

Andreas Schläpfer

List of Publications by Year in descending order

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139
papers

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47409

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docs citations

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8330
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#	ARTICLE	IF	CITATIONS
1	Phage Genome Diversity in a Biogas-Producing Microbiome Analyzed by Illumina and Nanopore GridION Sequencing. <i>Microorganisms</i> , 2022, 10, 368.	1.6	8
2	Exopolysaccharide Characterization of <i>Rhizobium favelukesii</i> LPU83 and Its Role in the Symbiosis With Alfalfa. <i>Frontiers in Plant Science</i> , 2021, 12, 642576.	1.7	7
3	Identification of Beneficial Microbial Consortia and Bioactive Compounds with Potential as Plant Biostimulants for a Sustainable Agriculture. <i>Microorganisms</i> , 2021, 9, 426.	1.6	37
4	Indicative Marker Microbiome Structures Deduced from the Taxonomic Inventory of 67 Full-Scale Anaerobic Digesters of 49 Agricultural Biogas Plants. <i>Microorganisms</i> , 2021, 9, 1457.	1.6	8
5	Genome Analyses of the Less Aggressive <i>Rhizoctonia solani</i> AG1-IB Isolates 1/2/21 and O8/2 Compared to the Reference AG1-IB Isolate 7/3/14. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 832.	1.5	5
6	Genome Analyses and Genome-Centered Metatranscriptomics of <i>Methanothermobacter wolfeii</i> Strain SIV6, Isolated from a Thermophilic Production-Scale Biogas Fermenter. <i>Microorganisms</i> , 2020, 8, 13.	1.6	8
7	Global transcriptome analysis of <i>Rhizobium favelukesii</i> LPU83 in response to acid stress. <i>FEMS Microbiology Ecology</i> , 2020, 97, .	1.3	10
8	The Role of <i>Petrimonas mucosa</i> ING2-E5AT in Mesophilic Biogas Reactor Systems as Deduced from Multiomics Analyses. <i>Microorganisms</i> , 2020, 8, 2024.	1.6	23
9	Impact of process temperature and organic loading rate on cellulolytic / hydrolytic biofilm microbiomes during biomethanation of ryegrass silage revealed by genome-centered metagenomics and metatranscriptomics. <i>Environmental Microbiomes</i> , 2020, 15, 7.	2.2	13
10	New insights from the biogas microbiome by comprehensive genome-resolved metagenomics of nearly 1600 species originating from multiple anaerobic digesters. <i>Biotechnology for Biofuels</i> , 2020, 13, 25.	6.2	136
11	Genetic Potential of the Biocontrol Agent <i>Pseudomonas brassicacearum</i> (Formerly <i>P. trivialis</i>) 3Re2-7 Unraveled by Genome Sequencing and Mining, Comparative Genomics and Transcriptomics. <i>Genes</i> , 2019, 10, 601.	1.0	32
12	A comprehensive analysis of the <i>Lactuca sativa</i> , L. transcriptome during different stages of the compatible interaction with <i>Rhizoctonia solani</i> . <i>Scientific Reports</i> , 2019, 9, 7221.	1.6	11
13	Effect of Long-Term Farming Practices on Agricultural Soil Microbiome Members Represented by Metagenomically Assembled Genomes (MAGs) and Their Predicted Plant-Beneficial Genes. <i>Genes</i> , 2019, 10, 424.	1.0	61
14	Insight into the structure, function and conjugative transfer of pLPU83a, an accessory plasmid of <i>Rhizobium favelukesii</i> LPU83. <i>Plasmid</i> , 2019, 103, 9-16.	0.4	10
15	Complete Genome Sequencing of <i>Acinetobacter baumannii</i> Strain K50 Discloses the Large Conjugative Plasmid pK50a Encoding Carbapenemase OXA-23 and Extended-Spectrum β -Lactamase GES-11. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	46
16	Complete Genome Sequence of the Novel Cellulolytic, Anaerobic, Thermophilic Bacterium <i>Herbivorax saccincola</i> Type Strain GGR1, Isolated from a Lab Scale Biogas Reactor as Established by Illumina and Nanopore MinION Sequencing. <i>Genome Announcements</i> , 2018, 6, .	0.8	10
17	Assembly of the <i>Lactuca sativa</i> , L. cv. Tizian draft genome sequence reveals differences within major resistance complex 1 as compared to the cv. Salinas reference genome. <i>Journal of Biotechnology</i> , 2018, 267, 12-18.	1.9	13
18	Metagenome, metatranscriptome, and metaproteome approaches unraveled compositions and functional relationships of microbial communities residing in biogas plants. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 5045-5063.	1.7	128

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19	Targeted <i>in situ</i> metatranscriptomics for selected taxa from mesophilic and thermophilic biogas plants. <i>Microbial Biotechnology</i> , 2018, 11, 667-679.	2.0	43
20	<i>Proteiniphilum saccharofermentans</i> str. M3/6T isolated from a laboratory biogas reactor is versatile in polysaccharide and oligopeptide utilization as deduced from genome-based metabolic reconstructions. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2018, 18, e00254.	2.1	30
21	Comparative genomic analysis of <i>Acinetobacter</i> spp. plasmids originating from clinical settings and environmental habitats. <i>Scientific Reports</i> , 2018, 8, 7783.	1.6	72
22	Fungal community profiles in agricultural soils of a long-term field trial under different tillage, fertilization and crop rotation conditions analyzed by high-throughput ITS-amplicon sequencing. <i>PLoS ONE</i> , 2018, 13, e0195345.	1.1	82
23	Characterization of <i>Bathyarchaeota</i> genomes assembled from metagenomes of biofilms residing in mesophilic and thermophilic biogas reactors. <i>Biotechnology for Biofuels</i> , 2018, 11, 167.	6.2	38
24	Genome sequence of <i>Methanobacterium congolense</i> strain Buetzberg, a hydrogenotrophic, methanogenic archaeon, isolated from a mesophilic industrial-scale biogas plant utilizing bio-waste. <i>Journal of Biotechnology</i> , 2017, 247, 1-5.	1.9	48
25	Genome Sequence of the Symbiotic Type Strain <i>Rhizobium tibeticum</i> CCBAU85039 T. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
26	The completely annotated genome and comparative genomics of the <i>Peptoniphilaceae</i> bacterium str. ING2-D1G, a novel acidogenic bacterium isolated from a mesophilic biogas reactor. <i>Journal of Biotechnology</i> , 2017, 257, 178-186.	1.9	2
27	Draft genome sequence of the potato pathogen <i>Rhizoctonia solani</i> AG3-PT isolate Ben3. <i>Archives of Microbiology</i> , 2017, 199, 1065-1068.	1.0	12
28	Bioinformatics for NGS-based metagenomics and the application to biogas research. <i>Journal of Biotechnology</i> , 2017, 261, 10-23.	1.9	84
29	Lifestyle-determining extrachromosomal replicon pAMV1 and its contribution to the carbon metabolism of the methylotrophic bacterium <i>Paracoccus aminovorans</i> JCM 7685. <i>Environmental Microbiology</i> , 2017, 19, 4536-4550.	1.8	40
30	Genome content, metabolic pathways and biotechnological potential of the psychrophilic Arctic bacterium <i>Psychrobacter</i> sp. DAB_AL43B, a source and a host of novel <i>Psychrobacter</i> -specific vectors. <i>Journal of Biotechnology</i> , 2017, 263, 64-74.	1.9	21
31	Transcriptomic buffering of cryptic genetic variation contributes to meningococcal virulence. <i>BMC Genomics</i> , 2017, 18, 282.	1.2	14
32	Identification of a novel mycovirus isolated from <i>Rhizoctonia solani</i> (AG 2-2 IV) provides further information about genome plasticity within the order Tymovirales. <i>Archives of Virology</i> , 2017, 162, 555-559.	0.9	15
33	Genomics and prevalence of bacterial and archaeal isolates from biogas-producing microbiomes. <i>Biotechnology for Biofuels</i> , 2017, 10, 264.	6.2	50
34	The <i>Rhizoctonia solani</i> AG1-IB (isolate 7/3/14) transcriptome during interaction with the host plant lettuce (<i>Lactuca sativa</i> L.). <i>PLoS ONE</i> , 2017, 12, e0177278.	1.1	28
35	Biphasic Study to Characterize Agricultural Biogas Plants by High-Throughput 16S rRNA Gene Amplicon Sequencing and Microscopic Analysis. <i>Journal of Microbiology and Biotechnology</i> , 2017, 27, 321-334.	0.9	31
36	DNA and RNA Extraction and Quantitative Real-Time PCR-Based Assays for Biogas Biocenoses in an Interlaboratory Comparison. <i>Bioengineering</i> , 2016, 3, 7.	1.6	23

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37	Complete Genome Sequence of the Methanogen <i>Methanoculleus bourgensis</i> BA1 Isolated from a Biogas Reactor. <i>Genome Announcements</i> , 2016, 4, .	0.8	11
38	Proteotyping of biogas plant microbiomes separates biogas plants according to process temperature and reactor type. <i>Biotechnology for Biofuels</i> , 2016, 9, 155.	6.2	80
39	Unraveling the microbiome of a thermophilic biogas plant by metagenome and metatranscriptome analysis complemented by characterization of bacterial and archaeal isolates. <i>Biotechnology for Biofuels</i> , 2016, 9, 171.	6.2	134
40	acdc – Automated Contamination Detection and Confidence estimation for single-cell genome data. <i>BMC Bioinformatics</i> , 2016, 17, 543.	1.2	22
41	Identification and genome reconstruction of abundant distinct taxa in microbiomes from one thermophilic and three mesophilic production-scale biogas plants. <i>Biotechnology for Biofuels</i> , 2016, 9, 156.	6.2	120
42	Finished genome sequence and methylome of the cyanide-degrading <i>Pseudomonas pseudoalcaligenes</i> strain CECT5344 as resolved by single-molecule real-time sequencing. <i>Journal of Biotechnology</i> , 2016, 232, 61-68.	1.9	20
43	Genome analysis of the sugar beet pathogen <i>Rhizoctonia solani</i> AG2-2IIIB revealed high numbers in secreted proteins and cell wall degrading enzymes. <i>BMC Genomics</i> , 2016, 17, 245.	1.2	69
44	Genomic characterization of <i>DeFluviitoga tunisiensis</i> L3, a key hydrolytic bacterium in a thermophilic biogas plant and its abundance as determined by metagenome fragment recruitment. <i>Journal of Biotechnology</i> , 2016, 232, 50-60.	1.9	53
45	Draft Genome Sequence of <i>Propionispora</i> sp. Strain 2/2-37, a New Xylan-Degrading Bacterium Isolated from a Mesophilic Biogas Reactor. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
46	Complete Genome Sequence of <i>Herbinix luporum</i> SD1D, a New Cellulose-Degrading Bacterium Isolated from a Thermophilic Biogas Reactor. <i>Genome Announcements</i> , 2016, 4, .	0.8	8
47	Efficiency and biotechnological aspects of biogas production from microalgal substrates. <i>Journal of Biotechnology</i> , 2016, 234, 7-26.	1.9	69
48	Genomics of high molecular weight plasmids isolated from an on-farm biopurification system. <i>Scientific Reports</i> , 2016, 6, 28284.	1.6	17
49	Comparative transcriptome analysis of the biocontrol strain <i>Bacillus amyloliquefaciens</i> FZB42 as response to biofilm formation analyzed by RNA sequencing. <i>Journal of Biotechnology</i> , 2016, 231, 212-223.	1.9	43
50	An integrated metagenome and -proteome analysis of the microbial community residing in a biogas production plant. <i>Journal of Biotechnology</i> , 2016, 231, 268-279.	1.9	33
51	Draft genome sequence of the sugar beet pathogen <i>Rhizoctonia solani</i> AG2-2IIIB strain BBA69670. <i>Journal of Biotechnology</i> , 2016, 222, 11-12.	1.9	20
52	Intraspecies Transfer of the Chromosomal <i>Acinetobacter baumannii</i> bla _{NDM-1} Carbapenemase Gene. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3032-3040.	1.4	65
53	Taxonomic analysis of the microbial community in stored sugar beets using high-throughput sequencing of different marker genes. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw004.	1.3	36
54	Complete genome analysis of <i>Clostridium bornimense</i> strain M2/40T: A new acidogenic <i>Clostridium</i> species isolated from a mesophilic two-phase laboratory-scale biogas reactor. <i>Journal of Biotechnology</i> , 2016, 232, 38-49.	1.9	19

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55	Deep Sequencing Analysis Reveals the Mycoviral Diversity of the Virome of an Avirulent Isolate of <i>Rhizoctonia solani</i> AG-2-2 IV. <i>PLoS ONE</i> , 2016, 11, e0165965.	1.1	58
56	Deeply sequenced metagenome and metatranscriptome of a biogas-producing microbial community from an agricultural production-scale biogas plant. <i>GigaScience</i> , 2015, 4, 33.	3.3	68
57	Fractionation of biogas plant sludge material improves metaproteomic characterization to investigate metabolic activity of microbial communities. <i>Proteomics</i> , 2015, 15, 3585-3589.	1.3	14
58	Genome-guided insight into the methylotrophy of <i>Paracoccus aminophilus</i> JCM 7686. <i>Frontiers in Microbiology</i> , 2015, 6, 852.	1.5	44
59	Development of a <i>Rhizoctonia solani</i> AG1-IB Specific Gene Model Enables Comparative Genome Analyses between Phytopathogenic <i>R. solani</i> AG1-IA, AG1-IB, AG3 and AG8 Isolates. <i>PLoS ONE</i> , 2015, 10, e0144769.	1.1	32
60	Characterization of a collection of plasmid-containing bacteria isolated from an on-farm biopurification system used for pesticide removal. <i>Plasmid</i> , 2015, 80, 16-23.	0.4	16
61	Comparative metagenomics of biogas-producing microbial communities from production-scale biogas plants operating under wet or dry fermentation conditions. <i>Biotechnology for Biofuels</i> , 2015, 8, 14.	6.2	159
62	Insights into the annotated genome sequence of <i>Methanoculleus bourgensis</i> MS2T, related to dominant methanogens in biogas-producing plants. <i>Journal of Biotechnology</i> , 2015, 201, 43-53.	1.9	35
63	Diversity and role of plasmids in adaptation of bacteria inhabiting the Lubin copper mine in Poland, an environment rich in heavy metals. <i>Frontiers in Microbiology</i> , 2015, 6, 152.	1.5	83
64	Improved genome sequence of the phytopathogenic fungus <i>Rhizoctonia solani</i> AG1-IB 7/3/14 as established by deep mate-pair sequencing on the MiSeq (Illumina) system. <i>Journal of Biotechnology</i> , 2015, 203, 19-21.	1.9	27
65	Successful heterologous expression of a novel chitinase identified by sequence analyses of the metagenome from a chitin-enriched soil sample. <i>Journal of Biotechnology</i> , 2015, 201, 60-68.	1.9	13
66	Complete genome sequence of the strain <i>Defluviitoga tunisiensis</i> L3, isolated from a thermophilic, production-scale biogas plant. <i>Journal of Biotechnology</i> , 2015, 203, 17-18.	1.9	58
67	Complete Genome Sequence of the Clinical Strain <i>Acinetobacter baumannii</i> R2090 Carrying the Chromosomally Encoded Metallo- β -Lactamase Gene <i>bla</i> _{NDM-1} . <i>Genome Announcements</i> , 2015, 3, .	0.8	1
68	Community shifts in a well-operating agricultural biogas plant: how process variations are handled by the microbiome. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 7791-7803.	1.7	64
69	Complete Genome Sequence of <i>Acinetobacter baumannii</i> CIP 70.10, a Susceptible Reference Strain for Comparative Genome Analyses. <i>Genome Announcements</i> , 2015, 3, .	0.8	11
70	Draft genome sequence of <i>Herbinix hemicellulosilytica</i> T3/55T, a new thermophilic cellulose degrading bacterium isolated from a thermophilic biogas reactor. <i>Journal of Biotechnology</i> , 2015, 214, 59-60.	1.9	21
71	Complete genome sequence of the novel <i>Porphyromonadaceae</i> bacterium strain ING2-E5B isolated from a mesophilic lab-scale biogas reactor. <i>Journal of Biotechnology</i> , 2015, 193, 34-36.	1.9	65
72	New FeFe-hydrogenase genes identified in a metagenomic fosmid library from a municipal wastewater treatment plant as revealed by high-throughput sequencing. <i>Research in Microbiology</i> , 2015, 166, 9-19.	1.0	12

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73	Identification of Oxygen-Responsive Transcripts in the Silage Inoculant <i>Lactobacillus buchneri</i> CD034 by RNA Sequencing. <i>PLoS ONE</i> , 2015, 10, e0134149.	1.1	19
74	Effect of the strain <i>Bacillus amyloliquefaciens</i> FZB42 on the microbial community in the rhizosphere of lettuce under field conditions analyzed by whole metagenome sequencing. <i>Frontiers in Microbiology</i> , 2014, 5, 252.	1.5	111
75	Rhizobial plasmid pLPU83a is able to switch between different transfer machineries depending on its genomic background. <i>FEMS Microbiology Ecology</i> , 2014, 88, 565-578.	1.3	24
76	Bacterial communities in chitin-amended soil as revealed by 16S rRNA gene based pyrosequencing. <i>Soil Biology and Biochemistry</i> , 2014, 76, 5-11.	4.2	32
77	Architecture and functions of a multipartite genome of the methylotrophic bacterium <i>Paracoccus aminophilus</i> JCM 7686, containing primary and secondary chromids. <i>BMC Genomics</i> , 2014, 15, 124.	1.2	51
78	Complete genome sequence of the cyanide-degrading bacterium <i>Pseudomonas pseudoalcaligenes</i> CECT5344. <i>Journal of Biotechnology</i> , 2014, 175, 67-68.	1.9	28
79	Towards molecular biomarkers for biogas production from lignocellulose-rich substrates. <i>Anaerobe</i> , 2014, 29, 10-21.	1.0	68
80	Complete genome sequence of <i>Peptoniphilus</i> sp. strain ING2-D1G isolated from a mesophilic lab-scale completely stirred tank reactor utilizing maize silage in co-digestion with pig and cattle manure for biomethanation. <i>Journal of Biotechnology</i> , 2014, 192, 59-61.	1.9	16
81	Complete genome sequence of the methanogenic neotype strain <i>Methanobacterium formicicum</i> MFT. <i>Journal of Biotechnology</i> , 2014, 192, 40-41.	1.9	19
82	First draft genome sequence of the amylolytic <i>Bacillus thermoamylovorans</i> wild-type strain 1A1 isolated from a thermophilic biogas plant. <i>Journal of Biotechnology</i> , 2014, 192, 154-155.	1.9	15
83	Complete genome sequence of the cellulolytic thermophile <i>Ruminoclostridium cellulosi</i> wild-type strain DG5 isolated from a thermophilic biogas plant. <i>Journal of Biotechnology</i> , 2014, 188, 136-137.	1.9	30
84	Transcriptome analysis of the phytopathogenic fungus <i>Rhizoctonia solani</i> AG1-IB 7/3/14 applying high-throughput sequencing of expressed sequence tags (ESTs). <i>Fungal Biology</i> , 2014, 118, 800-813.	1.1	32
85	Genome sequence of the acid-tolerant strain <i>Rhizobium</i> sp. LPU83. <i>Journal of Biotechnology</i> , 2014, 176, 40-41.	1.9	8
86	IncH-Type Plasmid Harboring <i>bla</i> _{CTX-M-15} , <i>bla</i> _{DHA-1} , and <i>qnrB4</i> Genes Recovered from Animal Isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 3768-3773.	1.4	19
87	Whole genome sequence of <i>Clostridium bornimense</i> strain M2/40 isolated from a lab-scale mesophilic two-phase biogas reactor digesting maize silage and wheat straw. <i>Journal of Biotechnology</i> , 2014, 184, 199-200.	1.9	8
88	Cultivation-Independent Screening Revealed Hot Spots of IncP-1, IncP-7 and IncP-9 Plasmid Occurrence in Different Environmental Habitats. <i>PLoS ONE</i> , 2014, 9, e89922.	1.1	31
89	Importance of rare taxa for bacterial diversity in the rhizosphere of <i>Bt</i> - and conventional maize varieties. <i>ISME Journal</i> , 2013, 7, 37-49.	4.4	105
90	Detailed analysis of metagenome datasets obtained from biogas-producing microbial communities residing in biogas reactors does not indicate the presence of putative pathogenic microorganisms. <i>Biotechnology for Biofuels</i> , 2013, 6, 49.	6.2	31

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91	Taxonomic Profiling and Metagenome Analysis of a Microbial Community from a Habitat Contaminated with Industrial Discharges. <i>Microbial Ecology</i> , 2013, 66, 533-550.	1.4	39
92	Metagenome analyses reveal the influence of the inoculant <i>Lactobacillus buchneri</i> CD034 on the microbial community involved in grass ensiling. <i>Journal of Biotechnology</i> , 2013, 167, 334-343.	1.9	102
93	MetaSAMS – A novel software platform for taxonomic classification, functional annotation and comparative analysis of metagenome datasets. <i>Journal of Biotechnology</i> , 2013, 167, 156-165.	1.9	17
94	Draft genome sequence of <i>Sinorhizobium meliloti</i> RU11/001, a model organism for flagellum structure, motility and chemotaxis. <i>Journal of Biotechnology</i> , 2013, 168, 731-733.	1.9	9
95	Draft genome sequence of the cellulolytic <i>Clostridium thermocellum</i> wild-type strain BC1 playing a role in cellulosic biomass degradation. <i>Journal of Biotechnology</i> , 2013, 168, 62-63.	1.9	21
96	Draft whole genome sequence of the cyanide-degrading bacterium <i>Pseudomonas pseudoalcaligenes</i> CECT 5344. <i>Environmental Microbiology</i> , 2013, 15, 253-270.	1.8	38
97	Establishment and interpretation of the genome sequence of the phytopathogenic fungus <i>Rhizoctonia solani</i> AG1-IB isolate 7/3/14. <i>Journal of Biotechnology</i> , 2013, 167, 142-155.	1.9	93
98	Complete genome sequence of the hydrogenotrophic Archaeon <i>Methanobacterium</i> sp. Mb1 isolated from a production-scale biogas plant. <i>Journal of Biotechnology</i> , 2013, 168, 734-736.	1.9	42
99	The IncF plasmid pRSB225 isolated from a municipal wastewater treatment plant's on-site preflooder combining antibiotic resistance and putative virulence functions is highly related to virulence plasmids identified in pathogenic <i>E. coli</i> isolates. <i>Plasmid</i> , 2013, 69, 127-137.	0.4	35
100	Metagenome and metaproteome analyses of microbial communities in mesophilic biogas-producing anaerobic batch fermentations indicate concerted plant carbohydrate degradation. <i>Systematic and Applied Microbiology</i> , 2013, 36, 330-338.	1.2	182
101	Complete sequence of broad-host-range plasmid pNOR-2000 harbouring the metallo- β -lactamase gene blaVIM-2 from <i>Pseudomonas aeruginosa</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 1060-1065.	1.3	40
102	Genome Sequence of a <i>Neisseria meningitidis</i> Capsule Null Locus Strain from the Clonal Complex of Sequence Type 198. <i>Journal of Bacteriology</i> , 2012, 194, 5144-5145.	1.0	7
103	Complete Genome Sequence of the Hydrogenotrophic, Methanogenic Archaeon <i>Methanoculleus bourgensis</i> Strain MS2 ^T , Isolated from a Sewage Sludge Digester. <i>Journal of Bacteriology</i> , 2012, 194, 5487-5488.	1.0	55
104	Profiling of the metabolically active community from a production-scale biogas plant by means of high-throughput metatranscriptome sequencing. <i>Journal of Biotechnology</i> , 2012, 158, 248-258.	1.9	198
105	Insights into the completely annotated genome of <i>Lactobacillus buchneri</i> CD034, a strain isolated from stable grass silage. <i>Journal of Biotechnology</i> , 2012, 161, 153-166.	1.9	85
106	IncP- β plasmids of <i>Comamonas</i> sp. and <i>Delftia</i> sp. strains isolated from a wastewater treatment plant mediate resistance to and decolorization of the triphenylmethane dye crystal violet. <i>Microbiology (United Kingdom)</i> , 2012, 158, 2060-2072.	0.7	20
107	Carbapenem-Hydrolyzing GES-5-Encoding Gene on Different Plasmid Types Recovered from a Bacterial Community in a Sewage Treatment Plant. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1292-1295.	1.4	34
108	Characterization of microbial biofilms in a thermophilic biogas system by high-throughput metagenome sequencing. <i>FEMS Microbiology Ecology</i> , 2012, 79, 785-799.	1.3	130

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109	The complete genome sequences of four new IncN plasmids from wastewater treatment plant effluent provide new insights into IncN plasmid diversity and evolution. <i>Plasmid</i> , 2012, 68, 13-24.	0.4	65
110	Comparative and Joint Analysis of Two Metagenomic Datasets from a Biogas Fermenter Obtained by 454-Pyrosequencing. <i>PLoS ONE</i> , 2011, 6, e14519.	1.1	208
111	Sequencing and comparative analysis of IncP-1 [±] antibiotic resistance plasmids reveal a highly conserved backbone and differences within accessory regions. <i>Journal of Biotechnology</i> , 2011, 155, 95-103.	1.9	19
112	The complete genome sequence of the dominant <i>Sinorhizobium meliloti</i> field isolate SM11 extends the <i>S. meliloti</i> pan-genome. <i>Journal of Biotechnology</i> , 2011, 155, 20-33.	1.9	56
113	Complete genome sequencing of <i>Agrobacterium</i> sp. H13-3, the former <i>Rhizobium lupini</i> H13-3, reveals a tripartite genome consisting of a circular and a linear chromosome and an accessory plasmid but lacking a tumor-inducing Ti-plasmid. <i>Journal of Biotechnology</i> , 2011, 155, 50-62.	1.9	112
114	First genomic analysis of the broad-host-range <i>Rhizobium</i> sp. LPU83 strain, a member of the low-genetic diversity Oregon-like <i>Rhizobium</i> sp. group. <i>Journal of Biotechnology</i> , 2011, 155, 3-10.	1.9	17
115	Bioinformatic Analysis Reveals High Diversity of Bacterial Genes for Laccase-Like Enzymes. <i>PLoS ONE</i> , 2011, 6, e25724.	1.1	115
116	Detection of 140 clinically relevant antibiotic-resistance genes in the plasmid metagenome of wastewater treatment plant bacteria showing reduced susceptibility to selected antibiotics. <i>Microbiology (United Kingdom)</i> , 2009, 155, 2306-2319.	0.7	411
117	Phylogenetic characterization of a biogas plant microbial community integrating clone library 16S-rDNA sequences and metagenome sequence data obtained by 454-pyrosequencing. <i>Journal of Biotechnology</i> , 2009, 142, 38-49.	1.9	248
118	Genetic diversity and composition of a plasmid metagenome from a wastewater treatment plant. <i>Journal of Biotechnology</i> , 2008, 136, 65-76.	1.9	87
119	Insight into the plasmid metagenome of wastewater treatment plant bacteria showing reduced susceptibility to antimicrobial drugs analysed by the 454-pyrosequencing technology. <i>Journal of Biotechnology</i> , 2008, 136, 54-64.	1.9	74
120	Comparative genomic hybridisation and ultrafast pyrosequencing revealed remarkable differences between the <i>Sinorhizobium meliloti</i> genomes of the model strain Rm1021 and the field isolate SM11. <i>Journal of Biotechnology</i> , 2008, 136, 31-37.	1.9	18
121	The metagenome of a biogas-producing microbial community of a production-scale biogas plant fermenter analysed by the 454-pyrosequencing technology. <i>Journal of Biotechnology</i> , 2008, 136, 77-90.	1.9	329
122	Taxonomic composition and gene content of a methane-producing microbial community isolated from a biogas reactor. <i>Journal of Biotechnology</i> , 2008, 136, 91-101.	1.9	202
123	Prevalence of pSmeSM11a-like plasmids in indigenous <i>Sinorhizobium meliloti</i> strains isolated in the course of a field release experiment with genetically modified <i>S. meliloti</i> strains. <i>FEMS Microbiology Ecology</i> , 2008, 63, 118-131.	1.3	21
124	Novel Macrolide Resistance Module Carried by the IncP-1 [±] Resistance Plasmid pRSB111, Isolated from a Wastewater Treatment Plant. <i>Antimicrobial Agents and Chemotherapy</i> , 2007, 51, 673-678.	1.4	32
125	IncP-1 [±] Plasmid pGNB1 Isolated from a Bacterial Community from a Wastewater Treatment Plant Mediates Decolorization of Triphenylmethane Dyes. <i>Applied and Environmental Microbiology</i> , 2007, 73, 6345-6350.	1.4	25
126	Sequence analysis of the 181-kb accessory plasmid pSmeSM11b, isolated from a dominant <i>Sinorhizobium meliloti</i> strain identified during a long-term field release experiment. <i>FEMS Microbiology Letters</i> , 2007, 271, 297-309.	0.7	27

#	ARTICLE	IF	CITATIONS
127	Genomics of IncP-1 antibiotic resistance plasmids isolated from wastewater treatment plants provides evidence for a widely accessible drug resistance gene pool. <i>FEMS Microbiology Reviews</i> , 2007, 31, 449-477.	3.9	312
128	Mobilizable IncQ-Related Plasmid Carrying a New Quinolone Resistance Gene, qnrS2, Isolated from the Bacterial Community of a Wastewater Treatment Plant. <i>Antimicrobial Agents and Chemotherapy</i> , 2006, 50, 3075-3080.	1.4	95
129	Sequence of the 68,869bp IncP-1 [±] plasmid pTB11 from a waste-water treatment plant reveals a highly conserved backbone, a Tn402-like integron and other transposable elements. <i>Plasmid</i> , 2005, 53, 218-238.	0.4	93
130	Plasmid pB8 is closely related to the prototype IncP-1 [±] plasmid R751 but transfers poorly to <i>Escherichia coli</i> and carries a new transposon encoding a small multidrug resistance efflux protein. <i>Plasmid</i> , 2005, 54, 135-148.	0.4	56
131	TLA-2, a Novel Ambler Class A Expanded-Spectrum β -Lactamase. <i>Antimicrobial Agents and Chemotherapy</i> , 2005, 49, 4767-4770.	1.4	13
132	Antibiotic multiresistance plasmid pRSB101 isolated from a wastewater treatment plant is related to plasmids residing in phytopathogenic bacteria and carries eight different resistance determinants including a multidrug transport system. <i>Microbiology (United Kingdom)</i> , 2004, 150, 3613-3630.	0.7	128
133	Different molecular rearrangements in the integron of the IncP-1 [±] resistance plasmid pB10 isolated from a wastewater treatment plant result in elevated β -lactam resistance levels. <i>Archives of Microbiology</i> , 2004, 182, 429-435.	1.0	15
134	Occurrence of integron-associated resistance gene cassettes located on antibiotic resistance plasmids isolated from a wastewater treatment plant. <i>FEMS Microbiology Ecology</i> , 2003, 45, 239-252.	1.3	187
135	The <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> <i>glnD</i> gene, encoding a uridylyltransferase/uridylyl-removing enzyme, is expressed in the root nodule but is not essential for nitrogen fixation. <i>Microbiology (United Kingdom)</i> , 2000, 146, 2987-2996.	0.7	18
136	Functional and Regulatory Analysis of the Two Copies of the <i>fixNOQP</i> Operon of <i>Rhizobium leguminosarum</i> Strain VF39. <i>Molecular Plant-Microbe Interactions</i> , 1997, 10, 605-616.	1.4	48
137	<i>Rhizobium leguminosarum</i> bv. <i>viciae</i> contains a second <i>fnr</i> / <i>fixK</i> like gene and an unusual <i>fixL</i> homologue. <i>Molecular Microbiology</i> , 1996, 21, 267-280.	1.2	58
138	An Fnr-like protein encoded in <i>Rhizobium leguminosarum</i> biovar <i>viciae</i> shows structural and functional homology to <i>Rhizobium meliloti</i> FixK. <i>Molecular Genetics and Genomics</i> , 1990, 223, 138-147.	2.4	79
139	The <i>Rhizobium meliloti</i> <i>fdxN</i> gene encoding a ferredoxin-like protein is necessary for nitrogen fixation and is cotranscribed with <i>nifA</i> and <i>nifB</i> . <i>Molecular Genetics and Genomics</i> , 1989, 216, 293-302.	2.4	60