Armin Ehrenreich

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

62 61 3,741 32 h-index g-index citations papers 62 5.8 4.88 4,145 avg, IF L-index ext. citations ext. papers

#	Paper	IF	Citations
62	The Roles of the Various Cellulose Biosynthesis Operons in ATCC 23769 <i>Applied and Environmental Microbiology</i> , 2022 , e0246021	4.8	1
61	Monitoring co-cultures of Clostridium carboxidivorans and Clostridium kluyveri by fluorescence in situ hybridization with specific 23S rRNA oligonucleotide probes. <i>Systematic and Applied Microbiology</i> , 2021 , 44, 126271	4.2	3
60	Synthetic co-culture of autotrophic Clostridium carboxidivorans and chain elongating Clostridium kluyveri monitored by flow cytometry. <i>Microbial Biotechnology</i> , 2021 ,	6.3	3
59	L-Erythrulose production with a multideletion strain of Gluconobacter oxydans. <i>Applied Microbiology and Biotechnology</i> , 2019 , 103, 4393-4404	5.7	7
58	An efficient method for markerless mutant generation by allelic exchange in and using suicide vectors. <i>Biotechnology for Biofuels</i> , 2019 , 12, 31	7.8	6
57	Restriction-deficient mutants and marker-less genomic modification for metabolic engineering of the solvent producer. <i>Biotechnology for Biofuels</i> , 2018 , 11, 264	7.8	6
56	Characterization of membrane-bound dehydrogenases of Gluconobacter oxydans 621H using a new system for their functional expression. <i>Applied Microbiology and Biotechnology</i> , 2017 , 101, 3189-3200	5.7	35
55	Expression of membrane-bound dehydrogenases from a mother of vinegar metagenome in Gluconobacter oxydans. <i>Applied Microbiology and Biotechnology</i> , 2017 , 101, 7901-7912	5.7	14
54	The Genomes of Acetic Acid Bacteria 2017 , 469-494		2
53	Markerless deletion of putative alanine dehydrogenase genes in Bacillus licheniformis using a codBA-based counterselection technique. <i>Microbiology (United Kingdom)</i> , 2017 , 163, 1532-1539	2.9	10
52	Gluconic acid: Properties, production methods and applications An excellent opportunity for agro-industrial by-products and waste bio-valorization. <i>Process Biochemistry</i> , 2016 , 51, 1891-1903	4.8	89
51	Identification of ecotype-specific marker genes for categorization of beer-spoiling Lactobacillus brevis. <i>Food Microbiology</i> , 2015 , 51, 130-8	6	11
50	Alternative hosts for functional (meta)genome analysis. <i>Applied Microbiology and Biotechnology</i> , 2014 , 98, 8099-109	5.7	66
49	Development of an in vivo methylation system for the solventogen Clostridium saccharobutylicum NCP 262 and analysis of two endonuclease mutants. <i>Journal of Biotechnology</i> , 2014 , 188, 97-9	3.7	17
48	Coping with anoxia: a comprehensive proteomic and transcriptomic survey of denitrification. <i>Journal of Proteome Research</i> , 2014 , 13, 4325-38	5.6	4
47	Temperature- and nitrogen source-dependent regulation of GlnR target genes in Listeria monocytogenes. <i>FEMS Microbiology Letters</i> , 2014 , 355, 131-41	2.9	8
46	Chemostat cultivation and transcriptional analyses of Clostridium acetobutylicum mutants with defects in the acid and acetone biosynthetic pathways. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 9777-94	5.7	12

(2010-2014)

45	Identification of genes essential for anaerobic growth of Listeria monocytogenes. <i>Microbiology</i> (United Kingdom), 2014 , 160, 752-765	2.9	36
44	Sequence similarity of Clostridium difficile strains by analysis of conserved genes and genome content is reflected by their ribotype affiliation. <i>PLoS ONE</i> , 2014 , 9, e86535	3.7	34
43	Size unlimited markerless deletions by a transconjugative plasmid-system in Bacillus licheniformis. Journal of Biotechnology, 2013 , 167, 365-9	3.7	16
42	Characterization of membrane-bound dehydrogenases from Gluconobacter oxydans 621H via whole-cell activity assays using multideletion strains. <i>Applied Microbiology and Biotechnology</i> , 2013 , 97, 6397-412	5.7	46
41	Metabolic engineering of Bacillus subtilis for growth on overflow metabolites. <i>Microbial Cell Factories</i> , 2013 , 12, 72	6.4	26
40	Importance of codB for new codA-based markerless gene deletion in Gluconobacter strains. <i>Applied Microbiology and Biotechnology</i> , 2013 , 97, 8341-9	5.7	31
39	Deletion of pyruvate decarboxylase by a new method for efficient markerless gene deletions in Gluconobacter oxydans. <i>Applied Microbiology and Biotechnology</i> , 2013 , 97, 2521-30	5.7	49
38	RACK1/Asc1p, a ribosomal node in cellular signaling. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 87-10!	57.6	31
37	Complete Genome Sequence of the Solvent Producer Clostridium saccharobutylicum NCP262 (DSM 13864). <i>Genome Announcements</i> , 2013 , 1,		20
36	Global transcriptional changes of Clostridium acetobutylicum cultures with increased butanol:acetone ratios. <i>New Biotechnology</i> , 2012 , 29, 485-93	6.4	41
35	A transcriptional study of acidogenic chemostat cells of Clostridium acetobutylicum-cellular behavior in adaptation to n-butanol. <i>Journal of Biotechnology</i> , 2012 , 161, 366-77	3.7	41
34	A transcriptional study of acidogenic chemostat cells of Clostridium acetobutylicumsolvent stress caused by a transient n-butanol pulse. <i>Journal of Biotechnology</i> , 2012 , 161, 354-65	3.7	50
33	Modifying the product pattern of Clostridium acetobutylicum: physiological effects of disrupting the acetate and acetone formation pathways. <i>Applied Microbiology and Biotechnology</i> , 2012 , 94, 743-54	5.7	70
32	Effect of iron limitation and fur gene inactivation on the transcriptional profile of the strict anaerobe Clostridium acetobutylicum. <i>Microbiology (United Kingdom)</i> , 2012 , 158, 1918-1929	2.9	29
31	Genome-wide gene expression analysis of the switch between acidogenesis and solventogenesis in continuous cultures of Clostridium acetobutylicum. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2011 , 20, 1-15	0.9	75
30	Proteomic and transcriptomic elucidation of the mutant ralstonia eutropha G+1 with regard to glucose utilization. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 2058-70	4.8	36
29	Facilitation of direct conditional knockout of essential genes in Bacillus licheniformis DSM13 by comparative genetic analysis and manipulation of genetic competence. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 5046-57	4.8	30
28	Genome-wide transcriptome analyses of the WnallgasVbacterium Ralstonia eutropha H16 with regard to polyhydroxyalkanoate metabolism. <i>Microbiology (United Kingdom)</i> , 2010 , 156, 2136-2152	2.9	78

27	Impact of multiple beta-ketothiolase deletion mutations in Ralstonia eutropha H16 on the composition of 3-mercaptopropionic acid-containing copolymers. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 5373-82	4.8	31
26	Characterization and inactivation of the membrane-bound polyol dehydrogenase in Gluconobacter oxydans DSM 7145 reveals a role in meso-erythritol oxidation. <i>Microbiology (United Kingdom)</i> , 2010 , 156, 1890-1899	2.9	13
25	Clostridium ljungdahlii represents a microbial production platform based on syngas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 13087-92	11.5	497
24	Regulation of acetoin and 2,3-butanediol utilization in Bacillus licheniformis. <i>Applied Microbiology and Biotechnology</i> , 2010 , 87, 2227-35	5.7	31
23	A proteomic and transcriptional view of acidogenic and solventogenic steady-state cells of Clostridium acetobutylicum in a chemostat culture. <i>Applied Microbiology and Biotechnology</i> , 2010 , 87, 2209-26	5.7	64
22	Investigations on the microbial catabolism of the organic sulfur compounds TDP and DTDP in Ralstonia eutropha H16 employing DNA microarrays. <i>Applied Microbiology and Biotechnology</i> , 2010 , 88, 1145-59	5.7	14
21	Transcriptional analysis of catabolite repression in Clostridium acetobutylicum growing on mixtures of D-glucose and D-xylose. <i>Journal of Biotechnology</i> , 2010 , 150, 315-23	3.7	67
20	The role of PerR in O2-affected gene expression of Clostridium acetobutylicum. <i>Journal of Bacteriology</i> , 2009 , 191, 6082-93	3.5	51
19	Physiology of acetic acid bacteria in light of the genome sequence of Gluconobacter oxydans. Journal of Molecular Microbiology and Biotechnology, 2009 , 16, 69-80	0.9	86
18	Cell physiology and protein secretion of Bacillus licheniformis compared to Bacillus subtilis. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2009 , 16, 53-68	0.9	23
17	The Genome of Acetic Acid Bacteria 2009 , 379-394		
16	Insights into the NrpR regulon in Methanosarcina mazei GI. Archives of Microbiology, 2008, 190, 319-32	3	25
15	The glucose and nitrogen starvation response of Bacillus licheniformis. <i>Proteomics</i> , 2007 , 7, 413-23	4.8	48
14	Identification of genes involved in salt adaptation in the archaeon Methanosarcina mazei Gil using genome-wide gene expression profiling. <i>FEMS Microbiology Letters</i> , 2007 , 277, 79-89	2.9	34
13	Transcriptional and metabolic responses of Bacillus subtilis to the availability of organic acids: transcription regulation is important but not sufficient to account for metabolic adaptation. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 499-507	4.8	58
12	DNA microarray technology for the microbiologist: an overview. <i>Applied Microbiology and Biotechnology</i> , 2006 , 73, 255-73	5.7	86
11	Cell envelope stress response in Bacillus licheniformis: integrating comparative genomics, transcriptional profiling, and regulon mining to decipher a complex regulatory network. <i>Journal of Bacteriology</i> , 2006 , 188, 7500-11	3.5	26
10	The extracellular proteome of Bacillus licheniformis grown in different media and under different nutrient starvation conditions. <i>Proteomics</i> , 2006 , 6, 268-81	4.8	99

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9	The phosphate-starvation response of Bacillus licheniformis. <i>Proteomics</i> , 2006 , 6, 3582-601	4.8	35	
8	Global transcriptional analysis of Methanosarcina mazei strain GII under different nitrogen availabilities. <i>Molecular Genetics and Genomics</i> , 2006 , 276, 41-55	3.1	48	
7	Complete genome sequence of the acetic acid bacterium Gluconobacter oxydans. <i>Nature Biotechnology</i> , 2005 , 23, 195-200	44.5	330	
6	DNA microarray analysis of Methanosarcina mazei GII reveals adaptation to different methanogenic substrates. <i>Molecular Genetics and Genomics</i> , 2005 , 273, 225-39	3.1	69	
5	A proteomic view of cell physiology of Bacillus licheniformis. <i>Proteomics</i> , 2004 , 4, 1465-90	4.8	62	
4	The complete genome sequence of Bacillus licheniformis DSM13, an organism with great industrial potential. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2004 , 7, 204-11	0.9	241	
3	Analysis of the domain structure and the DNA binding site of the transcriptional activator FhlA. <i>FEBS Journal</i> , 2000 , 267, 3672-84		23	
2	Ferrous iron oxidation by anoxygenic phototrophic bacteria. <i>Nature</i> , 1993 , 362, 834-836	50.4	559	
1	Selenoprotein synthesis in E. coli. Purification and characterisation of the enzyme catalysing selenium activation. <i>FEBS Journal</i> , 1992 , 206, 767-73		88	