Fabian M Commichau

List of Publications by Year
in descending order

72 papers	3,409 citations	159585 30 h-index	161849 54 g-index
81 all docs	81 docs citations	81 times ranked	3153 citing authors

#	Article	IF	Citations
1	Characterization of glyphosateâ€resistant <i>Burkholderia anthina</i> and <i>Burkholderia cenocepacia</i> isolates from a commercial RoundupÂ® solution. Environmental Microbiology Reports, 2022, 14, 70-84.	2.4	11
2	The <i>Bacillus</i> phage <scp>SPÎ²</scp> and its relatives: a temperate phage model system reveals new strains, species, prophage integration loci, conserved proteins and lysogeny management components. Environmental Microbiology, 2022, 24, 2098-2118.	3.8	19
3	Adaptation of<i>Listeria monocytogenes</i>to perturbation of<scp>câ€diâ€AMP</scp>metabolism underpins its role in osmoadaptation and identifies a fosfomycin uptake system. Environmental Microbiology, 2022, 24, 4466-4488.	3.8	5
4	Draft Genome Sequence of the Type Strain Bacillus subtilis subsp. <i>subtilis</i> DSM10. Microbiology Resource Announcements, 2021, 10, .	0.6	4
5	A <i>Bacillus subtilis</i>â€‰<scp>Î”<i>pdxT</i></scp> mutant suppresses vitamin <scp>B6</scp> limitation by acquiring mutations enhancing <scp><i>pdxS</i></scp> gene dosage and ammonium assimilation. Environmental Microbiology Reports, 2021, 13, 218-233.	2.4	5
6	Underground metabolism facilitates the evolution of novel pathways for vitamin B6 biosynthesis. Applied Microbiology and Biotechnology, 2021, 105, 2297-2305.	3.6	17
7	Molecular mechanisms underlying glyphosate resistance in bacteria. Environmental Microbiology, 2021, 23, 2891-2905.	3.8	24
8	The <i>Bacillus subtilis</i> Minimal Genome Compendium. ACS Synthetic Biology, 2021, 10, 2767-2771.	3.8	23
9	Complete Genome Sequence of the Prototrophic Bacillus subtilis subsp. <i>subtilis</i> Strain SP1. Microbiology Resource Announcements, 2020, 9, .	0.6	4
10	An extracytoplasmic protein and a moonlighting enzyme modulate synthesis of <scp>câ€diâ€AMP</scp> in <i>Listeria monocytogenes</i>. Environmental Microbiology, 2020, 22, 2771-2791.	3.8	20
11	Fermentative Production of Vitamin B6. , 2020, , 1-34.		0
12	Microbial cell factories for the sustainable manufacturing of B vitamins. Current Opinion in Biotechnology, 2019, 56, 18-29.	6.6	105
13	Variants of the Bacillus subtilis LysR-Type Regulator GltC With Altered Activator and Repressor Function. Frontiers in Microbiology, 2019, 10, 2321.	3.5	7
14	c-di-AMP assists osmoadaptation by regulating the Listeria monocytogenes potassium transporters KimA and KtrCD. Journal of Biological Chemistry, 2019, 294, 16020-16033.	3.4	41
15	Identification of the first glyphosate transporter by genomic adaptation. Environmental Microbiology, 2019, 21, 1287-1305.	3.8	36
16	Aurantimycin resistance genes contribute to survival of <i>Listeria monocytogenes </i>during life in the environment. Molecular Microbiology, 2019, 111, 1009-1024.	2.5	16
17	A Survey of Pyridoxal 5â€²-Phosphate-Dependent Proteins in the Gram-Positive Model Bacterium Bacillus subtilis. Frontiers in Molecular Biosciences, 2019, 6, 32.	3.5	36
18	Bacillus subtilis Spore Resistance to Simulated Mars Surface Conditions. Frontiers in Microbiology, 2019, 10, 333.	3.5	44

#	ARTICLE	IF	CITATIONS
19	The KupA and KupB Proteins of <i>Lactococcus lactis</i> IL1403 Are Novel c-di-AMP Receptor Proteins Responsible for Potassium Uptake. Journal of Bacteriology, 2019, 201, .	2.2	38
20	Harnessing Underground Metabolism for Pathway Development. Trends in Biotechnology, 2019, 37, 29-37.	9.3	29
21	Making and Breaking of an Essential Poison: the Cyclases and Phosphodiesterases That Produce and Degrade the Essential Second Messenger Cyclic di-AMP in Bacteria. Journal of Bacteriology, 2019, 201, .	2.2	90
22	Visualization of tandem repeat mutagenesis in Bacillus subtilis. DNA Repair, 2018, 63, 10-15.	2.8	9
23	Perspective of ions and messengers: an intricate link between potassium, glutamate, and cyclic di-AMP. Current Genetics, 2018, 64, 191-195.	1.7	41
24	Coping with an Essential Poison: a Genetic Suppressor Analysis Corroborates a Key Function of c-di-AMP in Controlling Potassium Ion Homeostasis in Gram-Positive Bacteria. Journal of Bacteriology, 2018, 200, .	2.2	22
25	A Delicate Connection: c-di-AMP Affects Cell Integrity by Controlling Osmolyte Transport. Trends in Microbiology, 2018, 26, 175-185.	7.7	88
26	A twoâ€step evolutionary process establishes a nonâ€native vitamin B6 pathway in <i>Bacillus subtilis</i>. Environmental Microbiology, 2018, 20, 156-168.	3.8	20
27	Changes of DNA topology affect the global transcription landscape and allow rapid growth of a Bacillus subtilis mutant lacking carbon catabolite repression. Metabolic Engineering, 2018, 45, 171-179.	7.0	18
28	Selective Pressure for Biofilm Formation in Bacillus subtilis: Differential Effect of Mutations in the Master Regulator SinR on Bistability. MBio, 2018, 9, .	4.1	21
29	Role of DNA Repair and Protective Components in Bacillus subtilis Spore Resistance to Inactivation by 400-nm-Wavelength Blue Light. Applied and Environmental Microbiology, 2018, 84, .	3.1	30
30	Control of potassium homeostasis is an essential function of the second messenger cyclic di-AMP in <i>Bacillus subtilis</i>. Science Signaling, 2017, 10, .	3.6	162
31	Vitamin B6 metabolism in microbes and approaches for fermentative production. Biotechnology Advances, 2017, 35, 31-40.	11.7	54
32	Hierarchical mutational events compensate for glutamate auxotrophy of a <scp><i>B</i></scp><i>acillus subtilis gltC</i> mutant. Environmental Microbiology Reports, 2017, 9, 279-289.	2.4	22
33	Large-scale reduction of the <i>Bacillus subtilis</i> genome: consequences for the transcriptional network, resource allocation, and metabolism. Genome Research, 2017, 27, 289-299.	5.5	137
34	The contribution of bacterial genome engineering to sustainable development. Microbial Biotechnology, 2017, 10, 1259-1263.	4.2	2
35	ThrR, a DNAâ€binding transcription factor involved in controlling threonine biosynthesis in <i>Bacillus subtilis</i>. Molecular Microbiology, 2016, 101, 879-893.	2.5	21
36	The Blueprint of a Minimal Cell: MiniBacillus. Microbiology and Molecular Biology Reviews, 2016, 80, 955-987.	6.6	54

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37	Saltâ€sensitivity of Ïƒ^H and Spo0A prevents sporulation of <scp><i>B</i></scp><i>acillus subtilis</i> at high osmolarity avoiding death during cellular differentiation. Molecular Microbiology, 2016, 100, 108-124.	2.5	25
38	Phenotypes Associated with the Essential Diadenylate Cyclase CdaA and Its Potential Regulator CdaR in the Human Pathogen Listeria monocytogenes. Journal of Bacteriology, 2016, 198, 416-426.	2.2	40
39	A jack of all trades: the multiple roles of the unique essential second messenger cyclic diâ€<scp>AMP</scp>. Molecular Microbiology, 2015, 97, 189-204.	2.5	121
40	Trigger Enzymes: Coordination of Metabolism and Virulence Gene Expression. Microbiology Spectrum, 2015, 3, .	3.0	34
41	Evidence for synergistic control of glutamate biosynthesis by glutamate dehydrogenases and glutamate in <scp><i>B</i></scp><i>acillus subtilis</i>. Environmental Microbiology, 2015, 17, 3379-3390.	3.8	35
42	Trigger Enzymes: Coordination of Metabolism and Virulence Gene Expression. , 2015, , 105-127.		1
43	Structural and Biochemical Analysis of the Essential Diadenylate Cyclase CdaA from Listeria monocytogenes. Journal of Biological Chemistry, 2015, 290, 6596-6606.	3.4	62
44	Engineering Bacillus subtilis for the conversion of the antimetabolite 4-hydroxy-l-threonine to pyridoxine. Metabolic Engineering, 2015, 29, 196-207.	7.0	40
45	A novel engineering tool in the Bacillus subtilis toolbox: inducer-free activation of gene expression by selection-driven promoter decryptification. Microbiology (United Kingdom), 2015, 161, 354-361.	1.8	8
46	<i>Bacillus subtilis</i>RecA and its accessory factors, RecF, RecO, RecR and RecX, are required for spore resistance to DNA double-strand break. Nucleic Acids Research, 2014, 42, 2295-2307.	14.5	33
47	Complex formation between malate dehydrogenase and isocitrate dehydrogenase from <i>BacillusÂsubtilis</i> is regulated by tricarboxylic acid cycle metabolites. FEBS Journal, 2014, 281, 1132-1143.	4.7	16
48	<i>Subti</i>Wikiâ€"a database for the model organism<i>Bacillus subtilis</i>that links pathway, interaction and expression information. Nucleic Acids Research, 2014, 42, D692-D698.	14.5	77
49	The Î³-Aminobutyrate Permease GabP Serves as the Third Proline Transporter of Bacillus subtilis. Journal of Bacteriology, 2014, 196, 515-526.	2.2	27
50	Bacillus subtilis and Escherichia coli essential genes and minimal cell factories after one decade of genome engineering. Microbiology (United Kingdom), 2014, 160, 2341-2351.	1.8	127
51	Overexpression of a non-native deoxyxylulose-dependent vitamin B6 pathway in Bacillus subtilis for the production of pyridoxine. Metabolic Engineering, 2014, 25, 38-49.	7.0	45
52	Monitoring Intraspecies Competition in a Bacterial Cell Population by Cocultivation of Fluorescently Labelled Strains. Journal of Visualized Experiments, 2014, , e51196.	0.3	5
53	Factors that mediate and prevent degradation of the inactive and unstable GudB protein in Bacillus subtilis. Frontiers in Microbiology, 2014, 5, 758.	3.5	13
54	Essential genes in Bacillus subtilis: a re-evaluation after ten years. Molecular BioSystems, 2013, 9, 1068.	2.9	95

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55	Selection-Driven Accumulation of Suppressor Mutants in Bacillus subtilis: The Apparent High Mutation Frequency of the Cryptic gudB Gene and the Rapid Clonal Expansion of gudB+ Suppressors Are Due to Growth under Selection. PLoS ONE, 2013, 8, e66120.	2.5	16
56	The resuscitation promotion concept extends to firmicutes. Microbiology (United Kingdom), 2013, 159, 1298-1300.	1.8	5
57	A Mystery Unraveled: Essentiality of RNase III in Bacillus subtilis Is Caused by Resident Prophages. PLoS Genetics, 2012, 8, e1003199.	3.5	6
58	A High-Frequency Mutation in Bacillus subtilis: Requirements for the Decryptification of the gudB Glutamate Dehydrogenase Gene. Journal of Bacteriology, 2012, 194, 1036-1044.	2.2	41
59	Control of glutamate homeostasis in <i>Bacillus subtilis</i>: a complex interplay between ammonium assimilation, glutamate biosynthesis and degradation. Molecular Microbiology, 2012, 85, 213-224.	2.5	127
60	Physical interactions between tricarboxylic acid cycle enzymes in Bacillus subtilis: Evidence for a metabolon. Metabolic Engineering, 2011, 13, 18-27.	7.0	94
61	RNase Y in Bacillus subtilis: a Natively Disordered Protein That Is the Functional Equivalent of RNase E from Escherichia coli. Journal of Bacteriology, 2011, 193, 5431-5441.	2.2	102
62	Functional Dissection of a Trigger Enzyme: Mutations of the Bacillus subtilis Glutamate Dehydrogenase RocG That Affect Differentially Its Catalytic Activity and Regulatory Properties. Journal of Molecular Biology, 2010, 400, 815-827.	4.2	41
63	In vitro Phosphorylation of Key Metabolic Enzymes from <i>Bacillus subtilis:</i> PrkC Phosphorylates Enzymes from Different Branches of Basic Metabolism. Journal of Molecular Microbiology and Biotechnology, 2010, 18, 129-140.	1.0	40
64	Novel Activities of Glycolytic Enzymes in Bacillus subtilis. Molecular and Cellular Proteomics, 2009, 8, 1350-1360.	3.8	221
65	Trigger enzymes: bifunctional proteins active in metabolism and in controlling gene expression. Molecular Microbiology, 2008, 67, 692-702.	2.5	116
66	Glutamate Metabolism in<i>Bacillus subtilis</i>: Gene Expression and Enzyme Activities Evolved To Avoid Futile Cycles and To Allow Rapid Responses to Perturbations of the System. Journal of Bacteriology, 2008, 190, 3557-3564.	2.2	90
67	Characterization of <i>Bacillus subtilis</i> Mutants with Carbon Source-Independent Glutamate Biosynthesis. Journal of Molecular Microbiology and Biotechnology, 2007, 12, 106-113.	1.0	29
68	SPINE: A method for the rapid detection and analysis of proteinâ€“protein interactions <i>in vivo</i>. Proteomics, 2007, 7, 4032-4035.	2.2	90
69	A regulatory proteinâ€“protein interaction governs glutamate biosynthesis in <i>Bacillus subtilis</i>: the glutamate dehydrogenase RocG moonlights in controlling the transcription factor GltC. Molecular Microbiology, 2007, 65, 642-654.	2.5	87
70	Regulatory links between carbon and nitrogen metabolism. Current Opinion in Microbiology, 2006, 9, 167-172.	5.1	171
71	Regulation of citB expression in Bacillus subtilis: integration of multiple metabolic signals in the citrate pool and by the general nitrogen regulatory system. Archives of Microbiology, 2006, 185, 136-146.	2.2	26
72	L-Proline Synthesis Mutants of Bacillus subtilis Overcome Osmotic Sensitivity by Genetically Adapting L-Arginine Metabolism. Frontiers in Microbiology, 0, 13, .	3.5	9