

Luis Miguel Rodriguez-R

List of Publications by Year in descending order

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53
papers

8,552
citations

172207

29
h-index

182168

51
g-index

75
all docs

75
docs citations

75
times ranked

10349
citing authors

#	ARTICLE	IF	CITATIONS
1	High throughput ANI analysis of 90K prokaryotic genomes reveals clear species boundaries. Nature Communications, 2018, 9, 5114.	5.8	2,816
2	Bypassing Cultivation To Identify Bacterial Species. Microbe Magazine, 2014, 9, 111-118.	0.4	581
3	Strengths and Limitations of 16S rRNA Gene Amplicon Sequencing in Revealing Temporal Microbial Community Dynamics. PLoS ONE, 2014, 9, e93827.	1.1	508
4	The Microbial Genomes Atlas (MiGA) webserver: taxonomic and gene diversity analysis of Archaea and Bacteria at the whole genome level. Nucleic Acids Research, 2018, 46, W282-W288.	6.5	458
5	MyTaxa: an advanced taxonomic classifier for genomic and metagenomic sequences. Nucleic Acids Research, 2014, 42, e73-e73.	6.5	445
6	Microbiome of the upper troposphere: Species composition and prevalence, effects of tropical storms, and atmospheric implications. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2575-2580.	3.3	377
7	Nonpareil: a redundancy-based approach to assess the level of coverage in metagenomic datasets. Bioinformatics, 2014, 30, 629-635.	1.8	186
8	SAR11 bacteria linked to ocean anoxia and nitrogen loss. Nature, 2016, 536, 179-183.	13.7	160
9	Shifts in bacterial communities of two caribbean reef-building coral species affected by white plague disease. ISME Journal, 2012, 6, 502-512.	4.4	155
10	Microbial community successional patterns in beach sands impacted by the Deepwater Horizon oil spill. ISME Journal, 2015, 9, 1928-1940.	4.4	155
11	Nonpareil 3: Fast Estimation of Metagenomic Coverage and Sequence Diversity. MSystems, 2018, 3, .	1.7	152
12	Detecting Nitrous Oxide Reductase (<i>nosZ</i>) Genes in Soil Metagenomes: Method Development and Implications for the Nitrogen Cycle. MBio, 2014, 5, e01193-14.	1.8	142
13	Estimating coverage in metagenomic data sets and why it matters. ISME Journal, 2014, 8, 2349-2351.	4.4	142
14	New insights from the biogas microbiome by comprehensive genome-resolved metagenomics of nearly 1600 species originating from multiple anaerobic digesters. Biotechnology for Biofuels, 2020, 13, 25.	6.2	136
15	Soil Microbial Community Responses to a Decade of Warming as Revealed by Comparative Metagenomics. Applied and Environmental Microbiology, 2014, 80, 1777-1786.	1.4	131
16	An Improved Method for TAL Effectors DNA-Binding Sites Prediction Reveals Functional Convergence in TAL Repertoires of Xanthomonas oryzae Strains. PLoS ONE, 2013, 8, e68464.	1.1	102
17	Biofilms on Hospital Shower Hoses: Characterization and Implications for Nosocomial Infections. Applied and Environmental Microbiology, 2016, 82, 2872-2883.	1.4	102
18	The Reliability of Metagenome-Assembled Genomes (MAGs) in Representing Natural Populations: Insights from Comparing MAGs against Isolate Genomes Derived from the Same Fecal Sample. Applied and Environmental Microbiology, 2021, 87, .	1.4	82

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19	Genomes-based phylogeny of the genus <i>Xanthomonas</i> . <i>BMC Microbiology</i> , 2012, 12, 43.	1.3	71
20	New Multilocus Variable-Number Tandem-Repeat Analysis Tool for Surveillance and Local Epidemiology of Bacterial Leaf Blight and Bacterial Leaf Streak of Rice Caused by <i>Xanthomonas oryzae</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 688-698.	1.4	69
21	Iterative subtractive binning of freshwater chronoserries metagenomes identifies over 400 novel species and their ecologic preferences. <i>Environmental Microbiology</i> , 2020, 22, 3394-3412.	1.8	69
22	Metagenomics Reveals Pervasive Bacterial Populations and Reduced Community Diversity across the Alaska Tundra Ecosystem. <i>Frontiers in Microbiology</i> , 2016, 7, 579.	1.5	66
23	Quantifying the Importance of the Rare Biosphere for Microbial Community Response to Organic Pollutants in a Freshwater Ecosystem. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	60
24	Development of a Variable Number of Tandem Repeats Typing Scheme for the Bacterial Rice Pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> . <i>Phytopathology</i> , 2012, 102, 948-956.	1.1	51
25	How Much Do rRNA Gene Surveys Underestimate Extant Bacterial Diversity?. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	47
26	â€œ <i>Candidatus</i> <i>Macondimonas diazotrophica</i> â€œ, a novel gammaproteobacterial genus dominating crude-oil-contaminated coastal sediments. <i>ISME Journal</i> , 2019, 13, 2129-2134.	4.4	46
27	Genomic Survey of Pathogenicity Determinants and VNTR Markers in the Cassava Bacterial Pathogen <i>Xanthomonas axonopodis</i> pv. <i>Manihotis</i> Strain CIO151. <i>PLoS ONE</i> , 2013, 8, e79704.	1.1	42
28	Quantifying the changes in genetic diversity within sequence-discrete bacterial populations across a spatial and temporal riverine gradient. <i>ISME Journal</i> , 2019, 13, 767-779.	4.4	40
29	ROcker: accurate detection and quantification of target genes in short-read metagenomic data sets by modeling sliding-window bitscores. <i>Nucleic Acids Research</i> , 2017, 45, gkw900.	6.5	37
30	Evaluation of metatranscriptomic protocols and application to the study of freshwater microbial communities. <i>Environmental Microbiology Reports</i> , 2014, 6, 640-655.	1.0	36
31	Reply to: â€œRe-evaluating the evidence for a universal genetic boundary among microbial speciesâ€œ. <i>Nature Communications</i> , 2021, 12, 4060.	5.8	36
32	Ecogenomic characterization of widespread, closely-related SAR11 clades of the freshwater genus â€œ <i>Candidatus</i> <i>Fonsibacter</i> â€œ and proposal of <i>Ca. Fonsibacter lacus</i> sp. nov. <i>Systematic and Applied Microbiology</i> , 2019, 42, 495-505.	1.2	33
33	Genomic Characterization and Copy Number Variation of <i>Bacillus anthracis</i> Plasmids pXO1 and pXO2 in a Historical Collection of 412 Strains. <i>MSystems</i> , 2018, 3, .	1.7	32
34	A Userâ€™s Guide to Quantitative and Comparative Analysis of Metagenomic Datasets. <i>Methods in Enzymology</i> , 2013, 531, 525-547.	0.4	28
35	Metagenomics as a Public Health Risk Assessment Tool in a Study of Natural Creek Sediments Influenced by Agricultural and Livestock Runoff: Potential and Limitations. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	27
36	imGLAD: accurate detection and quantification of target organisms in metagenomes. <i>PeerJ</i> , 2018, 6, e5882.	0.9	24

#	ARTICLE	IF	CITATIONS
37	Genome repository of oil systems: An interactive and searchable database that expands the catalogued diversity of crude oil-associated microbes. <i>Environmental Microbiology</i> , 2020, 22, 2094-2106.	1.8	21
38	Draft Genome Sequence of <i>Bacillus cereus</i> LA2007, a Human-Pathogenic Isolate Harboring Anthrax-Like Plasmids. <i>Genome Announcements</i> , 2017, 5, .	0.8	18
39	Targeted metabolic reconstruction: a novel approach for the characterization of plant-pathogen interactions. <i>Briefings in Bioinformatics</i> , 2011, 12, 151-162.	3.2	16
40	CRISPR elements provide a new framework for the genealogy of the citrus canker pathogen <i>Xanthomonas citri</i> pv. <i>citri</i> . <i>BMC Genomics</i> , 2019, 20, 917.	1.2	16
41	The type VI secretion system of <i>Xanthomonas phaseoli</i> pv. <i>manihotis</i> is involved in virulence and in vitro motility. <i>BMC Microbiology</i> , 2021, 21, 14.	1.3	16
42	Model-based Comparisons of the Abundance Dynamics of Bacterial Communities in Two Lakes. <i>Scientific Reports</i> , 2020, 10, 2423.	1.6	14
43	Analysis of Whole-Genome Sequences for the Prediction of Penicillin Resistance and β -Lactamase Activity in <i>Bacillus anthracis</i> . <i>MSystems</i> , 2018, 3, .	1.7	12
44	Toward shotgun metagenomic approaches for microbial source tracking sewage spills based on laboratory mesocosms. <i>Water Research</i> , 2022, 210, 117993.	5.3	12
45	Computational Biology in Colombia. <i>PLoS Computational Biology</i> , 2009, 5, e1000535.	1.5	9
46	Discovery of <i>Phytophthora infestans</i> Genes Expressed in Planta through Mining of cDNA Libraries. <i>PLoS ONE</i> , 2010, 5, e9847.	1.1	8
47	An RNAi in silico approach to find an optimal shRNA cocktail against HIV-1. <i>Virology Journal</i> , 2010, 7, 369.	1.4	6
48	Beach sand oil spills select for generalist microbial populations. <i>ISME Journal</i> , 2021, 15, 3418-3422.	4.4	3
49	Reply to Smith and Griffin: Methods, air flows, and conclusions are robust in the DeLeon-Rodriguez et al. study. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2085.	3.3	2
50	Identification and Classification of Prokaryotes using whole-genome sequences.. , 2021, , 217-230.		2
51	RecruitPlotEasy: An Advanced Read Recruitment Plot Tool for Assessing Metagenomic Population Abundance and Genetic Diversity. <i>Frontiers in Bioinformatics</i> , 2022, 1, .	1.0	2
52	ROcker Models for Reliable Detection and Typing of Short-Read Sequences Carrying β -Lactamase Genes. <i>MSystems</i> , 2022, 7, .	1.7	1
53	Transcriptomic and rRNA:rDNA Signatures of Environmental versus Enteric <i>Enterococcus faecalis</i> Isolates under Oligotrophic Freshwater Conditions. <i>Microbiology Spectrum</i> , 2021, 9, e0081721.	1.2	0