

Manoj Pillay

List of Publications by Year in descending order

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36
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3,774
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516710

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6189
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#	ARTICLE	IF	CITATIONS
1	IMG/M v.5.0: an integrated data management and comparative analysis system for microbial genomes and microbiomes. <i>Nucleic Acids Research</i> , 2019, 47, D666-D677.	14.5	799
2	IMG 4 version of the integrated microbial genomes comparative analysis system. <i>Nucleic Acids Research</i> , 2014, 42, D560-D567.	14.5	555
3	IMG/M: integrated genome and metagenome comparative data analysis system. <i>Nucleic Acids Research</i> , 2017, 45, D507-D516.	14.5	451
4	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
5	IMG/M 4 version of the integrated metagenome comparative analysis system. <i>Nucleic Acids Research</i> , 2014, 42, D568-D573.	14.5	270
6	An expression atlas of rice mRNAs and small RNAs. <i>Nature Biotechnology</i> , 2007, 25, 473-477.	17.5	246
7	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
8	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
9	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2016, 45, D457-D465.	14.5	177
10	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
11	Genome Data Provides High Support for Generic Boundaries in Burkholderia Sensu Lato. <i>Frontiers in Microbiology</i> , 2017, 8, 1154.	3.5	122
12	Supporting community annotation and user collaboration in the integrated microbial genomes (IMG) system. <i>BMC Genomics</i> , 2016, 17, 307.	2.8	54
13	Permanent draft genome of <i>Thiobacillus thioparus</i> DSM 505T, an obligately chemolithoautotrophic member of the Betaproteobacteria. <i>Standards in Genomic Sciences</i> , 2017, 12, 10.	1.5	34
14	Genomes of ubiquitous marine and hypersaline <i>Hydrogenovibrio</i> and <i>Thiomicrothrix</i> spp. encode a diversity of mechanisms to sustain chemolithoautotrophy in heterogeneous environments. <i>Environmental Microbiology</i> , 2018, 20, 2686-2708.	3.8	32
15	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
16	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
17	Draft genome sequence of <i>Dethiobacter alkaliphilus</i> strain AHT1T, a gram-positive sulfidogenic polyextremophile. <i>Standards in Genomic Sciences</i> , 2017, 12, 57.	1.5	16
18	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

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19	Draft Genome Sequence of <i>Frankia</i> Strain G2, a Nitrogen-Fixing Actinobacterium Isolated from <i>Casuarina equisetifolia</i> and Able To Nodulate Actinorrhizal Plants of the Order <i>Rhamnales</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	13
20	High-quality permanent draft genome sequence of the Bradyrhizobium elkanii type strain USDA 76T, isolated from Glycine max (L.) Merr. <i>Standards in Genomic Sciences</i> , 2017, 12, 26.	1.5	11
21	Complete genome sequence of Jiangella gansuensis strain YIM 002T (DSM 44835T), the type species of the genus Jiangella and source of new antibiotic compounds. <i>Standards in Genomic Sciences</i> , 2017, 12, 21.	1.5	9
22	High-quality permanent draft genome sequence of Ensifer 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
23	Draft genome of Paraburkholderia caballeronis TNe-841T, a free-living, nitrogen-fixing, tomato plant-associated bacterium. <i>Standards in Genomic Sciences</i> , 2017, 12, 80.	1.5	7
24	High-quality-draft genome sequence of the fermenting bacterium Anaerobium acetethylicum type strain GluBS11T (DSM 29698). <i>Standards in Genomic Sciences</i> , 2017, 12, 24.	1.5	6
25	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
26	One Complete and Seven Draft Genome Sequences of Subdivision 1 and 3 <i>Acidobacteria</i> Isolated from Soil. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	5
27	High-quality draft genome sequence of Flavobacterium suncheonense GH29-5T (DSM 17707T) isolated from greenhouse soil in South Korea, and emended description of Flavobacterium suncheonense GH29-5T. <i>Standards in Genomic Sciences</i> , 2016, 11, 42.	1.5	3
28	Complete Genome Sequence of <i>Nitrosomonas cryotolerans</i> ATCC 49181, a Phylogenetically Distinct Ammonia-Oxidizing Bacterium Isolated from Arctic Waters. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
29	Draft Genome of Burkholderia cenocepacia TAtl-371, a Strain from the Burkholderia cepacia Complex Retains Antagonism in Different Carbon and Nitrogen Sources. <i>Current Microbiology</i> , 2019, 76, 566-574.	2.2	3
30	An improved high-quality draft genome sequence of Carnobacterium inhibens subsp. inhibens strain K1T. <i>Standards in Genomic Sciences</i> , 2016, 11, 65.	1.5	2
31	High quality permanent draft genome sequence of Chryseobacterium bovis DSM 19482T, isolated from raw cow milk. <i>Standards in Genomic Sciences</i> , 2017, 12, 31.	1.5	2
32	Permanent Draft Genome Sequence of Desulfurococcus amylolyticus Strain Z-533 ^T , a Peptide and Starch Degradar Isolated from Thermal Springs in the Kamchatka Peninsula and Kunashir Island, Russia. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
33	High quality permanent draft genome sequence of Phaseolibacter flectens ATCC 12775T, a plant pathogen of French bean pods. <i>Standards in Genomic Sciences</i> , 2016, 11, 4.	1.5	1
34	Draft genome sequence of Marinobacterium rhizophilum CL-YJ9T (DSM 18822T), isolated from the rhizosphere of the coastal tidal-flat plant Suaeda japonica. <i>Standards in Genomic Sciences</i> , 2017, 12, 65.	1.5	1
35	Sodalis ligni Strain 159R Isolated from an Anaerobic Lignin-Degrading Consortium. <i>Microbiology Spectrum</i> , 2022, 10, e0234621.	3.0	1
36	High-Quality Draft Genome Sequence of Thermocrinis jamiesonii GBS1 ^T Isolated from Great Boiling Spring, Nevada. <i>Genome Announcements</i> , 2016, 4, .	0.8	0