

Prabhu B Patil

List of Publications by Year in descending order

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63
papers

2,713
citations

304602

22
h-index

197736

49
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73
all docs

73
docs citations

73
times ranked

3123
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylo-Taxonogenomics Supports Revision of Taxonomic Status of <i>Xanthomonas</i> Pathovars to <i>Xanthomonas citri</i> . <i>Phytopathology</i> , 2022, 112, 1201-1207.	1.1	9
2	Novel insights into the role of the mobilome in ecological diversification and success of <i>Staphylococcus haemolyticus</i> as an opportunistic pathogen. <i>Microbial Genomics</i> , 2022, 8, .	1.0	1
3	Genomic data resource of type strains of genus <i>Pseudoxanthomonas</i> . <i>Data in Brief</i> , 2022, 42, 108145.	0.5	5
4	Discerning the role of a functional arsenic-resistance cassette in the evolution and adaptation of a rice pathogen. <i>Microbial Genomics</i> , 2021, 7, .	1.0	1
5	Global transcriptome analysis of <i>Stenotrophomonas maltophilia</i> in response to growth at human body temperature. <i>Microbial Genomics</i> , 2021, 7, .	1.0	4
6	<i>Xanthomonas sontii</i> sp. nov., a non-pathogenic bacterium isolated from healthy basmati rice (<i>Oryza</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf .	0.7	22
7	Genome of <i>Bifidobacterium longum</i> NCIM 5672 provides insights into its acid-tolerance mechanism and probiotic properties. <i>Archives of Microbiology</i> , 2021, 203, 6109-6118.	1.0	9
8	Bacteriocin isolated from the natural inhabitant of <i>Allium cepa</i> against <i>Staphylococcus aureus</i> . <i>World Journal of Microbiology and Biotechnology</i> , 2021, 37, 20.	1.7	11
9	Deep phylo-taxono genomics reveals <i>Xylella</i> as a variant lineage of plant associated <i>Xanthomonas</i> and supports their taxonomic reunification along with <i>Stenotrophomonas</i> and <i>Pseudoxanthomonas</i> . <i>Genomics</i> , 2021, 113, 3989-4003.	1.3	17
10	Bacterial Populations in Subgingival Plaque Under Healthy and Diseased Conditions: Genomic Insights into Oral Adaptation Strategies by <i>Lactobacillus</i> sp. Strain DISK7. <i>Indian Journal of Microbiology</i> , 2020, 60, 78-86.	1.5	5
11	Evolutionary insights into adaptation of <i>Staphylococcus haemolyticus</i> to human and non-human niches. <i>Genomics</i> , 2020, 112, 2052-2062.	1.3	13
12	Phylogenomic Insights into Diversity and Evolution of Nonpathogenic <i>Xanthomonas</i> Strains Associated with Citrus. <i>MSphere</i> , 2020, 5, .	1.3	18
13	Exploring the Interplay of Resistance Nodulation Division Efflux Pumps, <i>Amp</i> C and <i>Opr</i> D in Antimicrobial Resistance of <i>Burkholderia cepacia</i> Complex in Clinical Isolates. <i>Microbial Drug Resistance</i> , 2020, 26, 1144-1152.	0.9	6
14	Surfactin Like Broad Spectrum Antimicrobial Lipopeptide Co-produced With Sublancin From <i>Bacillus subtilis</i> Strain A52: Dual Reservoir of Bioactives. <i>Frontiers in Microbiology</i> , 2020, 11, 1167.	1.5	26
15	Genomic insights into evolution of extensive drug resistance in <i>Stenotrophomonas maltophilia</i> complex. <i>Genomics</i> , 2020, 112, 4171-4178.	1.3	14
16	Extensive Genomic Rearrangements along with Distinct Mobilome and TALome are Associated with Extreme Pathotypes of a Rice Pathogen. <i>Genome Biology and Evolution</i> , 2020, 12, 3951-3956.	1.1	2
17	Molecular epidemiology of carbapenem-resistant <i>Acinetobacter baumannii</i> isolates reveals the emergence of blaOXA-23 and blaNDM-1 encoding international clones in India. <i>Infection, Genetics and Evolution</i> , 2019, 75, 103986.	1.0	26
18	Phylogenomics insights into order and families of Lysobacterales. <i>Access Microbiology</i> , 2019, 1, e000015.	0.2	22

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19	Complete genome dynamics of a dominant-lineage strain of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> harbouring a novel plasmid encoding a type IV secretion system. <i>Access Microbiology</i> , 2019, 1, e000063.	0.2	13
20	<i>Clostridium indicum</i> sp. nov., a novel anaerobic bacterium isolated from the sludge of an industrial effluent. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 672-678.	0.8	7
21	Purification, Characterization and in vitro Evaluation of Polymyxin A From <i>Paenibacillus dendritiformis</i> : An Underexplored Member of the Polymyxin Family. <i>Frontiers in Microbiology</i> , 2018, 9, 2864.	1.5	14
22	A Strain of an Emerging Indian <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Pathotype Defeats the Rice Bacterial Blight Resistance Gene xa13 Without Inducing a Clade III SWEET Gene and Is Nearly Identical to a Recent Thai Isolate. <i>Frontiers in Microbiology</i> , 2018, 9, 2703.	1.5	17
23	Complete genome sequence reveals evolutionary dynamics of an emerging and variant pathovar of <i>Xanthomonas euvesicatoria</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 3104-3109.	1.1	8
24	Phylogenomic Based Comparative Studies on Indian and American Commensal <i>Staphylococcus epidermidis</i> Isolates. <i>Frontiers in Microbiology</i> , 2018, 9, 333.	1.5	7
25	Isolation and characterization of a novel 1-aminocyclopropane-1-carboxylate (ACC) deaminase producing plant growth promoting marine Gammaproteobacteria from crops grown in brackish environments. Proposal for <i>Pokkaliibacter plantistimulans</i> gen. nov., sp. nov., Balneatricaceae fam. nov. in the order Oceanospirillales and an emended description of the genus <i>Balneatrix</i> . <i>Systematic and Applied Microbiology</i> , 2018, 41, 570-580.	1.2	19
26	<i>Pseudomonas fluvialis</i> sp. nov., a novel member of the genus <i>Pseudomonas</i> isolated from the river Ganges, India. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 402-408.	0.8	15
27	<i>Paenibacillus xerothermodurans</i> sp. nov., an extremely dry heat resistant spore forming bacterium isolated from the soil of Cape Canaveral, Florida. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3190-3196.	0.8	10
28	Taxonogenomics reveal multiple novel genomospecies associated with clinical isolates of <i>Stenotrophomonas maltophilia</i> . <i>Microbial Genomics</i> , 2018, 4, .	1.0	24
29	Population genomic insights into variation and evolution of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Scientific Reports</i> , 2017, 7, 40694.	1.6	45
30	Ecological and Evolutionary Insights into <i>Xanthomonas citri</i> Pathovar Diversity. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	41
31	Glimpse into the Genomes of Rice Endophytic Bacteria: Diversity and Distribution of Firmicutes. <i>Frontiers in Microbiology</i> , 2017, 7, 2115.	1.5	37
32	Genomics Reveals a Unique Clone of <i>Burkholderia cenocepacia</i> Harboring an Actively Excising Novel Genomic Island. <i>Frontiers in Microbiology</i> , 2017, 8, 590.	1.5	24
33	Genomic Resource and Genome Guided Comparison of Twenty Type Strains of the Genus <i>Methylobacterium</i> . <i>Canadian Journal of Biotechnology</i> , 2017, 1, 265-265.	0.3	0
34	Genome Sequence of Type Strains of Genus <i>Stenotrophomonas</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 309.	1.5	45
35	Genomic investigation reveals evolution and lifestyle adaptation of endophytic <i>Staphylococcus epidermidis</i> . <i>Scientific Reports</i> , 2016, 6, 19263.	1.6	39
36	Biochemical and genome sequence analyses of <i>Megasphaera</i> sp. strain DISK18 from dental plaque of a healthy individual reveals commensal lifestyle. <i>Scientific Reports</i> , 2016, 6, 33665.	1.6	23

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37	Methylobacterium indicum sp. nov., a facultative methylotrophic bacterium isolated from rice seed. Systematic and Applied Microbiology, 2016, 39, 25-32.	1.2	23
38	Characterization of the Antimicrobial Peptide Penisin, a Class Ia Novel Lantibiotic from Paenibacillus sp. Strain A3. Antimicrobial Agents and Chemotherapy, 2016, 60, 580-591.	1.4	73
39	Multilocus sequence analysis reveals high genetic diversity in clinical isolates of Burkholderia cepacia complex from India. Scientific Reports, 2016, 6, 35769.	1.6	10
40	Laterosporulin10: a novel defensin like Class IId bacteriocin from Brevibacillus sp. strain SKDU10 with inhibitory activity against microbial pathogens. Microbiology (United Kingdom), 2016, 162, 1286-1299.	0.7	58
41	Genome Sequence of Acinetobacter baumannii Strain 5021_13, Isolated from Cerebrospinal Fluid. Genome Announcements, 2015, 3, .	0.8	4
42	Genome Sequence of Acinetobacter baumannii Strain 10441_14 Belonging to ST451, Isolated from India. Genome Announcements, 2015, 3, .	0.8	4
43	The rice immune receptor XA21 recognizes a tyrosine-sulfated protein from a Gram-negative bacterium. Science Advances, 2015, 1, e1500245.	4.7	209
44	Genomic Resource of Rice Seed Associated Bacteria. Frontiers in Microbiology, 2015, 6, 1551.	1.5	58
45	Genomic Insights into the Evolutionary Origin of Xanthomonas axonopodis pv. citri and Its Ecological Relatives. Applied and Environmental Microbiology, 2014, 80, 6266-6279.	1.4	36
46	Genomic Flux in Xanthomonas Group of Plant Pathogenic Bacteria. , 2014, , 131-153.		2
47	Genomic Survey of Pathogenicity Determinants and VNTR Markers in the Cassava Bacterial Pathogen Xanthomonas axonopodis pv. Manihotis Strain CIO151. PLoS ONE, 2013, 8, e79704.	1.1	42
48	Genome Sequence of Pediococcus pentosaceus Strain IE-3. Journal of Bacteriology, 2012, 194, 4468-4468.	1.0	21
49	Genome Sequence of Brevibacillus laterosporus Strain GI-9. Journal of Bacteriology, 2012, 194, 1279-1279.	1.0	25
50	Genome Sequence of Xanthomonas citri pv. mangiferaeindicae Strain LMG 941. Journal of Bacteriology, 2012, 194, 3031-3031.	1.0	14
51	Identification, Purification and Characterization of Laterosporulin, a Novel Bacteriocin Produced by Brevibacillus sp. Strain GI-9. PLoS ONE, 2012, 7, e31498.	1.1	68
52	Genome Sequence of Xanthomonas axonopodis pv. punicae Strain LMG 859. Journal of Bacteriology, 2012, 194, 2395-2395.	1.0	18
53	Two New Complete Genome Sequences Offer Insight into Host and Tissue Specificity of Plant Pathogenic Xanthomonas spp. Journal of Bacteriology, 2011, 193, 5450-5464.	1.0	189
54	Comparative genomics reveals diversity among xanthomonads infecting tomato and pepper. BMC Genomics, 2011, 12, 146.	1.2	167

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55	The Evolution of Host Specialization in the Vertebrate Gut Symbiont <i>Lactobacillus reuteri</i> . PLoS Genetics, 2011, 7, e1001314.	1.5	270
56	Resolving the phylogenetic and taxonomic relationship of <i>Xanthomonas</i> and <i>Stenotrophomonas</i> strains using complete <i>rpoB</i> gene sequence. PLOS Currents, 2011, 3, RRN1239.	1.4	8
57	Diversification of the gut symbiont <i>Lactobacillus reuteri</i> as a result of host-driven evolution. ISME Journal, 2010, 4, 377-387.	4.4	254
58	Names: dropped to avoid prejudice, now useful again. Nature, 2008, 453, 450-450.	13.7	0
59	Genome sequence and rapid evolution of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A. BMC Genomics, 2008, 9, 204.	1.2	327
60	Genome sequence and rapid evolution of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A. BMC Genomics, 2008, 9, 534.	1.2	33
61	Acquisition and Evolution of Plant Pathogenesis-Associated Gene Clusters and Candidate Determinants of Tissue-Specificity in <i>Xanthomonas</i> . PLoS ONE, 2008, 3, e3828.	1.1	89
62	The role of horizontal transfer in the evolution of a highly variable lipopolysaccharide biosynthesis locus in xanthomonads that infect rice, citrus and crucifers. BMC Evolutionary Biology, 2007, 7, 243.	3.2	46
63	Variation suggestive of horizontal gene transfer at a lipopolysaccharide (<i>lps</i>) biosynthetic locus in <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> , the bacterial leaf blight pathogen of rice. BMC Microbiology, 2004, 4, 40.	1.3	44