molecular profiling of mucosal tissue associated microbiota in patients manifesting acute exacerbations and remission stage of ulcerative colitis. World Journal of Microbiology and Biotechnology, 2018, 34, 76.	1.7	53
54	Acquired Genetic Mechanisms of a Multiresistant Bacterium Isolated from a Treatment Plant Receiving Wastewater from Antibiotic Production. Applied and Environmental Microbiology, 2013, 79, 7256-7263.	1.4	52

#	Article	IF	CITATIONS
55	Differential Proteomics in Response to Low Temperature Diazotrophy of Himalayan Psychrophilic Nitrogen Fixing Pseudomonas migulae S10724 Strain. Current Microbiology, 2014, 68, 543-550.	1.0	52
56	Opportunities and challenges for gut microbiome studies in the Indian population. Microbiome, 2013, 1, 24 .	4.9	51
57	Peteryoungia gen. nov. with four new species combinations and description of Peteryoungia desertarenae sp. nov., and taxonomic revision of the genus Ciceribacter based on phylogenomics of Rhizobiaceae. Archives of Microbiology, 2021, 203, 3591-3604.	1.0	51
58	Kinetic modelling and microbial community assessment of anaerobic biphasic fixed film bioreactor treating distillery spent wash. Water Research, 2011, 45, 4248-4259.	5.3	50
59	Mountain-associated clade endemism in an ancient frog family (Nyctibatrachidae) on the Indian subcontinent. Molecular Phylogenetics and Evolution, 2012, 62, 839-847.	1.2	50
60	Gut, oral and skin microbiome of Indian patrilineal families reveal perceptible association with age. Scientific Reports, 2020, 10, 5685.	1.6	50
61	Anthropogenic Activities Induce Depletion in Microbial Communities at Urban Sites of the River Ganges. Current Microbiology, 2018, 75, 79-83.	1.0	49
62	Assessment of fungal diversity in deep-sea sediments by multiple primer approach. World Journal of Microbiology and Biotechnology, 2012, 28, 659-667.	1.7	48
63	Analysis of bacterial and fungal communities in Marcha and Thiat, traditionally prepared amylolytic starters of India. Scientific Reports, 2017, 7, 10967.	1.6	48
64	Bacterial diversity and community structure of Western Indian Himalayan red kidney bean (Phaseolus) Tj ETQq0		
04		0.8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Overlock 10 1 46
65	Studies on biosurfactant from Oceanobacillus sp. BRI 10 isolated from Antarctic sea water. Desalination, 2013, 318, 64-71.	4.0	Overlock 10 1
	Studies on biosurfactant from Oceanobacillus sp. BRI 10 isolated from Antarctic sea water.	0.0	
65	Studies on biosurfactant from Oceanobacillus sp. BRI 10 isolated from Antarctic sea water. Desalination, 2013, 318, 64-71. Diversity of Yeasts and Molds by Culture-Dependent and Culture-Independent Methods for Mycobiome Surveillance of Traditionally Prepared Dried Starters for the Production of Indian Alcoholic	4.0	45
65	Studies on biosurfactant from Oceanobacillus sp. BRI 10 isolated from Antarctic sea water. Desalination, 2013, 318, 64-71. Diversity of Yeasts and Molds by Culture-Dependent and Culture-Independent Methods for Mycobiome Surveillance of Traditionally Prepared Dried Starters for the Production of Indian Alcoholic Beverages. Frontiers in Microbiology, 2018, 9, 2237. Phylogenetic Analysis of Methanogenic Enrichment Cultures Obtained from Lonar Lake in India:	4.0	45 45
65 66 67	Studies on biosurfactant from Oceanobacillus sp. BRI 10 isolated from Antarctic sea water. Desalination, 2013, 318, 64-71. Diversity of Yeasts and Molds by Culture-Dependent and Culture-Independent Methods for Mycobiome Surveillance of Traditionally Prepared Dried Starters for the Production of Indian Alcoholic Beverages. Frontiers in Microbiology, 2018, 9, 2237. Phylogenetic Analysis of Methanogenic Enrichment Cultures Obtained from Lonar Lake in India: Isolation of Methanocalculus sp. and Methanoculleus sp Microbial Ecology, 2007, 54, 697-704. Comparative analysis of midgut bacterial communities of Aedes aegypti mosquito strains varying in	4.0 1.5	45 45 44
65 66 67 68	Studies on biosurfactant from Oceanobacillus sp. BRI 10 isolated from Antarctic sea water. Desalination, 2013, 318, 64-71. Diversity of Yeasts and Molds by Culture-Dependent and Culture-Independent Methods for Mycobiome Surveillance of Traditionally Prepared Dried Starters for the Production of Indian Alcoholic Beverages. Frontiers in Microbiology, 2018, 9, 2237. Phylogenetic Analysis of Methanogenic Enrichment Cultures Obtained from Lonar Lake in India: Isolation of Methanocalculus sp. and Methanoculleus sp Microbial Ecology, 2007, 54, 697-704. Comparative analysis of midgut bacterial communities of Aedes aegypti mosquito strains varying in vector competence to dengue virus. Parasitology Research, 2013, 112, 2627-2637. Metabolite profiling for biomarkers in Schistosoma haematobium infection and associated bladder	4.0 1.5 1.4	45 45 44 44
65 66 67 68	Studies on biosurfactant from Oceanobacillus sp. BRI 10 isolated from Antarctic sea water. Desalination, 2013, 318, 64-71. Diversity of Yeasts and Molds by Culture-Dependent and Culture-Independent Methods for Mycobiome Surveillance of Traditionally Prepared Dried Starters for the Production of Indian Alcoholic Beverages. Frontiers in Microbiology, 2018, 9, 2237. Phylogenetic Analysis of Methanogenic Enrichment Cultures Obtained from Lonar Lake in India: Isolation of Methanocalculus sp. and Methanoculleus sp Microbial Ecology, 2007, 54, 697-704. Comparative analysis of midgut bacterial communities of Aedes aegypti mosquito strains varying in vector competence to dengue virus. Parasitology Research, 2013, 112, 2627-2637. Metabolite profiling for biomarkers in Schistosoma haematobium infection and associated bladder pathologies. PLoS Neglected Tropical Diseases, 2018, 12, e0006452. Bacterial diversity in different regions of gastrointestinal tract of <scp>G</scp> iant <scp>A</scp> frican <scp>S</scp> nail (<i>><scp>A</scp>chatina fulica</i>). MicrobiologyOpen, 2012, 1,	4.0 1.5 1.4 0.6	45 45 44 44

#	Article	IF	Citations
73	Molecular microbial diversity of a soil sample and detection of ammonia oxidizers from Cape Evans, Mcmurdo Dry Valley, Antarctica. Microbiological Research, 2007, 162, 15-25.	2.5	41
74	Purification and characterization of an extreme halothermophilic protease from a halophilic bacterium Chromohalobacter sp. TVSP101. Brazilian Journal of Microbiology, 2009, 40, 12-19.	0.8	41
75	Characterization and identification of <i>Geobacillus</i> spp. isolated from Soldhar hot spring site of Garhwal Himalaya, India. Journal of Basic Microbiology, 2009, 49, 187-194.	1.8	41
76	Restoration of dysbiotic human gut microbiome for homeostasis. Life Sciences, 2021, 278, 119622.	2.0	41
77	Technicalities and Glitches of Terminal Restriction Fragment Length Polymorphism (T-RFLP). Indian Journal of Microbiology, 2014, 54, 255-261.	1.5	40
78	Molecular typing of fecal eukaryotic microbiota of human infants and their respective mothers. Journal of Biosciences, 2012, 37, 221-226.	0.5	39
79	Microbial Culture Collection (MCC) and International Depositary Authority (IDA) at National Centre for Cell Science, Pune. Indian Journal of Microbiology, 2014, 54, 129-133.	1.5	39
80	World's Largest Mass Bathing Event Influences the Bacterial Communities of Godavari, a Holy River of India. Microbial Ecology, 2018, 76, 706-718.	1.4	39
81	Biodegradation of 2-Nitrotoluene by Micrococcus sp. strain SMN-1. Biodegradation, 2011, 22, 95-102.	1.5	38
82	Evaluation of Probiotic Characteristics of Siderophoregenic Bacillus spp. Isolated from Dairy Waste. Applied Biochemistry and Biotechnology, 2010, 160, 140-155.	1.4	37
83	Surface Engineering of Polycaprolactone by Biomacromolecules and their Blood Compatibility. Journal of Biomaterials Applications, 2011, 26, 227-252.	1.2	37
84	Biodegradation of tributyl phosphate by novel bacteria isolated from enrichment cultures. Biodegradation, 2012, 23, 165-176.	1.5	37
85	A cross-sectional comparative study of gut bacterial community of Indian and Finnish children. Scientific Reports, 2017, 7, 10555.	1.6	37
86	Effect of repeated <i>in vitro </i> sub-culturing on the virulence of <i>Metarhizium anisopliae </i> equivalence and Technology, 2008, 18, 337-355.	0.5	36
87	Phylogenetic diversity of archaeal 16S rRNA and ammonia monooxygenase genes from tropical estuarine sediments on the central west coast of India. Research in Microbiology, 2010, 161, 177-186.	1.0	36
88	Changes in human gut flora with age: an Indian familial study. BMC Microbiology, 2012, 12, 222.	1.3	36
89	Implication of Arthrobacter and Enterobacter species for polycarbonate degradation. International Biodeterioration and Biodegradation, 2008, 61, 167-172.	1.9	35
90	Life in (and on) the rocks. Journal of Biosciences, 2012, 37, 3-11.	0.5	35

#	Article	IF	Citations
91	Salivary gland transcriptome analysis during Plasmodium infection in malaria vector Anopheles stephensi. International Journal of Infectious Diseases, 2009, 13, 636-646.	1.5	34
92	A Physical Map for an Asian Malaria Mosquito, Anopheles stephensi. American Journal of Tropical Medicine and Hygiene, 2010, 83, 1023-1027.	0.6	34
93	Determination of Wolbachia Diversity in Butterflies from Western Ghats, India, by a Multigene Approach. Applied and Environmental Microbiology, 2012, 78, 4458-4467.	1.4	34
94	Microbulbifer mangrovi sp. nov., a polysaccharide-degrading bacterium isolated from an Indian mangrove. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 2532-2537.	0.8	34
95	DNA barcoding reveals unprecedented diversity in Dancing Frogs of India (Micrixalidae, Micrixalus): a taxonomic revision with description of 14 new species. Ceylon Journal of Science (Biological) Tj ETQq1 1 0.7843	14ogBT/C	vestock 10 T
96	Degradation of a Plasticizer, di-n-Butylphthalate by Delftia sp. TBKNP-05. Current Microbiology, 2006, 52, 225-230.	1.0	32
97	A new endophytic species of Arthrinium (Apiosporaceae) from Jatropha podagrica. Mycoscience, 2014, 55, 118-123.	0.3	32
98	Sequence analysis of mitochondrial 16S ribosomal RNA gene fragment from seven mosquito species. Journal of Biosciences, 2000, 25, 361-366.	0.5	29
99	Biodegradation of Carbofuran phenol by free and immobilized cells of Klebsiella pneumoniae ATCC13883T. World Journal of Microbiology and Biotechnology, 2011, 27, 25-29.	1.7	29
100	Declination of Copper Toxicity in Pigeon Pea and Soil System by Growth-Promoting Proteus vulgaris KNP3 Strain. Current Microbiology, 2008, 57, 78-82.	1.0	28
101	Cold Stress and Nitrogen Deficiency Affected Protein Expression of Psychrotrophic Dyadobacter psychrophilus B2 and Pseudomonas jessenii MP1. Frontiers in Microbiology, 2017, 8, 430.	1.5	28
102	Psychrophilic Pseudomonas helmanticensis proteome under simulated cold stress. Cell Stress and Chaperones, 2020, 25, 1025-1032.	1.2	28
103	Genomic and functional features of the biosurfactant producing Bacillus sp. AM13. Functional and Integrative Genomics, 2016, 16, 557-566.	1.4	27
104	Molecular evidence and phylogenetic affiliations of Wolbachia in cockroachesâ~†. Molecular Phylogenetics and Evolution, 2007, 44, 1346-1351.	1.2	26
105	Insights into Diversity and Imputed Metabolic Potential of Bacterial Communities in the Continental Shelf of Agatti Island. PLoS ONE, 2015, 10, e0129864.	1.1	26
106	Molecular systematics of caeciliid caecilians (Amphibia: Gymnophiona) of the Western Ghats, India. Molecular Phylogenetics and Evolution, 2011, 59, 698-707.	1.2	24
107	Diversified diazotrophs associated with the rhizosphere of Western Indian Himalayan native red kidney beans (Phaseolus vulgaris L.). 3 Biotech, 2015, 5, 433-441.	1.1	24
108	Frankixalus, a New Rhacophorid Genus of Tree Hole Breeding Frogs with Oophagous Tadpoles. PLoS ONE, 2016, 11, e0145727.	1.1	24

#	Article	IF	Citations
109	Cultivable Microbial Diversity Associated With Cellular Phones. Frontiers in Microbiology, 2018, 9, 1229.	1.5	24
110	Description of Two New Cathepsin C Gene Mutations in Patients With Papillon-Lefà vre Syndrome. Journal of Periodontology, 2006, 77, 233-237.	1.7	23
111	Comparison of <i>Metarhizium</i> isolates for biocontrol of <i>Helicoverpa armigera</i> (Lepidoptera:) Tj ETQq1 1	0,784314	4 rgBT /Oved
112	Temporal bacterial diversity and detection of putative methanotrophs in surface mats of Lonar crater lake. Journal of Basic Microbiology, 2010, 50, 465-474.	1.8	23
113	Antimicrobial resistance dynamics andÂthe one-healthÂstrategy: a review. Environmental Chemistry Letters, 2021, 19, 2995-3007.	8.3	23
114	Molecular analyses of methanogen diversity associated with cattle dung. World Journal of Microbiology and Biotechnology, 2008, 24, 2973-2979.	1.7	22
115	Characterization of Microbulbifer Strain CMC-5, a New Biochemical Variant of Microbulbifer elongatus Type Strain DSM6810T Isolated from Decomposing Seaweeds. Current Microbiology, 2009, 59, 600-607.	1.0	22
116	<i>In vivo</i> modulation of foreign body response on polyurethane by surface entrapment technique. Journal of Biomedical Materials Research - Part A, 2010, 95A, 413-423.	2.1	22
117	Diversity of Wolbachiaâ€fin Odontotermesâ€fspp. (Termitidae) and Coptotermes heimiâ€f (Rhinotermitidae) using the multigene approach. FEMS Microbiology Letters, 2010, 307, 55-64.	0.7	22
118	Dynamics of midgut microflora and dengue virus impact on life history traits in Aedes aegypti. Acta Tropica, 2014, 140, 151-157.	0.9	22
119	MicFunPred: A conserved approach to predict functional profiles from 16S rRNA gene sequence data. Genomics, 2021, 113, 3635-3643.	1.3	22
120	Corynebacterium godavarianum sp. nov., isolated from the Godavari river, India. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 241-247.	0.8	22
121	The biocompatibility of sulfobetaine engineered polymethylmethacrylate by surface entrapment technique. Journal of Materials Science: Materials in Medicine, 2010, 21, 635-646.	1.7	21
122	Lactobacillus plantarum (VR1) isolated from an Ayurvedic medicine (Kutajarista) ameliorates in vitro cellular damage caused by Aeromonas veronii. BMC Microbiology, 2011, 11, 152.	1.3	21
123	DNA barcoding of nymphalid butterflies (Nymphalidae: Lepidoptera) from Western Ghats of India. Molecular Biology Reports, 2012, 39, 2375-2383.	1.0	21
124	In vitro antibacterial activity of Tabernaemontana alternifolia (Roxb) stem bark aqueous extracts against clinical isolates of methicillin resistant Staphylococcus aureus. Annals of Clinical Microbiology and Antimicrobials, 2013, 12, 26.	1.7	21
125	DNA barcoding of Pentatomomorpha bugs (Hemiptera: Heteroptera) from Western Ghats of India. Meta Gene, 2014, 2, 737-745.	0.3	21
126	Genome sequencing analysis reveals virulence-related gene content of <i>Ochrobactrum intermedium </i> strain 229E, a urease-positive strain isolated from the human gastric niche. FEMS Microbiology Letters, 2014, 359, 12-15.	0.7	21

#	Article	IF	Citations
127	Fictibacillus enclensis sp. nov., isolated from marine sediment. Antonie Van Leeuwenhoek, 2014, 105, 461-469.	0.7	21
128	Biomineralization Potential of <i>Bacillus subtilis, Rummeliibacillus Stabekisii</i> and <i>Staphylococcus Epidermidis</i> Strains <i>In Vitro</i> Isolated from Speleothems, Khasi Hill Caves, Meghalaya, India. Geomicrobiology Journal, 2018, 35, 675-694.	1.0	21
129	Genomic and physiological analyses of an indigenous strain, Enterococcus faecium 17OM39. Functional and Integrative Genomics, 2018, 18, 385-399.	1.4	21
130	Pea (Pisum sativum I.) Plant Shapes Its Rhizosphere Microbiome for Nutrient Uptake and Stress Amelioration in Acidic Soils of the North-East Region of India. Frontiers in Microbiology, 2020, 11, 968.	1.5	21
131	Factors influencing the gut microbiome in children: from infancy to childhood. Journal of Biosciences, 2019, 44, .	0.5	21
132	Molecular Characterization of Prokaryotic Communities Associated with Lonar Crater Basalts. Geomicrobiology Journal, 2014, 31, 519-528.	1.0	20
133	Enterobacillus tribolii gen. nov., sp. nov., a novel member of the family Enterobacteriaceae, isolated from the gut of a red flour beetle, Tribolium castaneum. Antonie Van Leeuwenhoek, 2015, 107, 1207-1216.	0.7	20
134	Enhanced Detoxification of Arsenic Under Carbon Starvation: A New Insight into Microbial Arsenic Physiology. Current Microbiology, 2017, 74, 614-622.	1.0	20
135	Draft Genome Sequences of Two Phytoplasma Strains Associated with Sugarcane Grassy Shoot (SCGS) and Bermuda Grass White Leaf (BGWL) Diseases. Molecular Plant-Microbe Interactions, 2020, 33, 715-717.	1.4	20
136	Recognition of B and Z forms of DNA by Escherichia coli DNA polymerase I. Journal of Molecular Biology, 1986, 190, 635-638.	2.0	19
137	Isolation and characterization of sulphate-reducing bacteria Desulfovibrio vulgaris from Vajreshwari thermal springs in Maharashtra, India. World Journal of Microbiology and Biotechnology, 2008, 24, 681-685.	1.7	19
138	Isolation of urease-positive Ochrobactrum intermedium in the stomach of a non-ulcer dyspeptic patient from north India. Journal of Microbiology, Immunology and Infection, 2008, 41, 183-6.	1.5	19
139	Helicobacter pylori in areas of gastric metaplasia in the gallbladder and isolation of H. pylori DNA from gallstones. Pathology, 2007, 39, 419-424.	0.3	18
140	TecoflexTM functionalization by curdlan and its effect on protein adsorption and bacterial and tissue cell adhesion. Journal of Materials Science: Materials in Medicine, 2009, 20, 1115-1129.	1.7	18
141	Biodegradation of 4-chlorobenzoic acid by Pseudomonas aeruginosa PA01 NC. Biodegradation, 2011, 22, 509-516.	1.5	18
142	Influence of endophytic fungal elicitation on production of inophyllum in suspension cultures of Calophyllum inophyllum L Plant Cell, Tissue and Organ Culture, 2011, 106, 345-352.	1.2	18
143	Draft genome of Ochrobactrum intermedium strain M86 isolated from non-ulcer dyspeptic individual from India. Gut Pathogens, 2013, 5, 7.	1.6	18
144	Conserved boundary elements from the Hox complex of mosquito, Anopheles gambiae. Nucleic Acids Research, 2013, 41, 804-816.	6.5	18

#	Article	IF	CITATIONS
145	Association of 16SrII-C and 16SrII-D subgroup phytoplasma strains with witches' broom disease of Parthenium hysterophorus and insect vector Orosius albicinctus in India. Australasian Plant Disease Notes, 2015, 10, 1.	0.4	18
146	Functional eubacteria species along with trans-domain gut inhabitants favour dysgenic diversity in oxalate stone disease. Scientific Reports, 2018, 8, 16598.	1.6	18
147	Secretor Status Is Strongly Associated with Microbial Alterations Observed during Pregnancy. PLoS ONE, 2015, 10, e0134623.	1.1	18
148	Subsaxibacter sediminis sp. nov., isolated from Arctic glacial sediment and emended description of the genus Subsaxibacter. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1678-1682.	0.8	17
149	Novel methanotroph diversity evidenced by molecular characterization of particulate methane monooxygenase A (pmoA) genes in a biogas reactor. Microbiological Research, 2009, 164, 536-544.	2.5	16
150	Alishewanella solinquinati sp. nov., Isolated from Soil Contaminated with Textile Dyes. Current Microbiology, 2013, 67, 454-459.	1.0	16
151	<p>Distribution of Pathogenic Yeasts in Different Clinical Samples: Their Identification, Antifungal Susceptibility Pattern, and Cell Invasion Assays</p> . Infection and Drug Resistance, 2020, Volume 13, 1133-1145.	1.1	16
152	Natrialba swarupiae sp. nov., a halophilic archaeon isolated from a hypersaline lake in India. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1876-1881.	0.8	16
153	Characterization of novel extracellular protease produced by marine bacterial isolate from the Indian Ocean. Brazilian Journal of Microbiology, 2011, 42, 1364-73.	0.8	16
154	Isolation, Identification and Optimization of a New Extracellular Lipase Producing Strain of Rhizopus sp Applied Biochemistry and Biotechnology, 2011, 164, 969-978.	1.4	15
155	A Variant Quorum Sensing System in Aeromonas veronii MTCC 3249. Sensors, 2012, 12, 3814-3830.	2.1	15
156	Human mitochondrial NDUFS3 protein bearing Leigh syndrome mutation is more prone to aggregation than its wild-type. Biochimie, 2013, 95, 2392-2403.	1.3	15
157	Microbial diversity of the Soldhar hot spring, India, assessed by analyzing 16S rRNA and protein-coding genes. Annals of Microbiology, 2015, 65, 1323-1332.	1.1	15
158	Draft genome sequence of Lactobacillus plantarum strains E2C2 and E2C5 isolated from human stool culture. Standards in Genomic Sciences, 2017, 12, 15.	1.5	15
159	Mining the Core Gut Microbiome from a Sample Indian Population. Indian Journal of Microbiology, 2019, 59, 90-95.	1.5	15
160	Comparative overview of red kidney bean (Phaseolus valgaris) rhizospheric bacterial diversity in perspective of altitudinal variations. Biologia (Poland), 2019, 74, 1405-1413.	0.8	15
161	Characterization of Insect Cell Lines: Heteroduplex Analysis Employing a Mitochondrial 16S Ribosomal RNA Gene Fragment. Analytical Biochemistry, 1997, 253, 65-69.	1.1	14
162	Microbiology of the insect gut: tales from mosquitoes and bees. Journal of Biosciences, 2006, 31, 293-295.	0.5	14

#	Article	IF	CITATIONS
163	Analysis of Mitochondrial DNA Sequences in Childhood Encephalomyopathies Reveals New Disease-Associated Variants. PLoS ONE, 2007, 2, e942.	1.1	14
164	Biochemical characterization of three putative ATPases from a new type IV secretion system of Aeromonas veronii plasmid pAC3249A. BMC Biochemistry, 2010, 11, 10.	4.4	14
165	Bacillus enclensis sp. nov., isolated from sediment sample. Antonie Van Leeuwenhoek, 2014, 105, 199-206.	0.7	14
166	Distribution and Evolutionary Impact of Wolbachia on Butterfly Hosts. Indian Journal of Microbiology, 2014, 54, 249-254.	1.5	14
167	Geochemistry Shapes Bacterial Communities and their Metabolic Potentials in Tertiary Coalbed. Geomicrobiology Journal, 2019, 36, 179-187.	1.0	14
168	Detection of Conjugation Related Type Four Secretion Machinery in Aeromonas culicicola. PLoS ONE, 2006, 1, e115.	1.1	13
169	Molecular and phylogenetic analysis of a novel salivary defensin cDNA from malaria vector Anopheles stephensi. Acta Tropica, 2008, 106, 75-79.	0.9	13
170	A new endophytic species of <i>Chaetomium</i> from <i>Jatropha podagrica</i> . Mycotaxon, 2013, 124, 117-126.	0.1	13
171	DIVERSITY IN GUT MICROFLORA OF <i>Helicoverpa armigera</i> POPULATIONS FROM DIFFERENT REGIONS IN RELATION TO BIOLOGICAL ACTIVITY OF <i>Bacillus thuringiensis</i> δâ€ENDOTOXIN Cry1Ac. Archives of Insect Biochemistry and Physiology, 2014, 87, 201-213.	0.6	13
172	Chemotaxis and physiological adaptation of an indigenous abiotic stress tolerant plant growth promoting Pseudomonas stutzeri: Amelioration of salt stress to Cicer arietinum. Biocatalysis and Agricultural Biotechnology, 2020, 27, 101652.	1.5	13
173	Cloning of two hexokinase isoenzyme sequences from Drosophila melanogaster. Insect Biochemistry and Molecular Biology, 2001, 31, 1165-1171.	1.2	12
174	The Biocompatibility of Sulfobetaine Engineered Poly (Ethylene Terephthalate) by Surface Entrapment Technique. Journal of Biomaterials Applications, 2010, 25, 119-143.	1.2	12
175	Bacillus filamentosus sp. nov., isolated from sediment sample. Antonie Van Leeuwenhoek, 2015, 107, 433-441.	0.7	12
176	A new species of <i>Scytonema</i> isolated from Bilaspur, Chhattisgarh, India. Journal of Systematics and Evolution, 2016, 54, 519-527.	1.6	12
177	Multilocus sequence typing of Ochrobactrum spp. isolated from gastric niche. Journal of Infection and Public Health, 2017, 10, 201-210.	1.9	12
178	Cultivation of Diverse Microorganisms from Hypersaline Lake and Impact of Delay in Sample Processing on Cell Viability. Current Microbiology, 2020, 77, 716-721.	1.0	12
179	Taxonomic profiling of bacterial community structure from coastal sediment of Alang–Sosiya shipbreaking yard near Bhavnagar, India. Marine Pollution Bulletin, 2015, 101, 736-745.	2.3	11
180	Mossambicus tilapia (Oreochromis mossambicus) collected from water bodies impacted by urban waste carries extended-spectrum beta-lactamases and integron-bearing gut bacteria. Journal of Biosciences, 2016, 41, 341-346.	0.5	11

#	Article	IF	Citations
181	Selection of potential bacterial strains to develop bacterial consortia for the remediation of e-waste and its in situ implications. Waste Management, 2018, 79, 526-536.	3.7	11
182	Understanding the association between the human gut, oral and skin microbiome and the Ayurvedic concept of prakriti. Journal of Biosciences, 2019, 44, 1.	0.5	11
183	Human gut-derived commensal suppresses generation of T-cell response to gliadin in humanized mice by modulating gut microbiota. Anaerobe, 2021, 68, 102237.	1.0	11
184	Extended Ecological Restoration of Bacterial Communities in the Godavari River During the COVID-19 Lockdown Period: a Spatiotemporal Meta-analysis. Microbial Ecology, 2021, 82, 365-376.	1.4	11
185	Bhargavaea indica sp. nov., a member of the phylum Firmicutes, isolated from Arabian Sea sediment. Journal of Microbiology, 2013, 51, 36-42.	1.3	10
186	Draft Genome Sequences of Yersinia pestis Strains from the 1994 Plague Epidemic of Surat and 2002 Shimla Outbreak in India. Indian Journal of Microbiology, 2014, 54, 480-482.	1.5	10
187	Efficacy of DNA barcoding for the species identification of spiders from Western Ghats of India. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2017, 28, 638-644.	0.7	10
188	Deep Sequencing Reveals Highly Variable Gut Microbial Composition of Invasive Fish Mossambicus Tilapia (Oreochromis mossambicus) Collected from Two Different Habitats. Indian Journal of Microbiology, 2017, 57, 235-240.	1.5	10
189	Traversing the "Omic―landscape of microbial halotolerance for key molecular processes and new insights. Critical Reviews in Microbiology, 2020, 46, 631-653.	2.7	10
190	Bacterial Communities Associated with the Biofilms Formed in High-Altitude Brackish Water PangongÂTso Located in the Himalayan Plateau. Current Microbiology, 2020, 77, 4072-4084.	1.0	10
191	Probing of unusual DNA structures in topologically constrained form V DNA: use of restriction enzymes as structural probe. Nucleic Acids Research, 1990, 18, 267-275.	6.5	9
192	Molecular and phylogenetic analysis of a novel family of fibrinogen-related proteins from mosquito Aedes albopictus cell line. Computational Biology and Chemistry, 2008, 32, 382-386.	1.1	9
193	Ĵμ-Caprolactam Utilization by Proteus sp. and Bordetella sp. Isolated From Solid Waste Dumpsites in Lagos State, Nigeria, First Report. Indian Journal of Microbiology, 2013, 53, 221-226.	1.5	9
194	Deinococcus enclensis sp. nov., isolated from a marine sediment sample. Antonie Van Leeuwenhoek, 2015, 107, 141-148.	0.7	9
195	Superoxide Dismutase 2 Polymorphisms and Osteoporosis in Asian Indians: A Genetic Association Analysis. Cellular and Molecular Biology Letters, 2015, 20, 685-97.	2.7	9
196	Comparative analysis of midgut bacterial communities in three aedine mosquito species from dengueâ€endemic and nonâ€endemic areas ofRajasthan,India. Medical and Veterinary Entomology, 2016, 30, 264-277.	0.7	9
197	Taxonomic description and draft genome of Pseudomonas sediminis sp. nov., isolated from the rhizospheric sediment of Phragmites karka. Journal of Microbiology, 2018, 56, 458-466.	1.3	9
198	Disruptions in oral and nasal microbiota in biomass and tobacco smoke associated chronic obstructive pulmonary disease. Archives of Microbiology, 2021, 203, 2087-2099.	1.0	9

#	Article	IF	CITATIONS
199	Limited Bacterial Diversity within a Treatment Plant Receiving Antibiotic-Containing Waste from Bulk Drug Production. PLoS ONE, 2016, 11, e0165914.	1.1	9
200	The Selenophosphate Synthetase Gene from Leishmania major. DNA Sequence, 2004, 15, 66-70.	0.7	8
201	Generation, annotation, and analysis of ESTs from midgut tissue of adult female Anopheles stephensi mosquitoes. BMC Genomics, 2009, 10, 386.	1.2	8
202	Optimization of Nutrients and Culture Conditions for Alkaline Protease Production Using Two Endophytic Micrococci: Micrococcus aloeverae and Micrococcus yunnanensis. Indian Journal of Microbiology, 2017, 57, 218-225.	1.5	8
203	Characterization of <i>Solibacillus silvestris</i> strain AM1 that produces amyloid bioemulsifier. Journal of Basic Microbiology, 2018, 58, 523-531.	1.8	8
204	Antimicrobial resistance pattern of microorganisms isolated and identified from Godavari River across the mass gathering event. Journal of Biosciences, 2019, 44, 1.	0.5	8
205	Contrasting Composition, Diversity and Predictive Metabolic Potential of the Rhizobacterial Microbiomes Associated with Native and Invasive Prosopis Congeners. Current Microbiology, 2021, 78, 2051-2060.	1.0	8
206	Chakrabartia godavariana gen. nov., sp. nov., a novel member of the family Sphingomonadaceae isolated from the Godavari River, India. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2452-2458.	0.8	8
207	Characterization of leptospira borgpetersenii isolates from field rats (rattus norvegicus) by 16s rrna and lipl32 gene sequencing. Brazilian Journal of Microbiology, 2010, 41, 150-7.	0.8	8
208	Analysis of reactive oxygen species and antioxidant defenses in complex I deficient patients revealed a specific increase in superoxide dismutase activity. Free Radical Research, 2008, 42, 415-427.	1.5	7
209	Carl Woese: from Biophysics to Evolutionary Microbiology. Indian Journal of Microbiology, 2013, 53, 247-252.	1.5	7
210	Response of cellular fatty acids to environmental stresses in endophytic Micrococcus spp Annals of Microbiology, 2015, 65, 2209-2218.	1.1	7
211	Selection of poly(R)-3-hydroxybutyric acid utilising bacteria by enrichment, optimisation and compatibility testing for consortia development. Chemistry and Ecology, 2016, 32, 583-597.	0.6	7
212	Diversity of Onygenalean Fungi in Keratin-Rich Habitats of Maharashtra (India) and Description of Three Novel Taxa. Mycopathologia, 2019, 185, 67-85.	1.3	7
213	New approaches for antituberculosis leads from Actinobacteria. Drug Discovery Today, 2020, 25, 2335-2342.	3.2	7
214	Gut microbial diversity during pregnancy and early infancy: an exploratory study in the Indian population. FEMS Microbiology Letters, 2020, 367, .	0.7	7
215	Benchmarking of 16S rRNA gene databases using known strain sequences. Bioinformation, 2021, 17, 377-391.	0.2	7
216	Sequence analysis of a few species of termites (Order: Isoptera) on the basis of partial characterization of COII gene. Molecular and Cellular Biochemistry, 2009, 331, 145-151.	1.4	6

#	Article	IF	CITATIONS
217	Wolbachia and termite association: present status and future implications. Journal of Biosciences, 2010, 35, 171-175.	0.5	6
218	Response of Haloalkaliphilic Archaeon Natronococcus Jeotgali RR17 to Hypergravity. Microgravity Science and Technology, 2017, 29, 191-200.	0.7	6
219	A new species of Scytonema isolated from Bilaspur, Chhattisgarh, India using the polyphasic approach. Plant Systematics and Evolution, 2017, 303, 249-258.	0.3	6
220	Range extension of Ferguson's Toad Duttaphrynus scaber (Schneider) (Amphibia: Anura: Bufonidae) up to the northern most limit of Western Ghats, with its advertisement call analysis. Journal of Threatened Taxa, 2013, 5, 4579-4585.	0.1	6
221	Isolation and characterization of Vagococcus sp from midgut of Culex quinquefasciatus (Say) mosquito. Journal of Vector Borne Diseases, 2015, 52, 52-7.	0.1	6
222	Understanding the association between the human gut, oral and skin microbiome and the Ayurvedic concept of prakriti. Journal of Biosciences, 2019, 44, .	0.5	6
223	Antimicrobial resistance pattern of microorganisms isolated and identified from Godavari River across the mass gathering event. Journal of Biosciences, 2019, 44, .	0.5	6
224	Microbial Community Structure at Different Fermentation Stages of Kutajarista, a Herbal Formulation. Indian Journal of Microbiology, 2013, 53, 11-17.	1.5	5
225	Genome sequencing of multidrug resistant novel Clostridium sp. BL8 reveals its potential for pathogenicity. Gut Pathogens, 2014, 6, 30.	1.6	5
226	Potential of Health and Demographic Surveillance System in Asthma and Chronic Obstructive Pulmonary Disease Microbiome Research. Frontiers in Public Health, 2017, 5, 196.	1.3	5
227	A Microcosm Model for the Study of Microbial Community Shift and Carbon Emission from Landfills. Indian Journal of Microbiology, 2022, 62, 195-203.	1.5	5
228	Analysis of 16S-23S Intergenic Spacer Regions andrrnOperon Copy Number ofAeromonas culicicolaMTCC 3249T. DNA Sequence, 2003, 14, 183-194.	0.7	4
229	Nonspecific PCR Amplification of the 16S rRNA Gene Segment in Different Bacteria by Use of Primers Specific for Campylobacter, Arcobacter, and Helicobacter spp. Journal of Clinical Microbiology, 2007, 45, 1376-1377.	1.8	4
230	Identification of putative innate immune related genes from a cell line of the mosquito Aedes albopictus following bacterial challenge. Innate Immunity, 2011, 17, 106-117.	1.1	4
231	Bacterial Diversity in the Metal-Rich Terrestrial Deep Subsurface Sediments of Krishna Godavari Basin, India. Geomicrobiology Journal, 2019, 36, 917-932.	1.0	4
232	Survey of Probiotic Preparations and Labeling Practices in Indian Market. Indian Journal of Medical Microbiology, 2018, 36, 116-119.	0.3	4
233	A comprehensive appraisal of evolutionary diversity in venomous Asian coralsnakes of the genus <i>Sinomicrurus</i> (Serpentes: Elapidae) using Bayesian coalescent inference and supervised machine learning. Journal of Zoological Systematics and Evolutionary Research, 2021, 59, 2212-2277.	0.6	4
234	Two-Dimensional Cell Separation: a High-Throughput Approach to Enhance the Culturability of Bacterial Cells from Environmental Samples. Microbiology Spectrum, 2022, 10, e0000722.	1,2	4

#	Article	IF	CITATIONS
235	PCR-SSCP and sequence analysis of three Odontotermes spp. (Order: Isoptera; Family: Termitidae) on the basis of partial 16SrRNA gene. Molecular and Cellular Biochemistry, 2009, 330, 153-162.	1.4	3
236	<i>Pseudofusicoccum adansoniae</i> isolated as an endophyte from <i>Jatropha podagrica:</i> new record for India. Mycotaxon, 2013, 123, 39-45.	0.1	3
237	Antibiotic susceptibility of human gut-derived facultative anaerobic bacteria is different under aerobic versus anaerobic test conditions. Microbes and Infection, 2021, 23, 104847.	1.0	3
238	Whole genome sequence of colistin-resistant Escherichia coli from western India. Medical Journal Armed Forces India, 2021, 77, 297-301.	0.3	3
239	Recent trend, biases and limitations of cultivation-based diversity studies of microbes. FEMS Microbiology Letters, 2021, 368, .	0.7	3
240	Insect cell line authentication by denaturing gradient gel electrophoresis. In Vitro Cellular and Developmental Biology - Animal, 1998, 34, 665-667.	0.7	2
241	Phylogenetic profiling of bacterial community from two intimately located sites in Balramgari, North-East coast of India. Indian Journal of Microbiology, 2009, 49, 169-187.	1.5	2
242	Transcriptome analysis of Anopheles stephensi embryo using expressed sequence tags. Journal of Biosciences, 2013, 38, 301-309.	0.5	2
243	Laboratory maintained and wild populations of Hydra differ in their microbiota. Annals of Microbiology, 2016, 66, 931-935.	1.1	2
244	Rectal administration of buttermilk processed with medicinal plants alters gut microbiome in obese individuals. Journal of Diabetes and Metabolic Disorders, 2021, 20, 1415-1427.	0.8	2
245	Manipulation and Assessment of Gut Microbiome for Metabolic Studies. Methods in Molecular Biology, 2014, 1194, 449-469.	0.4	2
246	Assessment of Airborne Microbial Community in Indian Cities during the Middle East Dust Storm. Current Science, 2019, 117, 1693.	0.4	2
247	Partial genomic organization of ribosomal protein S7 gene from malaria vector Anopheles stephensi. Insect Science, 2007, 14, 101-106.	1.5	1
248	New record of <l>Scedosporium</l> <l>dehoogii</l> from India. Mycotaxon, 2013, 124, 239-245.	0.1	1
249	IP and The Budapest Treatyâ€"Depositing Biological Material for Patent Purposes. , 2017, , 275-292.		1
250	Data on genome sequencing, assembly, annotation and genomic analysis of Rhodococcus rhodochrous strain SPC17 isolated from Lonar Lake. Data in Brief, 2020, 29, 105336.	0.5	1
251	Probiotics: A Mainstream Therapy for the Disease Suppression. , 2022, , 257-257.		1
252	Importance of Vision, Visibility and Viability of Microbial Resource Centres. Current Science, 2020, 119, 625.	0.4	1

#	Article	IF	CITATIONS
253	Natronococcus pandeyae sp. nov., a Novel Haloarchaeon from Sambhar Salt Lake. Current Microbiology, 2022, 79, 51.	1.0	1
254	Understanding Anopheles and Plasmodium interactions: lessons from the real world. Journal of Biosciences, 2007, 32, 1045-1047.	0.5	0
255	Mining Human Microbiome for Therapeutics. , 2019, , 573-613.		O
256	Integrated Genomic and Functional Characterization of the Anti-diabetic Potential of Arthrobacter sp. SW1. Current Microbiology, 2021, 78, 2577-2588.	1.0	0
257	Need to Explore Camel Milk as Probiotics. Current Science, 2018, 114, 425.	0.4	0
258	Surveillance of Root-associated Microbiome of Oxalogenic Colocasia esculenta (Linn) Plant Reveals Distinct Bacterial Species Diversity. Journal of Pure and Applied Microbiology, 2020, 14, 547-557.	0.3	0