

Alfred PÃ¼hler

List of Publications by Year in descending order

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407
papers

36,626
citations

3721

89
h-index

3997

176
g-index

415
all docs

415
docs citations

415
times ranked

23097
citing authors

#	ARTICLE	IF	CITATIONS
1	A Broad Host Range Mobilization System for In Vivo Genetic Engineering: Transposon Mutagenesis in Gram Negative Bacteria. <i>Bio/technology</i> , 1983, 1, 784-791.	1.9	6,523
2	Small mobilizable multi-purpose cloning vectors derived from the <i>Escherichia coli</i> plasmids pK18 and pK19: selection of defined deletions in the chromosome of <i>Corynebacterium glutamicum</i> . <i>Gene</i> , 1994, 145, 69-73.	1.0	2,547
3	The Composite Genome of the Legume Symbiont <i>Sinorhizobium meliloti</i> . <i>Science</i> , 2001, 293, 668-672.	6.0	1,098
4	The complete <i>Corynebacterium glutamicum</i> ATCC 13032 genome sequence and its impact on the production of l-aspartate-derived amino acids and vitamins. <i>Journal of Biotechnology</i> , 2003, 104, 5-25.	1.9	844
5	GenDB—an open source genome annotation system for prokaryote genomes. <i>Nucleic Acids Research</i> , 2003, 31, 2187-2195.	6.5	644
6	Genome sequence of the ubiquitous hydrocarbon-degrading marine bacterium <i>Alcanivorax borkumensis</i> . <i>Nature Biotechnology</i> , 2006, 24, 997-1004.	9.4	417
7	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
8	EDGAR: A software framework for the comparative analysis of prokaryotic genomes. <i>BMC Bioinformatics</i> , 2009, 10, 154.	1.2	401
9	Xanthan gum biosynthesis and application: a biochemical/genetic perspective. <i>Applied Microbiology and Biotechnology</i> , 1998, 50, 145-152.	1.7	356
10	Complete genome sequence of the myxobacterium <i>Sorangium cellulosum</i> . <i>Nature Biotechnology</i> , 2007, 25, 1281-1289.	9.4	354
11	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
12	Overlaps in the Transcriptional Profiles of <i>Medicago truncatula</i> Roots Inoculated with Two Different <i>Glomus</i> Fungi Provide Insights into the Genetic Program Activated during Arbuscular Mycorrhiza. <i>Plant Physiology</i> , 2005, 137, 1283-1301.	2.3	322
13	Insights into Genome Plasticity and Pathogenicity of the Plant Pathogenic Bacterium <i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> Revealed by the Complete Genome Sequence. <i>Journal of Bacteriology</i> , 2005, 187, 7254-7266.	1.0	321
14	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
15	Analysis of the chromosome sequence of the legume symbiont <i>Sinorhizobium meliloti</i> strain 1021. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 9877-9882.	3.3	304
16	Nucleotide sequence of a 24,206-base-pair DNA fragment carrying the entire nitrogen fixation gene cluster of <i>Klebsiella pneumoniae</i> . <i>Journal of Molecular Biology</i> , 1988, 203, 715-738.	2.0	290
17	The complete sequence of the 1,683-kb pSymB megaplasmid from the N ₂ -fixing endosymbiont <i>Sinorhizobium meliloti</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 9889-9894.	3.3	282
18	Expression Profiling in <i>Medicago truncatula</i> Identifies More Than 750 Genes Differentially Expressed during Nodulation, Including Many Potential Regulators of the Symbiotic Program. <i>Plant Physiology</i> , 2004, 136, 3159-3176.	2.3	269

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19	Relationship of <i>Bacillus amyloliquefaciens</i> clades associated with strains DSM 7T and FZB42T: a proposal for <i>Bacillus amyloliquefaciens</i> subsp. <i>amyloliquefaciens</i> subsp. nov. and <i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> subsp. nov. based on complete genome sequence comparisons. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 1786-1801.	0.8	265
20	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
21	A new family of RSF1010-derived expression and lac-fusion broad-host-range vectors for Gram-negative bacteria. <i>Gene</i> , 1990, 89, 37-46.	1.0	247
22	Comparison of a prototype magnetoresistive biosensor to standard fluorescent DNA detection. <i>Biosensors and Bioelectronics</i> , 2004, 19, 1149-1156.	5.3	239
23	The genome of <i>Xanthomonas campestris</i> pv. <i>campestris</i> B100 and its use for the reconstruction of metabolic pathways involved in xanthan biosynthesis. <i>Journal of Biotechnology</i> , 2008, 134, 33-45.	1.9	238
24	Complete genome of the mutualistic, N ₂ -fixing grass endophyte <i>Azoarcus</i> sp. strain BH72. <i>Nature Biotechnology</i> , 2006, 24, 1384-1390.	9.4	237
25	Efficient Electrotransformation of <i>Corynebacterium diphtheriae</i> with a Mini-Replicon Derived from the <i>Corynebacterium glutamicum</i> Plasmid pGA1. <i>Current Microbiology</i> , 2002, 45, 362-367.	1.0	235
26	Genomes of Stigonematalean Cyanobacteria (Subsection V) and the Evolution of Oxygenic Photosynthesis from Prokaryotes to Plastids. <i>Genome Biology and Evolution</i> , 2013, 5, 31-44.	1.1	234
27	Global Changes in Gene Expression in <i>Sinorhizobium meliloti</i> 1021 under Microoxic and Symbiotic Conditions. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 292-303.	1.4	230
28	High-frequency conjugal plasmid transfer from gram-negative <i>Escherichia coli</i> to various gram-positive coryneform bacteria. <i>Journal of Bacteriology</i> , 1990, 172, 1663-1666.	1.0	208
29	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
30	A vector system with temperature-sensitive replication for gene disruption and mutational cloning in streptomycetes. <i>Molecular Genetics and Genomics</i> , 1989, 219, 341-348.	2.4	202
31	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
32	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
33	Complete Genome Sequence and Analysis of the Multiresistant Nosocomial Pathogen <i>Corynebacterium jeikeium</i> K411, a Lipid-Requiring Bacterium of the Human Skin Flora. <i>Journal of Bacteriology</i> , 2005, 187, 4671-4682.	1.0	189
34	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
35	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
36	The development of plasmid-free strains of <i>Agrobacterium tumefaciens</i> by using incompatibility with a <i>Rhizobium meliloti</i> plasmid to eliminate pAtc58. <i>Plasmid</i> , 1985, 13, 99-105.	0.4	168

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37	Evaluation of the resolving power of three different DNA fingerprinting methods to discriminate among isolates of a natural <i>Rhizobium meliloti</i> population. <i>Journal of Applied Microbiology</i> , 1997, 82, 477-484.	1.4	168
38	Chinese hamster genome sequenced from sorted chromosomes. <i>Nature Biotechnology</i> , 2013, 31, 694-695.	9.4	160
39	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
40	Identification and mapping of nitrogen fixation genes of <i>Rhodobacter capsulatus</i> : duplication of a <i>nifA-nifB</i> region. <i>Journal of Bacteriology</i> , 1988, 170, 693-699.	1.0	153
41	The <i>clc</i> Element of <i>Pseudomonas</i> sp. Strain B13, a Genomic Island with Various Catabolic Properties. <i>Journal of Bacteriology</i> , 2006, 188, 1999-2013.	1.0	153
42	The Genome Sequence of the Tomato-Pathogenic Actinomycete <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> NCPPB382 Reveals a Large Island Involved in Pathogenicity. <i>Journal of Bacteriology</i> , 2008, 190, 2138-2149.	1.0	153
43	Transcriptome Profiling in Root Nodules and Arbuscular Mycorrhiza Identifies a Collection of Novel Genes Induced During <i>Medicago truncatula</i> Root Endosymbioses. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 1063-1077.	1.4	152
44	Genetic and biochemical analysis of the aspartokinase from <i>Corynebacterium glutamicum</i> . <i>Molecular Microbiology</i> , 1991, 5, 1197-1204.	1.2	146
45	Horizontal gene transfer as a biosafety issue: A natural phenomenon of public concern. <i>Journal of Biotechnology</i> , 1998, 64, 75-90.	1.9	146
46	High-quality genome sequence of <i>Pichia pastoris</i> CBS7435. <i>Journal of Biotechnology</i> , 2011, 154, 312-320.	1.9	146
47	New gentamicin-resistance and <i>lacZ</i> promoter-probe cassettes suitable for insertion mutagenesis and generation of transcriptional fusions. <i>Gene</i> , 1995, 162, 37-39.	1.0	141
48	The 32-kilobase <i>exp</i> gene cluster of <i>Rhizobium meliloti</i> directing the biosynthesis of galactoglucan: genetic organization and properties of the encoded gene products. <i>Journal of Bacteriology</i> , 1997, 179, 1375-1384.	1.0	139
49	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
50	Cloning of a phosphinothricin N-acetyltransferase gene from <i>Streptomyces viridochromogenes</i> TÅ14494 and its expression in <i>Streptomyces lividans</i> and <i>Escherichia coli</i> . <i>Gene</i> , 1988, 63, 65-74.	1.0	130
51	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
52	Genetic characterization and sequence analysis of the duplicated <i>nifA/nifB</i> gene region of <i>Rhodobacter capsulatus</i> . <i>Molecular Genetics and Genomics</i> , 1988, 212, 27-37.	2.4	129
53	The DtxR protein acting as dual transcriptional regulator directs a global regulatory network involved in iron metabolism of <i>Corynebacterium glutamicum</i> . <i>BMC Genomics</i> , 2006, 7, 21.	1.2	129
54	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

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55	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
56	Genome sequence completed of <i>Alcanivorax borkumensis</i> , a hydrocarbon-degrading bacterium that plays a global role in oil removal from marine systems. <i>Journal of Biotechnology</i> , 2003, 106, 215-220.	1.9	126
57	Direct selection for curing and deletion of <i>Rhizobium</i> plasmids using transposons carrying the <i>Bacillus subtilis</i> <i>sacB</i> gene. <i>Gene</i> , 1989, 78, 111-120.	1.0	125
58	The genetic organization and evolution of the broad host range mercury resistance plasmid pSB102 isolated from a microbial population residing in the rhizosphere of alfalfa. <i>Nucleic Acids Research</i> , 2001, 29, 5169-5181.	6.5	122
59	The Promoter of the <i>Vicia faba</i> L. Leghemoglobin Gene <i>VfLb29</i> Is Specifically Activated in the Infected Cells of Root Nodules and in the Arbuscule-Containing Cells of Mycorrhizal Roots from Different Legume and Nonlegume Plants. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 62-69.	1.4	122
60	The 27.8-kb R-plasmid pTET3 from <i>Corynebacterium glutamicum</i> encodes the aminoglycoside adenylyltransferase gene cassette <i>aadA9</i> and the regulated tetracycline efflux system Tet 33 flanked by active copies of the widespread insertion sequence IS6100. <i>Plasmid</i> , 2002, 48, 117-129.	0.4	120
61	Back to the Future of Soil Metagenomics. <i>Frontiers in Microbiology</i> , 2016, 7, 73.	1.5	120
62	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
63	The two megaplasmids of <i>Rhizobium meliloti</i> are involved in the effective nodulation of alfalfa. <i>Molecular Genetics and Genomics</i> , 1986, 202, 356-362.	2.4	119
64	Identification and sequence analysis of the <i>Rhizobium meliloti</i> <i>dctA</i> gene encoding the C4-dicarboxylate carrier. <i>Journal of Bacteriology</i> , 1989, 171, 5551-5560.	1.0	119
65	Identification of Two <i>prpDBC</i> Gene Clusters in <i>Corynebacterium glutamicum</i> and Their Involvement in Propionate Degradation via the 2-Methylcitrate Cycle. <i>Journal of Bacteriology</i> , 2002, 184, 2728-2739.	1.0	118
66	A family of high-copy-number plasmid vectors with single end-label sites for rapid nucleotide sequencing. <i>Gene</i> , 1988, 70, 171-179.	1.0	117
67	Phenotypic and molecular characterization of conjugative antibiotic resistance plasmids isolated from bacterial communities of activated sludge. <i>Molecular Genetics and Genomics</i> , 2000, 263, 471-482.	2.4	117
68	The lipopolysaccharides of the phytopathogen <i>Xanthomonas campestris</i> pv. <i>campestris</i> induce an oxidative burst reaction in cell cultures of <i>Nicotiana tabacum</i> . <i>Planta</i> , 2001, 213, 214-222.	1.6	114
69	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
70	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
71	The individual and common repertoire of DNA-binding transcriptional regulators of <i>Corynebacterium glutamicum</i> , <i>Corynebacterium efficiens</i> , <i>Corynebacterium diphtheriae</i> and <i>Corynebacterium jeikeium</i> deduced from the complete genome sequences. <i>BMC Genomics</i> , 2005, 6, 86.	1.2	108
72	Low-molecular-weight succinoglycan is predominantly produced by <i>Rhizobium meliloti</i> strains carrying a mutated ExoP protein characterized by a periplasmic N-terminal domain and a missing C-terminal domain. <i>Molecular Microbiology</i> , 1995, 16, 191-204.	1.2	106

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73	The <i>Medicago truncatula</i> Sucrose Synthase Gene MtSucS1 Is Activated Both in the Infected Region of Root Nodules and in the Cortex of Roots Colonized by Arbuscular Mycorrhizal Fungi. <i>Molecular Plant-Microbe Interactions</i> , 2003, 16, 903-915.	1.4	106
74	Proteome analysis of <i>Corynebacterium glutamicum</i> . <i>Electrophoresis</i> , 2001, 22, 1712-1723.	1.3	105
75	Two classes of <i>Rhizobium meliloti</i> infection mutants differ in exopolysaccharide production and in coinoculation properties with nodulation mutants. <i>Molecular Genetics and Genomics</i> , 1988, 211, 17-26.	2.4	103
76	Construction and validation of a <i>Sinorhizobium meliloti</i> whole genome DNA microarray: genome-wide profiling of osmoadaptive gene expression. <i>Journal of Biotechnology</i> , 2003, 106, 255-268.	1.9	103
77	Construction and validation of cDNA-based Mt6k-RIT macro- and microarrays to explore root endosymbioses in the model legume <i>Medicago truncatula</i> . <i>Journal of Biotechnology</i> , 2004, 108, 95-113.	1.9	103
78	Identification and analysis of the <i>Rhizobium meliloti</i> exoAMONP genes involved in exopolysaccharide biosynthesis and mapping of promoters located on the exoHKLAMONP fragment. <i>Molecular Genetics and Genomics</i> , 1993, 241-241, 367-379.	2.4	102
79	Next-generation sequencing of the Chinese hamster ovary microRNA transcriptome: Identification, annotation and profiling of microRNAs as targets for cellular engineering. <i>Journal of Biotechnology</i> , 2011, 153, 62-75.	1.9	102
80	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
81	EMMA: a platform for consistent storage and efficient analysis of microarray data. <i>Journal of Biotechnology</i> , 2003, 106, 135-146.	1.9	100
82	Genome sequence of <i>Desulfobacterium autotrophicum</i> HRM2, a marine sulfate reducer oxidizing organic carbon completely to carbon dioxide. <i>Environmental Microbiology</i> , 2009, 11, 1038-1055.	1.8	100
83	Promoter analysis of the <i>Xanthomonas campestris</i> pv. <i>campestris</i> gum operon directing biosynthesis of the xanthan polysaccharide. <i>Journal of Bacteriology</i> , 1996, 178, 4313-4318.	1.0	98
84	Horizontal gene transfer among bacteria in terrestrial and aquatic habitats as assessed by microcosm and field studies. <i>Biology and Fertility of Soils</i> , 1999, 29, 221-245.	2.3	97
85	Unraveling the Chinese hamster ovary cell line transcriptome by next-generation sequencing. <i>Journal of Biotechnology</i> , 2011, 156, 227-235.	1.9	96
86	Rational Design of a <i>Corynebacterium glutamicum</i> Pantothenate Production Strain and Its Characterization by Metabolic Flux Analysis and Genome-Wide Transcriptional Profiling. <i>Applied and Environmental Microbiology</i> , 2005, 71, 3255-3268.	1.4	95
87	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
88	The complete nucleotide sequence and environmental distribution of the cryptic, conjugative, broad-host-range plasmid pIPO2 isolated from bacteria of the wheat rhizosphere The GenBank accession number for the pIPO2T sequence reported in this paper is AJ297913.. <i>Microbiology (United Kingdom)</i> 147: 94-102	0.7	94
89	The <i>Corynebacterium xerosis</i> Composite Transposon Tn5432 Consists of Two Identical Insertion Sequences, Designated IS1249, Flanking the Erythromycin Resistance Gene ermCX. <i>Plasmid</i> , 1995, 34, 119-131.	0.4	93
90	Sequence of the 68,869bp IncP-1 \pm 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

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91	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
92	The McbR repressor modulated by the effector substance S-adenosylhomocysteine controls directly the transcription of a regulon involved in sulphur metabolism of <i>Corynebacterium glutamicum</i> ATCC 13032. <i>Molecular Microbiology</i> , 2005, 56, 871-887.	1.2	92
93	The DeoR-type transcriptional regulator SugR acts as a repressor for genes encoding the phosphoenolpyruvate:sugar phosphotransferase system (PTS) in <i>Corynebacterium glutamicum</i> . <i>BMC Molecular Biology</i> , 2007, 8, 104.	3.0	91
94	Manipulation of <i>Corynebacterium glutamicum</i> by Gene Disruption and Replacement. <i>Nature Biotechnology</i> , 1991, 9, 84-87.	9.4	90
95	Whole-Genome Sequence of <i>Listeria welshimeri</i> Reveals Common Steps in Genome Reduction with <i>Listeria innocua</i> as Compared to <i>Listeria monocytogenes</i> . <i>Journal of Bacteriology</i> , 2006, 188, 7405-7415.	1.0	89
96	The GlxR regulon of the amino acid producer <i>Corynebacterium glutamicum</i> : In silico and in vitro detection of DNA binding sites of a global transcription regulator. <i>Journal of Biotechnology</i> , 2008, 135, 340-350.	1.9	89
97	Genome-wide analysis of the l-methionine biosynthetic pathway in <i>Corynebacterium glutamicum</i> by targeted gene deletion and homologous complementation. <i>Journal of Biotechnology</i> , 2003, 104, 213-228.	1.9	88
98	Comparative genomics and transcriptomics of lineages I, II, and III strains of <i>Listeria monocytogenes</i> . <i>BMC Genomics</i> , 2012, 13, 144.	1.2	88
99	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
100	The putative transcriptional repressor McbR, member of the TetR-family, is involved in the regulation of the metabolic network directing the synthesis of sulfur containing amino acids in <i>Corynebacterium glutamicum</i> . <i>Journal of Biotechnology</i> , 2003, 103, 51-65.	1.9	85
101	Development of a <i>Corynebacterium glutamicum</i> DNA microarray and validation by genome-wide expression profiling during growth with propionate as carbon source. <i>Journal of Biotechnology</i> , 2003, 106, 269-286.	1.9	85
102	The missing link: <i>Bordetella petrii</i> is endowed with both the metabolic versatility of environmental bacteria and virulence traits of pathogenic <i>Bordetellae</i> . <i>BMC Genomics</i> , 2008, 9, 449.	1.2	85
103	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
104	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
105	Role of the Regulatory Gene <i>rirA</i> in the Transcriptional Response of <i>Sinorhizobium meliloti</i> to Iron Limitation. <i>Applied and Environmental Microbiology</i> , 2005, 71, 5969-5982.	1.4	82
106	The lifestyle of <i>Corynebacterium urealyticum</i> derived from its complete genome sequence established by pyrosequencing. <i>Journal of Biotechnology</i> , 2008, 136, 11-21.	1.9	81
107	The tetracycline resistance transposons Tn1721 and Tn1771 have three 38-base-pair repeats and generate five-base-pair direct repeats. <i>Molecular Genetics and Genomics</i> , 1981, 181, 87-94.	2.4	80
108	The <i>Vicia faba</i> Leghemoglobin Gene <i>VfLb29</i> Is Induced in Root Nodules and in Roots Colonized by the Arbuscular Mycorrhizal Fungus <i>Glomus fasciculatum</i> . <i>Molecular Plant-Microbe Interactions</i> , 1997, 10, 124-131.	1.4	80

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109	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
110	The time course of the transcriptomic response of <i>Sinorhizobium meliloti</i> 1021 following a shift to acidic pH. <i>BMC Microbiology</i> , 2009, 9, 37.	1.3	76
111	Biosynthesis of the exopolysaccharide galactoglucan in <i>Sinorhizobium meliloti</i> is subject to a complex control by the phosphate-dependent regulator PhoB and the proteins ExpG and MucR. <i>Microbiology (United Kingdom)</i> , 1999, 145, 603-611.	0.7	75
112	<i>Corynebacterium striatum</i> Chloramphenicol Resistance Transposon Tn5564: Genetic Organization and Transposition in <i>Corynebacterium glutamicum</i> . <i>Plasmid</i> , 1998, 40, 126-139.	0.4	74
113	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
114	The <i>Sinorhizobium meliloti</i> fur Gene Regulates, with Dependence on Mn(II), Transcription of the sitABCD Operon, Encoding a Metal-Type Transporter. <i>Journal of Bacteriology</i> , 2004, 186, 3609-3620.	1.0	73
115	Development of joint application strategies for two microbial gene finders. <i>Bioinformatics</i> , 2004, 20, 1622-1631.	1.8	72
116	Adaptation of <i>Corynebacterium glutamicum</i> to Ammonium Limitation: a Global Analysis Using Transcriptome and Proteome Techniques. <i>Applied and Environmental Microbiology</i> , 2005, 71, 2391-2402.	1.4	72
117	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
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