

Christian Rckert

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172
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187
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8,307
ext. citations

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avg, IF

5.31
L-index

#	Paper	IF	Citations
172	The subsystems approach to genome annotation and its use in the project to annotate 1000 genomes. <i>Nucleic Acids Research</i> , 2005 , 33, 5691-702	20.1	1485
171	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	3.7	750
170	An environmental bacterial taxon with a large and distinct metabolic repertoire. <i>Nature</i> , 2014 , 506, 58-63	30.4	421
169	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	11.6	360
168	Complete genome sequence of the myxobacterium <i>Sorangium cellulosum</i> . <i>Nature Biotechnology</i> , 2007 , 25, 1281-9	44.5	307
167	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, 7254-66	3.5	286
166	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	3.7	202
165	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, 2138-49	3.5	130
164	Comprehensive analysis of the <i>Corynebacterium glutamicum</i> transcriptome using an improved RNAseq technique. <i>BMC Genomics</i> , 2013 , 14, 888	4.5	127
163	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, 6006-15	4.8	110
162	Genome sequence of <i>B. amyloliquefaciens</i> type strain DSM7(T) reveals differences to plant-associated <i>B. amyloliquefaciens</i> FZB42. <i>Journal of Biotechnology</i> , 2011 , 155, 78-85	3.7	91
161	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	5.6	87
160	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, 871-87	4.1	86
159	The <i>Waddlia</i> genome: a window into chlamydial biology. <i>PLoS ONE</i> , 2010 , 5, e10890	3.7	82
158	The gene <i>ncgl2918</i> encodes a novel maleylpyruvate isomerase that needs mycothiol as cofactor and links mycothiol biosynthesis and gentisate assimilation in <i>Corynebacterium glutamicum</i> . <i>Journal of Biological Chemistry</i> , 2006 , 281, 10778-85	5.4	70
157	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	4.5	69
156	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	3.7	67

155	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, 126-39	3.7	64
154	Complete genome sequence of <i>Streptomyces lividans</i> TK24. <i>Journal of Biotechnology</i> , 2015 , 199, 21-2	3.7	62
153	The complete genome sequence of the acarbose producer <i>Actinoplanes</i> sp. SE50/110. <i>BMC Genomics</i> , 2012 , 13, 112	4.5	61
152	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> , 2012 , 164, 281-91	3.7	57
151	Comprehensive discovery and characterization of small RNAs in <i>Corynebacterium glutamicum</i> ATCC 13032. <i>BMC Genomics</i> , 2013 , 14, 714	4.5	52
150	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, 11-9	3.7	50
149	New natural products identified by combined genomics-metabolomics profiling of marine <i>Streptomyces</i> sp. MP131-18. <i>Scientific Reports</i> , 2017 , 7, 42382	4.9	49
148	Functional genomics and expression analysis of the <i>Corynebacterium glutamicum</i> <i>fpr2-cysIXHDNYZ</i> gene cluster involved in assimilatory sulphate reduction. <i>BMC Genomics</i> , 2005 , 6, 121	4.5	49
147	Single-bacterial genomics validates rich and varied specialized metabolism of uncultivated sponge symbionts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 1718-1723	11.5	45
146	<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	5.7	43
145	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, 729-30	3.7	40
144	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, 6818-27	3.5	39
143	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	4.5	39
142	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	4.5	37
141	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	3.7	37
140	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	4.5	36
139	Sulfate reduction in microorganisms-recent advances and biotechnological applications. <i>Current Opinion in Microbiology</i> , 2016 , 33, 140-146	7.9	33
138	Genome-based analysis of biosynthetic aminotransferase genes of <i>Corynebacterium glutamicum</i> . <i>Journal of Biotechnology</i> , 2003 , 104, 229-40	3.7	32

137	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	17.6	32
136	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	3.7	31
135	Adaptation of <i>Corynebacterium glutamicum</i> to salt-stress conditions. <i>Proteomics</i> , 2010 , 10, 445-57	4.8	31
134	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	9.7	30
133	Sequencing of high G+C microbial genomes using the ultrafast pyrosequencing technology. <i>Journal of Biotechnology</i> , 2011 , 155, 68-77	3.7	29
132	Arabitol metabolism of <i>Corynebacterium glutamicum</i> and its regulation by AtIR. <i>Journal of Bacteriology</i> , 2012 , 194, 941-55	3.5	29
131	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	4.5	29
130	Bioinformatics support for high-throughput proteomics. <i>Journal of Biotechnology</i> , 2003 , 106, 147-56	3.7	29
129	Monitoring global protein thiol-oxidation and protein S-mycothiolation in <i>Mycobacterium smegmatis</i> under hypochlorite stress. <i>Scientific Reports</i> , 2017 , 7, 1195	4.9	28
128	On the Enigma of Glutathione-Dependent Styrene Degradation in <i>Gordonia rubripertincta</i> CWB2. <i>Applied and Environmental Microbiology</i> , 2018 , 84,	4.8	27
127	Complete genome sequence of <i>Bacillus methanolicus</i> MGA3, a thermotolerant amino acid producing methylotroph. <i>Journal of Biotechnology</i> , 2014 , 188, 110-1	3.7	27
126	The transcriptional regulator SsuR activates expression of the <i>Corynebacterium glutamicum</i> sulphonate utilization genes in the absence of sulphate. <i>Molecular Microbiology</i> , 2005 , 58, 480-94	4.1	27
125	A multiproducer microbiome generates chemical diversity in the marine sponge. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 9508-9518	11.5	27
124	Isolation and genome sequencing of four Arctic marine <i>Psychrobacter</i> strains exhibiting multicopper oxidase activity. <i>BMC Genomics</i> , 2016 , 17, 117	4.5	26
123	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	3.7	26
122	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	5.7	25
121	Phenylacetic acid catabolism and its transcriptional regulation in <i>Corynebacterium glutamicum</i> . <i>Applied and Environmental Microbiology</i> , 2012 , 78, 5796-804	4.8	25
120	Complete genome sequence of <i>Saccharothrix espanaensis</i> DSM 44229(T) and comparison to the other completely sequenced <i>Pseudonocardia</i> spp. <i>BMC Genomics</i> , 2012 , 13, 465	4.5	24

119	Methanol-Essential Growth of : Adaptive Laboratory Evolution Overcomes Limitation due to Methanethiol Assimilation Pathway. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	24
118	Engineering L-arabinose metabolism in triacylglycerol-producing <i>Rhodococcus opacus</i> for lignocellulosic fuel production. <i>Metabolic Engineering</i> , 2015 , 30, 89-95	9.7	23
117	Molecular characterization of PrpR, the transcriptional activator of propionate catabolism in <i>Corynebacterium glutamicum</i> . <i>Journal of Biotechnology</i> , 2012 , 159, 1-11	3.7	23
116	Development of a Biosensor Concept to Detect the Production of Cluster-Specific Secondary Metabolites. <i>ACS Synthetic Biology</i> , 2017 , 6, 1026-1033	5.7	22
115	Complete genome sequence of the kirromycin producer <i>Streptomyces collinus</i> T1B65 consisting of a linear chromosome and two linear plasmids. <i>Journal of Biotechnology</i> , 2013 , 168, 739-40	3.7	21
114	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	4.7	21
113	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	4.5	21
112	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	3.7	20
111	Fast and reliable strain characterization of <i>Streptomyces lividans</i> through micro-scale cultivation. <i>Biotechnology and Bioengineering</i> , 2017 , 114, 2011-2022	4.9	18
110	Complete genome sequence of producer of the glycopeptide antibiotic Aculeximycin <i>Kutzneria albida</i> DSM 43870T, a representative of minor genus of Pseudonocardiaaceae. <i>BMC Genomics</i> , 2014 , 15, 885	4.5	18
109	High Quality Transcriptome Assembly of. <i>Frontiers in Molecular Biosciences</i> , 2018 , 5, 62	5.6	17
108	Genome Mining of sp. YIM 130001 Isolated From Lichen Affords New Thiopeptide Antibiotic. <i>Frontiers in Microbiology</i> , 2018 , 9, 3139	5.7	17
107	<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, 7720-9	4.8	16
106	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, 166-77	3.7	16
105	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	3.7	15
104	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. <i>Molecular Genetics and Genomics</i> , 2011 , 286, 247-59	3.1	15
103	Complete genome sequence of the actinobacterium <i>Amycolatopsis japonica</i> MG417-CF17(T) (=DSM 44213T) producing (S,S)-N,NPethylenediaminedisuccinic acid. <i>Journal of Biotechnology</i> , 2014 , 189, 46-7	3.7	14
102	Functional Characterization of a Small Alarmone Hydrolase in. <i>Frontiers in Microbiology</i> , 2018 , 9, 916	5.7	13

101	Multi-Omics and Targeted Approaches to Determine the Role of Cellular Proteases in Protein Secretion. <i>Frontiers in Microbiology</i> , 2018 , 9, 1174	5.7	13
100	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	6.3	13
99	Improving the genome annotation of the acarbose producer <i>Actinoplanes</i> sp. SE50/110 by sequencing enriched 5Pends of primary transcripts. <i>Journal of Biotechnology</i> , 2014 , 190, 85-95	3.7	13
98	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, 41-2	3.7	13
97	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	3.7	13
96	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	2.2	13
95	New Alpiniamides From sp. IB2014/011-12 Assembled by an Unusual Hybrid Non-ribosomal Peptide Synthetase -AT Polyketide Synthase Enzyme. <i>Frontiers in Microbiology</i> , 2018 , 9, 1959	5.7	12
94	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, 225-32	3.7	12
93	Impact of phenolic substrate and growth temperature on the <i>Arthrobacter chlorophenolicus</i> proteome. <i>Journal of Proteome Research</i> , 2009 , 8, 1953-64	5.6	12
92	Draft genome sequence of <i>Bacillus anthracis</i> UR-1, isolated from a German heroin user. <i>Journal of Bacteriology</i> , 2012 , 194, 5997-8	3.5	12
91	Draft genome sequence of <i>Wickerhamomyces ciferrii</i> NRRL Y-1031 F-60-10. <i>Eukaryotic Cell</i> , 2012 , 11, 1582-3		11
90	Transcriptomic and fluxomic changes in <i>Streptomyces lividans</i> producing heterologous protein. <i>Microbial Cell Factories</i> , 2018 , 17, 198	6.4	11
89	Exploiting <i>Hydrogenophaga pseudoflava</i> for aerobic syngas-based production of chemicals. <i>Metabolic Engineering</i> , 2019 , 55, 220-230	9.7	10
88	Draft genome sequence of <i>Bacillus anthracis</i> BF-1, isolated from Bavarian cattle. <i>Journal of Bacteriology</i> , 2012 , 194, 6360-1	3.5	10
87	Adaptive laboratory evolution accelerated glutarate production by <i>Corynebacterium glutamicum</i> . <i>Microbial Cell Factories</i> , 2021 , 20, 97	6.4	10
86	spp. From Ethiopia Producing Antimicrobial Compounds: Characterization via Bioassays, Genome Analyses, and Mass Spectrometry. <i>Frontiers in Microbiology</i> , 2018 , 9, 1270	5.7	9
85	Comprehensive subcellular topologies of polypeptides in <i>Streptomyces</i> . <i>Microbial Cell Factories</i> , 2018 , 17, 43	6.4	9
84	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 β -hydroxy streptomycin, and acarbose. <i>Journal of Biotechnology</i> , 2017 , 262, 84-88	3.7	9

83	Complete genome sequence of <i>Paenibacillus riograndensis</i> SBR5(T), a Gram-positive diazotrophic rhizobacterium. <i>Journal of Biotechnology</i> , 2015 , 207, 30-1	3.7	9
82	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, 5968-9	3.5	9
81	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	4.9	9
80	Physiological Response of to Indole. <i>Microorganisms</i> , 2020 , 8,	4.9	9
79	Characterization of Sigma Factor Genes in TK24 Using a Genomic Library-Based Approach for Multiple Gene Deletions. <i>Frontiers in Microbiology</i> , 2018 , 9, 3033	5.7	9
78	Baikalomycins A-C, New Aquayamycin-Type Angucyclines Isolated from Lake Baikal Derived sp. IB201691-2A. <i>Microorganisms</i> , 2020 , 8,	4.9	8
77	spp. From the Marine Sponge : Analyses of Secondary Metabolite Biosynthesis Gene Clusters and Some of Their Products. <i>Frontiers in Microbiology</i> , 2020 , 11, 437	5.7	8
76	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, 2204-18	3.5	8
75	Molecular Epidemiology of Multidrug-Resistant Bacteria Isolated from Libyan and Syrian Patients with War Injuries in Two Bundeswehr Hospitals in Germany. <i>European Journal of Microbiology and Immunology</i> , 2018 , 8, 1-11	4.6	8
74	Draft genome sequence of <i>Sinorhizobium meliloti</i> RU11/001, a model organism for flagellum structure, motility and chemotaxis. <i>Journal of Biotechnology</i> , 2013 , 168, 731-3	3.7	8
73	Draft Genome Sequence of <i>Streptomyces niveus</i> NCIMB 11891, Producer of the Aminocoumarin Antibiotic Novobiocin. <i>Genome Announcements</i> , 2014 , 2,		8
72	Whole-Genome Sequence of the Clinical Strain <i>Corynebacterium argenteorotense</i> DSM 44202, Isolated from a Human Throat Specimen. <i>Genome Announcements</i> , 2013 , 1,		8
71	Complete Genome Sequence of subsp. CCM 3239 (Formerly " CCM 3239"), a Producer of the Angucycline-Type Antibiotic Auricin. <i>Genome Announcements</i> , 2018 , 6,		7
70	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,		7
69	Genomic-Led Discovery of a Novel Glycopeptide Antibiotic by DSM 45129. <i>ACS Chemical Biology</i> , 2021 , 16, 915-928	4.9	7
68	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	3.7	6
67	Twenty-Five Years of Propagation in Suspension Cell Culture Results in Substantial Alterations of the Genome. <i>Genes</i> , 2019 , 10,	4.2	6
66	Genetic interrelations in the actinomycin biosynthetic gene clusters of IMRU 3720 and ATCC11523, producers of actinomycin X and actinomycin C. <i>Advances and Applications in Bioinformatics and Chemistry</i> , 2017 , 10, 29-46	1.5	6

65	Complete Genome Sequence of the Novel Cellulolytic, Anaerobic, Thermophilic Bacterium Type Strain GGR1, Isolated from a Lab Scale Biogas Reactor as Established by Illumina and Nanopore MinION Sequencing. <i>Genome Announcements</i> , 2018 , 6,		6
64	Draft Genome Sequence of <i>Streptomyces roseochromogenes</i> subsp. <i>oscitans</i> DS 12.976, Producer of the Aminocoumarin Antibiotic Clorobiocin. <i>Genome Announcements</i> , 2014 , 2,		6
63	Size exclusion chromatography: an improved method to harvest <i>Corynebacterium glutamicum</i> cells for the analysis of cytosolic metabolites. <i>Journal of Biotechnology</i> , 2011 , 154, 171-8	3.7	6
62	Secretome Dynamics in a Gram-Positive Bacterial Model. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 423-436	7.6	6
61	Towards a RassisPfor bacterial magnetosome biosynthesis: genome streamlining of <i>Magnetospirillum gryphiswaldense</i> by multiple deletions. <i>Microbial Cell Factories</i> , 2021 , 20, 35	6.4	6
60	<i>Actinoalloteichus fjordicus</i> sp. nov. isolated from marine sponges: phenotypic, chemotaxonomic and genomic characterisation. <i>Antonie Van Leeuwenhoek</i> , 2017 , 110, 1705-1717	2.1	5
59	Complete genome sequence of <i>Rhodococcus erythropolis</i> BG43 (DSM 46869), a degrader of <i>Pseudomonas aeruginosa</i> quorum sensing signal molecules. <i>Journal of Biotechnology</i> , 2015 , 211, 99-100	3.7	5
58	Class IV Lasso Peptides Synergistically Induce Proliferation of Cancer Cells and Sensitize Them to Doxorubicin. <i>IScience</i> , 2020 , 23, 101785	6.1	5
57	Sequence-based identification of inositol monophosphatase-like histidinol-phosphate phosphatases (HisN) in <i>Corynebacterium glutamicum</i> , Actinobacteria, and beyond. <i>BMC Microbiology</i> , 2017 , 17, 161	4.5	5
56	Perquinolines A-C: Unprecedented Bacterial Tetrahydroisoquinolines Involving an Intriguing Biosynthesis. <i>Angewandte Chemie - International Edition</i> , 2019 , 58, 12930-12934	16.4	5
55	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, 76-7	3.7	5
54	Genome sequence of the soil bacterium <i>Corynebacterium callunae</i> type strain DSM 20147(T). <i>Standards in Genomic Sciences</i> , 2015 , 10, 5		5
53	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, 81-3	3.7	5
52	Complete Genome Sequence of <i>Corynebacterium falsenii</i> DSM 44353 To Study the Evolution of <i>Corynebacterium</i> Cluster 3 Species. <i>Genome Announcements</i> , 2014 , 2,		5
51	Genome sequence of the squalene-degrading bacterium <i>Corynebacterium terpenotabidum</i> type strain Y-11(T) (= DSM 44721(T)). <i>Standards in Genomic Sciences</i> , 2014 , 9, 505-13		5
50	Genome sequence of the halotolerant bacterium <i>Corynebacterium halotolerans</i> type strain YIM 70093(T) (= DSM 44683(T)). <i>Standards in Genomic Sciences</i> , 2012 , 7, 284-93		5
49	<i>Corynebacterium crudilactis</i> sp. nov., isolated from raw cowB milk. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016 , 66, 5288-5293	2.2	5
48	Viennamycins: Lipopeptides Produced by a sp. <i>Journal of Natural Products</i> , 2020 , 83, 2381-2389	4.9	5

47	Screening of a genome-reduced <i>Corynebacterium glutamicum</i> strain library for improved heterologous cutinase secretion. <i>Microbial Biotechnology</i> , 2020 , 13, 2020-2031	6.3	5
46	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	4.9	5
45	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	5.7	5
44	Complete genome sequence of <i>Streptomyces</i> sp. CNQ-509, a prolific producer of meroterpenoid chemistry. <i>Journal of Biotechnology</i> , 2015 , 216, 140-1	3.7	4
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