

# Alfred Phler

## List of Publications by Citations

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#	Paper	IF	Citations
396	A Broad Host Range Mobilization System for In Vivo Genetic Engineering: Transposon Mutagenesis in Gram Negative Bacteria. <i>Bio/technology</i> , <b>1983</b> , 1, 784-791		5701
395	Small mobilizable multi-purpose cloning vectors derived from the Escherichia coli plasmids pK18 and pK19: selection of defined deletions in the chromosome of Corynebacterium glutamicum. <i>Gene</i> , <b>1994</b> , 145, 69-73	3.8	2103
394	The composite genome of the legume symbiont Sinorhizobium meliloti. <i>Science</i> , <b>2001</b> , 293, 668-72	33.3	984
393	The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins. <i>Journal of Biotechnology</i> , <b>2003</b> , 104, 5-25	3.7	750
392	GenDB--an open source genome annotation system for prokaryote genomes. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 2187-95	20.1	587
391	Genome sequence of the ubiquitous hydrocarbon-degrading marine bacterium Alcanivorax borkumensis. <i>Nature Biotechnology</i> , <b>2006</b> , 24, 997-1004	44.5	350
390	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> , <b>2009</b> , 155, 2306-2319	2.9	330
389	EDGAR: a software framework for the comparative analysis of prokaryotic genomes. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 154	3.6	317
388	Complete genome sequence of the myxobacterium Sorangium cellulosum. <i>Nature Biotechnology</i> , <b>2007</b> , 25, 1281-9	44.5	307
387	Xanthan gum biosynthesis and application: a biochemical/genetic perspective. <i>Applied Microbiology and Biotechnology</i> , <b>1998</b> , 50, 145-52	5.7	293
386	Overlaps in the transcriptional profiles of Medicago truncatula roots inoculated with two different Glomus fungi provide insights into the genetic program activated during arbuscular mycorrhiza. <i>Plant Physiology</i> , <b>2005</b> , 137, 1283-301	6.6	289
385	Insights into genome plasticity and pathogenicity of the plant pathogenic bacterium Xanthomonas campestris pv. vesicatoria revealed by the complete genome sequence. <i>Journal of Bacteriology</i> , <b>2005</b> , 187, 7254-66	3.5	286
384	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> , <b>2008</b> , 136, 77-90	3.7	280
383	Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2001</b> , 98, 9877-82	11.5	279
382	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> , <b>2007</b> , 31, 449-77	15.1	274
381	The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2001</b> , 98, 9889-94	11.5	263
380	Nucleotide sequence of a 24,206-base-pair DNA fragment carrying the entire nitrogen fixation gene cluster of Klebsiella pneumoniae. <i>Journal of Molecular Biology</i> , <b>1988</b> , 203, 715-38	6.5	243

379	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> , <b>2004</b> , 136, 3159-76	6.6	236
378	A new family of RSF1010-derived expression and lac-fusion broad-host-range vectors for gram-negative bacteria. <i>Gene</i> , <b>1990</b> , 89, 37-46	3.8	232
377	Efficient electrotransformation of <i>Corynebacterium diphtheriae</i> with a mini-replicon derived from the <i>Corynebacterium glutamicum</i> plasmid pGA1. <i>Current Microbiology</i> , <b>2002</b> , 45, 362-7	2.4	212
376	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> , <b>2009</b> , 142, 38-49	3.7	209
375	Comparison of a prototype magnetoresistive biosensor to standard fluorescent DNA detection. <i>Biosensors and Bioelectronics</i> , <b>2004</b> , 19, 1149-56	11.8	209
374	Global changes in gene expression in <i>Sinorhizobium meliloti</i> 1021 under microoxic and symbiotic conditions. <i>Molecular Plant-Microbe Interactions</i> , <b>2004</b> , 17, 292-303	3.6	204
373	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> , <b>2008</b> , 134, 33-45	3.7	202
372	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> , <b>2011</b> , 61, 1786-1801	2.2	200
371	Complete genome of the mutualistic, N <sub>2</sub> -fixing grass endophyte <i>Azoarcus</i> sp. strain BH72. <i>Nature Biotechnology</i> , <b>2006</b> , 24, 1385-91	44.5	199
370	Comparative and joint analysis of two metagenomic datasets from a biogas fermenter obtained by 454-pyrosequencing. <i>PLoS ONE</i> , <b>2011</b> , 6, e14519	3.7	187
369	Genomes of Stigonematalean cyanobacteria (subsection V) and the evolution of oxygenic photosynthesis from prokaryotes to plastids. <i>Genome Biology and Evolution</i> , <b>2013</b> , 5, 31-44	3.9	182
368	High-frequency conjugal plasmid transfer from gram-negative <i>Escherichia coli</i> to various gram-positive coryneform bacteria. <i>Journal of Bacteriology</i> , <b>1990</b> , 172, 1663-6	3.5	180
367	A vector system with temperature-sensitive replication for gene disruption and mutational cloning in streptomycetes. <i>Molecular Genetics and Genomics</i> , <b>1989</b> , 219, 341-348		179
366	Taxonomic composition and gene content of a methane-producing microbial community isolated from a biogas reactor. <i>Journal of Biotechnology</i> , <b>2008</b> , 136, 91-101	3.7	177
365	Profiling of the metabolically active community from a production-scale biogas plant by means of high-throughput metatranscriptome sequencing. <i>Journal of Biotechnology</i> , <b>2012</b> , 158, 248-58	3.7	170
364	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> , <b>2005</b> , 187, 4671-82	3.5	168
363	Occurrence of integron-associated resistance gene cassettes located on antibiotic resistance plasmids isolated from a wastewater treatment plant. <i>FEMS Microbiology Ecology</i> , <b>2003</b> , 45, 239-52	4.3	157
362	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> , <b>1985</b> , 13, 99-105	3.3	156

361	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> , <b>1997</b> , 82, 477-84	4.7	145
360	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> , <b>1988</b> , 170, 693-9	3.5	144
359	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> , <b>2004</b> , 17, 1063-77	3.6	142
358	Chinese hamster genome sequenced from sorted chromosomes. <i>Nature Biotechnology</i> , <b>2013</b> , 31, 694-5	44.5	141
357	New gentamicin-resistance and <i>lacZ</i> promoter-probe cassettes suitable for insertion mutagenesis and generation of transcriptional fusions. <i>Gene</i> , <b>1995</b> , 162, 37-9	3.8	133
356	Genetic and biochemical analysis of the aspartokinase from <i>Corynebacterium glutamicum</i> . <i>Molecular Microbiology</i> , <b>1991</b> , 5, 1197-204	4.1	133
355	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> , <b>2008</b> , 190, 2138-49	3.5	130
354	Horizontal gene transfer as a biosafety issue: a natural phenomenon of public concern. <i>Journal of Biotechnology</i> , <b>1998</b> , 64, 75-90	3.7	129
353	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> , <b>2013</b> , 36, 330-8	4.2	128
352	High-quality genome sequence of <i>Pichia pastoris</i> CBS7435. <i>Journal of Biotechnology</i> , <b>2011</b> , 154, 312-20	3.7	123
351	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> , <b>1997</b> , 179, 1375-84	3.5	123
350	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> , <b>2004</b> , 150, 3613-3630	2.9	120
349	Comparative metagenomics of biogas-producing microbial communities from production-scale biogas plants operating under wet or dry fermentation conditions. <i>Biotechnology for Biofuels</i> , <b>2015</b> , 8, 14	7.8	118
348	Cloning of a phosphinothricin N-acetyltransferase gene from <i>Streptomyces viridochromogenes</i> T894 and its expression in <i>Streptomyces lividans</i> and <i>Escherichia coli</i> . <i>Gene</i> , <b>1988</b> , 63, 65-74	3.8	115
347	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> , <b>1988</b> , 212, 27-37		114
346	A family of high-copy-number plasmid vectors with single end-label sites for rapid nucleotide sequencing. <i>Gene</i> , <b>1988</b> , 70, 171-9	3.8	113
345	The <i>clc</i> element of <i>Pseudomonas</i> sp. strain B13, a genomic island with various catabolic properties. <i>Journal of Bacteriology</i> , <b>2006</b> , 188, 1999-2013	3.5	112
344	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> , <b>2004</b> , 17, 62-9	3.6	109

343	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> , <b>2002</b> , 48, 117-29	3.3	108
342	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> , <b>1989</b> , 78, 111-20	3.8	108
341	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> , <b>2003</b> , 106, 215-20	3.7	107
340	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> , <b>2002</b> , 184, 2728-39	3.5	107
339	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> , <b>2001</b> , 213, 214-22	4.7	105
338	Phenotypic and molecular characterization of conjugative antibiotic resistance plasmids isolated from bacterial communities of activated sludge. <i>Molecular Genetics and Genomics</i> , <b>2000</b> , 263, 471-82		105
337	The two megaplasmids of <i>Rhizobium meliloti</i> are involved in the effective nodulation of alfalfa. <i>Molecular Genetics and Genomics</i> , <b>1986</b> , 202, 356-362		102
336	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> , <b>2016</b> , 9, 171	7.8	102
335	Characterization of microbial biofilms in a thermophilic biogas system by high-throughput metagenome sequencing. <i>FEMS Microbiology Ecology</i> , <b>2012</b> , 79, 785-99	4.3	101
334	Identification and sequence analysis of the <i>Rhizobium meliloti</i> <i>dctA</i> gene encoding the C4-dicarboxylate carrier. <i>Journal of Bacteriology</i> , <b>1989</b> , 171, 5551-60	3.5	101
333	EMMA: a platform for consistent storage and efficient analysis of microarray data. <i>Journal of Biotechnology</i> , <b>2003</b> , 106, 135-46	3.7	99
332	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> , <b>2006</b> , 7, 21	4.5	98
331	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> , <b>2003</b> , 106, 255-68	3.7	98
330	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> , <b>2004</b> , 108, 95-113	3.7	98
329	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> , <b>2005</b> , 6, 86	4.5	98
328	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> , <b>1995</b> , 16, 191-203	4.1	97
327	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> , <b>2011</b> , 153, 62-75	3.7	95
326	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> , <b>2003</b> , 16, 903-15	3.6	95

325	Proteome analysis of <i>Corynebacterium glutamicum</i> . <i>Electrophoresis</i> , <b>2001</b> , 22, 1712-23	3.6	94
324	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> , <b>2011</b> , 155, 50-62	3.7	90
323	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> , <b>1988</b> , 211, 17-26		90
322	Genome sequence of <i>Desulfobacterium autotrophicum</i> HRM2, a marine sulfate reducer oxidizing organic carbon completely to carbon dioxide. <i>Environmental Microbiology</i> , <b>2009</b> , 11, 1038-55	5.2	89
321	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> , <b>2001</b> , 29, 5169-81	20.1	89
320	Unraveling the Chinese hamster ovary cell line transcriptome by next-generation sequencing. <i>Journal of Biotechnology</i> , <b>2011</b> , 156, 227-35	3.7	88
319	Sequence of the 68,869 bp IncP-1alpha plasmid pTB11 from a waste-water treatment plant reveals a highly conserved backbone, a Tn402-like integron and other transposable elements. <i>Plasmid</i> , <b>2005</b> , 53, 218-38	3.3	88
318	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> , <b>1996</b> , 178, 4313-8	3.5	88
317	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> , <b>2005</b> , 56, 871-87	4.1	86
316	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> , <b>2005</b> , 71, 3255-68	4.8	85
315	Horizontal gene transfer among bacteria in terrestrial and aquatic habitats as assessed by microcosm and field studies. <i>Biology and Fertility of Soils</i> , <b>1999</b> , 29, 221-245	6.1	85
314	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> , <b>2008</b> , 135, 340-50	3.7	84
313	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> , <b>2006</b> , 50, 3075-80	5.9	83
312	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> , <b>1995</b> , 34, 119-331	3.3	83
311	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> , <b>1993</b> , 241, 367-79		82
310	Back to the Future of Soil Metagenomics. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 73	5.7	82
309	Metagenome, metatranscriptome, and metaproteome approaches unraveled compositions and functional relationships of microbial communities residing in biogas plants. <i>Applied Microbiology and Biotechnology</i> , <b>2018</b> , 102, 5045-5063	5.7	81
308	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> , <b>2003</b> , 103, 51-65	3.7	81

307	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> , <b>2007</b> , 8, 104	4.5	79
306	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> , <b>2003</b> , 106, 269-86	3.7	79
305	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> , <b>2006</b> , 188, 7405-15	3.5	77
304	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> , <b>2003</b> , 104, 213-28	3.7	76
303	Genetic diversity and composition of a plasmid metagenome from a wastewater treatment plant. <i>Journal of Biotechnology</i> , <b>2008</b> , 136, 65-76	3.7	74
302	Insights into the completely annotated genome of <i>Lactobacillus buchneri</i> CD034, a strain isolated from stable grass silage. <i>Journal of Biotechnology</i> , <b>2012</b> , 161, 153-66	3.7	73
301	The lifestyle of <i>Corynebacterium urealyticum</i> derived from its complete genome sequence established by pyrosequencing. <i>Journal of Biotechnology</i> , <b>2008</b> , 136, 11-21	3.7	73
300	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> , <b>2016</b> , 9, 156	7.8	73
299	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> , <b>1999</b> , 145 ( Pt 3), 603-611	2.9	72
298	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> , <b>2013</b> , 167, 334-43	3.7	71
297	Development of joint application strategies for two microbial gene finders. <i>Bioinformatics</i> , <b>2004</b> , 20, 1622-31	7.2	71
296	The complete nucleotide sequence and environmental distribution of the cryptic, conjugative, broad-host-range plasmid pIPO2 isolated from bacteria of the wheat rhizosphere. <i>Microbiology (United Kingdom)</i> , <b>2002</b> , 148, 1637-1653	2.9	71
295	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> , <b>2014</b> , 5, 252	5.7	70
294	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> , <b>2005</b> , 71, 5969-82	4.8	70
293	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> , <b>2008</b> , 136, 54-64	3.7	69
292	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> , <b>1990</b> , 223, 138-47		69
291	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> , <b>2013</b> , 167, 142-55	3.7	68
290	The <i>Vicia faba</i> leghemoglobin gene VFLb29 is induced in root nodules and in roots colonized by the arbuscular mycorrhizal fungus <i>Glomus fasciculatum</i> . <i>Molecular Plant-Microbe Interactions</i> , <b>1997</b> , 10, 124-31	3.6	68

289	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> , <b>2004</b> , 186, 3609-20	3.5	68
288	Strategy to sequence the genome of <i>Corynebacterium glutamicum</i> ATCC 13032: use of a cosmid and a bacterial artificial chromosome library. <i>Journal of Biotechnology</i> , <b>2002</b> , 95, 25-38	3.7	67
287	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> , <b>2008</b> , 9, 449	4.5	65
286	Organization and partial sequence of a DNA region of the <i>Rhizobium leguminosarum</i> symbiotic plasmid pRL6Jl containing the genes fixABC, nifA, nifB and a novel open reading frame. <i>Nucleic Acids Research</i> , <b>1987</b> , 15, 31-49	20.1	64
285	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> , <b>1981</b> , 181, 87-94		64
284	The time course of the transcriptomic response of <i>Sinorhizobium meliloti</i> 1021 following a shift to acidic pH. <i>BMC Microbiology</i> , <b>2009</b> , 9, 37	4.5	63
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282	EMMA 2--a MAGE-compliant system for the collaborative analysis and integration of microarray data. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 50	3.6	62
281	Manipulation of <i>Corynebacterium glutamicum</i> by gene disruption and replacement. <i>Nature Biotechnology</i> , <b>1991</b> , 9, 84-7	44.5	62
280	The complete genome sequence of the acarbose producer <i>Actinoplanes</i> sp. SE50/110. <i>BMC Genomics</i> , <b>2012</b> , 13, 112	4.5	61
279	Finding novel genes in bacterial communities isolated from the environment. <i>Bioinformatics</i> , <b>2006</b> , 22, e281-9	7.2	61
278	Adaptation of <i>Corynebacterium glutamicum</i> to ammonium limitation: a global analysis using transcriptome and proteome techniques. <i>Applied and Environmental Microbiology</i> , <b>2005</b> , 71, 2391-402	4.8	61
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276	Comparative genomics and transcriptomics of lineages I, II, and III strains of <i>Listeria monocytogenes</i> . <i>BMC Genomics</i> , <b>2012</b> , 13, 144	4.5	60
275	Combined transcriptome profiling reveals a novel family of arbuscular mycorrhizal-specific <i>Medicago truncatula</i> lectin genes. <i>Molecular Plant-Microbe Interactions</i> , <b>2005</b> , 18, 771-82	3.6	60
274	<i>Corynebacterium striatum</i> chloramphenicol resistance transposon Tn5564: genetic organization and transposition in <i>Corynebacterium glutamicum</i> . <i>Plasmid</i> , <b>1998</b> , 40, 126-39	3.3	59
273	The glycosylated cell surface protein Rpf2, containing a resuscitation-promoting factor motif, is involved in intercellular communication of <i>Corynebacterium glutamicum</i> . <i>Archives of Microbiology</i> , <b>2004</b> , 182, 299-312	3	59
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268	Extension of the <i>Rhizobium meliloti</i> succinoglycan biosynthesis gene cluster: identification of the <i>exsA</i> gene encoding an ABC transporter protein, and the <i>exsB</i> gene which probably codes for a regulator of succinoglycan biosynthesis. <i>Molecular Genetics and Genomics</i> , <b>1995</b> , 249, 487-97		58
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263	Identification and functional analysis of six mycolyltransferase genes of <i>Corynebacterium glutamicum</i> ATCC 13032: the genes <i>cop1</i> , <i>cmt1</i> , and <i>cmt2</i> can replace each other in the synthesis of trehalose dicorynomycolate, a component of the mycolic acid layer of the cell envelope. <i>Archives of Microbiology</i> , <b>2003</b> , 180, 33-44	3	53
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260	Construction of a public CHO cell line transcript database using versatile bioinformatics analysis pipelines. <i>PLoS ONE</i> , <b>2014</b> , 9, e85568	3.7	52
259	Comprehensive discovery and characterization of small RNAs in <i>Corynebacterium glutamicum</i> ATCC 13032. <i>BMC Genomics</i> , <b>2013</b> , 14, 714	4.5	52
258	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> , <b>2011</b> , 155, 20-33	3.7	52
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250	Characterization of the <i>Xanthomonas campestris</i> pv. <i>campestris</i> lipopolysaccharide substructures essential for elicitation of an oxidative burst in tobacco cells. <i>Molecular Plant-Microbe Interactions</i> , <b>2005</b> , 18, 674-81	3.6	48
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9	The tetAB genes of the <i>Corynebacterium striatum</i> R-plasmid pTP10 encode an ABC transporter and confer tetracycline, oxytetracycline and oxacillin resistance in <i>Corynebacterium glutamicum</i>		1
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