

Tobias Busche

List of Publications by Year in descending order

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74
papers

1,151
citations

471509

17
h-index

526287

27
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76
all docs

76
docs citations

76
times ranked

1219
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	Phage Genome Diversity in a Biogas-Producing Microbiome Analyzed by Illumina and Nanopore GridION Sequencing. <i>Microorganisms</i> , 2022, 10, 368.	3.6	8
3	Sigma regulatory network in <i>Rhodococcus erythropolis</i> CCM2595. <i>FEMS Microbiology Letters</i> , 2022, , .	1.8	3
4	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.	3.5	11
5	A Second Gamma-Glutamylpolyamine Synthetase, GlnA2, Is Involved in Polyamine Catabolism in <i>Streptomyces coelicolor</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 3752.	4.1	7
6	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
7	The Gut Microbial Composition Is Species-Specific and Individual-Specific in Two Species of Estrildid Finches, the Bengalese Finch and the Zebra Finch. <i>Frontiers in Microbiology</i> , 2021, 12, 619141.	3.5	13
8	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
9	Nanopore Sequencing Reveals Global Transcriptome Signatures of Mitochondrial and Ribosomal Gene Expressions in Various Human Cancer Stem-like Cell Populations. <i>Cancers</i> , 2021, 13, 1136.	3.7	14
10	Genomic and Transcriptomic Investigation of the Physiological Response of the Methylophilic <i>Bacillus methanolicus</i> to 5-Aminovalerate. <i>Frontiers in Microbiology</i> , 2021, 12, 664598.	3.5	3
11	Extensive Reannotation of the Genome of the Model Streptomyces <i>Streptomyces lividans</i> TK24 Based on Transcriptome and Proteome Information. <i>Frontiers in Microbiology</i> , 2021, 12, 604034.	3.5	5
12	Exploring the molecular content of CHO exosomes during bioprocessing. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 3673-3689.	3.6	21
13	Poly- and Monoamine Metabolism in <i>Streptomyces coelicolor</i> : The New Role of Glutamine Synthetase-Like Enzymes in the Survival under Environmental Stress. <i>Microbial Physiology</i> , 2021, 31, 233-247.	2.4	12
14	Adaptive laboratory evolution accelerated glutarate production by <i>Corynebacterium glutamicum</i> . <i>Microbial Cell Factories</i> , 2021, 20, 97.	4.0	19
15	Exposure to 1-Butanol Exemplifies the Response of the Thermoacidophilic Archaeon <i>Sulfolobus acidocaldarius</i> to Solvent Stress. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	8
16	Recombinant expression and characterization of novel P450s from <i>Actinosynnema mirum</i> . <i>Bioorganic and Medicinal Chemistry</i> , 2021, 42, 116241.	3.0	6
17	Isolation and Characterization of Barley (<i>Hordeum vulgare</i>) Extracellular Vesicles to Assess Their Role in RNA Spray-Based Crop Protection. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7212.	4.1	9
18	Functional Redundancy and Specialization of the Conserved Cold Shock Proteins in <i>Bacillus subtilis</i> . <i>Microorganisms</i> , 2021, 9, 1434.	3.6	7

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19	Coupling of the engineered DNA "mutator" 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
20	A novel plant-fungal association reveals fundamental sRNA and gene expression reprogramming at the onset of symbiosis. <i>BMC Biology</i> , 2021, 19, 171.	3.8	10
21	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
22	Multiple Occurrences of a 168-Nucleotide Deletion in SARS-CoV-2 ORF8, Unnoticed by Standard Amplicon Sequencing and Variant Calling Pipelines. <i>Viruses</i> , 2021, 13, 1870.	3.3	7
23	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
24	The Complex Transcriptional Landscape of Magnetosome Gene Clusters in <i>Magnetospirillum gryphiswaldense</i> . <i>MSystems</i> , 2021, 6, e0089321.	3.8	9
25	Comparative Analysis of Transcriptome and sRNAs Expression Patterns in the <i>Brachypodium distachyon</i> "Magnaporthe oryzae Pathosystems. <i>International Journal of Molecular Sciences</i> , 2021, 22, 650.	4.1	16
26	SPI2 T3SS effectors facilitate enterocyte apical to basolateral transmigration of <i>Salmonella</i> -containing vacuoles <i>in vivo</i> . <i>Gut Microbes</i> , 2021, 13, 1973836.	9.8	6
27	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
28	The two-Cys-type TetR repressor GbaA confers resistance under disulfide and electrophile stress in <i>Staphylococcus aureus</i> . <i>Free Radical Biology and Medicine</i> , 2021, 177, 120-131.	2.9	8
29	Complete Genome Sequence of the Nonmotile <i>Myxococcus xanthus</i> Strain NM. <i>Microbiology Resource Announcements</i> , 2021, 10, e0098921.	0.6	1
30	Activity-Based Protein Profiling for the Identification of Novel Carbohydrate-Active Enzymes Involved in Xylan Degradation in the Hyperthermophilic Euryarchaeon <i>Thermococcus</i> sp. Strain 2319x1E. <i>Frontiers in Microbiology</i> , 2021, 12, 734039.	3.5	6
31	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
32	The plant-derived naphthoquinone lapachol causes an oxidative stress response in <i>Staphylococcus aureus</i> . <i>Free Radical Biology and Medicine</i> , 2020, 158, 126-136.	2.9	26
33	Viennamycins: Lipopeptides Produced by a <i>Streptomyces</i> sp.. <i>Journal of Natural Products</i> , 2020, 83, 2381-2389.	3.0	17
34	Physiological Response of <i>Corynebacterium glutamicum</i> to Indole. <i>Microorganisms</i> , 2020, 8, 1945.	3.6	17
35	Class IV Lasso Peptides Synergistically Induce Proliferation of Cancer Cells and Sensitize Them to Doxorubicin. <i>IScience</i> , 2020, 23, 101785.	4.1	12
36	Revisiting the Growth Modulon of <i>Corynebacterium glutamicum</i> Under Glucose Limited Chemostat Conditions. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 584614.	4.1	7

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37	The alarmone (p)ppGpp confers tolerance to oxidative stress during the stationary phase by maintenance of redox and iron homeostasis in <i>Staphylococcus aureus</i> . <i>Free Radical Biology and Medicine</i> , 2020, 161, 351-364.	2.9	27
38	Genetic Engineering of <i>Oligotropha carboxidovorans</i> Strain OM5â€”A Promising Candidate for the Aerobic Utilization of Synthesis Gas. <i>ACS Synthetic Biology</i> , 2020, 9, 1426-1440.	3.8	14
39	The roseoflavin producer <i>Streptomyces davaonensis</i> has a high catalytic capacity and specific genetic adaptations with regard to the biosynthesis of riboflavin. <i>Environmental Microbiology</i> , 2020, 22, 3248-3265.	3.8	3
40	<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
41	RNA extraction from soil bacterium <i>Pseudomonas putida</i> and green alga <i>Raphidocelis subcapitata</i> after exposure to nanoscale zero valent iron. , 2020, , .		0
42	Effect of ribosome engineering on the transcription level and production of <i>S. albus</i> indigenous secondary metabolites. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 7097-7110.	3.6	23
43	Evaluation of vector systems and promoters for overexpression of the acarbose biosynthesis gene <i>acbC</i> in <i>Actinoplanes</i> sp. SE50/110. <i>Microbial Cell Factories</i> , 2019, 18, 114.	4.0	15
44	The genetic basis of 3-hydroxypropanoate metabolism in <i>Cupriavidus necator</i> H16. <i>Biotechnology for Biofuels</i> , 2019, 12, 150.	6.2	17
45	Identifying the Growth Modulon of <i>Corynebacterium glutamicum</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 974.	3.5	12
46	<i>Staphylococcus aureus</i> responds to allicin by global S-thioallylation â€” Role of the Brx/BSH/YpdA pathway and the disulfide reductase MerA to overcome allicin stress. <i>Free Radical Biology and Medicine</i> , 2019, 139, 55-69.	2.9	65
47	Physiology and Transcriptional Analysis of (p)ppGpp-Related Regulatory Effects in <i>Corynebacterium glutamicum</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2769.	3.5	8
48	Essentiality of the Maltase AmlE in Maltose Utilization and Its Transcriptional Regulation by the Repressor AmlR in the Acarbose-Producing Bacterium <i>Actinoplanes</i> sp. SE50/110. <i>Frontiers in Microbiology</i> , 2019, 10, 2448.	3.5	4
49	Secretome Dynamics in a Gram-Positive Bacterial Model. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 423-436.	3.8	12
50	Metabolic engineering to guide evolution â€” Creating a novel mode for L-valine production with <i>Corynebacterium glutamicum</i> . <i>Metabolic Engineering</i> , 2018, 47, 31-41.	7.0	41
51	Complete Genome Sequence of <i>Streptomyces lavendulae</i> subsp. <i>lavendulae</i> CCM 3239 (Formerly <i>Streptomyces aureofaciens</i> CCM 3239â€”), a Producer of the Angucycline-Type Antibiotic Auricin. <i>Genome Announcements</i> , 2018, 6, .	0.8	10
52	Differential transcriptomic analysis reveals hidden light response in <i>Streptomyces lividans</i> . <i>Biotechnology Progress</i> , 2018, 34, 287-292.	2.6	3
53	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
54	Transcriptomic and fluxomic changes in <i>Streptomyces lividans</i> producing heterologous protein. <i>Microbial Cell Factories</i> , 2018, 17, 198.	4.0	18

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55	Comparative Secretome Analyses of Human and Zoonotic <i>Staphylococcus aureus</i> Isolates CC8, CC22, and CC398. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2412-2433.	3.8	29
56	Transcriptome sequencing of the human pathogen <i>Corynebacterium diphtheriae</i> NCTC 13129 provides detailed insights into its transcriptional landscape and into DtxR-mediated transcriptional regulation. <i>BMC Genomics</i> , 2018, 19, 82.	2.8	26
57	RNAseq analysis of $\hat{\pm}$ -proteobacterium <i>Gluconobacter oxydans</i> 621H. <i>BMC Genomics</i> , 2018, 19, 24.	2.8	16
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.	3.5	29
59	<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
60	Deciphering the Adaptation of <i>Corynebacterium glutamicum</i> in Transition from Aerobiosis via Microaerobiosis to Anaerobiosis. <i>Genes</i> , 2018, 9, 297.	2.4	19
61	Comprehensive subcellular topologies of polypeptides in <i>Streptomyces</i> . <i>Microbial Cell Factories</i> , 2018, 17, 43.	4.0	19
62	Characterization of the small flavin-binding dodecin in the roseoflavin producer <i>Streptomyces davawensis</i> . <i>Microbiology (United Kingdom)</i> , 2018, 164, 908-919.	1.8	6
63	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
64	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
65	Fast and reliable strain characterization of <i>Streptomyces lividans</i> through micro-scale cultivation. <i>Biotechnology and Bioengineering</i> , 2017, 114, 2011-2022.	3.3	37
66	<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
67	Assignment of sigma factors of RNA polymerase to promoters in <i>Corynebacterium glutamicum</i> . <i>AMB Express</i> , 2017, 7, 133.	3.0	20
68	The transcriptional regulator LysG (Rv1985c) of <i>Mycobacterium tuberculosis</i> activates lysE (Rv1986) in a lysine-dependent manner. <i>PLoS ONE</i> , 2017, 12, e0186505.	2.5	6
69	Physiological roles of sigma factor SigD in <i>Corynebacterium glutamicum</i> . <i>BMC Microbiology</i> , 2017, 17, 158.	3.3	26
70	The guanidinobutyrase GbuA is essential for the alkylquinolone-regulated pyocyanin production during parasitic growth of <i>Pseudomonas aeruginosa</i> in co-culture with <i>Aeromonas hydrophila</i> . <i>Environmental Microbiology</i> , 2016, 18, 3550-3564.	3.8	10
71	An influence of the copy number of biosynthetic gene clusters on the production level of antibiotics in a heterologous host. <i>Journal of Biotechnology</i> , 2016, 232, 110-117.	3.8	18
72	Complete genome sequence of <i>Streptomyces reticuli</i> , an efficient degrader of crystalline cellulose. <i>Journal of Biotechnology</i> , 2016, 222, 13-14.	3.8	14

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73	Deciphering the Transcriptional Response Mediated by the Redox-Sensing System HbpS-SenS-SenR from <i>Streptomyces</i> . PLoS ONE, 2016, 11, e0159873.	2.5	7
74	Complete genome sequence of <i>Streptomyces lividans</i> TK24. Journal of Biotechnology, 2015, 199, 21-22.	3.8	96