

# Dieter Jahn

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4342054/publications.pdf>

Version: 2024-02-01

232  
papers

14,352  
citations

17440

63  
h-index

26613

107  
g-index

241  
all docs

241  
docs citations

241  
times ranked

14446  
citing authors

#	ARTICLE	IF	CITATIONS
1	JCat: a novel tool to adapt codon usage of a target gene to its potential expression host. <i>Nucleic Acids Research</i> , 2005, 33, W526-W531.	14.5	1,009
2	Microbial production of vitamin B 12. <i>Applied Microbiology and Biotechnology</i> , 2002, 58, 275-285.	3.6	555
3	RNA-Dependent Cysteine Biosynthesis in Archaea. <i>Science</i> , 2005, 307, 1969-1972.	12.6	468
4	PrediSi: prediction of signal peptides and their cleavage positions. <i>Nucleic Acids Research</i> , 2004, 32, W375-W379.	14.5	432
5	BRENDA, the ELIXIR core data resource in 2021: new developments and updates. <i>Nucleic Acids Research</i> , 2021, 49, D498-D508.	14.5	347
6	Virtual Footprint and PRODORIC: an integrative framework for regulon prediction in prokaryotes. <i>Bioinformatics</i> , 2005, 21, 4187-4189.	4.1	341
7	The biochemistry of heme biosynthesis. <i>Archives of Biochemistry and Biophysics</i> , 2008, 474, 238-251.	3.0	269
8	Structure and function of enzymes in heme biosynthesis. <i>Protein Science</i> , 2010, 19, 1137-1161.	7.6	264
9	Crystal structure of coproporphyrinogen III oxidase reveals cofactor geometry of Radical SAM enzymes. <i>EMBO Journal</i> , 2003, 22, 6214-6224.	7.8	259
10	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.	9.8	244
11	Prokaryotic Heme Biosynthesis: Multiple Pathways to a Common Essential Product. <i>Microbiology and Molecular Biology Reviews</i> , 2017, 81, .	6.6	236
12	Long-Term Anaerobic Survival of the Opportunistic Pathogen <i>Pseudomonas aeruginosa</i> via Pyruvate Fermentation. <i>Journal of Bacteriology</i> , 2004, 186, 4596-4604.	2.2	223
13	PRODORIC: prokaryotic database of gene regulation. <i>Nucleic Acids Research</i> , 2003, 31, 266-269.	14.5	220
14	Fermentative Metabolism of <i>Bacillus subtilis</i> : Physiology and Regulation of Gene Expression. <i>Journal of Bacteriology</i> , 2000, 182, 3072-3080.	2.2	219
15	<i>Bacillus megaterium</i> from simple soil bacterium to industrial protein production host. <i>Applied Microbiology and Biotechnology</i> , 2007, 76, 957-967.	3.6	215
16	Glutamyl-transfer RNA: a precursor of heme and chlorophyll biosynthesis. <i>Trends in Biochemical Sciences</i> , 1992, 17, 215-218.	7.5	199
17	Crystal structure of 5-aminolevulinatase synthase, the first enzyme of heme biosynthesis, and its link to XLSA in humans. <i>EMBO Journal</i> , 2005, 24, 3166-3177.	7.8	193
18	<i>Nanoarchaeum equitans</i> creates functional tRNAs from separate genes for their 5' and 3'-halves. <i>Nature</i> , 2005, 433, 537-541.	27.8	192

#	ARTICLE	IF	CITATIONS
19	Genome Sequences of the Biotechnologically Important <i>Bacillus megaterium</i> Strains QM B1551 and DSM319. <i>Journal of Bacteriology</i> , 2011, 193, 4199-4213.	2.2	155
20	Anaerobic adaptation in <i>Pseudomonas aeruginosa</i> : definition of the Anr and Dnr regulons. <i>Environmental Microbiology</i> , 2010, 12, 1719-1733.	3.8	153
21	Anaerobic physiology of <i>Pseudomonas aeruginosa</i> in the cystic fibrosis lung. <i>International Journal of Medical Microbiology</i> , 2010, 300, 549-556.	3.6	148
22	The Anaerobic Regulatory Network Required for <i>Pseudomonas aeruginosa</i> Nitrate Respiration. <i>Journal of Bacteriology</i> , 2007, 189, 4310-4314.	2.2	139
23	Oxygen-independent Coproporphyrinogen-III Oxidase HemN from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 34136-34142.	3.4	137
24	Structure Annotation of All Mass Spectra in Untargeted Metabolomics. <i>Analytical Chemistry</i> , 2019, 91, 2155-2162.	6.5	131
25	Nitrogen and Oxygen Regulation of <i>Bacillus subtilis</i> nasDEF Encoding NADH-Dependent Nitrite Reductase by TnrA and ResDE. <i>Journal of Bacteriology</i> , 1998, 180, 5344-5350.	2.2	128
26	The anaerobic life of <i>Bacillus subtilis</i> : Cloning of the genes encoding the respiratory nitrate reductase system. <i>FEMS Microbiology Letters</i> , 1995, 131, 219-225.	1.8	120
27	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.	3.7	115
28	V-shaped structure of glutamyl-tRNA reductase, the first enzyme of tRNA-dependent tetrapyrrole biosynthesis. <i>EMBO Journal</i> , 2001, 20, 6583-6590.	7.8	114
29	Metabolism the Difficile Way: The Key to the Success of the Pathogen <i>Clostridioides difficile</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 219.	3.5	106
30	The urgent need for microbiology literacy in society. <i>Environmental Microbiology</i> , 2019, 21, 1513-1528.	3.8	99
31	Production of medium chain length polyhydroxyalkanoate in metabolic flux optimized <i>Pseudomonas putida</i> . <i>Microbial Cell Factories</i> , 2014, 13, 88.	4.0	98
32	Structure and function of radical SAM enzymes. <i>Current Opinion in Chemical Biology</i> , 2004, 8, 468-476.	6.1	97
33	Heme biosynthesis is coupled to electron transport chains for energy generation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10436-10441.	7.1	95
34	Identification and functional analysis of enzymes required for precorrin-2 dehydrogenation and metal ion insertion in the biosynthesis of sirohaem and cobalamin in <i>Bacillus megaterium</i> . <i>Biochemical Journal</i> , 2003, 370, 505-516.	3.7	93
35	High resolution crystal structure of a Mg <sup>2+</sup> -dependent porphobilinogen synthase. <i>Journal of Molecular Biology</i> , 1999, 289, 591-602.	4.2	88
36	Characterization of a New Type of Phosphopantetheinyl Transferase for Fatty Acid and Siderophore Synthesis in <i>Pseudomonas aeruginosa</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 50293-50302.	3.4	88

#	ARTICLE	IF	CITATIONS
37	Bacterial heme biosynthesis and its biotechnological application. <i>Applied Microbiology and Biotechnology</i> , 2003, 63, 115-127.	3.6	87
38	High-Yield Intra- and Extracellular Protein Production Using <i>Bacillus megaterium</i> . <i>Applied and Environmental Microbiology</i> , 2010, 76, 4037-4046.	3.1	87
39	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.	3.4	86
40	Production and secretion of recombinant <i>Leuconostoc mesenteroides</i> dextran sucrose DsrS in <i>Bacillus megaterium</i> . <i>Biotechnology and Bioengineering</i> , 2005, 89, 206-218.	3.3	83
41	PRODORIC (release 2009): a database and tool platform for the analysis of gene regulation in prokaryotes. <i>Nucleic Acids Research</i> , 2009, 37, D61-D65.	14.5	83
42	Radical S-Adenosylmethionine Enzyme Coproporphyrinogen III Oxidase HemN. <i>Journal of Biological Chemistry</i> , 2005, 280, 29038-29046.	3.4	81
43	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.	3.3	81
44	Regulation of <i>Pseudomonas aeruginosa</i> hemF and hemN by the dual action of the redox response regulators Anr and Dnr. <i>Molecular Microbiology</i> , 1998, 29, 985-997.	2.5	80
45	The Fnr Regulon of <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2006, 188, 1103-1112.	2.2	80
46	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.	6.1	80
47	The <i>Escherichia coli</i> hemL gene encodes glutamate 1-semialdehyde aminotransferase. <i>Journal of Bacteriology</i> , 1991, 173, 3408-3413.	2.2	78
48	Crystal Structure of the Nitrogenase-like Dark Operative Protochlorophyllide Oxidoreductase Catalytic Complex (ChlN/ChlB) <sub>2</sub> . <i>Journal of Biological Chemistry</i> , 2010, 285, 27336-27345.	3.4	78
49	Cloning and characterization of the <i>Escherichia coli</i> hemN gene encoding the oxygen-independent coproporphyrinogen III oxidase. <i>Journal of Bacteriology</i> , 1995, 177, 3326-3331.	2.2	77
50	Isolation of the hemF operon containing the gene for the <i>Escherichia coli</i> aerobic coproporphyrinogen III oxidase by in vivo complementation of a yeast HEM13 mutant. <i>Journal of Bacteriology</i> , 1994, 176, 673-680.	2.2	75
51	Ammonification in <i>Bacillus subtilis</i> Utilizing Dissimilatory Nitrite Reductase Is Dependent on resDE. <i>Journal of Bacteriology</i> , 1998, 180, 186-189.	2.2	75
52	Metabolic engineering of cobalamin (vitamin B <sub>12</sub> ) production in <i>Bacillus megaterium</i> . <i>Microbial Biotechnology</i> , 2010, 3, 24-37.	4.2	75
53	You are what you talk: quorum sensing induces individual morphologies and cell division modes in <i>Dinoroseobacter shibae</i> . <i>ISME Journal</i> , 2013, 7, 2274-2286.	9.8	74
54	The Substrate Radical of <i>Escherichia coli</i> Oxygen-independent Coproporphyrinogen III Oxidase HemN. <i>Journal of Biological Chemistry</i> , 2006, 281, 15727-15734.	3.4	73

#	ARTICLE	IF	CITATIONS
55	Large-Scale <sup>13</sup> 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.	3.1	73
56	Oxygen-dependent Coproporphyrinogen III Oxidase (HemF) from <i>Escherichia coli</i> Is Stimulated by Manganese. <i>Journal of Biological Chemistry</i> , 2003, 278, 46625-46631.	3.4	71
57	Complex Formation between Glutamyl-tRNA Reductase and Glutamate-1-semialdehyde 2,1-Aminomutase in <i>Escherichia coli</i> during the Initial Reactions of Porphyrin Biosynthesis. <i>Journal of Biological Chemistry</i> , 2005, 280, 18568-18572.	3.4	70
58	Regulation of the Anaerobic Metabolism in <i>Bacillus subtilis</i> . <i>Advances in Microbial Physiology</i> , 2012, 61, 195-216.	2.4	70
59	Members of the genus <i>Arthrobacter</i> grow anaerobically using nitrate ammonification and fermentative processes: anaerobic adaptation of aerobic bacteria abundant in soil. <i>FEMS Microbiology Letters</i> , 2003, 223, 227-230.	1.8	69
60	Purification of human transcription factor III C and its binding to the gene for ribosomal 5S RNA. <i>Nucleic Acids Research</i> , 1989, 17, 5003-5016.	14.5	68
61	MetaQuant: a tool for the automatic quantification of GC/MS-based metabolome data. <i>Bioinformatics</i> , 2006, 22, 2962-2965.	4.1	67
62	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.	3.6	67
63	Metabolic Reprogramming of <i>Clostridioides difficile</i> During the Stationary Phase With the Induction of Toxin Production. <i>Frontiers in Microbiology</i> , 2018, 9, 1970.	3.5	67
64	Transcription complexes for various class III genes differ in parameters of formation and stability towards salt. <i>Journal of Molecular Biology</i> , 1987, 193, 303-313.	4.2	66
65	JVirGel: calculation of virtual two-dimensional protein gels. <i>Nucleic Acids Research</i> , 2003, 31, 3862-3865.	14.5	64
66	<i>Methanopyrus kandleri</i> Glutamyl-tRNA Reductase. <i>Journal of Biological Chemistry</i> , 1999, 274, 30679-30685.	3.4	63
67	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.	3.8	63
68	Activity and spectroscopic properties of the <i>Escherichia coli</i> glutamate 1-semialdehyde aminotransferase and the putative active site mutant K265R. <i>Biochemistry</i> , 1992, 31, 7143-7151.	2.5	61
69	High yield recombinant penicillin G amidase production and export into the growth medium using <i>Bacillus megaterium</i> . <i>Microbial Cell Factories</i> , 2006, 5, 36.	4.0	60
70	Systems Biology of Recombinant Protein Production Using <i>Bacillus megaterium</i> . <i>Methods in Enzymology</i> , 2011, 500, 165-195.	1.0	60
71	Robustness and Plasticity of Metabolic Pathway Flux among Uropathogenic Isolates of <i>Pseudomonas aeruginosa</i> . <i>PLoS ONE</i> , 2014, 9, e88368.	2.5	60
72	Protein Network of the <i>Pseudomonas aeruginosa</i> Denitrification Apparatus. <i>Journal of Bacteriology</i> , 2016, 198, 1401-1413.	2.2	60

#	ARTICLE	IF	CITATIONS
73	Testosterone-regulated expression of enzymes involved in steroid and aromatic hydrocarbon catabolism in <i>Comamonas testosteroni</i> . <i>Journal of Bacteriology</i> , 1997, 179, 5951-5955.	2.2	58
74	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.	3.3	58
75	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.	3.4	57
76	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
77	Structure of ADP-aluminium fluoride-stabilized protochlorophyllide oxidoreductase complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2094-2098.	7.1	56
78	<i>Escherichia coli</i> Glutamyl-tRNA Reductase. <i>Journal of Biological Chemistry</i> , 2002, 277, 48657-48663.	3.4	55
79	Codon optimized <i>Thermobifida fusca</i> hydrolase secreted by <i>Bacillus megaterium</i> . <i>Biotechnology and Bioengineering</i> , 2007, 96, 780-794.	3.3	55
80	Structure of Porphobilinogen Synthase from <i>Pseudomonas aeruginosa</i> in Complex with 5-Fluorolevulinic Acid Suggests a Double Schiff Base Mechanism. <i>Journal of Molecular Biology</i> , 2002, 320, 237-247.	4.2	54
81	<i>Bacillus subtilis</i> Fnr senses oxygen via a [4Fe-4S] cluster coordinated by three cysteine residues without change in the oligomeric state. <i>Molecular Microbiology</i> , 2006, 60, 1432-1445.	2.5	54
82	A short story about a big magic bug. <i>Bioengineered Bugs</i> , 2010, 1, 85-91.	1.7	53
83	Complex formation between glutamyl-tRNA synthetase and glutamyl-tRNA reductase during the tRNA-dependent synthesis of 5-aminolevulinic acid in <i>Chlamydomonas reinhardtii</i> . <i>FEBS Letters</i> , 1992, 314, 77-80.	2.8	50
84	A <i>Bacillus megaterium</i> Plasmid System for the Production, Export, and One-Step Purification of Affinity-Tagged Heterologous Levansucrase from Growth Medium. <i>Applied and Environmental Microbiology</i> , 2006, 72, 1677-1679.	3.1	50
85	Crystal Structure of a Non-discriminating Glutamyl-tRNA Synthetase. <i>Journal of Molecular Biology</i> , 2006, 361, 888-897.	4.2	50
86	SYSTEMONAS -- an integrated database for systems biology analysis of <i>Pseudomonas</i> . <i>Nucleic Acids Research</i> , 2007, 35, D533-D537.	14.5	50
87	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.	3.8	50
88	Characterization of the Cobaltochelate CbiXL. <i>Journal of Biological Chemistry</i> , 2003, 278, 41900-41907.	3.4	49
89	A T7 RNA polymerase-dependent gene expression system for <i>Bacillus megaterium</i> . <i>Applied Microbiology and Biotechnology</i> , 2009, 82, 1195-1203.	3.6	49
90	Iron Regulation in <i>Clostridioides difficile</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 3183.	3.5	49

#	ARTICLE	IF	CITATIONS
91	The Transcription Factor AlsR Binds and Regulates the Promoter of the alsSD Operon Responsible for Acetoin Formation in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2012, 194, 1100-1112.	2.2	48
92	Structural and functional comparison of HemN to other radical SAM enzymes. <i>Biological Chemistry</i> , 2005, 386, 971-80.	2.5	47
93	Genetic tools for the investigation of <i>Roseobacter</i> clade bacteria. <i>BMC Microbiology</i> , 2009, 9, 265.	3.3	47
94	Getting the big beast to work – Systems biotechnology of <i>Bacillus megaterium</i> for novel high-value proteins. <i>Journal of Biotechnology</i> , 2013, 163, 87-96.	3.8	47
95	Regulation of heme biosynthesis in non-phototrophic bacteria. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2002, 4, 287-94.	1.0	47
96	Changes in protein synthesis during the adaptation of <i>Bacillus subtilis</i> to anaerobic growth conditions This paper is dedicated to Professor Dr R. K. Thauer, Marburg, on the occasion of his 60th birthday.. <i>Microbiology (United Kingdom)</i> , 2000, 146, 97-105.	1.8	45
97	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.	3.4	45
98	Evolutionary Relationship between Initial Enzymes of Tetrapyrrole Biosynthesis. <i>Journal of Molecular Biology</i> , 2006, 358, 1212-1220.	4.2	44
99	Functional definition of the tobacco protoporphyrinogen IX oxidase substrate-binding site. <i>Biochemical Journal</i> , 2007, 402, 575-580.	3.7	44
100	Production of recombinant antibody fragments in <i>Bacillus megaterium</i> . <i>Microbial Cell Factories</i> , 2007, 6, 2.	4.0	44
101	Chimeric Nitrogenase-like Enzymes of (Bacterio)chlorophyll Biosynthesis. <i>Journal of Biological Chemistry</i> , 2009, 284, 15530-15540.	3.4	44
102	Genotypic and phenotypic characterization of <i>Pseudomonas aeruginosa</i> isolates from urinary tract infections. <i>International Journal of Medical Microbiology</i> , 2011, 301, 282-292.	3.6	43
103	Protein complex formation during denitrification by <i>Pseudomonas aeruginosa</i> . <i>Microbial Biotechnology</i> , 2017, 10, 1523-1534.	4.2	43
104	Heme Biosynthesis in <i>Methanosarcina barkeri</i> via a Pathway Involving Two Methylation Reactions. <i>Journal of Bacteriology</i> , 2006, 188, 8666-8668.	2.2	42
105	TLM-Tracker: software for cell segmentation, tracking and lineage analysis in time-lapse microscopy movies. <i>Bioinformatics</i> , 2012, 28, 2276-2277.	4.1	42
106	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.	3.6	42
107	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.	3.5	41
108	Nitrate-responsive NarX-NarL represses arginine-mediated induction of the <i>Pseudomonas aeruginosa</i> arginine fermentation arcDABC operon. <i>Microbiology (United Kingdom)</i> , 2008, 154, 3053-3060.	1.8	41

#	ARTICLE	IF	CITATIONS
109	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.	3.8	40
110	Aspartate 141 Is the Fourth Ligand of the Oxygen-sensing [4Fe-4S] <sup>2+</sup> Cluster of <i>Bacillus subtilis</i> Transcriptional Regulator Fnr. <i>Journal of Biological Chemistry</i> , 2011, 286, 2017-2021.	3.4	38
111	Coexpression of the type I signal peptidase gene <i>sipM</i> increases recombinant protein production and export in <i>Bacillus megaterium</i> MS941. <i>Biotechnology and Bioengineering</i> , 2005, 91, 616-621.	3.3	37
112	Complexity of macrophage metabolism in infection. <i>Current Opinion in Biotechnology</i> , 2021, 68, 231-239.	6.6	37
113	High yield production of extracellular recombinant levansucrase by <i>Bacillus megaterium</i> . <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 3343-3353.	3.6	36
114	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.	7.1	36
115	Regulatory and Metabolic Networks for the Adaptation of <i>Pseudomonas aeruginosa</i> Biofilms to Urinary Tract-Like Conditions. <i>PLoS ONE</i> , 2013, 8, e71845.	2.5	36
116	Production, Purification, and Characterization of a Mg <sup>2+</sup> -Responsive Porphobilinogen Synthase from <i>Pseudomonas aeruginosa</i> . <i>Biochemistry</i> , 1999, 38, 13968-13975.	2.5	35
117	<i>Pseudomonas aeruginosa</i> Contains a Novel Type V Porphobilinogen Synthase with No Required Catalytic Metal Ions. <i>Biochemistry</i> , 1999, 38, 13976-13982.	2.5	35
118	Lipase LipC affects motility, biofilm formation and rhamnolipid production in <i>Pseudomonas aeruginosa</i> . <i>FEMS Microbiology Letters</i> , 2010, 309, no-no.	1.8	35
119	Transcriptional Control of <i>Bacillus subtilis</i> <i>hemN</i> and <i>hemZ</i> . <i>Journal of Bacteriology</i> , 1999, 181, 5922-5929.	2.2	35
120	PRODORIC: state-of-the-art database of prokaryotic gene regulation. <i>Nucleic Acids Research</i> , 2022, 50, D295-D302.	14.5	34
121	Mechanism of a GatCAB Amidotransferase: Aspartyl-tRNA Synthetase Increases Its Affinity for Asp-tRNA <sup>Asn</sup> and Novel Aminoacyl-tRNA Analogues Are Competitive Inhibitors. <i>Biochemistry</i> , 2007, 46, 13190-13198.	2.5	33
122	Export, purification, and activities of affinity tagged <i>Lactobacillus reuteri</i> levansucrase produced by <i>Bacillus megaterium</i> . <i>Applied Microbiology and Biotechnology</i> , 2007, 74, 1062-1073.	3.6	33
123	Complex formation between protoporphyrinogen IX oxidase and ferrochelatase during haem biosynthesis in <i>Thermosynechococcus elongatus</i> . <i>Microbiology (United Kingdom)</i> , 2008, 154, 3707-3714.	1.8	33
124	Comprehensive molecular, genomic and phenotypic analysis of a major clone of <i>Enterococcus faecalis</i> MLST ST40. <i>BMC Genomics</i> , 2015, 16, 175.	2.8	33
125	Protochlorophyllide: a new photosensitizer for the photodynamic inactivation of Gram-positive and Gram-negative bacteria. <i>FEMS Microbiology Letters</i> , 2009, 290, 156-163.	1.8	32
126	The radical SAM protein HemW is a heme chaperone. <i>Journal of Biological Chemistry</i> , 2018, 293, 2558-2572.	3.4	32



#	ARTICLE	IF	CITATIONS
127	PRODORIC2: the bacterial gene regulation database in 2018. <i>Nucleic Acids Research</i> , 2018, 46, D320-D326.	14.5	32
128	tRNA Recognition by Glutamyl-tRNA Reductase. <i>Journal of Biological Chemistry</i> , 2004, 279, 34931-34937.	3.4	31
129	JVirGel 2.0: computational prediction of proteomes separated via two-dimensional gel electrophoresis under consideration of membrane and secreted proteins. <i>Bioinformatics</i> , 2006, 22, 2441-2443.	4.1	31
130	Expression of the <i>Chlamydomonas reinhardtii</i> chloroplast tRNA <sup>Glu</sup> gene in a homologous in vitro transcription system is independent of upstream promoter elements. <i>Archives of Biochemistry and Biophysics</i> , 1992, 298, 505-513.	3.0	30
131	<i>Bacillus subtilis</i> ResD Induces Expression of the Potential Regulatory Genes <i>yclJ</i> upon Oxygen Limitation. <i>Journal of Bacteriology</i> , 2004, 186, 6477-6484.	2.2	30
132	Substrate Recognition of Nitrogenase-like Dark Operative Protochlorophyllide Oxidoreductase from <i>Prochlorococcus marinus</i> . <i>Journal of Biological Chemistry</i> , 2008, 283, 29873-29881.	3.4	30
133	Proteome analysis of a recombinant <i>Bacillus megaterium</i> strain during heterologous production of a glucosyltransferase. <i>Proteome Science</i> , 2005, 3, 4.	1.7	29
134	The <i>Bacillus subtilis</i> <i>nrdeF</i> Genes, Encoding a Class Ib Ribonucleotide Reductase, Are Essential for Aerobic and Anaerobic Growth. <i>Applied and Environmental Microbiology</i> , 2006, 72, 5260-5265.	3.1	29
135	JProGO: a novel tool for the functional interpretation of prokaryotic microarray data using Gene Ontology information. <i>Nucleic Acids Research</i> , 2006, 34, W510-W515.	14.5	28
136	Yeast seryl-tRNA synthetase expressed in <i>Escherichia coli</i> recognizes bacterial serine-specific tRNAs in vivo. <i>FEBS Journal</i> , 1993, 214, 869-877.	0.2	27
137	<i>Lactococcus lactis</i> HemW (HemN) is a haem-binding protein with a putative role in haem trafficking. <i>Biochemical Journal</i> , 2012, 442, 335-343.	3.7	27
138	Modulation of Anaerobic Energy Metabolism of <i>Bacillus subtilis</i> by <i>arfM</i> ( <i>ywiD</i> ). <i>Journal of Bacteriology</i> , 2001, 183, 6815-6821.	2.2	26
139	Construction and characterization of nitrate and nitrite respiring <i>Pseudomonas putida</i> KT2440 strains for anoxic biotechnical applications. <i>Journal of Biotechnology</i> , 2013, 163, 155-165.	3.8	26
140	Transposon Mutagenesis Identified Chromosomal and Plasmid Genes Essential for Adaptation of the Marine Bacterium <i>Dinoroseobacter shibae</i> to Anaerobic Conditions. <i>Journal of Bacteriology</i> , 2013, 195, 4769-4777.	2.2	26
141	Acetate Dissimilation and Assimilation in <i>Mycobacterium tuberculosis</i> Depend on Carbon Availability. <i>Journal of Bacteriology</i> , 2015, 197, 3182-3190.	2.2	26
142	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.	3.1	26
143	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.	3.4	25
144	Biosynthesis of (Bacterio)chlorophylls. <i>Journal of Biological Chemistry</i> , 2010, 285, 8268-8277.	3.4	24

#	ARTICLE	IF	CITATIONS
145	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.	2.2	24
146	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.	3.5	24
147	A Precise Temperature-Responsive Bistable Switch Controlling <i>Yersinia</i> Virulence. <i>PLoS Pathogens</i> , 2016, 12, e1006091.	4.7	24
148	Wet chemical modification of PTFE implant surfaces with a specific cell adhesion molecule. <i>Chemical Communications</i> , 2002, , 2568-2569.	4.1	23
149	Protein and Vitamin Production in <i>Bacillus megaterium</i> . , 2005, , 205-223.		23
150	The <i>Alcaligenes eutrophus</i> hemN gene encoding the oxygen-independent coproporphyrinogen III oxidase, is required for heme biosynthesis during anaerobic growth. <i>Archives of Microbiology</i> , 1997, 169, 52-60.	2.2	20
151	Unstable Reaction Intermediates and Hysteresis during the Catalytic Cycle of 5-Aminolevulinate Synthase. <i>Journal of Biological Chemistry</i> , 2014, 289, 22915-22925.	3.4	20
152	Co-ordination of iron acquisition, iron porphyrin chelation and iron-protoporphyrin export via the cytochrome c biogenesis protein CcmC in <i>Pseudomonas fluorescens</i> . <i>Microbiology (United Kingdom)</i> , 2003, 149, 3543-3552.	1.8	20
153	Cloning, mapping and characterization of the <i>Pseudomonas aeruginosa</i> hemL gene. <i>Molecular Genetics and Genomics</i> , 1995, 248, 375-380.	2.4	19
154	Aminolaevulinic acid synthase of <i>Rhodobacter capsulatus</i> : high-resolution kinetic investigation of the structural basis for substrate binding and catalysis. <i>Biochemical Journal</i> , 2013, 451, 205-216.	3.7	19
155	Complete synthesis and transcription in vitro of a gene coding for human ribosomal 5S RNA. <i>Gene</i> , 1988, 64, 77-85.	2.2	18
156	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.	3.5	18
157	Structure and function of glutamyl-tRNA reductase, the first enzyme of tetrapyrrole biosynthesis in plants and prokaryotes. <i>Photosynthesis Research</i> , 2002, 74, 205-215.	2.9	17
158	A Tale of Two Acids: When Arginine Is a More Appropriate Acid than H <sub>3</sub> O <sup>+</sup> . <i>Journal of Physical Chemistry B</i> , 2010, 114, 8994-9001.	2.6	17
159	Iron-Sulfur Cluster-dependent Catalysis of Chlorophyllide a Oxidoreductase from <i>Roseobacter denitrificans</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 1141-1154.	3.4	17
160	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.	2.9	17
161	Tracking the Evolution of Porphobilinogen Synthase Metal Dependence in Vitro. <i>Journal of Molecular Biology</i> , 2005, 345, 1059-1070.	4.2	16
162	A protein database constructed from low-coverage genomic sequence of <i>Bacillus megaterium</i> and its use for accelerated proteomic analysis. <i>Journal of Biotechnology</i> , 2006, 124, 486-495.	3.8	16

#	ARTICLE	IF	CITATIONS
163	An Emergent Self-Organizing Map Based Analysis Pipeline for Comparative Metabolome Studies. In <i>Silico Biology</i> , 2009, 9, 163-178.	0.9	16
164	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.	3.8	16
165	ProdoNet: identification and visualization of prokaryotic gene regulatory and metabolic networks. <i>Nucleic Acids Research</i> , 2008, 36, W460-W464.	14.5	15
166	A phosphatidic acid-binding protein is important for lipid homeostasis and adaptation to anaerobic biofilm conditions in <i>Pseudomonas aeruginosa</i> . <i>Biochemical Journal</i> , 2018, 475, 1885-1907.	3.7	15
167	Redefining the <i>Clostridioides difficile</i> $\sigma^B$ Regulon: $\sigma^B$ Activates Genes Involved in Detoxifying Radicals That Can Result from the Exposure to Antimicrobials and Hydrogen Peroxide. <i>MSphere</i> , 2020, 5, .	2.9	15
168	Functionalization of an extended-gate field-effect transistor (EGFET) for bacteria detection. <i>Scientific Reports</i> , 2022, 12, 4397.	3.3	15
169	Glutamate recognition and hydride transfer by <i>Escherichia coli</i> glutamyl-tRNA reductase. <i>FEBS Journal</i> , 2007, 274, 4609-4614.	4.7	14
170	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.	3.7	14
171	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.	3.4	14
172	Virulence of <i>Agrobacterium tumefaciens</i> requires lipid homeostasis mediated by the lysyl-phosphatidylglycerol hydrolase AcvB. <i>Molecular Microbiology</i> , 2019, 111, 269-286.	2.5	14
173	Cellular levels of heme affect the activity of dimeric glutamyl-tRNA reductase. <i>Biochemical and Biophysical Research Communications</i> , 2011, 405, 134-139.	2.1	13
174	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.	3.4	13
175	PrsA2 (CD630_35000) of <i>Clostridioides difficile</i> Is an Active Parvulin-Type PPIase and a Virulence Modulator. <i>Frontiers in Microbiology</i> , 2018, 9, 2913.	3.5	13
176	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.	3.5	13
177	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.	2.5	13
178	The hemA gene encoding glutamyl-tRNA reductase from the archaeon <i>Methanobacterium thermoautotrophicum</i> strain Marburg. <i>Bioorganic and Medicinal Chemistry</i> , 1996, 4, 1089-1095.	3.0	12
179	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
180	Physical and immunological characterization of human transcription factor IIIA. <i>FEBS Journal</i> , 1990, 194, 167-174.	0.2	11

#	ARTICLE	IF	CITATIONS
181	Changes in Protein Synthesis as a Consequence of Heme Depletion in <i>Escherichia coli</i> . <i>Current Microbiology</i> , 1998, 37, 226-230.	2.2	11
182	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.	3.2	11
183	<i>Clostridioides difficile</i> Activates Human Mucosal-Associated Invariant T Cells. <i>Frontiers in Microbiology</i> , 2018, 9, 2532.	3.5	11
184	Crystal structures and protein engineering of three different penicillin G acylases from Gram-positive bacteria with different thermostability. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 7537-7552.	3.6	11
185	Biosynthesis of 5-Aminolevulinic Acid. , 2009, , 29-42.		10
186	Transfer RNA Involvement in Chlorophyll Biosynthesis. <i>Sub-Cellular Biochemistry</i> , 1991, 17, 235-264.	2.4	10
187	Ungewöhnliche Wege und umweltregulierte Gene der bakteriellen Häm biosynthese. <i>Die Naturwissenschaften</i> , 1996, 83, 389-400.	1.6	9
188	Systems Biology of Recombinant Protein Production in <i>Bacillus megaterium</i> . , 2010, 120, 133-161.		9
189	Microbial communities related to volatile organic compound emission in automobile air conditioning units. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 8777-8793.	3.6	9
190	<i>Leishmania major</i> possesses a unique HemG-type protoporphyrinogen IX oxidase. <i>Bioscience Reports</i> , 2014, 34, .	2.4	9
191	Evolutionary model for the unequal segregation of high copy plasmids. <i>PLoS Computational Biology</i> , 2019, 15, e1006724.	3.2	9
192	Transcriptome profiling of <i>degU</i> expression reveals unexpected regulatory patterns in <i>Bacillus megaterium</i> and discloses new targets for optimizing expression. <i>Applied Microbiology and Biotechnology</i> , 2011, 92, 583-596.	3.6	8
193	RirA of <i>Dinoroseobacter shibae</i> senses iron via a [3Fe <sup>4S</sup> ] <sub>1</sub> + cluster co-ordinated by three cysteine residues. <i>Biochemical Journal</i> , 2020, 477, 191-212.	3.7	8
194	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.	3.5	8
195	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.	3.8	8
196	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
197	Functional definition of the two effector binding sites, the oligomerization and DNA binding domains of the <i>Bacillus subtilis</i> LysR-type transcriptional regulator AlsR. <i>Molecular Microbiology</i> , 2018, 109, 845-864.	2.5	7
198	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.	3.5	7

#	ARTICLE	IF	CITATIONS
199	Pleiotropic <i>Clostridioides difficile</i> Cyclophilin PpiB Controls Cysteine-Tolerance, Toxin Production, the Central Metabolism and Multiple Stress Responses. <i>Frontiers in Pharmacology</i> , 2019, 10, 340.	3.5	7
200	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.	3.6	6
201	A Point Mutation in the Transcriptional Repressor PerR Results in a Constitutive Oxidative Stress Response in <i>Clostridioides difficile</i> 6301 <sup>™</sup> . <i>MSphere</i> , 2021, 6, .	2.9	6
202	Biosynthesis of Heme and Vitamin B12. , 2010, , 445-499.		5
203	GeneReporter <sup>™</sup> sequence-based document retrieval and annotation. <i>Bioinformatics</i> , 2011, 27, 1034-1035.	4.1	5
204	Genome Sequence of the Acute Urethral Catheter Isolate <i>Pseudomonas aeruginosa</i> MH38. <i>Genome Announcements</i> , 2014, 2, .	0.8	5
205	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.	1.7	5
206	Chimeric Interaction of Nitrogenase <sup>α</sup> -Like Reductases with the MoFe Protein of Nitrogenase. <i>ChemBioChem</i> , 2020, 21, 1733-1741.	2.6	5
207	Membrane Proteomics of <i>Pseudomonas aeruginosa</i> . <i>Methods in Molecular Biology</i> , 2014, 1149, 213-224.	0.9	5
208	Radical SAM Enzymes Involved in Tetrapyrrole Biosynthesis and Insertion. <i>ACS Bio &amp; Med Chem Au</i> , 2022, 2, 196-204.	3.7	5
209	Transfer RNA-Dependent Aminolevulinic Acid Formation: Structure and Function Of Glutamyl-tRNA Synthetase, Reductase and Glutamate-1-Semialdehyde-2,1-Aminomutase. , 2006, , 159-171.		4
210	Strepto-DB, a database for comparative genomics of group A (GAS) and B (GBS) streptococci, implemented with the novel database platform <sup>™</sup> Open Genome Resource <sup>™</sup> (OGeR). <i>Nucleic Acids Research</i> , 2009, 37, D494-D498.	14.5	4
211	Purification, crystallization and preliminary X-ray analysis of the effector domain of AlsR, an LysR-type transcriptional regulator from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 581-584.	0.7	3
212	Complete Genome Sequence of <i>Raoultella electrica</i> 1GB (DSM 102253 <sup>T</sup> ), Isolated from Anodic Biofilms of a Glucose-Fed Microbial Fuel Cell. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	3
213	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.	3.7	3
214	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.	0.9	3
215	An emergent self-organizing map based analysis pipeline for comparative metabolome studies. <i>In Silico Biology</i> , 2009, 9, 163-78.	0.9	3
216	Thiol Metabolism and Volatile Metabolome of <i>Clostridioides difficile</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	3

#	ARTICLE	IF	CITATIONS
217	Directed optimization of biocatalytic transglycosylation processes by the integration of genetic algorithms and fermentative approaches into a kinetic model. <i>Process Biochemistry</i> , 2009, 44, 1103-1114.	3.7	2
218	InFiRe " a novel computational method for the identification of insertion sites in transposon mutagenized bacterial genomes. <i>Bioinformatics</i> , 2012, 28, 306-310.	4.1	2
219	Interatomic Characterization of Protein-Protein Interactions in Membrane-Associated Mega-complexes. <i>Springer Protocols</i> , 2015, , 103-124.	0.3	2
220	Genome Sequence of the Urethral Isolate <i>Pseudomonas aeruginosa</i> RN21. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
221	Genome Sequence of the Urethral Catheter Isolate <i>Pseudomonas aeruginosa</i> MH19. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
222	Adaptation of <i>Dinoroseobacter shibae</i> to oxidative stress and the specific role of RirA. <i>PLoS ONE</i> , 2021, 16, e0248865.	2.5	2
223	The Biosynthesis of Hemes, Siroheme, Vitamin B12 and Linear Tetrapyrroles in <i>Pseudomonads</i> . , 2004, , 111-146.		2
224	Biosynthesis and Insertion of Heme. , 2019, , 201-228.		1
225	Bioenergetics Theory and Components   Heme Synthesis Three Ways. , 2021, , 74-88.		1
226	Ungewöhnliche Wege und umweltregulierte Gene der bakteriellen Hämmbiosynthese. <i>Die Naturwissenschaften</i> , 1996, 83, 389-400.	1.6	1
227	<i>Bacillus megaterium</i> as a recombinant protein production host. <i>Microbial Cell Factories</i> , 2006, 5, P74.	4.0	0
228	Einladung zum Wissenschaftsforum in Ulm. <i>Chemie in Unserer Zeit</i> , 2007, 41, 71-71.	0.1	0
229	From gene to product. <i>Journal of Biotechnology</i> , 2013, 163, 85-86.	3.8	0
230	Mikrobiologisches Wissen für alle bedeutet Klimaschutz!. <i>BioSpektrum</i> , 2019, 25, 595-595.	0.0	0
231	A Likelihood Ratio Test for Differential Metabolic Profiles in Multiple Intensity Measurements. <i>Lecture Notes in Computer Science</i> , 2007, , 485-492.	1.3	0
232	Biosynthesis and Insertion of Heme. , 2018, , 1-28.		0