

Manoj Pillay

List of Publications by Year in descending order

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36
papers

3,774
citations

516710

16
h-index

377865

34
g-index

36
all docs

36
docs citations

36
times ranked

6189
citing authors

#	ARTICLE	IF	CITATIONS
1	Sodalis ligni Strain 159R Isolated from an Anaerobic Lignin-Degrading Consortium. Microbiology Spectrum, 2022, 10, e0234621.	3.0	1
2	One Complete and Seven Draft Genome Sequences of Subdivision 1 and 3 <i>Acidobacteria</i> Isolated from Soil. Microbiology Resource Announcements, 2020, 9, .	0.6	5
3	Draft Genome of Burkholderia cenocepacia TAtl-371, a Strain from the Burkholderia cepacia Complex Retains Antagonism in Different Carbon and Nitrogen Sources. Current Microbiology, 2019, 76, 566-574.	2.2	3
4	IMG/M v.5.0: an integrated data management and comparative analysis system for microbial genomes and microbiomes. Nucleic Acids Research, 2019, 47, D666-D677.	14.5	799
5	Genomes of ubiquitous marine and hypersaline <i>Hydrogenovibrio</i> , <i>Thiomicrothrix</i> and <i>Thiomicrospira</i> spp. encode a diversity of mechanisms to sustain chemolithoautotrophy in heterogeneous environments. Environmental Microbiology, 2018, 20, 2686-2708.	3.8	32
6	Complete genome sequence of Jiangella gansuensis strain YIM 002T (DSM 44835T), the type species of the genus Jiangella and source of new antibiotic compounds. Standards in Genomic Sciences, 2017, 12, 21.	1.5	9
7	Permanent draft genome of Thiobacillus thioparus DSM 505T, an obligately chemolithoautotrophic member of the Betaproteobacteria. Standards in Genomic Sciences, 2017, 12, 10.	1.5	34
8	High quality permanent draft genome sequence of Chryseobacterium bovis DSM 19482T, isolated from raw cow milk. Standards in Genomic Sciences, 2017, 12, 31.	1.5	2
9	Permanent Draft Genome Sequence of Desulfurococcus amylolyticus Strain Z-533 ^T , a Peptide and Starch Degrader Isolated from Thermal Springs in the Kamchatka Peninsula and Kunashir Island, Russia. Genome Announcements, 2017, 5, .	0.8	2
10	Complete Genome Sequence of <i>Nitrosomonas cryotolerans</i> ATCC 49181, a Phylogenetically Distinct Ammonia-Oxidizing Bacterium Isolated from Arctic Waters. Genome Announcements, 2017, 5, .	0.8	3
11	High-quality-draft genome sequence of the fermenting bacterium Anaerobium acetethylicum type strain GluBS11T (DSM 29698). Standards in Genomic Sciences, 2017, 12, 24.	1.5	6
12	High-quality permanent draft genome sequence of the Bradyrhizobium elkanii type strain USDA 76T, isolated from Glycine max (L.) Merr. Standards in Genomic Sciences, 2017, 12, 26.	1.5	11
13	IMG/M: integrated genome and metagenome comparative data analysis system. Nucleic Acids Research, 2017, 45, D507-D516.	14.5	451
14	Genome Data Provides High Support for Generic Boundaries in Burkholderia Sensu Lato. Frontiers in Microbiology, 2017, 8, 1154.	3.5	122
15	Draft genome sequence of Dethiobacter alkaliphilus strain AHT1T, a gram-positive sulfidogenic polyextremophile. Standards in Genomic Sciences, 2017, 12, 57.	1.5	16
16	Draft genome sequence of Marinobacterium rhizophilum CL-YJ9T (DSM 18822T), isolated from the rhizosphere of the coastal tidal-flat plant Suaeda japonica. Standards in Genomic Sciences, 2017, 12, 65.	1.5	1
17	Draft genome of Paraburkholderia caballeronis TNe-841T, a free-living, nitrogen-fixing, tomato plant-associated bacterium. Standards in Genomic Sciences, 2017, 12, 80.	1.5	7
18	Draft Genome Sequence of <i>Frankia</i> Strain G2, a Nitrogen-Fixing Actinobacterium Isolated from <i>Casuarina equisetifolia</i> and Able To Nodulate Actinorhizal Plants of the Order <i>Rhamales</i> . Genome Announcements, 2016, 4, .	0.8	13

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19	Complete genome sequence of <i>Desulfurivibrio alkaliphilus</i> strain AHT2T, a haloalkaliphilic sulfidogen from Egyptian hypersaline alkaline lakes. <i>Standards in Genomic Sciences</i> , 2016, 11, 67.	1.5	26
20	High-Quality Draft Genomes from <i>Thermus caliditerrae</i> YIM 77777 and <i>T.Âtengchongensis</i> YIM 77401, Isolates from Tengchong, China. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
21	Permanent draft genome of <i>Thermithiobacillus tepidarius</i> DSM 3134T, a moderately thermophilic, obligately chemolithoautotrophic member of the Acidithiobacillia. <i>Standards in Genomic Sciences</i> , 2016, 11, 74.	1.5	15
22	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2016, 45, D457-D465.	14.5	177
23	Complete genome of <i>Nitrosospira briensis</i> C-128, an ammonia-oxidizing bacterium from agricultural soil. <i>Standards in Genomic Sciences</i> , 2016, 11, 46.	1.5	22
24	High-Quality Draft Genome Sequence of <i>Thermocrinis jamiesonii</i> GBS1 Isolated from Great Boiling Spring, Nevada. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
25	An improved high-quality draft genome sequence of <i>Carnobacterium inhibens</i> subsp. <i>inhibens</i> strain K1T. <i>Standards in Genomic Sciences</i> , 2016, 11, 65.	1.5	2
26	High-quality permanent draft genome sequence of <i>Ensifer</i> sp. PC2, isolated from a nitrogen-fixing root nodule of the legume tree (Khejri) native to the Thar Desert of India. <i>Standards in Genomic Sciences</i> , 2016, 11, 43.	1.5	7
27	The standard operating procedure of the DOE-JGI Metagenome Annotation Pipeline (MAP v.4). <i>Standards in Genomic Sciences</i> , 2016, 11, 17.	1.5	161
28	High-quality draft genome sequence of <i>Flavobacterium suncheonense</i> GH29-5T (DSM 17707T) isolated from greenhouse soil in South Korea, and emended description of <i>Flavobacterium suncheonense</i> GH29-5T. <i>Standards in Genomic Sciences</i> , 2016, 11, 42.	1.5	3
29	Supporting community annotation and user collaboration in the integrated microbial genomes (IMG) system. <i>BMC Genomics</i> , 2016, 17, 307.	2.8	54
30	High quality permanent draft genome sequence of <i>Phaseolibacter flectens</i> ATCC 12775T, a plant pathogen of French bean pods. <i>Standards in Genomic Sciences</i> , 2016, 11, 4.	1.5	1
31	The standard operating procedure of the DOE-JGI Microbial Genome Annotation Pipeline (MGAP v.4). <i>Standards in Genomic Sciences</i> , 2015, 10, 86.	1.5	287
32	IMG/M 4 version of the integrated metagenome comparative analysis system. <i>Nucleic Acids Research</i> , 2014, 42, D568-D573.	14.5	270
33	IMG 4 version of the integrated microbial genomes comparative analysis system. <i>Nucleic Acids Research</i> , 2014, 42, D560-D567.	14.5	555
34	Distinct size distribution of endogenous siRNAs in maize: Evidence from deep sequencing in the <i>mop1-1</i> mutant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 14958-14963.	7.1	208
35	Genome-wide analysis for discovery of rice microRNAs reveals natural antisense microRNAs (nat-miRNAs). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 4951-4956.	7.1	218
36	An expression atlas of rice mRNAs and small RNAs. <i>Nature Biotechnology</i> , 2007, 25, 473-477.	17.5	246