Edoardo Puglisi

List of Publications by Year in descending order

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95 papers 3,314 citations

147566 31 h-index 53 g-index

101 all docs

101 docs citations

times ranked

101

4687 citing authors

#	Article	IF	CITATIONS
1	Evolution of microbial communities and nutritional content of fermented Amaranthus sp. leaves. International Journal of Food Microbiology, 2022, 362, 109445.	2.1	3
2	Land-use change affects the diversity and functionality of soil bacterial communities in semi-arid Chaco region, Argentina. Applied Soil Ecology, 2022, 172, 104362.	2.1	19
3	The treatment of the organic fraction of municipal solid waste (OFMSW) as a possible source of micro- and nano-plastics and bioplastics in agroecosystems: a review. Chemical and Biological Technologies in Agriculture, 2022, 9, .	1.9	6
4	Nitrogen use efficiency, rhizosphere bacterial community, and root metabolome reprogramming due to maize seed treatment with microbial biostimulants. Physiologia Plantarum, 2022, 174, e13679.	2.6	13
5	Anaerobic digestion and aerobic composting of rigid biopolymers in bio-waste treatment: fate and effects on the final compost. Bioresource Technology, 2022, 351, 126934.	4.8	23
6	Ecotoxicological effects of a synthetic and a natural insecticide on earthworms and soil bacterial community. Environmental Advances, 2022, 8, 100225.	2.2	4
7	Integrated Phenotypic-Genotypic Analysis of Candidate Probiotic Weissella CibariaÂStrains Isolated from Dairy Cows in Kuwait. Probiotics and Antimicrobial Proteins, 2021, 13, 809-823.	1.9	8
8	Silvopastoral systems in dry Chaco, Argentina: Impact on soil chemical parameters and bacterial communities. Soil Use and Management, 2021, 37, 866-878.	2.6	5
9	Smallholder Farmers' Practices and African Indigenous Vegetables Affect Soil Microbial Biodiversity and Enzyme Activities in Lake Naivasha Basin, Kenya. Biology, 2021, 10, 44.	1.3	4
10	Reducing N Fertilization without Yield Penalties in Maize with a Commercially Available Seed Dressing. Agronomy, 2021, 11, 407.	1.3	5
11	Integrated Genomic and Greenhouse Assessment of a Novel Plant Growth-Promoting Rhizobacterium for Tomato Plant. Frontiers in Plant Science, 2021, 12, 660620.	1.7	12
12	Acute and chronic effects of Titanium dioxide (TiO2) PM1 on honey bee gut microbiota under laboratory conditions. Scientific Reports, 2021, 11, 5946.	1.6	12
13	Potential role of microbiome in Chronic Fatigue Syndrome/Myalgic Encephalomyelits (CFS/ME). Scientific Reports, 2021, 11, 7043.	1.6	42
14	Bioaugmented Phytoremediation of Metal-Contaminated Soils and Sediments by Hemp and Giant Reed. Frontiers in Microbiology, 2021, 12, 645893.	1.5	28
15	Low density polyethylene degradation by filamentous fungi. Environmental Pollution, 2021, 274, 116548.	3.7	52
16	The extracellular DNA can baffle the assessment of soil bacterial community, but the effect varies with microscale spatial distribution. FEMS Microbiology Letters, 2021, 368, .	0.7	4
17	Bacterial community profiling of floating plastics from South Mediterranean sites: First evidence of effects on mussels as possible vehicles of transmission. Journal of Hazardous Materials, 2021, 411, 125079.	6.5	13
18	Lactic Acid Bacteria Strains Differently Modulate Gut Microbiota and Metabolic and Immunological Parameters in High-Fat Diet-Fed Mice. Frontiers in Nutrition, 2021, 8, 718564.	1.6	14

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19	The hidden effects of agrochemicals on plant metabolism and root-associated microorganisms. Plant Science, 2021, 311, 111012.	1.7	17
20	Fermentation as a tool for increasing food security and nutritional quality of indigenous African leafy vegetables: the case of Cucurbita sp Food Microbiology, 2021, 99, 103820.	2.1	18
21	Combined Impact of No-Till and Cover Crops with or without Short-Term Water Stress as Revealed by Physicochemical and Microbiological Indicators. Biology, 2021, 10, 23.	1.3	4
22	Pedosedimentary and microbial investigation of a karst sequence record. Science of the Total Environment, 2021, , 151297.	3.9	1
23	Epiphytic Microbial Community and Post-Harvest Characteristics of Strawberry Fruits as Affected by Plant Nutritional Regime with Silicon. Agronomy, 2021, 11, 2407.	1.3	2
24	Biodiversity and technological-functional potential of lactic acid bacteria isolated from spontaneously fermented chia sourdough. International Journal of Food Microbiology, 2020, 316, 108425.	2.1	32
25	Sustainability Perspectives of Vigna unguiculata L. Walp. Cultivation under No Tillage and Water Stress Conditions. Plants, 2020, 9, 48.	1.6	19
26	<i>Enterococcus faecalis</i> and <i>Vibrio harveyi</i> colonize low-density polyethylene and biodegradable plastics under marine conditions. FEMS Microbiology Letters, 2020, 367, .	0.7	10
27	Sub-Lethal Effects of Pesticides on the DNA of Soil Organisms as Early Ecotoxicological Biomarkers. Frontiers in Microbiology, 2020, 11, 1892.	1.5	26
28	Biopolymers modulate microbial communities in municipal organic waste digestion. FEMS Microbiology Ecology, 2020, 96, .	1.3	17
29	Isolation and Screening of Extracellular PGPR from the Rhizosphere of Tomato Plants after Long-Term Reduced Tillage and Cover Crops. Plants, 2020, 9, 668.	1.6	27
30	Fate of Biodegradable Polymers Under Industrial Conditions for Anaerobic Digestion and Aerobic Composting of Food Waste. Journal of Polymers and the Environment, 2020, 28, 2539-2550.	2.4	49
31	Selective bacterial colonization processes on polyethylene waste samples in an abandoned landfill site. Scientific Reports, 2019, 9, 14138.	1.6	77
32	Characterization of Bifidobacterium species in feaces of the Egyptian fruit bat: Description of B. vespertilionis sp. nov. and B. rousetti sp. nov Systematic and Applied Microbiology, 2019, 42, 126017.	1.2	22
33	Genome Sequence Announcement of Lactobacillus vaginalis LMG S-26419, Isolated from a Healthy Woman. Microbiology Resource Announcements, 2019, 8, .	0.3	0
34	Azadirachtin and trifloxystrobin had no inhibitory effects on key soil microbial functions even at high dose rates. Applied Soil Ecology, 2019, 137, 29-38.	2.1	17
35	Prebiotic supplementation over a cold season and during antibiotic treatment specifically modulates the gut microbiota composition of 3-6 year-old children. Beneficial Microbes, 2019, 10, 253-263.	1.0	26
36	Modulation of microbial consortia enriched from different polluted environments during petroleum biodegradation. Biodegradation, 2018, 29, 187-209.	1.5	30

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37	Draft Genome Sequences of Strains TRE 1, TRE D, TRE H, and TRI 7, Isolated from Tamarins and Belonging to Four Putative Novel Bifidobacterium Species. Genome Announcements, 2018, 6, .	0.8	1
38	Effective carbon sequestration in Italian agricultural soils by <i>in situ</i> polymerization of soil organic matter under biomimetic photocatalysis. Land Degradation and Development, 2018, 29, 485-494.	1.8	24
39	Bifidobacterium primatium sp. nov., Bifidobacterium scaligerum sp. nov., Bifidobacterium felsineum sp. nov. and Bifidobacterium simiarum sp. nov.: Four novel taxa isolated from the faeces of the cotton top tamarin (Saguinus oedipus) and the emperor tamarin (Saguinus imperator). Systematic and Applied Microbiology, 2018, 41, 593-603.	1.2	38
40	Molecular and Microbiological Insights on the Enrichment Procedures for the Isolation of Petroleum Degrading Bacteria and Fungi. Frontiers in Microbiology, 2018, 9, 2543.	1.5	56
41	Blame It on the Metabolite: 3,5-Dichloroaniline Rather than the Parent Compound Is Responsible for the Decreasing Diversity and Function of Soil Microorganisms. Applied and Environmental Microbiology, 2018, 84, .	1.4	41
42	Genome Sequence of Azospirillum brasilense REC3, Isolated from Strawberry Plants. Genome Announcements, 2018, 6, .	0.8	5
43	Butyric acid producing clostridia in cheese – Towards the completion of knowledge by means of an amalgamate of methodologies. International Dairy Journal, 2018, 86, 86-95.	1.5	13
44	Gut microbiota profile in systemic sclerosis patients with and without clinical evidence of gastrointestinal involvement. Scientific Reports, 2017, 7, 14874.	1.6	65
45	Infant Early Gut Colonization by Lachnospiraceae: High Frequency of Ruminococcus gnavus. Frontiers in Pediatrics, 2016, 4, 57.	0.9	93
46	Genome Sequence of Acidovorax avenae Strain T10 $_61$ Associated with Sugarcane Red Stripe in Argentina. Genome Announcements, 2016, 4, .	0.8	8
47	Mutations in rpoB sequences of Actinobacteria: a confounding factor in conjugal transfer experiments. International Journal of Antimicrobial Agents, 2016, 47, 105-106.	1.1	0
48	Effects of geographic area, feedstock, temperature, and operating time on microbial communities of six full-scale biogas plants. Bioresource Technology, 2016, 218, 980-990.	4.8	43
49	Microbial ecology involved in the ripening of naturally fermented llama meat sausages. A focus on lactobacilli diversity. International Journal of Food Microbiology, 2016, 236, 17-25.	2.1	47
50	Detailed analyses of the bacterial populations in processed cocoa beans of different geographic origin, subject to varied fermentation conditions. International Journal of Food Microbiology, 2016, 236, 98-106.	2.1	46
51	Protease encoding microbial communities and protease activity of the rhizosphere and bulk soils of two maize lines with different N uptake efficiency. Soil Biology and Biochemistry, 2016, 96, 176-179.	4.2	49
52	Transcriptome analysis of Bacillus thuringiensis spore life, germination and cell outgrowth in a vegetable-based food model. Food Microbiology, 2016, 55, 73-85.	2.1	28
53	Manganese and iron as structuring parameters of microbial communities in Arctic marine sediments from the Baffin Bay. FEMS Microbiology Ecology, 2015, 91, .	1.3	23
54	Ecology of antibiotic resistant coagulase-negative staphylococci isolated from the production chain of a typical Italian salami. Food Control, 2015, 53, 14-22.	2.8	16

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55	Microbial analyses of traditional Italian salami reveal microorganisms transfer from the natural casing to the meat matrix. International Journal of Food Microbiology, 2015, 207, 57-65.	2.1	56
56	High-throughput assessment of bacterial ecology in hog, cow and ovine casings used in sausages production. International Journal of Food Microbiology, 2015, 212, 49-59.	2.1	26
57	Understanding the bacterial communities of hard cheese with blowing defect. Food Microbiology, 2015, 52, 106-118.	2.1	72
58	Comparing natural and selected starter cultures in meat and cheese fermentations. Current Opinion in Food Science, 2015, 2, 118-122.	4.1	47
59	Changes in soil bacterial communities and diversity in response to long-term silver exposure. FEMS Microbiology Ecology, 2015, 91, fiv114.	1.3	67
60	Bacterial diversity in typical Italian salami at different ripening stages as revealed by high-throughput sequencing of 16S rRNA amplicons. Food Microbiology, 2015, 46, 342-356.	2.1	191
61	Changes in bacterial and archaeal community assemblages along an ombrotrophic peat bog profile. Biology and Fertility of Soils, 2014, 50, 815-826.	2.3	14
62	Bacterial diversity in a contaminated Alpine glacier as determined by culture-based and molecular approaches. Science of the Total Environment, 2014, 497-498, 50-59.	3.9	12
63	Rhizosphere microbial diversity as influenced by humic substance amendments and chemical composition of rhizodeposits. Journal of Geochemical Exploration, 2013, 129, 82-94.	1.5	54
64	Soil microbial diversity patterns of a lowland spring environment. FEMS Microbiology Ecology, 2013, 86, 172-184.	1.3	29
65	EUROSOIL 2012 bioremediation session: preface to special issue. Biodegradation, 2013, 24, 451-453.	1.5	2
66	Draft Genome Sequence of Clostridium tyrobutyricum Strain UC7086, Isolated from Grana Padano Cheese with Late-Blowing Defect. Genome Announcements, 2013, 1, .	0.8	18
67	Draft Genome Sequence of Vancomycin-Heteroresistant Staphylococcus epidermidis Strain UC7032, Isolated from Food. Genome Announcements, 2013, 1, .	0.8	4
68	Adaptation of Soil Microorganisms to Trace Element Contamination: A Review of Mechanisms, Methodologies, and Consequences for Risk Assessment and Remediation. Critical Reviews in Environmental Science and Technology, 2012, 42, 2435-2470.	6.6	29
69	Response of microbial organisms (aquatic and terrestrial) to pesticides. EFSA Supporting Publications, 2012, 9, 359E.	0.3	16
70	Response of Ammonia Oxidizing Bacteria and Archaea to Acute Zinc Stress and Different Moisture Regimes in Soil. Microbial Ecology, 2012, 64, 1028-1037.	1.4	25
71	Potential nitrification, nitrate reductase, and \hat{l}^2 -galactosidase activities as indicators of restoration of ecological functions in a Zn-contaminated soil. Biology and Fertility of Soils, 2012, 48, 923-931.	2.3	7
72	Impact of Fungicides on the Diversity and Function of Non-target Ammonia-Oxidizing Microorganisms Residing in a Litter Soil Cover. Microbial Ecology, 2012, 64, 692-701.	1.4	35

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73	Effects of Methods of Carbon Sequestration in Soil on Biochemical Indicators of Soil Quality., 2012,, 179-207.		4
74	Soil enzymology: classical and molecular approaches. Biology and Fertility of Soils, 2012, 48, 743-762.	2.3	493
75	Soil Bacterial Diversity Screening Using Single 16S rRNA Gene V Regions Coupled with Multi-Million Read Generating Sequencing Technologies. PLoS ONE, 2012, 7, e42671.	1.1	92
76	Bioremediation and Mitigation of Organic Contaminants in the Era of Climate Changes., 2012,, 467-485.		1
77	Relative sensitivity of different soil biological properties to zinc. Soil Biology and Biochemistry, 2011, 43, 1798-1807.	4.2	25
78	Transcriptional Response of Rhodococcus aetherivorans I24 to Polychlorinated Biphenyl-Contaminated Sediments. Microbial Ecology, 2010, 60, 505-515.	1.4	12
79	Conformational Distribution of Dissolved Organic Matter Released from Compost by Repeated Water Extractions. Compost Science and Utilization, 2010, 18, 105-110.	1.2	4
80	Soil monitoring of pentachlorophenol by bioavailability and ecotoxicity measurements. Journal of Environmental Monitoring, 2010, 12, 1575.	2.1	9
81	Bioaccessibility, bioavailability and ecotoxicity of pentachlorophenol in compost amended soils. Chemosphere, 2009, 77, 80-86.	4.2	23
82	Effects of a humic acid and its size-fractions on the bacterial community of soil rhizosphere under maize (Zea mays L.). Chemosphere, 2009, 77, 829-837.	4.2	63
83	Carbon deposition in soil rhizosphere following amendments with compost and its soluble fractions, as evaluated by combined soil–plant rhizobox and reporter gene systems. Chemosphere, 2008, 73, 1292-1299.	4.2	47
84	Bioavailability and degradation of phenanthrene in compost amended soils. Chemosphere, 2007, 67, 548-556.	4.2	113
85	EXTRACTION AND BIOANALYSIS OF THE ECOTOXICOLOGICALLY RELEVANT FRACTION OF CONTAMINANTS IN SEDIMENTS. Environmental Toxicology and Chemistry, 2007, 26, 2122.	2.2	32
86	Monitoring tricyclazole residues in rice paddy watersheds. Chemosphere, 2006, 62, 303-314.	4.2	74
87	Description of chemical and biological soil characteristics of two fields subjected to different agricultural management under mediterranean conditions. Italian Journal of Agronomy, 2006, 1, 379.	0.4	2
88	Development and validation of numerical indexes integrating enzyme activities of soils. Soil Biology and Biochemistry, 2006, 38, 1673-1681.	4.2	132
89	Changes in chemical and biological soil properties as induced by anthropogenic disturbance: A case study of an agricultural soil under recurrent flooding by wastewaters. Soil Biology and Biochemistry, 2006, 38, 2069-2080.	4.2	61
90	A soil alteration index based on phospholipid fatty acids. Chemosphere, 2005, 61, 1548-1557.	4.2	41

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91	A model assessing bioavailability of persistent organic pollutants in soil. , 2005, , 39-49.		1
92	Effect of air-drying treatment on enzymatic activities of soils affected by anthropogenic activities. Biology and Fertility of Soils, 2003, 38, 327-332.	2.3	29
93	Cholesterol, $\hat{l}^2\hat{a}\in S$ itosterol, Ergosterol, and Coprostanol in Agricultural Soils. Journal of Environmental Quality, 2003, 32, 466-471.	1.0	32
94	Non-exhaustive extraction techniques (NEETs) for bioavailability assessment of organic hydrophobic compounds in soils. Agronomy for Sustainable Development, 2003, 23, 755-756.	0.8	17
95	Cholesterol, \hat{l}^2 -Sitosterol, Ergosterol, and Coprostanol in Agricultural Soils. Journal of Environmental Quality, 2003, 32, 466.	1.0	13