

Luiz Fernando Wurdig Roesch

List of Publications by Year in descending order

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Version: 2024-02-01

93
papers

5,626
citations

136950

32
h-index

79698

73
g-index

103
all docs

103
docs citations

103
times ranked

8566
citing authors

#	ARTICLE	IF	CITATIONS
1	Meconium microbiota predicts clinical early-onset neonatal sepsis in preterm neonates. Journal of Maternal-Fetal and Neonatal Medicine, 2022, 35, 1935-1943.	1.5	11
2	Soybean crop incorporation in irrigated rice cultivation improves nitrogen availability, soil microbial diversity and activity, and growth of ryegrass. Applied Soil Ecology, 2022, 170, 104313.	4.3	14
3	Ammonia volatilization and Sporosarcina genus abundance in an Oxisol enriched with urea, compost and biochar. Applied Soil Ecology, 2022, 176, 104494.	4.3	5
4	Depression phenotype identified by using single nucleotide exact amplicon sequence variants of the human gut microbiome. Molecular Psychiatry, 2021, 26, 4277-4287.	7.9	46
5	Artificially intelligent soil quality and health indices for "next generation" food production systems.. Trends in Food Science and Technology, 2021, 107, 195-200.	15.1	9
6	Altered bacteria community dominance reduces tolerance to resident fungus and seed to seedling growth performance in maize (Zea mays L. var. DKB 177). Microbiological Research, 2021, 243, 126643.	5.3	4
7	Insights into the structure and role of seed-borne bacteriome during maize germination. FEMS Microbiology Ecology, 2021, 97, .	2.7	14
8	A long-term no-tillage system can increase enzymatic activity and maintain bacterial richness in paddy fields. Land Degradation and Development, 2021, 32, 2257-2268.	3.9	27
9	Whole Plastome Sequences of Two Drug-Type Cannabis: Insights Into the Use of Plastid in Forensic Analyses. Journal of Forensic Sciences, 2020, 65, 259-265.	1.6	6
10	Defining microbial biomarkers for risk of preterm labor. Brazilian Journal of Microbiology, 2020, 51, 151-159.	2.0	12
11	<scp>pime</scp>: A package for discovery of novel differences among microbial communities. Molecular Ecology Resources, 2020, 20, 415-428.	4.8	38
12	Environmental contamination alters the intestinal microbial community of the livebearer killifish Phalloceros caudimaculatus. Heliyon, 2020, 6, e04190.	3.2	13
13	Editorial: Microbe-Mediated Processes in Soils. Frontiers in Environmental Science, 2020, 8, .	3.3	3
14	Meconium microbiome and its relation to neonatal growth and head circumference catch-up in preterm infants. PLoS ONE, 2020, 15, e0238632.	2.5	13
15	Microbial patterns in rumen are associated with gain of weight in beef cattle. Antonie Van Leeuwenhoek, 2020, 113, 1299-1312.	1.7	8
16	Is the gut microbiota dysbiotic in patients with classical homocystinuria?. Biochimie, 2020, 173, 3-11.	2.6	10
17	Long-term farming systems modulate multi-trophic responses. Science of the Total Environment, 2019, 646, 480-490.	8.0	18
18	Genetic risk for autoimmunity is associated with distinct changes in the human gut microbiome. Nature Communications, 2019, 10, 3621.	12.8	132

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19	The vaginal microbial communities of healthy expectant Brazilian mothers and its correlation with the newborn's gut colonization. <i>World Journal of Microbiology and Biotechnology</i> , 2019, 35, 159.	3.6	18
20	Influence of own mother's milk and different proportions of formula on intestinal microbiota of very preterm newborns. <i>PLoS ONE</i> , 2019, 14, e0217296.	2.5	21
21	High-throughput sequencing analysis of <i>Eugenia uniflora</i> : insights into repetitive DNA, gene content and potential biotechnological applications. <i>3 Biotech</i> , 2019, 9, 200.	2.2	5
22	Hepatic glycogen storage diseases are associated to microbial dysbiosis. <i>PLoS ONE</i> , 2019, 14, e0214582.	2.5	17
23	Moisture Is More Important than Temperature for Assembly of Both Potentially Active and Whole Prokaryotic Communities in Subtropical Grassland. <i>Microbial Ecology</i> , 2019, 77, 460-470.	2.8	28
24	Recycling organic residues in agriculture impacts soil-borne microbial community structure, function and N ₂ O emissions. <i>Science of the Total Environment</i> , 2018, 631-632, 1089-1099.	8.0	45
25	Aliphatic Hydrocarbon Enhances Phenanthrene Degradation by Autochthonous Prokaryotic Communities from a Pristine Seawater. <i>Microbial Ecology</i> , 2018, 75, 688-700.	2.8	10
26	Differences in bacterial composition between men's and women's restrooms and other common areas within a public building. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 551-561.	1.7	9
27	Characterization and Phylogenetic Analysis of Chloroplast and Mitochondria Genomes from the Antarctic Polytrichaceae Species <i>Polytrichum juniperinum</i> and <i>Polytrichum strictum</i> . <i>Diversity</i> , 2018, 10, 89.	1.7	2
28	The microbiome and inborn errors of metabolism: Why we should look carefully at their interplay?. <i>Genetics and Molecular Biology</i> , 2018, 41, 515-532.	1.3	14
29	Characterization of Plastidial and Nuclear SSR Markers for Understanding Invasion Histories and Genetic Diversity of <i>Schinus molle</i> L. <i>Biology</i> , 2018, 7, 43.	2.8	4
30	Do probiotics effectively ameliorate glycemic control during gestational diabetes? A systematic review. <i>Archives of Gynecology and Obstetrics</i> , 2018, 298, 477-485.	1.7	22
31	Genetic Risk for Type 1 Diabetes Profoundly Influences the Core Gut Microbiome in Children. <i>Diabetes</i> , 2018, 67, 209-LB.	0.6	2
32	Seasonal dynamics alter taxonomical and functional microbial profiles in Pampa biome soils under natural grasslands. <i>PeerJ</i> , 2018, 6, e4991.	2.0	27
33	BTW "Bioinformatics Through Windows: an easy-to-install package to analyze marker gene data. <i>PeerJ</i> , 2018, 6, e5299.	2.0	13
34	Draft genome of <i>Nocardia farcinica</i> TRH1, a linear and polycyclic aromatic hydrocarbon-degrading bacterium isolated from the coast of Trindade Island, Brazil. <i>Brazilian Journal of Microbiology</i> , 2017, 48, 391-392.	2.0	9
35	Bioinformatics for Microbiome Research: Concepts, Strategies, and Advances. , 2017, , 111-123.		3
36	The Brazilian Microbiome Project. , 2017, , 1-6.		2

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37	The Brazilian Soil Microbiome. , 2017, , 21-39.		2
38	Low Microbial Diversity and Abnormal Microbial Succession Is Associated with Necrotizing Enterocolitis in Preterm Infants. <i>Frontiers in Microbiology</i> , 2017, 8, 2243.	3.5	72
39	Replacement of native vegetation alters the soil microbial structure in the Pampa biome. <i>Scientia Agricola</i> , 2017, 74, 77-84.	1.2	13
40	Diversity and composition of vaginal microbiota of pregnant women at risk for transmitting Group B <i>Streptococcus</i> treated with intrapartum penicillin. <i>PLoS ONE</i> , 2017, 12, e0169916.	2.5	19
41	USO DE PRÃ%, PRÃ“ E SIMBIÃ“TICOS COMO COADJUVANTES NO TRATAMENTO DO CÃ,NCER COLORRETAL. <i>Clinical and Biomedical Research</i> , 2017, 37, 232-246.	0.1	1
42	Back to the Future of Soil Metagenomics. <i>Frontiers in Microbiology</i> , 2016, 7, 73.	3.5	120
43	Phenylketonuria and Gut Microbiota: A Controlled Study Based on Next-Generation Sequencing. <i>PLoS ONE</i> , 2016, 11, e0157513.	2.5	52
44	BMPOS: a Flexible and User-Friendly Tool Sets for Microbiome Studies. <i>Microbial Ecology</i> , 2016, 72, 443-447.	2.8	45
45	Temporal variability of soil microbial communities after application of dicyandiamide-treated swine slurry and mineral fertilizers. <i>Soil Biology and Biochemistry</i> , 2016, 97, 71-82.	8.8	55
46	Misguided phylogenetic comparisons using DGGE excised bands may contaminate public sequence databases. <i>Journal of Microbiological Methods</i> , 2016, 126, 18-23.	1.6	3
47	Lettuce and rhizosphere microbiome responses to growth promoting<i>Pseudomonas</i>species under field conditions. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw197.	2.7	68
48	A Step Forward to Empower Global Microbiome Research Through Local Leadership. <i>Trends in Microbiology</i> , 2016, 24, 767-771.	7.7	12
49	Draft Genome of <i>Rhodococcus rhodochrous</i> TRN7, Isolated from the Coast of Trindade Island, Brazil. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
50	Fungal Community Assembly in the Amazonian Dark Earth. <i>Microbial Ecology</i> , 2016, 71, 962-973.	2.8	35
51	Relationship between honeybee nutrition and their microbial communities. <i>Antonie Van Leeuwenhoek</i> , 2015, 107, 921-933.	1.7	36
52	Microbiome studies need local leaders. <i>Nature</i> , 2015, 528, 39-39.	27.8	14
53	Distribution and Interaction Patterns of Bacterial Communities in an Ornithogenic Soil of Seymour Island, Antarctica. <i>Microbial Ecology</i> , 2015, 69, 684-694.	2.8	18
54	Network topology reveals high connectance levels and few key microbial genera within soils. <i>Frontiers in Environmental Science</i> , 2014, 2, .	3.3	226

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55	Brazilian Microbiome Project: Revealing the Unexplored Microbial Diversity—Challenges and Prospects. <i>Microbial Ecology</i> , 2014, 67, 237-241.	2.8	119
56	Data analysis for 16S microbial profiling from different benchtop sequencing platforms. <i>Journal of Microbiological Methods</i> , 2014, 107, 30-37.	1.6	221
57	Modeling distribution of <i>Schinus molle</i> L. in the Brazilian Pampa: insights on vegetation dynamics and conservation of the biome. <i>Annals of Forest Research</i> , 2014, 57, 1.	1.1	6
58	Desempenho agrônômico a campo de híbridos de milho inoculados com <i>Azospirillum</i> . <i>Revista Ceres</i> , 2014, 61, 209-218.	0.4	43
59	Land-use change and soil type are drivers of fungal and archaeal communities in the Pampa biome. <i>World Journal of Microbiology and Biotechnology</i> , 2013, 29, 223-233.	3.6	40
60	Shifts in soil bacterial community after eight years of land-use change. <i>Systematic and Applied Microbiology</i> , 2013, 36, 137-144.	2.8	93
61	Changes in Diversity, Abundance, and Structure of Soil Bacterial Communities in Brazilian Savanna Under Different Land Use Systems. <i>Microbial Ecology</i> , 2013, 66, 593-607.	2.8	97
62	Thirty years of Brazilian research in Antarctica: ups, downs and perspectives. <i>Scientometrics</i> , 2013, 95, 325-331.	3.0	10
63	Soil-Borne Bacterial Structure and Diversity Does Not Reflect Community Activity in Pampa Biome. <i>PLoS ONE</i> , 2013, 8, e76465.	2.5	52
64	Properties of catechol 1,2-dioxygenase in the cell free extract and immobilized extract of <i>Mycobacterium fortuitum</i> . <i>Brazilian Journal of Microbiology</i> , 2013, 44, 291-297.	2.0	22
65	Pyrosequencing Reveals Shared Bacterial Taxa Across Continents. <i>INCT-APA Annual Activity Report</i> , 2013, , 72-76.	0.0	1
66	Soil bacterial community abundance and diversity in ice-free areas of Keller Peninsula, Antarctica. <i>Applied Soil Ecology</i> , 2012, 61, 7-15.	4.3	36
67	Low sequencing efforts bias analyses of shared taxa in microbial communities. <i>Folia Microbiologica</i> , 2012, 57, 409-413.	2.3	27
68	Mapping and Geopositioning Methods in Ice-Free Areas Antarctica. <i>INCT-APA Annual Activity Report</i> , 2012, , 49-52.	0.0	0
69	Rethinking microbial diversity analysis in the high throughput sequencing era. <i>Journal of Microbiological Methods</i> , 2011, 86, 42-51.	1.6	262
70	Genetic variability of soybean bradyrhizobia populations under different soil managements. <i>Biology and Fertility of Soils</i> , 2011, 47, 357-362.	4.3	23
71	Impact of biodiesel on biodeterioration of stored Brazilian diesel oil. <i>International Biodeterioration and Biodegradation</i> , 2011, 65, 172-178.	3.9	90
72	Biogeography of diazotrophic bacteria in soils. <i>World Journal of Microbiology and Biotechnology</i> , 2010, 26, 1503-1508.	3.6	11

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73	PANGAEA: pipeline for analysis of next generation amplicons. ISME Journal, 2010, 4, 852-861.	9.8	103
74	Vegetal communities from ice-free areas of copacabana, king george island, antarctica. INCT-APA Annual Activity Report, 2010, , 25-26.	0.0	1
75	Plant communities from ice-free areas of demay point, King George Island, Antarctica. INCT-APA Annual Activity Report, 2010, , 58-62.	0.0	2
76	Global patterns in soil bacterial community composition across a continental scale. INCT-APA Annual Activity Report, 2010, , 63-67.	0.0	0
77	Influence of Fecal Sample Storage on Bacterial Community Diversity. Open Microbiology Journal, 2009, 3, 40-46.	0.7	118
78	Confirmation of the Sequence of <i>Candidatus</i> Liberibacter asiaticus TM and Assessment of Microbial Diversity in Huanglongbing-Infected Citrus Phloem Using a Metagenomic Approach. Molecular Plant-Microbe Interactions, 2009, 22, 1624-1634.	2.6	95
79	Culture-independent identification of gut bacteria correlated with the onset of diabetes in a rat model. ISME Journal, 2009, 3, 536-548.	9.8	211
80	The Brazilian Pampa: A Fragile Biome. Diversity, 2009, 1, 182-198.	1.7	172
81	Biodiversity of diazotrophic bacteria within the soil, root and stem of field-grown maize. Plant and Soil, 2008, 302, 91-104.	3.7	128
82	Distantly sampled soils carry few species in common. ISME Journal, 2008, 2, 901-910.	9.8	137
83	Complete Genome Sequence of the N2-Fixing Broad Host Range Endophyte <i>Klebsiella pneumoniae</i> 342 and Virulence Predictions Verified in Mice. PLoS Genetics, 2008, 4, e1000141.	3.5	253
84	Diversity of Nitrogen Fixing Bacterial Community Assessed by Molecular and Microbiological Techniques. Current Plant Science and Biotechnology in Agriculture, 2008, , 309-311.	0.0	0
85	Ocorrência de bactérias diazotróficas associadas a cultivares de sorgo forrageiro. Ciencia Rural, 2007, 37, 727-733.	0.5	10
86	Diversidade de bactérias diazotróficas endofíticas associadas a plantas de milho. Revista Brasileira De Ciencia Do Solo, 2007, 31, 1367-1380.	1.3	15
87	Pyrosequencing enumerates and contrasts soil microbial diversity. ISME Journal, 2007, 1, 283-290.	9.8	1,615
88	Screening of diazotrophic bacteria <i>Azopirillum</i> spp. for nitrogen fixation and auxin production in multiple field sites in southern Brazil. World Journal of Microbiology and Biotechnology, 2007, 23, 1377-1383.	3.6	36
89	Occurrence and distribution of nitrogen fixing bacterial community associated with oat (<i>Avena</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	4.3	63
90	Characterization of diazotrophic bacteria associated with maize: effect of plant genotype, ontogeny and nitrogen-supply. World Journal of Microbiology and Biotechnology, 2006, 22, 967-974.	3.6	53

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91	Relationship Between In Vitro Enhanced Nitrogenase Activity of an Azospirillum brasilense Sp7 Mutant and Its Growth-Promoting Activities In Situ. Current Microbiology, 2006, 53, 43-47.	2.2	5
92	Reinoculação de bactérias diazotróficas aumentando o crescimento de plantas de trigo. Ciencia Rural, 2005, 35, 1201-1204.	0.5	14
93	Identificação de cultivares de milho eficientes na absorção de nitrogênio e na associação com bactérias diazotróficas. Ciencia Rural, 2005, 35, 924-927.	0.5	8