

# Leonardo Erijman

## List of Publications by Year in descending order

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Version: 2024-02-01

45  
papers

1,567  
citations

331670

21  
h-index

315739

38  
g-index

49  
all docs

49  
docs citations

49  
times ranked

2152  
citing authors

#	ARTICLE	IF	CITATIONS
1	Industrial activated sludge exhibit unique bacterial community composition at high taxonomic ranks. <i>Water Research</i> , 2013, 47, 3854-3864.	11.3	183
2	Continuous biosorption of Cu and Zn by immobilized waste biomass <i>Sargassum</i> sp.. <i>Process Biochemistry</i> , 2001, 36, 869-873.	3.7	147
3	Oligomeric protein associations: transition from stochastic to deterministic equilibrium. <i>Biochemistry</i> , 1991, 30, 1595-1599.	2.5	77
4	Bacterial Indicator of Agricultural Management for Soil under No-Till Crop Production. <i>PLoS ONE</i> , 2012, 7, e51075.	2.5	77
5	Crop monoculture rather than agriculture reduces the spatial turnover of soil bacterial communities at a regional scale. <i>Environmental Microbiology</i> , 2015, 17, 678-688.	3.8	71
6	Protein kinase C in <i>Trypanosoma cruzi</i> epimastigote forms: partial purification and characterization. <i>Molecular and Biochemical Parasitology</i> , 1989, 36, 101-108.	1.1	67
7	High quality residues from cover crops favor changes in microbial community and enhance C and N sequestration. <i>Global Ecology and Conservation</i> , 2016, 6, 242-256.	2.1	61
8	Soil microbial communities and glyphosate decay in soils with different herbicide application history. <i>Science of the Total Environment</i> , 2018, 634, 974-982.	8.0	59
9	Balance of Neutral and Deterministic Components in the Dynamics of Activated Sludge Floc Assembly. <i>Microbial Ecology</i> , 2011, 61, 486-495.	2.8	58
10	Bacterial taxa abundance pattern in an industrial wastewater treatment system determined by the full rRNA cycle approach. <i>Environmental Microbiology</i> , 2007, 9, 1780-1789.	3.8	56
11	Shotgun Metagenomic Profiles Have a High Capacity To Discriminate Samples of Activated Sludge According to Wastewater Type. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5186-5196.	3.1	52
12	Bacterial community shifts in nonylphenol polyethoxylates-enriched activated sludge. <i>Water Research</i> , 2004, 38, 2077-2086.	11.3	51
13	Diversity of nitrifying bacteria in a full-scale petroleum refinery wastewater treatment plant experiencing unstable nitrification. <i>Journal of Hazardous Materials</i> , 2010, 181, 281-288.	12.4	48
14	The Bias Associated with Amplicon Sequencing Does Not Affect the Quantitative Assessment of Bacterial Community Dynamics. <i>PLoS ONE</i> , 2014, 9, e99722.	2.5	45
15	Performance of planar and cylindrical carbon electrodes at sedimentary microbial fuel cells. <i>Bioresource Technology</i> , 2012, 126, 328-335.	9.6	43
16	Replicability of dominant bacterial populations after long-term surfactant-enrichment in lab-scale activated sludge. <i>Environmental Microbiology</i> , 2006, 8, 625-638.	3.8	42
17	Molecular monitoring of microbial diversity in an UASB reactor. <i>International Biodeterioration and Biodegradation</i> , 2003, 52, 7-12.	3.9	41
18	Reversible Stalling of Transcription Elongation Complexes by High Pressure. <i>Biophysical Journal</i> , 1998, 75, 453-462.	0.5	38

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19	Reversible dissociation and conformational stability of dimeric ribulose biphosphate carboxylase. <i>Biochemistry</i> , 1993, 32, 5187-5195.	2.5	36
20	Nonrandom Assembly of Bacterial Populations in Activated Sludge Flocs. <i>Microbial Ecology</i> , 2010, 59, 436-444.	2.8	25
21	Time Series Genome-Centric Analysis Unveils Bacterial Response to Operational Disturbance in Activated Sludge. <i>MSystems</i> , 2019, 4, .	3.8	23
22	USE OF SENSITIZED FLUORESCENCE FOR THE STUDY OF THE EXCHANGE OF SUBUNITS IN PROTEIN AGGREGATES. <i>Photochemistry and Photobiology</i> , 1993, 57, 411-415.	2.5	22
23	The influence of soil properties on denitrifying bacterial communities and denitrification potential in no-till production farms under contrasting management in the Argentinean Pampas. <i>Applied Soil Ecology</i> , 2014, 75, 172-180.	4.3	22
24	Heterogeneity of E. coli RNA Polymerase Revealed by High Pressure. <i>Journal of Molecular Biology</i> , 1995, 253, 259-265.	4.2	16
25	Microbiome network analysis of co-occurrence patterns in anaerobic co-digestion of sewage sludge and food waste. <i>Water Science and Technology</i> , 2019, 79, 1956-1965.	2.5	16
26	Molecular Recognition by Calmodulin: Pressure-Induced Reorganization of a Novel Calmodulin~Peptide Complex. <i>Biochemistry</i> , 1996, 35, 1599-1605.	2.5	14
27	Impacts of switching tillage to no-tillage and vice versa on soil structure, enzyme activities and prokaryotic community profiles in Argentinean semi-arid soils. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	14
28	Analysis of Dissociation and Unfolding of Oligomeric Proteins Using a Flat Bed Gel Electrophoresis at High Pressure. <i>Analytical Biochemistry</i> , 1994, 218, 364-369.	2.4	13
29	Quantitative assessment of phenol hydroxylase diversity in bioreactors using a functional gene analysis. <i>Applied Microbiology and Biotechnology</i> , 2008, 78, 863-872.	3.6	13
30	Draft Genome Sequences of Type Strain <i>Sediminibacterium salmoneum</i> NJ-44 and <i>Sediminibacterium</i> sp. Strain C3, a Novel Strain Isolated from Activated Sludge. <i>Genome Announcements</i> , 2014, 2, .	0.8	13
31	Extracellular hydrolytic potential drives microbiome shifts during anaerobic co-digestion of sewage sludge and food waste. <i>Bioresource Technology</i> , 2022, 343, 126102.	9.6	13
32	Microbiomes and glyphosate biodegradation in edaphic and aquatic environments: recent issues and trends. <i>World Journal of Microbiology and Biotechnology</i> , 2022, 38, 98.	3.6	13
33	Long-run bacteria-phage coexistence dynamics under natural habitat conditions in an environmental biotechnology system. <i>ISME Journal</i> , 2021, 15, 636-648.	9.8	12
34	Anaerobic nonylphenol ethoxylate degradation coupled to nitrate reduction in a modified biodegradability batch test. <i>Chemosphere</i> , 2007, 68, 2136-2143.	8.2	11
35	Phosphorescence Emission of 7-Azatriptophan and 5-Hydroxytryptophan in Fluid Solutions and in $\pm$ 2RNA Polymerase. <i>Biochemical and Biophysical Research Communications</i> , 1998, 248, 347-351.	2.1	10
36	Impact of non-ionic surfactant on the long-term development of lab-scale-activated sludge bacterial communities. <i>Research in Microbiology</i> , 2007, 158, 712-717.	2.1	10

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37	Maintenance of phenol hydroxylase genotypes at high diversity in bioreactors exposed to step increases in phenol loading. <i>FEMS Microbiology Ecology</i> , 2010, 73, no-no.	2.7	10
38	High pressure electrophoresis in narrow bore glass tubes: One- and two-dimensional separations of protein subunits. <i>Review of Scientific Instruments</i> , 1996, 67, 813-817.	1.3	9
39	Glyphosate Biodegradation Potential in Soil Based on Glycine Oxidase Gene (thiO) from <i>Bradyrhizobium</i> . <i>Current Microbiology</i> , 2021, 78, 1991-2000.	2.2	9
40	Modulation of Maize Rhizosphere Microbiota Composition by Inoculation with <i>Azospirillum argentinense</i> Az39 (Formerly <i>A. brasilense</i> Az39). <i>Journal of Soil Science and Plant Nutrition</i> , 2022, 22, 3553-3567.	3.4	8
41	Expression of stress-related proteins in <i>Sediminibacterium</i> sp. growing under planktonic conditions. <i>Journal of Basic Microbiology</i> , 2015, 55, 1134-1140.	3.3	7
42	A rapid and simple protocol for concentration of SARS-CoV-2 from sewage. <i>Journal of Virological Methods</i> , 2021, 297, 114272.	2.1	6
43	New methods for spectrofluorometer monochromator wavelength calibration. <i>Journal of Proteomics</i> , 1988, 17, 61-66.	2.4	3
44	Genetic Approaches for Improving Performance of Microbial Fuel Cells: Part A. , 2018, , 243-285.		0
45	Editorial: Meta-omic Approaches to the Complex Anaerobic Communities in Wastewater Treatment Plants and Digesters. <i>Frontiers in Microbiology</i> , 2021, 12, 664716.	3.5	0