

Christian RÃ¼ckert

List of Publications by Year in descending order

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109
papers

7,879
citations

109321

35
h-index

51608

86
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116
all docs

116
docs citations

116
times ranked

10362
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	<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
5	Complete Genome Sequence of the Nonmotile <i>Myxococcus xanthus</i> Strain NM. <i>Microbiology Resource Announcements</i> , 2021, 10, e0098921.	0.6	1
6	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
7	<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
8	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
9	Viennamycins: Lipopeptides Produced by a <i>Streptomyces</i> sp.. <i>Journal of Natural Products</i> , 2020, 83, 2381-2389.	3.0	17
10	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
11	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
12	pSETT4, an Improved λ C31-Based Integrative Vector System for Actinoplanes sp. SE50/110. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
13	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
14	Perquinolines A-C: Unprecedented Bacterial Tetrahydroisoquinolines Involving an Intriguing Biosynthesis. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 12930-12934.	13.8	10
15	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
16	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
17	Secretome Dynamics in a Gram-Positive Bacterial Model. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 423-436.	3.8	12
18	<i>Streptomyces dysidea</i> sp. nov., isolated from a marine Mediterranean sponge <i>Dysidea tupha</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	1.7	6

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19	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
20	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
21	Complete Genome Sequence of <i>Streptomyces lavendulae</i> subsp. <i>lavendulae</i> CCM 3239 (Formerly <i>Streptomyces aureofaciens</i> CCM 3239), a Producer of the Angucycline-Type Antibiotic Auricin. <i>Genome Announcements</i> , 2018, 6, .	0.8	10
22	Draft Genome Sequence of <i>Streptomyces</i> sp. Strain DH-12, a Soilborne Isolate from the Thar Desert with Broad-Spectrum Antibacterial Activity. <i>Genome Announcements</i> , 2018, 6, .	0.8	5
23	Transcriptomic and fluxomic changes in <i>Streptomyces lividans</i> producing heterologous protein. <i>Microbial Cell Factories</i> , 2018, 17, 198.	4.0	18
24	High Quality de Novo Transcriptome Assembly of <i>Croton tiglium</i> . <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 62.	3.5	48
25	Functional Characterization of a Small Alarmone Hydrolase in <i>Corynebacterium glutamicum</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 916.	3.5	25
26	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
27	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
28	Complete Draft Genome Sequence of the Actinobacterium <i>Nocardiopsis sinuspersici</i> UTMC102 (DSM Tj ETQq0 0 0 rgBT /Overlock 10 T	0.8	1
29	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
30	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
31	<i>Streptomyces phaeopurpureus</i> Shinobu 1957 (Approved Lists 1980) and <i>Streptomyces griseorubiginosus</i> (Ryabova and Preobrazhenskaya 1957) Pridham et al. 1958 (Approved Lists 1980) are heterotypic subjective synonyms. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 3111-3116.	1.7	5
32	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
33	Sulfate reduction in microorganisms – recent advances and biotechnological applications. <i>Current Opinion in Microbiology</i> , 2016, 33, 140-146.	5.1	59
34	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
35	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
36	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

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37	Complete genome sequence of <i>Streptomyces lividans</i> TK24. <i>Journal of Biotechnology</i> , 2015, 199, 21-22.	3.8	96
38	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
39	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
40	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
41	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
42	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
43	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
44	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
45	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
46	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
47	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
48	An environmental bacterial taxon with a large and distinct metabolic repertoire. <i>Nature</i> , 2014, 506, 58-62.	27.8	530
49	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
50	Complete genome sequence of the actinobacterium <i>Amycolatopsis japonica</i> MG417-CF17T (=DSM 44213T) producing (S,S)-N,N'-ethylene-diaminedisuccinic acid. <i>Journal of Biotechnology</i> , 2014, 189, 46-47.	3.8	16
51	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
52	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.	3.8	14
53	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
54	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

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55	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
56	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.	3.8	23
57	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
58	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
59	Comprehensive analysis of the <i>Corynebacterium glutamicum</i> transcriptome using an improved RNAseq technique. <i>BMC Genomics</i> , 2013, 14, 888.	2.8	175
60	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
61	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
62	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
63	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
64	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
65	Comprehensive discovery and characterization of small RNAs in <i>Corynebacterium glutamicum</i> ATCC 13032. <i>BMC Genomics</i> , 2013, 14, 714.	2.8	61
66	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
67	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
68	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
69	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
70	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
71	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
72	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

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73	Arabitol Metabolism of <i>Corynebacterium glutamicum</i> and Its Regulation by AtIR. <i>Journal of Bacteriology</i> , 2012, 194, 941-955.	2.2	32
74	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
75	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
76	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
77	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
78	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
79	The complete genome sequence of the acarbose producer <i>Actinoplanes</i> sp. SE50/110. <i>BMC Genomics</i> , 2012, 13, 112.	2.8	69
80	Complete genome sequence of <i>Saccharothrix espanaensis</i> DSM 44229T and comparison to the other completely sequenced <i>Pseudonocardia</i> spp. <i>BMC Genomics</i> , 2012, 13, 465.	2.8	32
81	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
82	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
83	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
84	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
85	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
86	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
87	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
88	Sequencing of high G+C microbial genomes using the ultrafast pyrosequencing technology. <i>Journal of Biotechnology</i> , 2011, 155, 68-77.	3.8	29
89	Adaptation of <i>Corynebacterium glutamicum</i> to salt stress conditions. <i>Proteomics</i> , 2010, 10, 445-457.	2.2	34
90	The <i>Waddlia</i> Genome: A Window into Chlamydial Biology. <i>PLoS ONE</i> , 2010, 5, e10890.	2.5	104

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91	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
92	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
93	The missing link: <i>Bordetella petrii</i> is endowed with both the metabolic versatility of environmental bacteria and virulence traits of pathogenic <i>Bordetellae</i> . <i>BMC Genomics</i> , 2008, 9, 449.	2.8	85
94	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.	2.8	45
95	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
96	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
97	Complete genome sequence of the myxobacterium <i>Sorangium cellulosum</i> . <i>Nature Biotechnology</i> , 2007, 25, 1281-1289.	17.5	354
98	Bioinformatic evaluation of L-arginine catabolic pathways in 24 cyanobacteria and transcriptional analysis of genes encoding enzymes of L-arginine catabolism in the cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>BMC Genomics</i> , 2007, 8, 437.	2.8	40
99	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
100	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
101	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.	2.5	92
102	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, 480-494.	2.5	30
103	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
104	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
105	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
106	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.	3.8	844
107	Genome-based analysis of biosynthetic aminotransferase genes of <i>Corynebacterium glutamicum</i> . <i>Journal of Biotechnology</i> , 2003, 104, 229-240.	3.8	33
108	Bioinformatics support for high-throughput proteomics. <i>Journal of Biotechnology</i> , 2003, 106, 147-156.	3.8	31

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109	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