Thomas Schweder

List of Publications by Year
in descending order

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113 papers	7,096 citations	71102 41 h-index	66911 78 g-index
122 all docs	122 docs citations	122 times ranked	7640 citing authors

#	Article	IF	Citations
1	Substrate-Controlled Succession of Marine Bacterioplankton Populations Induced by a Phytoplankton Bloom. Science, 2012, 336, 608-611.	12.6	1,304
2	Physiological responses to mixing in large scale bioreactors. Journal of Biotechnology, 2001, 85, 175-185.	3.8	394
3	Physiological Proteomics of the Uncultured Endosymbiont of Riftia pachyptila. Science, 2007, 315, 247-250.	12.6	207
4	Metaproteomics of a gutless marine worm and its symbiotic microbial community reveal unusual pathways for carbon and energy use. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1173-82.	7.1	191
5	Niches of two polysaccharide-degrading Polaribacter isolates from the North Sea during a spring diatom bloom. ISME Journal, 2015, 9, 1410-1422.	9.8	182
6	Verrucomicrobia use hundreds of enzymes to digest the algal polysaccharide fucoidan. Nature Microbiology, 2020, 5, 1026-1039.	13.3	182
7	Functional characterization of polysaccharide utilization loci in the marine Bacteroidetes â€˜Gramella forsetiiâ€™ KT0803. ISME Journal, 2014, 8, 1492-1502.	9.8	177
8	Functional Analysis of the Magnetosome Island in Magnetospirillum gryphiswaldense: The mamAB Operon Is Sufficient for Magnetite Biomineralization. PLoS ONE, 2011, 6, e25561.	2.5	155
9	Polysaccharide utilization loci of North Sea Flavobacteriia as basis for using SusC/D-protein expression for predicting major phytoplankton glycans. ISME Journal, 2019, 13, 76-91.	9.8	139
10	Automated Detection and Quantitation of Bacterial RNA by Using Electrical Microarrays. Analytical Chemistry, 2006, 78, 4794-4802.	6.5	136
11	The Genome of the Obligate Intracellular Parasite Trachipleistophora hominis: New Insights into Microsporidian Genome Dynamics and Reductive Evolution. PLoS Pathogens, 2012, 8, e1002979.	4.7	127
12	In marine Bacteroidetes the bulk of glycan degradation during algae blooms is mediated by few clades using a restricted set of genes. ISME Journal, 2019, 13, 2800-2816.	9.8	125
13	Monitoring of genes that respond to process-related stress in large-scale bioprocesses. Biotechnology and Bioengineering, 1999, 65, 151-159.	3.3	124
14	Staphylococcal serine proteaseâ€“like proteins are pacemakers of allergic airway reactions to Staphylococcus aureus. Journal of Allergy and Clinical Immunology, 2017, 139, 492-500.e8.	2.9	118
15	Monitoring of genes that respond to overproduction of an insoluble recombinant protein inEscherichia coli glucose-limited fed-batch fermentations. Biotechnology and Bioengineering, 2000, 70, 217-224.	3.3	117
16	Metabolic and physiological interdependencies in the Bathymodiolus azoricus symbiosis. ISME Journal, 2017, 11, 463-477.	9.8	116
17	The extracellular proteome ofBacillus licheniformis grown in different media and under different nutrient starvation conditions. Proteomics, 2006, 6, 268-281.	2.2	104
18	Genome-wide transcriptional profiling of the Bacillus subtilis cold-shock response. Microbiology (United Kingdom), 2002, 148, 3441-3455.	1.8	100

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19	A marine bacterial enzymatic cascade degrades the algal polysaccharide ulvan. Nature Chemical Biology, 2019, 15, 803-812.	8.0	97
20	Isolation and characterization of marine psychrophilic phage-host systems from Arctic sea ice. Extremophiles, 2003, 7, 377-384.	2.3	93
21	Adaptive mechanisms that provide competitive advantages to marine bacteroidetes during microalgal blooms. ISME Journal, 2018, 12, 2894-2906.	9.8	84
22	Electric chips for rapid detection and quantification of nucleic acids. Biosensors and Bioelectronics, 2004, 19, 537-546.	10.1	82
23	Physiological homogeneity among the endosymbionts of Riftia pachyptila and Tevnia jerichonana revealed by proteogenomics. ISME Journal, 2012, 6, 766-776.	9.8	80
24	Biphasic cellular adaptations and ecological implications of Alteromonas macleodii degrading a mixture of algal polysaccharides. ISME Journal, 2019, 13, 92-103.	9.8	74
25	Cloning of two pectate lyase genes from the marine Antarctic bacterium Pseudoalteromonas haloplanktis strain ANT/505 and characterization of the enzymes. Extremophiles, 2001, 5, 35-44.	2.3	67
26	A proteomic view of cell physiology ofBacillus licheniformis. Proteomics, 2004, 4, 1465-1490.	2.2	64
27	Deletion of a fur -Like Gene Affects Iron Homeostasis and Magnetosome Formation in Magnetospirillum gryphiswaldense. Journal of Bacteriology, 2010, 192, 4192-4204.	2.2	64
28	Proteome and transcriptome based analysis of Bacillus subtilis cells overproducing an insoluble heterologous protein. Applied Microbiology and Biotechnology, 2001, 55, 326-332.	3.6	61
29	Diatom fucan polysaccharide precipitates carbon during algal blooms. Nature Communications, 2021, 12, 1150.	12.8	58
30	Quality control of inclusion bodies in Escherichia coli. Microbial Cell Factories, 2010, 9, 41.	4.0	57
31	Aquatic adaptation of a laterally acquired pectin degradation pathway in marine gammaproteobacteria. Environmental Microbiology, 2017, 19, 2320-2333.	3.8	57
32	A twoâ€compartment bioreactor system made of commercial parts for bioprocess scaleâ€down studies: Impact of oscillations on Bacillus subtilis fedâ€batch cultivations. Biotechnology Journal, 2011, 6, 1009-1017.	3.5	56
33	Stress Responses of the Industrial Workhorse Bacillus licheniformis to Osmotic Challenges. PLoS ONE, 2013, 8, e80956.	2.5	56
34	Nitrogen fixation in a chemoautotrophic lucinid symbiosis. Nature Microbiology, 2017, 2, 16193.	13.3	56
35	Bacillus subtilis as heterologous host for the secretory production of the non-ribosomal cyclodepsipeptide enniatin. Applied Microbiology and Biotechnology, 2015, 99, 681-691.	3.6	55
36	The glucose and nitrogen starvation response of Bacillus licheniformis. Proteomics, 2007, 7, 413-423.	2.2	54

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37	Abundant toxin-related genes in the genomes of beneficial symbionts from deep-sea hydrothermal vent mussels. ELife, 2015, 4, e07966.	6.0	50
38	Characterization of a thaumarchaeal symbiont that drives incomplete nitrification in the tropical spongeIanthella basta. Environmental Microbiology, 2019, 21, 3831-3854.	3.8	50
39	Microbial metalâ€sulfide oxidation in inactive hydrothermal vent chimneys suggested by metagenomic and metaproteomic analyses. Environmental Microbiology, 2019, 21, 682-701.	3.8	50
40	Cloning, expression, and characterization of a chitinase gene from the Antarctic psychrotolerant bacterium Vibrio sp. strain Fi:7. Extremophiles, 2001, 5, 119-126.	2.3	47
41	Characterization and optimization of Bacillus subtilis ATCC 6051 as an expression host. Journal of Biotechnology, 2013, 163, 97-104.	3.8	47
42	Oxidative demethylation of algal carbohydrates by cytochrome P450 monooxygenases. Nature Chemical Biology, 2018, 14, 342-344.	8.0	47
43	An acetoin-regulated expression system of Bacillussubtilis. Applied Microbiology and Biotechnology, 2006, 73, 895-903.	3.6	46
44	High level expression of a recombinant phospholipase C from Bacillus cereus in Bacillus subtilis. Applied Microbiology and Biotechnology, 2007, 74, 634-639.	3.6	43
45	Genomic and proteomic profiles of biofilms on microplastics are decoupled from artificial surface properties. Environmental Microbiology, 2021, 23, 3099-3115.	3.8	43
46	Changing expression patterns of TonB-dependent transporters suggest shifts in polysaccharide consumption over the course of a spring phytoplankton bloom. ISME Journal, 2021, 15, 2336-2350.	9.8	42
47	Genome and proteome characterization of the psychrophilic Flavobacterium bacteriophage 11b. Extremophiles, 2007, 11, 95-104.	2.3	41
48	Biochemical characterization of an ulvan lyase from the marine flavobacterium Formosa agariphila KMM 3901T. Applied Microbiology and Biotechnology, 2018, 102, 6987-6996.	3.6	41
49	Insight into the evolution of microbial metabolism from the deep-branching bacterium, Thermovibrio ammonificans. ELife, 2017, 6, .	6.0	40
50	Regulation of acetoin and 2,3-butanediol utilization in Bacillus licheniformis. Applied Microbiology and Biotechnology, 2010, 87, 2227-2235.	3.6	38
51	Metabolic engineering of Bacillus subtilis for growth on overflow metabolites. Microbial Cell Factories, 2013, 12, 72.	4.0	38
52	Host-Microbe Interactions in the Chemosynthetic Riftia pachyptila Symbiosis. MBio, 2019, 10, .	4.1	38
53	Role of the general stress response during strong overexpression of a heterologous gene in Escherichia coli. Applied Microbiology and Biotechnology, 2002, 58, 330-337.	3.6	37
54	Global expression profiling ofBacillus subtilis cells during industrial-close fed-batch fermentations with different nitrogen sources. Biotechnology and Bioengineering, 2005, 92, 277-298.	3.3	37

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55	The phosphate-starvation response ofBacillus licheniformis. Proteomics, 2006, 6, 3582-3601.	2.2	37
56	Fed-batch process for the psychrotolerant marine bacterium Pseudoalteromonas haloplanktis. Microbial Cell Factories, 2010, 9, 72.	4.0	36
57	Metaproteogenomic Profiling of Microbial Communities Colonizing Actively Venting Hydrothermal Chimneys. Frontiers in Microbiology, 2018, 9, 680.	3.5	36
58	Effects of Halide Ions on the Carbamidocyclophane Biosynthesis in Nostoc sp. CAVN2. Marine Drugs, 2016, 14, 21.	4.6	35
59	Status quo in physiological proteomics of the unculturedRiftia pachyptilaendosymbiont. Proteomics, 2011, 11, 3106-3117.	2.2	34
60	The peroxide stress response of Bacillus licheniformis. Proteomics, 2011, 11, 2851-2866.	2.2	32
61	Genome sequence of the sulfur-oxidizing Bathymodiolus thermophilus gill endosymbiont. Standards in Genomic Sciences, 2017, 12, 50.	1.5	32
62	An expression vector system providing plasmid stability and conditional suicide of plasmid-containing cells. Applied Microbiology and Biotechnology, 1992, 38, 91-3.	3.6	31
63	Regulation of the expression of the cold shock proteins CspB and CspC in Bacillus subtilis. Molecular Genetics and Genomics, 1999, 262, 351-354.	2.4	31
64	Bacillus pumilus Reveals a Remarkably High Resistance to Hydrogen Peroxide Provoked Oxidative Stress. PLoS ONE, 2014, 9, e85625.	2.5	31
65	Alphaâ€•and betaâ€mannan utilization by marine Bacteroidetes. Environmental Microbiology, 2018, 20, 4127-4140.	3.8	31
66	Detailed proteome analysis of growing cells of the planctomycete Rhodopirellula baltica SH1^T. Proteomics, 2008, 8, 1608-1623.	2.2	30
67	Cytoplasmic and Periplasmic Proteomic Signatures of Exponentially Growing Cells of the Psychrophilic Bacterium Pseudoalteromonas haloplanktis TAC125. Applied and Environmental Microbiology, 2011, 77, 1276-1283.	3.1	30
68	Proteomics of marine bacteria. Electrophoresis, 2008, 29, 2603-2616.	2.4	28
69	Cell Physiology and Protein Secretion of <i>Bacillus licheniformis</i> Compared to<i> Bacillus subtilis</i>. Journal of Molecular Microbiology and Biotechnology, 2009, 16, 53-68.	1.0	28
70	Application of an electric DNA-chip for the expression analysis of bioprocess-relevant marker genes ofBacillus subtilis. Biotechnology and Bioengineering, 2005, 92, 299-307.	3.3	27
71	Heterologous expression, refolding and functional characterization of two antifreeze proteins from Fragilariopsis cylindrus (Bacillariophyceae). Cryobiology, 2011, 63, 220-228.	0.7	27
72	Production of the polyketide 6-deoxyerythronolide B in the heterologous host Bacillus subtilis. Applied Microbiology and Biotechnology, 2016, 100, 1209-1220.	3.6	27

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73	Diverse events have transferred genes for edible seaweed digestion from marine to human gut bacteria. Cell Host and Microbe, 2022, 30, 314-328.e11.	11.0	25
74	Biotransformation of bisphenol A analogues by the biphenyl-degrading bacterium Cupriavidus basilensisÂ- a structure-biotransformation relationship. Applied Microbiology and Biotechnology, 2020, 104, 3569-3583.	3.6	24
75	Analysis of the expression and function of the Ïƒ B -dependent general stress regulon of Bacillus subtilis during slow growth. Archives of Microbiology, 1999, 171, 439-443.	2.2	21
76	Monitoring of Stress Responses. Advances in Biochemical Engineering/Biotechnology, 2004, 89, 47-71.	1.1	21
77	Proteomic identification of a two-component regulatory system in Pseudoalteromonas haloplanktis TAC125. Extremophiles, 2006, 10, 483-491.	2.3	20
78	The role of thioredoxin TrxA in Bacillus subtilis: A proteomics and transcriptomics approach. Proteomics, 2008, 8, 2676-2690.	2.2	20
79	A proteomic view of cell physiology of the industrial workhorse Bacillus licheniformis. Journal of Biotechnology, 2014, 191, 139-149.	3.8	20
80	Biopearling of Interconnected Outer Membrane Vesicle Chains by a Marine Flavobacterium. Applied and Environmental Microbiology, 2019, 85, .	3.1	20
81	The oxygen-independent metabolism of cyclic monoterpenes in Castellaniella defragrans 65Phen. BMC Microbiology, 2014, 14, 164.	3.3	19
82	Cold induction of the Bacillus subtilis bkd operon is mediated by increased mRNA stability. Molecular Genetics and Genomics, 2004, 272, 98-107.	2.1	18
83	The response of Bacillus licheniformis to heat and ethanol stress and the role of the SigB regulon. Proteomics, 2013, 13, 2140-2161.	2.2	18
84	Exploiting fine-scale genetic and physiological variation of closely related microbes to reveal unknown enzyme functions. Journal of Biological Chemistry, 2017, 292, 13056-13067.	3.4	18
85	Improved sandwich-hybridization assay for an electrical DNA-chip-based monitoring of bioprocess-relevant marker genes. Applied Microbiology and Biotechnology, 2008, 78, 719-728.	3.6	17
86	Electrical protein array chips for the detection of staphylococcal virulence factors. Applied Microbiology and Biotechnology, 2010, 85, 1619-1627.	3.6	17
87	Bacterial symbiont subpopulations have different roles in a deep-sea symbiosis. ELife, 2021, 10, .	6.0	17
88	Transcriptomic and proteomic insight into the mechanism of cyclooctasulfurâ€•versus thiosulfateâ€oxidation by the chemolithoautotroph Sulfurimonas denitrificans. Environmental Microbiology, 2019, 21, 244-258.	3.8	16
89	Comparative proteomics of related symbiotic mussel species reveals high variability of hostâ€“symbiont interactions. ISME Journal, 2020, 14, 649-656.	9.8	15
90	An optimized technique for rapid genome modifications of Bacillus subtilis. Journal of Microbiological Methods, 2013, 95, 350-352.	1.6	14

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91	Linalool isomerase, a membrane-anchored enzyme in the anaerobic monoterpene degradation in Thauera linaloolentis 47Lol. BMC Biochemistry, 2016, 17, 6.	4.4	14
92	Screening for New Metabolites from Marine Microorganisms. Advances in Biochemical Engineering/Biotechnology, 2005, 96, 1-48.	1.1	13
93	Cell surface proteome of the marine planctomycete <scp>R</scp>hodopirellula baltica. Proteomics, 2012, 12, 1781-1791.	2.2	13
94	Proteomic profiles and kinetics of development of bacteriophage T4 and its rI and rIII mutants in slowly growing Escherichia coli. Journal of General Virology, 2013, 94, 896-905.	2.9	13
95	The anaerobic linalool metabolism in Thauera linaloolentis 47 Lol. BMC Microbiology, 2016, 16, 76.	3.3	13
96	Bioprocess monitoring by marker gene analysis. Biotechnology Journal, 2011, 6, 926-933.	3.5	12
97	Stepwise optimization of a low-temperature Bacillus subtilis expression system for â€œdifficult to expressâ€•proteins. Applied Microbiology and Biotechnology, 2015, 99, 6363-6376.	3.6	12
98	An auto-inducible phosphate-controlled expression system of Bacillus licheniformis. BMC Biotechnology, 2019, 19, 3.	3.3	10
99	Reaching out in anticipation: bacterial membrane extensions represent a permanent investment in polysaccharide sensing and utilization. Environmental Microbiology, 2021, 23, 3149-3163.	3.8	10
100	Atâ€‹ine Monitoring of Bioprocessâ€Relevant Marker Genes. Engineering in Life Sciences, 2007, 7, 373-379.	3.6	8
101	A new carbohydrate-active oligosaccharide dehydratase is involved in the degradation of ulvan. Journal of Biological Chemistry, 2021, 297, 101210.	3.4	8
102	Methanosaeta and â€œ Candidatus Velamenicoccus archaeovorusâ€• Applied and Environmental Microbiology, 2022, 88, e0240721.	3.1	7
103	A host-vector toolbox for improved secretory protein overproduction in Bacillus subtilis. Applied Microbiology and Biotechnology, 2022, 106, 5137-5151.	3.6	7
104	Suitability of different Î²-galactosidases as reporter enzymes in Bacillus subtilis. Applied Microbiology and Biotechnology, 2012, 93, 381-392.	3.6	6
105	Highâ€resolution proteome maps of Bacillus licheniformis cells growing in minimal medium. Proteomics, 2015, 15, 2629-2633.	2.2	6
106	A Phosphate Starvation-Inducible Ribonuclease of Bacillus licheniformis. Journal of Microbiology and Biotechnology, 2016, 26, 1464-1472.	2.1	6
107	Novel developments for improved detection of specific mRNAs by DNA chips. Applied Microbiology and Biotechnology, 2008, 80, 953-63.	3.6	5
108	Sensitive detection of idiotypic platelet-reactive alloantibodies by an electrical protein chip. Biosensors and Bioelectronics, 2012, 36, 207-211.	10.1	4

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109	Connecting Algal Polysaccharide Degradation to Formaldehyde Detoxification. ChemBioChem, 2022, 23, .	2.6	3
110	Bacillus pumilus KatX2 confers enhanced hydrogen peroxide resistance to a Bacillus subtilis PkatA::katX2 mutant strain. Microbial Cell Factories, 2017, 16, 72.	4.0	2
111	Monitoring of stress responses. Microbial Cell Factories, 2006, 5, S23.	4.0	1
112	Characterization of the Thermophilic Starch Degrading Petrotoga Strain 64G3 and the Expression of its Î±-amylase Gene. Biotechnology, 2012, 11, 199-208.	0.1	1
113	Monitoring of Genes that Respond to Overproduction of Insoluble Recombinant Proteins in Escherichia Coli and Bacillus Subtilis. , 2001, , 359-369.		0