

dbCAN2: a meta server for automated carbohydrate-act

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Citation Report

#	ARTICLE	IF	CITATIONS
2	Freshwater carbon and nutrient cycles revealed through reconstructed population genomes. PeerJ, 2018, 6, e6075.	0.9	64
3	Prediction of pathogenesis-related secreted proteins from <i>Stemphylium lycopersici</i> . BMC Microbiology, 2018, 18, 191.	1.3	21
4	Fiber-associated spirochetes are major agents of hemicellulose degradation in the hindgut of wood-feeding higher termites. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11996-E12004.	3.3	90
5	Fucoidan Sulfatases from Marine Bacterium <i>Wenyngzhuangia fucanilytica</i> CZ1127T. Biomolecules, 2018, 8, 98.	1.8	29
6	Ega3 from the fungal pathogen <i>Aspergillus fumigatus</i> is an endo- α -1,4-galactosaminidase that disrupts microbial biofilms. Journal of Biological Chemistry, 2019, 294, 13833-13849.	1.6	35
7	Compendium of 4,941 rumen metagenome-assembled genomes for rumen microbiome biology and enzyme discovery. Nature Biotechnology, 2019, 37, 953-961.	9.4	353
8	The secretome of two representative lignocellulose-decay basidiomycetes growing on sugarcane bagasse solid-state cultures. Enzyme and Microbial Technology, 2019, 130, 109370.	1.6	15
9	A marine bacterial enzymatic cascade degrades the algal polysaccharide ulvan. Nature Chemical Biology, 2019, 15, 803-812.	3.9	97
10	Enzymes of early-diverging, zoosporic fungi. Applied Microbiology and Biotechnology, 2019, 103, 6885-6902.	1.7	30
11	A Diverse Repertoire of Exopolysaccharide Biosynthesis Gene Clusters in <i>Lactobacillus</i> Revealed by Comparative Analysis in 106 Sequenced Genomes. Microorganisms, 2019, 7, 444.	1.6	50
12	Discovery, activity and characterisation of an AA10 lytic polysaccharide oxygenase from the shipworm symbiont <i>Teredinibacter turnerae</i> . Biotechnology for Biofuels, 2019, 12, 232.	6.2	27
13	Draft genome sequence of fastidious pathogen <i>Ceratobasidium theobromae</i> , which causes vascular-streak dieback in <i>Theobroma cacao</i> . Fungal Biology and Biotechnology, 2019, 6, 14.	2.5	10
14	Comparative transcriptomics of <i>Gymnosporangium</i> spp. teliospores reveals a conserved genetic program at this specific stage of the rust fungal life cycle. BMC Genomics, 2019, 20, 723.	1.2	6
15	Characterization of fructooligosaccharide-degrading enzymes in human commensal <i>Bifidobacterium longum</i> and <i>Anaerostipes caccae</i> . Biochemical and Biophysical Research Communications, 2019, 518, 294-298.	1.0	16
16	A Genome-Centric Approach Reveals a Novel Glycosyltransferase from the GA A07 Strain of <i>Bacillus thuringiensis</i> Responsible for Catalyzing 15-O-Glycosylation of Ganoderic Acid A. International Journal of Molecular Sciences, 2019, 20, 5192.	1.8	8
17	Bioinformatics for Marine Products: An Overview of Resources, Bottlenecks, and Perspectives. Marine Drugs, 2019, 17, 576.	2.2	26
18	Carbo-loading in <i>Coccidioides</i> spp.: a quantitative analysis of CAZyme abundance and resulting glycan populations. Glycobiology, 2019, 30, 186-197.	1.3	7
19	Microbial metabolisms in an abyssal ferromanganese crust from the Takuyo-Daigo Seamount as revealed by metagenomics. PLoS ONE, 2019, 14, e0224888.	1.1	14

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20	Species-wide Metabolic Interaction Network for Understanding Natural Lignocellulose Digestion in Termite Gut Microbiota. <i>Scientific Reports</i> , 2019, 9, 16329.	1.6	28
21	Recovery of the Gut Microbiota after Antibiotics Depends on Host Diet, Community Context, and Environmental Reservoirs. <i>Cell Host and Microbe</i> , 2019, 26, 650-665.e4.	5.1	166
22	Complete genome sequencing of <i>Shigella</i> sp. PAMC 28760: Identification of CAZyme genes and analysis of their potential role in glycogen metabolism for cold survival adaptation. <i>Microbial Pathogenesis</i> , 2019, 137, 103759.	1.3	15
23	<i>Pleurotus eryngii</i> Genomes Reveal Evolution and Adaptation to the Gobi Desert Environment. <i>Frontiers in Microbiology</i> , 2019, 10, 2024.	1.5	19
24	Biochemical characterization and mutational analysis of silkworm <i>Bombyx mori</i> Î²-1,4-N-acetylgalactosaminyltransferase and insight into the substrate specificity of Î²-1,4-galactosyltransferase family enzymes. <i>Insect Biochemistry and Molecular Biology</i> , 2019, 115, 103254.	1.2	9
25	The genome of the migratory nematode, <i>Radopholus similis</i> , reveals signatures of close association to the sedentary cyst nematodes. <i>PLoS ONE</i> , 2019, 14, e0224391.	1.1	13
26	Active Fungal Communities in Asymptomatic <i>Eucalyptus grandis</i> Stems Differ between a Susceptible and Resistant Clone. <i>Microorganisms</i> , 2019, 7, 375.	1.6	6
27	Genomic Insights into the Fungal Lignocellulolytic Machinery of <i>Flammulina rossica</i> . <i>Microorganisms</i> , 2019, 7, 421.	1.6	5
28	Top-Down Enrichment Guides in Formation of Synthetic Microbial Consortia for Biomass Degradation. <i>ACS Synthetic Biology</i> , 2019, 8, 2174-2185.	1.9	74
29	Revealing the metabolic capacity of <i>Streblomastix strix</i> and its bacterial symbionts using single-cell metagenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19675-19684.	3.3	40
30	In Silico Analysis of <i>Gardnerella</i> Genomespecies Detected in the Setting of Bacterial Vaginosis. <i>Clinical Chemistry</i> , 2019, 65, 1375-1387.	1.5	24
31	Macroalga-Derived Alginate Oligosaccharide Alters Intestinal Bacteria of Atlantic Salmon. <i>Frontiers in Microbiology</i> , 2019, 10, 2037.	1.5	49
32	Sequence and Structural Analysis of AA9 and AA10 LPMOs: An Insight into the Basis of Substrate Specificity and Regioselectivity. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4594.	1.8	15
33	Genome Insights into the Novel Species <i>Microvirga brassicacearum</i> , a Rapeseed Endophyte with Biotechnological Potential. <i>Microorganisms</i> , 2019, 7, 354.	1.6	30
34	Mining of Sucrose Synthases from <i>Glycyrrhiza uralensis</i> and Their Application in the Construction of an Efficient UDP-Recycling System. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 11694-11702.	2.4	16
35	The pH optimum of soil exoenzymes adapt to long term changes in soil pH. <i>Soil Biology and Biochemistry</i> , 2019, 138, 107601.	4.2	73
36	Two Trifunctional Leloir Glycosyltransferases as Biocatalysts for Natural Products Glycodiversification. <i>Organic Letters</i> , 2019, 21, 8058-8064.	2.4	19
37	Draft Genome Sequence of Acidobacteria Group 1 <i>Acidipila</i> sp. Strain EB88, Isolated from Forest Soil. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	10

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38	Modular Assembly of Polysaccharide-Degrading Marine Microbial Communities. <i>Current Biology</i> , 2019, 29, 1528-1535.e6.	1.8	144
39	Molecular mechanism of <i>Aspergillus fumigatus</i> biofilm disruption by fungal and bacterial glycoside hydrolases. <i>Journal of Biological Chemistry</i> , 2019, 294, 10760-10772.	1.6	50
40	Draft Genome Sequence of the Wood-Decaying Fungus <i>Xylaria</i> sp. BCC 1067. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
41	Effect of Long-Term Farming Practices on Agricultural Soil Microbiome Members Represented by Metagenomically Assembled Genomes (MAGs) and Their Predicted Plant-Beneficial Genes. <i>Genes</i> , 2019, 10, 424.	1.0	61
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43	Mediterranean grassland soil C-N compound turnover is dependent on rainfall and depth, and is mediated by genomically divergent microorganisms. <i>Nature Microbiology</i> , 2019, 4, 1356-1367.	5.9	170
44	Wood Modification by Furfuryl Alcohol Resulted in a Delayed Decomposition Response in <i>Rhodonia</i> (<i>Postia</i>) <i>placenta</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	13
45	Peptide-based functional annotation of carbohydrate-active enzymes by conserved unique peptide patterns (CUPP). <i>Biotechnology for Biofuels</i> , 2019, 12, 102.	6.2	55
46	Sulfate-Reducing Bacteria That Produce Exopolymers Thrive in the Calcifying Zone of a Hypersaline Cyanobacterial Mat. <i>Frontiers in Microbiology</i> , 2019, 10, 862.	1.5	54
47	Draft Genome Sequence of <i>Agarivorans</i> sp. Strain Toyoura001, Isolated from an Abalone Gut. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4
48	Draft Genome Sequences of Two Glycoalkaloid-Degrading <i>Arthrobacter</i> Strains Isolated from Green Potato Peel. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4
49	Genomic analysis of ant domatia-associated melanized fungi (Chaetothyriales, Ascomycota). <i>Mycological Progress</i> , 2019, 18, 541-552.	0.5	17
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53	Bioinformatics applied to biotechnology: A review towards bioenergy research. <i>Biomass and Bioenergy</i> , 2019, 123, 195-224.	2.9	17
54	Adaptations of <i>Alteromonas</i> sp. 76-1 to Polysaccharide Degradation: A CAZyme Plasmid for Ulvan Degradation and Two Alginolytic Systems. <i>Frontiers in Microbiology</i> , 2019, 10, 504.	1.5	30
55	Genome Sequencing of <i>Cladobotryum protrusum</i> Provides Insights into the Evolution and Pathogenic Mechanisms of the Cobweb Disease Pathogen on Cultivated Mushroom. <i>Genes</i> , 2019, 10, 124.	1.0	25

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56	Whole Genome Sequence of the Commercially Relevant Mushroom Strain <i>Agaricus bisporus</i> var. <i>bisporus</i> ARP23. G3: Genes, Genomes, Genetics, 2019, 9, 3057-3066.	0.8	13
57	Draft Genome Sequence of <i>Clostridium estertheticum</i> subsp. <i>laramiense</i> DSM 14864 ^T , Isolated from Spoiled Uncooked Beef. Microbiology Resource Announcements, 2019, 8, .	0.3	13
58	Structural Identity of Galactooligosaccharide Molecules Selectively Utilized by Single Cultures of Probiotic Bacterial Strains. Journal of Agricultural and Food Chemistry, 2019, 67, 13969-13977.	2.4	29
59	The host generalist phytopathogenic fungus <i>Sclerotinia sclerotiorum</i> differentially expresses multiple metabolic enzymes on two different plant hosts. Scientific Reports, 2019, 9, 19966.	1.6	21
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62	Comparative Genomics and CAZyme Genome Repertoires of Marine <i>Zobellia amurskyensis</i> KMM 3526T and <i>Zobellia laminariae</i> KMM 3676T. Marine Drugs, 2019, 17, 661.	2.2	27
63	Metagenomics of Atacama Lithobiontic Extremophile Life Unveils Highlights on Fungal Communities, Biogeochemical Cycles and Carbohydrate-Active Enzymes. Microorganisms, 2019, 7, 619.	1.6	28
64	Plant cell wall degradation in insects: Recent progress on endogenous enzymes revealed by multi-omics technologies. Advances in Insect Physiology, 2019, , 97-136.	1.1	33
65	Division of labor in honey bee gut microbiota for plant polysaccharide digestion. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25909-25916.	3.3	191
66	Assembly, annotation, and comparison of <i>Macrophomina phaseolina</i> isolates from strawberry and other hosts. BMC Genomics, 2019, 20, 802.	1.2	16
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71	Complete Genome Sequence of <i>Saccharospirillum mangrovi</i> HK-33T Sheds Light on the Ecological Role of a Bacterium in Mangrove Sediment Environment. Current Microbiology, 2019, 76, 231-236.	1.0	4
72	Expression of the GAF Sensor, Carbohydrate-Active Enzymes, Elicitins, and RXLRs Differs Markedly Between Two <i>Phytophthora cactorum</i> Isolates. Phytopathology, 2019, 109, 726-735.	1.1	7
73	High-throughput screening for texturing <i>Lactococcus</i> strains. FEMS Microbiology Letters, 2019, 366, .	0.7	20

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74	Biochemical Reconstruction of a Metabolic Pathway from a Marine Bacterium Reveals Its Mechanism of Pectin Depolymerization. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	23
75	Genomic analysis of a lignocellulose degrading strain from the underexplored genus <i>Meridianimaribacter</i> . <i>Genomics</i> , 2020, 112, 952-960.	1.3	20
76	Applications of plant-based fermented foods and their microbes. <i>Current Opinion in Biotechnology</i> , 2020, 61, 45-52.	3.3	60
77	Complete genome sequence of <i>Dyadobacter</i> sp. 32, isolated from a culture of the freshwater diatom <i>Cymbella microcephala</i> . <i>Marine Genomics</i> , 2020, 52, 100720.	0.4	0
78	Shedding light on biogas: Phototrophic biofilms in anaerobic digesters hold potential for improved biogas production. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126024.	1.2	9
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81	Genomic Sequencing of <i>Phyllosticta citriasiana</i> Provides Insight Into Its Conservation and Diversification With Two Closely Related <i>Phyllosticta</i> Species Associated With Citrus. <i>Frontiers in Microbiology</i> , 2019, 10, 2979.	1.5	15
82	Description of three bacterial strains belonging to the new genus <i>Novipirellula</i> gen. nov., reclassification of <i>Rhodopirellula rosea</i> and <i>Rhodopirellula caenicola</i> and readjustment of the genus threshold of the phylogenetic marker <i>rpoB</i> for <i>Planctomycetaceae</i> . <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1779-1795.	0.7	56
83	Characterization of <i>Glaciecola</i> sp. enzymes involved in the late steps of degradation of sulfated polysaccharide ulvan extracted from <i>Ulva ohnoi</i> . <i>Biochemical and Biophysical Research Communications</i> , 2020, 523, 441-445.	1.0	8
84	<i>Alienimonas californiensis</i> gen. nov. sp. nov., a novel <i>Planctomycete</i> isolated from the kelp forest in Monterey Bay. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1751-1766.	0.7	40
85	PreDSLpmo: A neural network-based prediction tool for functional annotation of lytic polysaccharide monooxygenases. <i>Journal of Biotechnology</i> , 2020, 308, 148-155.	1.9	0
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87	eCAMI: simultaneous classification and motif identification for enzyme annotation. <i>Bioinformatics</i> , 2020, 36, 2068-2075.	1.8	27
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89	Conserved unique peptide patterns (CUPP) online platform: peptide-based functional annotation of carbohydrate active enzymes. <i>Nucleic Acids Research</i> , 2020, 48, W110-W115.	6.5	35
90	Genome-wide identification and functional analysis of the horizontally transferred genes in <i>Penicillium</i> . <i>Genomics</i> , 2020, 112, 5037-5043.	1.3	2
91	Genome-Centric Metagenomic Insights into the Impact of Alkaline/Acid and Thermal Sludge Pretreatment on the Microbiome in Digestion Sludge. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	12

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92	Glucosylation prevents plant defense activation in phloem-feeding insects. <i>Nature Chemical Biology</i> , 2020, 16, 1420-1426.	3.9	30
93	Genomic characterization of a diazotrophic microbiota associated with maize aerial root mucilage. <i>PLoS ONE</i> , 2020, 15, e0239677.	1.1	13
94	A Need for Improved Cellulase Identification from Metagenomic Sequence Data. <i>Applied and Environmental Microbiology</i> , 2020, 87, .	1.4	2
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97	Metabolic Response of <i>Faecalibacterium prausnitzii</i> to Cell-Free Supernatants from Lactic Acid Bacteria. <i>Microorganisms</i> , 2020, 8, 1528.	1.6	16
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99	First Draft Genome Resource for the Tomato Black Leaf Mold Pathogen <i>Pseudocercospora fuligena</i> . <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1441-1445.	1.4	3
100	<i>Paenibacillus lycopersici</i> sp. nov. and <i>Paenibacillus rhizovicinus</i> sp. nov., isolated from the rhizosphere of tomato (<i>Solanum lycopersicum</i>). <i>Journal of Microbiology</i> , 2020, 58, 832-840.	1.3	4
101	The gut microbiome stability is altered by probiotic ingestion and improved by the continuous supplementation of galactooligosaccharide. <i>Gut Microbes</i> , 2020, 12, 1785252.	4.3	39
102	Genomic Analysis of Diverse Members of the Fungal Genus <i>Monosporascus</i> Reveals Novel Lineages, Unique Genome Content and a Potential Bacterial Associate. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2573-2583.	0.8	5
103	Comparative Genomics of <i>Stenotrophomonas maltophilia</i> and <i>Stenotrophomonas rhizophila</i> Revealed Characteristic Features of Both Species. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4922.	1.8	21
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105	Multi-omic Directed Discovery of Cellulosomes, Polysaccharide Utilization Loci, and Lignocellulases from an Enriched Rumen Anaerobic Consortium. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	20
106	Draft genome assembly of <i>Passalora sequoiae</i> a needle blight pathogen on Leyland cypress. <i>BMC Research Notes</i> , 2020, 13, 505.	0.6	0
107	Thermogenic hydrocarbon biodegradation by diverse depth-stratified microbial populations at a Scotian Basin cold seep. <i>Nature Communications</i> , 2020, 11, 5825.	5.8	72
108	Genome Mining and Evaluation of the Biocontrol Potential of <i>Pseudomonas fluorescens</i> BRZ63, a New Endophyte of Oilseed Rape (<i>Brassica napus</i> L.) against Fungal Pathogens. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8740.	1.8	37
109	Combinatorial Glycomic Analyses to Direct CAZyme Discovery for the Tailored Degradation of Canola Meal Non-Starch Dietary Polysaccharides. <i>Microorganisms</i> , 2020, 8, 1888.	1.6	12

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111	DRAM for distilling microbial metabolism to automate the curation of microbiome function. Nucleic Acids Research, 2020, 48, 8883-8900.	6.5	410
112	Vast Differences in Strain-Level Diversity in the Gut Microbiota of Two Closely Related Honey Bee Species. Current Biology, 2020, 30, 2520-2531.e7.	1.8	63
113	Comparative Analysis of Microbial Community Structure and Function in the Gut of Wild and Captive Amur Tiger. Frontiers in Microbiology, 2020, 11, 1665.	1.5	39
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115	Reference Genome Assembly for Australian <i>Ascochyta rabiei</i> Isolate ArME14. G3: Genes, Genomes, Genetics, 2020, 10, 2131-2140.	0.8	15
116	Draft Genome Sequence of <i>Clostridium estertheticum</i> -Like Strain FP3, Isolated from Spoiled Uncooked Lamb. Microbiology Resource Announcements, 2020, 9, .	0.3	3
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118	Succession of <i>Bifidobacterium longum</i> Strains in Response to a Changing Early Life Nutritional Environment Reveals Dietary Substrate Adaptations. IScience, 2020, 23, 101368.	1.9	26
119	<i>Tenuifilum thalassicum</i> gen. nov., sp. nov., a novel moderate thermophilic anaerobic bacterium from a Kunashir Island shallow hot spring representing a new family Tenuifilaceae fam. nov. in the class Bacteroidia. Systematic and Applied Microbiology, 2020, 43, 126126.	1.2	22
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124	Inducible expression of agar-degrading genes in a marine bacterium <i>Catenovulum maritimus</i> Q1T and characterization of a β -agarase. Applied Microbiology and Biotechnology, 2020, 104, 10541-10553.	1.7	6
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126	Deciphering the Infectious Process of <i>Colletotrichum lupini</i> in Lupin through Transcriptomic and Proteomic Analysis. Microorganisms, 2020, 8, 1621.	1.6	18
127	Distinct Polysaccharide Utilization Determines Interspecies Competition between Intestinal <i>Prevotella</i> spp.. Cell Host and Microbe, 2020, 28, 838-852.e6.	5.1	86

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129	Metagenomic and Metatranscriptomic Analyses Revealed Uncultured Bacteroidales Populations as the Dominant Proteolytic Amino Acid Degradors in Anaerobic Digesters. <i>Frontiers in Microbiology</i> , 2020, 11, 593006.	1.5	57
130	Comparative genomic analysis reveals metabolic diversity of different <i>Paenibacillus</i> groups. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 10133-10143.	1.7	5
131	The Effector Repertoire of the Hop Downy Mildew Pathogen <i>Pseudoperonospora humuli</i> . <i>Frontiers in Genetics</i> , 2020, 11, 910.	1.1	9
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133	Characterization of sponge-associated <i>Verrucomicrobia</i> : microcompartment-based sugar utilization and enhanced toxin-antitoxin modules as features of host-associated <i>Opitutales</i> . <i>Environmental Microbiology</i> , 2020, 22, 4669-4688.	1.8	26
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145	<i>Lactobacillus Mucosae</i> Strain Promoted by a High-Fiber Diet in Genetic Obese Child Alleviates Lipid Metabolism and Modifies Gut Microbiota in ApoE ^{-/-} Mice on a Western Diet. <i>Microorganisms</i> , 2020, 8, 1225.	1.6	22

#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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201	Responses of <i>Acidobacteria Granulicella</i> sp. WH15 to High Carbon Revealed by Integrated Omics Analyses. <i>Microorganisms</i> , 2020, 8, 244.	1.6	8
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#	ARTICLE	IF	CITATIONS
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220	Comparative Genomics, Pangenome, and Phylogenomic Analyses of <i>Brenneria</i> spp., and Delineation of <i>Brenneria izadpanahii</i> sp. nov.. <i>Phytopathology</i> , 2021, 111, 78-95.	1.1	11
221	Genomics and metatranscriptomics of biogeochemical cycling and degradation of lignin-derived aromatic compounds in thermal swamp sediment. <i>ISME Journal</i> , 2021, 15, 879-893.	4.4	34
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#	ARTICLE	IF	CITATIONS
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237	<scp>TMTâ€MS</scp>/<scp>MS</scp> proteomic analysis of the carbohydrateâ€active enzymes in the fruiting body of <i>Pleurotus tuoliensis</i> during storage. <i>Journal of the Science of Food and Agriculture</i> , 2021, 101, 1879-1891.	1.7	10
238	dbCAN-PUL: a database of experimentally characterized CAZyme gene clusters and their substrates. <i>Nucleic Acids Research</i> , 2021, 49, D523-D528.	6.5	55
239	Genomic Sequence Resource of <i>Alternaria alternata</i> Strain B3 Causing Leaf Blight on <i>Ophiopogon japonicus</i>. <i>Plant Disease</i> , 2021, 105, 684-687.	0.7	7
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251	Combined whole cell wall analysis and streamlined in silico carbohydrate-active enzyme discovery to improve biocatalytic conversion of agricultural crop residues. <i>Biotechnology for Biofuels</i> , 2021, 14, 16.	6.2	15
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255	Phytoplankton consortia as a blueprint for mutually beneficial eukaryote-bacteria ecosystems based on the biocoenosis of <i>Botryococcus</i> consortia. <i>Scientific Reports</i> , 2021, 11, 1726.	1.6	12

#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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