

# Alfred Phler

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

396  
papers

31,112  
citations

83  
h-index

164  
g-index

415  
ext. papers

34,161  
ext. citations

4.8  
avg, IF

6.58  
L-index

#	Paper	IF	Citations
396	Genome Analyses of the Less Aggressive 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> , <b>2021</b> , 7,	5.6	2
395	Indicative Marker Microbiome Structures Deduced from the Taxonomic Inventory of 67 Full-Scale Anaerobic Digesters of 49 Agricultural Biogas Plants. <i>Microorganisms</i> , <b>2021</b> , 9,	4.9	1
394	Implementing FAIR data management within the German Network for Bioinformatics Infrastructure (de.NBI) exemplified by selected use cases. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	4
393	Exopolysaccharide Characterization of LPU83 and Its Role in the Symbiosis With Alfalfa. <i>Frontiers in Plant Science</i> , <b>2021</b> , 12, 642576	6.2	4
392	ExoS/ChvI Two-Component Signal-Transduction System Activated in the Absence of Bacterial Phosphatidylcholine. <i>Frontiers in Plant Science</i> , <b>2021</b> , 12, 678976	6.2	2
391	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> , <b>2020</b> , 15, 7	5.6	6
390	Absence of the highly expressed small carbohydrate-binding protein Cgt improves the acarbose formation in <i>Actinoplanes</i> sp. SE50/110. <i>Applied Microbiology and Biotechnology</i> , <b>2020</b> , 104, 5395-5408	5.7	2
389	A maltose-regulated large genomic region is activated by the transcriptional regulator MalT in <i>Actinoplanes</i> sp. SE50/110. <i>Applied Microbiology and Biotechnology</i> , <b>2020</b> , 104, 9283-9294	5.7	
388	Global transcriptome analysis of <i>Rhizobium favelukesii</i> LPU83 in response to acid stress. <i>FEMS Microbiology Ecology</i> , <b>2020</b> , 97,	4.3	6
387	The expression of the acarbose biosynthesis gene cluster in <i>Actinoplanes</i> sp. SE50/110 is dependent on the growth phase. <i>BMC Genomics</i> , <b>2020</b> , 21, 818	4.5	1
386	The Role of ING2-E5A in Mesophilic Biogas Reactor Systems as Deduced from Multiomics Analyses. <i>Microorganisms</i> , <b>2020</b> , 8,	4.9	6
385	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> , <b>2019</b> , 9, 7221	4.9	10
384	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> , <b>2019</b> , 10,	4.2	31
383	Insight into the structure, function and conjugative transfer of pLPU83a, an accessory plasmid of <i>Rhizobium favelukesii</i> LPU83. <i>Plasmid</i> , <b>2019</b> , 103, 9-16	3.3	7
382	Genetic Potential of the Biocontrol Agent (Formerly ) 3Re2-7 Unraveled by Genome Sequencing and Mining, Comparative Genomics and Transcriptomics. <i>Genes</i> , <b>2019</b> , 10,	4.2	18
381	Evaluation of vector systems and promoters for overexpression of the acarbose biosynthesis gene <i>acbC</i> in <i>Actinoplanes</i> sp. SE50/110. <i>Microbial Cell Factories</i> , <b>2019</b> , 18, 114	6.4	8
380	de.NBI Cloud federation through ELIXIR AAI. <i>F1000Research</i> , <b>2019</b> , 8, 842	3.6	7

379	Genome Analyses and Genome-Centered Metatranscriptomics of Strain SIV6, Isolated from a Thermophilic Production-Scale Biogas Fermenter. <i>Microorganisms</i> , <b>2019</b> , 8,	4.9	4
378	Essentiality of the Maltase AmlE in Maltose Utilization and Its Transcriptional Regulation by the Repressor AmlR in the Acarbose-Producing Bacterium sp. SE50/110. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 2448	5.7	3
377	Complete Genome Sequencing of Acinetobacter baumannii Strain K50 Discloses the Large Conjugative Plasmid pK50a Encoding Carbapenemase OXA-23 and Extended-Spectrum $\beta$ -Lactamase GES-11. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2018</b> , 62,	5.9	17
376	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. <i>Journal of Biotechnology</i> , <b>2018</b> , 267, 12-18	3.7	11
375	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
374	Characterization of genomes assembled from metagenomes of biofilms residing in mesophilic and thermophilic biogas reactors. <i>Biotechnology for Biofuels</i> , <b>2018</b> , 11, 167	7.8	22
373	Targeted in situ metatranscriptomics for selected taxa from mesophilic and thermophilic biogas plants. <i>Microbial Biotechnology</i> , <b>2018</b> , 11, 667-679	6.3	25
372	str. M3/6 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> , <b>2018</b> , 18, e00254	5.3	14
371	Comparative genomic analysis of Acinetobacter spp. plasmids originating from clinical settings and environmental habitats. <i>Scientific Reports</i> , <b>2018</b> , 8, 7783	4.9	27
370	Comparative transcription profiling of two fermentation cultures of Xanthomonas campestris pv. campestris B100 sampled in the growth and in the stationary phase. <i>Applied Microbiology and Biotechnology</i> , <b>2018</b> , 102, 6613-6625	5.7	5
369	Genome sequence of Methanobacterium congolense strain Buetzberg, a hydrogenotrophic, methanogenic archaeon, isolated from a mesophilic industrial-scale biogas plant utilizing bio-waste. <i>Journal of Biotechnology</i> , <b>2017</b> , 247, 1-5	3.7	38
368	Genome Sequence of the Symbiotic Type Strain Rhizobium tibeticum CCBAU85039T. <i>Genome Announcements</i> , <b>2017</b> , 5,		1
367	A metabolomic approach to characterize the acid-tolerance response in Sinorhizobium meliloti. <i>Metabolomics</i> , <b>2017</b> , 13, 1	4.7	8
366	Genome improvement of the acarbose producer Actinoplanes sp. SE50/110 and annotation refinement based on RNA-seq analysis. <i>Journal of Biotechnology</i> , <b>2017</b> , 251, 112-123	3.7	9
365	Refined annotation of the complete genome of the phytopathogenic and xanthan producing Xanthomonas campestris pv. campestris strain B100 based on RNA sequence data. <i>Journal of Biotechnology</i> , <b>2017</b> , 253, 55-61	3.7	6
364	The completely annotated genome and comparative genomics of the Peptoniphilaceae bacterium str. ING2-D1G, a novel acidogenic bacterium isolated from a mesophilic biogas reactor. <i>Journal of Biotechnology</i> , <b>2017</b> , 257, 178-186	3.7	1
363	Draft genome sequence of the potato pathogen Rhizoctonia solani AG3-PT isolate Ben3. <i>Archives of Microbiology</i> , <b>2017</b> , 199, 1065-1068	3	8
362	The Rhizoctonia solani AG1-IB (isolate 7/3/14) transcriptome during interaction with the host plant lettuce (Lactuca sativa L.). <i>PLoS ONE</i> , <b>2017</b> , 12, e0177278	3.7	20

361	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> , <b>2017</b> , 19, 4536-4550	5.2	12
360	The complete genome sequence of the actinobacterium <i>Streptomyces glaucescens</i> GLA.O (DSM 40922) carrying gene clusters for the biosynthesis of tetracenomycin C, 5 $\alpha$ -hydroxy streptomycin, and acarbose. <i>Journal of Biotechnology</i> , <b>2017</b> , 262, 84-88	3.7	9
359	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> , <b>2017</b> , 263, 64-74	3.7	7
358	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> , <b>2017</b> , 162, 555-559	3.6	7
357	Genomics and prevalence of bacterial and archaeal isolates from biogas-producing microbiomes. <i>Biotechnology for Biofuels</i> , <b>2017</b> , 10, 264	7.8	26
356	The MalR type regulator AcrC is a transcriptional repressor of acarbose biosynthetic genes in <i>Actinoplanes</i> sp. SE50/110. <i>BMC Genomics</i> , <b>2017</b> , 18, 562	4.5	8
355	A community proposal to integrate proteomics activities in ELIXIR. <i>F1000Research</i> , <b>2017</b> , 6,	3.6	10
354	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> , <b>2017</b> , 27, 321-334	3.3	25
353	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> , <b>2016</b> , 4,		1
352	Complete Genome Sequence of <i>Herbinix luporum</i> SD1D, a New Cellulose-Degrading Bacterium Isolated from a Thermophilic Biogas Reactor. <i>Genome Announcements</i> , <b>2016</b> , 4,		6
351	Genomics of high molecular weight plasmids isolated from an on-farm biopurification system. <i>Scientific Reports</i> , <b>2016</b> , 6, 28284	4.9	12
350	The influence of a modified lipopolysaccharide O-antigen on the biosynthesis of xanthan in <i>Xanthomonas campestris</i> pv. <i>campestris</i> B100. <i>BMC Microbiology</i> , <b>2016</b> , 16, 93	4.5	10
349	Complete Genome Sequence of the Barley Pathogen <i>Xanthomonas translucens</i> pv. <i>translucens</i> DSM 18974T (ATCC 19319T). <i>Genome Announcements</i> , <b>2016</b> , 4,		15
348	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> , <b>2016</b> , 231, 212-223	3.7	29
347	An integrated metagenome and -proteome analysis of the microbial community residing in a biogas production plant. <i>Journal of Biotechnology</i> , <b>2016</b> , 231, 268-279	3.7	29
346	Targeted genome editing in the rare actinomycete <i>Actinoplanes</i> sp. SE50/110 by using the CRISPR/Cas9 System. <i>Journal of Biotechnology</i> , <b>2016</b> , 231, 122-128	3.7	31
345	Comparative proteome analysis of <i>Actinoplanes</i> sp. SE50/110 grown with maltose or glucose shows minor differences for acarbose biosynthesis proteins but major differences for saccharide transporters. <i>Journal of Proteomics</i> , <b>2016</b> , 131, 140-148	3.9	15
344	Genome wide transcription start sites analysis of <i>Xanthomonas campestris</i> pv. <i>campestris</i> B100 with insights into the gum gene cluster directing the biosynthesis of the exopolysaccharide xanthan. <i>Journal of Biotechnology</i> , <b>2016</b> , 225, 18-28	3.7	31

343	Draft genome sequence of the sugar beet pathogen <i>Rhizoctonia solani</i> AG2-2IIIB strain BBA69670. <i>Journal of Biotechnology</i> , <b>2016</b> , 222, 11-2	3.7	13
342	Intraspecies Transfer of the Chromosomal <i>Acinetobacter baumannii</i> blaNDM-1 Carbapenemase Gene. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2016</b> , 60, 3032-40	5.9	49
341	Taxonomic analysis of the microbial community in stored sugar beets using high-throughput sequencing of different marker genes. <i>FEMS Microbiology Ecology</i> , <b>2016</b> , 92,	4.3	25
340	Complete genome analysis of <i>Clostridium bornimense</i> strain M2/40(T): A new acidogenic <i>Clostridium</i> species isolated from a mesophilic two-phase laboratory-scale biogas reactor. <i>Journal of Biotechnology</i> , <b>2016</b> , 232, 38-49	3.7	13
339	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> , <b>2016</b> , 11, e0165965	3.7	37
338	<i>Rhizobium favelukesii</i> sp. nov., isolated from the root nodules of alfalfa ( <i>Medicago sativa</i> L). <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2016</b> , 66, 4451-4457	2.2	17
337	Complete Genome Sequence of the Methanogen <i>Methanoculleus bourgensis</i> BA1 Isolated from a Biogas Reactor. <i>Genome Announcements</i> , <b>2016</b> , 4,		7
336	Back to the Future of Soil Metagenomics. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 73	5.7	82
335	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
334	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
333	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> , <b>2016</b> , 232, 61-8	3.7	11
332	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> , <b>2016</b> , 17, 245	4.5	52
331	Genomic characterization of <i>Deffluviitoga 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> , <b>2016</b> , 232, 50-60	3.7	38
330	Applying DNA affinity chromatography to specifically screen for sucrose-related DNA-binding transcriptional regulators of <i>Xanthomonas campestris</i> . <i>Journal of Biotechnology</i> , <b>2016</b> , 232, 89-98	3.7	3
329	Genetic engineering in <i>Actinoplanes</i> sp. SE50/110 - development of an intergeneric conjugation system for the introduction of actinophage-based integrative vectors. <i>Journal of Biotechnology</i> , <b>2016</b> , 232, 79-88	3.7	13
328	The structure of the <i>Cyberlindnera jadinii</i> genome and its relation to <i>Candida utilis</i> analyzed by the occurrence of single nucleotide polymorphisms. <i>Journal of Biotechnology</i> , <b>2015</b> , 211, 20-30	3.7	6
327	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> , <b>2015</b> , 6, 152	5.7	38
326	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> , <b>2015</b> , 203, 19-21	3.7	20

325	Genome Sequence of the Urethral Catheter Isolate <i>Pseudomonas aeruginosa</i> MH19. <i>Genome Announcements</i> , <b>2015</b> , 3,		2
324	Comprehensive proteome analysis of <i>Actinoplanes</i> sp. SE50/110 highlighting the location of proteins encoded by the acarbose and the pyochelin biosynthesis gene cluster. <i>Journal of Proteomics</i> , <b>2015</b> , 125, 1-16	3.9	14
323	Complete genome sequence of the strain <i>DeFluviitoga tunisiensis</i> L3, isolated from a thermophilic, production-scale biogas plant. <i>Journal of Biotechnology</i> , <b>2015</b> , 203, 17-8	3.7	35
322	Draft genome of the xanthan producer <i>Xanthomonas campestris</i> NRRL B-1459 (ATCC 13951). <i>Journal of Biotechnology</i> , <b>2015</b> , 204, 45-6	3.7	17
321	Complete Genome Sequence of the Clinical Strain <i>Acinetobacter baumannii</i> R2090 Carrying the Chromosomally Encoded Metallo- $\beta$ -Lactamase Gene blaNDM-1. <i>Genome Announcements</i> , <b>2015</b> , 3,		1
320	Community shifts in a well-operating agricultural biogas plant: how process variations are handled by the microbiome. <i>Applied Microbiology and Biotechnology</i> , <b>2015</b> , 99, 7791-803	5.7	48
319	Complete Genome Sequence of <i>Acinetobacter baumannii</i> CIP 70.10, a Susceptible Reference Strain for Comparative Genome Analyses. <i>Genome Announcements</i> , <b>2015</b> , 3,		9
318	Draft genome sequence of <i>Herbinix hemicellulosilytica</i> T3/55 T, a new thermophilic cellulose degrading bacterium isolated from a thermophilic biogas reactor. <i>Journal of Biotechnology</i> , <b>2015</b> , 214, 59-60	3.7	18
317	Complete genome sequence of the novel Porphyromonadaceae bacterium strain ING2-E5B isolated from a mesophilic lab-scale biogas reactor. <i>Journal of Biotechnology</i> , <b>2015</b> , 193, 34-6	3.7	53
316	Deeply sequenced metagenome and metatranscriptome of a biogas-producing microbial community from an agricultural production-scale biogas plant. <i>GigaScience</i> , <b>2015</b> , 4, 33	7.6	53
315	Genome-guided insight into the methylotrophy of <i>Paracoccus aminophilus</i> JCM 7686. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 852	5.7	24
314	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> , <b>2015</b> , 10, e0144769	3.7	28
313	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
312	Draft Genome Sequence of <i>Pseudomonas aeruginosa</i> Strain WS136, a Highly Cytotoxic ExoS-Positive Wound Isolate Recovered from <i>Pyoderma Gangrenosum</i> . <i>Genome Announcements</i> , <b>2015</b> , 3,		2
311	Genome Sequence of the Urethral Isolate <i>Pseudomonas aeruginosa</i> RN21. <i>Genome Announcements</i> , <b>2015</b> , 3,		2
310	Insights into the annotated genome sequence of <i>Methanoculleus bourgensis</i> MS2(T), related to dominant methanogens in biogas-producing plants. <i>Journal of Biotechnology</i> , <b>2015</b> , 201, 43-53	3.7	25
309	The <i>Sinorhizobium fredii</i> HH103 Genome: A Comparative Analysis With <i>S. fredii</i> Strains Differing in Their Symbiotic Behavior With Soybean. <i>Molecular Plant-Microbe Interactions</i> , <b>2015</b> , 28, 811-24	3.6	39
308	Complete genome sequence of the actinobacterium <i>Streptomyces glaucescens</i> GLA.O (DSM 40922) consisting of a linear chromosome and one linear plasmid. <i>Journal of Biotechnology</i> , <b>2015</b> , 194, 81-3	3.7	5

307	Identification of Oxygen-Responsive Transcripts in the Silage Inoculant <i>Lactobacillus buchneri</i> CD034 by RNA Sequencing. <i>PLoS ONE</i> , <b>2015</b> , 10, e0134149	3.7	12
306	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> , <b>2014</b> , 15, 124	4.5	33
305	Complete genome sequence of the cyanide-degrading bacterium <i>Pseudomonas pseudoalcaligenes</i> CECT5344. <i>Journal of Biotechnology</i> , <b>2014</b> , 175, 67-8	3.7	18
304	Improving the genome annotation of the acarbose producer <i>Actinoplanes</i> sp. SE50/110 by sequencing enriched 5Rends of primary transcripts. <i>Journal of Biotechnology</i> , <b>2014</b> , 190, 85-95	3.7	13
303	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> , <b>2014</b> , 192 Pt A, 59-61	3.7	13
302	Complete genome sequence of the methanogenic neotype strain <i>Methanobacterium formicicum</i> MF(T.). <i>Journal of Biotechnology</i> , <b>2014</b> , 192 Pt A, 40-1	3.7	17
301	First draft genome sequence of the amyolytic <i>Bacillus thermoamylovorans</i> wild-type strain 1A1 isolated from a thermophilic biogas plant. <i>Journal of Biotechnology</i> , <b>2014</b> , 192 Pt A, 154-5	3.7	8
300	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> , <b>2014</b> , 188, 136-7	3.7	26
299	Metabolic flux pattern of glucose utilization by <i>Xanthomonas campestris</i> pv. <i>campestris</i> : prevalent role of the Entner-Doudoroff pathway and minor fluxes through the pentose phosphate pathway and glycolysis. <i>Molecular BioSystems</i> , <b>2014</b> , 10, 2663-76		22
298	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> , <b>2014</b> , 118, 800-13	2.8	27
297	Complete genome sequence of the actinobacterium <i>Actinoplanes friuliensis</i> HAG 010964, producer of the lipopeptide antibiotic friulimycin. <i>Journal of Biotechnology</i> , <b>2014</b> , 178, 41-2	3.7	13
296	Genome sequence of the acid-tolerant strain <i>Rhizobium</i> sp. LPU83. <i>Journal of Biotechnology</i> , <b>2014</b> , 176, 40-1	3.7	8
295	IncH-type plasmid harboring bla CTX-M-15, bla DHA-1, and qnrB4 genes recovered from animal isolates. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2014</b> , 58, 3768-73	5.9	18
294	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> , <b>2014</b> , 184, 199-200	3.7	8
293	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
292	The crystal structures of apo and cAMP-bound GlxR from <i>Corynebacterium glutamicum</i> reveal structural and dynamic changes upon cAMP binding in CRP/FNR family transcription factors. <i>PLoS ONE</i> , <b>2014</b> , 9, e113265	3.7	21
291	Genome Sequence of the Small-Colony Variant <i>Pseudomonas aeruginosa</i> MH27, Isolated from a Chronic Urethral Catheter Infection. <i>Genome Announcements</i> , <b>2014</b> , 2,		7
290	Genome Sequence of the Acute Urethral Catheter Isolate <i>Pseudomonas aeruginosa</i> MH38. <i>Genome Announcements</i> , <b>2014</b> , 2,		4

289	Draft Genome Sequence of <i>Pseudomonas aeruginosa</i> Strain WS394, a Multidrug-Resistant and Highly Cytotoxic Wound Isolate from Chronic Ulcus Cruris. <i>Genome Announcements</i> , <b>2014</b> , 2,		1
288	5.2 Functional -Omics for Cell Lines and Processes: The -Omics Technologies on the Example of CHO Cells <b>2014</b> , 326-367		
287	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
286	Rhizobial plasmid pLPU83a is able to switch between different transfer machineries depending on its genomic background. <i>FEMS Microbiology Ecology</i> , <b>2014</b> , 88, 565-78	4.3	17
285	Carbon source dependent biosynthesis of acarbose metabolites in <i>Actinoplanes</i> sp. SE50/110. <i>Journal of Biotechnology</i> , <b>2014</b> , 191, 113-20	3.7	17
284	Discovery of transcription start sites in the Chinese hamster genome by next-generation RNA sequencing. <i>Journal of Biotechnology</i> , <b>2014</b> , 190, 64-75	3.7	7
283	Synthetic Biology ¶Towards an Engineering Science. <i>European Review</i> , <b>2014</b> , 22, S102-S112		0.3
282	Transcriptome analyses of CHO cells with the next-generation microarray CHO41K: development and validation by analysing the influence of the growth stimulating substance IGF-1 substitute LongR(3.). <i>Journal of Biotechnology</i> , <b>2014</b> , 178, 23-31	3.7	12
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166	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
165	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
164	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

163	The transcriptional regulator SsuR activates expression of the <i>Corynebacterium glutamicum</i> sulphonate utilization genes in the absence of sulphate. <i>Molecular Microbiology</i> , <b>2005</b> , 58, 480-94	4.1	27
162	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
161	Plasmid pB8 is closely related to the prototype IncP-1beta 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> , <b>2005</b> , 54, 135-48	3.3	53
160	Functional genomics and expression analysis of the <i>Corynebacterium glutamicum</i> fpr2-cysIXHDNYZ gene cluster involved in assimilatory sulphate reduction. <i>BMC Genomics</i> , <b>2005</b> , 6, 121	4.5	49
159	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
158	EST sequencing and time course microarray hybridizations identify more than 700 <i>Medicago truncatula</i> genes with developmental expression regulation in flowers and pods. <i>Planta</i> , <b>2005</b> , 222, 269-87	4.7	34
157	The promoter of the leghaemoglobin gene Vflb29: functional analysis and identification of modules necessary for its activation in the infected cells of root nodules and in the arbuscule-containing cells of mycorrhizal roots. <i>Journal of Experimental Botany</i> , <b>2005</b> , 56, 799-806	7	57
156	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
155	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
154	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> , <b>2005</b> , 137, 1283-301	6.6	289
153	BACCardI--a tool for the validation of genomic assemblies, assisting genome finishing and intergenome comparison. <i>Bioinformatics</i> , <b>2005</b> , 21, 853-9	7.2	32
152	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
151	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
150	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
149	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
148	What can bacterial genome research teach us about bacteria-plant interactions?. <i>Current Opinion in Plant Biology</i> , <b>2004</b> , 7, 137-47	9.9	55
147	Comparative genomics identified two conserved DNA modules in a corynebacterial plasmid family present in clinical isolates of the opportunistic human pathogen <i>Corynebacterium jeikeium</i> . <i>Plasmid</i> , <b>2004</b> , 52, 102-18	3.3	23
146	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

145	Different molecular rearrangements in the integron of the IncP-1 beta resistance plasmid pB10 isolated from a wastewater treatment plant result in elevated beta-lactam resistance levels. <i>Archives of Microbiology</i> , <b>2004</b> , 182, 429-35	3	14
144	Comparing expression level-dependent features in codon usage with protein abundance: an analysis of predictive proteomics. <i>Proteomics</i> , <b>2004</b> , 4, 46-58	4.8	15
143	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
142	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
141	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
140	Classification of hyper-variable <i>Corynebacterium glutamicum</i> surface-layer proteins by sequence analyses and atomic force microscopy. <i>Journal of Biotechnology</i> , <b>2004</b> , 112, 177-93	3.7	33
139	Single molecule force spectroscopy on ligand-DNA complexes: from molecular binding mechanisms to biosensor applications. <i>Journal of Biotechnology</i> , <b>2004</b> , 112, 5-12	3.7	28
138	Development of joint application strategies for two microbial gene finders. <i>Bioinformatics</i> , <b>2004</b> , 20, 1622-31	7.2	71
137	The promoter of the <i>Vicia faba</i> L. leghemoglobin gene Vflb29 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
136	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
135	Identification and functional analysis of six mycolyltransferase genes of <i>Corynebacterium glutamicum</i> ATCC 13032: the genes cop1, cmt1, and cmt2 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
134	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
133	Genomics insights into symbiotic nitrogen fixation. <i>Current Opinion in Biotechnology</i> , <b>2003</b> , 14, 200-5	11.4	38
132	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
131	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> , <b>2003</b> , 104, 5-25	3.7	750
130	Identification and characterization of the last two unknown genes, dapC and dapF, in the succinylase branch of the L-lysine biosynthesis of <i>Corynebacterium glutamicum</i> . <i>Journal of Biotechnology</i> , <b>2003</b> , 104, 199-211	3.7	36
129	Plasmids in <i>Corynebacterium glutamicum</i> and their molecular classification by comparative genomics. <i>Journal of Biotechnology</i> , <b>2003</b> , 104, 27-40	3.7	43
128	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



127	Genome-based analysis of biosynthetic aminotransferase genes of <i>Corynebacterium glutamicum</i> . <i>Journal of Biotechnology</i> , <b>2003</b> , 104, 229-40	3.7	32
126	GenDB--an open source genome annotation system for prokaryote genomes. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 2187-95	20.1	587
125	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
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122	Building a BRIDGE for the integration of heterogeneous data from functional genomics into a platform for systems biology. <i>Journal of Biotechnology</i> , <b>2003</b> , 106, 157-67	3.7	22
121	Whole genome shotgun sequencing guided by bioinformatics pipelines--an optimized approach for an established technique. <i>Journal of Biotechnology</i> , <b>2003</b> , 106, 121-33	3.7	25
120	Bioinformatics support for high-throughput proteomics. <i>Journal of Biotechnology</i> , <b>2003</b> , 106, 147-56	3.7	29
119	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
118	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
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98	The <i>exbD2</i> gene as well as the iron-uptake genes <i>tonB</i> , <i>exbB</i> and <i>exbD1</i> of <i>Xanthomonas campestris</i> pv. <i>campestris</i> are essential for the induction of a hypersensitive response on pepper ( <i>Capsicum annuum</i> ). <i>Microbiology (United Kingdom)</i> , <b>2000</b> , 146 ( Pt 5), 1053-1060	2.9	34
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88	Genetic basis of enterobacterial repetitive intergenic consensus (ERIC)-PCR fingerprint pattern in <i>Sinorhizobium meliloti</i> and identification of <i>S. meliloti</i> employing PCR primers derived from an ERIC-PCR fragment. <i>Archives of Microbiology</i> , <b>1999</b> , 172, 22-30	3	15
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83	<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
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70	The persistence of bioluminescent <i>Rhizobium meliloti</i> strains L1 (RecA-) and L33 (RecA+) in non-sterile microcosms depends on the soil type, on the co-cultivation of the host legume alfalfa and on the presence of an indigenous <i>R. meliloti</i> population. <i>Plant and Soil</i> , <b>1997</b> , 188, 257-266	4.2	12
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68	Symbiotic suppression of the <i>Medicago sativa</i> plant defence system by <i>Rhizobium meliloti</i> oligosaccharides <b>1997</b> , 111-114		9
67	Analysis of genes expressed in root nodules of broad bean ( <i>Vicia faba</i> L.) <b>1997</b> , 91-94		2
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65	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
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59	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
58	The insertion sequence element ISRm2011-2 belongs to the IS630-Tc1 family of transposable elements and is abundant in <i>Rhizobium meliloti</i> . <i>Gene</i> , <b>1995</b> , 163, 59-64	3.8	31
57	A <i>Rhizobium Meliloti</i> Ferredoxin (FdxN) Purified from <i>Escherichia Coli</i> Donates Electrons to <i>Rhodobacter Capsulatus</i> Nitrogenase. <i>FEBS Journal</i> , <b>1995</b> , 231, 742-746		1
56	Molekulargenetik am Beispiel Aminosäure-produzierender <i>Corynebakterien</i> . <i>Biologie in Unserer Zeit</i> , <b>1995</b> , 25, 221-229	0.1	1

55	A Rhizobium meliloti ferredoxin (FdxN) purified from Escherichia coli donates electrons to Rhodobacter capsulatus nitrogenase. <i>FEBS Journal</i> , <b>1995</b> , 231, 742-6		8
54	The new class II transposon Tn163 is plasmid-borne in two unrelated Rhizobium leguminosarum biovar viciae strains. <i>Molecular Genetics and Genomics</i> , <b>1994</b> , 242, 505-16		15
53	Corynebacterium glutamicum DNA is subjected to methylation-restriction in Escherichia coli. <i>FEMS Microbiology Letters</i> , <b>1994</b> , 123, 343-7	2.9	45
52	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
51	Regulatory aspects of the C4-dicarboxylate transport in Rhizobium meliloti: Transcriptional activation and dependence on effective symbiosis. <i>Journal of Plant Physiology</i> , <b>1993</b> , 141, 18-27	3.6	23
50	Analysis of the Rhizobium meliloti exoH/exoK/exoL fragment: ExoK shows homology to excreted endo-beta-1,3-1,4-glucanases and ExoH resembles membrane proteins. <i>Molecular Genetics and Genomics</i> , <b>1993</b> , 238, 145-54		49
49	The membrane topology of the Rhizobium meliloti C4-dicarboxylate permease (DctA) as derived from protein fusions with Escherichia coli K12 alkaline phosphatase (PhoA) and beta-galactosidase (LacZ). <i>Molecular Genetics and Genomics</i> , <b>1993</b> , 241, 106-14		33
48	Identification and analysis of the Rhizobium meliloti 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
47	Synthesis of the ferredoxin-like protein FdxN from Rhizobium meliloti bacteroids as a fusion protein in Escherichia coli. <i>Canadian Journal of Microbiology</i> , <b>1992</b> , 38, 534-40	3.2	2
46	The Rhizobium meliloti pmi gene encodes a new type of phosphomannose isomerase. <i>Gene</i> , <b>1992</b> , 122, 35-43	3.8	25
45	High frequency, heat treatment-induced inactivation of the phosphinothricin resistance gene in transgenic single cell suspension cultures of Medicago sativa. <i>Molecular Genetics and Genomics</i> , <b>1992</b> , 235, 189-96		40
44	Functional analysis of the cysteine motifs in the ferredoxin-like protein FdxN of Rhizobium meliloti involved in symbiotic nitrogen fixation. <i>Molecular Genetics and Genomics</i> , <b>1992</b> , 233, 33-41		19
43	Genetic Improvement of Rhizobium Strains <b>1992</b> , 265-285		3
42	Characterization of recA genes and recA mutants of Rhizobium meliloti and Rhizobium leguminosarum biovar viciae. <i>Molecular Genetics and Genomics</i> , <b>1991</b> , 229, 86-95		37
41	Genetic and biochemical analysis of the aspartokinase from Corynebacterium glutamicum. <i>Molecular Microbiology</i> , <b>1991</b> , 5, 1197-204	4.1	133
40	Characterization of pGA1, a new plasmid from Corynebacterium glutamicum LP-6. <i>Gene</i> , <b>1991</b> , 107, 69-74	3.8	33
39	Manipulation of Corynebacterium glutamicum by gene disruption and replacement. <i>Nature Biotechnology</i> , <b>1991</b> , 9, 84-7	44.5	62
38	Genetic Analysis of Different Resistance Mechanisms Against the Herbicidal Antibiotic Phosphinothricyl-Alanyl-Alanine <b>1991</b> , 171-183		2

37	Cooperative Action of Rhizobium meliloti Nodulation and Infection Mutants during the Process of Forming Mixed Infected Alfalfa Nodules. <i>Plant Cell</i> , <b>1990</b> , 2, 139	11.6	6
36	High-frequency conjugal plasmid transfer from gram-negative Escherichia coli to various gram-positive coryneform bacteria. <i>Journal of Bacteriology</i> , <b>1990</b> , 172, 1663-6	3.5	180
35	Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum. <i>Molecular Genetics and Genomics</i> , <b>1990</b> , 224, 317-24		59
34	An Fnr-like protein encoded in Rhizobium leguminosarum biovar viciae shows structural and functional homology to Rhizobium meliloti FixK. <i>Molecular Genetics and Genomics</i> , <b>1990</b> , 223, 138-47		69
33	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
32	Conjugal Transfer of Megaplasmid 2 between Rhizobium meliloti Strains in Alfalfa Nodules. <i>Applied and Environmental Microbiology</i> , <b>1990</b> , 56, 2354-2359	4.8	29
31	The Rhizobium meliloti fdxN gene encoding a ferredoxin-like protein is necessary for nitrogen fixation and is cotranscribed with nifA and nifB. <i>Molecular Genetics and Genomics</i> , <b>1989</b> , 216, 293-302		52
30	Electrotransformation of intact and osmotically sensitive cells of Corynebacterium glutamicum. <i>Applied Microbiology and Biotechnology</i> , <b>1989</b> , 30, 283	5.7	37
29	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
28	Direct selection for curing and deletion of Rhizobium plasmids using transposons carrying the Bacillus subtilis sacB gene. <i>Gene</i> , <b>1989</b> , 78, 111-20	3.8	108
27	ISR1, a transposable DNA sequence resident in Rhizobium class IV strains, shows structural characteristics of classical insertion elements. <i>Plasmid</i> , <b>1989</b> , 21, 120-8	3.3	23
26	Identification and sequence analysis of the Rhizobium meliloti dctA gene encoding the C4-dicarboxylate carrier. <i>Journal of Bacteriology</i> , <b>1989</b> , 171, 5551-60	3.5	101
25	Genetic characterization and sequence analysis of the duplicated nifA/nifB gene region of Rhodobacter capsulatus. <i>Molecular Genetics and Genomics</i> , <b>1988</b> , 212, 27-37		114
24	Two classes of Rhizobium meliloti 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
23	The minimal replicon of the Streptomyces ghanaensis plasmid pSG5 identified by subcloning and Tn5 mutagenesis. <i>Molecular Genetics and Genomics</i> , <b>1988</b> , 211, 424-9		45
22	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
21	Cloning of a phosphinothricin N-acetyltransferase gene from Streptomyces viridochromogenes T894 and its expression in Streptomyces lividans and Escherichia coli. <i>Gene</i> , <b>1988</b> , 63, 65-74	3.8	115
20	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

19	Identification and mapping of nitrogen fixation genes of <i>Rhodobacter capsulatus</i> : duplication of a nifA-nifB region. <i>Journal of Bacteriology</i> , <b>1988</b> , 170, 693-9	3.5	144
18	Organization and partial sequence of a DNA region of the <i>Rhizobium leguminosarum</i> symbiotic plasmid pRL6JI 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
17	Conserved sequence motifs in the untranslated 3' end of leghemoglobin transcripts isolated from broadbean nodules. <i>Plant Science</i> , <b>1987</b> , 49, 137-143	5.3	15
16	Genes of lithoautotrophic metabolism are clustered on the megaplasmid pHG1 in <i>Alcaligenes eutrophus</i> . <i>Molecular Genetics and Genomics</i> , <b>1987</b> , 210, 122-128		40
15	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
14	Mapping and expression of a regulatory nitrogen fixation gene (fix D) of <i>Rhizobium meliloti</i> . <i>EMBO Journal</i> , <b>1985</b> , 4, 2751-2756	13	32
13	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
12	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
11	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
10	Expression of plant tumor-specific proteins in minicells of <i>Escherichia coli</i> : a fusion protein of lysopine dehydrogenase with chloramphenicol acetyltransferase. <i>Nucleic Acids Research</i> , <b>1981</b> , 9, 5187-202 <sup>20.1</sup>		48
9	Identification of the repressor and repressor bypass (antirepressor) polypeptides of bacteriophage P1 synthesized in infected minicells. <i>Molecular Genetics and Genomics</i> , <b>1980</b> , 178, 149-54		20
8	Transposon mutagenesis of the gene encoding the bacteriophage P1 restriction endonuclease. Co-linearity of the gene and gene product. <i>Journal of Molecular Biology</i> , <b>1980</b> , 144, 387-96	6.5	11
7	Characterization of plasmids isolated from <i>Rhizobium meliloti</i> . <i>Archives of Microbiology</i> , <b>1979</b> , 121, 1-7	3	16
6	Fertility inhibition in <i>Rhizobium lupini</i> by the resistance plasmid RP4. <i>Molecular Genetics and Genomics</i> , <b>1978</b> , 162, 163-71		8
5	Characterization of a nosocomially significant, multiple drug-resistant strain of <i>Serratia marcescens</i> . <i>Chemotherapy</i> , <b>1976</b> , 22, 297-312	3.2	14
4	Physical map of circular mitochondrial DNA from <i>Neurospora crassa</i> . <i>FEBS Letters</i> , <b>1975</b> , 60, 119-21	3.8	13
3	Denaturation map of the circular mitochondrial genome of <i>Neurospora crassa</i> . <i>Nucleic Acids and Protein Synthesis</i> , <b>1975</b> , 402, 270-8		23
2	The <i>Sinorhizobium meliloti</i> insertion sequence (IS) elements ISRm102F34-1/ISRm7 and ISRm220-13-5 belong to a new family of insertion sequence elements		1

1 The tetAB genes of the *Corynebacterium striatum* R-plasmid pTP10 encode an ABC transporter and confer tetracycline, oxytetracycline and oxacillin resistance in *Corynebacterium glutamicum*

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