

Armin Ehrenreich

List of Publications by Citations

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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

papers

3,741

citations

32

h-index

61

g-index

62

ext. papers

4,145

ext. citations

5.8

avg, IF

4.88

L-index

#	Paper	IF	Citations
62	Ferrous iron oxidation by anoxygenic phototrophic bacteria. <i>Nature</i> , 1993 , 362, 834-836	50.4	559
61	<i>Clostridium ljungdahlii</i> 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
60	Complete genome sequence of the acetic acid bacterium <i>Gluconobacter oxydans</i> . <i>Nature Biotechnology</i> , 2005 , 23, 195-200	44.5	330
59	The complete genome sequence of <i>Bacillus licheniformis</i> DSM13, an organism with great industrial potential. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2004 , 7, 204-11	0.9	241
58	The extracellular proteome of <i>Bacillus licheniformis</i> grown in different media and under different nutrient starvation conditions. <i>Proteomics</i> , 2006 , 6, 268-81	4.8	99
57	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
56	Selenoprotein synthesis in <i>E. coli</i> . Purification and characterisation of the enzyme catalysing selenium activation. <i>FEBS Journal</i> , 1992 , 206, 767-73		88
55	Physiology of acetic acid bacteria in light of the genome sequence of <i>Gluconobacter oxydans</i> . <i>Journal of Molecular Microbiology and Biotechnology</i> , 2009 , 16, 69-80	0.9	86
54	DNA microarray technology for the microbiologist: an overview. <i>Applied Microbiology and Biotechnology</i> , 2006 , 73, 255-73	5.7	86
53	Genome-wide transcriptome analyses of the <i>Knallgas</i> bacterium <i>Ralstonia eutropha</i> H16 with regard to polyhydroxyalkanoate metabolism. <i>Microbiology (United Kingdom)</i> , 2010 , 156, 2136-2152	2.9	78
52	Genome-wide gene expression analysis of the switch between acidogenesis and solventogenesis in continuous cultures of <i>Clostridium acetobutylicum</i> . <i>Journal of Molecular Microbiology and Biotechnology</i> , 2011 , 20, 1-15	0.9	75
51	Modifying the product pattern of <i>Clostridium acetobutylicum</i> : physiological effects of disrupting the acetate and acetone formation pathways. <i>Applied Microbiology and Biotechnology</i> , 2012 , 94, 743-54	5.7	70
50	DNA microarray analysis of <i>Methanosarcina mazei</i> G11 reveals adaptation to different methanogenic substrates. <i>Molecular Genetics and Genomics</i> , 2005 , 273, 225-39	3.1	69
49	Transcriptional analysis of catabolite repression in <i>Clostridium acetobutylicum</i> growing on mixtures of D-glucose and D-xylose. <i>Journal of Biotechnology</i> , 2010 , 150, 315-23	3.7	67
48	Alternative hosts for functional (meta)genome analysis. <i>Applied Microbiology and Biotechnology</i> , 2014 , 98, 8099-109	5.7	66
47	A proteomic and transcriptional view of acidogenic and solventogenic steady-state cells of <i>Clostridium acetobutylicum</i> in a chemostat culture. <i>Applied Microbiology and Biotechnology</i> , 2010 , 87, 2209-26	5.7	64
46	A proteomic view of cell physiology of <i>Bacillus licheniformis</i> . <i>Proteomics</i> , 2004 , 4, 1465-90	4.8	62

45	Transcriptional and metabolic responses of <i>Bacillus subtilis</i> to the availability of organic acids: transcription regulation is important but not sufficient to account for metabolic adaptation. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 499-507	4.8	58
44	The role of PerR in O ₂ -affected gene expression of <i>Clostridium acetobutylicum</i> . <i>Journal of Bacteriology</i> , 2009 , 191, 6082-93	3.5	51
43	A transcriptional study of acidogenic chemostat cells of <i>Clostridium acetobutylicum</i> --solvent stress caused by a transient n-butanol pulse. <i>Journal of Biotechnology</i> , 2012 , 161, 354-65	3.7	50
42	Deletion of pyruvate decarboxylase by a new method for efficient markerless gene deletions in <i>Gluconobacter oxydans</i> . <i>Applied Microbiology and Biotechnology</i> , 2013 , 97, 2521-30	5.7	49
41	The glucose and nitrogen starvation response of <i>Bacillus licheniformis</i> . <i>Proteomics</i> , 2007 , 7, 413-23	4.8	48
40	Global transcriptional analysis of <i>Methanosarcina mazei</i> strain G1 under different nitrogen availabilities. <i>Molecular Genetics and Genomics</i> , 2006 , 276, 41-55	3.1	48
39	Characterization of membrane-bound dehydrogenases from <i>Gluconobacter oxydans</i> 621H via whole-cell activity assays using multideletion strains. <i>Applied Microbiology and Biotechnology</i> , 2013 , 97, 6397-412	5.7	46
38	Global transcriptional changes of <i>Clostridium acetobutylicum</i> cultures with increased butanol:acetone ratios. <i>New Biotechnology</i> , 2012 , 29, 485-93	6.4	41
37	A transcriptional study of acidogenic chemostat cells of <i>Clostridium acetobutylicum</i> --cellular behavior in adaptation to n-butanol. <i>Journal of Biotechnology</i> , 2012 , 161, 366-77	3.7	41
36	Identification of genes essential for anaerobic growth of <i>Listeria monocytogenes</i> . <i>Microbiology (United Kingdom)</i> , 2014 , 160, 752-765	2.9	36
35	Proteomic and transcriptomic elucidation of the mutant <i>Ralstonia eutropha</i> G+1 with regard to glucose utilization. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 2058-70	4.8	36
34	Characterization of membrane-bound dehydrogenases of <i>Gluconobacter oxydans</i> 621H using a new system for their functional expression. <i>Applied Microbiology and Biotechnology</i> , 2017 , 101, 3189-3200	5.7	35
33	The phosphate-starvation response of <i>Bacillus licheniformis</i> . <i>Proteomics</i> , 2006 , 6, 3582-601	4.8	35
32	Identification of genes involved in salt adaptation in the archaeon <i>Methanosarcina mazei</i> G1 using genome-wide gene expression profiling. <i>FEMS Microbiology Letters</i> , 2007 , 277, 79-89	2.9	34
31	Sequence similarity of <i>Clostridium difficile</i> 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
30	Importance of <i>codB</i> for new <i>codA</i> -based markerless gene deletion in <i>Gluconobacter</i> strains. <i>Applied Microbiology and Biotechnology</i> , 2013 , 97, 8341-9	5.7	31
29	RACK1/Asc1p, a ribosomal node in cellular signaling. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 87-1057.6		31
28	Impact of multiple beta-ketothiolase deletion mutations in <i>Ralstonia eutropha</i> H16 on the composition of 3-mercaptopropionic acid-containing copolymers. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 5373-82	4.8	31

27	Regulation of acetoin and 2,3-butanediol utilization in <i>Bacillus licheniformis</i> . <i>Applied Microbiology and Biotechnology</i> , 2010 , 87, 2227-35	5.7	31
26	Facilitation of direct conditional knockout of essential genes in <i>Bacillus licheniformis</i> DSM13 by comparative genetic analysis and manipulation of genetic competence. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 5046-57	4.8	30
25	Effect of iron limitation and fur gene inactivation on the transcriptional profile of the strict anaerobe <i>Clostridium acetobutylicum</i> . <i>Microbiology (United Kingdom)</i> , 2012 , 158, 1918-1929	2.9	29
24	Metabolic engineering of <i>Bacillus subtilis</i> for growth on overflow metabolites. <i>Microbial Cell Factories</i> , 2013 , 12, 72	6.4	26
23	Cell envelope stress response in <i>Bacillus licheniformis</i> : 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
22	Insights into the NrpR regulon in <i>Methanosarcina mazei</i> G β . <i>Archives of Microbiology</i> , 2008 , 190, 319-323	3	25
21	Cell physiology and protein secretion of <i>Bacillus licheniformis</i> compared to <i>Bacillus subtilis</i> . <i>Journal of Molecular Microbiology and Biotechnology</i> , 2009 , 16, 53-68	0.9	23
20	Analysis of the domain structure and the DNA binding site of the transcriptional activator FhIA. <i>FEBS Journal</i> , 2000 , 267, 3672-84		23
19	Complete Genome Sequence of the Solvent Producer <i>Clostridium saccharobutylicum</i> NCP262 (DSM 13864). <i>Genome Announcements</i> , 2013 , 1,		20
18	Development of an in vivo methylation system for the solventogen <i>Clostridium saccharobutylicum</i> NCP 262 and analysis of two endonuclease mutants. <i>Journal of Biotechnology</i> , 2014 , 188, 97-9	3.7	17
17	Size unlimited markerless deletions by a transconjugative plasmid-system in <i>Bacillus licheniformis</i> . <i>Journal of Biotechnology</i> , 2013 , 167, 365-9	3.7	16
16	Expression of membrane-bound dehydrogenases from a mother of vinegar metagenome in <i>Gluconobacter oxydans</i> . <i>Applied Microbiology and Biotechnology</i> , 2017 , 101, 7901-7912	5.7	14
15	Investigations on the microbial catabolism of the organic sulfur compounds TDP and DTDP in <i>Ralstonia eutropha</i> H16 employing DNA microarrays. <i>Applied Microbiology and Biotechnology</i> , 2010 , 88, 1145-59	5.7	14
14	Characterization and inactivation of the membrane-bound polyol dehydrogenase in <i>Gluconobacter oxydans</i> DSM 7145 reveals a role in meso-erythritol oxidation. <i>Microbiology (United Kingdom)</i> , 2010 , 156, 1890-1899	2.9	13
13	Chemostat cultivation and transcriptional analyses of <i>Clostridium acetobutylicum</i> mutants with defects in the acid and acetone biosynthetic pathways. <i>Applied Microbiology and Biotechnology</i> , 2014 , 98, 9777-94	5.7	12
12	Identification of ecotype-specific marker genes for categorization of beer-spoiling <i>Lactobacillus brevis</i> . <i>Food Microbiology</i> , 2015 , 51, 130-8	6	11
11	Markerless deletion of putative alanine dehydrogenase genes in <i>Bacillus licheniformis</i> using a codBA-based counterselection technique. <i>Microbiology (United Kingdom)</i> , 2017 , 163, 1532-1539	2.9	10
10	Temperature- and nitrogen source-dependent regulation of GlnR target genes in <i>Listeria monocytogenes</i> . <i>FEMS Microbiology Letters</i> , 2014 , 355, 131-41	2.9	8

9	L-Erythrulose production with a multideletion strain of <i>Gluconobacter oxydans</i> . <i>Applied Microbiology and Biotechnology</i> , 2019 , 103, 4393-4404	5.7	7
8	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
7	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
6	Coping with anoxia: a comprehensive proteomic and transcriptomic survey of denitrification. <i>Journal of Proteome Research</i> , 2014 , 13, 4325-38	5.6	4
5	Monitoring co-cultures of <i>Clostridium carboxidivorans</i> and <i>Clostridium kluveri</i> by fluorescence in situ hybridization with specific 23S rRNA oligonucleotide probes. <i>Systematic and Applied Microbiology</i> , 2021 , 44, 126271	4.2	3
4	Synthetic co-culture of autotrophic <i>Clostridium carboxidivorans</i> and chain elongating <i>Clostridium kluveri</i> monitored by flow cytometry. <i>Microbial Biotechnology</i> , 2021 ,	6.3	3
3	The Genomes of Acetic Acid Bacteria 2017 , 469-494		2
2	The Roles of the Various Cellulose Biosynthesis Operons in ATCC 23769.. <i>Applied and Environmental Microbiology</i> , 2022 , e0246021	4.8	1
1	The Genome of Acetic Acid Bacteria 2009 , 379-394		