

Anke Becker

List of Publications by Year in descending order

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149
papers

8,921
citations

34016

52
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48187

88
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160
all docs

160
docs citations

160
times ranked

7651
citing authors

#	ARTICLE	IF	CITATIONS
1	The Composite Genome of the Legume Symbiont <i>Sinorhizobium meliloti</i> . <i>Science</i> , 2001, 293, 668-672.	6.0	1,098
2	Overlaps in the Transcriptional Profiles of <i>Medicago truncatula</i> Roots Inoculated with Two Different <i>Glomus</i> Fungi Provide Insights into the Genetic Program Activated during Arbuscular Mycorrhiza. <i>Plant Physiology</i> , 2005, 137, 1283-1301.	2.3	322
3	Expression Profiling in <i>Medicago truncatula</i> Identifies More Than 750 Genes Differentially Expressed during Nodulation, Including Many Potential Regulators of the Symbiotic Program. <i>Plant Physiology</i> , 2004, 136, 3159-3176.	2.3	269
4	Relationship of <i>Bacillus amyloliquefaciens</i> clades associated with strains DSM 7T and FZB42T: a proposal for <i>Bacillus amyloliquefaciens</i> subsp. <i>amyloliquefaciens</i> subsp. nov. and <i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> subsp. nov. based on complete genome sequence comparisons. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 1786-1801.	0.8	265
5	The genome of <i>Xanthomonas campestris</i> pv. <i>campestris</i> B100 and its use for the reconstruction of metabolic pathways involved in xanthan biosynthesis. <i>Journal of Biotechnology</i> , 2008, 134, 33-45.	1.9	238
6	Global Changes in Gene Expression in <i>Sinorhizobium meliloti</i> 1021 under Microoxic and Symbiotic Conditions. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 292-303.	1.4	230
7	<i>Xanthomonas campestris</i> pv. <i>campestris</i> gum Mutants: Effects on Xanthan Biosynthesis and Plant Virulence. <i>Journal of Bacteriology</i> , 1998, 180, 1607-1617.	1.0	221
8	Global mapping of transcription start sites and promoter motifs in the symbiotic α -proteobacterium <i>Sinorhizobium meliloti</i> 1021. <i>BMC Genomics</i> , 2013, 14, 156.	1.2	163
9	Transcriptomic profiling of <i>Bacillus amyloliquefaciens</i> FZB42 in response to maize root exudates. <i>BMC Microbiology</i> , 2012, 12, 116.	1.3	151
10	Mechanistic insights into host adaptation, virulence and epidemiology of the phytopathogen <i>Xanthomonas</i> . <i>FEMS Microbiology Reviews</i> , 2020, 44, 1-32.	3.9	148
11	Transcriptome profiling uncovers metabolic and regulatory processes occurring during the transition from desiccation-sensitive to desiccation-tolerant stages in <i>Medicago truncatula</i> seeds. <i>Plant Journal</i> , 2006, 47, 735-750.	2.8	142
12	New gentamicin-resistance and <i>lacZ</i> promoter-probe cassettes suitable for insertion mutagenesis and generation of transcriptional fusions. <i>Gene</i> , 1995, 162, 37-39.	1.0	141
13	Linking Plant Nutritional Status to Plant-Microbe Interactions. <i>PLoS ONE</i> , 2013, 8, e68555.	1.1	138
14	Transcriptome Profiling Reveals the Importance of Plasmid pSymB for Osmoadaptation of <i>Sinorhizobium meliloti</i> . <i>Journal of Bacteriology</i> , 2006, 188, 7617-7625.	1.0	129
15	Genome-wide identification of transcriptional start sites in the haloarchaeon <i>Haloferax volcanii</i> based on differential RNA-Seq (dRNA-Seq). <i>BMC Genomics</i> , 2016, 17, 629.	1.2	125
16	The LuxR Homolog ExpR, in Combination with the Sin Quorum Sensing System, Plays a Central Role in <i>Sinorhizobium meliloti</i> Gene Expression. <i>Journal of Bacteriology</i> , 2004, 186, 5460-5472.	1.0	123
17	Low-molecular-weight succinoglycan is predominantly produced by <i>Rhizobium meliloti</i> strains carrying a mutated ExoP protein characterized by a periplasmic N-terminal domain and a missing C-terminal domain. <i>Molecular Microbiology</i> , 1995, 16, 191-204.	1.2	106
18	<i>Sinorhizobium meliloti</i> ExoR and ExoS Proteins Regulate both Succinoglycan and Flagellum Production. <i>Journal of Bacteriology</i> , 2004, 186, 6042-6049.	1.0	106

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19	Transcriptomic analysis of responses to exudates reveal genes required for rhizosphere competence of the endophyte <i>Azoarcus</i> sp. strain BH72. <i>Environmental Microbiology</i> , 2012, 14, 2775-2787.	1.8	105
20	<i>Sinorhizobium meliloti</i> Regulator MucR Couples Exopolysaccharide Synthesis and Motility. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 1498-1509.	1.4	104
21	A genome-wide survey of sRNAs in the symbiotic nitrogen-fixing alpha-proteobacterium <i>Sinorhizobium meliloti</i> . <i>BMC Genomics</i> , 2010, 11, 245.	1.2	104
22	Construction and validation of a <i>Sinorhizobium meliloti</i> whole genome DNA microarray: genome-wide profiling of osmoadaptive gene expression. <i>Journal of Biotechnology</i> , 2003, 106, 255-268.	1.9	103
23	Construction and validation of cDNA-based Mt6k-RIT macro- and microarrays to explore root endosymbioses in the model legume <i>Medicago truncatula</i> . <i>Journal of Biotechnology</i> , 2004, 108, 95-113.	1.9	103
24	Identification and analysis of the <i>Rhizobium meliloti</i> exoAMONP genes involved in exopolysaccharide biosynthesis and mapping of promoters located on the exoHKLAMONP fragment. <i>Molecular Genetics and Genomics</i> , 1993, 241-241, 367-379.	2.4	102
25	Recent Advances in Studies on Structure and Symbiosis-Related Function of Rhizobial K-Antigens and Lipopolysaccharides. <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 899-905.	1.4	92
26	Profiling of histone H3 lysine 9 trimethylation levels predicts transcription factor activity and survival in acute myeloid leukemia. <i>Blood</i> , 2010, 116, 3564-3571.	0.6	90
27	Development of a <i>Corynebacterium glutamicum</i> DNA microarray and validation by genome-wide expression profiling during growth with propionate as carbon source. <i>Journal of Biotechnology</i> , 2003, 106, 269-286.	1.9	85
28	Construction of a Large Signature-Tagged Mini-Tn5 Transposon Library and Its Application to Mutagenesis of <i>Sinorhizobium meliloti</i> . <i>Applied and Environmental Microbiology</i> , 2006, 72, 4329-4337.	1.4	84
29	Specific binding of the regulatory protein ExpG to promoter regions of the galactoglucan biosynthesis gene cluster of <i>Sinorhizobium meliloti</i> - a combined molecular biology and force spectroscopy investigation. <i>Journal of Structural Biology</i> , 2003, 143, 145-152.	1.3	82
30	The Molecular Weight Distribution of Succinoglycan Produced by <i>Sinorhizobium meliloti</i> Is Influenced by Specific Tyrosine Phosphorylation and ATPase Activity of the Cytoplasmic Domain of the ExoP Protein. <i>Journal of Bacteriology</i> , 2001, 183, 5163-5170.	1.0	78
31	Biosynthesis of the exopolysaccharide galactoglucan in <i>Sinorhizobium meliloti</i> is subject to a complex control by the phosphate-dependent regulator PhoB and the proteins ExpG and MucR. <i>Microbiology (United Kingdom)</i> , 1999, 145, 603-611.	0.7	75
32	Analysis of the <i>Rhizobium meliloti</i> Genes <i>exoU</i> , <i>exoV</i> , <i>exoW</i> , <i>exoT</i> , and <i>exoI</i> Involved in Exopolysaccharide Biosynthesis and Nodule Invasion: <i>exoU</i> and <i>exoW</i> Probably Encode Glucosyltransferases. <i>Molecular Plant-Microbe Interactions</i> , 1993, 6, 735.	1.4	74
33	The <i>Sinorhizobium meliloti</i> <i>fur</i> Gene Regulates, with Dependence on Mn(II), Transcription of the <i>sitABCD</i> Operon, Encoding a Metal-Type Transporter. <i>Journal of Bacteriology</i> , 2004, 186, 3609-3620.	1.0	73
34	Striking Complexity of Lipopolysaccharide Defects in a Collection of <i>Sinorhizobium meliloti</i> Mutants. <i>Journal of Bacteriology</i> , 2003, 185, 3853-3862.	1.0	72
35	Genome-wide analysis of histone H3 acetylation patterns in AML identifies PRDX2 as an epigenetically silenced tumor suppressor gene. <i>Blood</i> , 2012, 119, 2346-2357.	0.6	72
36	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> , 1995, 249, 487-497.	2.4	70

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37	The <scp>DivK</scp>, <scp>CbrA</scp> and <scp>PleC</scp> system controls <scp>DivK</scp> phosphorylation and symbiosis in <i>Sinorhizobium meliloti</i>. <i>Molecular Microbiology</i> , 2013, 90, 54-71.	1.2	68
38	Competitive and Cooperative Effects in Quorum-Sensing-Regulated Galactoglucan Biosynthesis in <i>Sinorhizobium meliloti</i>. <i>Journal of Bacteriology</i> , 2008, 190, 5308-5317.	1.0	67
39	Symbiotic properties and first analyses of the genomic sequence of the fast growing model strain <i>Sinorhizobium fredii</i> HH103 nodulating soybean. <i>Journal of Biotechnology</i> , 2011, 155, 11-19.	1.9	67
40	Small RNA sX13: A Multifaceted Regulator of Virulence in the Plant Pathogen <i>Xanthomonas</i> . <i>PLoS Pathogens</i> , 2013, 9, e1003626.	2.1	67
41	Analysis of the <i>Rhizobium meliloti</i> <i>exoH/exoK/exoL</i> fragment: ExoK shows homology to excreted endo- β -1,3-1,4-glucanases and ExoH resembles membrane proteins. <i>Molecular Genetics and Genomics</i> , 1993, 238-238, 145-154.	2.4	66
42	Transcriptional profiling of the marine oil-degrading bacterium <i>Alcanivorax borkumensis</i> during growth on n-alkanes. <i>FEMS Microbiology Letters</i> , 2011, 319, 160-168.	0.7	65
43	Genome-wide profiling of Hfq-binding RNAs uncovers extensive post-transcriptional rewiring of major stress response and symbiotic regulons in <i>Sinorhizobium meliloti</i>. <i>RNA Biology</i> , 2014, 11, 563-579.	1.5	65
44	Virulence Evolution of the Human Pathogen <i>Neisseria meningitidis</i> by Recombination in the Core and Accessory Genome. <i>PLoS ONE</i> , 2011, 6, e18441.	1.1	65
45	Two New <i>Sinorhizobium meliloti</i> LysR-Type Transcriptional Regulators Required for Nodulation. <i>Journal of Bacteriology</i> , 2005, 187, 4562-4572.	1.0	64
46	Identification of Genes Relevant to Symbiosis and Competitiveness in <i>Sinorhizobium meliloti</i> Using Signature-Tagged Mutants. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 219-231.	1.4	63
47	Prediction of <i>Sinorhizobium meliloti</i> sRNA genes and experimental detection in strain 2011. <i>BMC Genomics</i> , 2008, 9, 416.	1.2	58
48	AraC-like transcriptional activator CuxR binds c-di-GMP by a PilZ-like mechanism to regulate extracellular polysaccharide production. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4822-E4831.	3.3	58
49	<i>Sinorhizobium meliloti</i> <i>acpXL</i> Mutant Lacks the C28 Hydroxylated Fatty Acid Moiety of Lipid A and Does Not Express a Slow Migrating Form of Lipopolysaccharide. <i>Journal of Biological Chemistry</i> , 2003, 278, 12946-12954.	1.6	56
50	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
51	Cyclic Di-GMP Regulates Multiple Cellular Functions in the Symbiotic Alphaproteobacterium <i>Sinorhizobium meliloti</i> . <i>Journal of Bacteriology</i> , 2016, 198, 521-535.	1.0	56
52	The Role of Microbial Surface Polysaccharides in the <i>Rhizobium</i> -Legume Interaction. <i>Sub-Cellular Biochemistry</i> , 1998, 29, 73-116.	1.0	55
53	Genome Sequence of the Soybean Symbiont <i>Sinorhizobium fredii</i> HH103. <i>Journal of Bacteriology</i> , 2012, 194, 1617-1618.	1.0	54
54	Novel <i>Sinorhizobium meliloti</i> quorum sensing positive and negative regulatory feedback mechanisms respond to phosphate availability. <i>Molecular Microbiology</i> , 2009, 74, 1238-1256.	1.2	53

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55	Fine-Tuning of Galactoglucan Biosynthesis in <i>Sinorhizobium meliloti</i> by Differential WggR (ExpC)-, PhoB-, and MucR-Dependent Regulation of Two Promoters. <i>Journal of Bacteriology</i> , 2008, 190, 3456-3466.	1.0	52
56	ppGpp in <i>Sinorhizobium meliloti</i> : biosynthesis in response to sudden nutritional downshifts and modulation of the transcriptome. <i>Molecular Microbiology</i> , 2011, 81, 1233-1254.	1.2	52
57	Single-Molecule Experiments in Synthetic Biology: An Approach to the Affinity Ranking of DNA-Binding Peptides. <i>Angewandte Chemie - International Edition</i> , 2005, 44, 3921-3924.	7.2	51
58	Challenges and perspectives in combinatorial assembly of novel exopolysaccharide biosynthesis pathways. <i>Frontiers in Microbiology</i> , 2015, 6, 687.	1.5	51
59	A Stress-Induced Small RNA Modulates Alpha-Rhizobial Cell Cycle Progression. <i>PLoS Genetics</i> , 2015, 11, e1005153.	1.5	51
60	Comparative Genome Biology of a Serogroup B Carriage and Disease Strain Supports a Polygenic Nature of Meningococcal Virulence. <i>Journal of Bacteriology</i> , 2010, 192, 5363-5377.	1.0	50
61	Development of bioinformatic tools to support EST-sequencing, in silico- and microarray-based transcriptome profiling in mycorrhizal symbioses. <i>Phytochemistry</i> , 2007, 68, 19-32.	1.4	49
62	Phenotypic Heterogeneity in Bacterial Quorum Sensing Systems. <i>Journal of Molecular Biology</i> , 2019, 431, 4530-4546.	2.0	49
63	Temporal Expression Program of Quorum Sensing-Based Transcription Regulation in <i>Sinorhizobium meliloti</i> . <i>Journal of Bacteriology</i> , 2013, 195, 3224-3236.	1.0	48
64	Transcript Profiling Reveals New Insights into the Acclimation of the Mesophilic Fresh-Water Cyanobacterium <i>Synechococcus elongatus</i> PCC 7942 to Iron Starvation. <i>Plant Physiology</i> , 2008, 147, 747-763.	2.3	47
65	Quantitative Proteomic Analysis of the Hfq-Regulon in <i>Sinorhizobium meliloti</i> 2011. <i>PLoS ONE</i> , 2012, 7, e48494.	1.1	46
66	Rhizobial homologs of the fatty acid transporter FadL facilitate perception of long-chain acyl-homoserine lactone signals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 10702-10707.	3.3	45
67	Large-scale genetic variation of the symbiosis-required megaplasmid pSymA revealed by comparative genomic analysis of <i>Sinorhizobium meliloti</i> natural strains. <i>BMC Genomics</i> , 2005, 6, 158.	1.2	44
68	Effector-Stimulated Single Molecule Protein-DNA Interactions of a Quorum-Sensing System in <i>Sinorhizobium meliloti</i> . <i>Biophysical Journal</i> , 2007, 92, 4391-4400.	0.2	44
69	Riboregulation in plant-associated \hat{I}_{\pm} -proteobacteria. <i>RNA Biology</i> , 2014, 11, 550-562.	1.5	43
70	Detailed studies of the binding mechanism of the <i>Sinorhizobium meliloti</i> transcriptional activator ExpG to DNA. <i>Microbiology (United Kingdom)</i> , 2005, 151, 259-268.	0.7	41
71	A portal for rhizobial genomes: RhizoGATE integrates a <i>Sinorhizobium meliloti</i> genome annotation update with postgenome data. <i>Journal of Biotechnology</i> , 2009, 140, 45-50.	1.9	38
72	Spatiotemporal choreography of chromosome and megaplasmids in the <i>Sinorhizobium meliloti</i> cell cycle. <i>Molecular Microbiology</i> , 2016, 100, 808-823.	1.2	37

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73	Identification of <i>Xanthomonas campestris</i> pv. <i>campestris</i> galactose utilization genes from transcriptome data. <i>Journal of Biotechnology</i> , 2008, 135, 309-317.	1.9	36
74	Insights into the Extracytoplasmic Stress Response of <i>Xanthomonas campestris</i> pv. <i>campestris</i> : Role and Regulation of σ^E -Dependent Activity. <i>Journal of Bacteriology</i> , 2011, 193, 246-264.	1.0	36
75	Expression of small RNAs in Rhizobiales and protection of a small RNA and its degradation products by Hfq in <i>Sinorhizobium meliloti</i> . <i>Biochemical and Biophysical Research Communications</i> , 2009, 390, 331-336.	1.0	35
76	RNase E Affects the Expression of the Acyl-Homoserine Lactone Synthase Gene <i>sinI</i> in <i>Sinorhizobium meliloti</i> . <i>Journal of Bacteriology</i> , 2014, 196, 1435-1447.	1.0	34
77	Specificity traits consistent with legume-rhizobia coevolution displayed by <i>Ensifer meliloti</i> rhizosphere colonization. <i>Environmental Microbiology</i> , 2017, 19, 3423-3438.	1.8	33
78	Expansion and re-classification of the extracytoplasmic function (ECF) σ factor family. <i>Nucleic Acids Research</i> , 2021, 49, 986-1005.	6.5	32
79	Rhizobium-Initiated Rice Growth Inhibition Caused by Nitric Oxide Accumulation. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 283-292.	1.4	30
80	Genome sequence of the endophytic strain <i>Enterobacter</i> sp. J49, a potential biofertilizer for peanut and maize. <i>Genomics</i> , 2019, 111, 913-920.	1.3	30
81	Conservation and Occurrence of Trans-Encoded sRNAs in the Rhizobiales. <i>Genes</i> , 2011, 2, 925-956.	1.0	29
82	A Family of Single Copy <i>repABC</i> -Type Shuttle Vectors Stably Maintained in the Alpha-Proteobacterium <i>Sinorhizobium meliloti</i> . <i>ACS Synthetic Biology</i> , 2017, 6, 968-984.	1.9	29
83	<i>Sinorhizobium meliloti</i> YbeY is an endoribonuclease with unprecedented catalytic features, acting as silencing enzyme in riboregulation. <i>Nucleic Acids Research</i> , 2017, 45, 1371-1391.	6.5	29
84	Two-step chromosome segregation in the stalked budding bacterium <i>Hyphomonas neptunium</i> . <i>Nature Communications</i> , 2019, 10, 3290.	5.8	29
85	Increased HDAC1 deposition at hematopoietic promoters in AML and its association with patient survival. <i>Leukemia Research</i> , 2011, 35, 620-625.	0.4	28
86	RhizoRegNet—A database of rhizobial transcription factors and regulatory networks. <i>Journal of Biotechnology</i> , 2011, 155, 127-134.	1.9	27
87	Deletion of the Sm1 encoding motif in the <i>lsm</i> gene results in distinct changes in the transcriptome and enhanced swarming activity of <i>Haloferax</i> cells. <i>Biochimie</i> , 2015, 117, 129-137.	1.3	27
88	A conserved σ -proteobacterial small RNA contributes to osmoadaptation and symbiotic efficiency of rhizobia on legume roots. <i>Environmental Microbiology</i> , 2017, 19, 2661-2680.	1.8	27
89	Classification of phenotypic subpopulations in isogenic bacterial cultures by triple promoter probing at single cell level. <i>Journal of Biotechnology</i> , 2015, 198, 3-14.	1.9	25
90	Reverse Engineering of an Affinity-Switchable Molecular Interaction Characterized by Atomic Force Microscopy Single-Molecule Force Spectroscopy. <i>Langmuir</i> , 2008, 24, 1365-1370.	1.6	24

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91	Creation and Characterization of a Genomically Hybrid Strain in the Nitrogen-Fixing Symbiotic Bacterium <i>Sinorhizobium meliloti</i> . ACS Synthetic Biology, 2018, 7, 2365-2378.	1.9	24
92	Regulation of succinoglycan and galactoglucan biosynthesis in <i>Sinorhizobium meliloti</i> . Journal of Molecular Microbiology and Biotechnology, 2002, 4, 187-90.	1.0	24
93	Insights into the Noncoding RNome of Nitrogen-Fixing Endosymbiotic $\hat{\pm}$ -Proteobacteria. Molecular Plant-Microbe Interactions, 2013, 26, 160-167.	1.4	23
94	Transcriptional reprogramming and phenotypical changes associated with growth of <i>Xanthomonas campestris</i> pv. <i>campestris</i> in cabbage xylem sap. FEMS Microbiology Ecology, 2014, 89, 527-541.	1.3	23
95	Antisense transcription of symbiotic genes in <i>Sinorhizobium meliloti</i> . Symbiosis, 2015, 67, 55-67.	1.2	23
96	Detection and segmentation of morphologically complex eukaryotic cells in fluorescence microscopy images via feature pyramid fusion. PLoS Computational Biology, 2020, 16, e1008179.	1.5	23
97	MESA: automated assessment of synthetic DNA fragments and simulation of DNA synthesis, storage, sequencing and PCR errors. Bioinformatics, 2020, 36, 3322-3326.	1.8	22
98	Evidence for <i>Escherichia coli</i> Diguanylate Cyclase DgcZ Interlinking Surface Sensing and Adhesion via Multiple Regulatory Routes. Journal of Bacteriology, 2016, 198, 2524-2535.	1.0	21
99	Unipolar Peptidoglycan Synthesis in the <i>Rhizobiales</i> Requires an Essential Class A Penicillin-Binding Protein. MBio, 2021, 12, e0234621.	1.8	21
100	Cyclic mononucleotide- and Clr-dependent gene regulation in <i>Sinorhizobium meliloti</i> . Microbiology (United Kingdom), 2016, 162, 1840-1856.	0.7	21
101	The Gellan Gum Biosynthetic Genes <i>gelC</i> and <i>gelE</i> Encode Two Separate Polypeptides Homologous to the Activator and the Kinase Domains of Tyrosine Autokinases. Journal of Molecular Microbiology and Biotechnology, 2004, 8, 43-57.	1.0	20
102	Under the influence of the active deodorant ingredient 4-hydroxy-3-methoxybenzyl alcohol, the skin bacterium <i>Corynebacterium jeikeium</i> moderately responds with differential gene expression. Journal of Biotechnology, 2006, 127, 21-33.	1.9	20
103	Environmental Factors Affecting the Expression of <i>pilAB</i> as Well as the Proteome and Transcriptome of the Grass Endophyte <i>Azoarcus</i> sp. Strain BH72. PLoS ONE, 2012, 7, e30421.	1.1	20
104	Regulation of Polyhydroxybutyrate Accumulation in <i>Sinorhizobium meliloti</i> by the <i>Trans</i> -Encoded Small RNA <i>MmgR</i> . Journal of Bacteriology, 2017, 199, .	1.0	20
105	Design and Control of Extrachromosomal Elements in <i>Methylobacterium extorquens</i> AM1. ACS Synthetic Biology, 2019, 8, 2451-2456.	1.9	20
106	Genome-enabled determination of amino acid biosynthesis in <i>Xanthomonas campestris</i> pv. <i>campestris</i> and identification of biosynthetic pathways for alanine, glycine, and isoleucine by ¹³ C-isotopologue profiling. Molecular Genetics and Genomics, 2011, 286, 247-59.	1.0	19
107	Cloning-free genome engineering in <i>Sinorhizobium meliloti</i> advances applications of <i>Cre/loxP</i> site-specific recombination. Journal of Biotechnology, 2016, 233, 160-170.	1.9	19
108	A Bifunctional UDP-Sugar 4-Epimerase Supports Biosynthesis of Multiple Cell Surface Polysaccharides in <i>Sinorhizobium meliloti</i> . Journal of Bacteriology, 2019, 201, .	1.0	19

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109	Four Promoters Subject to Regulation by ExoR and PhoB Direct Transcription of the <i>Sinorhizobium meliloti</i> <i>exoYFQ</i> Operon Involved in the Biosynthesis of Succinoglycan. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2004, 7, 115-132.	1.0	18
110	Comparative genomic hybridisation and ultrafast pyrosequencing revealed remarkable differences between the <i>Sinorhizobium meliloti</i> genomes of the model strain Rm1021 and the field isolate SM11. <i>Journal of Biotechnology</i> , 2008, 136, 31-37.	1.9	18
111	Analysis of the interaction of <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> with its host plant tomato by genome-wide expression profiling. <i>Journal of Biotechnology</i> , 2012, 160, 42-54.	1.9	18
112	Tol-Pal System and Rgs Proteins Interact to Promote Unipolar Growth and Cell Division in <i>Sinorhizobium meliloti</i> . <i>MBio</i> , 2020, 11, .	1.8	18
113	Probing DNA-peptide interaction forces at the single-molecule level. <i>Journal of Peptide Science</i> , 2006, 12, 836-842.	0.8	17
114	Production of Succinoglycan Polymer in <i>Sinorhizobium meliloti</i> Is Affected by SMB21506 and Requires the N-terminal Domain of ExoP. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 1656-1668.	1.4	17
115	Single-Molecule Experiments to Elucidate the Minimal Requirement for DNA Recognition by Transcription Factor Epitopes. <i>Small</i> , 2009, 5, 484-495.	5.2	16
116	Seven-transmembrane receptor protein RgsP and cell wall-binding protein RgsM promote unipolar growth in Rhizobiales. <i>PLoS Genetics</i> , 2018, 14, e1007594.	1.5	16
117	NT-CRISPR, combining natural transformation and CRISPR-Cas9 counterselection for markerless and scarless genome editing in <i>Vibrio natriegens</i> . <i>Communications Biology</i> , 2022, 5, 265.	2.0	16
118	ZomB is essential for flagellar motor reversals in <i>Shewanella putrefaciens</i> and <i>Vibrio parahaemolyticus</i> . <i>Molecular Microbiology</i> , 2018, 109, 694-709.	1.2	15
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