

Alfred PÃ¼hler

List of Publications by Year in descending order

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407
papers

36,626
citations

3721

89
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3997

176
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415
all docs

415
docs citations

415
times ranked

23097
citing authors

#	ARTICLE	IF	CITATIONS
1	Two Flagellar mutants of <i>Xanthomonas campestris</i> are characterized by enhanced xanthan production and higher xanthan viscosity. <i>Journal of Biotechnology</i> , 2022, 347, 9-17.	1.9	3
2	Implementing FAIR data management within the German Network for Bioinformatics Infrastructure (de.NBI) exemplified by selected use cases. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	18
3	Exopolysaccharide Characterization of <i>Rhizobium favelukesii</i> LPU83 and Its Role in the Symbiosis With Alfalfa. <i>Frontiers in Plant Science</i> , 2021, 12, 642576.	1.7	7
4	Indicative Marker Microbiome Structures Deduced from the Taxonomic Inventory of 67 Full-Scale Anaerobic Digesters of 49 Agricultural Biogas Plants. <i>Microorganisms</i> , 2021, 9, 1457.	1.6	8
5	ExoS/ChvI Two-Component Signal-Transduction System Activated in the Absence of Bacterial Phosphatidylcholine. <i>Frontiers in Plant Science</i> , 2021, 12, 678976.	1.7	14
6	Genome Analyses of the Less Aggressive <i>Rhizoctonia solani</i> AG1-IB Isolates 1/2/21 and O8/2 Compared to the Reference AG1-IB Isolate 7/3/14. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 832.	1.5	5
7	Genome Analyses and Genome-Centered Metatranscriptomics of <i>Methanothermobacter wolfeii</i> Strain SIV6, Isolated from a Thermophilic Production-Scale Biogas Fermenter. <i>Microorganisms</i> , 2020, 8, 13.	1.6	8
8	A maltose-regulated large genomic region is activated by the transcriptional regulator MaltI in <i>Actinoplanes</i> sp. SE50/110. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 9283-9294.	1.7	0
9	Global transcriptome analysis of <i>Rhizobium favelukesii</i> LPU83 in response to acid stress. <i>FEMS Microbiology Ecology</i> , 2020, 97, .	1.3	10
10	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> , 2020, 21, 818.	1.2	3
11	The Role of <i>Petrimonas mucosa</i> ING2-E5AT in Mesophilic Biogas Reactor Systems as Deduced from Multiomics Analyses. <i>Microorganisms</i> , 2020, 8, 2024.	1.6	23
12	pSETT4, an Improved λ C31-Based Integrative Vector System for <i>Actinoplanes</i> sp. SE50/110. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
13	Impact of process temperature and organic loading rate on cellulolytic / hydrolytic biofilm microbiomes during biomethanation of ryegrass silage revealed by genome-centered metagenomics and metatranscriptomics. <i>Environmental Microbiomes</i> , 2020, 15, 7.	2.2	13
14	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> , 2020, 104, 5395-5408.	1.7	2
15	Genetic Potential of the Biocontrol Agent <i>Pseudomonas brassicacearum</i> (Formerly <i>P. trivialis</i>) 3Re2-7 Unraveled by Genome Sequencing and Mining, <i>Comparative Genomics and Transcriptomics</i> . <i>Genes</i> , 2019, 10, 601.	1.0	32
16	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> , 2019, 18, 114.	1.9	15
17	A comprehensive analysis of the <i>Lactuca sativa</i> , <i>L.</i> transcriptome during different stages of the compatible interaction with <i>Rhizoctonia solani</i> . <i>Scientific Reports</i> , 2019, 9, 7221.	1.6	11
18	Effect of Long-Term Farming Practices on Agricultural Soil Microbiome Members Represented by Metagenomically Assembled Genomes (MAGs) and Their Predicted Plant-Beneficial Genes. <i>Genes</i> , 2019, 10, 424.	1.0	61

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19	Insight into the structure, function and conjugative transfer of pLPU83a, an accessory plasmid of <i>Rhizobium favelukesii</i> LPU83. <i>Plasmid</i> , 2019, 103, 9-16.	0.4	10
20	Essentiality of the Maltase AmIE in Maltose Utilization and Its Transcriptional Regulation by the Repressor AmIR in the Acarbose-Producing Bacterium <i>Actinoplanes</i> sp. SE50/110. <i>Frontiers in Microbiology</i> , 2019, 10, 2448.	1.5	4
21	de.NBI Cloud federation through ELIXIR AAI. <i>F1000Research</i> , 2019, 8, 842.	0.8	13
22	Complete Genome Sequencing of <i>Acinetobacter baumannii</i> Strain K50 Discloses the Large Conjugative Plasmid pK50a Encoding Carbapenemase OXA-23 and Extended-Spectrum β -Lactamase GES-11. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	46
23	Assembly of the <i>Lactuca sativa</i> , L. cv. Tizian draft genome sequence reveals differences within major resistance complex 1 as compared to the cv. Salinas reference genome. <i>Journal of Biotechnology</i> , 2018, 267, 12-18.	1.9	13
24	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
25	Targeted <i>in situ</i> metatranscriptomics for selected taxa from mesophilic and thermophilic biogas plants. <i>Microbial Biotechnology</i> , 2018, 11, 667-679.	2.0	43
26	<i>Proteiniphilum saccharofermentans</i> str. M3/6T isolated from a laboratory biogas reactor is versatile in polysaccharide and oligopeptide utilization as deduced from genome-based metabolic reconstructions. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2018, 18, e00254.	2.1	30
27	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
28	Comparative transcription profiling of two fermentation cultures of <i>Xanthomonas campestris</i> pv. <i>campestris</i> B100 sampled in the growth and in the stationary phase. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 6613-6625.	1.7	8
29	Characterization of <i>Bathyarchaeota</i> genomes assembled from metagenomes of biofilms residing in mesophilic and thermophilic biogas reactors. <i>Biotechnology for Biofuels</i> , 2018, 11, 167.	6.2	38
30	Genome sequence of <i>Methanobacterium congolense</i> strain Buetzberg, a hydrogenotrophic, methanogenic archaeon, isolated from a mesophilic industrial-scale biogas plant utilizing bio-waste. <i>Journal of Biotechnology</i> , 2017, 247, 1-5.	1.9	48
31	Genome Sequence of the Symbiotic Type Strain <i>Rhizobium tibeticum</i> CCBAU85039 T. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
32	A metabolomic approach to characterize the acid-tolerance response in <i>Sinorhizobium meliloti</i> . <i>Metabolomics</i> , 2017, 13, 1.	1.4	10
33	Genome improvement of the acarbose producer <i>Actinoplanes</i> sp. SE50/110 and annotation refinement based on RNA-seq analysis. <i>Journal of Biotechnology</i> , 2017, 251, 112-123.	1.9	13
34	Refined annotation of the complete genome of the phytopathogenic and xanthan producing <i>Xanthomonas campestris</i> pv. <i>campestris</i> strain B100 based on RNA sequence data. <i>Journal of Biotechnology</i> , 2017, 253, 55-61.	1.9	7
35	The completely annotated genome and comparative genomics of the <i>Peptoniphilaceae</i> bacterium str. INC2-D1G, a novel acidogenic bacterium isolated from a mesophilic biogas reactor. <i>Journal of Biotechnology</i> , 2017, 257, 178-186.	1.9	2
36	Draft genome sequence of the potato pathogen <i>Rhizoctonia solani</i> AG3-PT isolate Ben3. <i>Archives of Microbiology</i> , 2017, 199, 1065-1068.	1.0	12

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37	Lifestyleâ€determining extrachromosomal replicon pAMV1 and its contribution to the carbon metabolism of the methylotrophic bacterium <i>Paracoccus aminovorans</i> JCM 7685. <i>Environmental Microbiology</i> , 2017, 19, 4536-4550.	1.8	40
38	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'-hydroxy streptomycin, and acarbose. <i>Journal of Biotechnology</i> , 2017, 262, 84-88.	1.9	10
39	Genome content, metabolic pathways and biotechnological potential of the psychrophilic Arctic bacterium <i>Psychrobacter</i> sp. DAB_AL43B, a source and a host of novel <i>Psychrobacter</i> -specific vectors. <i>Journal of Biotechnology</i> , 2017, 263, 64-74.	1.9	21
40	Identification of a novel mycovirus isolated from <i>Rhizoctonia solani</i> (AG 2-2 IV) provides further information about genome plasticity within the order Tymovirales. <i>Archives of Virology</i> , 2017, 162, 555-559.	0.9	15
41	Genomics and prevalence of bacterial and archaeal isolates from biogas-producing microbiomes. <i>Biotechnology for Biofuels</i> , 2017, 10, 264.	6.2	50
42	The MalR type regulator AcrC is a transcriptional repressor of acarbose biosynthetic genes in <i>Actinoplanes</i> sp. SE50/110. <i>BMC Genomics</i> , 2017, 18, 562.	1.2	15
43	The <i>Rhizoctonia solani</i> AG1-IB (isolate 7/3/14) transcriptome during interaction with the host plant lettuce (<i>Lactuca sativa</i> L.). <i>PLoS ONE</i> , 2017, 12, e0177278.	1.1	28
44	A community proposal to integrate proteomics activities in ELIXIR. <i>F1000Research</i> , 2017, 6, 875.	0.8	13
45	Biphasic Study to Characterize Agricultural Biogas Plants by High-Throughput 16S rRNA Gene Amplicon Sequencing and Microscopic Analysis. <i>Journal of Microbiology and Biotechnology</i> , 2017, 27, 321-334.	0.9	31
46	Complete Genome Sequence of the Methanogen <i>Methanoculleus bourgensis</i> BA1 Isolated from a Biogas Reactor. <i>Genome Announcements</i> , 2016, 4, .	0.8	11
47	Back to the Future of Soil Metagenomics. <i>Frontiers in Microbiology</i> , 2016, 7, 73.	1.5	120
48	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
49	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
50	Finished genome sequence and methylome of the cyanide-degrading <i>Pseudomonas pseudoalcaligenes</i> strain CECT5344 as resolved by single-molecule real-time sequencing. <i>Journal of Biotechnology</i> , 2016, 232, 61-68.	1.9	20
51	Genome analysis of the sugar beet pathogen <i>Rhizoctonia solani</i> AG2-2IIIB revealed high numbers in secreted proteins and cell wall degrading enzymes. <i>BMC Genomics</i> , 2016, 17, 245.	1.2	69
52	Genomic characterization of <i>DeFluviitoga tunisiensis</i> L3, a key hydrolytic bacterium in a thermophilic biogas plant and its abundance as determined by metagenome fragment recruitment. <i>Journal of Biotechnology</i> , 2016, 232, 50-60.	1.9	53
53	Applying DNA affinity chromatography to specifically screen for sucrose-related DNA-binding transcriptional regulators of <i>Xanthomonas campestris</i> . <i>Journal of Biotechnology</i> , 2016, 232, 89-98.	1.9	3
54	Genetic engineering in <i>Actinoplanes</i> sp. SE50/110 âˆ™ development of an intergeneric conjugation system for the introduction of actinophage-based integrative vectors. <i>Journal of Biotechnology</i> , 2016, 232, 79-88.	1.9	17

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55	Draft Genome Sequence of <i>Propionispora</i> sp. Strain 2/2-37, a New Xylan-Degrading Bacterium Isolated from a Mesophilic Biogas Reactor. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
56	Complete Genome Sequence of <i>Herbinix luporum</i> SD1D, a New Cellulose-Degrading Bacterium Isolated from a Thermophilic Biogas Reactor. <i>Genome Announcements</i> , 2016, 4, .	0.8	8
57	Genomics of high molecular weight plasmids isolated from an on-farm biopurification system. <i>Scientific Reports</i> , 2016, 6, 28284.	1.6	17
58	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> , 2016, 16, 93.	1.3	13
59	Complete Genome Sequence of the Barley Pathogen <i>Xanthomonas translucens</i> pv. <i>translucens</i> DSM 18974 ^T (ATCC 19319 ^T). <i>Genome Announcements</i> , 2016, 4, .	0.8	24
60	Comparative transcriptome analysis of the biocontrol strain <i>Bacillus amyloliquefaciens</i> FZB42 as response to biofilm formation analyzed by RNA sequencing. <i>Journal of Biotechnology</i> , 2016, 231, 212-223.	1.9	43
61	An integrated metagenome and -proteome analysis of the microbial community residing in a biogas production plant. <i>Journal of Biotechnology</i> , 2016, 231, 268-279.	1.9	33
62	Targeted genome editing in the rare actinomycete <i>Actinoplanes</i> sp. SE50/110 by using the CRISPR/Cas9 System. <i>Journal of Biotechnology</i> , 2016, 231, 122-128.	1.9	39
63	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> , 2016, 131, 140-148.	1.2	21
64	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> , 2016, 225, 18-28.	1.9	38
65	Draft genome sequence of the sugar beet pathogen <i>Rhizoctonia solani</i> AG2-IIIIB strain BBA69670. <i>Journal of Biotechnology</i> , 2016, 222, 11-12.	1.9	20
66	Intraspecies Transfer of the Chromosomal <i>Acinetobacter baumannii</i> <i>bla</i> _{NDM-1} Carbapenemase Gene. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3032-3040.	1.4	65
67	Taxonomic analysis of the microbial community in stored sugar beets using high-throughput sequencing of different marker genes. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv004.	1.3	36
68	Complete genome analysis of <i>Clostridium bornimense</i> strain M2/40T: A new acidogenic <i>Clostridium</i> species isolated from a mesophilic two-phase laboratory-scale biogas reactor. <i>Journal of Biotechnology</i> , 2016, 232, 38-49.	1.9	19
69	<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> , 2016, 66, 4451-4457.	0.8	27
70	Deep Sequencing Analysis Reveals the Mycoviral Diversity of the Virome of an Avirulent Isolate of <i>Rhizoctonia solani</i> AG-2-2 IV. <i>PLoS ONE</i> , 2016, 11, e0165965.	1.1	58
71	Deeply sequenced metagenome and metatranscriptome of a biogas-producing microbial community from an agricultural production-scale biogas plant. <i>GigaScience</i> , 2015, 4, 33.	3.3	68
72	Genome-guided insight into the methylotrophy of <i>Paracoccus aminophilus</i> JCM 7686. <i>Frontiers in Microbiology</i> , 2015, 6, 852.	1.5	44

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73	Development of a <i>Rhizoctonia solani</i> AG1-IB Specific Gene Model Enables Comparative Genome Analyses between Phytopathogenic <i>R. solani</i> AG1-IA, AG1-IB, AG3 and AG8 Isolates. <i>PLoS ONE</i> , 2015, 10, e0144769.	1.1	32
74	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
75	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> , 2015, 3, .	0.8	3
76	Genome Sequence of the Urethral Isolate <i>Pseudomonas aeruginosa</i> RN21. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
77	Insights into the annotated genome sequence of <i>Methanoculleus bourgensis</i> MS2T, related to dominant methanogens in biogas-producing plants. <i>Journal of Biotechnology</i> , 2015, 201, 43-53.	1.9	35
78	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> , 2015, 28, 811-824.	1.4	56
79	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> , 2015, 194, 81-83.	1.9	7
80	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> , 2015, 211, 20-30.	1.9	10
81	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
82	Improved genome sequence of the phytopathogenic fungus <i>Rhizoctonia solani</i> AG1-IB 7/3/14 as established by deep mate-pair sequencing on the MiSeq (Illumina) system. <i>Journal of Biotechnology</i> , 2015, 203, 19-21.	1.9	27
83	Genome Sequence of the Urethral Catheter Isolate <i>Pseudomonas aeruginosa</i> MH19. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
84	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> , 2015, 125, 1-16.	1.2	17
85	Complete genome sequence of the strain <i>Defluviitoga tunisiensis</i> L3, isolated from a thermophilic, production-scale biogas plant. <i>Journal of Biotechnology</i> , 2015, 203, 17-18.	1.9	58
86	Draft genome of the xanthan producer <i>Xanthomonas campestris</i> NRRL B-1459 (ATCC 13951). <i>Journal of Biotechnology</i> , 2015, 204, 45-46.	1.9	19
87	Complete Genome Sequence of the Clinical Strain <i>Acinetobacter baumannii</i> R2090 Carrying the Chromosomally Encoded Metallo- β -Lactamase Gene <i>bla</i> _{NDM-1} . <i>Genome Announcements</i> , 2015, 3, .	0.8	1
88	Community shifts in a well-operating agricultural biogas plant: how process variations are handled by the microbiome. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 7791-7803.	1.7	64
89	Complete Genome Sequence of <i>Acinetobacter baumannii</i> CIP 70.10, a Susceptible Reference Strain for Comparative Genome Analyses. <i>Genome Announcements</i> , 2015, 3, .	0.8	11
90	Draft genome sequence of <i>Herbinix hemicellulosilytica</i> T3/55T, a new thermophilic cellulose degrading bacterium isolated from a thermophilic biogas reactor. <i>Journal of Biotechnology</i> , 2015, 214, 59-60.	1.9	21

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91	Complete genome sequence of the novel Porphyromonadaceae bacterium strain ING2-E5B isolated from a mesophilic lab-scale biogas reactor. <i>Journal of Biotechnology</i> , 2015, 193, 34-36.	1.9	65
92	Identification of Oxygen-Responsive Transcripts in the Silage Inoculant <i>Lactobacillus buchneri</i> CD034 by RNA Sequencing. <i>PLoS ONE</i> , 2015, 10, e0134149.	1.1	19
93	Construction of a Public CHO Cell Line Transcript Database Using Versatile Bioinformatics Analysis Pipelines. <i>PLoS ONE</i> , 2014, 9, e85568.	1.1	57
94	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> , 2014, 9, e113265.	1.1	27
95	Genome Sequence of the Small-Colony Variant <i>Pseudomonas aeruginosa</i> MH27, Isolated from a Chronic Urethral Catheter Infection. <i>Genome Announcements</i> , 2014, 2, .	0.8	7
96	Genome Sequence of the Acute Urethral Catheter Isolate <i>Pseudomonas aeruginosa</i> MH38. <i>Genome Announcements</i> , 2014, 2, .	0.8	5
97	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> , 2014, 2, .	0.8	1
98	5.2 Functional -Omics for Cell Lines and Processes: The -Omics Technologies on the Example of CHO Cells. , 2014, , 326-367.		0
99	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
100	Rhizobial plasmid pLPU83a is able to switch between different transfer machineries depending on its genomic background. <i>FEMS Microbiology Ecology</i> , 2014, 88, 565-578.	1.3	24
101	Carbon source dependent biosynthesis of acarbose metabolites in <i>Actinoplanes</i> sp. SE50/110. <i>Journal of Biotechnology</i> , 2014, 191, 113-120.	1.9	21
102	Discovery of transcription start sites in the Chinese hamster genome by next-generation RNA sequencing. <i>Journal of Biotechnology</i> , 2014, 190, 64-75.	1.9	9
103	Synthetic Biology – Towards an Engineering Science. <i>European Review</i> , 2014, 22, S102-S112.	0.4	1
104	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 LongR3. <i>Journal of Biotechnology</i> , 2014, 178, 23-31.	1.9	14
105	Architecture and functions of a multipartite genome of the methylotrophic bacterium <i>Paracoccus aminophilus</i> JCM 7686, containing primary and secondary chromids. <i>BMC Genomics</i> , 2014, 15, 124.	1.2	51
106	Complete genome sequence of the cyanide-degrading bacterium <i>Pseudomonas pseudoalcaligenes</i> CECT5344. <i>Journal of Biotechnology</i> , 2014, 175, 67-68.	1.9	28
107	Improving the genome annotation of the acarbose producer <i>Actinoplanes</i> sp. SE50/110 by sequencing enriched 5'-ends of primary transcripts. <i>Journal of Biotechnology</i> , 2014, 190, 85-95.	1.9	15
108	Complete genome sequence of <i>Peptoniphilus</i> sp. strain ING2-D1G isolated from a mesophilic lab-scale completely stirred tank reactor utilizing maize silage in co-digestion with pig and cattle manure for biomethanation. <i>Journal of Biotechnology</i> , 2014, 192, 59-61.	1.9	16

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109	Complete genome sequence of the methanogenic neotype strain <i>Methanobacterium formicicum</i> MFT. <i>Journal of Biotechnology</i> , 2014, 192, 40-41.	1.9	19
110	First draft genome sequence of the amylolytic <i>Bacillus thermoamylovorans</i> wild-type strain 1A1 isolated from a thermophilic biogas plant. <i>Journal of Biotechnology</i> , 2014, 192, 154-155.	1.9	15
111	Complete genome sequence of the cellulolytic thermophile <i>Ruminoclostridium cellulosi</i> wild-type strain DG5 isolated from a thermophilic biogas plant. <i>Journal of Biotechnology</i> , 2014, 188, 136-137.	1.9	30
112	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> , 2014, 10, 2663-2676.	2.9	28
113	Transcriptome analysis of the phytopathogenic fungus <i>Rhizoctonia solani</i> AG1-IB 7/3/14 applying high-throughput sequencing of expressed sequence tags (ESTs). <i>Fungal Biology</i> , 2014, 118, 800-813.	1.1	32
114	Complete genome sequence of the actinobacterium <i>Actinoplanes friuliensis</i> HAG 010964, producer of the lipopeptide antibiotic friulimycin. <i>Journal of Biotechnology</i> , 2014, 178, 41-42.	1.9	13
115	Genome sequence of the acid-tolerant strain <i>Rhizobium</i> sp. LPU83. <i>Journal of Biotechnology</i> , 2014, 176, 40-41.	1.9	8
116	IncH-Type Plasmid Harboring <i>bla</i> _{CTX-M-15} , <i>bla</i> _{DHA-1} , and <i>qnrB4</i> Genes Recovered from Animal Isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 3768-3773.	1.4	19
117	Whole genome sequence of <i>Clostridium bornimense</i> strain M2/40 isolated from a lab-scale mesophilic two-phase biogas reactor digesting maize silage and wheat straw. <i>Journal of Biotechnology</i> , 2014, 184, 199-200.	1.9	8
118	Detailed analysis of metagenome datasets obtained from biogas-producing microbial communities residing in biogas reactors does not indicate the presence of putative pathogenic microorganisms. <i>Biotechnology for Biofuels</i> , 2013, 6, 49.	6.2	31
119	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
120	Chinese hamster genome sequenced from sorted chromosomes. <i>Nature Biotechnology</i> , 2013, 31, 694-695.	9.4	160
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362	The <i>Rhizobium meliloti</i> pmi gene encodes a new type of phosphomannose isomerase. <i>Gene</i> , 1992, 122, 35-43.	1.0	28
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364	Functional analysis of the cysteine motifs in the ferredoxin-like protein FdxN of <i>Rhizobium meliloti</i> involved in symbiotic nitrogen fixation. <i>Molecular Genetics and Genomics</i> , 1992, 233, 33-41.	2.4	21
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367	Characterization of pGA1, a new plasmid from <i>Corynebacterium glutamicum</i> LP-6. <i>Gene</i> , 1991, 107, 69-74.	1.0	36
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373	Aspartokinase genes <i>lysC¹</i> and <i>lysC²</i> overlap and are adjacent to the aspartate β -semialdehyde dehydrogenase gene <i>asd</i> in <i>Corynebacterium glutamicum</i> . <i>Molecular Genetics and Genomics</i> , 1990, 224, 317-324.	2.4	67
374	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
375	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
376	Conjugal Transfer of Megaplasmid 2 between <i>Rhizobium meliloti</i> Strains in Alfalfa Nodules. <i>Applied and Environmental Microbiology</i> , 1990, 56, 2354-2359.	1.4	40
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378	The <i>Rhizobium meliloti</i> <i>fdxN</i> gene encoding a ferredoxin-like protein is necessary for nitrogen fixation and is cotranscribed with <i>nifA</i> and <i>nifB</i> . <i>Molecular Genetics and Genomics</i> , 1989, 216, 293-302.	2.4	60

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380	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
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385	The minimal replicon of the <i>Streptomyces ghanaensis</i> plasmid pSG5 identified by subcloning and Tn5 mutagenesis. <i>Molecular Genetics and Genomics</i> , 1988, 211, 424-429.	2.4	49
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395	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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398	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> , 1981, 9, 5187-5202.	6.5	52
399	Identification of the repressor and repressor bypass (antirepressor) polypeptides of bacteriophage P1 synthesized in infected minicells. <i>Molecular Genetics and Genomics</i> , 1980, 178, 149-154.	2.4	23
400	Transposon mutagenesis of the gene encoding the bacteriophage P1 restriction endonuclease. <i>Journal of Molecular Biology</i> , 1980, 144, 387-396.	2.0	13
401	Characterization of plasmids isolated from <i>Rhizobium meliloti</i> . <i>Archives of Microbiology</i> , 1979, 121, 1-7.	1.0	20
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403	Characterization of a Nosocomially Significant, Multiple Drug-Resistant Strain of <i>Serratia marcescens</i> . <i>Chemotherapy</i> , 1976, 22, 297-312.	0.8	17
404	Physical map of circular mitochondrial DNA from <i>Neurospora crassa</i> . <i>FEBS Letters</i> , 1975, 60, 119-121.	1.3	13
405	Denaturation map of the circular mitochondrial genome of <i>Neurospora crassa</i> . <i>Nucleic Acids and Protein Synthesis</i> , 1975, 402, 270-278.	1.7	26
406	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. , 0, .		1
407	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> . , 0, .		1