

# Wolfgang Liebl

## List of Publications by Year in descending order

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163  
papers

6,663  
citations

66343

42  
h-index

76900

74  
g-index

168  
all docs

168  
docs citations

168  
times ranked

6570  
citing authors

#	ARTICLE	IF	CITATIONS
1	Towards valorization of pectin-rich agro-industrial residues: Engineering of <i>Saccharomyces cerevisiae</i> for co-fermentation of d-galacturonic acid and glycerol. <i>Metabolic Engineering</i> , 2022, 69, 1-14.	7.0	9
2	Synthetic co-culture of autotrophic <i>Clostridium carboxidivorans</i> and chain elongating <i>Clostridium kluyveri</i> monitored by flow cytometry. <i>Microbial Biotechnology</i> , 2022, 15, 1471-1485.	4.2	16
3	Molecular biology: Fantastic toolkits to improve knowledge and application of acetic acid bacteria. <i>Biotechnology Advances</i> , 2022, 58, 107911.	11.7	10
4	Unusual substrate specificity in GH family 12: structure-function analysis of glucanases Bgh12A and Xgh12B from <i>Aspergillus cervinus</i> , and Egh12 from <i>Thielavia terrestris</i> . <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 1493-1509.	3.6	4
5	The Roles of the Various Cellulose Biosynthesis Operons in <i>Komagataeibacter hansenii</i> ATCC 23769. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0246021.	3.1	12
6	Oxidative Fermentation of Acetic Acid Bacteria and Its Products. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	8
7	Complete Utilization of the Major Carbon Sources Present in Sugar Beet Pulp Hydrolysates by the Oleaginous Red Yeasts <i>Rhodotorula toruloides</i> and <i>R. mucilaginosa</i> . <i>Journal of Fungi (Basel)</i> , 2022, 8, 1071-1081.	0.784314	10
8	Draft Genome Sequence of <i>Clostridium beijerinckii</i> Strain mbf-VZ-132, Isolated from an Environmental Soil Sample. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	0
9	Draft Genome Sequence of <i>Mobilitalea sibirica</i> Strain P3M-3, the Sole Representative of the Genus <i>Mobilitalea</i> . <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	1
10	Characterization of Two $\alpha$ -L-Arabinofuranosidases from <i>Acetivibrio mesophilus</i> and Their Synergistic Effect in Degradation of Arabinose-Containing Substrates. <i>Microorganisms</i> , 2021, 9, 1467.	3.6	8
11	Identification of New Chromosomal Loci Involved in com Genes Expression and Natural Transformation in the Actinobacterial Model Organism <i>Micrococcus luteus</i> . <i>Genes</i> , 2021, 12, 1307.	2.4	1
12	Monitoring co-cultures of <i>Clostridium carboxidivorans</i> and <i>Clostridium kluyveri</i> by fluorescence in situ hybridization with specific 23S rRNA oligonucleotide probes. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126271.	2.8	8
13	<i>Variimorphobacter saccharofermentans</i> gen. nov., sp. nov., a new member of the family Lachnospiraceae, isolated from a maize-fed biogas fermenter. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	12
14	A Novel Primer Mixture for GH48 Genes: Quantification and Identification of Truly Cellulolytic Bacteria in Biogas Fermenters. <i>Microorganisms</i> , 2020, 8, 1297.	3.6	3
15	Milling byproducts are an economically viable substrate for butanol production using clostridial ABE fermentation. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 8679-8689.	3.6	8
16	Importance of <i>Defluviitalea raffinosedens</i> for Hydrolytic Biomass Degradation in Co-Culture with <i>Hungateiclostridium thermocellum</i> . <i>Microorganisms</i> , 2020, 8, 915.	3.6	13
17	Draft Genome Sequence of <i>Paenibacillus polymyxa</i> DSM 292, a Gram-Positive, Spore-Forming Soil Bacterium with High Biotechnological Potential. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
18	Meltome atlas thermal proteome stability across the tree of life. <i>Nature Methods</i> , 2020, 17, 495-503.	19.0	152

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19	Distribution and diversity of olefins and olefin-biosynthesis genes in Gram-positive bacteria. <i>Biotechnology for Biofuels</i> , 2020, 13, 70.	6.2	6
20	<i>Anaerospaera multitolerans</i> sp. nov., a salt-tolerant member of the family Peptoniphilaceae isolated from a mesophilically operated biogas fermenter fed with maize silage. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1217-1223.	1.7	6
21	Novel endo-(1,4)- $\beta$ -glucanase Bgh12A and xyloglucanase Xgh12B from <i>Aspergillus cervinus</i> belong to GH12 subgroup I and II, respectively. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 7553-7566.	3.6	11
22	Amino acids as nutritional factors and (p)ppGpp as an alarmone of the stringent response regulate natural transformation in <i>Micrococcus luteus</i> . <i>Scientific Reports</i> , 2019, 9, 11030.	3.3	5
23	Comparison of sampling techniques and different media for the enrichment and isolation of cellulolytic organisms from biogas fermenters. <i>Systematic and Applied Microbiology</i> , 2019, 42, 481-487.	2.8	5
24	Draft Genome Sequence of <i>Anaerospaera</i> sp. Strain GS7-6-2, a Coccal Bacterium Isolated from a Biogas-Related Environment. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
25	L-Erythrose production with a multideletion strain of <i>Gluconobacter oxydans</i> . <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 4393-4404.	3.6	13
26	An efficient method for markerless mutant generation by allelic exchange in <i>Clostridium acetobutylicum</i> and <i>Clostridium saccharobutylicum</i> using suicide vectors. <i>Biotechnology for Biofuels</i> , 2019, 12, 31.	6.2	11
27	Biochemical characterisation of four rhamnosidases from thermophilic bacteria of the genera <i>Thermotoga</i> , <i>Caldicellulosiruptor</i> and <i>Thermoclostridium</i> . <i>Scientific Reports</i> , 2019, 9, 15924.	3.3	13
28	<i>Hungateiclostridium mesophilum</i> sp. nov., a mesophilic, cellulolytic and spore-forming bacterium isolated from a biogas fermenter fed with maize silage. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3567-3573.	1.7	22
29	<i>Ruminiclostridium herbifermentans</i> sp. nov., a mesophilic and moderately thermophilic cellulolytic and xylanolytic bacterium isolated from a lab-scale biogas fermenter fed with maize silage. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	1.7	10
30	Handling gene and protein names in the age of bioinformatics: the special challenge of secreted multimodular bacterial enzymes such as the <i>cbhA/cbh9A</i> gene of <i>Clostridium thermocellum</i> . <i>World Journal of Microbiology and Biotechnology</i> , 2018, 34, 42.	3.6	2
31	Complete Genome Sequence of the Novel Cellulolytic, Anaerobic, Thermophilic Bacterium <i>Herbivorax saccincola</i> Type Strain GGR1, Isolated from a Lab Scale Biogas Reactor as Established by Illumina and Nanopore MinION Sequencing. <i>Genome Announcements</i> , 2018, 6, .	0.8	10
32	Evaluation of promoter sequences for the secretory production of a <i>Clostridium thermocellum</i> cellulase in <i>Paenibacillus polymyxa</i> . <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 10147-10159.	3.6	7
33	Restriction-deficient mutants and marker-less genomic modification for metabolic engineering of the solvent producer <i>Clostridium saccharobutylicum</i> . <i>Biotechnology for Biofuels</i> , 2018, 11, 264.	6.2	12
34	Variances in cellular sedimentation behavior as an effective enrichment method of hydrocarbon-overproducing <i>Micrococcus luteus</i> strains. <i>Biotechnology for Biofuels</i> , 2018, 11, 288.	6.2	0
35	Addition of $\beta$ -galactosidase boosts the xyloglucan degradation capability of endoglucanase Cel9D from <i>Clostridium thermocellum</i> . <i>Biotechnology for Biofuels</i> , 2018, 11, 238.	6.2	6
36	Transmating: conjugative transfer of a new broad host range expression vector to various <i>Bacillus</i> species using a single protocol. <i>BMC Microbiology</i> , 2018, 18, 56.	3.3	15

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37	Impact of Branched-Chain Amino Acid Catabolism on Fatty Acid and Alkene Biosynthesis in <i>Micrococcus luteus</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 374.	3.5	29
38	The hemicellulose-degrading enzyme system of the thermophilic bacterium <i>Clostridium stercorarium</i> : comparative characterisation and addition of new hemicellulolytic glycoside hydrolases. <i>Biotechnology for Biofuels</i> , 2018, 11, 229.	6.2	62
39	Optimizing the composition of a synthetic cellulosome complex for the hydrolysis of softwood pulp: identification of the enzymatic core functions and biochemical complex characterization. <i>Biotechnology for Biofuels</i> , 2018, 11, 220.	6.2	19
40	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.	3.6	44
41	Thermostable multifunctional GH74 xyloglucanase from <i>Myceliophthora thermophila</i> : high-level expression in <i>Pichia pastoris</i> and characterization of the recombinant protein. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 5653-5666.	3.6	21
42	A new method to evaluate temperature vs. pH activity profiles for biotechnological relevant enzymes. <i>Biotechnology for Biofuels</i> , 2017, 10, 234.	6.2	39
43	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.	3.6	17
44	HPAEC-PAD for oligosaccharide analysis—novel insights into analyte sensitivity and response stability. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 7169-7181.	3.7	26
45	Identification of endoxylanase XynE from <i>Clostridium thermocellum</i> as the first xylanase of glycoside hydrolase family GH141. <i>Scientific Reports</i> , 2017, 7, 11178.	3.3	27
46	The Genomes of Acetic Acid Bacteria. , 2017, , 469-494.		3
47	A metagenome-derived thermostable $\beta$ -glucanase with an unusual module architecture which defines the new glycoside hydrolase family GH148. <i>Scientific Reports</i> , 2017, 7, 17306.	3.3	15
48	Genomics and prevalence of bacterial and archaeal isolates from biogas-producing microbiomes. <i>Biotechnology for Biofuels</i> , 2017, 10, 264.	6.2	50
49	Comparative characterization of all cellulosomal cellulases from <i>Clostridium thermocellum</i> reveals high diversity in endoglucanase product formation essential for complex activity. <i>Biotechnology for Biofuels</i> , 2017, 10, 240.	6.2	45
50	Novel archaeal thermostable cellulases from an oil reservoir metagenome. <i>AMB Express</i> , 2017, 7, 183.	3.0	38
51	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.	1.8	12
52	DNA and RNA Extraction and Quantitative Real-Time PCR-Based Assays for Biogas Biocenoses in an Interlaboratory Comparison. <i>Bioengineering</i> , 2016, 3, 7.	3.5	23
53	Unraveling the microbiome of a thermophilic biogas plant by metagenome and metatranscriptome analysis complemented by characterization of bacterial and archaeal isolates. <i>Biotechnology for Biofuels</i> , 2016, 9, 171.	6.2	134
54	Draft Genome Sequence of <i>Propionispora</i> sp. Strain 2/2-37, a New Xylan-Degrading Bacterium Isolated from a Mesophilic Biogas Reactor. <i>Genome Announcements</i> , 2016, 4, .	0.8	1

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55	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.	3.7	133
56	Complete Genome Sequence of <i>Herbinix luporum</i> SD1D, a New Cellulose-Degrading Bacterium Isolated from a Thermophilic Biogas Reactor. <i>Genome Announcements</i> , 2016, 4, .	0.8	8
57	Flow cytometric sorting of fecal bacteria after in situ hybridization with polynucleotide probes. <i>Systematic and Applied Microbiology</i> , 2016, 39, 464-475.	2.8	10
58	Structural basis for cellulose binding by the type A carbohydrate-binding module 64 of <i>Picrochaeta thermophila</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 855-858.	2.6	16
59	<i>Herbivorax saccincola</i> gen. nov., sp. nov., a cellulolytic, anaerobic, thermophilic bacterium isolated via in sacco enrichments from a lab-scale biogas reactor. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 4458-4463.	1.7	35
60	Functional Screening of Hydrolytic Activities Reveals an Extremely Thermostable Cellulase from a Deep-Sea Archaeon. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 95.	4.1	26
61	Identification of novel esterase-active enzymes from hot environments by use of the host bacterium <i>Thermus thermophilus</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 275.	3.5	65
62	<i>Herbinix hemicellulosilytica</i> gen. nov., sp. nov., a thermophilic cellulose-degrading bacterium isolated from a thermophilic biogas reactor. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 2365-2371.	1.7	90
63	Complete Genome Sequence of the Linear Plasmid pJD12 Hosted by <i>Micrococcus</i> sp. D12, Isolated from a High-Altitude Volcanic Lake in Argentina. <i>Genome Announcements</i> , 2015, 3, .	0.8	11
64	The consequence of an additional NADH dehydrogenase paralog on the growth of <i>Gluconobacter oxydans</i> DSM3504. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 375-386.	3.6	21
65	Novel Flp pilus biogenesis-dependent natural transformation. <i>Frontiers in Microbiology</i> , 2015, 6, 84.	3.5	33
66	Characterization of chromosomal and megaplasmid partitioning loci in <i>Thermus thermophilus</i> HB27. <i>BMC Genomics</i> , 2015, 16, 317.	2.8	8
67	Draft genome sequence of <i>Herbinix hemicellulosilytica</i> T3/55T, a new thermophilic cellulose degrading bacterium isolated from a thermophilic biogas reactor. <i>Journal of Biotechnology</i> , 2015, 214, 59-60.	3.8	21
68	Differences in biomass degradation between newly isolated environmental strains of <i>Clostridium thermocellum</i> and heterogeneity in the size of the cellulosomal scaffoldin. <i>Systematic and Applied Microbiology</i> , 2015, 38, 424-432.	2.8	16
69	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, 9777-9794.	3.6	12
70	First draft genome sequence of the amylolytic <i>Bacillus thermoamylovorans</i> wild-type strain 1A1 isolated from a thermophilic biogas plant. <i>Journal of Biotechnology</i> , 2014, 192, 154-155.	3.8	15
71	Alternative hosts for functional (meta)genome analysis. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 8099-8109.	3.6	77
72	Complete genome sequence of the cellulolytic thermophile <i>Ruminoclostridium cellulosi</i> wild-type strain DG5 isolated from a thermophilic biogas plant. <i>Journal of Biotechnology</i> , 2014, 188, 136-137.	3.8	30

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73	Genetic analysis of lipolytic activities in <i>Thermus thermophilus</i> HB27. <i>Journal of Biotechnology</i> , 2014, 191, 150-157.	3.8	13
74	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, 97-99.	3.8	18
75	Comparative genotyping of <i>Clostridium thermocellum</i> strains isolated from biogas plants: Genetic markers and characterization of cellulolytic potential. <i>Systematic and Applied Microbiology</i> , 2014, 37, 311-319.	2.8	24
76	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.	2.5	39
77	Size unlimited markerless deletions by a transconjugative plasmid-system in <i>Bacillus licheniformis</i> . <i>Journal of Biotechnology</i> , 2013, 167, 365-369.	3.8	23
78	Toxicity of indoxyl derivative accumulation in bacteria and its use as a new counterselection principle. <i>Systematic and Applied Microbiology</i> , 2013, 36, 585-592.	2.8	20
79	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, 6397-6412.	3.6	56
80	Extrachromosomal genetic elements in <i>Micrococcus</i> . <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 63-75.	3.6	36
81	Comparative direct infusion ion mobility mass spectrometry profiling of <i>Thermus thermophilus</i> wild-type and mutant $\Delta$ trcC carotenoid extracts. <i>Analytical and Bioanalytical Chemistry</i> , 2013, 405, 9843-9848.	3.7	9
82	Screening and Expression of Genes from Metagenomes. <i>Advances in Applied Microbiology</i> , 2013, 83, 1-68.	2.4	43
83	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, 8341-8349.	3.6	46
84	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, 2521-2530.	3.6	56
85	Complete Genome Sequence of <i>Clostridium stercorarium</i> subsp. <i>stercorarium</i> Strain DSM 8532, a Thermophilic Degrader of Plant Cell Wall Fibers. <i>Genome Announcements</i> , 2013, 1, e0007313.	0.8	18
86	Complete Genome Sequence of the Solvent Producer <i>Clostridium saccharobutylicum</i> NCP262 (DSM Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.8	21
87	Thermostable Xylanase and $\alpha$ -Glucanase Derived from the Metagenome of the Avachinsky Crater in Kamchatka (Russia). <i>Current Biotechnology</i> , 2013, 2, 284-293.	0.4	8
88	Involvement of Two Latex-Clearing Proteins during Rubber Degradation and Insights into the Subsequent Degradation Pathway Revealed by the Genome Sequence of <i>Gordonia polyisoprenivorans</i> Strain VH2. <i>Applied and Environmental Microbiology</i> , 2012, 78, 2874-2887.	3.1	78
89	Structure-functional analysis of the <i>Dictyoglomus</i> cell envelope. <i>Systematic and Applied Microbiology</i> , 2012, 35, 279-290.	2.8	10
90	Metagenomic cellulases highly tolerant towards the presence of ionic liquids-linking thermostability and halotolerance. <i>Applied Microbiology and Biotechnology</i> , 2012, 95, 135-146.	3.6	83

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91	Biochemie 2010. Nachrichten Aus Der Chemie, 2011, 59, 297-318.	0.0	0
92	Characterization of Plasmid pPO1 from the Hyperacidophile <i>Picrophilus oshimae</i> . Archaea, 2011, 2011, 1-4.	2.3	5
93	Genomic analysis reveals <i>Lactobacillus sanfranciscensis</i> as stable element in traditional sourdoughs. Microbial Cell Factories, 2011, 10, S6.	4.0	101
94	Proteomic analysis of the extremely thermoacidophilic archaeon <i>Picrophilus torridus</i> at pH and temperature values close to its growth limit. Proteomics, 2011, 11, 4559-4568.	2.2	13
95	Novel Family of Carbohydrate-Binding Modules Revealed by the Genome Sequence of <i>Spirochaeta thermophila</i> DSM 6192. Applied and Environmental Microbiology, 2011, 77, 5483-5489.	3.1	12
96	Genome-Wide Gene Expression Analysis of the Switch between Acidogenesis and Solventogenesis in Continuous Cultures of <i>Clostridium acetobutylicum</i> . Journal of Molecular Microbiology and Biotechnology, 2011, 20, 1-15.	1.0	82
97	Metagenomics. Encyclopedia of Earth Sciences Series, 2011, , 553-558.	0.1	2
98	<i>Clostridium ljungdahlii</i> represents a microbial production platform based on syngas. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 13087-13092.	7.1	594
99	Hyperthermostable acetyl xylan esterase. Microbial Biotechnology, 2010, 3, 84-92.	4.2	25
100	Transcriptional analysis of catabolite repression in <i>Clostridium acetobutylicum</i> growing on mixtures of d-glucose and d-xylose. Journal of Biotechnology, 2010, 150, 315-323.	3.8	76
101	The complete genome sequence of the algal symbiont <i>Dinoroseobacter shibae</i> : a hitchhiker's guide to life in the sea. ISME Journal, 2010, 4, 61-77.	9.8	244
102	Genome Sequence of the Polysaccharide-Degrading, Thermophilic Anaerobe <i>Spirochaeta thermophila</i> DSM 6192. Journal of Bacteriology, 2010, 192, 6492-6493.	2.2	19
103	Characterization and inactivation of the membrane-bound polyol dehydrogenase in <i>Gluconobacter oxydans</i> DSM 7145 reveals a role in meso-erythritol oxidation. Microbiology (United Kingdom), 2010, 156, 1890-1899.	1.8	17
104	The Genome of a <i>Bacillus</i> Isolate Causing Anthrax in Chimpanzees Combines Chromosomal Properties of <i>B. cereus</i> with <i>B. anthracis</i> Virulence Plasmids. PLoS ONE, 2010, 5, e10986.	2.5	157
105	Rapid Access to Genes of Biotechnologically Useful Enzymes by Partial Genome Sequencing: The Thermoalkaliphile <i>Anaerobranca gottschalkii</i> . Journal of Molecular Microbiology and Biotechnology, 2009, 16, 81-90.	1.0	7
106	A two-host fosmid system for functional screening of (meta)genomic libraries from extreme thermophiles. Systematic and Applied Microbiology, 2009, 32, 177-185.	2.8	65
107	Phytate utilization by genetically engineered lysine-producing <i>Corynebacterium glutamicum</i> . Journal of Biotechnology, 2008, 134, 211-217.	3.8	4
108	Xylanase Attachment to the Cell Wall of the Hyperthermophilic Bacterium <i>Thermotoga maritima</i> . Journal of Bacteriology, 2008, 190, 1350-1358.	2.2	34

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109	Insights into extreme thermoacidophily based on genome analysis of <i>Picrophilus torridus</i> and other thermoacidophilic archaea. <i>Journal of Biotechnology</i> , 2006, 126, 3-10.	3.8	49
110	Identification and Characterization of a Novel Intracellular Alkaline $\alpha$ -Amylase from the Hyperthermophilic Bacterium <i>Thermotoga maritima</i> MSB8. <i>Applied and Environmental Microbiology</i> , 2006, 72, 2206-2211.	3.1	60
111	Structure of the novel $\alpha$ -amylase AmyC from <i>Thermotoga maritima</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 262-270.	2.5	34
112	Comparative characterization of deletion derivatives of the modular xylanase XynA of <i>Thermotoga maritima</i> . <i>Extremophiles</i> , 2006, 10, 373-381.	2.3	20
113	Molecular and Biochemical Characterization of $\alpha$ -Glucosidase and $\alpha$ -Mannosidase and Their Clustered Genes from the Thermoacidophilic Archaeon <i>Picrophilus torridus</i> . <i>Journal of Bacteriology</i> , 2006, 188, 7123-7131.	2.2	43
114	<i>Corynebacterium</i> -Nonmedical. , 2006, , 796-818.		20
115	Properties of the recombinant glucose/galactose dehydrogenase from the extreme thermoacidophile, <i>Picrophilus torridus</i> . <i>FEBS Journal</i> , 2005, 272, 1054-1062.	4.7	32
116	AmyA, an $\alpha$ -Amylase with $\alpha$ -Cyclodextrin-Forming Activity, and AmyB from the Thermoalkaliphilic Organism <i>Anaerobranca gottschalkii</i> : Two $\alpha$ -Amylases Adapted to Their Different Cellular Localizations. <i>Applied and Environmental Microbiology</i> , 2005, 71, 3709-3715.	3.1	27
117	Genome sequence of <i>Picrophilus torridus</i> and its implications for life around pH 0. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9091-9096.	7.1	231
118	Cloning, Sequencing, and Characterization of a Heat- and Alkali-Stable Type I Pullulanase from <i>Anaerobranca gottschalkii</i> . <i>Applied and Environmental Microbiology</i> , 2004, 70, 3407-3416.	3.1	70
119	Genomics taken to the extreme. <i>Nature Biotechnology</i> , 2004, 22, 524-525.	17.5	9
120	Title is missing!. <i>Molecular Biology</i> , 2003, 37, 686-694.	1.3	4
121	Title is missing!. <i>Molecular Biology</i> , 2003, 37, 678-685.	1.3	6
122	Crystal Structure of <i>Thermotoga maritima</i> $\alpha$ -Glucosidase AglA Defines a New Clan of NAD <sup>+</sup> -dependent Glycosidases. <i>Journal of Biological Chemistry</i> , 2003, 278, 19151-19158.	3.4	56
123	Genetic dissection of trehalose biosynthesis in <i>Corynebacterium glutamicum</i> : inactivation of trehalose production leads to impaired growth and an altered cell wall lipid composition. <i>Microbiology (United Kingdom)</i> , 2003, 149, 1659-1673.	1.8	86
124	Comparative Analysis of the Recombinant $\alpha$ -Glucosidases from the <i>Thermotoga neapolitana</i> and <i>Thermotoga maritima</i> Maltodextrin Utilization Gene Clusters. <i>Biocatalysis and Biotransformation</i> , 2003, 21, 147-158.	2.0	3
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