Blaz Stres

List of Publications by Year in descending order

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55 papers	21,245 citations	304368 22 h-index	197535 49 g-index
56 all docs	56 docs citations	56 times ranked	27589 citing authors

#	Article	IF	Citations
1	Introducing mothur: Open-Source, Platform-Independent, Community-Supported Software for Describing and Comparing Microbial Communities. Applied and Environmental Microbiology, 2009, 75, 7537-7541.	1.4	18,390
2	Quantitative Detection of the nosZ Gene, Encoding Nitrous Oxide Reductase, and Comparison of the Abundances of 16S rRNA, narG , nirK , and nosZ Genes in Soils. Applied and Environmental Microbiology, 2006, 72, 5181-5189.	1.4	828
3	Phylogenetic Analysis of Nitrite, Nitric Oxide, and Nitrous Oxide Respiratory Enzymes Reveal a Complex Evolutionary History for Denitrification. Molecular Biology and Evolution, 2008, 25, 1955-1966.	3.5	424
4	Rhizosphere bacteria and fungi associated with plant growth in soils of three replanted apple orchards. Plant and Soil, 2015, 395, 317-333.	1.8	200
5	Influence of temperature and soil water content on bacterial, archaeal and denitrifying microbial communities in drained fen grassland soil microcosms. FEMS Microbiology Ecology, 2008, 66, 110-122.	1.3	177
6	Applications of Machine Learning in Human Microbiome Studies: A Review on Feature Selection, Biomarker Identification, Disease Prediction and Treatment. Frontiers in Microbiology, 2021, 12, 634511.	1.5	157
7	Nitrous Oxide Reductase (nosZ) Gene Fragments Differ between Native and Cultivated Michigan Soils. Applied and Environmental Microbiology, 2004, 70, 301-309.	1.4	94
8	The Core Gut Microbiome of Black Soldier Fly (Hermetia illucens) Larvae Raised on Low-Bioburden Diets. Frontiers in Microbiology, 2020, 11, 993.	1.5	91
9	Emissions of CO2, CH4 and N2O from Southern European peatlands. Soil Biology and Biochemistry, 2010, 42, 1437-1446.	4.2	76
10	Recently Deglaciated High-Altitude Soils of the Himalaya: Diverse Environments, Heterogenous Bacterial Communities and Long-Range Dust Inputs from the Upper Troposphere. PLoS ONE, 2013, 8, e76440.	1.1	66
11	Microbial activity and community structure in two drained fen soils in the Ljubljana Marsh. Soil Biology and Biochemistry, 2006, 38, 2762-2771.	4.2	62
12	Frequent freeze-thaw cycles yield diminished yet resistant and responsive microbial communities in two temperate soils: a laboratory experiment. FEMS Microbiology Ecology, 2010, 74, 323-335.	1.3	59
13	Statistical and Machine Learning Techniques in Human Microbiome Studies: Contemporary Challenges and Solutions. Frontiers in Microbiology, 2021, 12, 635781.	1.5	51
14	Ecological and conventional viticulture gives rise to distinct fungal and bacterial microbial communities in vineyard soils. Applied Soil Ecology, 2017, 113, 86-95.	2.1	39
15	Biotic and abiotic processes contribute to successful anaerobic degradation of cyanide by UASB reactor biomass treating brewery waste water. Water Research, 2013, 47, 3644-3653.	5.3	36
16	Impact of Processed Food (Canteen and Oil Wastes) on the Development of Black Soldier Fly (Hermetia) Tj ETQq0 0 0 rgBT /Overlock 10	1.5	36
17	Addressing case specific biogas plant tasks: Industry oriented methane yields derived from 5L Automatic Methane Potential Test Systems in batch or semi-continuous tests using realistic inocula, substrate particle sizes and organic loading. Bioresource Technology, 2014, 153, 180-188.	4.8	35
18	Hypoxia and Inactivity Related Physiological Changes (Constipation, Inflammation) Are Not Reflected at the Level of Gut Metabolites and Butyrate Producing Microbial Community: The PlanHab Study. Frontiers in Physiology, 2017, 8, 250.	1.3	32

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19	Reanalysis of microbiomes in soils affected by apple replant disease (ARD): Old foes and novel suspects lead to the proposal of extended model of disease development. Applied Soil Ecology, 2018, 129, 24-33.	2.1	30
20	Diversity and seasonal variations of mycorrhiza and rhizosphere bacteria in three common plant species at the Slovenian Ljubljana Marsh. Biology and Fertility of Soils, 2009, 45, 573-583.	2.3	26
21	Potential for valorization of dehydrated paper pulp sludge for biogas production: Addition of selected hydrolytic enzymes in semi-continuous anaerobic digestion assays. Energy, 2017, 126, 326-334.	4.5	26
22	Intestinal Metagenomes and Metabolomes in Healthy Young Males: Inactivity and Hypoxia Generated Negative Physiological Symptoms Precede Microbial Dysbiosis. Frontiers in Physiology, 2018, 9, 198.	1.3	25
23	Methane Yield Database: Online infrastructure and bioresource for methane yield data and related metadata. Bioresource Technology, 2015, 189, 217-223.	4.8	21
24	Transformations of mineral nitrogen applied to peat soil during sequential oxic/anoxic cycling. Soil Biology and Biochemistry, 2010, 42, 1338-1346.	4.2	20
25	Hypoxia and inactivity related physiological changes precede or take place in absence of significant rearrangements in bacterial community structure: The PlanHab randomized trial pilot study. PLoS ONE, 2017, 12, e0188556.	1.1	20
26	Effect of the Nursing Mother on the Gut Microbiome of the Offspring During Early Mouse Development. Microbial Ecology, 2019, 78, 517-527.	1.4	17
27	Integral analysis of hydrodynamic cavitation effects on waste activated sludge characteristics, potentially toxic metals, microorganisms and identification of microplastics. Science of the Total Environment, 2022, 806, 151414.	3.9	17
28	Spinal Muscular Atrophy after Nusinersen Therapy: Improved Physiology in Pediatric Patients with No Significant Change in Urine, Serum, and Liquor 1H-NMR Metabolomes in Comparison to an Age-Matched, Healthy Cohort. Metabolites, 2021, 11, 206.	1.3	16
29	Community effort endorsing multiscale modelling, multiscale data science and multiscale computing for systems medicine. Briefings in Bioinformatics, 2019, 20, 1057-1062.	3.2	15
30	1H NMR metabolomics of microbial metabolites in the four MW agricultural biogas plant reactors: A case study of inhibition mirroring the acute rumen acidosis symptoms. Journal of Environmental Management, 2018, 222, 428-435.	3.8	14
31	Shift in the paradigm towards next-generation microbiology. FEMS Microbiology Letters, 2019, 366, .	0.7	12
32	Computational Framework for High-Quality Production and Large-Scale Evolutionary Analysis of Metagenome Assembled Genomes. Molecular Biology and Evolution, 2020, 37, 593-598.	3.5	11
33	Mechanistic Modeling and Multiscale Applications for Precision Medicine: Theory and Practice. Network and Systems Medicine, 2020, 3, 36-56.	2.7	11
34	BEsTRF: a tool for optimal resolution of terminal-restriction fragment length polymorphism analysis based on user-defined primer-enzyme-sequence databases. Bioinformatics, 2009, 25, 1556-1558.	1.8	10
35	Mixture of primary and secondary municipal wastewater sludge as a short-term substrate in 2 MW agricultural biogas plant: site-specific sustainability of enzymatic and ultrasound pretreatments. Journal of Chemical Technology and Biotechnology, 2016, 91, 2769-2778.	1.6	10
36	New Frontiers in Soil Microbiology: How To Link Structure and Function of Microbial Communities?. , 2006, , 1-22.		9

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37	Systems View of Deconditioning During Spaceflight Simulation in the PlanHab Project: The Departure of Urine 1 H-NMR Metabolomes From Healthy State in Young Males Subjected to Bedrest Inactivity and Hypoxia. Frontiers in Physiology, 2020, 11, 532271.	1.3	9
38	An Early Stage Researcher's Primer on Systems Medicine Terminology. Network and Systems Medicine, 2021, 4, 2-50.	2.7	9
39	Microbial community dynamics in mesophilic and thermophilic batch reactors under methanogenic, phenyl acid-forming conditions. Biotechnology for Biofuels, 2020, 13, 81.	6.2	8
40	Lignin intermediates lead to phenyl acid formation and microbial community shifts in meso- and thermophilic batch reactors. Biotechnology for Biofuels, 2021, 14, 27.	6.2	8
41	The Importance of Objective Stool Classification in Fecal 1H-NMR Metabolomics: Exponential Increase in Stool Crosslinking Is Mirrored in Systemic Inflammation and Associated to Fecal Acetate and Methionine. Metabolites, 2021, 11, 172.	1.3	8
42	Composition of the cutaneous bacterial community of a cave amphibian,Proteus anguinus. FEMS Microbiology Ecology, 2019, 95, .	1.3	7
43	Full-scale agricultural biogas plant metal content and process parameters in relation to bacterial and archaeal microbial communities over 2.5 year span. Journal of Environmental Management, 2018, 213, 566-574.	3.8	6
44	Original Leaf Colonisers Shape Fungal Decomposer Communities of Phragmites australis in Intermittent Habitats. Journal of Fungi (Basel, Switzerland), 2022, 8, 284.	1.5	6
45	Exercise and Interorgan Communication: Short-Term Exercise Training Blunts Differences in Consecutive Daily Urine 1H-NMR Metabolomic Signatures between Physically Active and Inactive Individuals. Metabolites, 2022, 12, 473.	1.3	4
46	Distinct approaches for the detection and removal of chimeric 16S rRNA sequences can significantly affect the outcome of between-site comparisons. Aquatic Microbial Ecology, 2012, 66, 13-21.	0.9	3
47	Organisms of the Nitrogen Cycle Under Extreme Conditions: Low Temperature, Salinity, pH Value and Water Stress. , 2007, , 369-379.		2
48	Clustering and Classification of Human Microbiome Data: Evaluating the Impact of Different Settings in Bioinformatics Workflows. , 2019, , .		2
49	Broad diversity of bacteria degrading 17ÃŸ-estradiol-3-sulfate isolated from river sediment and biofilm at a wastewater treatment plant discharge. Archives of Microbiology, 2021, 203, 4209-4219.	1.0	2
50	Student performance study: the outcomes of metabolic, molecular and physical-chemical characterization of intestinal tract microbiome on a four mammalian species model. Acta Agriculturae Slovenica, 2014, , 91-98.	0.2	2
51	Urine and Fecal 1H-NMR Metabolomes Differ Significantly between Pre-Term and Full-Term Born Physically Fit Healthy Adult Males. Metabolites, 2022, 12, 536.	1.3	2
52	The impact of crude glycerol from biodiesel production and its trace element content on biomethane production in a batch experiment: modelling as a step towards impartial routine comparison of results. Acta Hydrotechnica, 2021, , 11-24.	0.4	1
53	General Unified Microbiome Profiling Pipeline (GUMPP) for Large Scale, Streamlined and Reproducible Analysis of Bacterial 16S rRNA Data to Predicted Microbial Metagenomes, Enzymatic Reactions and Metabolic Pathways. Metabolites, 2021, 11, 336.	1.3	1
54	Antibiotic-resistantsoilbacteria in high-altitude (5000-6000 m) soilsoftheHimalaya. Acta Agriculturae Slovenica, 2010, 96, .	0.2	0

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55	DNA encoding for an efficient 'Omics processing. Computer Methods and Programs in Biomedicine, 2010, 100, 175-190.	2.6	0