

Christian RÃ¼ckert

List of Publications by Year in descending order

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181
papers

9,020
citations

87888

38
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46799

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187
all docs

187
docs citations

187
times ranked

11151
citing authors

#	ARTICLE	IF	CITATIONS
1	Biosynthetic Potential of the Endophytic Fungus <i>Helotiales</i> sp. BL73 Revealed via Compound Identification and Genome Mining. <i>Applied and Environmental Microbiology</i> , 2022, 88, aem0251021.	3.1	7
2	Seventeen <i>Ustilaginaceae</i> High-Quality Genome Sequences Allow Phylogenomic Analysis and Provide Insights into Secondary Metabolite Synthesis. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 269.	3.5	11
3	High quality genome sequences of thirteen <i>Hypoxylaceae</i> (Ascomycota) strengthen the phylogenetic family backbone and enable the discovery of new taxa. <i>Fungal Diversity</i> , 2021, 106, 7-28.	12.3	65
4	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.	3.3	12
5	Identification and elimination of genomic regions irrelevant for magnetosome biosynthesis by large-scale deletion in <i>Magnetospirillum gryphiswaldense</i> . <i>BMC Microbiology</i> , 2021, 21, 65.	3.3	8
6	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.	4.0	16
7	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.	3.3	14
8	Optimizing recombinering in <i>Corynebacterium glutamicum</i> . <i>Biotechnology and Bioengineering</i> , 2021, 118, 2255-2264.	3.3	13
9	Genomic-Led Discovery of a Novel Glycopeptide Antibiotic by <i>Nonomuraea coxensis</i> DSM 45129. <i>ACS Chemical Biology</i> , 2021, 16, 915-928.	3.4	16
10	Extensive Reannotation of the Genome of the Model Streptomyccete <i>Streptomyces lividans</i> TK24 Based on Transcriptome and Proteome Information. <i>Frontiers in Microbiology</i> , 2021, 12, 604034.	3.5	5
11	Complete genome sequence of <i>Streptomyces cyanogenus</i> S136, producer of anticancer angucycline landomycin A. <i>3 Biotech</i> , 2021, 11, 282.	2.2	3
12	Adaptive laboratory evolution accelerated glutarate production by <i>Corynebacterium glutamicum</i> . <i>Microbial Cell Factories</i> , 2021, 20, 97.	4.0	19
13	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.	3.3	15
14	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.	4.0	11
15	Coupling of the engineered DNA "emutator" to a biosensor as a new paradigm for activation of silent biosynthetic gene clusters in <i>Streptomyces</i> . <i>Nucleic Acids Research</i> , 2021, 49, 8396-8405.	14.5	5
16	<i>Streptomonospora litoralis</i> sp. nov., a halophilic thiopeptides producer isolated from sand collected at Cuxhaven beach. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 1483-1496.	1.7	6
17	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, .	1.7	13
18	The linear plasmid pSA3239 is essential for the replication of the <i>Streptomyces lavendulae</i> subsp. <i>lavendulae</i> CCM 3239 chromosome. <i>Research in Microbiology</i> , 2021, 172, 103870.	2.1	1

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19	Heterologous production of β -Carotene in <i>Corynebacterium glutamicum</i> using a multi-copy chromosomal integration method. <i>Bioresource Technology</i> , 2021, 341, 125782.	9.6	17
20	Estimation of pathogenic potential of an environmental <i>Pseudomonas aeruginosa</i> isolate using comparative genomics. <i>Scientific Reports</i> , 2021, 11, 1370.	3.3	5
21	Complete Genome Sequence of Ovine <i>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.	3.6	13
22	Establishment of a near-contiguous genome sequence of the citric acid producing yeast <i>Yarrowia lipolytica</i> DSM 3286 with resolution of rDNA clusters and telomeres. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab085.	3.2	4
23	Complete Genome Sequence of the Nonmotile <i>Myxococcus xanthus</i> Strain NM. <i>Microbiology Resource Announcements</i> , 2021, 10, e0098921.	0.6	1
24	Whole-Genome Sequence of <i>Streptococcus pyogenes</i> Strain 591, Belonging to the Genotype <i>emm</i> 49. <i>Microbiology Resource Announcements</i> , 2021, 10, e0081621.	0.6	5
25	<i>Paralysiella testudinis</i> gen. nov., sp. nov., isolated from the cloaca of a toad-headed turtle (<i>Mesoclemmys nasuta</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	9
26	Construction of an IS-Free <i>Corynebacterium glutamicum</i> ATCC 13032 Chassis Strain and Random Mutagenesis Using the Endogenous IS <i>Cg1</i> Transposase. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 751334.	4.1	5
27	Mutant Strains of <i>Escherichia coli</i> and Methicillin-Resistant <i>Staphylococcus aureus</i> Obtained by Laboratory Selection To Survive on Metallic Copper Surfaces. <i>Applied and Environmental Microbiology</i> , 2020, 87, .	3.1	4
28	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.	2.8	14
29	Viennamycins: Lipopeptides Produced by a <i>Streptomyces</i> sp.. <i>Journal of Natural Products</i> , 2020, 83, 2381-2389.	3.0	17
30	Screening of a genome-reduced <i>Corynebacterium glutamicum</i> strain library for improved heterologous cutinase secretion. <i>Microbial Biotechnology</i> , 2020, 13, 2020-2031.	4.2	17
31	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.	3.3	22
32	Physiological Response of <i>Corynebacterium glutamicum</i> to Indole. <i>Microorganisms</i> , 2020, 8, 1945.	3.6	17
33	Class IV Lasso Peptides Synergistically Induce Proliferation of Cancer Cells and Sensitize Them to Doxorubicin. <i>IScience</i> , 2020, 23, 101785.	4.1	12
34	pSETT4, an Improved ϕ C31-Based Integrative Vector System for Actinoplanes sp. SE50/110. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
35	Complete Genome Sequence of the Cryptophycin-Producing Cyanobacterium <i>Nostoc</i> sp. Strain ATCC 53789. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	6
36	Baikalomycins A-C, New Aquayamycin-Type Angucyclines Isolated from Lake Baikal Derived <i>Streptomyces</i> sp. IB201691-2A. <i>Microorganisms</i> , 2020, 8, 680.	3.6	19

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37	<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.	3.5	25
38	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.	7.1	71
39	<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.	1.7	12
40	<i>Prauserella flavalba</i> sp. nov., a novel species of the genus <i>Prauserella</i> , isolated from alkaline soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 380-387.	1.7	6
41	<i>Corynebacterium urogenitale</i> sp. nov. isolated from the genital tract of a cow. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3625-3632.	1.7	9
42	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.	4.1	38
43	Back Cover Image, Volume 117, Number 12, December 2020. <i>Biotechnology and Bioengineering</i> , 2020, 117, .	3.3	0
44	Perquinolineâ€¦: neuartige bakterielle Tetrahydroisochinoline mit einer bemerkenswerten Biosynthese. <i>Angewandte Chemie</i> , 2019, 131, 13063-13068.	2.0	0
45	Perquinolines Aâ€¦C: Unprecedented Bacterial Tetrahydroisoquinolines Involving an Intriguing Biosynthesis. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 12930-12934.	13.8	10
46	Exploiting <i>Hydrogenophaga pseudoflava</i> for aerobic syngas-based production of chemicals. <i>Metabolic Engineering</i> , 2019, 55, 220-230.	7.0	28
47	Whole-Genome Sequence of <i>Pseudoalteromonas</i> sp. NC201, a Probiotic Strain for <i>Litopenaeus stylirostris</i> Hatcheries in New Caledonia. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	3
48	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.	2.4	15
49	Secretome Dynamics in a Gram-Positive Bacterial Model. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 423-436.	3.8	12
50	Classification of three corynebacterial strains isolated from the Northern Bald Ibis (<i>Geronticus tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 23</i>) <i>Corynebacterium gerontici</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2928-2935.	1.7	21
51	<i>Streptomyces dysidea</i> sp. nov., isolated from a marine Mediterranean sponge <i>Dysidea tupa</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	1.7	6
52	Metabolic engineering to guide evolution â€œ Creating a novel mode for L-valine production with <i>Corynebacterium glutamicum</i> . <i>Metabolic Engineering</i> , 2018, 47, 31-41.	7.0	41
53	Complete Genome Sequence of the Novel Cellulolytic, Anaerobic, Thermophilic Bacterium <i>Herbivorax saccincola</i> Type Strain GGR1, Isolated from a Lab Scale Biogas Reactor as Established by Illumina and Nanopore MinION Sequencing. <i>Genome Announcements</i> , 2018, 6, .	0.8	10
54	On the Enigma of Glutathione-Dependent Styrene Degradation in <i>Gordonia rubripertincta</i> CWB2. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	38

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55	Complete Genome Sequence of <i>Streptomyces lavendulae</i> subsp. <i>lavendulae</i> CCM 3239 (Formerly <i>Streptomyces aureofaciens</i>), a Producer of the Angucycline-Type Antibiotic Auricin. <i>Genome Announcements</i> , 2018, 6, .	0.8	10
56	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.	7.1	70
57	Isolation and whole genome analysis of endospore-forming bacteria from heroin. <i>Forensic Science International: Genetics</i> , 2018, 32, 1-6.	3.1	6
58	<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.	3.8	63
59	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.	3.5	23
60	Transcriptomic and fluxomic changes in <i>Streptomyces lividans</i> producing heterologous protein. <i>Microbial Cell Factories</i> , 2018, 17, 198.	4.0	18
61	Genome Mining of <i>Streptomyces</i> sp. YIM 130001 Isolated From Lichen Affords New Thiopeptide Antibiotic. <i>Frontiers in Microbiology</i> , 2018, 9, 3139.	3.5	26
62	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.	3.6	8
63	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.	2.8	10
64	High Quality de Novo Transcriptome Assembly of <i>Croton tiglium</i> . <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 62.	3.5	48
65	Functional Characterization of a Small Alarmone Hydrolase in <i>Corynebacterium glutamicum</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 916.	3.5	25
66	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.	3.5	29
67	<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.	3.5	14
68	Genomics-Based Insights Into the Biosynthesis and Unusually High Accumulation of Free Fatty Acids by <i>Streptomyces</i> sp. NP10. <i>Frontiers in Microbiology</i> , 2018, 9, 1302.	3.5	3
69	Synthetic Biology Ethics at iGEM: iGEMer Perspectives. <i>Trends in Biotechnology</i> , 2018, 36, 985-987.	9.3	7
70	Comprehensive subcellular topologies of polypeptides in <i>Streptomyces</i> . <i>Microbial Cell Factories</i> , 2018, 17, 43.	4.0	19
71	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.	4.7	26
72	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.	3.5	19

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73	Taxonomic analyses of members of the <i>Streptomyces cinnabarinus</i> cluster, description of <i>Streptomyces cinnabarinus</i> sp. nov. and <i>Streptomyces davaonensis</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 382-393.	1.7	26
74	Development of a Biosensor Concept to Detect the Production of Cluster-Specific Secondary Metabolites. <i>ACS Synthetic Biology</i> , 2017, 6, 1026-1033.	3.8	28
75	New natural products identified by combined genomics-metabolomics profiling of marine <i>Streptomyces</i> sp. MP131-18. <i>Scientific Reports</i> , 2017, 7, 42382.	3.3	86
76	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.	3.8	27
77	Monitoring global protein thiol-oxidation and protein S-mycothiolation in <i>Mycobacterium smegmatis</i> under hypochlorite stress. <i>Scientific Reports</i> , 2017, 7, 1195.	3.3	47
78	Fast and reliable strain characterization of <i>Streptomyces lividans</i> through microscale cultivation. <i>Biotechnology and Bioengineering</i> , 2017, 114, 2011-2022.	3.3	37
79	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.	3.8	7
80	Complete Draft Genome Sequence of the Actinobacterium <i>Nocardiosis sinuspersici</i> UTMC102 (DSM) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.8	1
81	<i>Actinoalloteichus fjordicus</i> sp. nov. isolated from marine sponges: phenotypic, chemotaxonomic and genomic characterisation. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 1705-1717.	1.7	7
82	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.	3.8	10
83	Complete Genome Sequence of the <i>Streptococcus gallolyticus</i> subsp. <i>gallolyticus</i> Strain DSM 16831. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
84	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.	3.3	7
85	Genetic interrelations in the actinomycin biosynthetic gene clusters of <i>Streptomyces antibioticus</i> IMRU 3720 and <i>Streptomyces chrysomallus</i> ATCC11523, producers of actinomycin X and actinomycin C. <i>Advances and Applications in Bioinformatics and Chemistry</i> , 2017, Volume 10, 29-46.	2.6	7
86	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.	2.5	19
87	Sulfate reduction in microorganisms – recent advances and biotechnological applications. <i>Current Opinion in Microbiology</i> , 2016, 33, 140-146.	5.1	59
88	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
89	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.	2.2	12
90	Isolation and genome sequencing of four Arctic marine <i>Psychrobacter</i> strains exhibiting multicopper oxidase activity. <i>BMC Genomics</i> , 2016, 17, 117.	2.8	34

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91	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.	3.8	38
92	<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.	1.7	12
93	Deciphering the Transcriptional Response Mediated by the Redox-Sensing System HbpS-SenS-SenR from <i>Streptomyces</i> . <i>PLoS ONE</i> , 2016, 11, e0159873.	2.5	7
94	Genome sequence of the soil bacterium <i>Corynebacterium callunae</i> type strain DSM 20147T. <i>Standards in Genomic Sciences</i> , 2015, 10, 5.	1.5	8
95	Complete Genome Sequence of the Type Strain <i>Corynebacterium mustelae</i> DSM 45274, Isolated from Various Tissues of a Male Ferret with Lethal Sepsis. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
96	Complete genome sequence of <i>Paenibacillus riograndensis</i> SBR5T, a Gram-positive diazotrophic rhizobacterium. <i>Journal of Biotechnology</i> , 2015, 207, 30-31.	3.8	13
97	Complete Genome Sequence and Annotation of <i>Corynebacterium singulare</i> DSM 44357, Isolated from a Human Semen Specimen. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
98	Complete Genome Sequence of <i>Corynebacterium camporealensis</i> DSM 44610, Isolated from the Milk of a Manchega Sheep with Subclinical Mastitis. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
99	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
100	Virulence Factor Genes Detected in the Complete Genome Sequence of <i>Corynebacterium uterequi</i> DSM 45634, Isolated from the Uterus of a Maiden Mare. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
101	Complete Genome Sequence of the Type Strain <i>Corynebacterium testudinoris</i> DSM 44614, Recovered from Necrotic Lesions in the Mouth of a Tortoise. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
102	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.	3.8	7
103	Complete genome sequence of <i>Streptomyces lividans</i> TK24. <i>Journal of Biotechnology</i> , 2015, 199, 21-22.	3.8	96
104	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.	2.8	49
105	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.	3.5	102
106	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.	3.8	6
107	Engineering l-arabinose metabolism in triacylglycerol-producing <i>Rhodococcus opacus</i> for lignocellulosic fuel production. <i>Metabolic Engineering</i> , 2015, 30, 89-95.	7.0	26
108	<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.	3.1	26

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109	Complete genome sequence of <i>Streptomyces</i> sp. CNQ-509, a prolific producer of meroterpenoid chemistry. <i>Journal of Biotechnology</i> , 2015, 216, 140-141.	3.8	4
110	Complete Genome Sequence of the Type Strain <i>Corynebacterium epidermidicantis</i> DSM 45586, Isolated from the Skin of a Dog Suffering from Pruritus. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
111	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.	1.7	10
112	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.	2.5	51
113	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
114	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, .	0.8	5
115	Complete Genome Sequence of <i>Corynebacterium imitans</i> DSM 44264, Isolated from a Five-Month-Old Boy with Suspected Pharyngeal Diphtheria. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
116	Draft Genome Sequence of <i>Streptomyces niveus</i> NCIMB 11891, Producer of the Aminocoumarin Antibiotic Novobiocin. <i>Genome Announcements</i> , 2014, 2, .	0.8	8
117	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, .	0.8	8
118	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.	2.8	26
119	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.	3.8	15
120	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.	3.6	30
121	An environmental bacterial taxon with a large and distinct metabolic repertoire. <i>Nature</i> , 2014, 506, 58-62.	27.8	530
122	Complete genome sequence of <i>Corynebacterium vitaeruminis</i> DSM 20294T, isolated from the cow rumen as a vitamin B producer. <i>Journal of Biotechnology</i> , 2014, 189, 70-71.	3.8	8
123	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.	3.8	16
124	Complete genome sequence of <i>Bacillus methanolicus</i> MGA3, a thermotolerant amino acid producing methylotroph. <i>Journal of Biotechnology</i> , 2014, 188, 110-111.	3.8	31
125	Complete genome sequence of <i>Corynebacterium casei</i> LMC S-19264T (=DSM 44701T), isolated from a smear-ripened cheese. <i>Journal of Biotechnology</i> , 2014, 189, 76-77.	3.8	14
126	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.	3.8	46

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127	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.	3.8	13
128	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.	3.8	26
129	Complete Genome Sequence of <i>Corynebacterium ureicelerivorans</i> DSM 45051, a Lipophilic and Urea-Splitting Isolate from the Blood Culture of a Septicemia Patient. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
130	Complete genome sequence of the kirromycin producer <i>Streptomyces collinus</i> TÄ¼ 365 consisting of a linear chromosome and two linear plasmids. <i>Journal of Biotechnology</i> , 2013, 168, 739-740.	3.8	23
131	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.	3.1	142
132	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, 731-733.	3.8	9
133	Comprehensive analysis of the <i>Corynebacterium glutamicum</i> transcriptome using an improved RNAseq technique. <i>BMC Genomics</i> , 2013, 14, 888.	2.8	175
134	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.	3.8	20
135	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.	3.8	70
136	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.	3.8	51
137	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.	3.8	16
138	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.	2.8	27
139	Comprehensive discovery and characterization of small RNAs in <i>Corynebacterium glutamicum</i> ATCC 13032. <i>BMC Genomics</i> , 2013, 14, 714.	2.8	61
140	Whole-Genome Sequence of the Clinical Strain <i>Corynebacterium argenteratense</i> DSM 44202, Isolated from a Human Throat Specimen. <i>Genome Announcements</i> , 2013, 1, .	0.8	12
141	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.	8.4	425
142	Genome sequence of the marine bacterium <i>Corynebacterium maris</i> type strain Coryn-1T (= DSM 45190T). <i>Standards in Genomic Sciences</i> , 2013, 8, 516-524.	1.5	2
143	Genome sequence of the squalene-degrading bacterium <i>Corynebacterium terpenotabidum</i> type strain Y-11T (= DSM 44721T). <i>Standards in Genomic Sciences</i> , 2013, 9, 505-513.	1.5	7
144	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.	2.2	12

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145	Draft Genome Sequence of <i>Bacillus anthracis</i> BF-1, Isolated from Bavarian Cattle. <i>Journal of Bacteriology</i> , 2012, 194, 6360-6361.	2.2	11
146	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.	2.2	42
147	Arabitol Metabolism of <i>Corynebacterium glutamicum</i> and Its Regulation by AtIR. <i>Journal of Bacteriology</i> , 2012, 194, 941-955.	2.2	32
148	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
149	Phenylacetic Acid Catabolism and Its Transcriptional Regulation in <i>Corynebacterium glutamicum</i> . <i>Applied and Environmental Microbiology</i> , 2012, 78, 5796-5804.	3.1	32
150	Genome sequence of the halotolerant bacterium <i>Corynebacterium halotolerans</i> type strain YIM 70093T (= DSM 44683T). <i>Standards in Genomic Sciences</i> , 2012, 7, 284-293.	1.5	9
151	Molecular characterization of PrpR, the transcriptional activator of propionate catabolism in <i>Corynebacterium glutamicum</i> . <i>Journal of Biotechnology</i> , 2012, 159, 1-11.	3.8	31
152	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.	2.2	15
153	The complete genome sequence of the acarbose producer <i>Actinoplanes</i> sp. SE50/110. <i>BMC Genomics</i> , 2012, 13, 112.	2.8	69
154	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.	2.8	32
155	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.	3.0	23
156	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.	2.1	19
157	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.	2.8	41
158	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.	3.8	78
159	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, 171-178.	3.8	8
160	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.	3.8	107
161	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.	3.8	67
162	Sequencing of high G+C microbial genomes using the ultrafast pyrosequencing technology. <i>Journal of Biotechnology</i> , 2011, 155, 68-77.	3.8	29

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163	Adaptation of <i>Corynebacterium glutamicum</i> to salt stress conditions. <i>Proteomics</i> , 2010, 10, 445-457.	2.2	34
164	The <i>Waddlia</i> Genome: A Window into Chlamydial Biology. <i>PLoS ONE</i> , 2010, 5, e10890.	2.5	104
165	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.	2.8	90
166	Impact of Phenolic Substrate and Growth Temperature on the <i>Arthrobacter chlorophenicus</i> Proteome. <i>Journal of Proteome Research</i> , 2009, 8, 1953-1964.	3.7	13
167	The dual transcriptional regulator <i>CysR</i> in <i>Corynebacterium glutamicum</i> ATCC 13032 controls a subset of genes of the <i>McbR</i> regulon in response to the availability of sulphide acceptor molecules. <i>BMC Genomics</i> , 2008, 9, 483.	2.8	45
168	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.	3.8	238
169	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.	2.2	153
170	Complete genome sequence of the myxobacterium <i>Sorangium cellulosum</i> . <i>Nature Biotechnology</i> , 2007, 25, 1281-1289.	17.5	354
171	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.	2.8	35
172	The Gene <i>ncgl2918</i> 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.	3.4	74
173	The <i>McbR</i> repressor modulated by the effector substance <i>S</i> -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.	2.5	92
174	The transcriptional regulator <i>SsuR</i> activates expression of the <i>Corynebacterium glutamicum</i> sulphonate utilization genes in the absence of sulphate. <i>Molecular Microbiology</i> , 2005, 58, 480-494.	2.5	30
175	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.	2.8	61
176	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.	14.5	1,806
177	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.	2.2	321
178	The complete <i>Corynebacterium glutamicum</i> ATCC 13032 genome sequence and its impact on the production of <i>l</i> -aspartate-derived amino acids and vitamins. <i>Journal of Biotechnology</i> , 2003, 104, 5-25.	3.8	844
179	Genome-based analysis of biosynthetic aminotransferase genes of <i>Corynebacterium glutamicum</i> . <i>Journal of Biotechnology</i> , 2003, 104, 229-240.	3.8	33
180	Bioinformatics support for high-throughput proteomics. <i>Journal of Biotechnology</i> , 2003, 106, 147-156.	3.8	31

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181	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.	3.8	70