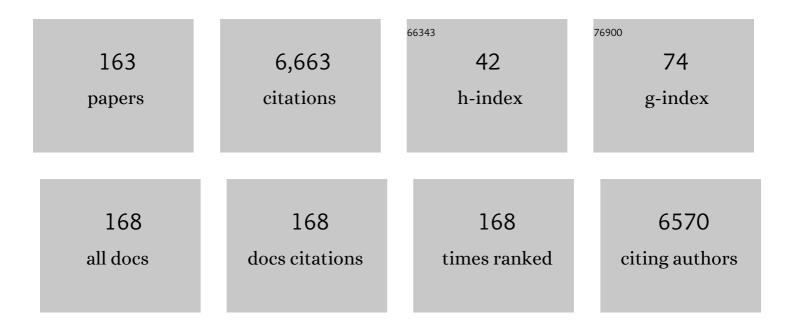
Wolfgang Liebl

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6425187/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	<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
2	Thermophilic Adaptation of Proteins. Critical Reviews in Biochemistry and Molecular Biology, 2001, 36, 39-106.	5.2	338
3	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
4	Genome sequence ofPicrophilus torridusand its implications for life around pH 0. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 9091-9096.	7.1	231
5	A family of Corynebacterium glutamicum/Escherichia coli shuttle vectors for cloning, controlled gene expression, and promoter probing. Gene, 1991, 102, 93-98.	2.2	215
6	Direct Cloning from Enrichment Cultures, a Reliable Strategy for Isolation of Complete Operons and Genes from Microbial Consortia. Applied and Environmental Microbiology, 2001, 67, 89-99.	3.1	168
7	The Genome of a Bacillus Isolate Causing Anthrax in Chimpanzees Combines Chromosomal Properties of B. cereus with B. anthracis Virulence Plasmids. PLoS ONE, 2010, 5, e10986.	2.5	157
8	Meltome atlas—thermal proteome stability across the tree of life. Nature Methods, 2020, 17, 495-503.	19.0	152
9	Identification of a novel cellulose-binding domain the multidomain 120 kDa xylanase XynA of the hyperthermophilic bacterium Thermotoga maritima. Molecular Microbiology, 1995, 15, 431-444.	2.5	146
10	Unraveling the microbiome of a thermophilic biogas plant by metagenome and metatranscriptome analysis complemented by characterization of bacterial and archaeal isolates. Biotechnology for Biofuels, 2016, 9, 171.	6.2	134
11	Gluconic acid: Properties, production methods and applications—An excellent opportunity for agro-industrial by-products and waste bio-valorization. Process Biochemistry, 2016, 51, 1891-1903.	3.7	133
12	Purification and characterization of a novel thermostable 4-alpha-glucanotransferase of Thermotoga maritima cloned in Escherichia coli. FEBS Journal, 1992, 207, 81-88.	0.2	103
13	Genomic analysis reveals Lactobacillus sanfranciscensis as stable element in traditional sourdoughs. Microbial Cell Factories, 2011, 10, S6.	4.0	101
14	Herbinix hemicellulosilytica gen. nov., sp. nov., a thermophilic cellulose-degrading bacterium isolated from a thermophilic biogas reactor. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 2365-2371.	1.7	90
15	Isolation and analysis of genes for amylolytic enzymes of the hyperthermophilic bacteriumThermotoga maritima. FEMS Microbiology Letters, 1998, 158, 9-15.	1.8	88
16	Genetic dissection of trehalose biosynthesis in Corynebacterium glutamicum: inactivation of trehalose production leads to impaired growth and an altered cell wall lipid composition. Microbiology (United Kingdom), 2003, 149, 1659-1673.	1.8	86
17	Metagenomic cellulases highly tolerant towards the presence of ionic liquids—linking thermostability and halotolerance. Applied Microbiology and Biotechnology, 2012, 95, 135-146.	3.6	83
18	Genome-Wide Gene Expression Analysis of the Switch between Acidogenesis and Solventogenesis in Continuous Cultures of Clostridium acetobutylicum. Journal of Molecular Microbiology and Biotechnology, 2011, 20, 1-15.	1.0	82

#	Article	IF	CITATIONS
19	Studies on lipase directed export of Escherichia coli β-lactamase in Staphylococcus carnosus. Molecular Genetics and Genomics, 1986, 204, 166-173.	2.4	81
20	Involvement of Two Latex-Clearing Proteins during Rubber Degradation and Insights into the Subsequent Degradation Pathway Revealed by the Genome Sequence of Gordonia polyisoprenivorans Strain VH2. Applied and Environmental Microbiology, 2012, 78, 2874-2887.	3.1	78
21	Nucleotide sequence and fine structural analysis of theCorynebacterium glutamicum hom-thrBoperon. Molecular Microbiology, 1988, 2, 63-72.	2.5	77
22	Alternative hosts for functional (meta)genome analysis. Applied Microbiology and Biotechnology, 2014, 98, 8099-8109.	3.6	77
23	Transcriptional analysis of catabolite repression in Clostridium acetobutylicum growing on mixtures of d-glucose and d-xylose. Journal of Biotechnology, 2010, 150, 315-323.	3.8	76
24	Crystal Structure of Thermotoga maritima 4-α-Glucanotransferase and its Acarbose Complex: Implications for Substrate Specificity and Catalysis. Journal of Molecular Biology, 2002, 321, 149-162.	4.2	71
25	Cloning, Sequencing, and Characterization of a Heat- and Alkali-Stable Type I Pullulanase from <i>Anaerobranca gottschalkii</i> . Applied and Environmental Microbiology, 2004, 70, 3407-3416.	3.1	70
26	Requirement of chelating compounds for the growth of Corynebacterium glutamicum in synthetic media. Applied Microbiology and Biotechnology, 1989, 32, 205-210.	3.6	66
27	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
28	Identification of novel esterase-active enzymes from hot environments by use of the host bacterium Thermus thermophilus. Frontiers in Microbiology, 2015, 6, 275.	3.5	65
29	The hemicellulose-degrading enzyme system of the thermophilic bacterium Clostridium stercorarium: comparative characterisation and addition of new hemicellulolytic glycoside hydrolases. Biotechnology for Biofuels, 2018, 11, 229.	6.2	62
30	Identification and Characterization of a Novel Intracellular Alkaline α-Amylase from the Hyperthermophilic Bacterium Thermotoga maritima MSB8. Applied and Environmental Microbiology, 2006, 72, 2206-2211.	3.1	60
31	The thermostabilizing domain of the modular xylanase XynA of Thermotoga maritima represents a novel type of binding domain with affinity for soluble xylan and mixed-linkage beta-1,3/beta-1,4-glucan. Molecular Microbiology, 2000, 36, 898-912.	2.5	57
32	Isolation and analysis of a gene encoding αâ€glucuronidase, an enzyme with a novel primary structure involved in the breakdown of xylan. Molecular Microbiology, 1997, 23, 267-279.	2.5	56
33	Crystal Structure of Thermotoga maritima α-Glucosidase AglA Defines a New Clan of NAD+-dependent Glycosidases. Journal of Biological Chemistry, 2003, 278, 19151-19158.	3.4	56
34	Characterization of membrane-bound dehydrogenases from Gluconobacter oxydans 621H via whole-cell activity assays using multideletion strains. Applied Microbiology and Biotechnology, 2013, 97, 6397-6412.	3.6	56
35	Deletion of pyruvate decarboxylase by a new method for efficient markerless gene deletions in Gluconobacter oxydans. Applied Microbiology and Biotechnology, 2013, 97, 2521-2530.	3.6	56
36	Studies on the utilization of lactose by Corynebacterium glutamicum, bearing the lactose operon of Escherichia coli. Archives of Microbiology, 1991, 155, 607-612.	2.2	54

#	Article	IF	CITATIONS
37	Genomics and prevalence of bacterial and archaeal isolates from biogas-producing microbiomes. Biotechnology for Biofuels, 2017, 10, 264.	6.2	50
38	Insights into extreme thermoacidophily based on genome analysis of Picrophilus torridus and other thermoacidophilic archaea. Journal of Biotechnology, 2006, 126, 3-10.	3.8	49
39	Purification and properties of recombinant ?-glucosidase of the hyperthermophilic bacterium Thermotoga maritima. Applied Microbiology and Biotechnology, 1993, 40, 44.	3.6	48
40	Xylanase XynA from the hyperthermophilic bacterium <i>Thermotoga maritima</i> : Structure and stability of the recombinant enzyme and its isolated celluloseâ€binding domain. Protein Science, 1997, 6, 1718-1726.	7.6	47
41	Thermotoga maritima AglA, an extremely thermostable NAD+-, Mn2+-, and thiol-dependent α-glucosidase. Extremophiles, 2000, 4, 189-200.	2.3	46
42	Importance of codB for new codA-based markerless gene deletion in Gluconobacter strains. Applied Microbiology and Biotechnology, 2013, 97, 8341-8349.	3.6	46
43	The l-lactate dehydrogenase gene of the hyperthermophilic bacterium Thermotoga maritima cloned by complementation in Escherichia coli. FEBS Journal, 1993, 216, 709-715.	0.2	45
44	Properties of an α-galactosidase, and Structure of its Gene galA, within an α- and β-galactoside Utilization Gene Cluster of the Hyperthermophilic Bacterium Thermotoga maritima. Systematic and Applied Microbiology, 1998, 21, 1-11.	2.8	45
45	Comparative characterization of all cellulosomal cellulases from Clostridium thermocellum reveals high diversity in endoglucanase product formation essential for complex activity. Biotechnology for Biofuels, 2017, 10, 240.	6.2	45
46	Characterization of membrane-bound dehydrogenases of Gluconobacter oxydans 621H using a new system for their functional expression. Applied Microbiology and Biotechnology, 2017, 101, 3189-3200.	3.6	44
47	Molecular and Biochemical Characterization of α-Glucosidase and α-Mannosidase and Their Clustered Genes from the Thermoacidophilic Archaeon Picrophilus torridus. Journal of Bacteriology, 2006, 188, 7123-7131.	2.2	43
48	Screening and Expression of Genes from Metagenomes. Advances in Applied Microbiology, 2013, 83, 1-68.	2.4	43
49	Pullulanase from the hyperthermophilic bacterium Thermotoga maritima: purification by β-cyclodextrin affinity chromatography. Biomedical Applications, 2000, 737, 245-251.	1.7	42
50	Comparative amino acid sequence analysis of Thermotoga maritima Î ² -glucosidase (BglA) deduced from the nucleotide sequence of the gene indicates distant relationship between Î ² -glucosidases of the BGA family and other families of Î ² -1,4-glycosyl hydrolases. Molecular Genetics and Genomics, 1994, 242, 111-115.	2.4	41
51	A new method to evaluate temperature vs. pH activity profiles for biotechnological relevant enzymes. Biotechnology for Biofuels, 2017, 10, 234.	6.2	39
52	Sequence Similarity of Clostridium difficile Strains by Analysis of Conserved Genes and Genome Content Is Reflected by Their Ribotype Affiliation. PLoS ONE, 2014, 9, e86535.	2.5	39
53	Novel archaeal thermostable cellulases from an oil reservoir metagenome. AMB Express, 2017, 7, 183.	3.0	38
54	Cloning and characterization of β-galactoside and β-glucoside hydrolysing enzymes of Thermotoga maritima. FEMS Microbiology Letters, 1993, 109, 131-137.	1.8	37

#	Article	IF	CITATIONS
55	Maltose-binding protein from the hyperthermophilic bacterium Thermotoga maritima: stability and binding properties. Journal of Molecular Biology, 2000, 295, 279-288.	4.2	36
56	Extrachromosomal genetic elements in Micrococcus. Applied Microbiology and Biotechnology, 2013, 97, 63-75.	3.6	36
57	Herbivorax saccincola gen. nov., sp. nov., a cellulolytic, anaerobic, thermophilic bacterium isolated via in sacco enrichments from a lab-scale biogas reactor. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4458-4463.	1.7	35
58	Structure of the novel α-amylase AmyC fromThermotoga maritima. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 262-270.	2.5	34
59	Xylanase Attachment to the Cell Wall of the Hyperthermophilic Bacterium <i>Thermotoga maritima</i> . Journal of Bacteriology, 2008, 190, 1350-1358.	2.2	34
60	Cloning and characterization of β-galactoside and β-glucoside hydrolysing enzymes of Thermotoga maritima. FEMS Microbiology Letters, 1993, 109, 131-137.	1.8	34
61	Novel Flp pilus biogenesis-dependent natural transformation. Frontiers in Microbiology, 2015, 6, 84.	3.5	33
62	Nucleotide sequence ofarfBofClostridium stercorarium, and prediction of catalytic residues of α-l-arabinofuranosidases based on local similarity with several families of glycosyl hydrolases. FEMS Microbiology Letters, 1998, 164, 337-343.	1.8	32
63	Properties of the recombinant glucose/galactose dehydrogenase from the extreme thermoacidophile, Picrophilus torridus. FEBS Journal, 2005, 272, 1054-1062.	4.7	32
64	Thermotoga maritima maltosyltransferase, a novel type of maltodextrin glycosyltransferase acting on starch and malto-oligosaccharides. FEBS Journal, 1998, 258, 1050-1058.	0.2	30
65	Complete genome sequence of the cellulolytic thermophile Ruminoclostridium cellulosi wild-type strain DG5 isolated from a thermophilic biogas plant. Journal of Biotechnology, 2014, 188, 136-137.	3.8	30
66	Impact of Branched-Chain Amino Acid Catabolism on Fatty Acid and Alkene Biosynthesis in Micrococcus luteus. Frontiers in Microbiology, 2018, 9, 374.	3.5	29
67	AmyA, an α-Amylase with β-Cyclodextrin-Forming Activity, and AmyB from the Thermoalkaliphilic Organism <i>Anaerobranca gottschalkii</i> : Two ݱ-Amylases Adapted to Their Different Cellular Localizations. Applied and Environmental Microbiology, 2005, 71, 3709-3715.	3.1	27
68	Identification of endoxylanase XynE from Clostridium thermocellum as the first xylanase of glycoside hydrolase family GH141. Scientific Reports, 2017, 7, 11178.	3.3	27
69	Identification of residues important for NAD+binding by theThermotoga maritimaα-glucosidase AgIA, a member of glycoside hydrolase family 4. FEBS Letters, 2002, 517, 267-271.	2.8	26
70	Functional Screening of Hydrolytic Activities Reveals an Extremely Thermostable Cellulase from a Deep-Sea Archaeon. Frontiers in Bioengineering and Biotechnology, 2015, 3, 95.	4.1	26
71	HPAEC-PAD for oligosaccharide analysis—novel insights into analyte sensitivity and response stability. Analytical and Bioanalytical Chemistry, 2017, 409, 7169-7181.	3.7	26
72	Hyperthermostable acetyl xylan esterase. Microbial Biotechnology, 2010, 3, 84-92.	4.2	25

#	Article	IF	CITATIONS
73	A histidine gene cluster of the hyperthermophile Thermotoga maritima : sequence analysis and evolutionary significance. Extremophiles, 1998, 2, 379-389.	2.3	24
74	Comparative genotyping of Clostridium thermocellum strains isolated from biogas plants: Genetic markers and characterization of cellulolytic potential. Systematic and Applied Microbiology, 2014, 37, 311-319.	2.8	24
75	Size unlimited markerless deletions by a transconjugative plasmid-system in Bacillus licheniformis. Journal of Biotechnology, 2013, 167, 365-369.	3.8	23
76	DNA and RNA Extraction and Quantitative Real-Time PCR-Based Assays for Biogas Biocenoses in an Interlaboratory Comparison. Bioengineering, 2016, 3, 7.	3.5	23
77	Hungateiclostridium mesophilum sp. nov., a mesophilic, cellulolytic and spore-forming bacterium isolated from a biogas fermenter fed with maize silage. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 3567-3573.	1.7	22
78	Complete Genome Sequence of the Solvent Producer Clostridium saccharobutylicum NCP262 (DSM) Tj ETQqO	0 0 rgBT /(Overlock 10 Tf
79	The consequence of an additional NADH dehydrogenase paralog on the growth of Gluconobacter oxydans DSM3504. Applied Microbiology and Biotechnology, 2015, 99, 375-386.	3.6	21
80	Draft genome sequence of Herbinix hemicellulosilytica T3/55T, a new thermophilic cellulose degrading bacterium isolated from a thermophilic biogas reactor. Journal of Biotechnology, 2015, 214, 59-60.	3.8	21
81	Thermostable multifunctional GH74 xyloglucanase from Myceliophthora thermophila: high-level expression in Pichia pastoris and characterization of the recombinant protein. Applied Microbiology and Biotechnology, 2017, 101, 5653-5666.	3.6	21
82	Comparative characterization of deletion derivatives of the modular xylanase XynA of Thermotoga maritima. Extremophiles, 2006, 10, 373-381.	2.3	20
83	Toxicity of indoxyl derivative accumulation in bacteria and its use as a new counterselection principle. Systematic and Applied Microbiology, 2013, 36, 585-592.	2.8	20
84	CorynebacteriumNonmedical. , 2006, , 796-818.		20
85	Glutamate dehydrogenase from the hyperthermophilic bacterium Thermotoga maritima: molecular characterization and phylogenetic implications. Extremophiles, 1997, 1, 53-61.	2.3	19
86	Genome Sequence of the Polysaccharide-Degrading, Thermophilic Anaerobe <i>Spirochaeta thermophila</i> DSM 6192. Journal of Bacteriology, 2010, 192, 6492-6493.	2.2	19
87	Optimizing the composition of a synthetic cellulosome complex for the hydrolysis of softwood pulp: identification of the enzymatic core functions and biochemical complex characterization. Biotechnology for Biofuels, 2018, 11, 220.	6.2	19
88	Complete Genome Sequence of Clostridium stercorarium subsp. <i>stercorarium</i> Strain DSM 8532, a Thermophilic Degrader of Plant Cell Wall Fibers. Genome Announcements, 2013, 1, e0007313.	0.8	18
89	Development of an in vivo methylation system for the solventogen Clostridium saccharobutylicum NCP 262 and analysis of two endonuclease mutants. Journal of Biotechnology, 2014, 188, 97-99.	3.8	18
90	Sinorhizobium melilotistrain 1021bioSandbdhAgene transcriptions are both affected by biotin available in defined medium. FEMS Microbiology Letters, 2000, 182, 41-44.	1.8	17

#	Article	IF	CITATIONS
91	Characterization and inactivation of the membrane-bound polyol dehydrogenase in Gluconobacter oxydans DSM 7145 reveals a role in meso-erythritol oxidation. Microbiology (United Kingdom), 2010, 156, 1890-1899.	1.8	17
92	Expression of membrane-bound dehydrogenases from a mother of vinegar metagenome in Gluconobacter oxydans. Applied Microbiology and Biotechnology, 2017, 101, 7901-7912.	3.6	17
93	Complete Utilization of the Major Carbon Sources Present in Sugar Beet Pulp Hydrolysates by the Oleaginous Red Yeasts Rhodotorula toruloides and R. mucilaginosa. Journal of Fungi (Basel,) Tj ETQq1 1 0.784314	ഷ്യങ⊺ /Ove	e døck 10 Tf
94	Plasmid-borne macrolide resistance in Micrococcus luteus a aThe GenBank accession number for the sequence reported in this paper is AF462611 Microbiology (United Kingdom), 2002, 148, 2479-2487.	1.8	17
95	Expression in Escherichia coli and Structure of the Gene Encoding 4-α-Glucanotransferase from Thermotoga maritima. Classification of Maltodextrin Glycosyltransferases into Two Distantly Related Enzyme Subfamilies. Systematic and Applied Microbiology, 1994, 17, 297-305.	2.8	16
96	Differences in biomass degradation between newly isolated environmental strains of Clostridium thermocellum and heterogeneity in the size of the cellulosomal scaffoldin. Systematic and Applied Microbiology, 2015, 38, 424-432.	2.8	16
97	Structural basis for cellulose binding by the type A carbohydrateâ€binding module 64 of <scp><i>S</i></scp> <i>pirochaeta thermophila</i> . Proteins: Structure, Function and Bioinformatics, 2016, 84, 855-858.	2.6	16
98	Synthetic coâ€culture of autotrophic <i>Clostridium carboxidivorans</i> and chain elongating <i>Clostridium kluyveri</i> monitored by flow cytometry. Microbial Biotechnology, 2022, 15, 1471-1485.	4.2	16
99	Cellulolytic enzymes from Thermotoga species. Methods in Enzymology, 2001, 330, 290-300.	1.0	15
100	First draft genome sequence of the amylolytic Bacillus thermoamylovorans wild-type strain 1A1 isolated from a thermophilic biogas plant. Journal of Biotechnology, 2014, 192, 154-155.	3.8	15
101	A metagenome-derived thermostable \hat{l}^2 -glucanase with an unusual module architecture which defines the new glycoside hydrolase family GH148. Scientific Reports, 2017, 7, 17306.	3.3	15
102	Transmating: conjugative transfer of a new broad host range expression vector to various Bacillus species using a single protocol. BMC Microbiology, 2018, 18, 56.	3.3	15
103	The crystal structure of Thermotoga maritima maltosyltransferase and its implications for the molecular basis of the novel transfer specificity 1 1Edited by R. Huber. Journal of Molecular Biology, 2001, 312, 119-131.	4.2	14
104	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
105	Genetic analysis of lipolytic activities in Thermus thermophilus HB27. Journal of Biotechnology, 2014, 191, 150-157.	3.8	13
106	L-Erythrulose production with a multideletion strain of Gluconobacter oxydans. Applied Microbiology and Biotechnology, 2019, 103, 4393-4404.	3.6	13
107	Biochemical characterisation of four rhamnosidases from thermophilic bacteria of the genera Thermotoga, Caldicellulosiruptor and Thermoclostridium. Scientific Reports, 2019, 9, 15924.	3.3	13
108	Importance of Defluviitalea raffinosedens for Hydrolytic Biomass Degradation in Co-Culture with Hungateiclostridium thermocellum. Microorganisms, 2020, 8, 915.	3.6	13

#	Article	IF	CITATIONS
109	Novel Family of Carbohydrate-Binding Modules Revealed by the Genome Sequence of Spirochaeta thermophila DSM 6192. Applied and Environmental Microbiology, 2011, 77, 5483-5489.	3.1	12
110	Chemostat cultivation and transcriptional analyses of Clostridium acetobutylicum mutants with defects in the acid and acetone biosynthetic pathways. Applied Microbiology and Biotechnology, 2014, 98, 9777-9794.	3.6	12
111	Restriction-deficient mutants and marker-less genomic modification for metabolic engineering of the solvent producer Clostridium saccharobutylicum. Biotechnology for Biofuels, 2018, 11, 264.	6.2	12
112	Markerless deletion of putative alanine dehydrogenase genes in Bacillus licheniformis using a codBA-based counterselection technique. Microbiology (United Kingdom), 2017, 163, 1532-1539.	1.8	12
113	Variimorphobacter saccharofermentans gen. nov., sp. nov., a new member of the family Lachnospiraceae, isolated from a maize-fed biogas fermenter. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	1.7	12
114	The Roles of the Various Cellulose Biosynthesis Operons in <i>Komagataeibacter hansenii</i> ATCC 23769. Applied and Environmental Microbiology, 2022, 88, e0246021.	3.1	12
115	Complete Genome Sequence of the Linear Plasmid pJD12 Hosted by <i>Micrococcus</i> sp. D12, Isolated from a High-Altitude Volcanic Lake in Argentina. Genome Announcements, 2015, 3, .	0.8	11
116	Novel endo-(1,4)-β-glucanase Bgh12A and xyloglucanase Xgh12B from Aspergillus cervinus belong to GH12 subgroup I and II, respectively. Applied Microbiology and Biotechnology, 2019, 103, 7553-7566.	3.6	11
117	An efficient method for markerless mutant generation by allelic exchange in Clostridium acetobutylicum and Clostridium saccharobutylicum using suicide vectors. Biotechnology for Biofuels, 2019, 12, 31.	6.2	11
118	Structure–functional analysis of the Dictyoglomus cell envelope. Systematic and Applied Microbiology, 2012, 35, 279-290.	2.8	10
119	Flow cytometric sorting of fecal bacteria after in situ hybridization with polynucleotide probes. Systematic and Applied Microbiology, 2016, 39, 464-475.	2.8	10
120	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. Genome Announcements, 2018, 6, .	0.8	10
121	Ruminiclostridium herbifermentans sp. nov., a mesophilic and moderately thermophilic cellulolytic and xylanolytic bacterium isolated from a lab-scale biogas fermenter fed with maize silage. International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	1.7	10
122	Molecular biology: Fantastic toolkits to improve knowledge and application of acetic acid bacteria. Biotechnology Advances, 2022, 58, 107911.	11.7	10
123	Genomics taken to the extreme. Nature Biotechnology, 2004, 22, 524-525.	17.5	9
124	Comparative direct infusion ion mobility mass spectrometry profiling of Thermus thermophilus wild-type and mutant â^†cruC carotenoid extracts. Analytical and Bioanalytical Chemistry, 2013, 405, 9843-9848.	3.7	9
125	Isolation and analysis of genes for amylolytic enzymes of the hyperthermophilic bacterium Thermotoga maritima. FEMS Microbiology Letters, 1998, 158, 9-15.	1.8	9
126	Towards valorization of pectin-rich agro-industrial residues: Engineering of Saccharomyces cerevisiae for co-fermentation of d-galacturonic acid and glycerol. Metabolic Engineering, 2022, 69, 1-14.	7.0	9

#	Article	IF	CITATIONS
127	Characterization of chromosomal and megaplasmid partitioning loci in Thermus thermophilus HB27. BMC Genomics, 2015, 16, 317.	2.8	8
128	Complete Genome Sequence of <i>Herbinix luporum</i> SD1D, a New Cellulose-Degrading Bacterium Isolated from a Thermophilic Biogas Reactor. Genome Announcements, 2016, 4, .	0.8	8
129	Milling byproducts are an economically viable substrate for butanol production using clostridial ABE fermentation. Applied Microbiology and Biotechnology, 2020, 104, 8679-8689.	3.6	8
130	Characterization of Two α-l-Arabinofuranosidases from Acetivibrio mesophilus and Their Synergistic Effect in Degradation of Arabinose-Containing Substrates. Microorganisms, 2021, 9, 1467.	3.6	8
131	Thermostable Xylanase and β-Glucanase Derived from the Metagenome of the Avachinsky Crater in Kamchatka (Russia). Current Biotechnology, 2013, 2, 284-293.	0.4	8
132	Monitoring co-cultures of Clostridium carboxidivorans and Clostridium kluyveri by fluorescence in situ hybridization with specific 23S rRNA oligonucleotide probes. Systematic and Applied Microbiology, 2021, 44, 126271.	2.8	8
133	Oxidative Fermentation of Acetic Acid Bacteria and Its Products. Frontiers in Microbiology, 2022, 13, .	3.5	8
134	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
135	Evaluation of promoter sequences for the secretory production of a Clostridium thermocellum cellulase in Paenibacillus polymyxa. Applied Microbiology and Biotechnology, 2018, 102, 10147-10159.	3.6	7
136	Acceptor Specificity of 4-α-Glucanotransferase of Thermotoga Maritima. Biocatalysis, 1994, 11, 105-115.	0.9	6
137	Title is missing!. Molecular Biology, 2003, 37, 678-685.	1.3	6
138	Addition of β-galactosidase boosts the xyloglucan degradation capability of endoglucanase Cel9D from Clostridium thermocellum. Biotechnology for Biofuels, 2018, 11, 238.	6.2	6
139	Distribution and diversity of olefins and olefin-biosynthesis genes in Gram-positive bacteria. Biotechnology for Biofuels, 2020, 13, 70.	6.2	6
140	Anaerosphaera multitolerans sp. nov., a salt-tolerant member of the family Peptoniphilaceae isolated from a mesophilically operated biogas fermenter fed with maize silage. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1217-1223.	1.7	6
141	Characterization of Plasmid pPO1 from the Hyperacidophile <i>Picrophilus oshimae</i> . Archaea, 2011, 2011, 1-4.	2.3	5
142	Amino acids as nutritional factors and (p)ppGpp as an alarmone of the stringent response regulate natural transformation in Micrococcus luteus. Scientific Reports, 2019, 9, 11030.	3.3	5
143	Comparison of sampling techniques and different media for the enrichment and isolation of cellulolytic organisms from biogas fermenters. Systematic and Applied Microbiology, 2019, 42, 481-487.	2.8	5
144	Molecular characterization of the Sinorhizobium meliloti nlp D gene. Archives of Microbiology, 2000, 174, 292-295.	2.2	4

#	Article	IF	CITATIONS
145	Crystallization and preliminary X-ray crystallographic studies on 4-α-glucanotransferase fromThermotoga maritima. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1046-1047.	2.5	4
146	Title is missing!. Molecular Biology, 2003, 37, 686-694.	1.3	4
147	Phytate utilization by genetically engineered lysine-producing Corynebacterium glutamicum. Journal of Biotechnology, 2008, 134, 211-217.	3.8	4
148	Unusual substrate specificity in GH family 12: structure–function analysis of glucanases Bgh12A and Xgh12B from Aspergillus cervinus, and Egh12 from Thielavia terrestris. Applied Microbiology and Biotechnology, 2022, 106, 1493-1509.	3.6	4
149	Comparative Analysis of the Recombinant α-Glucosidases from theThermotoga neapolitanaandThermotoga maritimaMaltodextrin Utilization Gene Clusters. Biocatalysis and Biotransformation, 2003, 21, 147-158.	2.0	3
150	The Genomes of Acetic Acid Bacteria. , 2017, , 469-494.		3
151	A Novel Primer Mixture for CH48 Genes: Quantification and Identification of Truly Cellulolytic Bacteria in Biogas Fermenters. Microorganisms, 2020, 8, 1297.	3.6	3
152	Crystallization and preliminary X-ray crystallographic studies on maltosyltransferase fromThermotoga maritima. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1049-1050.	2.5	2
153	Handling gene and protein names in the age of bioinformatics: the special challenge of secreted multimodular bacterial enzymes such as the cbhA/cbh9A gene of Clostridium thermocellum. World Journal of Microbiology and Biotechnology, 2018, 34, 42.	3.6	2
154	Draft Genome Sequence of <i>Anaerosphaera</i> sp. Strain GS7-6-2, a Coccal Bacterium Isolated from a Biogas-Related Environment. Microbiology Resource Announcements, 2019, 8, .	0.6	2
155	Metagenomics. Encyclopedia of Earth Sciences Series, 2011, , 553-558.	0.1	2
156	Biochemical and Structural Characterization of Thermostable GH159 Glycoside Hydrolases Exhibiting α-L-Arabinofuranosidase Activity. Frontiers in Molecular Biosciences, 0, 9, .	3.5	2
157	Draft Genome Sequence of <i>Propionispora</i> sp. Strain 2/2-37, a New Xylan-Degrading Bacterium Isolated from a Mesophilic Biogas Reactor. Genome Announcements, 2016, 4, .	0.8	1
158	Draft Genome Sequence of Paenibacillus polymyxa DSM 292, a Gram-Positive, Spore-Forming Soil Bacterium with High Biotechnological Potential. Microbiology Resource Announcements, 2020, 9, .	0.6	1
159	Draft Genome Sequence of Mobilitalea sibirica Strain P3M-3 ^T , the Sole Representative of the Genus <i>Mobilitalea</i> . Microbiology Resource Announcements, 2021, 10, .	0.6	1
160	Identification of New Chromosomal Loci Involved in com Genes Expression and Natural Transformation in the Actinobacterial Model Organism Micrococcus luteus. Genes, 2021, 12, 1307.	2.4	1
161	Biochemie 2010. Nachrichten Aus Der Chemie, 2011, 59, 297-318.	0.0	0
162	Variances in cellular sedimentation behavior as an effective enrichment method of hydrocarbon-overproducing Micrococcus luteus strains. Biotechnology for Biofuels, 2018, 11, 288.	6.2	0

#	Article	IF	CITATIONS
163	Draft Genome Sequence of Clostridium beijerinckii Strain mbf-VZ-132, Isolated from an Environmental Soil Sample. Microbiology Resource Announcements, 2021, 10, .	0.6	0