

Andreas DÃ¶tsch

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

3,139
citations

201575

27
h-index

189801

50
g-index

51
all docs

51
docs citations

51
times ranked

4432
citing authors

#	ARTICLE	IF	CITATIONS
1	Gut Microbiome Composition in Obese and Non-Obese Persons: A Systematic Review and Meta-Analysis. <i>Nutrients</i> , 2022, 14, 12.	1.7	121
2	The Core Human Microbiome: Does It Exist and How Can We Find It? A Critical Review of the Concept. <i>Nutrients</i> , 2022, 14, 2872.	1.7	16
3	Microbiological findings in early and late implant loss: an observational clinical case-controlled study. <i>BMC Oral Health</i> , 2021, 21, 112.	0.8	16
4	Identification and Characterization of Human Observational Studies in Nutritional Epidemiology on Gut Microbiomics for Joint Data Analysis. <i>Nutrients</i> , 2021, 13, 3292.	1.7	6
5	Influence of salt concentration and iodized table salt on the microbiota of fermented cucumbers. <i>Food Microbiology</i> , 2020, 92, 103552.	2.1	19
6	From an extremophilic community to an electroautotrophic production strain: identifying a novel <i>Knallgas</i> bacterium as cathodic biofilm biocatalyst. <i>ISME Journal</i> , 2020, 14, 1125-1140.	4.4	28
7	Specific Wheat Fractions Influence Hepatic Fat Metabolism in Diet-Induced Obese Mice. <i>Nutrients</i> , 2019, 11, 2348.	1.7	9
8	Draft Genome Sequences of Type Strains of <i>Gordonibacter faecihominis</i> , <i>Paraeggerthella hongkongensis</i> , <i>Parvibacter caecicola</i> , <i>Slackia equolifaciens</i> , <i>Slackia faecicanis</i> , and <i>Slackia isoflavonicvertens</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	9
9	Efficient Extraction from Mice Feces for NMR Metabolomics Measurements with Special Emphasis on SCFAs. <i>Metabolites</i> , 2019, 9, 55.	1.3	8
10	Efficient Bioelectrochemical Conversion of Industrial Wastewater by Specific Strain Isolation and Community Adaptation. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 23.	2.0	4
11	The influence of an anti-inflammatory diet on gingivitis. A randomized controlled trial. <i>Journal of Clinical Periodontology</i> , 2019, 46, 481-490.	2.3	85
12	Live-dead discrimination analysis, qPCR assessment for opportunistic pathogens, and population analysis at ozone wastewater treatment plants. <i>Environmental Pollution</i> , 2018, 232, 571-579.	3.7	57
13	Does the antidiabetic drug metformin affect embryo development and the health of brown trout (<i>Salmo trutta f. fario</i>)?. <i>Environmental Sciences Europe</i> , 2018, 30, 48.	2.6	29
14	Draft Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Enteritidis MS 501, a Potential Human Pathogen Isolated from Red Lettuce (<i>Lactuca sativa</i> var. <i>capitata</i>) in Karlsruhe, Germany. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	4
15	Insights into the variability of microbial community composition and micropollutant degradation in diverse biological wastewater treatment systems. <i>Water Research</i> , 2018, 143, 313-324.	5.3	81
16	Impact of dental cement on the peri-implant biofilm—microbial comparison of two different cements in an in vivo observational study. <i>Clinical Implant Dentistry and Related Research</i> , 2018, 20, 806-813.	1.6	19
17	Resilience, Dynamics, and Interactions within a Model Multispecies Exoelectrogenic-Biofilm Community. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	37
18	Ability of phages to infect <i>Acinetobacter calcoaceticus</i> – <i>Acinetobacter baumannii</i> complex species through acquisition of different pectate lyase depolymerase domains. <i>Environmental Microbiology</i> , 2017, 19, 5060-5077.	1.8	81

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19	Profiling 5-tolyltriazole biodegrading sludge communities using next-generation sequencing and denaturing gradient gel electrophoresis. <i>Systematic and Applied Microbiology</i> , 2017, 40, 508-515.	1.2	8
20	Investigation on the anaerobic propionate degradation by <i>Escherichia coli</i> K12. <i>Molecular Microbiology</i> , 2017, 103, 55-66.	1.2	20
21	A Genotypic Analysis of Five <i>P. aeruginosa</i> Strains after Biofilm Infection by Phages Targeting Different Cell Surface Receptors. <i>Frontiers in Microbiology</i> , 2017, 8, 1229.	1.5	41
22	Enzyme-Mediated Quenching of the <i>Pseudomonas</i> Quinolone Signal (PQS) Promotes Biofilm Formation of <i>Pseudomonas aeruginosa</i> by Increasing Iron Availability. <i>Frontiers in Microbiology</i> , 2016, 7, 1978.	1.5	23
23	RNASeq Based Transcriptional Profiling of <i>Pseudomonas aeruginosa</i> PA14 after Short- and Long-Term Anoxic Cultivation in Synthetic Cystic Fibrosis Sputum Medium. <i>PLoS ONE</i> , 2016, 11, e0147811.	1.1	42
24	Effect of dental cements on peri-implant microbial community: comparison of the microbial communities inhabiting the peri-implant tissue when using different luting cements. <i>Clinical Oral Implants Research</i> , 2016, 27, e161-e166.	1.9	17
25	Transcriptome Profiling of Antimicrobial Resistance in <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 4722-4733.	1.4	67
26	Ozone treatment of conditioned wastewater selects antibiotic resistance genes, opportunistic bacteria, and induce strong population shifts. <i>Science of the Total Environment</i> , 2016, 559, 103-112.	3.9	206
27	Zellfreie Biom mineralisation: Charakterisierung molekularer Komponenten der Biom mineralisation mittels Biotyping von Coccolithophoriden. <i>Chemie-Ingenieur-Technik</i> , 2016, 88, 1405-1406.	0.4	0
28	A dynamic periplasmic electron transfer network enables respiratory flexibility beyond a thermodynamic regulatory regime. <i>ISME Journal</i> , 2015, 9, 1802-1811.	4.4	134
29	Elucidation of Sigma Factor-Associated Networks in <i>Pseudomonas aeruginosa</i> Reveals a Modular Architecture with Limited and Function-Specific Crosstalk. <i>PLoS Pathogens</i> , 2015, 11, e1004744.	2.1	134
30	Constitutive production of c-di-GMP is associated with mutations in a variant of <i>Pseudomonas aeruginosa</i> with altered membrane composition. <i>Science Signaling</i> , 2015, 8, ra36.	1.6	49
31	The <i>Pseudomonas aeruginosa</i> Transcriptional Landscape Is Shaped by Environmental Heterogeneity and Genetic Variation. <i>MBio</i> , 2015, 6, e00749.	1.8	73
32	<i>Pseudomonas aeruginosa</i> LysR PA4203 Regulator NmoR Acts as a Repressor of the PA4202 <i>nmoA</i> Gene, Encoding a Nitronate Monooxygenase. <i>Journal of Bacteriology</i> , 2015, 197, 1026-1039.	1.0	9
33	Whole genome and transcriptome analyses of environmental antibiotic sensitive and multi-resistant <i>Pseudomonas aeruginosa</i> isolates exposed to waste water and tap water. <i>Microbial Biotechnology</i> , 2015, 8, 116-130.	2.0	21
34	Knockout of Extracytoplasmic Function Sigma Factor ECF-10 Affects Stress Resistance and Biofilm Formation in <i>Pseudomonas putida</i> KT2440. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4911-4919.	1.4	27
35	The peptide chain release factor methyltransferase <i>PrmC</i> is essential for pathogenicity and environmental adaptation of <i>Pseudomonas aeruginosa</i> PA14. <i>Environmental Microbiology</i> , 2013, 15, 597-609.	1.8	21
36	Quantitative Contributions of Target Alteration and Decreased Drug Accumulation to <i>Pseudomonas aeruginosa</i> Fluoroquinolone Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 1361-1368.	1.4	130

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37	The YfiB/NR Signal Transduction Mechanism Reveals Novel Targets for the Evolution of Persistent <i>Pseudomonas aeruginosa</i> in Cystic Fibrosis Airways. <i>PLoS Pathogens</i> , 2012, 8, e1002760.	2.1	105
38	Global regulation of gene expression by OxyR in an important human opportunistic pathogen. <i>Nucleic Acids Research</i> , 2012, 40, 4320-4333.	6.5	189
39	The <i>Pseudomonas aeruginosa</i> Transcriptome in Planktonic Cultures and Static Biofilms Using RNA Sequencing. <i>PLoS ONE</i> , 2012, 7, e31092.	1.1	212
40	Mutation in Elongation Factor G Confers Resistance to the Antibiotic Argyrin in the Opportunistic Pathogen <i>Pseudomonas aeruginosa</i> . <i>ChemBioChem</i> , 2012, 13, 2339-2345.	1.3	30
41	Phenotypic and Genome-Wide Analysis of an Antibiotic-Resistant Small Colony Variant (SCV) of <i>Pseudomonas aeruginosa</i> . <i>PLoS ONE</i> , 2011, 6, e29276.	1.1	81
42	iDynoMiCS: next-generation individual-based modelling of biofilms. <i>Environmental Microbiology</i> , 2011, 13, 2416-2434.	1.8	217
43	Evolutionary conservation of essential and highly expressed genes in <i>Pseudomonas aeruginosa</i> . <i>BMC Genomics</i> , 2010, 11, 234.	1.2	48
44	Damage of <i>Streptococcus mutans</i> biofilms by carolacton, a secondary metabolite from the myxobacterium <i>Sorangium cellulosum</i> . <i>BMC Microbiology</i> , 2010, 10, 199.	1.3	79
45	Genetic determinants of <i>Pseudomonas aeruginosa</i> biofilm establishment. <i>Microbiology (United Kingdom)</i> 151: 1078-1091	0.7	97
46	Global Genotype-Phenotype Correlations in <i>Pseudomonas aeruginosa</i> . <i>PLoS Pathogens</i> , 2010, 6, e1001074.	2.1	12
47	β -Lactam Resistance Response Triggered by Inactivation of a Nonessential Penicillin-Binding Protein. <i>PLoS Pathogens</i> , 2009, 5, e1000353.	2.1	258
48	Evaluation of a microarray-hybridization based method applicable for discovery of single nucleotide polymorphisms (SNPs) in the <i>Pseudomonas aeruginosa</i> genome. <i>BMC Genomics</i> , 2009, 10, 29.	1.2	22
49	Genomewide Identification of Genetic Determinants of Antimicrobial Drug Resistance in <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 2522-2531.	1.4	108
50	A mathematical model for growth and osmoregulation in halophilic bacteria. <i>Microbiology (United Kingdom)</i> 151: 1078-1091	0.7	28