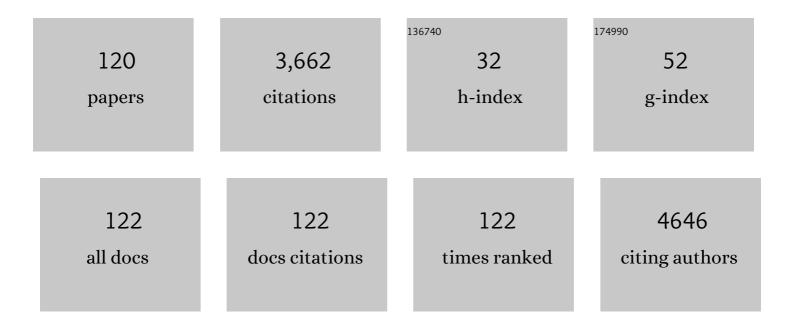
V M De Oliveira

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Hydrogen and organic acid production from dark fermentation of sugarcane vinasse without buffers in mesophilic and thermophilic conditions. Journal of Chemical Technology and Biotechnology, 2022, 97, 1585-1596.	1.6	6
2	Hydrogen and organic acid production from dark fermentation of cheese whey without buffers under mesophilic condition. Journal of Environmental Management, 2022, 304, 114253.	3.8	15
3	Antarctic environments as a source of bacterial and fungal therapeutic enzymes. Anais Da Academia Brasileira De Ciencias, 2022, 94, e20210452.	0.3	0
4	Antarctic organisms as a source of antimicrobial compounds: a patent review. Anais Da Academia Brasileira De Ciencias, 2022, 94, e20210840.	0.3	3
5	Potential for resistance to freezing by non-virulent bacteria isolated from Antarctica. Anais Da Academia Brasileira De Ciencias, 2022, 94, e20210459.	0.3	1
6	Extracellular hydrolytic enzymes produced by yeasts from Antarctic lichens. Anais Da Academia Brasileira De Ciencias, 2022, 94, e20210540.	0.3	7
7	Interactive analysis of biosurfactants in fruit-waste fermentation samples using BioSurfDB and MEGAN. Scientific Reports, 2022, 12, 7769.	1.6	3
8	A genomic catalog of Earth's microbiomes. Nature Biotechnology, 2021, 39, 499-509.	9.4	457
9	Marine associated microbial consortium applied to RBBR textile dye detoxification and decolorization: Combined approach and metatranscriptomic analysis. Chemosphere, 2021, 267, 129190.	4.2	15
10	Dynamics of microbial stress responses driven by abiotic changes along a temporal gradient in Deception Island, Maritime Antarctica. Science of the Total Environment, 2021, 758, 143671.	3.9	9
11	Microbiome taxonomic and functional profiles of two domestic sewage treatment systems. Biodegradation, 2021, 32, 17-36.	1.5	7
12	Pigments from Antarctic bacteria and their biotechnological applications. Critical Reviews in Biotechnology, 2021, 41, 809-826.	5.1	31
13	Antarctic lichens as a source of phosphate-solubilizing bacteria. Extremophiles, 2021, 25, 181-191.	0.9	6
14	Enzymatic routes to hydrogen and organic acids production from banana waste fermentation by autochthonous bacteria: Optimization of pH and temperature. International Journal of Hydrogen Energy, 2021, 46, 8454-8468.	3.8	21
15	Evaluation of anaerobic and anoxic reactors installed in serial to treat fish tank effluent. Revista Ambiente & Ãgua, 2021, 16, 1.	0.1	0
16	Pharmaceutical biotechnological potential of filamentous fungi isolated from textile industry. Archives of Microbiology, 2021, 203, 3933-3944.	1.0	4
17	Antimicrobial activity against Microcystis aeruginosa and degradation of microcystin-LR by bacteria isolated from Antarctica. Environmental Science and Pollution Research, 2021, 28, 52381-52391.	2.7	7
18	Effect of biostimulation and bioaugmentation on hydrocarbon degradation and detoxification of diesel-contaminated soil: a microcosm study. Journal of Microbiology, 2021, 59, 634-643.	1.3	4

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19	Cold-adapted chitinases from Antarctic bacteria: Taxonomic assessment and enzyme production optimization. Biocatalysis and Agricultural Biotechnology, 2021, 34, 102029.	1.5	5
20	Fibrinolytic enzymes from extremophilic microorganisms in the development of new thrombolytic therapies: Technological Prospecting. Recent Patents on Biotechnology, 2021, 15, .	0.4	0
21	Technological Prospecting: Mapping Patents on L-asparaginases from Extremophilic Microorganisms. Recent Patents on Biotechnology, 2021, 15, .	0.4	1
22	New Insights into Controlling Homoacetogenesis in the Co-digestion of Coffee Waste: Effect of Operational Conditions and Characterization of Microbial Communities. Applied Biochemistry and Biotechnology, 2021, , 1.	1.4	2
23	Mangrove soil as a source for novel xylanase and amylase as determined by cultivation-dependent and cultivation-independent methods. Brazilian Journal of Microbiology, 2020, 51, 217-228.	0.8	16
24	Optimization of key factors affecting hydrogen production from coffee waste using factorial design and metagenomic analysis of the microbial community. International Journal of Hydrogen Energy, 2020, 45, 4205-4222.	3.8	34
25	Taxonomic and functional diversity of the microbiome in a jet fuel contaminated site as revealed by combined application of in situ microcosms with metagenomic analysis. Science of the Total Environment, 2020, 708, 135152.	3.9	20
26	Characterization of amylase produced by cold-adapted bacteria from Antarctic samples. Biocatalysis and Agricultural Biotechnology, 2020, 23, 101452.	1.5	21
27	Exploring the genetic potential of a fosmid metagenomic library from an oil-impacted mangrove sediment for metabolism of aromatic compounds. Ecotoxicology and Environmental Safety, 2020, 189, 109974.	2.9	16
28	Undecane production by cold-adapted bacteria from Antarctica. Extremophiles, 2020, 24, 863-873.	0.9	3
29	Metagenomic Insights Into the Mechanisms for Biodegradation of Polycyclic Aromatic Hydrocarbons in the Oil Supply Chain. Frontiers in Microbiology, 2020, 11, 561506.	1.5	40
30	Actinobacteria from Antarctica as a source for anticancer discovery. Scientific Reports, 2020, 10, 13870.	1.6	38
31	Anaerobic reactor applied to laundry wastewater treatment: Unveiling the microbial community by gene and genome-centric approaches. International Biodeterioration and Biodegradation, 2020, 149, 104916.	1.9	15
32	Physicochemical characterization of Pseudomonas stutzeri UFV5 and analysis of its transcriptome under heterotrophic nitrification/aerobic denitrification pathway induction condition. Scientific Reports, 2020, 10, 2215.	1.6	17
33	In depth metagenomic analysis in contrasting oil wells reveals syntrophic bacterial and archaeal associations for oil biodegradation in petroleum reservoirs. Science of the Total Environment, 2020, 715, 136646.	3.9	28
34	The influence of upflow velocity and hydraulic retention time changes on taxonomic and functional characterization in Fluidized Bed Reactor treating commercial laundry wastewater in co-digestion with domestic sewage. Biodegradation, 2020, 31, 73-89.	1.5	12
35	Metagenomic analysis of autochthonous microbial biomass from banana waste: Screening design of factors that affect hydrogen production. Biomass and Bioenergy, 2020, 138, 105573.	2.9	24
36	Heterotrophic nitrifying/aerobic denitrifying bacteria: Ammonium removal under different physical-chemical conditions and molecular characterization. Journal of Environmental Management, 2019, 248, 109294.	3.8	57

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37	Hydrogen, alcohols and volatile fatty acids from the co-digestion of coffee waste (coffee pulp, husk,) Tj ETQq1 1 Hydrogen Energy, 2019, 44, 21434-21450.	0.784314 3.8	rgBT /Over 50
38	The Challenge of Making Wastewater Treatment Plants Composed by Anaerobic Reactors Capable of Removing Nitrogen. Water, Air, and Soil Pollution, 2019, 230, 1.	1.1	5
39	Unveiling resistome profiles in the sediments of an Antarctic volcanic island. Environmental Pollution, 2019, 255, 113240.	3.7	15
40	Laundry wastewater and domestic sewage pilot-scale anaerobic treatment: Microbial community resilience regarding sulfide production. Journal of Environmental Management, 2019, 251, 109495.	3.8	27
41	Antarctic Fungi as Producers of Pigments. , 2019, , 305-318.		6
42	Hydrocarbon-associated substrates reveal promising fungi for poly (ethylene terephthalate) (PET) depolymerization. Brazilian Journal of Microbiology, 2019, 50, 633-648.	0.8	19
43	Microbial enhanced oil recovery using a biosurfactant produced by Bacillus safensis isolated from mangrove microbiota - Part I biosurfactant characterization and oil displacement test. Journal of Petroleum Science and Engineering, 2019, 180, 950-957.	2.1	25
44	Land Use and Seasonal Effects on the Soil Microbiome of a Brazilian Dry Forest. Frontiers in Microbiology, 2019, 10, 648.	1.5	61
45	The metagenomic landscape of xenobiotics biodegradation in mangrove sediments. Ecotoxicology and Environmental Safety, 2019, 179, 232-240.	2.9	17
46	Wide diversity of methane and short-chain alkane metabolisms in uncultured archaea. Nature Microbiology, 2019, 4, 603-613.	5.9	187
47	Chemical Characterization and Biotechnological Applicability of Pigments Isolated from Antarctic Bacteria. Marine Biotechnology, 2019, 21, 416-429.	1.1	31
48	Comparative metatranscriptomic analysis of anaerobic digesters treating anionic surfactant contaminated wastewater. Science of the Total Environment, 2019, 649, 482-494.	3.9	33
49	Pigments in an iridescent bacterium, Cellulophaga fucicola, isolated from Antarctica. Antonie Van Leeuwenhoek, 2019, 112, 479-490.	0.7	9
50	Warming weakens facilitative interactions between decomposers and detritivores, and modifies freshwater ecosystem functioning. Global Change Biology, 2018, 24, 3170-3186.	4.2	27
51	Integrated diversity analysis of the microbial community in a reverse osmosis system from a Brazilian oil refinery. Systematic and Applied Microbiology, 2018, 41, 473-486.	1.2	11
52	Effect of salinity in heterotrophic nitrification/aerobic denitrification performed by acclimated microbiota from oil-produced water biological treatment system. International Biodeterioration and Biodegradation, 2018, 130, 1-7.	1.9	52
53	Bacteria from Antarctic environments: diversity and detection of antimicrobial, antiproliferative, and antiparasitic activities. Polar Biology, 2018, 41, 1505-1519.	0.5	33
54	Exploring the potential of halophilic bacteria from oil terminal environments for biosurfactant production and hydrocarbon degradation under high-salinity conditions. International Biodeterioration and Biodegradation, 2018, 126, 231-242.	1.9	60

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55	Microbes and Petroleum Bioremediation. , 2018, , 97-123.		2
56	Antimicrobial, antiparasitic and antiproliferative effects of the extract of Bacillus safensis SG-32 isolated from a Brazilian oil reservoir. African Journal of Microbiology Research, 2018, 12, 897-907.	0.4	2
57	Microbial functional responses to long-term anthropogenic impact in mangrove soils. Ecotoxicology and Environmental Safety, 2018, 160, 231-239.	2.9	19
58	Environmental change and predator diversity drive alpha and beta diversity in freshwater macro and microorganisms. Global Change Biology, 2018, 24, 3715-3728.	4.2	32
59	Anaerobic co-digestion of commercial laundry wastewater and domestic sewage in a pilot-scale EGSB reactor: The influence of surfactant concentration on microbial diversity. International Biodeterioration and Biodegradation, 2018, 127, 77-86.	1.9	46
60	Microbial diversity of a fullâ€scale UASB reactor applied to poultry slaughterhouse wastewater treatment: integration of 16S rRNA gene amplicon and shotgun metagenomic sequencing. MicrobiologyOpen, 2017, 6, e00443.	1.2	43
61	Metagenomic analysis of the microbiome in three different bioreactor configurations applied to commercial laundry wastewater treatment. Science of the Total Environment, 2017, 587-588, 389-398.	3.9	45
62	Ammonium removal from high-salinity oilfield-produced water: assessing the microbial community dynamics at increasing salt concentrations. Applied Microbiology and Biotechnology, 2017, 101, 859-870.	1.7	25
63	Functional metagenomics of oil-impacted mangrove sediments reveals high abundance of hydrolases of biotechnological interest. World Journal of Microbiology and Biotechnology, 2017, 33, 141.	1.7	20
64	Diversity of aromatic hydroxylating dioxygenase genes in mangrove microbiome and their biogeographic patterns across global sites. MicrobiologyOpen, 2017, 6, e00490.	1.2	11
65	Microbial diversity in degraded and non-degraded petroleum samples and comparison across oil reservoirs at local and global scales. Extremophiles, 2017, 21, 211-229.	0.9	34
66	Potential of semiarid soil from Caatinga biome as a novel source for mining lignocellulose-degrading enzymes. FEMS Microbiology Ecology, 2017, 93, fiw248.	1.3	15
67	Taxonomic and functional patterns across soil microbial communities of global biomes. Science of the Total Environment, 2017, 609, 1064-1074.	3.9	32
68	Functional and genetic characterization of hydrocarbon biodegrader and exopolymer-producing clones from a petroleum reservoir metagenomic library. Environmental Technology (United Kingdom), 2017, 38, 1139-1150.	1.2	3
69	A Novel Multifunctional β-N-Acetylhexosaminidase Revealed through Metagenomics of an Oil-Spilled Mangrove. Bioengineering, 2017, 4, 62.	1.6	13
70	Bioaugmentation strategy employing a microbial consortium immobilized in chitosan beads for oil degradation in mesocosm scale. Marine Pollution Bulletin, 2016, 107, 107-117.	2.3	50
71	Enzymatic potential of heterotrophic bacteria from a neutral copper mine drainage. Brazilian Journal of Microbiology, 2016, 47, 846-852.	0.8	5
72	Anthropogenic impact on mangrove sediments triggers differential responses in the heavy metals and antibiotic resistomes of microbial communities. Environmental Pollution, 2016, 216, 460-469.	3.7	80

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73	Evaluation of bacterial diversity recovered from petroleum samples using different physical matrices. Brazilian Journal of Microbiology, 2016, 47, 712-723.	0.8	10
74	Detoxification of Atrazine by Endophytic Streptomyces sp. Isolated from Sugarcane and Detection of Nontoxic Metabolite. Bulletin of Environmental Contamination and Toxicology, 2015, 95, 803-809.	1.3	18
75	Identification of oxidoreductases from the petroleum Bacillus safensis strain. Biotechnology Reports (Amsterdam, Netherlands), 2015, 8, 152-159.	2.1	17
76	Genomic and chemical insights into biosurfactant production by the mangrove-derived strain Bacillus safensis CCMA-560. Applied Microbiology and Biotechnology, 2015, 99, 3155-3167.	1.7	30
77	Slurry Phase Biological Treatment of Latosol Contaminated with Phthalates, Adipate, and Alcohols. Journal of Environmental Engineering, ASCE, 2015, 141, 04014046.	0.7	2
78	Compositional profile of α / βâ€hydrolase fold proteins in mangrove soil metagenomes: prevalence of epoxide hydrolases and haloalkane dehalogenases in oilâ€contaminated sites. Microbial Biotechnology, 2015, 8, 604-613.	2.0	17
79	The use of the carbon/nitrogen ratio and specific organic loading rate as tools for improving biohydrogen production in fixed-bed reactors. Biotechnology Reports (Amsterdam, Netherlands), 2015, 5, 46-54.	2.1	106
80	Molecular diversity of fungal and bacterial communities in the marine sponge <i>Dragmacidon reticulatum</i> . Journal of Basic Microbiology, 2015, 55, 207-220.	1.8	17
81	New FeFe-hydrogenase genes identified in a metagenomic fosmid library from a municipal wastewater treatment plant as revealed by high-throughput sequencing. Research in Microbiology, 2015, 166, 9-19.	1.0	12
82	Classification and Identification of Petroleum Microorganisms by MALDI-TOF Mass Spectrometry. Journal of the Brazilian Chemical Society, 2015, , .	0.6	2
83	New Hydrocarbon Degradation Pathways in the Microbial Metagenome from Brazilian Petroleum Reservoirs. PLoS ONE, 2014, 9, e90087.	1.1	83
84	Bioremediation potential of microorganisms derived from petroleum reservoirs. Marine Pollution Bulletin, 2014, 89, 191-200.	2.3	61
85	Production and Properties of a Surface-Active Lipopeptide Produced by a New Marine Brevibacterium luteolum Strain. Applied Biochemistry and Biotechnology, 2014, 174, 2245-2256.	1.4	29
86	Culturable bacterial diversity from a feed water of a reverse osmosis system, evaluation of biofilm formation and biocontrol using phages. World Journal of Microbiology and Biotechnology, 2014, 30, 2689-2700.	1.7	25
87	Genome Sequence of Bacillus safensis CFA06, Isolated from Biodegraded Petroleum in Brazil. Genome Announcements, 2014, 2, .	0.8	5
88	Chromosome numbers and karyotypes ofCatasetumspecies (Orchidaceae). Plant Biosystems, 2014, 148, 499-507.	0.8	1
89	The Effect of Biomass Immobilization Support Material and Bed Porosity on Hydrogen Production in an Upflow Anaerobic Packed-Bed Bioreactor. Applied Biochemistry and Biotechnology, 2013, 170, 1348-1366.	1.4	45
90	Investigation of the FeFe-hydrogenase gene diversity combined with phylogenetic microbial community analysis of an anaerobic domestic sewage sludge. World Journal of Microbiology and Biotechnology, 2013, 29, 2003-2014.	1.7	10

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91	Diversity analyses of microbial communities in petroleum samples from Brazilian oil fields. International Biodeterioration and Biodegradation, 2013, 81, 57-70.	1.9	84
92	Draft Genome Sequence of the Biosurfactant-Producing Bacterium Gordonia amicalis Strain CCMA-559, Isolated from Petroleum-Impacted Sediment. Genome Announcements, 2013, 1, .	0.8	5
93	Draft Genome Sequence of Bacillus pumilus CCMA-560, Isolated from an Oil-Contaminated Mangrove Swamp. Genome Announcements, 2013, 1, .	0.8	8
94	Identification of Genes and Pathways Related to Phenol Degradation in Metagenomic Libraries from Petroleum Refinery Wastewater. PLoS ONE, 2013, 8, e61811.	1.1	47
95	Taxonomic Diversity and Biodegradation Potential of Bacteria Isolated from Oil Reservoirs of an Offshore Southern Brazilian Basin. Journal of Petroleum & Environmental Biotechnology, 2013, 03, .	0.3	4
96	Diversity of Hydrocarbon-Related Catabolic Genes in Oil Samples from Potiguar Basin (Rn, Brazil). Journal of Petroleum & Environmental Biotechnology, 2013, 04, .	0.3	1
97	Phylogenetic and functional diversity of metagenomic libraries of phenol degrading sludge from petroleum refinery wastewater treatment system. AMB Express, 2012, 2, 18.	1.4	55
98	Correlation of soil microbial community responses to contamination with crude oil with and without chromium and copper. International Biodeterioration and Biodegradation, 2012, 70, 104-110.	1.9	21
99	Could petroleum biodegradation be a joint achievement of aerobic and anaerobic microrganisms in deep sea reservoirs?. AMB Express, 2011, 1, 47.	1.4	37
100	Cultivation-independent methods applied to the microbial prospection of oil and gas in soil from a sedimentary basin in Brazil. AMB Express, 2011, 1, 35.	1.4	22
101	The potential for hydrocarbon biodegradation and production of extracellular polymeric substances by aerobic bacteria isolated from a Brazilian petroleum reservoir. World Journal of Microbiology and Biotechnology, 2011, 27, 1513-1518.	1.7	29
102	Molecular analysis of microbial diversity in corrosion samples from energy transmission towers. Biofouling, 2011, 27, 435-447.	0.8	13
103	Searching for monooxygenases and hydrolases in bacteria from an extreme environment. Applied Microbiology and Biotechnology, 2010, 87, 319-329.	1.7	16
104	Screening and Production Study of Microbial Xylanase Producers from Brazilian Cerrado. Applied Biochemistry and Biotechnology, 2010, 161, 333-346.	1.4	53
105	Microbial diversity associated with algae, ascidians and sponges from the north coast of São Paulo state, Brazil. Microbiological Research, 2010, 165, 466-482.	2.5	137
106	Treatment of linear alkylbenzene sulfonate in a horizontal anaerobic immobilized biomass reactor. Bioresource Technology, 2010, 101, 606-612.	4.8	33
107	Screening for hydrocarbon biodegraders in a metagenomic clone library derived from Brazilian petroleum reservoirs. Organic Geochemistry, 2010, 41, 675-681.	0.9	43
108	Reprint of: Screening for hydrocarbon biodegraders in a metagenomic clone library derived from Brazilian petroleum reservoirs. Organic Geochemistry, 2010, 41, 1067-1073.	0.9	10

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109	Monitoring the Bacterial Community Dynamics in a Petroleum Refinery Wastewater Membrane Bioreactor Fed with a High Phenolic Load. Journal of Microbiology and Biotechnology, 2010, 20, 21-29.	0.9	24
110	Isolation, biodegradation ability and molecular detection of hydrocarbon degrading bacteria in petroleum samples from a Brazilian offshore basin. Organic Geochemistry, 2009, 40, 574-588.	0.9	45
111	Evaluation of the microbial diversity in a horizontal-flow anaerobic immobilized biomass reactor treating linear alkylbenzene sulfonate. Biodegradation, 2008, 19, 375-385.	1.5	38
112	Bacterial diversity characterization in petroleum samples from Brazilian reservoirs. Brazilian Journal of Microbiology, 2008, 39, 445-452.	0.8	30
113	Interaction of endophytic diazotrophic bacteria and Fusarium oxysporum f. sp. cubense on plantlets of banana â€~Maça'. Plant and Soil, 2007, 298, 47-56.	1.8	27
114	Analysis of the composition of bacterial communities in oil reservoirs from a southern offshore Brazilian basin. Antonie Van Leeuwenhoek, 2007, 91, 253-266.	0.7	85
115	A ribosomal RNA gene intergenic spacer based PCR and DGGE fingerprinting method for the analysis of specific rhizobial communities in soil. Journal of Microbiological Methods, 2006, 64, 366-379.	0.7	25
116	Biodegradation and detoxification of -nitrophenol by Rhodococcus wratislaviensis. International Biodeterioration and Biodegradation, 2005, 55, 103-108.	1.9	81
117	Isolation and characterization of alachlor-degrading actinomycetes from soil. Antonie Van Leeuwenhoek, 2005, 87, 81-89.	0.7	25
118	Relationship between cyclohexyl-alkanoic acids and the acidothermophilic bacterium Alicyclobacillus spp.: Evidence from Brazilian oils. Organic Geochemistry, 2005, 36, 1443-1453.	0.9	11
119	Discrimination ofRhizobium tropici and R. leguminosarumstrains by PCRâ€specific amplification of 16S–23S rDNA spacer region fragments and denaturing gradient gel electrophoresis (DGGE). Letters in Applied Microbiology, 1999, 28, 137-141.	1.0	23
120	Evaluation of the diversity of rhizobia in Brazilian agricultural soils cultivated with soybeans. Applied Soil Ecology, 1999, 13, 159-167.	2.1	42