

Dieter Jahn

List of Publications by Year in descending order

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232
papers

14,352
citations

20036

63
h-index

30277

107
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241
all docs

241
docs citations

241
times ranked

16001
citing authors

#	ARTICLE	IF	CITATIONS
1	PRODORIC: state-of-the-art database of prokaryotic gene regulation. <i>Nucleic Acids Research</i> , 2022, 50, D295-D302.	6.5	34
2	Cellular adaptation of <i>Clostridioides difficile</i> to high salinity encompasses a compatible solute-responsive change in cell morphology. <i>Environmental Microbiology</i> , 2022, 24, 1499-1517.	1.8	8
3	Radical SAM Enzymes Involved in Tetrapyrrole Biosynthesis and Insertion. <i>ACS Bio & Med Chem Au</i> , 2022, 2, 196-204.	1.7	5
4	Functionalization of an extended-gate field-effect transistor (EGFET) for bacteria detection. <i>Scientific Reports</i> , 2022, 12, 4397.	1.6	15
5	A Point Mutation in the Transcriptional Repressor PerR Results in a Constitutive Oxidative Stress Response in <i>Clostridioides difficile</i> 630 ¹ . <i>MSphere</i> , 2021, 6, .	1.3	6
6	Adaptation of <i>Dinoroseobacter shibae</i> to oxidative stress and the specific role of RirA. <i>PLoS ONE</i> , 2021, 16, e0248865.	1.1	2
7	Complexity of macrophage metabolism in infection. <i>Current Opinion in Biotechnology</i> , 2021, 68, 231-239.	3.3	37
8	What's a Biofilm? How the Choice of the Biofilm Model Impacts the Protein Inventory of <i>Clostridioides difficile</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 682111.	1.5	13
9	The "beauty in the beast" the multiple uses of <i>Priestia megaterium</i> in biotechnology. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 5719-5737.	1.7	42
10	Bioenergetics Theory and Components Heme Synthesis Three Ways. , 2021, , 74-88.		1
11	Influence of L-lactate and low glucose concentrations on the metabolism and the toxin formation of <i>Clostridioides difficile</i> . <i>PLoS ONE</i> , 2021, 16, e0244988.	1.1	13
12	BRENDA, the ELIXIR core data resource in 2021: new developments and updates. <i>Nucleic Acids Research</i> , 2021, 49, D498-D508.	6.5	347
13	The Influence of Genes on the "Killer Plasmid" of <i>Dinoroseobacter shibae</i> on Its Symbiosis With the Dinoflagellate <i>Prorocentrum minimum</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 804767.	1.5	8
14	Chimeric Interaction of Nitrogenase-Like Reductases with the MoFe Protein of Nitrogenase. <i>ChemBioChem</i> , 2020, 21, 1733-1741.	1.3	5
15	Involvement of Lactate and Pyruvate in the Anti-Inflammatory Effects Exerted by Voluntary Activation of the Sympathetic Nervous System. <i>Metabolites</i> , 2020, 10, 148.	1.3	17
16	RirA of <i>Dinoroseobacter shibae</i> senses iron via a [3Fe ^{4S}] ₁ cluster co-ordinated by three cysteine residues. <i>Biochemical Journal</i> , 2020, 477, 191-212.	1.7	8
17	Mg-protoporphyrin IX monomethyl ester cyclase from <i>Rhodobacter capsulatus</i> : radical SAM-dependent synthesis of the isocyclic ring of bacteriochlorophylls. <i>Biochemical Journal</i> , 2020, 477, 4635-4654.	1.7	3
18	Redefining the <i>Clostridioides difficile</i> "B" Regulon: "B" Activates Genes Involved in Detoxifying Radicals That Can Result from the Exposure to Antimicrobials and Hydrogen Peroxide. <i>MSphere</i> , 2020, 5, .	1.3	15

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19	Mikrobiologisches Wissen für alle bedeutet Klimaschutz!. BioSpektrum, 2019, 25, 595-595.	0.0	0
20	Crystal structures and protein engineering of three different penicillin G acylases from Gram-positive bacteria with different thermostability. Applied Microbiology and Biotechnology, 2019, 103, 7537-7552.	1.7	11
21	Pleiotropic Clostridioides difficile Cyclophilin PpiB Controls Cysteine-Tolerance, Toxin Production, the Central Metabolism and Multiple Stress Responses. Frontiers in Pharmacology, 2019, 10, 340.	1.6	7
22	Biosynthesis and Insertion of Heme. , 2019, , 201-228.		1
23	Metabolism the Difficile Way: The Key to the Success of the Pathogen Clostridioides difficile. Frontiers in Microbiology, 2019, 10, 219.	1.5	106
24	The urgent need for microbiology literacy in society. Environmental Microbiology, 2019, 21, 1513-1528.	1.8	99
25	Evolutionary model for the unequal segregation of high copy plasmids. PLoS Computational Biology, 2019, 15, e1006724.	1.5	9
26	Complete Genome Sequence of Raoultella electrica 1GB (DSM 102253 ^T), Isolated from Anodic Biofilms of a Glucose-Fed Microbial Fuel Cell. Microbiology Resource Announcements, 2019, 8, .	0.3	3
27	Structure Annotation of All Mass Spectra in Untargeted Metabolomics. Analytical Chemistry, 2019, 91, 2155-2162.	3.2	131
28	Virulence of Agrobacterium tumefaciens requires lipid homeostasis mediated by the lysylphosphatidylglycerol hydrolase AcvB. Molecular Microbiology, 2019, 111, 269-286.	1.2	14
29	The radical SAM protein HemW is a heme chaperone. Journal of Biological Chemistry, 2018, 293, 2558-2572.	1.6	32
30	A phosphatidic acid-binding protein is important for lipid homeostasis and adaptation to anaerobic biofilm conditions in Pseudomonas aeruginosa. Biochemical Journal, 2018, 475, 1885-1907.	1.7	15
31	Clostridioides difficile Activates Human Mucosal-Associated Invariant T Cells. Frontiers in Microbiology, 2018, 9, 2532.	1.5	11
32	Iron Regulation in Clostridioides difficile. Frontiers in Microbiology, 2018, 9, 3183.	1.5	49
33	PrsA2 (CD630_35000) of Clostridioides difficile Is an Active Parvulin-Type PPlase and a Virulence Modulator. Frontiers in Microbiology, 2018, 9, 2913.	1.5	13
34	Metabolic Reprogramming of Clostridioides difficile During the Stationary Phase With the Induction of Toxin Production. Frontiers in Microbiology, 2018, 9, 1970.	1.5	67
35	PRODORIC2: the bacterial gene regulation database in 2018. Nucleic Acids Research, 2018, 46, D320-D326.	6.5	32
36	Functional definition of the two effector binding sites, the oligomerization and DNA binding domains of the Bacillus subtilis LysR-type transcriptional regulator AlsR. Molecular Microbiology, 2018, 109, 845-864.	1.2	7

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37	Chemiosmotic Energy Conservation in <i>Dinoroseobacter shibae</i> : Proton Translocation Driven by Aerobic Respiration, Denitrification, and Photosynthetic Light Reaction. <i>Frontiers in Microbiology</i> , 2018, 9, 903.	1.5	7
38	Biosynthesis and Insertion of Heme. , 2018, , 1-28.		0
39	Prokaryotic Heme Biosynthesis: Multiple Pathways to a Common Essential Product. <i>Microbiology and Molecular Biology Reviews</i> , 2017, 81, .	2.9	236
40	High metabolic versatility of different toxigenic and non-toxigenic <i>Clostridioides difficile</i> isolates. <i>International Journal of Medical Microbiology</i> , 2017, 307, 311-320.	1.5	67
41	Protein complex formation during denitrification by <i>Pseudomonas aeruginosa</i> . <i>Microbial Biotechnology</i> , 2017, 10, 1523-1534.	2.0	43
42	Heme and nitric oxide binding by the transcriptional regulator DnrF from the marine bacterium <i>Dinoroseobacter shibae</i> increases napD promoter affinity. <i>Journal of Biological Chemistry</i> , 2017, 292, 15468-15480.	1.6	14
43	Comprehensive comparison of in silico MS/MS fragmentation tools of the CASMI contest: database boosting is needed to achieve 93% accuracy. <i>Journal of Cheminformatics</i> , 2017, 9, 32.	2.8	80
44	FnrL and Three Dnr Regulators Are Used for the Metabolic Adaptation to Low Oxygen Tension in <i>Dinoroseobacter shibae</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 642.	1.5	18
45	Gene Flow Across Genus Barriers – Conjugation of <i>Dinoroseobacter shibae</i> 's 191-kb Killer Plasmid into <i>Phaeobacter inhibens</i> and AHL-mediated Expression of Type IV Secretion Systems. <i>Frontiers in Microbiology</i> , 2016, 7, 742.	1.5	24
46	A Precise Temperature-Responsive Bistable Switch Controlling <i>Yersinia</i> Virulence. <i>PLoS Pathogens</i> , 2016, 12, e1006091.	2.1	24
47	Biosynthesis of Violacein, Structure and Function of L-Tryptophan Oxidase VioA from <i>Chromobacterium violaceum</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 20068-20084.	1.6	45
48	Complete genome sequence of the bioleaching bacterium <i>Leptospirillum</i> sp. group II strain CF-1. <i>Journal of Biotechnology</i> , 2016, 222, 21-22.	1.9	16
49	Protein Network of the <i>Pseudomonas aeruginosa</i> Denitrification Apparatus. <i>Journal of Bacteriology</i> , 2016, 198, 1401-1413.	1.0	60
50	Interatomic Characterization of Protein-Protein Interactions in Membrane-Associated Mega-complexes. <i>Springer Protocols</i> , 2015, , 103-124.	0.1	2
51	Genome Sequence of the Urethral Isolate <i>Pseudomonas aeruginosa</i> RN21. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
52	Acetate Dissimilation and Assimilation in <i>Mycobacterium tuberculosis</i> Depend on Carbon Availability. <i>Journal of Bacteriology</i> , 2015, 197, 3182-3190.	1.0	26
53	A Periplasmic Complex of the Nitrite Reductase NirS, the Chaperone DnaK, and the Flagellum Protein FliC Is Essential for Flagellum Assembly and Motility in <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2015, 197, 3066-3075.	1.0	24
54	Large-Scale ¹³ C Flux Profiling Reveals Conservation of the Entner-Doudoroff Pathway as a Glycolytic Strategy among Marine Bacteria That Use Glucose. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2408-2422.	1.4	73

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55	Genome Sequence of the Urethral Catheter Isolate <i>Pseudomonas aeruginosa</i> MH19. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
56	Comprehensive molecular, genomic and phenotypic analysis of a major clone of <i>Enterococcus faecalis</i> MLST ST40. <i>BMC Genomics</i> , 2015, 16, 175.	1.2	33
57	A Metaproteomics Approach to Elucidate Host and Pathogen Protein Expression during Catheter-Associated Urinary Tract Infections (CAUTIs). <i>Molecular and Cellular Proteomics</i> , 2015, 14, 989-1008.	2.5	63
58	Iron-Sulfur Cluster-dependent Catalysis of Chlorophyllide a Oxidoreductase from <i>Roseobacter denitrificans</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 1141-1154.	1.6	17
59	Polar Fixation of Plasmids during Recombinant Protein Production in <i>Bacillus megaterium</i> Results in Population Heterogeneity. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5976-5986.	1.4	26
60	Structures of two bacterial resistance factors mediating tRNA-dependent aminoacylation of phosphatidylglycerol with lysine or alanine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10691-10696.	3.3	36
61	Broadened Substrate Specificity of 3-Hydroxyethyl Bacteriochlorophyllide a Dehydrogenase (BchC) Indicates a New Route for the Biosynthesis of Bacteriochlorophyll a. <i>Journal of Biological Chemistry</i> , 2015, 290, 19697-19709.	1.6	13
62	Robustness and Plasticity of Metabolic Pathway Flux among Uropathogenic Isolates of <i>Pseudomonas aeruginosa</i> . <i>PLoS ONE</i> , 2014, 9, e88368.	1.1	60
63	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
64	Genome Sequence of the Acute Urethral Catheter Isolate <i>Pseudomonas aeruginosa</i> MH38. <i>Genome Announcements</i> , 2014, 2, .	0.8	5
65	Modelling and analysis of a gene-regulatory feed-forward loop with basal expression of the second regulator. <i>Journal of Theoretical Biology</i> , 2014, 363, 290-299.	0.8	5
66	<i>Leishmania major</i> possesses a unique HemG-type protoporphyrinogen IX oxidase. <i>Bioscience Reports</i> , 2014, 34, .	1.1	9
67	Production of medium chain length polyhydroxyalkanoate in metabolic flux optimized <i>Pseudomonas putida</i> . <i>Microbial Cell Factories</i> , 2014, 13, 88.	1.9	98
68	Gene Regulatory and Metabolic Adaptation Processes of <i>Dinoroseobacter shibae</i> DFL12T during Oxygen Depletion. <i>Journal of Biological Chemistry</i> , 2014, 289, 13219-13231.	1.6	25
69	Unstable Reaction Intermediates and Hysteresis during the Catalytic Cycle of 5-Aminolevulinate Synthase. <i>Journal of Biological Chemistry</i> , 2014, 289, 22915-22925.	1.6	20
70	Membrane Proteomics of <i>Pseudomonas aeruginosa</i> . <i>Methods in Molecular Biology</i> , 2014, 1149, 213-224.	0.4	5
71	Microbial communities related to volatile organic compound emission in automobile air conditioning units. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 8777-8793.	1.7	9
72	High yield production of extracellular recombinant levansucrase by <i>Bacillus megaterium</i> . <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 3343-3353.	1.7	36

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73	You are what you talk: quorum sensing induces individual morphologies and cell division modes in <i>Dinoroseobacter shibae</i> . ISME Journal, 2013, 7, 2274-2286.	4.4	74
74	From gene to product. Journal of Biotechnology, 2013, 163, 85-86.	1.9	0
75	Construction and characterization of nitrate and nitrite respiring <i>Pseudomonas putida</i> KT2440 strains for anoxic biotechnical applications. Journal of Biotechnology, 2013, 163, 155-165.	1.9	26
76	Getting the big beast to work – Systems biotechnology of <i>Bacillus megaterium</i> for novel high-value proteins. Journal of Biotechnology, 2013, 163, 87-96.	1.9	47
77	Aminolaevulinic acid synthase of <i>Rhodobacter capsulatus</i> : high-resolution kinetic investigation of the structural basis for substrate binding and catalysis. Biochemical Journal, 2013, 451, 205-216.	1.7	19
78	Structure of ADP-aluminium fluoride-stabilized protochlorophyllide oxidoreductase complex. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2094-2098.	3.3	56
79	Purification, crystallization and preliminary X-ray analysis of the effector domain of AlsR, an LysR-type transcriptional regulator from <i>Bacillus subtilis</i> . Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 581-584.	0.7	3
80	Transposon Mutagenesis Identified Chromosomal and Plasmid Genes Essential for Adaptation of the Marine Bacterium <i>Dinoroseobacter shibae</i> to Anaerobic Conditions. Journal of Bacteriology, 2013, 195, 4769-4777.	1.0	26
81	Regulatory and Metabolic Networks for the Adaptation of <i>Pseudomonas aeruginosa</i> Biofilms to Urinary Tract-Like Conditions. PLoS ONE, 2013, 8, e71845.	1.1	36
82	TLM-Tracker: software for cell segmentation, tracking and lineage analysis in time-lapse microscopy movies. Bioinformatics, 2012, 28, 2276-2277.	1.8	42
83	The Transcription Factor AlsR Binds and Regulates the Promoter of the alsSD Operon Responsible for Acetoin Formation in <i>Bacillus subtilis</i> . Journal of Bacteriology, 2012, 194, 1100-1112.	1.0	48
84	InFiRe – a novel computational method for the identification of insertion sites in transposon mutagenized bacterial genomes. Bioinformatics, 2012, 28, 306-310.	1.8	2
85	<i>Lactococcus lactis</i> HemW (HemN) is a haem-binding protein with a putative role in haem trafficking. Biochemical Journal, 2012, 442, 335-343.	1.7	27
86	Regulation of the Anaerobic Metabolism in <i>Bacillus subtilis</i> . Advances in Microbial Physiology, 2012, 61, 195-216.	1.0	70
87	Systems Biology of Recombinant Protein Production Using <i>Bacillus megaterium</i> . Methods in Enzymology, 2011, 500, 165-195.	0.4	60
88	Cellular levels of heme affect the activity of dimeric glutamyl-tRNA reductase. Biochemical and Biophysical Research Communications, 2011, 405, 134-139.	1.0	13
89	Genotypic and phenotypic characterization of <i>Pseudomonas aeruginosa</i> isolates from urinary tract infections. International Journal of Medical Microbiology, 2011, 301, 282-292.	1.5	43
90	Transcriptome profiling of degU expression reveals unexpected regulatory patterns in <i>Bacillus megaterium</i> and discloses new targets for optimizing expression. Applied Microbiology and Biotechnology, 2011, 92, 583-596.	1.7	8

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91	Genome Sequences of the Biotechnologically Important <i>Bacillus megaterium</i> Strains QM B1551 and DSM319. <i>Journal of Bacteriology</i> , 2011, 193, 4199-4213.	1.0	155
92	GeneReporter™ sequence-based document retrieval and annotation. <i>Bioinformatics</i> , 2011, 27, 1034-1035.	1.8	5
93	Aspartate 141 Is the Fourth Ligand of the Oxygen-sensing [4Fe-4S] ²⁺ Cluster of <i>Bacillus subtilis</i> Transcriptional Regulator Fnr. <i>Journal of Biological Chemistry</i> , 2011, 286, 2017-2021.	1.6	38
94	Polysaccharide Synthesis of the Levansucrase SacB from <i>Bacillus megaterium</i> Is Controlled by Distinct Surface Motifs. <i>Journal of Biological Chemistry</i> , 2011, 286, 17593-17600.	1.6	86
95	Anaerobic adaptation in <i>Pseudomonas aeruginosa</i> : definition of the Anr and Dnr regulons. <i>Environmental Microbiology</i> , 2010, 12, 1719-1733.	1.8	153
96	Systems Biology of Recombinant Protein Production in <i>Bacillus megaterium</i> . , 2010, 120, 133-161.		9
97	Application of <i>Escherichia coli</i> phage K1E DNA-dependent RNA polymerase for in vitro RNA synthesis and in vivo protein production in <i>Bacillus megaterium</i> . <i>Applied Microbiology and Biotechnology</i> , 2010, 88, 529-539.	1.7	6
98	Characterization of JG024, a <i>Pseudomonas aeruginosa</i> PB1-like broad host range phage under simulated infection conditions. <i>BMC Microbiology</i> , 2010, 10, 301.	1.3	81
99	Metabolic engineering of cobalamin (vitamin B ₁₂) production in <i>Bacillus megaterium</i> . <i>Microbial Biotechnology</i> , 2010, 3, 24-37.	2.0	75
100	Structures of the nucleotide-binding domain of the human ABCB6 transporter and its complexes with nucleotides. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 979-987.	2.5	12
101	Structure and function of enzymes in heme biosynthesis. <i>Protein Science</i> , 2010, 19, 1137-1161.	3.1	264
102	Lipase LipC affects motility, biofilm formation and rhamnolipid production in <i>Pseudomonas aeruginosa</i> . <i>FEMS Microbiology Letters</i> , 2010, 309, no-no.	0.7	35
103	The complete genome sequence of the algal symbiont <i>Dinoroseobacter shibae</i> : a hitchhiker's guide to life in the sea. <i>ISME Journal</i> , 2010, 4, 61-77.	4.4	244
104	A Novel Pathway for the Biosynthesis of Heme in <i>Archaea</i> : Genome-Based Bioinformatic Predictions and Experimental Evidence. <i>Archaea</i> , 2010, 2010, 1-15.	2.3	56
105	Biosynthesis of (Bacterio)chlorophylls. <i>Journal of Biological Chemistry</i> , 2010, 285, 8268-8277.	1.6	24
106	Structure of the Heme Biosynthetic <i>Pseudomonas aeruginosa</i> Porphobilinogen Synthase in Complex with the Antibiotic Alaremycin. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 267-272.	1.4	11
107	High-Yield Intra- and Extracellular Protein Production Using <i>Bacillus megaterium</i> . <i>Applied and Environmental Microbiology</i> , 2010, 76, 4037-4046.	1.4	87
108	Crystal Structure of the Nitrogenase-like Dark Operative Protochlorophyllide Oxidoreductase Catalytic Complex (ChlN/ChlB) ₂ . <i>Journal of Biological Chemistry</i> , 2010, 285, 27336-27345.	1.6	78

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109	Heme biosynthesis is coupled to electron transport chains for energy generation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10436-10441.	3.3	95
110	A short story about a big magic bug. Bioengineered Bugs, 2010, 1, 85-91.	2.0	53
111	Biosynthesis of Heme and Vitamin B12. , 2010, , 445-499.		5
112	A Tale of Two Acids: When Arginine Is a More Appropriate Acid than H3O+. Journal of Physical Chemistry B, 2010, 114, 8994-9001.	1.2	17
113	Anaerobic physiology of Pseudomonas aeruginosa in the cystic fibrosis lung. International Journal of Medical Microbiology, 2010, 300, 549-556.	1.5	148
114	Protochlorophyllide: a new photosensitizer for the photodynamic inactivation of Gram-positive and Gram-negative bacteria. FEMS Microbiology Letters, 2009, 290, 156-163.	0.7	32
115	Chimeric Nitrogenase-like Enzymes of (Bacterio)chlorophyll Biosynthesis. Journal of Biological Chemistry, 2009, 284, 15530-15540.	1.6	44
116	An Emergent Self-Organizing Map Based Analysis Pipeline for Comparative Metabolome Studies. In Silico Biology, 2009, 9, 163-178.	0.4	16
117	Strepto-DB, a database for comparative genomics of group A (GAS) and B (GBS) streptococci, implemented with the novel database platform "Open Genome Resource"™ (OGeR). Nucleic Acids Research, 2009, 37, D494-D498.	6.5	4
118	PRODORIC (release 2009): a database and tool platform for the analysis of gene regulation in prokaryotes. Nucleic Acids Research, 2009, 37, D61-D65.	6.5	83
119	Genetic tools for the investigation of Roseobacter clade bacteria. BMC Microbiology, 2009, 9, 265.	1.3	47
120	Directed optimization of biocatalytic transglycosylation processes by the integration of genetic algorithms and fermentative approaches into a kinetic model. Process Biochemistry, 2009, 44, 1103-1114.	1.8	2
121	A T7 RNA polymerase-dependent gene expression system for Bacillus megaterium. Applied Microbiology and Biotechnology, 2009, 82, 1195-1203.	1.7	49
122	Biosynthesis of 5-Aminolevulinic Acid. , 2009, , 29-42.		10
123	An emergent self-organizing map based analysis pipeline for comparative metabolome studies. In Silico Biology, 2009, 9, 163-78.	0.4	3
124	The biochemistry of heme biosynthesis. Archives of Biochemistry and Biophysics, 2008, 474, 238-251.	1.4	269
125	Complex formation between protoporphyrinogen IX oxidase and ferrochelatase during haem biosynthesis in Thermosynechococcus elongatus. Microbiology (United Kingdom), 2008, 154, 3707-3714.	0.7	33
126	Nitrate-responsive NarX-NarL represses arginine-mediated induction of the Pseudomonas aeruginosa arginine fermentation arcDABC operon. Microbiology (United Kingdom), 2008, 154, 3053-3060.	0.7	41

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127	Substrate Recognition of Nitrogenase-like Dark Operative Protochlorophyllide Oxidoreductase from <i>Prochlorococcus marinus</i> . <i>Journal of Biological Chemistry</i> , 2008, 283, 29873-29881.	1.6	30
128	ProdoNet: identification and visualization of prokaryotic gene regulatory and metabolic networks. <i>Nucleic Acids Research</i> , 2008, 36, W460-W464.	6.5	15
129	ATP-driven Reduction by Dark-operative Protochlorophyllide Oxidoreductase from <i>Chlorobium tepidum</i> Mechanistically Resembles Nitrogenase Catalysis. <i>Journal of Biological Chemistry</i> , 2008, 283, 10559-10567.	1.6	57
130	Identification and characterization of the <i>Arabidopsis</i> gene encoding the tetrapyrrole biosynthesis enzyme uroporphyrinogen III synthase. <i>Biochemical Journal</i> , 2008, 410, 291-299.	1.7	14
131	ROSY—a flexible and universal database and bioinformatics tool platform for <i>Roseobacter</i> related species. <i>In Silico Biology</i> , 2008, 8, 177-86.	0.4	3
132	The Anaerobic Regulatory Network Required for <i>Pseudomonas aeruginosa</i> Nitrate Respiration. <i>Journal of Bacteriology</i> , 2007, 189, 4310-4314.	1.0	139
133	SYSTEMONAS – an integrated database for systems biology analysis of <i>Pseudomonas</i> . <i>Nucleic Acids Research</i> , 2007, 35, D533-D537.	6.5	50
134	Functional definition of the tobacco protoporphyrinogen IX oxidase substrate-binding site. <i>Biochemical Journal</i> , 2007, 402, 575-580.	1.7	44
135	A sucrose-inducible promoter system for the intra- and extracellular protein production in <i>Bacillus megaterium</i> . <i>Journal of Biotechnology</i> , 2007, 132, 426-430.	1.9	50
136	Effect of different carbon sources on central metabolic fluxes and the recombinant production of a hydrolase from <i>Thermobifida fusca</i> in <i>Bacillus megaterium</i> . <i>Journal of Biotechnology</i> , 2007, 132, 385-394.	1.9	40
137	Mechanism of a GatCAB Amidotransferase: Aspartyl-tRNA Synthetase Increases Its Affinity for Asp-tRNA ^{Asn} and Novel Aminoacyl-tRNA Analogues Are Competitive Inhibitors. <i>Biochemistry</i> , 2007, 46, 13190-13198.	1.2	33
138	Insights into polymer versus oligosaccharide synthesis: mutagenesis and mechanistic studies of a novel levansucrase from <i>Bacillus megaterium</i> . <i>Biochemical Journal</i> , 2007, 407, 189-198.	1.7	115
139	Production of recombinant antibody fragments in <i>Bacillus megaterium</i> . <i>Microbial Cell Factories</i> , 2007, 6, 2.	1.9	44
140	Einladung zum Wissenschaftsforum in Ulm. <i>Chemie in Unserer Zeit</i> , 2007, 41, 71-71.	0.1	0
141	Plasmid system for the intracellular production and purification of affinity-tagged proteins in <i>Bacillus megaterium</i> . <i>Biotechnology and Bioengineering</i> , 2007, 96, 525-537.	1.7	58
142	Codon optimized <i>Thermobifida fusca</i> hydrolase secreted by <i>Bacillus megaterium</i> . <i>Biotechnology and Bioengineering</i> , 2007, 96, 780-794.	1.7	55
143	Glutamate recognition and hydride transfer by <i>Escherichia coli</i> glutamyl-tRNA reductase. <i>FEBS Journal</i> , 2007, 274, 4609-4614.	2.2	14
144	D-Mannitol production by resting state whole cell biotransformation of D-fructose by heterologous mannitol and formate dehydrogenase gene expression in <i>Bacillus megaterium</i> . <i>Biotechnology Journal</i> , 2007, 2, 1408-1416.	1.8	41

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