JÃ¶rg StÃ¼lke

List of Publications by Year
in descending order

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98 papers	7,885 citations	50276 46 h-index	56724 83 g-index
107 all docs	107 docs citations	107 times ranked	6611 citing authors

#	Article	IF	Citations
1	The current state of <i>Subti</i>Wiki, the database for the model organism <i>Bacillus subtilis</i>. Nucleic Acids Research, 2022, 50, D875-D882.	14.5	89
2	Sustained Control of Pyruvate Carboxylase by the Essential Second Messenger Cyclic di-AMP in Bacillus subtilis. MBio, 2022, , e0360221.	4.1	11
3	A Central Role for Magnesium Homeostasis during Adaptation to Osmotic Stress. MBio, 2022, 13, e0009222.	4.1	17
4	A meet-up of two second messengers: the c-di-AMP receptor DarB controls (p)ppGpp synthesis in Bacillus subtilis. Nature Communications, 2021, 12, 1210.	12.8	35
5	Influence of the ABC Transporter YtrBCDEF of Bacillus subtilis on Competence, Biofilm Formation and Cell Wall Thickness. Frontiers in Microbiology, 2021, 12, 587035.	3.5	11
6	Quasi-essentiality of RNase Y in<i>Bacillus subtilis</i>is caused by its critical role in the control of mRNA homeostasis. Nucleic Acids Research, 2021, 49, 7088-7102.	14.5	12
7	Functional Redundancy and Specialization of the Conserved Cold Shock Proteins in Bacillus subtilis. Microorganisms, 2021, 9, 1434.	3.6	7
8	Unchaining mini <i>Bacillus</i> Strain PG10: Relief of FlgM-Mediated Repression of Autolysin Genes. Applied and Environmental Microbiology, 2021, 87, e0112321.	3.1	5
9	Syn Wiki : Functional annotation of the first artificial organism Mycoplasma mycoides JCVIâ€syn3A. Protein Science, 2021, , .	7.6	8
10	The <i>Bacillus subtilis</i> Minimal Genome Compendium. ACS Synthetic Biology, 2021, 10, 2767-2771.	3.8	23
11	Essentiality of c-di-AMP in Bacillus subtilis: Bypassing mutations converge in potassium and glutamate homeostasis. PLoS Genetics, 2021, 17, e1009092.	3.5	28
12	Diurnal metabolic control in cyanobacteria requires perception of second messenger signaling molecule c-di-AMP by the carbon control protein SbtB. Science Advances, 2021, 7, eabk0568.	10.3	26
13	Comparison of Proteomic Responses as Global Approach to Antibiotic Mechanism of Action Elucidation. Antimicrobial Agents and Chemotherapy, 2020, 65, .	3.2	23
14	In-cell architecture of an actively transcribing-translating expressome. Science, 2020, 369, 554-557.	12.6	192
15	Resistance to serine in <i>Bacillus subtilis</i>: identification of the serine transporter <scp>YbeC</scp> and of a metabolic network that links serine and threonine metabolism. Environmental Microbiology, 2020, 22, 3937-3949.	3.8	16
16	Mini<i>Bacillus</i> PG10 as a Convenient and Effective Production Host for Lantibiotics. ACS Synthetic Biology, 2020, 9, 1833-1842.	3.8	30
17	Cyclic di-AMP Signaling in Bacteria. Annual Review of Microbiology, 2020, 74, 159-179.	7.3	106
18	Two Ways To Convert a Low-Affinity Potassium Channel to High Affinity: Control of <i>Bacillus subtilis</i> KtrCD by Glutamate. Journal of Bacteriology, 2020, 202, .	2.2	20

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19	Characterization of an Immunoglobulin Binding Protein (IbpM) From Mycoplasma pneumoniae. Frontiers in Microbiology, 2020, 11, 685.	3.5	17
20	Topoisomerase IV can functionally replace all type 1A topoisomerases in Bacillus subtilis. Nucleic Acids Research, 2019, 47, 5231-5242.	14.5	29
21	Determination of the Gene Regulatory Network of a Genome-Reduced Bacterium Highlights Alternative Regulation Independent of Transcription Factors. Cell Systems, 2019, 9, 143-158.e13.	6.2	36
22	Recent Advances and Current Trends in Nucleotide Second Messenger Signaling in Bacteria. Journal of Molecular Biology, 2019, 431, 908-927.	4.2	41
23	Sustained sensing in potassium homeostasis: Cyclic di-AMP controls potassium uptake by KimA at the levels of expression and activity. Journal of Biological Chemistry, 2019, 294, 9605-9614.	3.4	66
24	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
25	Editorial. Journal of Molecular Biology, 2019, 431, 4529.	4.2	0
26	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
27	Less Is More: Toward a Genome-Reduced <i>Bacillus</i> Cell Factory for â€œDifficult Proteinsâ€. ACS Synthetic Biology, 2019, 8, 99-108.	3.8	58
28	Perspective of ions and messengers: an intricate link between potassium, glutamate, and cyclic di-AMP. Current Genetics, 2018, 64, 191-195.	1.7	41
29	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
30	A Delicate Connection: c-di-AMP Affects Cell Integrity by Controlling Osmolyte Transport. Trends in Microbiology, 2018, 26, 175-185.	7.7	88
31	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
32	Genetic Engineering of Lactococcus lactis Co-producing Antigen and the Mucosal Adjuvant 3â€² 5â€²- cyclic di Adenosine Monophosphate (c-di-AMP) as a Design Strategy to Develop a Mucosal Vaccine Prototype. Frontiers in Microbiology, 2018, 9, 2100.	3.5	18
33	The DEAD-Box RNA Helicases of Bacillus subtilis as a Model to Evaluate Genetic Compensation Among Duplicate Genes. Frontiers in Microbiology, 2018, 9, 2261.	3.5	3
34	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
35	SubtiWiki in 2018: from genes and proteins to functional network annotation of the model organism Bacillus subtilis. Nucleic Acids Research, 2018, 46, D743-D748.	14.5	228
36	Development of a replicating plasmid based on the native oriC in Mycoplasma pneumoniae. Microbiology (United Kingdom), 2018, 164, 1372-1382.	1.8	6

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37	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
38	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
39	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
40	Identification of c-di-AMP-Binding Proteins Using Magnetic Beads. Methods in Molecular Biology, 2017, 1657, 347-359.	0.9	4
41	The contribution of bacterial genome engineering to sustainable development. Microbial Biotechnology, 2017, 10, 1259-1263.	4.2	2
42	Adaptation of <i>Bacillus subtilis</i> to Life at Extreme Potassium Limitation. MBio, 2017, 8, .	4.1	49
43	The Highly Conserved Asp23 Family Protein YqhY Plays a Role in Lipid Biosynthesis in Bacillus subtilis. Frontiers in Microbiology, 2017, 8, 883.	3.5	15
44	Identification of the Components Involved in Cyclic Di-AMP Signaling in Mycoplasma pneumoniae. Frontiers in Microbiology, 2017, 8, 1328.	3.5	42
45	Second Messenger Signaling in Bacillus subtilis: Accumulation of Cyclic di-AMP Inhibits Biofilm Formation. Frontiers in Microbiology, 2016, 7, 804.	3.5	61
46	Localization of Components of the RNA-Degrading Machine in Bacillus subtilis. Frontiers in Microbiology, 2016, 07, 1492.	3.5	40
47	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
48	Complete Genome Sequence of <i>Bacillus subtilis</i> subsp. <i>subtilis</i> Strain â^†6. Genome Announcements, 2016, 4, .	0.8	8
49	The Blueprint of a Minimal Cell: MiniBacillus. Microbiology and Molecular Biology Reviews, 2016, 80, 955-987.	6.6	54
50	<i>Subti</i>Wiki 2.0â€"an integrated database for the model organism<i>Bacillus subtilis</i>. Nucleic Acids Research, 2016, 44, D654-D662.	14.5	87
51	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
52	Minor Causeâ€"Major Effect: A Novel Mode of Control of Bistable Gene Expression. PLoS Genetics, 2015, 11, e1005229.	3.5	1
53	Identification, Characterization, and Structure Analysis of the Cyclic di-AMP-binding PII-like Signal Transduction Protein DarA. Journal of Biological Chemistry, 2015, 290, 3069-3080.	3.4	69
54	Structural and Biochemical Analysis of the Essential Diadenylate Cyclase CdaA from Listeria monocytogenes. Journal of Biological Chemistry, 2015, 290, 6596-6606.	3.4	62

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55	Defining a minimal cell: essentiality of small <scp>ORF</scp> s and nc <scp>RNA</scp> s in a genomeâ€reduced bacterium. Molecular Systems Biology, 2015, 11, 780.	7.2	133
56	An Essential Poison: Synthesis and Degradation of Cyclic Di-AMP in Bacillus subtilis. Journal of Bacteriology, 2015, 197, 3265-3274.	2.2	105
57	Impact of Hfq on the Bacillus subtilis Transcriptome. PLoS ONE, 2014, 9, e98661.	2.5	40
58	The protein tyrosine kinases EpsB and PtkA differentially affect biofilm formation in Bacillus subtilis. Microbiology (United Kingdom), 2014, 160, 682-691.	1.8	48
59	Mutational activation of the <scp>RocR</scp> activator and of a cryptic <scp><i>rocDEF</i></scp> promoter bypass loss of the initial steps of proline biosynthesis in <i><scp>B</scp>acillus subtilis</i>. Environmental Microbiology, 2014, 16, 701-717.	3.8	29
60	The YmdB Phosphodiesterase Is a Global Regulator of Late Adaptive Responses in Bacillus subtilis. Journal of Bacteriology, 2014, 196, 265-275.	2.2	69
61	Adaptation of <scp><i>B</i></scp><i>acillus subtilis</i> carbon core metabolism to simultaneous nutrient limitation and osmotic challenge: a multiâ€omics perspective. Environmental Microbiology, 2014, 16, 1898-1917.	3.8	83
62	<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
63	Control of the Diadenylate Cyclase CdaS in Bacillus subtilis. Journal of Biological Chemistry, 2014, 289, 21098-21107.	3.4	58
64	Phosphotransferase protein EIIANtr interacts with SpoT, a key enzyme of the stringent response, in Ralstonia eutropha H16. Microbiology (United Kingdom), 2014, 160, 711-722.	1.8	42
65	DEAD-Box RNA Helicases in Bacillus subtilis Have Multiple Functions and Act Independently from Each Other. Journal of Bacteriology, 2013, 195, 534-544.	2.2	69
66	Essential genes in Bacillus subtilis: a re-evaluation after ten years. Molecular BioSystems, 2013, 9, 1068.	2.9	95
67	Cyclic Di-AMP Homeostasis in Bacillus subtilis. Journal of Biological Chemistry, 2013, 288, 2004-2017.	3.4	181
68	Two Roles for Aconitase in the Regulation of Tricarboxylic Acid Branch Gene Expression in Bacillus subtilis. Journal of Bacteriology, 2013, 195, 1525-1537.	2.2	24
69	SubtiWiki--a comprehensive community resource for the model organism Bacillus subtilis. Nucleic Acids Research, 2012, 40, D1278-D1287.	14.5	77
70	Crossâ€talk between phosphorylation and lysine acetylation in a genomeâ€reduced bacterium. Molecular Systems Biology, 2012, 8, 571.	7.2	169
71	Condition-Dependent Transcriptome Reveals High-Level Regulatory Architecture in <i>Bacillus subtilis</i>. Science, 2012, 335, 1103-1106.	12.6	809
72	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

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73	RNA degradation in <i>Bacillus subtilis</i>: an interplay of essential endoâ€•and exoribonucleases. Molecular Microbiology, 2012, 84, 1005-1017.	2.5	97
74	RNA processing in <i>Bacillus subtilis</i>: identification of targets of the essential RNase Y. Molecular Microbiology, 2011, 81, 1459-1473.	2.5	89
75	SPABBATS: A pathway-discovery method based on Boolean satisfiability that facilitates the characterization of suppressor mutants. BMC Systems Biology, 2011, 5, 5.	3.0	19
76	Physical interactions between tricarboxylic acid cycle enzymes in Bacillus subtilis: Evidence for a metabolon. Metabolic Engineering, 2011, 13, 18-27.	7.0	94
77	A Novel Factor Controlling Bistability in Bacillus subtilis: the YmdB Protein Affects Flagellin Expression and Biofilm Formation. Journal of Bacteriology, 2011, 193, 5997-6007.	2.2	87
78	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
79	The RNA degradosome in <i>Bacillus subtilis</i>: identification of CshA as the major RNA helicase in the multiprotein complex. Molecular Microbiology, 2010, 77, 958-971.	2.5	129
80	Connecting parts with processes: SubtiWiki and SubtiPathways integrate gene and pathway annotation for Bacillus subtilis. Microbiology (United Kingdom), 2010, 156, 849-859.	1.8	41
81	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
82	A community-curated consensual annotation that is continuously updated: the Bacillus subtilis centred wiki SubtiWiki. Database: the Journal of Biological Databases and Curation, 2009, 2009, bap012-bap012.	3.0	35
83	Novel Activities of Glycolytic Enzymes in Bacillus subtilis. Molecular and Cellular Proteomics, 2009, 8, 1350-1360.	3.8	221
84	Carbon catabolite repression in bacteria: many ways to make the most out of nutrients. Nature Reviews Microbiology, 2008, 6, 613-624.	28.6	1,346
85	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
86	Transcriptional and Metabolic Responses of <i>Bacillus subtilis</i> to the Availability of Organic Acids: Transcription Regulation Is Important but Not Sufficient To Account for Metabolic Adaptation. Applied and Environmental Microbiology, 2007, 73, 499-507.	3.1	76
87	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
88	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
89	Keeping signals straight in transcription regulation: specificity determinants for the interaction of a family of conserved bacterial RNAâ€"protein couples. Nucleic Acids Research, 2006, 34, 6102-6115.	14.5	21
90	Multiple-Mutation Reaction: a Method for Simultaneous Introduction of Multiple Mutations into the<i>glpK</i>Gene of<i>Mycoplasma pneumoniae</i>. Applied and Environmental Microbiology, 2005, 71, 4097-4100.	3.1	48

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91	The RsbRST Stress Module in Bacteria: A Signalling System That May Interact with Different Output Modules. Journal of Molecular Microbiology and Biotechnology, 2005, 9, 65-76.	1.0	69
92	In Vivo Activity of Enzymatic and Regulatory Components of the Phosphoenolpyruvate:Sugar Phosphotransferase System in <i>Mycoplasma pneumoniae</i>. Journal of Bacteriology, 2004, 186, 7936-7943.	2.2	50
93	<i>Mycoplasma pneumoniae</i> HPr kinase/phosphorylase. FEBS Journal, 2004, 271, 367-374.	0.2	48
94	The regulatory link between carbon and nitrogen metabolism in Bacillus subtilis: regulation of the gltAB operon by the catabolite control protein CcpA. Microbiology (United Kingdom), 2003, 149, 3001-3009.	1.8	78
95	Expression of the glycolytic gapA operon in Bacillus subtilis: differential syntheses of proteins encoded by the operon. Microbiology (United Kingdom), 2003, 149, 751-761.	1.8	70
96	Ammonium utilization in Bacillus subtilis: transport and regulatory functions of NrgA and NrgB. Microbiology (United Kingdom), 2003, 149, 3289-3297.	1.8	93
97	The general stress protein Ctc of Bacillus subtilis is a ribosomal protein. Journal of Molecular Microbiology and Biotechnology, 2002, 4, 495-501.	1.0	42
98	Induction of the <i>Bacillus subtilis ptsGHI </i>operon by glucose is controlled by a novel antiterminator, GlcT. Molecular Microbiology, 1997, 25, 65-78.	2.5	163