

# Christian RÃ¼ckert

## List of Publications by Year in descending order

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181  
papers

9,020  
citations

87723

38  
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46693

89  
g-index

187  
all docs

187  
docs citations

187  
times ranked

11151  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Subsystems Approach to Genome Annotation and its Use in the Project to Annotate 1000 Genomes. <i>Nucleic Acids Research</i> , 2005, 33, 5691-5702.	6.5	1,806
2	The complete <i>Corynebacterium glutamicum</i> ATCC 13032 genome sequence and its impact on the production of l-aspartate-derived amino acids and vitamins. <i>Journal of Biotechnology</i> , 2003, 104, 5-25.	1.9	844
3	An environmental bacterial taxon with a large and distinct metabolic repertoire. <i>Nature</i> , 2014, 506, 58-62.	13.7	530
4	Whole Genome Sequencing versus Traditional Genotyping for Investigation of a <i>Mycobacterium tuberculosis</i> Outbreak: A Longitudinal Molecular Epidemiological Study. <i>PLoS Medicine</i> , 2013, 10, e1001387.	3.9	425
5	Complete genome sequence of the myxobacterium <i>Sorangium cellulosum</i> . <i>Nature Biotechnology</i> , 2007, 25, 1281-1289.	9.4	354
6	Insights into Genome Plasticity and Pathogenicity of the Plant Pathogenic Bacterium <i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> Revealed by the Complete Genome Sequence. <i>Journal of Bacteriology</i> , 2005, 187, 7254-7266.	1.0	321
7	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
8	Comprehensive analysis of the <i>Corynebacterium glutamicum</i> transcriptome using an improved RNAseq technique. <i>BMC Genomics</i> , 2013, 14, 888.	1.2	175
9	The Genome Sequence of the Tomato-Pathogenic Actinomycete <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> NCPPB382 Reveals a Large Island Involved in Pathogenicity. <i>Journal of Bacteriology</i> , 2008, 190, 2138-2149.	1.0	153
10	Construction of a Prophage-Free Variant of <i>Corynebacterium glutamicum</i> ATCC 13032 for Use as a Platform Strain for Basic Research and Industrial Biotechnology. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6006-6015.	1.4	142
11	Genome sequence of <i>B. amyloliquefaciens</i> type strain DSM7T reveals differences to plant-associated <i>B. amyloliquefaciens</i> FZB42. <i>Journal of Biotechnology</i> , 2011, 155, 78-85.	1.9	107
12	The <i>Waddlia</i> Genome: A Window into Chlamydial Biology. <i>PLoS ONE</i> , 2010, 5, e10890.	1.1	104
13	Chassis organism from <i>Corynebacterium glutamicum</i> – a top-down approach to identify and delete irrelevant gene clusters. <i>Biotechnology Journal</i> , 2015, 10, 290-301.	1.8	102
14	Complete genome sequence of <i>Streptomyces lividans</i> TK24. <i>Journal of Biotechnology</i> , 2015, 199, 21-22.	1.9	96
15	The McbR repressor modulated by the effector substance S-adenosylhomocysteine controls directly the transcription of a regulon involved in sulphur metabolism of <i>Corynebacterium glutamicum</i> ATCC 13032. <i>Molecular Microbiology</i> , 2005, 56, 871-887.	1.2	92
16	Functional genomics of pH homeostasis in <i>Corynebacterium glutamicum</i> revealed novel links between pH response, oxidative stress, iron homeostasis and methionine synthesis. <i>BMC Genomics</i> , 2009, 10, 621.	1.2	90
17	New natural products identified by combined genomics-metabolomics profiling of marine <i>Streptomyces</i> sp. MP131-18. <i>Scientific Reports</i> , 2017, 7, 42382.	1.6	86
18	RamA and RamB are global transcriptional regulators in <i>Corynebacterium glutamicum</i> and control genes for enzymes of the central metabolism. <i>Journal of Biotechnology</i> , 2011, 154, 126-139.	1.9	78

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19	The Gene ncgl2918 Encodes a Novel Maleylpyruvate Isomerase That Needs Mycothiol as Cofactor and Links Mycothiol Biosynthesis and Gentsiate Assimilation in <i>Corynebacterium glutamicum</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 10778-10785.	1.6	74
20	A multiproducer microbiome generates chemical diversity in the marine sponge <i>Mycale hentscheli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9508-9518.	3.3	71
21	Strategy to sequence the genome of <i>Corynebacterium glutamicum</i> ATCC 13032: use of a cosmid and a bacterial artificial chromosome library. <i>Journal of Biotechnology</i> , 2002, 95, 25-38.	1.9	70
22	Genome sequence of the plant growth promoting strain <i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> B9601-Y2 and expression of mersacidin and other secondary metabolites. <i>Journal of Biotechnology</i> , 2013, 164, 281-291.	1.9	70
23	Single-bacterial genomics validates rich and varied specialized metabolism of uncultivated <i>Entotheonella</i> sponge symbionts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1718-1723.	3.3	70
24	The complete genome sequence of the acarbose producer <i>Actinoplanes</i> sp. SE50/110. <i>BMC Genomics</i> , 2012, 13, 112.	1.2	69
25	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
26	High quality genome sequences of thirteen Hypoxylaceae (Ascomycota) strengthen the phylogenetic family backbone and enable the discovery of new taxa. <i>Fungal Diversity</i> , 2021, 106, 7-28.	4.7	65
27	<i>Corynebacterium glutamicum</i> Chassis C1*: Building and Testing a Novel Platform Host for Synthetic Biology and Industrial Biotechnology. <i>ACS Synthetic Biology</i> , 2018, 7, 132-144.	1.9	63
28	Functional genomics and expression analysis of the <i>Corynebacterium glutamicum</i> fpr2-cysIXHDNYZ gene cluster involved in assimilatory sulphate reduction. <i>BMC Genomics</i> , 2005, 6, 121.	1.2	61
29	Comprehensive discovery and characterization of small RNAs in <i>Corynebacterium glutamicum</i> ATCC 13032. <i>BMC Genomics</i> , 2013, 14, 714.	1.2	61
30	Sulfate reduction in microorganisms – recent advances and biotechnological applications. <i>Current Opinion in Microbiology</i> , 2016, 33, 140-146.	2.3	59
31	Complete genome sequence of <i>Pseudomonas</i> sp. strain VLB120 a solvent tolerant, styrene degrading bacterium, isolated from forest soil. <i>Journal of Biotechnology</i> , 2013, 168, 729-730.	1.9	51
32	Genomics of Sponge-Associated <i>Streptomyces</i> spp. Closely Related to <i>Streptomyces albus</i> J1074: Insights into Marine Adaptation and Secondary Metabolite Biosynthesis Potential. <i>PLoS ONE</i> , 2014, 9, e96719.	1.1	51
33	Transcriptome analysis of thermophilic methylotrophic <i>Bacillus methanolicus</i> MGA3 using RNA-sequencing provides detailed insights into its previously uncharted transcriptional landscape. <i>BMC Genomics</i> , 2015, 16, 73.	1.2	49
34	High Quality de Novo Transcriptome Assembly of <i>Croton tiglium</i> . <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 62.	1.6	48
35	Monitoring global protein thiol-oxidation and protein S-mycothiolation in <i>Mycobacterium smegmatis</i> under hypochlorite stress. <i>Scientific Reports</i> , 2017, 7, 1195.	1.6	47
36	Transcriptional response of <i>Corynebacterium glutamicum</i> ATCC 13032 to hydrogen peroxide stress and characterization of the OxyR regulon. <i>Journal of Biotechnology</i> , 2014, 190, 40-54.	1.9	46

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37	The dual transcriptional regulator CysR in <i>Corynebacterium glutamicum</i> ATCC 13032 controls a subset of genes of the McbR regulon in response to the availability of sulphide acceptor molecules. <i>BMC Genomics</i> , 2008, 9, 483.	1.2	45
38	Genome Sequence of the Bacterium <i>Streptomyces davawensis</i> JCM 4913 and Heterologous Production of the Unique Antibiotic Roseoflavin. <i>Journal of Bacteriology</i> , 2012, 194, 6818-6827.	1.0	42
39	Complete genome and comparative analysis of <i>Streptococcus gallolyticus</i> subsp. <i>gallolyticus</i> , an emerging pathogen of infective endocarditis. <i>BMC Genomics</i> , 2011, 12, 400.	1.2	41
40	Metabolic engineering to guide evolution – Creating a novel mode for L-valine production with <i>Corynebacterium glutamicum</i> . <i>Metabolic Engineering</i> , 2018, 47, 31-41.	3.6	41
41	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
42	On the Enigma of Glutathione-Dependent Styrene Degradation in <i>Gordonia rubripertincta</i> CWB2. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	38
43	Methanol-Essential Growth of <i>Corynebacterium glutamicum</i> : Adaptive Laboratory Evolution Overcomes Limitation due to Methanethiol Assimilation Pathway. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3617.	1.8	38
44	Fast and reliable strain characterization of <i>Streptomyces lividans</i> through microscale cultivation. <i>Biotechnology and Bioengineering</i> , 2017, 114, 2011-2022.	1.7	37
45	Random mutagenesis in <i>Corynebacterium glutamicum</i> ATCC 13032 using an IS6100-based transposon vector identified the last unknown gene in the histidine biosynthesis pathway. <i>BMC Genomics</i> , 2006, 7, 205.	1.2	35
46	Adaptation of <i>Corynebacterium glutamicum</i> to salt stress conditions. <i>Proteomics</i> , 2010, 10, 445-457.	1.3	34
47	Isolation and genome sequencing of four Arctic marine <i>Psychrobacter</i> strains exhibiting multicopper oxidase activity. <i>BMC Genomics</i> , 2016, 17, 117.	1.2	34
48	Genome-based analysis of biosynthetic aminotransferase genes of <i>Corynebacterium glutamicum</i> . <i>Journal of Biotechnology</i> , 2003, 104, 229-240.	1.9	33
49	Arabitol Metabolism of <i>Corynebacterium glutamicum</i> and Its Regulation by AtIR. <i>Journal of Bacteriology</i> , 2012, 194, 941-955.	1.0	32
50	Phenylacetic Acid Catabolism and Its Transcriptional Regulation in <i>Corynebacterium glutamicum</i> . <i>Applied and Environmental Microbiology</i> , 2012, 78, 5796-5804.	1.4	32
51	Complete genome sequence of <i>Saccharothrix espanaensis</i> DSM 44229T and comparison to the other completely sequenced <i>Pseudonocardiaceae</i> . <i>BMC Genomics</i> , 2012, 13, 465.	1.2	32
52	Bioinformatics support for high-throughput proteomics. <i>Journal of Biotechnology</i> , 2003, 106, 147-156.	1.9	31
53	Molecular characterization of PrpR, the transcriptional activator of propionate catabolism in <i>Corynebacterium glutamicum</i> . <i>Journal of Biotechnology</i> , 2012, 159, 1-11.	1.9	31
54	Complete genome sequence of <i>Bacillus methanolicus</i> MGA3, a thermotolerant amino acid producing methylotroph. <i>Journal of Biotechnology</i> , 2014, 188, 110-111.	1.9	31

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55	The transcriptional regulator SsuR activates expression of the Corynebacterium glutamicum sulphonate utilization genes in the absence of sulphate. <i>Molecular Microbiology</i> , 2005, 58, 480-494.	1.2	30
56	Genome rearrangements of <i>Streptomyces albus</i> J1074 lead to the carotenoid gene cluster activation. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 795-806.	1.7	30
57	Sequencing of high G+C microbial genomes using the ultrafast pyrosequencing technology. <i>Journal of Biotechnology</i> , 2011, 155, 68-77.	1.9	29
58	Multi-Omics and Targeted Approaches to Determine the Role of Cellular Proteases in <i>Streptomyces</i> Protein Secretion. <i>Frontiers in Microbiology</i> , 2018, 9, 1174.	1.5	29
59	Development of a Biosensor Concept to Detect the Production of Cluster-Specific Secondary Metabolites. <i>ACS Synthetic Biology</i> , 2017, 6, 1026-1033.	1.9	28
60	Exploiting <i>Hydrogenophaga pseudoflava</i> for aerobic syngas-based production of chemicals. <i>Metabolic Engineering</i> , 2019, 55, 220-230.	3.6	28
61	A novel type of N-acetylglutamate synthase is involved in the first step of arginine biosynthesis in <i>Corynebacterium glutamicum</i> . <i>BMC Genomics</i> , 2013, 14, 713.	1.2	27
62	Genome-wide determination of transcription start sites reveals new insights into promoter structures in the actinomycete <i>Corynebacterium glutamicum</i> . <i>Journal of Biotechnology</i> , 2017, 257, 99-109.	1.9	27
63	Complete genome sequence of producer of the glycopeptide antibiotic Aculeximycin <i>Kutzneria albida</i> DSM 43870T, a representative of minor genus of Pseudonocardiaceae. <i>BMC Genomics</i> , 2014, 15, 885.	1.2	26
64	Transcriptome sequencing revealed the transcriptional organization at ribosome-mediated attenuation sites in <i>Corynebacterium glutamicum</i> and identified a novel attenuator involved in aromatic amino acid biosynthesis. <i>Journal of Biotechnology</i> , 2014, 190, 55-63.	1.9	26
65	Engineering l-arabinose metabolism in triacylglycerol-producing <i>Rhodococcus opacus</i> for lignocellulosic fuel production. <i>Metabolic Engineering</i> , 2015, 30, 89-95.	3.6	26
66	<i>Rhodococcus erythropolis</i> BG43 Genes Mediating <i>Pseudomonas aeruginosa</i> Quinolone Signal Degradation and Virulence Factor Attenuation. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7720-7729.	1.4	26
67	Genome Mining of <i>Streptomyces</i> sp. YIM 130001 Isolated From Lichen Affords New Thiopeptide Antibiotic. <i>Frontiers in Microbiology</i> , 2018, 9, 3139.	1.5	26
68	Auxotrophy to Xeno-DNA: an exploration of combinatorial mechanisms for a high-fidelity biosafety system for synthetic biology applications. <i>Journal of Biological Engineering</i> , 2018, 12, 13.	2.0	26
69	Taxonomic analyses of members of the <i>Streptomyces cinnabarinus</i> cluster, description of <i>Streptomyces cinnabarigriseus</i> sp. nov. and <i>Streptomyces davaonensis</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 382-393.	0.8	26
70	Functional Characterization of a Small Alarmone Hydrolase in <i>Corynebacterium glutamicum</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 916.	1.5	25
71	<i>Streptomyces</i> spp. From the Marine Sponge <i>Antho dichotoma</i> : Analyses of Secondary Metabolite Biosynthesis Gene Clusters and Some of Their Products. <i>Frontiers in Microbiology</i> , 2020, 11, 437.	1.5	25
72	MSEA: metabolite set enrichment analysis in the MeltDB metabolomics software platform: metabolic profiling of <i>Corynebacterium glutamicum</i> as an example. <i>Metabolomics</i> , 2012, 8, 310-322.	1.4	23

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73	Complete genome sequence of the kirromycin producer <i>Streptomyces collinus</i> TÅ¼ 365 consisting of a linear chromosome and two linear plasmids. <i>Journal of Biotechnology</i> , 2013, 168, 739-740.	1.9	23
74	Characterization of Sigma Factor Genes in <i>Streptomyces lividans</i> TK24 Using a Genomic Library-Based Approach for Multiple Gene Deletions. <i>Frontiers in Microbiology</i> , 2018, 9, 3033.	1.5	23
75	Microparticles globally reprogram <i>Streptomyces albus</i> toward accelerated morphogenesis, streamlined carbon core metabolism, and enhanced production of the antituberculosis polyketide pamamycin. <i>Biotechnology and Bioengineering</i> , 2020, 117, 3858-3875.	1.7	22
76	Classification of three corynebacterial strains isolated from the Northern Bald Ibis ( <i>Geronticus tinnuncius</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 632 <i>Corynebacterium gerontici</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2928-2935.	0.8	21
77	Comparative RNA-sequencing of the acarbose producer <i>Actinoplanes</i> sp. SE50/110 cultivated in different growth media. <i>Journal of Biotechnology</i> , 2013, 167, 166-177.	1.9	20
78	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 <sup>13</sup> C-isotopologue profiling. <i>Molecular Genetics and Genomics</i> , 2011, 286, 247-59.	1.0	19
79	Comprehensive subcellular topologies of polypeptides in <i>Streptomyces</i> . <i>Microbial Cell Factories</i> , 2018, 17, 43.	1.9	19
80	New Alpiniamides From <i>Streptomyces</i> sp. IB2014/011-12 Assembled by an Unusual Hybrid Non-ribosomal Peptide Synthetase Trans-AT Polyketide Synthase Enzyme. <i>Frontiers in Microbiology</i> , 2018, 9, 1959.	1.5	19
81	Baikalomycins A-C, New Aquayamycin-Type Angucyclines Isolated from Lake Baikal Derived <i>Streptomyces</i> sp. IB201691-2A. <i>Microorganisms</i> , 2020, 8, 680.	1.6	19
82	Adaptive laboratory evolution accelerated glutarate production by <i>Corynebacterium glutamicum</i> . <i>Microbial Cell Factories</i> , 2021, 20, 97.	1.9	19
83	Whole Genome Sequencing of 39 Invasive <i>Streptococcus pneumoniae</i> Sequence Type 199 Isolates Revealed Switches from Serotype 19A to 15B. <i>PLoS ONE</i> , 2017, 12, e0169370.	1.1	19
84	Transcriptomic and fluxomic changes in <i>Streptomyces lividans</i> producing heterologous protein. <i>Microbial Cell Factories</i> , 2018, 17, 198.	1.9	18
85	Viennamycins: Lipopeptides Produced by a <i>Streptomyces</i> sp.. <i>Journal of Natural Products</i> , 2020, 83, 2381-2389.	1.5	17
86	Screening of a genome-reduced <i>Corynebacterium glutamicum</i> strain library for improved heterologous cutinase secretion. <i>Microbial Biotechnology</i> , 2020, 13, 2020-2031.	2.0	17
87	Physiological Response of <i>Corynebacterium glutamicum</i> to Indole. <i>Microorganisms</i> , 2020, 8, 1945.	1.6	17
88	Heterologous production of $\beta$ -Carotene in <i>Corynebacterium glutamicum</i> using a multi-copy chromosomal integration method. <i>Bioresource Technology</i> , 2021, 341, 125782.	4.8	17
89	A propionate-inducible expression system based on the <i>Corynebacterium glutamicum</i> prpD2 promoter and PrpR activator and its application for the redirection of amino acid biosynthesis pathways. <i>Journal of Biotechnology</i> , 2013, 163, 225-232.	1.9	16
90	Complete genome sequence of the actinobacterium <i>Amycolatopsis japonica</i> MG417-CF17T (=DSM 44213T) producing (S,S)-N,N'-ethylenediaminedisuccinic acid. <i>Journal of Biotechnology</i> , 2014, 189, 46-47.	1.9	16

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91	Towards a 'chassis' for bacterial magnetosome biosynthesis: genome streamlining of <i>Magnetospirillum gryphiswaldense</i> by multiple deletions. <i>Microbial Cell Factories</i> , 2021, 20, 35.	1.9	16
92	Genomic-Led Discovery of a Novel Glycopeptide Antibiotic by <i>Nonomuraea coxensis</i> DSM 45129. <i>ACS Chemical Biology</i> , 2021, 16, 915-928.	1.6	16
93	Draft Genome Sequence of <i>Turicella otitidis</i> ATCC 51513, Isolated from Middle Ear Fluid from a Child with Otitis Media. <i>Journal of Bacteriology</i> , 2012, 194, 5968-5969.	1.0	15
94	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
95	Twenty-Five Years of Propagation in Suspension Cell Culture Results in Substantial Alterations of the <i>Arabidopsis thaliana</i> Genome. <i>Genes</i> , 2019, 10, 671.	1.0	15
96	Microparticles enhance the formation of seven major classes of natural products in native and metabolically engineered actinobacteria through accelerated morphological development. <i>Biotechnology and Bioengineering</i> , 2021, 118, 3076-3093.	1.7	15
97	Complete genome sequence of <i>Corynebacterium casei</i> LMG S-19264T (=DSM 44701T), isolated from a smear-ripened cheese. <i>Journal of Biotechnology</i> , 2014, 189, 76-77.	1.9	14
98	<i>Streptomyces</i> spp. From Ethiopia Producing Antimicrobial Compounds: Characterization via Bioassays, Genome Analyses, and Mass Spectrometry. <i>Frontiers in Microbiology</i> , 2018, 9, 1270.	1.5	14
99	High diversity of <i>Vibrio</i> spp. associated with different ecological niches in a marine aquaria system and description of <i>Vibrio aquimaris</i> sp. nov. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126123.	1.2	14
100	Eliciting the silent lucensomycin biosynthetic pathway in <i>Streptomyces cyanogenus</i> S136 via manipulation of the global regulatory gene <i>adpA</i> . <i>Scientific Reports</i> , 2021, 11, 3507.	1.6	14
101	Impact of Phenolic Substrate and Growth Temperature on the <i>Arthrobacter chlorophenolicus</i> Proteome. <i>Journal of Proteome Research</i> , 2009, 8, 1953-1964.	1.8	13
102	Draft Genome Sequence of <i>Wickerhamomyces ciferrii</i> NRRL Y-1031 F-60-10. <i>Eukaryotic Cell</i> , 2012, 11, 1582-1583.	3.4	13
103	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
104	Complete genome sequence of <i>Paenibacillus riograndensis</i> SBR5T, a Gram-positive diazotrophic rhizobacterium. <i>Journal of Biotechnology</i> , 2015, 207, 30-31.	1.9	13
105	Optimizing recombinering in <i>Corynebacterium glutamicum</i> . <i>Biotechnology and Bioengineering</i> , 2021, 118, 2255-2264.	1.7	13
106	Classification of three corynebacterial strains isolated from a small paddock in North Rhine-Westphalia: proposal of <i>Corynebacterium kalinowskii</i> sp. nov., <i>Corynebacterium comes</i> sp. nov. and <i>Corynebacterium occultum</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	13
107	Complete Genome Sequence of <i>Ovine Mycobacterium avium</i> subsp. <i>paratuberculosis</i> Strain JIII-386 (MAP-S/type III) and Its Comparison to MAP-S/type I, MAP-C, and <i>M. avium</i> Complex Genomes. <i>Microorganisms</i> , 2021, 9, 70.	1.6	13
108	Draft Genome Sequence of <i>Bacillus anthracis</i> UR-1, Isolated from a German Heroin User. <i>Journal of Bacteriology</i> , 2012, 194, 5997-5998.	1.0	12



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109	Whole-Genome Sequence of the Clinical Strain <i>Corynebacterium argentoratense</i> DSM 44202, Isolated from a Human Throat Specimen. <i>Genome Announcements</i> , 2013, 1, .	0.8	12
110	Transcription of Sialic Acid Catabolism Genes in <i>Corynebacterium glutamicum</i> Is Subject to Catabolite Repression and Control by the Transcriptional Repressor NanR. <i>Journal of Bacteriology</i> , 2016, 198, 2204-2218.	1.0	12
111	Secretome Dynamics in a Gram-Positive Bacterial Model. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 423-436.	2.5	12
112	Class IV Lasso Peptides Synergistically Induce Proliferation of Cancer Cells and Sensitize Them to Doxorubicin. <i>IScience</i> , 2020, 23, 101785.	1.9	12
113	Phytoplankton consortia as a blueprint for mutually beneficial eukaryote-bacteria ecosystems based on the biocoenosis of <i>Botryococcus</i> consortia. <i>Scientific Reports</i> , 2021, 11, 1726.	1.6	12
114	<i>Corynebacterium crudilactis</i> sp. nov., isolated from raw cow's milk. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 5288-5293.	0.8	12
115	<i>Corynebacterium endometrii</i> sp. nov., isolated from the uterus of a cow with endometritis. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 146-152.	0.8	12
116	Draft Genome Sequence of <i>Bacillus anthracis</i> BF-1, Isolated from Bavarian Cattle. <i>Journal of Bacteriology</i> , 2012, 194, 6360-6361.	1.0	11
117	Complete genome sequence of the actinomycete <i>Actinoalloteichus hymeniacidonis</i> type strain HPA 177T isolated from a marine sponge. <i>Standards in Genomic Sciences</i> , 2016, 11, 91.	1.5	11
118	Superior production of heavy pamamycin derivatives using a <i>bkdR</i> deletion mutant of <i>Streptomyces albus</i> J1074/R2. <i>Microbial Cell Factories</i> , 2021, 20, 111.	1.9	11
119	Seventeen Ustilaginaceae High-Quality Genome Sequences Allow Phylogenomic Analysis and Provide Insights into Secondary Metabolite Synthesis. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 269.	1.5	11
120	Revisiting <i>Corynebacterium glyciniphilum</i> (ex Kubota et al., 1972) sp. nov., nom. rev., isolated from putrefied banana. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 177-182.	0.8	10
121	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
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