Gergely Maroti

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4169639/publications.pdf

Version: 2024-02-01

136950 114465 4,618 108 32 63 citations h-index g-index papers 123 123 123 5148 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Microbiomes in supragingival biofilms and saliva of adolescents with gingivitis and gingival health. Oral Diseases, 2022, 28, 2000-2014.	3.0	7
2	Identification of Inflammatory and Regulatory Cytokines IL-1α-, IL-4-, IL-6-, IL-12-, IL-13-, IL-17A-, TNF-α-, and IFN-γ-Producing Cells in the Milk of Dairy Cows with Subclinical and Clinical Mastitis. Pathogens, 2022, 11, 372.	2.8	10
3	Adaptation and phenotypic diversification of Bacillus thuringiensis biofilm are accompanied by fuzzy spreader morphotypes. Npj Biofilms and Microbiomes, 2022, 8, 27.	6.4	4
4	Mitochondrial Side Effects of Surgical Prophylactic Antibiotics Ceftriaxone and Rifaximin Lead to Bowel Mucosal Damage. International Journal of Molecular Sciences, 2022, 23, 5064.	4.1	2
5	Experimental evolution of Bacillus subtilis on Arabidopsis thaliana roots reveals fast adaptation and improved root colonization. IScience, 2022, 25, 104406.	4.1	20
6	Development of a Microalgae-Based Continuous Starch-to-Hydrogen Conversion Approach. Fermentation, 2022, 8, 294.	3.0	11
7	Nocardioides carbamazepini sp. nov., an ibuprofen degrader isolated from a biofilm bacterial community enriched on carbamazepine. Systematic and Applied Microbiology, 2022, 45, 126339.	2.8	10
8	Evaluation of the biostimulant effects of two Chlorophyta microalgae on tomato (Solanum) Tj ETQq0 0 0 rgBT /C	Overlock 1	.0 Т <u>f</u> ₂ 50 462 То
9	Pervasive prophage recombination occurs during evolution of spore-forming <i>Bacilli</i> ISME Journal, 2021, 15, 1344-1358.	9.8	26
10	Genomic and Chemical Diversity of Bacillus subtilis Secondary Metabolites against Plant Pathogenic Fungi. MSystems, $2021, 6, .$	3.8	55
11	Impact of Rap-Phr system abundance on adaptation of Bacillus subtilis. Communications Biology, 2021, 4, 468.	4.4	18
12	Biomolecule composition and draft genome of a novel, high-lipid producing Scenedesmaceae microalga. Algal Research, 2021, 54, 102181.	4.6	4
13	Strain-Specific Biostimulant Effects of Chlorella and Chlamydomonas Green Microalgae on Medicago truncatula. Plants, 2021, 10, 1060.	3.5	19
14	Early response of methanogenic archaea to H2 as evaluated by metagenomics and metatranscriptomics. Microbial Cell Factories, 2021, 20, 127.	4.0	14
15	Comparison of monocultures and a mixed culture of three Chlorellaceae strains to optimize biomass production and biochemical content in microalgae grown in a greenhouse. Journal of Applied Phycology, 2021, 33, 2755-2766.	2.8	6
16	Fructose, glucose and fat interrelationships with metabolic pathway regulation and effects on the gut microbiota. Acta Veterinaria Hungarica, 2021, 69, 134-156.	0.5	2
17	Methane production from green and woody biomass using short rotation willow genotypes for bioenergy generation. Bioresource Technology, 2021, 333, 125223.	9.6	11
18	Diversification of <scp><i>Bacillus subtilis</i></scp> during experimental evolution on <i><scp><4 scp>and the complementarity in root colonization of evolved subpopulations. Environmental Microbiology, 2021, 23, 6122-6136.</scp></i>	3.8	26

#	Article	IF	Citations
19	Perturbation of the mucosa-associated anaerobic gut microbiota in streptozotocin-induced diabetic rats. Acta Biologica Szegediensis, 2021, 65, 75-84.	0.3	4
20	Genome-centric investigation of anaerobic digestion using sustainable second and third generation substrates. Journal of Biotechnology, 2021, 339, 53-64.	3.8	12
21	Assessment of Nitrate Removal Capacity of Two Selected Eukaryotic Green Microalgae. Cells, 2021, 10, 2490.	4.1	8
22	Comparative and phylogenomic analysis of nuclear and organelle genes in cryptic Coelastrella vacuolata MACC-549 green algae. Algal Research, 2021, 58, 102380.	4.6	4
23	Adaptation of Bacillus thuringiensis to Plant Colonization Affects Differentiation and Toxicity. MSystems, 2021, 6, e0086421.	3.8	16
24	Mobile Antimicrobial Resistance Genes in Probiotics. Antibiotics, 2021, 10, 1287.	3.7	22
25	Development of Stable Mixed Microbiota for High Yield Power to Methane Conversion. Energies, 2021, 14, 7336.	3.1	7
26	Genome analysis provides insights into microaerobic toluene-degradation pathway of Zoogloea oleivorans BucT. Archives of Microbiology, 2020, 202, 421-426.	2.2	16
27	Microaerobic conditions caused the overwhelming dominance of Acinetobacter spp. and the marginalization of Rhodococcus spp. in diesel fuel/crude oil mixture-amended enrichment cultures. Archives of Microbiology, 2020, 202, 329-342.	2.2	33
28	Chlorella vulgaris and Its Phycosphere in Wastewater: Microalgae-Bacteria Interactions During Nutrient Removal. Frontiers in Bioengineering and Biotechnology, 2020, 8, 557572.	4.1	34
29	Cheaters shape the evolution of phenotypic heterogeneity in <i>Bacillus subtilis</i> biofilms. ISME Journal, 2020, 14, 2302-2312.	9.8	23
30	A case study of salivary microbiome in smokers and non-smokers in Hungary: analysis by shotgun metagenome sequencing. Journal of Oral Microbiology, 2020, 12, 1773067.	2.7	18
31	Complete Genome Sequences of 13 Bacillus subtilis Soil Isolates for Studying Secondary Metabolite Diversity. Microbiology Resource Announcements, 2020, 9, .	0.6	13
32	Virulence Traits of Inpatient Campylobacter jejuni Isolates, and a Transcriptomic Approach to Identify Potential Genes Maintaining Intracellular Survival. Microorganisms, 2020, 8, 531.	3.6	14
33	Surfactin production is not essential for pellicle and root-associated biofilm development of Bacillus subtilis. Biofilm, 2020, 2, 100021.	3.8	33
34	Genome Analysis of a Historical Shigella dysenteriae Serotype 1 Strain Carrying a Conserved Stx Prophage Region. Frontiers in Microbiology, 2020, 11, 614793.	3.5	1
35	A glimpse of antimicrobial resistance gene diversity in kefir and yoghurt. Scientific Reports, 2020, 10, 22458.	3.3	27
36	Phylogenetic re-evaluation of previously identified Chlamydomonas (Chlorophyta,) Tj ETQq0 0 0 rgBT /Overlock	10 Tf 50 6	7 Td (Chlamyo

3

molecular data. South African Journal of Botany, 2019, 125, 16-23.

36

#	Article	IF	CITATIONS
37	R18C is a new viable P2-like bacteriophage of rabbit origin infecting Citrobacter rodentium and Shigella sonnei strains. Archives of Virology, 2019, 164, 3157-3160.	2.1	4
38	Integrated evolutionary analysis reveals antimicrobial peptides with limited resistance. Nature Communications, 2019, 10, 4538.	12.8	222
39	Exploitation of Algal-Bacterial Consortia in Combined Biohydrogen Generation and Wastewater Treatment. Frontiers in Energy Research, 2019, 7, .	2.3	41
40	The reclassification of 37 strains from The Mosonmagyaróvár Algal Culture Collection, Hungary, which were previously identified as Anabaena (Cyanobacteria, Nostocaceae). South African Journal of Botany, 2019, 123, 333-340.	2.5	0
41	Characterization of Core Microbiomes and Functional Profiles of Mesophilic Anaerobic Digesters Fed With Chlorella vulgaris Green Microalgae and Maize Silage. Frontiers in Energy Research, 2019, 7, .	2.3	19
42	Microbial Community Rearrangements in Power-to-Biomethane Reactors Employing Mesophilic Biogas Digestate. Frontiers in Energy Research, 2019, 7, .	2.3	19
43	Salinity Stress Responses and Adaptation Mechanisms in Eukaryotic Green Microalgae. Cells, 2019, 8, 1657.	4.1	156
44	Evolution of exploitative interactions during diversification in Bacillus subtilis biofilms. FEMS Microbiology Ecology, 2018, 94, .	2.7	33
45	Starvation- and xenobiotic-related transcriptomic responses of the sulfanilic acid-degrading bacterium, Novosphingobium resinovorum SA1. Applied Microbiology and Biotechnology, 2018, 102, 305-318.	3.6	12
46	Antimicrobial Activity of NCR Plant Peptides Strongly Depends on the Test Assays. Frontiers in Microbiology, 2018, 9, 2600.	3.5	33
47	Collapse of genetic division of labour and evolution of autonomy in pellicle biofilms. Nature Microbiology, 2018, 3, 1451-1460.	13.3	51
48	The Planktonic Core Microbiome and Core Functions in the Cattle Rumen by Next Generation Sequencing. Frontiers in Microbiology, 2018, 9, 2285.	3 . 5	62
49	Aerobic and oxygen-limited enrichment of BTEX-degrading biofilm bacteria: dominance of Malikia versus Acidovorax species. Environmental Science and Pollution Research, 2018, 25, 32178-32195.	5. 3	25
50	Anaerobic gaseous biofuel production using microalgal biomass – A review. Anaerobe, 2018, 52, 1-8.	2.1	53
51	Kinetics of Targeted Phage Rescue in a Mouse Model of Systemic <i>Escherichia coli</i> K1. BioMed Research International, 2018, 2018, 1-8.	1.9	18
52	De novo evolved interference competition promotes the spread of biofilm defectors. Nature Communications, 2017, 8, 15127.	12.8	60
53	Bioaugmentation of the thermophilic anaerobic biodegradation of cellulose and corn stover. Anaerobe, 2017, 46, 104-113.	2.1	37
54	Factors influencing algal photobiohydrogen production in algal-bacterial co-cultures. Algal Research, 2017, 28, 161-171.	4.6	30

#	Article	IF	Citations
55	Complete genome sequence of Novosphingobium resinovorum SA1, a versatile xenobiotic-degrading bacterium capable of utilizing sulfanilic acid. Journal of Biotechnology, 2017, 241, 76-80.	3.8	27
56	Comparative Genomic and Phylogenetic Analysis of a Shiga Toxin Producing Shigella sonnei (STSS) Strain. Frontiers in Cellular and Infection Microbiology, 2017, 7, 229.	3.9	18
57	Comparative Analysis of the Bacterial Membrane Disruption Effect of Two Natural Plant Antimicrobial Peptides. Frontiers in Microbiology, 2017, 8, 51.	3.5	80
58	Biofilm Forming Bacteria during Thermal Water Reinjection. Geofluids, 2017, 2017, 1-7.	0.7	6
59	Draft Genome Sequence of the Soil Isolate Lysinibacillus fusiformis M5, a Potential Hypoxanthine Producer. Genome Announcements, 2016, 4, .	0.8	6
60	Cytolethal distending toxin producing Escherichia coli O157:H43 strain T22 represents a novel evolutionary lineage within the O157 serogroup. Infection, Genetics and Evolution, 2016, 46, 110-117.	2.3	3
61	Comparative analysis of the Shiga toxin converting bacteriophage first detected in Shigella sonnei. Infection, Genetics and Evolution, 2016, 37, 150-157.	2.3	31
62	HupO, a Novel Regulator Involved in Thiosulfate-Responsive Control of HupSL [NiFe]-Hydrogenase Synthesis in Thiocapsa roseopersicina. Applied and Environmental Microbiology, 2016, 82, 2039-2049.	3.1	4
63	Polyphasic analysis of an Azoarcus-Leptothrix-dominated bacterial biofilm developed on stainless steel surface in a gasoline-contaminated hypoxic groundwater. Environmental Science and Pollution Research, 2016, 23, 9019-9035.	5.3	30
64	Surpassing the current limitations of biohydrogen production systems: The case for a novel hybrid approach. Bioresource Technology, 2016, 204, 192-201.	9.6	64
65	Diversity of Microbial Communities in Biogas Reactors. Current Biochemical Engineering, 2016, 3, 177-187.	1.3	7
66	Plant cysteine-rich peptides that inhibit pathogen growth and control rhizobial differentiation in legume nodules. Current Opinion in Plant Biology, 2015, 26, 57-63.	7.1	92
67	Exploitation of algal-bacterial associations in a two-stage biohydrogen and biogas generation process. Biotechnology for Biofuels, 2015, 8, 59.	6.2	75
68	Metagenome changes in the mesophilic biogas-producing community during fermentation of the green alga Scenedesmus obliquus. Journal of Biotechnology, 2015, 215, 52-61.	3.8	66
69	Pilot bioreactor system for rapid test of different industrial wastewater efficiency in hydrogen production through dark fermentation. Journal of Biotechnology, 2015, 208, S118.	3.8	1
70	Metabolic responses of Rhodococcus erythropolis PR4 grown on diesel oil and various hydrocarbons. Applied Microbiology and Biotechnology, 2015, 99, 9745-9759.	3.6	58
71	Temperature-dependent transformation of biogas-producing microbial communities points to the increased importance of hydrogenotrophic methanogenesis under thermophilic operation. Bioresource Technology, 2015, 177, 375-380.	9.6	110
72	Augmented biogas production from protein-rich substrates and associated metagenomic changes. Bioresource Technology, 2015, 178, 254-261.	9.6	68

#	Article	IF	Citations
73	A novel transducible chimeric phage from Escherichia coli O157:H7 Sakai strain encoding Stx1 production. Infection, Genetics and Evolution, 2015, 29, 42-47.	2.3	12
74	An Acidophilic Bacterial-Archaeal-Fungal Ecosystem Linked to Formation of Ferruginous Crusts and Stalactites. Geomicrobiology Journal, 2014, 31, 407-418.	2.0	12
75	Bacterial symbionts enhance photo-fermentative hydrogen evolution of Chlamydomonas algae. Green Chemistry, 2014, 16, 4716-4727.	9.0	75
76	Revealing the factors influencing a fermentative biohydrogen production process using industrial wastewater as fermentation substrate. Biotechnology for Biofuels, 2014, 7, 139.	6.2	43
77	Heterologous functionality and roles of conserved cysteine motifs of the [NiFe]-hydrogenase accessory protein, HupK/HoxV. International Journal of Hydrogen Energy, 2014, 39, 18556-18564.	7.1	1
78	Effect of light on growth and endogenous hormones in Chlorella minutissima (Trebouxiophyceae). Plant Physiology and Biochemistry, 2014, 79, 66-76.	5.8	77
79	Production of a defensin-like antifungal protein NFAP from Neosartorya fischeri in Pichia pastoris and its antifungal activity against filamentous fungal isolates from human infections. Protein Expression and Purification, 2014, 94, 79-84.	1.3	31
80	Simultaneous biohydrogen production and wastewater treatment based on the selective enrichment of the fermentation ecosystem. International Journal of Hydrogen Energy, 2014, 39, 1502-1510.	7.1	19
81	<i>Medicago truncatula</i> symbiotic peptide NCR247 contributes to bacteroid differentiation through multiple mechanisms. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5183-5188.	7.1	161
82	Monitoring of thermophilic adaptation of mesophilic anaerobe fermentation of sugar beet pressed pulp. Bioresource Technology, 2014, 166, 288-294.	9.6	17
83	Nitrogen-fixing Rhizobium-legume symbiosis: are polyploidy and host peptide-governed symbiont differentiation general principles of endosymbiosis?. Frontiers in Microbiology, 2014, 5, 326.	3.5	84
84	Regionally Distinct Alterations in the Composition of the Gut Microbiota in Rats with Streptozotocin-Induced Diabetes. PLoS ONE, 2014, 9, e110440.	2.5	60
85	Draft Genome Sequence of an Escherichia coli O157:H43 Strain Isolated from Cattle. Genome Announcements, 2013, 1 , .	0.8	6
86	Antimicrobial Nodule-Specific Cysteine-Rich Peptides Induce Membrane Depolarization-Associated Changes in the Transcriptome of Sinorhizobium meliloti. Applied and Environmental Microbiology, 2013, 79, 6737-6746.	3.1	112
87	The long polar fimbriae operon and its flanking regions in bovineEscherichia coliO157:H43 and STEC O136:H12 strains. Pathogens and Disease, 2013, 68, 1-7.	2.0	2
88	Sequence Variability of P2-Like Prophage Genomes Carrying the Cytolethal Distending Toxin V Operon in Escherichia coli O157. Applied and Environmental Microbiology, 2013, 79, 4958-4964.	3.1	20
89	Biogas Production from Protein-Rich Biomass: Fed-Batch Anaerobic Fermentation of Casein and of Pig Blood and Associated Changes in Microbial Community Composition. PLoS ONE, 2013, 8, e77265.	2.5	104
90	Characterization of a biogas-producing microbial community by short-read next generation DNA sequencing. Biotechnology for Biofuels, 2012, 5, 41.	6.2	328

#	Article	IF	Citations
91	Analyses of the Large Subunit Histidine-Rich Motif Expose an Alternative Proton Transfer Pathway in [NiFe] Hydrogenases. PLoS ONE, 2012, 7, e34666.	2.5	30
92	Isolation of new Pseudomonas tolaasii bacteriophages and genomic investigation of the lytic phage BF7. FEMS Microbiology Letters, 2012, 332, 162-169.	1.8	20
93	Innate immunity effectors and virulence factors in symbiosis. Current Opinion in Microbiology, 2011, 14, 76-81.	5.1	24
94	Natural roles of antimicrobial peptides in microbes, plants and animals. Research in Microbiology, 2011, 162, 363-374.	2.1	232
95	Specificity and selectivity of HypC chaperonins and endopeptidases in the molecular assembly machinery of [NiFe] hydrogenases of Thiocapsa roseopersicina. International Journal of Hydrogen Energy, 2010, 35, 3358-3370.	7.1	8
96	Plant Peptides Govern Terminal Differentiation of Bacteria in Symbiosis. Science, 2010, 327, 1122-1126.	12.6	525
97	A Second Soluble Hox-Type NiFe Enzyme Completes the Hydrogenase Set in <i>Thiocapsa roseopersicina </i> BBS. Applied and Environmental Microbiology, 2010, 76, 5113-5123.	3.1	26
98	Discovery of [NiFe] Hydrogenase Genes in Metagenomic DNA: Cloning and Heterologous Expression in <i>Thiocapsa roseopersicina</i> . Applied and Environmental Microbiology, 2009, 75, 5821-5830.	3.1	36
99	A novel approach for biohydrogen production. International Journal of Hydrogen Energy, 2006, 31, 1460-1468.	7.1	96
100	Anaerobic regulation of hydrogenase transcription in different bacteria. Biochemical Society Transactions, 2005, 33, 36-38.	3.4	11
101	The hydrogenases of Thiocapsa roseopersicina. Biochemical Society Transactions, 2005, 33, 61-63.	3.4	18
102	Hydrogen independent expression of hupSL genes in Thiocapsa roseopersicina BBS. FEBS Journal, 2005, 272, 4807-4816.	4.7	18
103	An FNR-Type Regulator Controls the Anaerobic Expression of Hyn Hydrogenase in Thiocapsa roseopersicina. Journal of Bacteriology, 2005, 187, 2618-2627.	2.2	13
104	Cyanobacterial-Type, Heteropentameric, NAD ⁺ -Reducing NiFe Hydrogenase in the Purple Sulfur Photosynthetic Bacterium <i>Thiocapsa roseopersicina</i> . Applied and Environmental Microbiology, 2004, 70, 722-728.	3.1	68
105	Modular Broad-Host-Range Expression Vectors for Single-Protein and Protein Complex Purification. Applied and Environmental Microbiology, 2004, 70, 712-721.	3.1	34
106	Improvement of biohydrogen production and intensification of biogas formation. Reviews in Environmental Science and Biotechnology, 2004, 3, 321-330.	8.1	18
107	Accessory proteins functioning selectively and pleiotropically in the biosynthesis of [NiFe] hydrogenases inThiocapsa roseopersicina. FEBS Journal, 2003, 270, 2218-2227.	0.2	37
108	Hydrogenases, accessory genes and the regulation of 6NiFe9 hydrogenase biosynthesis in Thiocapsa roseopersicina. International Journal of Hydrogen Energy, 2002, 27, 1463-1469.	7.1	27