Andreas SchlÃ¼ter

List of Publications by Year
in descending order

139 papers	7,861 citations	41344 49 h-index	58581 82 g-index
145 all docs	145 docs citations	145 times ranked	7523 citing authors

#	Article	IF	Citations
1	Phage Genome Diversity in a Biogas-Producing Microbiome Analyzed by Illumina and Nanopore GridION Sequencing. Microorganisms, 2022, 10, 368.	3.6	8
2	Exopolysaccharide Characterization of Rhizobium favelukesii LPU83 and Its Role in the Symbiosis With Alfalfa. Frontiers in Plant Science, 2021, 12, 642576.	3.6	7
3	Identification of Beneficial Microbial Consortia and Bioactive Compounds with Potential as Plant Biostimulants for a Sustainable Agriculture. Microorganisms, 2021, 9, 426.	3.6	37
4	Indicative Marker Microbiome Structures Deduced from the Taxonomic Inventory of 67 Full-Scale Anaerobic Digesters of 49 Agricultural Biogas Plants. Microorganisms, 2021, 9, 1457.	3.6	8
5	Genome Analyses of the Less Aggressive Rhizoctonia solani AG1-IB Isolates 1/2/21 and O8/2 Compared to the Reference AG1-IB Isolate 7/3/14. Journal of Fungi (Basel, Switzerland), 2021, 7, 832.	3.5	5
6	Genome Analyses and Genome-Centered Metatranscriptomics of Methanothermobacter wolfeii Strain SIV6, Isolated from a Thermophilic Production-Scale Biogas Fermenter. Microorganisms, 2020, 8, 13.	3.6	8
7	Global transcriptome analysis of Rhizobium favelukesii LPU83 in response to acid stress. FEMS Microbiology Ecology, 2020, 97, .	2.7	10
8	The Role of Petrimonas mucosa ING2-E5AT in Mesophilic Biogas Reactor Systems as Deduced from Multiomics Analyses. Microorganisms, 2020, 8, 2024.	3.6	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. Environmental Microbiomes, 2020, 15, 7.	5.0	13
10	New insights from the biogas microbiome by comprehensive genome-resolved metagenomics of nearly 1600 species originating from multiple anaerobic digesters. Biotechnology for Biofuels, 2020, 13, 25.	6.2	136
11	Genetic Potential of the Biocontrol Agent Pseudomonas brassicacearum (Formerly P. trivialis) 3Re2-7 Unraveled by Genome Sequencing and Mining, Comparative Genomics and Transcriptomics. Genes, 2019, 10, 601.	2.4	32
12	A comprehensive analysis of the Lactuca sativa, L. transcriptome during different stages of the compatible interaction with Rhizoctonia solani. Scientific Reports, 2019, 9, 7221.	3.3	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. Genes, 2019, 10, 424.	2.4	61
14	Insight into the structure, function and conjugative transfer of pLPU83a, an accessory plasmid of Rhizobium favelukesii LPU83. Plasmid, 2019, 103, 9-16.	1.4	10
15	Complete Genome Sequencing of Acinetobacter baumannii Strain K50 Discloses the Large Conjugative Plasmid pK50a Encoding Carbapenemase OXA-23 and Extended-Spectrum Î²-Lactamase GES-11. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	46
16	Complete Genome Sequence of the Novel Cellulolytic, Anaerobic, Thermophilic Bacterium Herbivorax saccincola Type Strain GGR1, Isolated from a Lab Scale Biogas Reactor as Established by Illumina and Nanopore MinION Sequencing. Genome Announcements, 2018, 6, .	0.8	10
17	Assembly of the Lactuca sativa, L. cv. Tizian draft genome sequence reveals differences within major resistance complex 1 as compared to the cv. Salinas reference genome. Journal of Biotechnology, 2018, 267, 12-18.	3.8	13
18	Metagenome, metatranscriptome, and metaproteome approaches unraveled compositions and functional relationships of microbial communities residing in biogas plants. Applied Microbiology and Biotechnology, 2018, 102, 5045-5063.	3.6	128

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19	Targeted inÂsitu metatranscriptomics for selected taxa from mesophilic and thermophilic biogas plants. Microbial Biotechnology, 2018, 11, 667-679.	4.2	43
20	Proteiniphilum saccharofermentans str. M3/6T isolated from a laboratory biogas reactor is versatile in polysaccharide and oligopeptide utilization as deduced from genome-based metabolic reconstructions. Biotechnology Reports (Amsterdam, Netherlands), 2018, 18, e00254.	4.4	30
21	Comparative genomic analysis of Acinetobacter spp. plasmids originating from clinical settings and environmental habitats. Scientific Reports, 2018, 8, 7783.	3.3	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. PLoS ONE, 2018, 13, e0195345.	2.5	82
23	Characterization of Bathyarchaeota genomes assembled from metagenomes of biofilms residing in mesophilic and thermophilic biogas reactors. Biotechnology for Biofuels, 2018, 11, 167.	6.2	38
24	Genome sequence of Methanobacterium congolense strain Buetzberg, a hydrogenotrophic, methanogenic archaeon, isolated from a mesophilic industrial-scale biogas plant utilizing bio-waste. Journal of Biotechnology, 2017, 247, 1-5.	3.8	48
25	Genome Sequence of the Symbiotic Type Strain Rhizobium tibeticum CCBAU85039 T. Genome Announcements, 2017, 5, .	0.8	2
26	The completely annotated genome and comparative genomics of the Peptoniphilaceae bacterium str. ING2-D1G, a novel acidogenic bacterium isolated from a mesophilic biogas reactor. Journal of Biotechnology, 2017, 257, 178-186.	3.8	2
27	Draft genome sequence of the potato pathogen Rhizoctonia solani AG3-PT isolate Ben3. Archives of Microbiology, 2017, 199, 1065-1068.	2.2	12
28	Bioinformatics for NGS-based metagenomics and the application to biogas research. Journal of Biotechnology, 2017, 261, 10-23.	3.8	84
29	Lifestyleâ€determining extrachromosomal replicon pAMV1 and its contribution to the carbon metabolism of the methylotrophic bacterium Paracoccus aminovorans JCM 7685. Environmental Microbiology, 2017, 19, 4536-4550.	3.8	40
30	Genome content, metabolic pathways and biotechnological potential of the psychrophilic Arctic bacterium Psychrobacter sp. DAB_AL43B, a source and a host of novel Psychrobacter -specific vectors. Journal of Biotechnology, 2017, 263, 64-74.	3.8	21
31	Transcriptomic buffering of cryptic genetic variation contributes to meningococcal virulence. BMC Genomics, 2017, 18, 282.	2.8	14
32	Identification of a novel mycovirus isolated from Rhizoctonia solani (AG 2-2 IV) provides further information about genome plasticity within the order Tymovirales. Archives of Virology, 2017, 162, 555-559.	2.1	15
33	Genomics and prevalence of bacterial and archaeal isolates from biogas-producing microbiomes. Biotechnology for Biofuels, 2017, 10, 264.	6.2	50
34	The Rhizoctonia solani AG1-IB (isolate 7/3/14) transcriptome during interaction with the host plant lettuce (Lactuca sativa L.). PLoS ONE, 2017, 12, e0177278.	2.5	28
35	Biphasic Study to Characterize Agricultural Biogas Plants by High-Throughput 16S rRNA Gene Amplicon Sequencing and Microscopic Analysis. Journal of Microbiology and Biotechnology, 2017, 27, 321-334.	2.1	31
36	DNA and RNA Extraction and Quantitative Real-Time PCR-Based Assays for Biogas Biocenoses in an Interlaboratory Comparison. Bioengineering, 2016, 3, 7.	3.5	23

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37	Complete Genome Sequence of the Methanogen Methanoculleus bourgensis BA1 Isolated from a Biogas Reactor. Genome Announcements, 2016, 4, .	0.8	11
38	Proteotyping of biogas plant microbiomes separates biogas plants according to process temperature and reactor type. Biotechnology for Biofuels, 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. Biotechnology for Biofuels, 2016, 9, 171.	6.2	134
40	acdc â€“ Automated Contamination Detection and Confidence estimation for single-cell genome data. BMC Bioinformatics, 2016, 17, 543.	2.6	22
41	Identification and genome reconstruction of abundant distinct taxa in microbiomes from one thermophilic and three mesophilic production-scale biogas plants. Biotechnology for Biofuels, 2016, 9, 156.	6.2	120
42	Finished genome sequence and methylome of the cyanide-degrading Pseudomonas pseudoalcaligenes strain CECT5344 as resolved by single-molecule real-time sequencing. Journal of Biotechnology, 2016, 232, 61-68.	3.8	20
43	Genome analysis of the sugar beet pathogen Rhizoctonia solani AG2-2IIIB revealed high numbers in secreted proteins and cell wall degrading enzymes. BMC Genomics, 2016, 17, 245.	2.8	69
44	Genomic characterization of Defluviitoga tunisiensis L3, a key hydrolytic bacterium in a thermophilic biogas plant and its abundance as determined by metagenome fragment recruitment. Journal of Biotechnology, 2016, 232, 50-60.	3.8	53
45	Draft Genome Sequence of Propionispora sp. Strain 2/2-37, a New Xylan-Degrading Bacterium Isolated from a Mesophilic Biogas Reactor. Genome Announcements, 2016, 4, .	0.8	1
46	Complete Genome Sequence of Herbinix luporum SD1D, a New Cellulose-Degrading Bacterium Isolated from a Thermophilic Biogas Reactor. Genome Announcements, 2016, 4, .	0.8	8
47	Efficiency and biotechnological aspects of biogas production from microalgal substrates. Journal of Biotechnology, 2016, 234, 7-26.	3.8	69
48	Genomics of high molecular weight plasmids isolated from an on-farm biopurification system. Scientific Reports, 2016, 6, 28284.	3.3	17
49	Comparative transcriptome analysis of the biocontrol strain Bacillus amyloliquefaciens FZB42 as response to biofilm formation analyzed by RNA sequencing. Journal of Biotechnology, 2016, 231, 212-223.	3.8	43
50	An integrated metagenome and -proteome analysis of the microbial community residing in a biogas production plant. Journal of Biotechnology, 2016, 231, 268-279.	3.8	33
51	Draft genome sequence of the sugar beet pathogen Rhizoctonia solani AG2-2IIIB strain BBA69670. Journal of Biotechnology, 2016, 222, 11-12.	3.8	20
52	Intraspecies Transfer of the Chromosomal Acinetobacter baumannii bla _{NDM-1} Carbapenemase Gene. Antimicrobial Agents and Chemotherapy, 2016, 60, 3032-3040.	3.2	65
53	Taxonomic analysis of the microbial community in stored sugar beets using high-throughput sequencing of different marker genes. FEMS Microbiology Ecology, 2016, 92, fiw004.	2.7	36
54	Complete genome analysis of Clostridium bornimense strain M2/40T: A new acidogenic Clostridium species isolated from a mesophilic two-phase laboratory-scale biogas reactor. Journal of Biotechnology, 2016, 232, 38-49.	3.8	19

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55	Deep Sequencing Analysis Reveals the Mycoviral Diversity of the Virome of an Avirulent Isolate of Rhizoctonia solani AG-2-2 IV. PLoS ONE, 2016, 11, e0165965.	2.5	58
56	Deeply sequenced metagenome and metatranscriptome of a biogas-producing microbial community from an agricultural production-scale biogas plant. GigaScience, 2015, 4, 33.	6.4	68
57	Fractionation of biogas plant sludge material improves metaproteomic characterization to investigate metabolic activity of microbial communities. Proteomics, 2015, 15, 3585-3589.	2.2	14
58	Genome-guided insight into the methylotrophy of Paracoccus aminophilus JCM 7686. Frontiers in Microbiology, 2015, 6, 852.	3.5	44
59	Development of a Rhizoctonia solani AG1-IB Specific Gene Model Enables Comparative Genome Analyses between Phytopathogenic R. solani AG1-IA, AG1-IB, AG3 and AG8 Isolates. PLoS ONE, 2015, 10, e0144769.	2.5	32
60	Characterization of a collection of plasmid-containing bacteria isolated from an on-farm biopurification system used for pesticide removal. Plasmid, 2015, 80, 16-23.	1.4	16
61	Comparative metagenomics of biogas-producing microbial communities from production-scale biogas plants operating under wet or dry fermentation conditions. Biotechnology for Biofuels, 2015, 8, 14.	6.2	159
62	Insights into the annotated genome sequence of Methanoculleus bourgensis MS2T, related to dominant methanogens in biogas-producing plants. Journal of Biotechnology, 2015, 201, 43-53.	3.8	35
63	Diversity and role of plasmids in adaptation of bacteria inhabiting the Lubin copper mine in Poland, an environment rich in heavy metals. Frontiers in Microbiology, 2015, 6, 152.	3.5	83
64	Improved genome sequence of the phytopathogenic fungus Rhizoctonia solani AG1-IB 7/3/14 as established by deep mate-pair sequencing on the MiSeq (Illumina) system. Journal of Biotechnology, 2015, 203, 19-21.	3.8	27
65	Successful heterologous expression of a novel chitinase identified by sequence analyses of the metagenome from a chitin-enriched soil sample. Journal of Biotechnology, 2015, 201, 60-68.	3.8	13
66	Complete genome sequence of the strain Defluviitoga tunisiensis L3, isolated from a thermophilic, production-scale biogas plant. Journal of Biotechnology, 2015, 203, 17-18.	3.8	58
67	Complete Genome Sequence of the Clinical Strain Acinetobacter baumannii R2090 Carrying the Chromosomally Encoded Metallo-Î²-Lactamase Gene bla _{NDM-1}. Genome Announcements, 2015, 3, .	0.8	1
68	Community shifts in a well-operating agricultural biogas plant: how process variations are handled by the microbiome. Applied Microbiology and Biotechnology, 2015, 99, 7791-7803.	3.6	64
69	Complete Genome Sequence of Acinetobacter baumannii CIP 70.10, a Susceptible Reference Strain for Comparative Genome Analyses. Genome Announcements, 2015, 3, .	0.8	11
70	Draft genome sequence of Herbinix hemicellulosilytica T3/55T, a new thermophilic cellulose degrading bacterium isolated from a thermophilic biogas reactor. Journal of Biotechnology, 2015, 214, 59-60.	3.8	21
71	Complete genome sequence of the novel Porphyromonadaceae bacterium strain ING2-E5B isolated from a mesophilic lab-scale biogas reactor. Journal of Biotechnology, 2015, 193, 34-36.	3.8	65
72	New FeFe-hydrogenase genes identified in a metagenomic fosmid library from a municipal wastewater treatment plant as revealed by high-throughput sequencing. Research in Microbiology, 2015, 166, 9-19.	2.1	12

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73	Identification of Oxygen-Responsive Transcripts in the Silage Inoculant Lactobacillus buchneri CD034 by RNA Sequencing. PLoS ONE, 2015, 10, e0134149.	2.5	19
74	Effect of the strain Bacillus amyloliquefaciens FZB42 on the microbial community in the rhizosphere of lettuce under field conditions analyzed by whole metagenome sequencing. Frontiers in Microbiology, 2014, 5, 252.	3.5	111
75	Rhizobial plasmid pLPU83a is able to switch between different transfer machineries depending on its genomic background. FEMS Microbiology Ecology, 2014, 88, 565-578.	2.7	24
76	Bacterial communities in chitin-amended soil as revealed by 16S rRNA gene based pyrosequencing. Soil Biology and Biochemistry, 2014, 76, 5-11.	8.8	32
77	Architecture and functions of a multipartite genome of the methylotrophic bacterium Paracoccus aminophilus JCM 7686, containing primary and secondary chromids. BMC Genomics, 2014, 15, 124.	2.8	51
78	Complete genome sequence of the cyanide-degrading bacterium Pseudomonas pseudoalcaligenes CECT5344. Journal of Biotechnology, 2014, 175, 67-68.	3.8	28
79	Towards molecular biomarkers for biogas production from lignocellulose-rich substrates. Anaerobe, 2014, 29, 10-21.	2.1	68
80	Complete genome sequence of Peptoniphilus 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. Journal of Biotechnology, 2014, 192, 59-61.	3.8	16
81	Complete genome sequence of the methanogenic neotype strain Methanobacterium formicicum MFT. Journal of Biotechnology, 2014, 192, 40-41.	3.8	19
82	First draft genome sequence of the amylolytic Bacillus thermoamylovorans wild-type strain 1A1 isolated from a thermophilic biogas plant. Journal of Biotechnology, 2014, 192, 154-155.	3.8	15
83	Complete genome sequence of the cellulolytic thermophile Ruminoclostridium cellulosi wild-type strain DG5 isolated from a thermophilic biogas plant. Journal of Biotechnology, 2014, 188, 136-137.	3.8	30
84	Transcriptome analysis of the phytopathogenic fungus Rhizoctonia solani AG1-IB 7/3/14 applying high-throughput sequencing of expressed sequence tags (ESTs). Fungal Biology, 2014, 118, 800-813.	2.5	32
85	Genome sequence of the acid-tolerant strain Rhizobium sp. LPU83. Journal of Biotechnology, 2014, 176, 40-41.	3.8	8
86	IncH-Type Plasmid Harboring bla _{CTX-M-15} , bla _{DHA-1} , and qnrB4 Genes Recovered from Animal Isolates. Antimicrobial Agents and Chemotherapy, 2014, 58, 3768-3773.	3.2	19
87	Whole genome sequence of Clostridium bornimense strain M2/40 isolated from a lab-scale mesophilic two-phase biogas reactor digesting maize silage and wheat straw. Journal of Biotechnology, 2014, 184, 199-200.	3.8	8
88	Cultivation-Independent Screening Revealed Hot Spots of IncP-1, IncP-7 and IncP-9 Plasmid Occurrence in Different Environmental Habitats. PLoS ONE, 2014, 9, e89922.	2.5	31
89	Importance of rare taxa for bacterial diversity in the rhizosphere of Bt- and conventional maize varieties. ISME Journal, 2013, 7, 37-49.	9.8	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. Biotechnology for Biofuels, 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. Microbial Ecology, 2013, 66, 533-550.	2.8	39
92	Metagenome analyses reveal the influence of the inoculant Lactobacillus buchneri CD034 on the microbial community involved in grass ensiling. Journal of Biotechnology, 2013, 167, 334-343.	3.8	102
93	MetaSAMSâ€"A novel software platform for taxonomic classification, functional annotation and comparative analysis of metagenome datasets. Journal of Biotechnology, 2013, 167, 156-165.	3.8	17
94	Draft genome sequence of Sinorhizobium meliloti RU11/001, a model organism for flagellum structure, motility and chemotaxis. Journal of Biotechnology, 2013, 168, 731-733.	3.8	9
95	Draft genome sequence of the cellulolytic Clostridium thermocellum wild-type strain BC1 playing a role in cellulosic biomass degradation. Journal of Biotechnology, 2013, 168, 62-63.	3.8	21
96	Draft whole genome sequence of the cyanideâ€degrading bacterium <scp>P</scp>seudomonas pseudoalcaligenes<scp>CECT</scp>5344. Environmental Microbiology, 2013, 15, 253-270.	3.8	38
97	Establishment and interpretation of the genome sequence of the phytopathogenic fungus Rhizoctonia solani AG1-IB isolate 7/3/14. Journal of Biotechnology, 2013, 167, 142-155.	3.8	93
98	Complete genome sequence of the hydrogenotrophic Archaeon Methanobacterium sp. Mb1 isolated from a production-scale biogas plant. Journal of Biotechnology, 2013, 168, 734-736.	3.8	42
99	The IncF plasmid pRSB225 isolated from a municipal wastewater treatment plantâ€™s on-site preflooder combining antibiotic resistance and putative virulence functions is highly related to virulence plasmids identified in pathogenic E. coli isolates. Plasmid, 2013, 69, 127-137.	1.4	35
100	Metagenome and metaproteome analyses of microbial communities in mesophilic biogas-producing anaerobic batch fermentations indicate concerted plant carbohydrate degradation. Systematic and Applied Microbiology, 2013, 36, 330-338.	2.8	182
101	Complete sequence of broad-host-range plasmid pNOR-2000 harbouring the metallo-Î²-lactamase gene blaVIM-2 from Pseudomonas aeruginosa. Journal of Antimicrobial Chemotherapy, 2013, 68, 1060-1065.	3.0	40
102	Genome Sequence of a Neisseria meningitidis Capsule Null Locus Strain from the Clonal Complex of Sequence Type 198. Journal of Bacteriology, 2012, 194, 5144-5145.	2.2	7
103	Complete Genome Sequence of the Hydrogenotrophic, Methanogenic Archaeon Methanoculleus bourgensis Strain MS2 ^T , Isolated from a Sewage Sludge Digester. Journal of Bacteriology, 2012, 194, 5487-5488.	2.2	55
104	Profiling of the metabolically active community from a production-scale biogas plant by means of high-throughput metatranscriptome sequencing. Journal of Biotechnology, 2012, 158, 248-258.	3.8	198
105	Insights into the completely annotated genome of Lactobacillus buchneri CD034, a strain isolated from stable grass silage. Journal of Biotechnology, 2012, 161, 153-166.	3.8	85
106	IncP-1Î² plasmids of Comamonas sp. and Delftia sp. strains isolated from a wastewater treatment plant mediate resistance to and decolorization of the triphenylmethane dye crystal violet. Microbiology (United Kingdom), 2012, 158, 2060-2072.	1.8	20
107	Carbapenem-Hydrolyzing GES-5-Encoding Gene on Different Plasmid Types Recovered from a Bacterial Community in a Sewage Treatment Plant. Applied and Environmental Microbiology, 2012, 78, 1292-1295.	3.1	34
108	Characterization of microbial biofilms in a thermophilic biogas system by high-throughput metagenome sequencing. FEMS Microbiology Ecology, 2012, 79, 785-799.	2.7	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. Plasmid, 2012, 68, 13-24.	1.4	65
110	Comparative and Joint Analysis of Two Metagenomic Datasets from a Biogas Fermenter Obtained by 454-Pyrosequencing. PLoS ONE, 2011, 6, e14519.	2.5	208
111	Sequencing and comparative analysis of IncP-1Î± antibiotic resistance plasmids reveal a highly conserved backbone and differences within accessory regions. Journal of Biotechnology, 2011, 155, 95-103.	3.8	19
112	The complete genome sequence of the dominant Sinorhizobium meliloti field isolate SM11 extends the S. meliloti pan-genome. Journal of Biotechnology, 2011, 155, 20-33.	3.8	56
113	Complete genome sequencing of Agrobacterium sp. H13-3, the former Rhizobium lupini 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. Journal of Biotechnology, 2011, 155, 50-62.	3.8	112
114	First genomic analysis of the broad-host-range Rhizobium sp. LPU83 strain, a member of the low-genetic diversity Oregon-like Rhizobium sp. group. Journal of Biotechnology, 2011, 155, 3-10.	3.8	17
115	Bioinformatic Analysis Reveals High Diversity of Bacterial Genes for Laccase-Like Enzymes. PLoS ONE, 2011, 6, e25724.	2.5	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. Microbiology (United Kingdom), 2009, 155, 2306-2319.	1.8	411
117	Phylogenetic characterization of a biogas plant microbial community integrating clone library 16S-rDNA sequences and metagenome sequence data obtained by 454-pyrosequencing. Journal of Biotechnology, 2009, 142, 38-49.	3.8	248
118	Genetic diversity and composition of a plasmid metagenome from a wastewater treatment plant. Journal of Biotechnology, 2008, 136, 65-76.	3.8	87
119	Insight into the plasmid metagenome of wastewater treatment plant bacteria showing reduced susceptibility to antimicrobial drugs analysed by the 454-pyrosequencing technology. Journal of Biotechnology, 2008, 136, 54-64.	3.8	74
120	Comparative genomic hybridisation and ultrafast pyrosequencing revealed remarkable differences between the Sinorhizobium meliloti genomes of the model strain Rm1021 and the field isolate SM11. Journal of Biotechnology, 2008, 136, 31-37.	3.8	18
121	The metagenome of a biogas-producing microbial community of a production-scale biogas plant fermenter analysed by the 454-pyrosequencing technology. Journal of Biotechnology, 2008, 136, 77-90.	3.8	329
122	Taxonomic composition and gene content of a methane-producing microbial community isolated from a biogas reactor. Journal of Biotechnology, 2008, 136, 91-101.	3.8	202
123	Prevalence of pSmeSM11a-like plasmids in indigenous Sinorhizobium meliloti strains isolated in the course of a field release experiment with genetically modified S. meliloti strains. FEMS Microbiology Ecology, 2008, 63, 118-131.	2.7	21
124	Novel Macrolide Resistance Module Carried by the IncP-1Î² Resistance Plasmid pRSB111, Isolated from a Wastewater Treatment Plant. Antimicrobial Agents and Chemotherapy, 2007, 51, 673-678.	3.2	32
125	IncP-1Î² Plasmid pGNB1 Isolated from a Bacterial Community from a Wastewater Treatment Plant Mediates Decolorization of Triphenylmethane Dyes. Applied and Environmental Microbiology, 2007, 73, 6345-6350.	3.1	25
126	Sequence analysis of the 181-kb accessory plasmid pSmeSM11b, isolated from a dominantSinorhizobium melilotistrain identified during a long-term field release experiment. FEMS Microbiology Letters, 2007, 271, 297-309.	1.8	27

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127	Genomics of IncP-1 antibiotic resistance plasmids isolated from wastewater treatment plants provides evidence for a widely accessible drug resistance gene pool. FEMS Microbiology Reviews, 2007, 31, 449-477.	8.6	312
128	Mobilizable IncQ-Related Plasmid Carrying a New Quinolone Resistance Gene, qnrS2 , Isolated from the Bacterial Community of a Wastewater Treatment Plant. Antimicrobial Agents and Chemotherapy, 2006, 50, 3075-3080.	3.2	95
129	Sequence of the 68,869bp IncP-1Î± plasmid pTB11 from a waste-water treatment plant reveals a highly conserved backbone, a Tn402-like integron and other transposable elements. Plasmid, 2005, 53, 218-238.	1.4	93
130	Plasmid pB8 is closely related to the prototype IncP-1Î² plasmid R751 but transfers poorly to Escherichia coli and carries a new transposon encoding a small multidrug resistance efflux protein. Plasmid, 2005, 54, 135-148.	1.4	56
131	TLA-2, a Novel Ambler Class A Expanded-Spectrum Î²-Lactamase. Antimicrobial Agents and Chemotherapy, 2005, 49, 4767-4770.	3.2	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. Microbiology (United Kingdom), 2004, 150, 3613-3630.	1.8	128
133	Different molecular rearrangements in the integron of the IncP-1? resistance plasmid pB10 isolated from a wastewater treatment plant result in elevated ?-lactam resistance levels. Archives of Microbiology, 2004, 182, 429-435.	2.2	15
134	Occurrence of integron-associated resistance gene cassettes located on antibiotic resistance plasmids isolated from a wastewater treatment plant. FEMS Microbiology Ecology, 2003, 45, 239-252.	2.7	187
135	The Rhizobium leguminosarum bv. viciae glnD gene, encoding a uridylyltransferase/uridylyl-removing enzyme, is expressed in the root nodule but is not essential for nitrogen fixation. Microbiology (United Kingdom), 2000, 146, 2987-2996.	1.8	18
136	Functional and Regulatory Analysis of the Two Copies of the fixNOQP Operon of Rhizobium leguminosarum Strain VF39. Molecular Plant-Microbe Interactions, 1997, 10, 605-616.	2.6	48
137	Rhizobium leguminosarum bv. viciae contains a second fnr / fixK â€like gene and an unusual fixL homologue. Molecular Microbiology, 1996, 21, 267-280.	2.5	58
138	An Fnr-like protein encoded in Rhizobium leguminosarum biovar viciae shows structural and functional homology to Rhizobium meliloti FixK. Molecular Genetics and Genomics, 1990, 223, 138-147.	2.4	79
139	The Rhizobium meliloti fdxN gene encoding a ferredoxin-like protein is necessary for nitrogen fixation and is cotranscribed with nifA and nifB. Molecular Genetics and Genomics, 1989, 216, 293-302.	2.4	60