

KAAS: an automatic genome annotation and pathway re

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Citation Report

#	ARTICLE	IF	CITATIONS
1	KEGG for linking genomes to life and the environment. <i>Nucleic Acids Research</i> , 2007, 36, D480-D484.	6.5	5,451
2	Current trends in the bioinformatic sequence analysis of metabolic pathways in prokaryotes. <i>Briefings in Bioinformatics</i> , 2007, 9, 34-45.	3.2	4
3	Gene Annotation and Pathway Mapping in KEGG. <i>Methods in Molecular Biology</i> , 2007, 396, 71-91.	0.4	238
4	AnEnPi: identification and annotation of analogous enzymes. <i>BMC Bioinformatics</i> , 2008, 9, 544.	1.2	28
5	The RAST Server: Rapid Annotations using Subsystems Technology. <i>BMC Genomics</i> , 2008, 9, 75.	1.2	9,977
6	Chromatophore Genome Sequence of <i>Paulinella</i> Sheds Light on Acquisition of Photosynthesis by Eukaryotes. <i>Current Biology</i> , 2008, 18, 410-418.	1.8	325
7	An Introduction to Metabolic Networks and Their Structural Analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008, 5, 594-617.	1.9	103
8	KEGG Atlas mapping for global analysis of metabolic pathways. <i>Nucleic Acids Research</i> , 2008, 36, W423-W426.	6.5	445
9	Metabolomics- and Proteomics-Assisted Genome Annotation and Analysis of the Draft Metabolic Network of <i>Chlamydomonas reinhardtii</i> . <i>Genetics</i> , 2008, 179, 157-166.	1.2	141
10	An approach of orthology detection from homologous sequences under minimum evolution. <i>Nucleic Acids Research</i> , 2008, 36, e110-e110.	6.5	26
11	SubpathwayMiner: a software package for flexible identification of pathways. <i>Nucleic Acids Research</i> , 2009, 37, e131-e131.	6.5	195
12	Simultaneous inference of biological networks of multiple species from genome-wide data and evolutionary information: a semi-supervised approach. <i>Bioinformatics</i> , 2009, 25, 2962-2968.	1.8	45
13	Genomic Survey of the Non-Cultivable Opportunistic Human Pathogen, <i>Enterocytozoon bieneusi</i> . <i>PLoS Pathogens</i> , 2009, 5, e1000261.	2.1	119
14	Comparative Genomic Characterization of <i>Francisella tularensis</i> Strains Belonging to Low and High Virulence Subspecies. <i>PLoS Pathogens</i> , 2009, 5, e1000459.	2.1	112
15	In response to "Can sugars be produced from fatty acids? A test case for pathway analysis tools". <i>Bioinformatics</i> , 2009, 25, 3202-3205.	1.8	9
16	A Parsimony Approach to Biological Pathway Reconstruction/Inference for Genomes and Metagenomes. <i>PLoS Computational Biology</i> , 2009, 5, e1000465.	1.5	481
17	Metabolic Network Model of a Human Oral Pathogen. <i>Journal of Bacteriology</i> , 2009, 191, 74-90.	1.0	67
18	TTA Lynx: a web-based service for analysis of actinomycete genes containing rare TTA codon. <i>Bioinformatics</i> , 2009, 25, 2432-2433.	1.8	19

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19	Nematode.net update 2008: improvements enabling more efficient data mining and comparative nematode genomics. <i>Nucleic Acids Research</i> , 2009, 37, D571-D578.	6.5	33
20	The High Throughput Sequence Annotation Service (HT-SAS) – the shortcut from sequence to true Medline words. <i>BMC Bioinformatics</i> , 2009, 10, 148.	1.2	4
21	The Genome Reverse Compiler: an explorative annotation tool. <i>BMC Bioinformatics</i> , 2009, 10, 35.	1.2	14
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27	Evolutionary Convergence and Nitrogen Metabolism in <i>Blattabacterium</i> strain Bge, Primary Endosymbiont of the Cockroach <i>Blattella germanica</i> . <i>PLoS Genetics</i> , 2009, 5, e1000721.	1.5	134
28	Graph methods for the investigation of metabolic networks in parasitology. <i>Parasitology</i> , 2010, 137, 1393-1407.	0.7	21
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37	Transcriptome analysis of the oil-rich seed of the bioenergy crop <i>Jatropha curcas</i> L. BMC Genomics, 2010, 11, 462.	1.2	118
38	Gene discovery for the bark beetle-vectored fungal tree pathogen <i>Grosmannia clavigera</i> . BMC Genomics, 2010, 11, 536.	1.2	25
39	Transcriptome analysis of the <i>Cryptocaryon irritans</i> tomont stage identifies potential genes for the detection and control of cryptocaryonosis. BMC Genomics, 2010, 11, 76.	1.2	38
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50	Genome Sequence of the Pea Aphid <i>Acyrtosiphon pisum</i> . PLoS Biology, 2010, 8, e1000313.	2.6	913
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62	RefNetBuilder: a platform for construction of integrated reference gene regulatory networks from expressed sequence tags. <i>BMC Bioinformatics</i> , 2011, 12, S20.	1.2	5
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81	iGepros: an integrated gene and protein annotation server for biological nature exploration. <i>BMC Bioinformatics</i> , 2011, 12, S6.	1.2	11
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111	Genome Sequence of <i>Staphylococcus capitis</i> QN1, Which Causes Infective Endocarditis. <i>Journal of Bacteriology</i> , 2012, 194, 4469-4470.	1.0	8

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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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562	Draft Genome Sequence of <i>Staphylococcus sciuri</i> subsp. <i>sciuri</i> Strain Z8, Isolated from Human Skin. <i>Genome Announcements</i> , 2015, 3, .	0.8	10
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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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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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963	Proteome Bioinformatics. <i>Methods in Molecular Biology</i> , 2017, , .	0.4	5

#	ARTICLE	IF	CITATIONS
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978	<i>Panax ginseng</i> genome examination for ginsenoside biosynthesis. <i>GigaScience</i> , 2017, 6, 1-15.	3.3	150
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982	De novo transcriptomic and metabolomic analysis of docosahexaenoic acid (DHA)-producing <i>Cryptocodinium cohnii</i> during fed-batch fermentation. <i>Algal Research</i> , 2017, 26, 380-391.	2.4	38

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1018	Comparative genome and transcriptome analysis reveals distinctive surface characteristics and unique physiological potentials of <i>Pseudomonas aeruginosa</i> ATCC 27853. <i>BMC Genomics</i> , 2017, 18, 459.	1.2	33

#	ARTICLE	IF	CITATIONS
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1020	CottonFGD: an integrated functional genomics database for cotton. <i>BMC Plant Biology</i> , 2017, 17, 101.	1.6	271
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1038	The genome of <i>Onchocerca volvulus</i> , agent of river blindness. <i>Nature Microbiology</i> , 2017, 2, 16216.	5.9	107
1039	<i>Phytophthora megakarya</i> and <i>Phytophthora palmivora</i> , Closely Related Causal Agents of Cacao Black Pod Rot, Underwent Increases in Genome Sizes and Gene Numbers by Different Mechanisms. <i>Genome Biology and Evolution</i> , 2017, 9, 536-557.	1.1	71
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1052	Development and Application of Transcriptome-Derived Microsatellites in <i>Actinidia eriantha</i> (Actinidiaceae). <i>Frontiers in Plant Science</i> , 2017, 8, 1383.	1.7	18
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#	ARTICLE	IF	CITATIONS
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1094	Transcriptome changes induced by abiotic stresses in <i>Artemisia annua</i> . <i>Scientific Reports</i> , 2018, 8, 3423.	1.6	36
1096	Comparative transcriptome analysis reveals an early gene expression profile that contributes to cold resistance in <i>Hevea brasiliensis</i> (the Para rubber tree). <i>Tree Physiology</i> , 2018, 38, 1409-1423.	1.4	26
1097	Comparative Study of Withanolide Biosynthesis-Related miRNAs in Root and Leaf Tissues of <i>Withania somnifera</i> . <i>Applied Biochemistry and Biotechnology</i> , 2018, 185, 1145-1159.	1.4	25
1098	Comparative proteomic analysis of ovaries from Huoyan geese between pre-laying and laying periods using an iTRAQ-based approach. <i>Poultry Science</i> , 2018, 97, 2170-2182.	1.5	8
1099	Cladogenesis and Genomic Streamlining in Extracellular Endosymbionts of Tropical Stink Bugs. <i>Genome Biology and Evolution</i> , 2018, 10, 680-693.	1.1	21
1100	Genetic and phenotypic analysis of carbohydrate metabolism and transport in <i>Lactobacillus reuteri</i> . <i>International Journal of Food Microbiology</i> , 2018, 272, 12-21.	2.1	53
1101	Comparative subtractive proteomics based ranking for antibiotic targets against the dirtiest superbug: <i>Acinetobacter baumannii</i> . <i>Journal of Molecular Graphics and Modelling</i> , 2018, 82, 74-92.	1.3	39
1102	Genome sequence and comparative analysis of <i>Bacillus cereus</i> BC04, reveals genetic diversity and alterations for antimicrobial resistance. <i>Functional and Integrative Genomics</i> , 2018, 18, 477-487.	1.4	4
1103	Phylogenetic analyses of the genes involved in carotenoid biosynthesis in algae. <i>Acta Oceanologica Sinica</i> , 2018, 37, 89-101.	0.4	13
1104	<i>Pseudomonas gallaeciensis</i> sp. nov., isolated from crude-oil-contaminated intertidal sand samples after the Prestige oil spill. <i>Systematic and Applied Microbiology</i> , 2018, 41, 340-347.	1.2	27
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1106	TodoFirGene: Developing Transcriptome Resources for Genetic Analysis of <i>Abies sachalinensis</i> . <i>Plant and Cell Physiology</i> , 2018, 59, 1276-1284.	1.5	17
1107	<i>In silico</i> characterization of broad range proteases produced by <i>Serratia marcescens</i> EGD-HP20. <i>Journal of Basic Microbiology</i> , 2018, 58, 492-500.	1.8	7
1108	The phosphorylated redox proteome of <i>Chlamydomonas reinhardtii</i> : Revealing novel means for regulation of protein structure and function. <i>Redox Biology</i> , 2018, 17, 35-46.	3.9	29
1109	Genome Sequence of a Heterotrophic Nitrifier and Aerobic Denitrifier, <i>Paracoccus denitrificans</i> Strain ISTOD1, Isolated from Wastewater. <i>Genome Announcements</i> , 2018, 6, .	0.8	11

#	ARTICLE	IF	CITATIONS
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1111	Comparative analyses of co-evolving host-parasite associations reveal unique gene expression patterns underlying slavemaker raiding and host defensive phenotypes. <i>Scientific Reports</i> , 2018, 8, 1951.	1.6	15
1112	Obtaining high-quality draft genomes from uncultured microbes by cleaning and co-assembly of single-cell amplified genomes. <i>Scientific Reports</i> , 2018, 8, 2059.	1.6	48
1113	Transcriptomic profiling reveals pigment regulation during peanut testa development. <i>Plant Physiology and Biochemistry</i> , 2018, 125, 116-125.	2.8	15
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1116	Multi-Omics Driven Assembly and Annotation of the Sandalwood ( <i>Santalum album</i> ) Genome. <i>Plant Physiology</i> , 2018, 176, 2772-2788.	2.3	45
1117	Multiple losses of photosynthesis and convergent reductive genome evolution in the colourless green alga <i>Prototheca</i> . <i>Scientific Reports</i> , 2018, 8, 940.	1.6	46
1118	Genomic and functional characterisation of two <i>Enterococcus</i> strains isolated from Cotija cheese and their potential role in ripening. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2251-2267.	1.7	14
1119	The systematic analysis of ultraconserved genomic regions in the budding yeast. <i>Bioinformatics</i> , 2018, 34, 361-366.	1.8	1
1121	Multiple Roots of Fruiting Body Formation in Amoebozoa. <i>Genome Biology and Evolution</i> , 2018, 10, 591-606.	1.1	39
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1123	Comparative transcriptomics uncovers differences in photoautotrophic versus photoheterotrophic modes of nutrition in relation to secondary metabolites biosynthesis in <i>Swertia chirayita</i> . <i>Molecular Biology Reports</i> , 2018, 45, 77-98.	1.0	12
1124	Transcriptomic analysis of changes in gene expression of immune proteins of gill tissue in response to low environmental temperature in fathead minnows ( <i>Pimephales promelas</i> ). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2018, 25, 109-117.	0.4	7
1125	Genomic comparison between members of the <i>Salinibacteraceae</i> family, and description of a new species of <i>Salinibacter</i> ( <i>Salinibacter altiplanensis</i> sp. nov.) isolated from high altitude hypersaline environments of the Argentinian Altiplano. <i>Systematic and Applied Microbiology</i> , 2018, 41, 198-212.	1.2	29
1126	Examination of gene repertoires and physiological responses to iron and light limitation in Southern Ocean diatoms. <i>Polar Biology</i> , 2018, 41, 679-696.	0.5	28
1127	Comparative transcriptomic analysis of shrimp hemocytes in response to acute hepatopancreas necrosis disease (AHPND) causing <i>Vibrio parahaemolyticus</i> infection. <i>Fish and Shellfish Immunology</i> , 2018, 74, 10-18.	1.6	47
1128	Subtractive genome analysis for in silico identification and characterization of novel drug targets in <i>Streptococcus pneumoniae</i> strain JJA. <i>Microbial Pathogenesis</i> , 2018, 115, 194-198.	1.3	37

#	ARTICLE	IF	CITATIONS
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1130	Comparative proteomics of the larval and adult stages of the model cestode parasite <i>Mesocestoides corti</i> . <i>Journal of Proteomics</i> , 2018, 175, 127-135.	1.2	21
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1132	Genome sequence and comparative analysis of <i>Jiangella alba</i> YIM 61503T isolated from a medicinal plant <i>Maytenus austroyunnanensis</i> . <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 667-678.	0.7	1
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1140	Ginseng Genome Database: an open-access platform for genomics of <i>Panax ginseng</i> . <i>BMC Plant Biology</i> , 2018, 18, 62.	1.6	73
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1143	Transcriptome profiling analysis revealed co-regulation of multiple pathways in jujube during infection by <i>Candidatus Phytoplasma ziziphi</i> . <i>Gene</i> , 2018, 665, 82-95.	1.0	31
1144	MetExplore: collaborative edition and exploration of metabolic networks. <i>Nucleic Acids Research</i> , 2018, 46, W495-W502.	6.5	101
1145	Comparative transcriptomic analysis identifies genes responsible for fruit count and oil yield in the oil tea plant <i>Camellia chekiangoleosa</i> . <i>Scientific Reports</i> , 2018, 8, 6637.	1.6	16
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#	ARTICLE	IF	CITATIONS
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1148	Genomic Understanding of an Infectious Brain Disease from the Desert. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 909-922.	0.8	39
1149	Discovering microRNAs and their targets in the red flour beetle <i>Tribolium castaneum</i> from expressed sequence tags. <i>Meta Gene</i> , 2018, 17, 61-67.	0.3	0
1150	Analysis of microRNA and Gene Expression Profiles in Alzheimer's Disease: A Meta-Analysis Approach. <i>Scientific Reports</i> , 2018, 8, 4767.	1.6	119
1151	Tracing Genomic Divergence of <i>Vibrio</i> Bacteria in the <i>Harveyi</i> Clade. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	8
1152	Fruit of three kiwifruit ( <i>Actinidia chinensis</i> ) cultivars differ in their degreening response to temperature after harvest. <i>Postharvest Biology and Technology</i> , 2018, 141, 16-23.	2.9	18
1153	Prioritization of potential drug targets against <i>P. aeruginosa</i> by core proteomic analysis using computational subtractive genomics and Protein-Protein interaction network. <i>Computational Biology and Chemistry</i> , 2018, 74, 115-122.	1.1	47
1154	A benzene-degrading nitrate-reducing microbial consortium displays aerobic and anaerobic benzene degradation pathways. <i>Scientific Reports</i> , 2018, 8, 4490.	1.6	74
1155	Genome sequencing and biodegradation characteristics of the n-butyl benzyl phthalate degrading bacterium- <i>Rhodococcus</i> sp. HS-D2. <i>International Biodeterioration and Biodegradation</i> , 2018, 128, 56-62.	1.9	23
1156	EumicrobeDBLite: a lightweight genomic resource and analytic platform for draft oomycete genomes. <i>Molecular Plant Pathology</i> , 2018, 19, 227-237.	2.0	24
1157	Identification and comparison of long non-coding RNAs in the silk gland between domestic and wild silkworms. <i>Insect Science</i> , 2018, 25, 604-616.	1.5	37
1158	Transcriptomes of <i>Podophyllum hexandrum</i> unravel candidate miRNAs and their association with the biosynthesis of secondary metabolites. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2018, 27, 46-54.	0.9	9
1159	Proteomics in plasma of ovariectomized rats and those exposed to estradiol valerate. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2018, 178, 1-12.	1.2	10
1160	Complete genome sequence of <i>Pseudoalteromonas espejiana</i> DSM9414T, an amino-acid-requiring strain from seawater. <i>Marine Genomics</i> , 2018, 38, 21-23.	0.4	1
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1162	Changes in fenugreek transcriptome induced by methyl jasmonate and steroid precursors revealed by RNA-Seq. <i>Genomics</i> , 2018, 110, 267-276.	1.3	16
1163	Sex-biased miRNAs of yellow catfish ( <i>Pelteobagrus fulvidraco</i> ) and their potential role in reproductive development. <i>Aquaculture</i> , 2018, 485, 73-80.	1.7	11
1164	Comparative transcriptomic analysis of larval and adult Malpighian tubules from the cotton bollworm <i>Helicoverpa armigera</i> . <i>Insect Science</i> , 2018, 25, 991-1005.	1.5	10

#	ARTICLE	IF	CITATIONS
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1166	Transcriptome profiling of PeCRY1 transgenic <i>Populus tomentosa</i> . <i>Genes and Genomics</i> , 2018, 40, 349-359.	0.5	4
1167	Metabolic versatility of small archaea Micrarchaeota and Parvarchaeota. <i>ISME Journal</i> , 2018, 12, 756-775.	4.4	91
1168	Metabolic Model Reconstruction and Analysis of an Artificial Microbial Ecosystem. <i>Methods in Molecular Biology</i> , 2018, 1716, 219-238.	0.4	1
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1174	Characterization and antifungal activity against <i>Pestalotiopsis</i> of a fusaricidin-type compound produced by <i>Paenibacillus polymyxa</i> Y-1. <i>Pesticide Biochemistry and Physiology</i> , 2018, 147, 67-74.	1.6	19
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1176	Draft Genome Sequence of <i>Candidatus</i> <i>Spirobacillus cienkowskii</i> , a Pathogen of Freshwater <i>Daphnia</i> Species, Reconstructed from Hemolymph Metagenomic Reads. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	13
1177	First complete genome sequence in <i>Arborophila</i> and comparative genomics reveals the evolutionary adaptation of Hainan Partridge ( <i>Arborophila ardens</i> ). <i>Avian Research</i> , 2018, 9, .	0.5	2
1178	Draft Genome Sequence of <i>Phaeobacter</i> sp. Strain JL2872, Isolated from Surface Waters in the South China Sea. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	0
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1180	Draft Genome Sequence of the Plant Growth-Promoting Rhizobacterium <i>Pseudomonas protegens</i> Strain BNJ-SS-45, Isolated from Rhizosphere Soil of Wheat ( <i>Triticum aestivum</i> ). <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	1
1181	Draft Genome Sequence of <i>Pelagicola</i> sp. Strain LXJ1103, Isolated from Coastal Surface Seawater. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	0
1182	Combining multiple functional annotation tools increases coverage of metabolic annotation. <i>BMC Genomics</i> , 2018, 19, 948.	1.2	35
1183	A transcriptomic snapshot of early molecular communication between <i>Pasteuria penetrans</i> and <i>Meloidogyne incognita</i> . <i>BMC Genomics</i> , 2018, 19, 850.	1.2	7

#	ARTICLE	IF	CITATIONS
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1186	CLAME: a new alignment-based binning algorithm allows the genomic description of a novel Xanthomonadaceae from the Colombian Andes. <i>BMC Genomics</i> , 2018, 19, 858.	1.2	2
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1188	Mechanisms of (photo)toxicity of TiO <sub>2</sub> nanomaterials (NM103, NM104, NM105): using high-throughput gene expression in <i>Enchytraeus crypticus</i> . <i>Nanoscale</i> , 2018, 10, 21960-21970.	2.8	17
1189	De novo transcriptome sequencing and SSR markers development for <i>Cedrela balansae</i> C.DC., a native tree species of northwest Argentina. <i>PLoS ONE</i> , 2018, 13, e0203768.	1.1	5
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1197	Genome-wide identification of flowering time genes associated with vernalization and the regulatory flowering networks in Chinese cabbage. <i>Plant Biotechnology Reports</i> , 2018, 12, 347-363.	0.9	10
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1200	Comparative Transcriptional Profiling and Physiological Responses of Two Contrasting Oat Genotypes under Salt Stress. <i>Scientific Reports</i> , 2018, 8, 16248.	1.6	25
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#	ARTICLE	IF	CITATIONS
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1216	An Improved Genome-Scale Metabolic Model of <i>Arthrospira platensis</i> C1 (iAK888) and Its Application in Glycogen Overproduction. <i>Metabolites</i> , 2018, 8, 84.	1.3	13
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1219	Dietary Probiotic Effect of <i>Lactococcus lactis</i> WFLU12 on Low-Molecular-Weight Metabolites and Growth of Olive Flounder ( <i>Paralichthys olivaceus</i> ). <i>Frontiers in Microbiology</i> , 2018, 9, 2059.	1.5	38

#	ARTICLE	IF	CITATIONS
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1222	The Transcriptomic Responses of <i>Pinus massoniana</i> to Drought Stress. <i>Forests</i> , 2018, 9, 326.	0.9	45
1223	Quantitative Proteomics Analysis of Lettuce ( <i>Lactuca sativa</i> L.) Reveals Molecular Basis-Associated Auxin and Photosynthesis with Bolting Induced by High Temperature. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2967.	1.8	22
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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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1362	MAPLE Enables Functional Assessment of Microbiota in Various Environments. , 2019, , 85-119.		4
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1373	De novo assembly of a chromosome-level reference genome of red-spotted grouper ( <i>Epinephelus</i> ) Tj ETQq1 1 0.784314 rgBT /Ov 2.2 48	2.2	48
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1389	Transcriptomic response in symptomless roots of clubroot infected kohlrabi ( <i>Brassica oleracea</i> var.) Tj ETQq1 1 0.784314 rgBT /Overl 1.6 39		
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1417	Transcriptomic analysis of Chlorimuron-ethyl degrading bacterial strain <i>Klebsiella jilinsis</i> 2N3. <i>Ecotoxicology and Environmental Safety</i> , 2019, 183, 109581.	2.9	23

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1498	Comparative genomics reveals the unique evolutionary status of <i>Plasmodiophora brassicae</i> and the essential role of GPCR signaling pathways. <i>Phytopathology Research</i> , 2019, 1, .	0.9	17
1499	Proteomics and microstructure profiling of goat milk protein after homogenization. <i>Journal of Dairy Science</i> , 2019, 102, 3839-3850.	1.4	23
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#	ARTICLE	IF	CITATIONS
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1528	Midgut de novo transcriptome analysis and gene expression profiling of <i>Achaea janata</i> larvae exposed with <i>Bacillus thuringiensis</i> (Bt)-based biopesticide formulation. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 30, 81-90.	0.4	7
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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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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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1756	Draft Genome Sequence of the Carboxydrotrophic Alphaproteobacterium <i>Aminobacter carboxidus</i> Type Strain DSM 1086. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
1757	Conserved Imprinted Genes between Intra-Subspecies and Inter-Subspecies Are Involved in Energy Metabolism and Seed Development in Rice. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9618.	1.8	8
1758	Functional Changes of the Community of Microbes With Ni-Dependent Enzyme Genes Accompany Adaptation of the Ruminant Microbiome to Urea-Supplemented Diets. <i>Frontiers in Microbiology</i> , 2020, 11, 596681.	1.5	4
1759	Eco-evolutionary Dynamics Set the Tempo and Trajectory of Metabolic Evolution in Multispecies Communities. <i>Current Biology</i> , 2020, 30, 4984-4988.e4.	1.8	17
1760	Assessment of Safety and Probiotic Traits of <i>Enterococcus durans</i> OSY-EGY, Isolated From Egyptian Artisanal Cheese, Using Comparative Genomics and Phenotypic Analyses. <i>Frontiers in Microbiology</i> , 2020, 11, 608314.	1.5	25

#	ARTICLE	IF	CITATIONS
1761	An Earliest Endosymbiont, <i>Wolbachia massiliensis</i> sp. nov., Strain PL13 from the Bed Bug ( <i>Cimex</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 8064.	1.8	23
1763	The draft genome of the blood pheasant ( <i>Thaginis cruentus</i> ): Phylogeny and high-altitude adaptation. <i>Ecology and Evolution</i> , 2020, 10, 11440-11452.	0.8	1
1764	HpeNet: Co-expression Network Database for de novo Transcriptome Assembly of <i>Paeonia lactiflora</i> Pall. <i>Frontiers in Genetics</i> , 2020, 11, 570138.	1.1	6
1765	RNA-Seq and secondary metabolite analyses reveal a putative defence-transcriptome in Norway spruce ( <i>Picea abies</i> ) against needle bladder rust ( <i>Chrysomyxa rhododendri</i> ) infection. <i>BMC Genomics</i> , 2020, 21, 336.	1.2	13
1766	Delineation of a Subgroup of the Genus <i>Paraburkholderia</i> , Including <i>P. Atterae</i> DSM 17804T, <i>P. Hospita</i> DSM 17164T, and Four Soil-Isolated Fungiphiles, Reveals Remarkable Genomic and Ecological Features—Proposal for the Definition of a <i>P. Hospita</i> Species Cluster. <i>Genome Biology and Evolution</i> , 2020, 12, 325-344.	1.1	12
1767	Genome analysis of plant growth-promoting rhizobacterium <i>Pseudomonas chlororaphis</i> subsp. <i>aurantiaca</i> JD37 and insights from comparison of genomics with three <i>Pseudomonas</i> strains. <i>Microbiological Research</i> , 2020, 237, 126483.	2.5	26
1768	Genome diversification in globally distributed novel marine Proteobacteria is linked to environmental adaptation. <i>ISME Journal</i> , 2020, 14, 2060-2077.	4.4	106
1769	Chromosome-level genome assembly of a cyprinid fish <i>Onychostoma macrolepis</i> by integration of nanopore sequencing, Bionano and Hi-C technology. <i>Molecular Ecology Resources</i> , 2020, 20, 1361-1371.	2.2	27
1770	Genome Comparison Identifies Different <i>Bacillus</i> Species in a Bast Fibre-Retting Bacterial Consortium and Provides Insights into Pectin Degrading Genes. <i>Scientific Reports</i> , 2020, 10, 8169.	1.6	22
1771	Progression of regeneration in demosponge <i>Cinachyrella cf. cavernosa</i> based on wound location. <i>Hydrobiologia</i> , 2020, 847, 2555-2571.	1.0	1
1772	iMarmot: an integrative platform for comparative and functional genomics of marmots. <i>BMC Genomics</i> , 2020, 21, 266.	1.2	3
1773	Bioinformatics Resources for Plant Abiotic Stress Responses: State of the Art and Opportunities in the Fast Evolving -Omics Era. <i>Plants</i> , 2020, 9, 591.	1.6	25
1774	&lt;p&gt;Discovery of Potential Plasma Biomarkers for Tuberculosis in HIV-Infected Patients by Data-Independent Acquisition-Based Quantitative Proteomics&lt;/p&gt;. <i>Infection and Drug Resistance</i> , 2020, Volume 13, 1185-1196.	1.1	4
1775	Gibberellin Promotes Bolting and Flowering via the Floral Integrators <i>RsFT</i> and <i>RsSOC1-1</i> under Marginal Vernalization in Radish. <i>Plants</i> , 2020, 9, 594.	1.6	13
1776	Similar yet different: phylogenomic analysis to delineate <i>Salmonella</i> and <i>Citrobacter</i> species boundaries. <i>BMC Genomics</i> , 2020, 21, 377.	1.2	15
1777	Effect of Praziquantel on <i>Schistosoma mekongi</i> Proteome and Phosphoproteome. <i>Pathogens</i> , 2020, 9, 417.	1.2	7
1778	Vitellogenins and choriogenins are biomarkers for monitoring <i>Oryzias curvinotus</i> juveniles exposed to 17 $\beta$ - estradiol. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2020, 236, 108800.	1.3	6
1779	Parallel reductive genome evolution in <i>Desulfovibrio</i> ectosymbionts independently acquired by <i>Trichonympha</i> protists in the termite gut. <i>ISME Journal</i> , 2020, 14, 2288-2301.	4.4	10

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1781	A computational subtractive genome analysis for the characterization of novel drug targets in <i>Klebsiella pneumonia</i> strain PittNDM01. <i>Microbial Pathogenesis</i> , 2020, 146, 104245.	1.3	1
1782	Comparative transcriptome profiling and co-expression network analysis reveals functionally coordinated genes associated with metabolic processes of <i>Andrographis paniculata</i> . <i>Plant Gene</i> , 2020, 23, 100234.	1.4	6
1783	Transcriptome analyses provide insights into the homeostatic regulation of axillary buds in upland cotton ( <i>G. hirsutum</i> L.). <i>BMC Plant Biology</i> , 2020, 20, 228.	1.6	5
1784	Negative Correlation between Lipid Content and Antibiotic Activity in <i>Streptomyces</i> : General Rule and Exceptions. <i>Antibiotics</i> , 2020, 9, 280.	1.5	6
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1786	Novel cultivated endophytic Verrucomicrobia reveal deep-rooting traits of bacteria to associate with plants. <i>Scientific Reports</i> , 2020, 10, 8692.	1.6	30
1787	Dataset of transcriptome assembly of date palm embryogenic calli and functional annotation. <i>Data in Brief</i> , 2020, 31, 105760.	0.5	4
1788	Shifts in the Bacterial Population and Ecosystem Functions in Response to Vegetation in the Yellow River Delta Wetlands. <i>MSystems</i> , 2020, 5, .	1.7	19
1789	Transcriptome Profiling of <i>Haloxylon persicum</i> (Bunge ex Boiss and Buhse) an Endangered Plant Species under PEG-Induced Drought Stress. <i>Genes</i> , 2020, 11, 640.	1.0	8
1790	A systematic strategy for the investigation of vaccines and drugs targeting bacteria. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1525-1538.	1.9	13
1791	Transcriptome profiling of the flowering transition in saffron ( <i>Crocus sativus</i> L.). <i>Scientific Reports</i> , 2020, 10, 9680.	1.6	28
1792	Interaction of <i>Varroa destructor</i> and Sublethal Clothianidin Doses during the Larval Stage on Subsequent Adult Honey Bee ( <i>Apis mellifera</i> L.) Health, Cellular Immunity, Deformed Wing Virus Levels and Differential Gene Expression. <i>Microorganisms</i> , 2020, 8, 858.	1.6	8
1793	Novel partiti-like viruses are conditional mutualistic symbionts in their normal lepidopteran host, African armyworm, but parasitic in a novel host, Fall armyworm. <i>PLoS Pathogens</i> , 2020, 16, e1008467.	2.1	34
1794	Comparative transcriptome analysis of MeJA-responsive AP2/ERF transcription factors involved in notoginsenosides biosynthesis. <i>3 Biotech</i> , 2020, 10, 290.	1.1	8
1795	Revealing biomass heterosis in the allodiploid <i>xBrassicoraphanus</i> , a hybrid between <i>Brassica rapa</i> and <i>Raphanus sativus</i> , through integrated transcriptome and metabolites analysis. <i>BMC Plant Biology</i> , 2020, 20, 252.	1.6	13
1796	Abnormal expression of bHLH3 disrupts a flavonoid homeostasis network, causing differences in pigment composition among mulberry fruits. <i>Horticulture Research</i> , 2020, 7, 83.	2.9	82
1797	De novo RNA sequencing analysis of <i>Aeluropus littoralis</i> halophyte plant under salinity stress. <i>Scientific Reports</i> , 2020, 10, 9148.	1.6	14

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1803	Identification and qualitative characterization of new therapeutic targets in <i>Stenotrophomonas maltophilia</i> through in silico proteome exploration. <i>Microbial Pathogenesis</i> , 2020, 149, 104293.	1.3	11
1804	Effects of Low-Dose Antibiotics on Gut Immunity and Antibiotic Resistomes in Weaned Piglets. <i>Frontiers in Immunology</i> , 2020, 11, 903.	2.2	13
1805	Analysis of Dynamic Global Transcriptional Atlas Reveals Common Regulatory Networks of Hormones and Photosynthesis Across <i>Nicotiana</i> Varieties in Response to Long-Term Drought. <i>Frontiers in Plant Science</i> , 2020, 11, 672.	1.7	13
1806	Representational Difference Analysis of Transcripts Involved in Jervine Biosynthesis. <i>Life</i> , 2020, 10, 88.	1.1	7
1807	Comparative transcriptomic analysis of deep- and shallow-water barnacle species ( <i>Cirripedia</i> ). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10</i> 2020, 21, 240.	1.2	18
1808	Comprehensive Phosphoproteomic Analysis of Pepper Fruit Development Provides Insight into Plant Signaling Transduction. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1962.	1.8	11
1809	Transcriptome Analysis and Identification of Genes Related to Biosynthesis of Anthocyanins and Kaempferitrin in Kenaf ( <i>Hibiscus cannabinus</i> L.). <i>Journal of Plant Biology</i> , 2020, 63, 51-62.	0.9	9
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1812	Development of Microsatellite Markers for a Dioecious <i>Herpetospermum pedunculatum</i> (Cucurbitaceae). <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432090826.	0.6	2
1813	The draft genome of a new <i>Verminephrobacter eiseniae</i> strain: a nephridial symbiont of earthworms. <i>Annals of Microbiology</i> , 2020, 70, .	1.1	3
1814	OsMYB80 Regulates Anther Development and Pollen Fertility by Targeting Multiple Biological Pathways. <i>Plant and Cell Physiology</i> , 2020, 61, 988-1004.	1.5	47
1815	Oral Microbiota Profile Associates with Sugar Intake and Taste Preference Genes. <i>Nutrients</i> , 2020, 12, 681.	1.7	38

#	ARTICLE	IF	CITATIONS
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1817	Relational dynamics obtained through simulation studies of thioredoxin reductase: From a multi-drug resistant <i>Entamoeba histolytica</i> . <i>Journal of Molecular Liquids</i> , 2020, 307, 112939.	2.3	4
1818	<i>Drosophila</i> -associated bacteria differentially shape the nutritional requirements of their host during juvenile growth. <i>PLoS Biology</i> , 2020, 18, e3000681.	2.6	79
1819	Combined transcriptomic and metabolomic analyses uncover rearranged gene expression and metabolite metabolism in tobacco during cold acclimation. <i>Scientific Reports</i> , 2020, 10, 5242.	1.6	29
1820	High-quality genome assembly and transcriptome of <i>Ancherythroculter nigrocauda</i> , an endemic Chinese cyprinid species. <i>Molecular Ecology Resources</i> , 2020, 20, 882-891.	2.2	11
1821	Gene correlation networks reveal the transcriptomic response to elevated nitrogen in a photosynthetic sponge. <i>Molecular Ecology</i> , 2020, 29, 1452-1462.	2.0	4
1822	In silico evolution of <i>Aspergillus niger</i> organic acid production suggests strategies for switching acid output. <i>Biotechnology for Biofuels</i> , 2020, 13, 27.	6.2	14
1823	Co-Expression Network Analysis of Spleen Transcriptome in Rock Bream ( <i>Oplegnathus fasciatus</i> ) Naturally Infected with Rock Bream Iridovirus (RBIV). <i>International Journal of Molecular Sciences</i> , 2020, 21, 1707.	1.8	17
1824	Neotropical termite microbiomes as sources of novel plant cell wall degrading enzymes. <i>Scientific Reports</i> , 2020, 10, 3864.	1.6	28
1825	Comparative transcriptomics revealed differential regulation of defense related genes in <i>Brassica juncea</i> leading to successful and unsuccessful infestation by aphid species. <i>Scientific Reports</i> , 2020, 10, 10583.	1.6	14
1826	Comparative Genomics Uncovers the Genetic Diversity and Characters of <i>Veillonella atypica</i> and Provides Insights Into Its Potential Applications. <i>Frontiers in Microbiology</i> , 2020, 11, 1219.	1.5	10
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1828	<i>Deinococcus detaillensis</i> sp. nov., isolated from humus soil in Antarctica. <i>Archives of Microbiology</i> , 2020, 202, 2493-2498.	1.0	8
1829	Differences in gene expression profiles at the early stage of <i>Solanum lycopersicum</i> infection with mild and severe variants of potato spindle tuber viroid. <i>Virus Research</i> , 2020, 286, 198090.	1.1	8
1830	<i>Orthosiphon stamineus</i> Proteins Alleviate Pentylene-tetrazol-Induced Seizures in Zebrafish. <i>Biomedicines</i> , 2020, 8, 191.	1.4	12
1831	Efficient System Wide Metabolic Pathway Comparisons in Multiple Microbes Using Genome to KEGG Orthology (G2KO) Pipeline Tool. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2020, 12, 311-322.	2.2	11
1832	Reducing the nicotine content of tobacco by grafting with eggplant. <i>BMC Plant Biology</i> , 2020, 20, 285.	1.6	6
1833	RNA-Seq analysis and development of SSR and KASP markers in lentil ( <i>Lens culinaris</i> Medikus subsp.) Tj ETQq1 1 0.784314 rgBT /Overbo 2.3 15	2.3	15

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1836	-Omic Analysis of the <i>Sepia officinalis</i> White Body: New Insights into Multifunctionality and Haematopoiesis Regulation. <i>Journal of Proteome Research</i> , 2020, 19, 3072-3087.	1.8	1
1837	Subtractive genomics approach towards the identification of novel therapeutic targets against human <i>Bartonella bacilliformis</i> . <i>Informatics in Medicine Unlocked</i> , 2020, 20, 100385.	1.9	13
1838	Genomic basis of homoploid hybrid speciation within chestnut trees. <i>Nature Communications</i> , 2020, 11, 3375.	5.8	41
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1840	Iron metabolic pathways in the processes of sponge plasticity. <i>PLoS ONE</i> , 2020, 15, e0228722.	1.1	11
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1842	Chromosomal-level assembly of <i>Juglans sigillata</i> genome using Nanopore, BioNano, and Hi-C analysis. <i>GigaScience</i> , 2020, 9, .	3.3	33
1843	Comparative analysis of bovine maternal corpus luteum microRNAs with aberrant and normal developed cloned fetus at late gestation. <i>Genes and Genomics</i> , 2020, 42, 283-290.	0.5	0
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1845	Mutation of genes for cell membrane synthesis in <i>Corynebacterium glutamicum</i> causes temperature-sensitive trait and promotes L-glutamate excretion. <i>Biotechnology and Biotechnological Equipment</i> , 2020, 34, 38-47.	0.5	7
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1847	Transcriptome profiles of phytohormone-related genes in <i>Populus tomentosa</i> vegetative buds from endodormancy to ecodormancy. <i>South African Journal of Botany</i> , 2020, 130, 430-439.	1.2	2
1848	Physiological and transcriptomic analysis provide novel insight into cobalt stress responses in willow. <i>Scientific Reports</i> , 2020, 10, 2308.	1.6	15
1849	Meta-omics Provides Insights into the Impact of Hydrocarbon Contamination on Microbial Mat Functioning. <i>Microbial Ecology</i> , 2020, 80, 286-295.	1.4	15
1850	Extreme Genome and Nervous System Streamlining in the Invertebrate Parasite <i>Intoshia variabilis</i> . <i>Current Biology</i> , 2020, 30, 1292-1298.e3.	1.8	35
1851	Interaction of field realistic doses of clothianidin and <i>Varroa destructor</i> parasitism on adult honey bee ( <i>Apis mellifera</i> L.) health and neural gene expression, and antagonistic effects on differentially expressed genes. <i>PLoS ONE</i> , 2020, 15, e0229030.	1.1	26
1852	EcoToxModules: Custom Gene Sets to Organize and Analyze Toxicogenomics Data from Ecological Species. <i>Environmental Science &amp; Technology</i> , 2020, 54, 4376-4387.	4.6	16

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1854	De novo transcriptome analysis of halotolerant bacterium <i>Staphylococcus</i> sp. strain P-TSB-70 isolated from East coast of India: In search of salt stress tolerant genes. <i>PLoS ONE</i> , 2020, 15, e0228199.	1.1	10
1855	Ultradeep Microbial Communities at 4.4 km within Crystalline Bedrock: Implications for Habitability in a Planetary Context. <i>Life</i> , 2020, 10, 2.	1.1	33
1856	Genome based safety assessment for <i>Bacillus coagulans</i> strain LBSC (DSM 17654) for probiotic application. <i>International Journal of Food Microbiology</i> , 2020, 318, 108523.	2.1	30
1857	Insights into ecological roles and potential evolution of Mlr-dependent microcystin-degrading bacteria. <i>Science of the Total Environment</i> , 2020, 710, 136401.	3.9	20
1858	Paralogization and New Protein Architectures in Planctomycetes Bacteria with Complex Cell Structures. <i>Molecular Biology and Evolution</i> , 2020, 37, 1020-1040.	3.5	6
1859	Genome-resolved metagenomics analysis provides insights into the ecological role of Thaumarchaeota in the Amazon River and its plume. <i>BMC Microbiology</i> , 2020, 20, 13.	1.3	15
1860	Identification of putative Type-I sex pheromone biosynthesis-related genes expressed in the female pheromone gland of <i>Streltziella insularis</i> . <i>PLoS ONE</i> , 2020, 15, e0227666.	1.1	4
1861	Transcriptome analysis of potato shoots, roots and stolons under nitrogen stress. <i>Scientific Reports</i> , 2020, 10, 1152.	1.6	61
1862	Proteomic and lipidomic analysis of exosomes derived from ovarian cancer cells and ovarian surface epithelial cells. <i>Journal of Ovarian Research</i> , 2020, 13, 9.	1.3	57
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1864	Increased replication of dissimilatory nitrate-reducing bacteria leads to decreased anammox bioreactor performance. <i>Microbiome</i> , 2020, 8, 7.	4.9	42
1865	Genomic, metabolic and phenotypic variability shapes ecological differentiation and intraspecies interactions of <i>Alteromonas macleodii</i> . <i>Scientific Reports</i> , 2020, 10, 809.	1.6	48
1866	Hitherto Unknown Terpene Synthase Organization in Taxol-Producing Endophytic Bacteria Isolated from Marine Macroalgae. <i>Current Microbiology</i> , 2020, 77, 918-923.	1.0	12
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1868	<i>Casimicrobium huifangae</i> gen. nov., sp. nov., a Ubiquitous "Most-Wanted" Core Bacterial Taxon from Municipal Wastewater Treatment Plants. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	26
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1870	Defining the Environmental Adaptations of Genus <i>Devosia</i> : Insights into its Expansive Short Peptide Transport System and Positively Selected Genes. <i>Scientific Reports</i> , 2020, 10, 1151.	1.6	54



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1872	De novo transcriptomic analysis predicts the effects of phenolic compounds in Ba River on the liver of female sharpbelly ( <i>Hemiculter lucidus</i> ). <i>Environmental Pollution</i> , 2020, 264, 114642.	3.7	8
1873	Molecular Response to High Hydrostatic Pressure: Time-Series Transcriptomic Analysis of Shallow-Water Sea Cucumber <i>Apostichopus japonicus</i> . <i>Frontiers in Genetics</i> , 2020, 11, 355.	1.1	2
1874	Comparative Transcriptome Analyses of <i>Schistosoma japonicum</i> Derived From SCID Mice and BALB/c Mice: Clues to the Abnormality in Parasite Growth and Development. <i>Frontiers in Microbiology</i> , 2020, 11, 274.	1.5	5
1875	Genome- and Community-Level Interaction Insights into Carbon Utilization and Element Cycling Functions of <i>Hydrothermarchaeota</i> in Hydrothermal Sediment. <i>MSystems</i> , 2020, 5, .	1.7	75
1876	Integrated Transcriptional and Proteomic Profiling Reveals Potential Amino Acid Transporters Targeted by Nitrogen Limitation Adaptation. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2171.	1.8	4
1877	Genome sequence of <i>Gossypium herbaceum</i> and genome updates of <i>Gossypium arboreum</i> and <i>Gossypium hirsutum</i> provide insights into cotton A-genome evolution. <i>Nature Genetics</i> , 2020, 52, 516-524.	9.4	240
1878	De novo transcriptome assembly and analysis of <i>Phragmites karka</i> , an invasive halophyte, to study the mechanism of salinity stress tolerance. <i>Scientific Reports</i> , 2020, 10, 5192.	1.6	24
1879	From the Inside Out: an Epibiotic <i>Bdellovibrio</i> Predator with an Expanded Genomic Complement. <i>Journal of Bacteriology</i> , 2020, 202, .	1.0	14
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1881	Comparative Metatranscriptomics of Periodontitis Supports a Common Polymicrobial Shift in Metabolic Function and Identifies Novel Putative Disease-Associated ncRNAs. <i>Frontiers in Microbiology</i> , 2020, 11, 482.	1.5	16
1882	Proteomics of <i>Brucella</i> . <i>Proteomes</i> , 2020, 8, 8.	1.7	5
1883	Draft Genome Assembly for the Tibetan Black Bear ( <i>Ursus thibetanus thibetanus</i> ). <i>Frontiers in Genetics</i> , 2020, 11, 231.	1.1	8
1884	Reverse vaccinology and drug target identification through pan-genomics. , 2020, , 317-333.		5
1885	Interactions between <i>Lactobacillus plantarum</i> NCU116 and its environments based on extracellular proteins and polysaccharides prediction by comparative analysis. <i>Genomics</i> , 2020, 112, 3579-3587.	1.3	8
1886	Sugar-regulated susceptibility of tomato fruit to <i>Colletotrichum</i> and <i>Penicillium</i> requires differential mechanisms of pathogenicity and fruit responses. <i>Environmental Microbiology</i> , 2020, 22, 2870-2891.	1.8	5
1887	Comprehensive transcriptome analyses of two <i>Oocystis</i> algae provide insights into the adaptation to Qinghai-Tibet Plateau. <i>Journal of Systematics and Evolution</i> , 2021, 59, 1209-1219.	1.6	9
1888	A Zeaxanthin-Producing Bacterium Isolated from the Algal Phycosphere Protects Coral Endosymbionts from Environmental Stress. <i>MBio</i> , 2020, 11, .	1.8	49

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1889	Postnatal Gut Immunity and Microbiota Development Is Minimally Affected by Prenatal Inflammation in Preterm Pigs. <i>Frontiers in Immunology</i> , 2020, 11, 420.	2.2	11
1890	Characterization of Nuclear and Mitochondrial Genomes of Two Tobacco Endophytic Fungi <i>Leptosphaerulina chartarum</i> and <i>Curvularia trifolii</i> and Their Contributions to Phylogenetic Implications in the Pleosporales. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2461.	1.8	7
1891	The P2RY12 receptor promotes VSMC-derived foam cell formation by inhibiting autophagy in advanced atherosclerosis. <i>Autophagy</i> , 2021, 17, 980-1000.	4.3	95
1892	Delineating Novel Therapeutic Drug and Vaccine Targets for <i>Staphylococcus cornubiensis</i> NW1T Through Computational Analysis. <i>International Journal of Peptide Research and Therapeutics</i> , 2021, 27, 181-195.	0.9	9
1893	Toward a high-quality pan-genome landscape of <i>Bacillus subtilis</i> by removal of confounding strains. <i>Briefings in Bioinformatics</i> , 2021, 22, 1951-1971.	3.2	46
1894	Genome sequence of an uncharted halophilic bacterium <i>Robertkochia marina</i> with deciphering its phosphate-solubilizing ability. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 251-256.	0.8	5
1895	Characterization of a novel <i>Pantoea</i> symbiont allows inference of a pattern of convergent genome reduction in bacteria associated with Pentatomidae. <i>Environmental Microbiology</i> , 2021, 23, 36-50.	1.8	12
1896	Complete genome sequence and comparative genome analysis of <i>Alcanivorax</i> sp. IO_7, a marine alkane-degrading bacterium isolated from hydrothermally-influenced deep seawater of southwest Indian ridge. <i>Genomics</i> , 2021, 113, 884-891.	1.3	14
1897	Effects of salinity on growth, hematological parameters, gill microstructure and transcriptome of fat greenling <i>Hexagrammos otakii</i> . <i>Aquaculture</i> , 2021, 531, 735945.	1.7	15
1898	Growth Performance and Transcriptomic Response of Warm-Acclimated Hybrid Abalone <i>Haliotis rufescens</i> (♀) × <i>H. corrugata</i> (♂). <i>Marine Biotechnology</i> , 2021, 23, 62-76.	1.1	11
1899	Transcriptomic and Proteomic Analyses of <i>Nepenthes ampullaria</i> and <i>Nepenthes rafflesiana</i> Reveal Parental Molecular Expression in the Pitchers of Their Hybrid, <i>Nepenthes</i> × <i>hookeriana</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 625507.	1.7	12
1900	The molecular mechanisms that determine different degrees of polyphagy in the <i>Bemisia tabaci</i> species complex. <i>Evolutionary Applications</i> , 2021, 14, 807-820.	1.5	12
1901	Whole-Genome Transcriptome Analyses of Native Symbionts Reveal Host Coral Genomic Novelty for Establishing Coral-Algae Symbioses. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	23
1902	Assessment of the microbial community and biocide resistance profile in production and injection waters from an Andean oil reservoir in Colombia. <i>International Biodeterioration and Biodegradation</i> , 2021, 157, 105137.	1.9	5
1903	Quantitative acetylome analysis reveals involvement of glucosyltransferase acetylation in <i>Streptococcus mutans</i> biofilm formation. <i>Environmental Microbiology Reports</i> , 2021, 13, 86-97.	1.0	18
1904	Diversification of methanogens into hyperalkaline serpentinizing environments through adaptations to minimize oxidant limitation. <i>ISME Journal</i> , 2021, 15, 1121-1135.	4.4	37
1905	Synchronization of proline, ascorbate and oxidative stress pathways under the combination of salinity and heat in tomato plants. <i>Environmental and Experimental Botany</i> , 2021, 183, 104351.	2.0	35
1906	Effects of nitrogen deficiency on the transcriptome of the oleaginous alga <i>Parachlorella kessleri</i> TY. <i>European Journal of Phycology</i> , 2021, 56, 203-215.	0.9	1

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1907	Protein oxidation analysis based on comparative proteomic of Russian sturgeon ( <i>Acipenser tjuvatensis</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 742 T	2.8	15
1908	On microbial community of <i>Pyropia haitanensis</i> by metagenomic analysis. <i>Journal of Oceanology and Limnology</i> , 2021, 39, 1091-1102.	0.6	6
1909	Chromosome-level de novo genome assembly of <i>Sarcophaga peregrina</i> provides insights into the evolutionary adaptation of flesh flies. <i>Molecular Ecology Resources</i> , 2021, 21, 251-262.	2.2	16
1911	The Methods and Tools for Molecular Network Construction. , 2021, , 14-28.		0
1912	Advances and Challenges in Metatranscriptomic Analysis. , 2021, , 453-469.		2
1913	Complementary transcriptomic and proteomic analyses reveal the cellular and molecular processes that drive growth and development of <i>Fasciola hepatica</i> in the host liver. <i>BMC Genomics</i> , 2021, 22, 46.	1.2	28
1914	Transcriptome characterization and generation of marker resource for Himalayan vulnerable species, <i>Ulmus wallichiana</i> . <i>Molecular Biology Reports</i> , 2021, 48, 721-729.	1.0	3
1915	Exploring the Role of a Cytokinin-Activating Enzyme LONELY GUY in Unicellular Microalga <i>Chlorella variabilis</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 611871.	1.7	8
1916	Orthology-Based Estimate of the Contribution of Horizontal Gene Transfer from Distantly Related Bacteria to the Intraspecific Diversity and Differentiation of <i>Xylella fastidiosa</i> . <i>Pathogens</i> , 2021, 10, 46.	1.2	6
1917	iTRAQ-based proteomic analysis of the hippocampus of pentylenetetrazole-kindled epileptic rats. <i>International Journal of Developmental Neuroscience</i> , 2021, 81, 125-141.	0.7	5
1918	Methylome and transcriptome analysis reveals candidate genes for tuber shape variation in tissue culture-derived potato. <i>Plant Growth Regulation</i> , 2021, 93, 319-332.	1.8	2
1919	Know your enemy – transcriptome of myxozoan <i>Tetracapsuloides bryosalmonae</i> reveals potential drug targets against proliferative kidney disease in salmonids. <i>Parasitology</i> , 2021, 148, 726-739.	0.7	9
1920	Genome analysis of a halophilic bacterium <i>Halomonas malpeensis</i> YU-PRIM-29T reveals its exopolysaccharide and pigment producing capabilities. <i>Scientific Reports</i> , 2021, 11, 1749.	1.6	12
1921	Proteomics of exhaled breath condensate in lung cancer and controls using data-independent acquisition (DIA): a pilot study. <i>Journal of Breath Research</i> , 2021, 15, 026002.	1.5	10
1922	Transcriptomic time-series analysis of cold- and heat-shock response in psychrotrophic lactic acid bacteria. <i>BMC Genomics</i> , 2021, 22, 28.	1.2	16
1923	Next Generation Sequencing. , 2021, , 277-302.		0
1925	CAMAMED: a pipeline for composition-aware mapping-based analysis of metagenomic data. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqaa107.	1.5	4
1926	BULKED SEGREGANT RNA SEQUENCING (BSR-SEQ) IDENTIFIES A NOVEL ALLELE ASSOCIATED WITH WEEPING TRAITS IN <i>PRUNUS MUME</i> . <i>Frontiers of Agricultural Science and Engineering</i> , 2021, ,	0.9	2

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1927	RNA-Seq-based high-resolution linkage map reveals the genetic architecture of fruiting body development in shiitake mushroom, <i>Lentinula edodes</i> . <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1641-1653.	1.9	12
1928	Sequencing, de novo assembly and annotation of <i>Digitalis ferruginea</i> subsp. <i>schischkinii</i> transcriptome. <i>Molecular Biology Reports</i> , 2021, 48, 127-137.	1.0	4
1929	The draft genome sequence of the grove snail <i>Cepaea nemoralis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	15
1930	Host susceptibility factors render ripe tomato fruit vulnerable to fungal disease despite active immune responses. <i>Journal of Experimental Botany</i> , 2021, 72, 2696-2709.	2.4	32
1931	Genome-wide genetic marker analysis and genotyping of <i>Escherichia fergusonii</i> strain OTSVEF-60. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 989-1004.	0.8	14
1933	Hologenome analysis reveals dual symbiosis in the deep-sea hydrothermal vent snail <i>Gigantopelta aegis</i> . <i>Nature Communications</i> , 2021, 12, 1165.	5.8	38
1934	Pangenomics of the Symbiotic Rhizobiales. Core and Accessory Functions Across a Group Endowed with High Levels of Genomic Plasticity. <i>Microorganisms</i> , 2021, 9, 407.	1.6	5
1936	Isolation and Functional Analysis of Genes Involved in Polyacylated Anthocyanin Biosynthesis in Blue <i>Senecio cruentus</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 640746.	1.7	11
1937	Proteomic analysis of decidua in patients with recurrent pregnancy loss (RPL) reveals mitochondrial oxidative stress dysfunction. <i>Clinical Proteomics</i> , 2021, 18, 9.	1.1	18
1938	Comparison of the Microsatellite Distribution Patterns in the Genomes of <i>Euarchontoglires</i> at the Taxonomic Level. <i>Frontiers in Genetics</i> , 2021, 12, 622724.	1.1	11
1940	Identification of Stress-Related Genes and a Comparative Analysis of the Amino Acid Compositions of Translated Coding Sequences Based on Draft Genome Sequences of Antarctic Yeasts. <i>Frontiers in Microbiology</i> , 2021, 12, 623171.	1.5	6
1941	A highly contiguous reference genome assembly for <i>Colletotrichum falcatum</i> pathotype Cf08 causing red rot disease in sugarcane. <i>3 Biotech</i> , 2021, 11, 148.	1.1	0
1943	High-pressure processing-induced transcriptome response during recovery of <i>Listeria monocytogenes</i> . <i>BMC Genomics</i> , 2021, 22, 117.	1.2	18
1944	Production and Excretion of Polyamines To Tolerate High Ammonia, a Case Study on Soil Ammonia-Oxidizing Archaeon <i>Candidatus Nitrosocosmicus agrestis</i> . <i>MSystems</i> , 2021, 6, .	1.7	15
1945	Genome Guided Bioprospecting of Extremely Halophilic <i>Haloferax</i> sp. AS1 for CAZymes, Bioremediation and Study Metabolic Versatility. <i>Proceedings of the National Academy of Sciences India Section B - Biological Sciences</i> , 2021, 91, 297-305.	0.4	0
1946	Unique niche-specific adaptation of fructophilic lactic acid bacteria and proposal of three <i>Apilactobacillus</i> species as novel members of the group. <i>BMC Microbiology</i> , 2021, 21, 41.	1.3	19
1947	Enrichment of novel <i>Verrucomicrobia</i> , <i>Bacteroidetes</i> , and <i>Krumholzibacteria</i> in an oxygen-limited methane and iron-fed bioreactor inoculated with Bothnian Sea sediments. <i>MicrobiologyOpen</i> , 2021, 10, e1175.	1.2	16
1948	Comparative transcriptome analysis of <i>Rheum australe</i> , an endangered medicinal herb, growing in its natural habitat and those grown in controlled growth chambers. <i>Scientific Reports</i> , 2021, 11, 3702.	1.6	11

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1949	Identifications of immune-responsive genes for adaptative traits by comparative transcriptome analysis of spleen tissue from Kazakh and Suffolk sheep. <i>Scientific Reports</i> , 2021, 11, 3157.	1.6	9
1950	An RNA-seq Analysis Reveals Differential Transcriptional Responses to Different Light Qualities in Leaf Color of <i>Camellia sinensis</i> cv. Huangjinya. <i>Journal of Plant Growth Regulation</i> , 0, , 1.	2.8	9
1951	Infection trains the host for microbiota-enhanced resistance to pathogens. <i>Cell</i> , 2021, 184, 615-627.e17.	13.5	148
1952	Bacteria and Metabolic Potential in Karst Caves Revealed by Intensive Bacterial Cultivation and Genome Assembly. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	12
1953	In Silico Identification of Protein in <i>Ralstonia solanacearum</i> , A Bacterial Wilt Pathogen for Drug Target by Subtractive Genomic Analysis. <i>Bioscience Biotechnology Research Communications</i> , 2021, 14, 291-297.	0.1	2
1954	De novo transcriptome reveals blood coagulation/antithrombin factors and infection mechanisms in <i>Angiostrongylus cantonensis</i> adult worms. <i>Parasitology</i> , 2021, 148, 857-870.	0.7	0
1955	Impact of exogenous caffeine on regulatory networks of microRNAs in response to <i>Colletotrichum gloeosporioides</i> in tea plant. <i>Scientia Horticulturae</i> , 2021, 279, 109914.	1.7	11
1956	<i>Iodidimonas gelatinilytica</i> sp. nov., aerobic iodide-oxidizing bacteria isolated from brine water and surface seawater. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 625-631.	0.7	11
1957	Comparative transcriptomic analysis of the different developmental stages of ovary in red swamp crayfish <i>Procambarus clarkii</i> . <i>BMC Genomics</i> , 2021, 22, 199.	1.2	8
1958	Draft genome sequencing of the foxglove aphid ( <i>Aulacorthum solani</i> Kaltentbach), a vector of potato viruses, provides insights on virulence genes. <i>Journal of Asia-Pacific Entomology</i> , 2021, 24, 93-93.	0.4	3
1960	Key aroma compounds and metabolic profiling of <i>Debaryomyces hansenii</i> L1â€¦â€¦fermented Flos Sophorae. <i>Journal of Food Biochemistry</i> , 2021, 45, e13711.	1.2	5
1961	Use of data-independent acquisition mass spectrometry for comparative proteomics analyses of sera from pregnant women with intrahepatic cholestasis of pregnancy. <i>Journal of Proteomics</i> , 2021, 236, 104124.	1.2	7
1962	Global analysis of lysine 2-hydroxyisobutyrylation in wheat root. <i>Scientific Reports</i> , 2021, 11, 6327.	1.6	7
1963	Comparative transcriptome analysis infers bulb derived in vitro cultures as a promising source for sipeimine biosynthesis in <i>Fritillaria cirrhosa</i> D. Don (Liliaceae, syn. <i>Fritillaria roylei</i> Hook.) - High value Himalayan medicinal herb. <i>Phytochemistry</i> , 2021, 183, 112631.	1.4	20
1964	De novo transcriptome assemblies of <i>Epicauta tibialis</i> provide insights into the sexual dimorphism in the production of cantharidin. <i>Archives of Insect Biochemistry and Physiology</i> , 2021, 106, e21784.	0.6	3
1967	De novo genome assembly of <i>Bacillus altitudinis</i> 19RS3 and <i>Bacillus altitudinis</i> T5S-T4, two plant growth-promoting bacteria isolated from <i>Ilex paraguariensis</i> St. Hil. (yerba mate). <i>PLoS ONE</i> , 2021, 16, e0248274.	1.1	11
1968	Comparative transcriptome analysis of short-term responses to salt and glycerol hyperosmotic stress in the green alga <i>Dunaliella salina</i> . <i>Algal Research</i> , 2021, 53, 102147.	2.4	10
1969	Transcriptional profiling of two contrasting genotypes uncovers molecular mechanisms underlying salt tolerance in alfalfa. <i>Scientific Reports</i> , 2021, 11, 5210.	1.6	13

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1972	Transcriptome and Comparative Chloroplast Genome Analysis of Vincetoxicum versicolor: Insights Into Molecular Evolution and Phylogenetic Implication. <i>Frontiers in Genetics</i> , 2021, 12, 602528.	1.1	10
1973	Predicted Input of Uncultured Fungal Symbionts to a Lichen Symbiosis from Metagenome-Assembled Genomes. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	19
1974	Diversity of Conopeptides and Conoenzymes from the Venom Duct of the Marine Cone Snail <i>Conus bayani</i> as Determined from Transcriptomic and Proteomic Analyses. <i>Marine Drugs</i> , 2021, 19, 202.	2.2	3
1975	Distinct morpho-physiological and biochemical features of arid and hyper-arid ecotypes of <i>Ziziphus nummularia</i> under drought suggest its higher tolerance compared with semi-arid ecotype. <i>Tree Physiology</i> , 2021, 41, 2063-2081.	1.4	2
1976	Description of <i>Candidatus Mesopelagibacter carboxydoxydans</i> and <i>Candidatus Anoxipelagibacter denitrificans</i> : Nitrate-reducing SAR11 genera that dominate mesopelagic and anoxic marine zones. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126185.	1.2	14
1978	SNP markers associated with resistance to frosty pod and black pod rot diseases in an F1 population of <i>Theobroma cacao</i> L.. <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	0.6	11
1979	Transcriptome profiling of <i>Cysticercus Pisiformis</i> provides insight into responses to host bile acids. <i>Parasitology International</i> , 2021, 81, 102246.	0.6	2
1980	<i>Eudiplozoon nipponicum</i> (Monogenea, Diplozoidae) and its adaptation to haematophagy as revealed by transcriptome and secretome profiling. <i>BMC Genomics</i> , 2021, 22, 274.	1.2	13
1981	Genomic insights into the molecular mechanisms of a <i>Pseudomonas</i> strain significant in its survival in Kongsfjorden, an Arctic fjord. <i>Molecular Genetics and Genomics</i> , 2021, 296, 893-903.	1.0	3
1982	Simultaneous nitrate and sulfate dependent anaerobic oxidation of methane linking carbon, nitrogen and sulfur cycles. <i>Water Research</i> , 2021, 194, 116928.	5.3	43
1983	Incipient genome erosion and metabolic streamlining for antibiotic production in a defensive symbiont. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	12
1985	Genome sequencing and comparative genomic analysis of highly and weakly aggressive strains of <i>Sclerotium rolfsii</i> , the causal agent of peanut stem rot. <i>BMC Genomics</i> , 2021, 22, 276.	1.2	20
1986	Whole Genome Sequence and Gene Annotation Resource for <i>Didymella bellidis</i> Associated with Tea Leaf Spot. <i>Plant Disease</i> , 2021, 105, 1168-1170.	0.7	3
1987	Large-Scale Phylogenomic Analyses Reveal the Monophyly of Bryophytes and Neoproterozoic Origin of Land Plants. <i>Molecular Biology and Evolution</i> , 2021, 38, 3332-3344.	3.5	56
1988	Gene Expression Differences Between Developmental Stages of the Fall Armyworm ( <i>Spodoptera</i> ) Tj ETQq0 0 0 rgBTj/Overlock 2 10 Tf 50 1	0.9	2
1989	Multiple concurrent and convergent stages of genome reduction in bacterial symbionts across a stink bug family. <i>Scientific Reports</i> , 2021, 11, 7731.	1.6	7
1990	Active Microbiome Structure and Functional Analyses of Freshwater Benthic Biofilm Samples Influenced by RNA Extraction Methods. <i>Frontiers in Microbiology</i> , 2021, 12, 588025.	1.5	2
1991	Limonoid biosynthesis 3: Functional characterization of crucial genes involved in neem limonoid biosynthesis. <i>Phytochemistry</i> , 2021, 184, 112669.	1.4	12

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1992	CAZymes in <i>Maribacter dokdonensis</i> 62â€“1 From the Patagonian Shelf: Genomics and Physiology Compared to Related Flavobacteria and a Co-occurring <i>Alteromonas</i> Strain. <i>Frontiers in Microbiology</i> , 2021, 12, 628055.	1.5	13
1993	<i>Comamonas suwonensis</i> sp. nov., isolated from stream water in the Republic of Korea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	8
1994	Characterization and Engineering of <i>Pseudomonas chlororaphis</i> LX24 with High Production of 2-Hydroxyphenazine. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 4778-4784.	2.4	6
1995	Sex-Biased Gene Expression and Evolution in the Cerebrum and Syrinx of Chinese Hwamei ( <i>Garrulax</i> ) Tj ETQq1 1 0.784314 rgBT /Over	1.0	1
1996	Single and Double Mutations in Tomato Ripening Transcription Factors Have Distinct Effects on Fruit Development and Quality Traits. <i>Frontiers in Plant Science</i> , 2021, 12, 647035.	1.7	16
1997	An Atlas of Genomic Resources for Studying Rosaceae Fruits and Ornamentals. <i>Frontiers in Plant Science</i> , 2021, 12, 644881.	1.7	5
1998	Niche-specific adaptation of <i>Lactobacillus helveticus</i> strains isolated from malt whisky and dairy fermentations. <i>Microbial Genomics</i> , 2021, 7, .	1.0	5
1999	Functional annotations of ESTs of <i>Stevia rebaudiana</i> involved in abiotic stress signaling through computational approach. <i>Saudi Journal of Biological Sciences</i> , 2021, 28, 2602-2612.	1.8	1
2001	Transcriptome Sequence Reveals Candidate Genes Involving in the Post-Harvest Hardening of Trifoliolate Yam <i>Dioscorea dumetorum</i> . <i>Plants</i> , 2021, 10, 787.	1.6	10
2002	A genome wide transcriptional study of <i>Populus alba</i> x <i>P. tremula</i> var. <i>glandulosa</i> in response to nitrogen deficiency stress. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 1277-1293.	1.4	5
2004	A high-quality carabid genome assembly provides insights into beetle genome evolution and cold adaptation. <i>Molecular Ecology Resources</i> , 2021, 21, 2145-2165.	2.2	13
2005	Assessment of changes in genetic transcriptome in nasal epithelial cells exposed to ozone-aged black carbon and pollen allergen by high-throughput transcriptomics. <i>Allergy, Asthma and Clinical Immunology</i> , 2021, 17, 52.	0.9	2
2006	Multiple cellular compartments engagement in <i>Nicotiana benthamiana</i> -peanut stunt virus-satRNA interactions revealed by systems biology approach. <i>Plant Cell Reports</i> , 2021, 40, 1247-1267.	2.8	4
2007	Microbiome Analysis Reveals Diversity and Function of <i>Mollicutes</i> Associated with the Eastern Oyster, <i>Crassostrea virginica</i> . <i>MSphere</i> , 2021, 6, .	1.3	21
2008	<i>Nepenthes Ã— ventrata</i> Transcriptome Profiling Reveals a Similarity Between the Evolutionary Origins of Carnivorous Traps and Floral Organs. <i>Frontiers in Plant Science</i> , 2021, 12, 643137.	1.7	4
2009	Resilience in Greenland intertidal <i>Mytilus</i> : The hidden stress defense. <i>Science of the Total Environment</i> , 2021, 767, 144366.	3.9	25
2010	Draft genome sequence of the pulse crop blackgram [ <i>Vigna mungo</i> (L.) Hepper] reveals potential R-genes. <i>Scientific Reports</i> , 2021, 11, 11247.	1.6	20
2011	Vulture Genomes Reveal Molecular Adaptations Underlying Obligate Scavenging and Low Levels of Genetic Diversity. <i>Molecular Biology and Evolution</i> , 2021, 38, 3649-3663.	3.5	9

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2012	Comprehensive Phosphoproteomic Analysis of <i>Nostoc flagelliforme</i> in Response to Dehydration Provides Insights into Plant ROS Signaling Transduction. <i>ACS Omega</i> , 2021, 6, 13554-13566.	1.6	7
2014	De novo transcriptome assembly of the deep-sea hydrothermal vent, shrimp <i>Rimicaris exoculate</i> (Crustacea: Decapoda), from the south Mid-Atlantic Ridge. <i>Marine Genomics</i> , 2021, 60, 100876.	0.4	0
2015	Physiological and Genomic Analysis of <i>Bacillus pumilus</i> UAMX Isolated from the Gastrointestinal Tract of Overweight Individuals. <i>Microorganisms</i> , 2021, 9, 1076.	1.6	2
2016	Secretome characterization of clinical isolates from the <i>Mycobacterium abscessus</i> complex provides insight into antigenic differences. <i>BMC Genomics</i> , 2021, 22, 385.	1.2	2
2017	Comprehensive Volatilome and Metabolome Signatures of Colorectal Cancer in Urine: A Systematic Review and Meta-Analysis. <i>Cancers</i> , 2021, 13, 2534.	1.7	19
2018	Identification of Olfactory Genes From the Greater Wax Moth by Antennal Transcriptome Analysis. <i>Frontiers in Physiology</i> , 2021, 12, 663040.	1.3	11
2019	Transcriptional Response in the Digestive Gland of the King Scallop ( <i>Pecten maximus</i> ) After the Injection of Domoic Acid. <i>Toxins</i> , 2021, 13, 339.	1.5	9
2020	Proteomic Analysis Reveals That Placenta-Specific Protein 9 Inhibits Proliferation and Stimulates Motility of Human Bronchial Epithelial Cells. <i>Frontiers in Oncology</i> , 2021, 11, 628480.	1.3	6
2021	Kinome analyses of <i>Candida albicans</i> , <i>C. parapsilosis</i> and <i>C. tropicalis</i> enable novel kinases as therapeutic drug targets in candidiasis. <i>Gene</i> , 2021, 780, 145530.	1.0	3
2022	Draft genome of the Korean smelt <i>Hypomesus nipponensis</i> and its transcriptomic responses to heat stress in the liver and muscle. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	1
2023	Comprehensive phylogeny of <i>Konosirus punctatus</i> (Clupeiformes: Clupeidae) based on transcriptomic data. <i>Bioscience Reports</i> , 2021, 41, .	1.1	2
2024	De novo transcriptome sequencing assisted identification of terpene synthases from black pepper ( <i>Piper nigrum</i> ) berry. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 1153-1161.	1.4	6
2025	<i>Sphingobacterium lumbrici</i> sp. nov., a novel bacterium isolated from wormcast of <i>Eisenia foetida</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	2
2026	Unveiling the CHO surfaceome: Identification of cell surface proteins reveals cell aggregation-relevant mechanisms. <i>Biotechnology and Bioengineering</i> , 2021, 118, 3015-3028.	1.7	6
2027	Sweet spheres: succession and <i>CAZyme</i> expression of marine bacterial communities colonizing a mix of alginate and pectin particles. <i>Environmental Microbiology</i> , 2021, 23, 3130-3148.	1.8	17
2028	Transcriptome analysis reveals the importance of exogenous nutrition in regulating antioxidant defenses during the mouth-opening stage in oviparous fish. <i>Fish Physiology and Biochemistry</i> , 2021, 47, 1087-1103.	0.9	8
2029	Chromosome-level assembly of southern catfish ( <i>Silurus meridionalis</i> ) provides insights into visual adaptation to nocturnal and benthic lifestyles. <i>Molecular Ecology Resources</i> , 2021, 21, 1575-1592.	2.2	20
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2034	The Genomic Impact of Mycoheterotrophy in Orchids. Frontiers in Plant Science, 2021, 12, 632033.	1.7	9
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2037	Review of Machine Learning Methods for the Prediction and Reconstruction of Metabolic Pathways. Frontiers in Molecular Biosciences, 2021, 8, 634141.	1.6	15
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2045	Subtractive proteomics approach to Unravel the druggable proteins of the emerging pathogen <i>Waddlia chondrophila</i> and drug repositioning on its MurB protein. Heliyon, 2021, 7, e07320.	1.4	2
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2047	Global mRNA and miRNA Analysis Reveal Key Processes in the Initial Response to Infection with WSSV in the Pacific Whiteleg Shrimp. Viruses, 2021, 13, 1140.	1.5	11
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2058	Substrate-dependent competition and cooperation relationships between <i>Geobacter</i> and <i>Dehalococcoides</i> for their organohalide respiration. <i>ISME Communications</i> , 2021, 1, .	1.7	27
2060	Integrated Analysis of mRNA and miRNA Changes in Two <i>Haliotis diversicolor</i> Genotypes and Their Hybrid. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	3
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2065	Insights Into the Mechanisms Implicated in <i>Pinus pinaster</i> Resistance to Pinewood Nematode. <i>Frontiers in Plant Science</i> , 2021, 12, 690857.	1.7	15
2066	Quantitative proteomic analyses reveal that energy metabolism and protein biosynthesis reinitiation are responsible for the initiation of bolting induced by high temperature in lettuce ( <i>Lactuca sativa</i> L.). <i>BMC Genomics</i> , 2021, 22, 427.	1.2	8
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2071	Enhancing nitrogen removal from anaerobically-digested swine wastewater through integration of <i>Miriophyllum aquaticum</i> and free nitrous acid-based technology in a constructed wetland. <i>Science of the Total Environment</i> , 2021, 779, 146441.	3.9	6
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2079	A chromosome-level genome assembly of the yellowfin seabream ( <i>Acanthopagrus latus</i> ; Hottuyn, 1782) provides insights into its osmoregulation and sex reversal. Genomics, 2021, 113, 1617-1627.	1.3	13
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2083	New Insights From Transcriptomic Data Reveal Differential Effects of CO <sub>2</sub> Acidification Stress on Photosynthesis of an Endosymbiotic Dinoflagellate in hospite. Frontiers in Microbiology, 2021, 12, 666510.	1.5	4
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2086	Genomic and transcriptomic analyses reveal metabolic complementarity between whiteflies and their symbionts. Insect Science, 2022, 29, 539-549.	1.5	9
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2090	TRAPID 2.0: a web application for taxonomic and functional analysis of <i>de novo</i> transcriptomes. Nucleic Acids Research, 2021, 49, e101-e101.	6.5	21
2091	Large-scale protein level comparison of Deltaproteobacteria reveals cohesive metabolic groups. ISME Journal, 2022, 16, 307-320.	4.4	71

#	ARTICLE	IF	CITATIONS
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2095	Comparative Analysis of PacBio and Oxford Nanopore Sequencing Technologies for Transcriptomic Landscape Identification of <i>Penaeus monodon</i> . <i>Life</i> , 2021, 11, 862.	1.1	7
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2100	Genome-wide analysis of HECT E3 ubiquitin ligase gene family in <i>Solanum lycopersicum</i> . <i>Scientific Reports</i> , 2021, 11, 15891.	1.6	10
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2102	Identification and expression pattern of lentil HSPs under different abiotic stresses. <i>Plant Biotechnology Reports</i> , 2021, 15, 609-625.	0.9	4
2103	Potential therapeutic targets of <i>Klebsiella pneumoniae</i> : a multi-omics review perspective. <i>Briefings in Functional Genomics</i> , 2022, 21, 63-77.	1.3	31
2104	Transcriptome profile of <i>Dunaliella salina</i> in Yuncheng Salt Lake reveals salt-stress-related genes under different salinity stresses. <i>Journal of Oceanology and Limnology</i> , 2021, 39, 2336-2362.	0.6	7
2105	Genome and transcriptome assemblies of the kuruma shrimp, <i>Marsupenaeus japonicus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	20
2106	clusterProfiler 4.0: A universal enrichment tool for interpreting omics data. <i>Innovation(China)</i> , 2021, 2, 100141.	5.2	2,743
2107	Genome Analysis of <i>Phytophthora nicotianae</i> JM01 Provides Insights into Its Pathogenicity Mechanisms. <i>Plants</i> , 2021, 10, 1620.	1.6	4
2108	Overdominance at the Gene Expression Level Plays a Critical Role in the Hybrid Root Growth of <i>Brassica napus</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 9246.	1.8	9
2109	Transcriptomic analysis of a wild and a cultivated varieties of <i>Capsicum annuum</i> over fruit development and ripening. <i>PLoS ONE</i> , 2021, 16, e0256319.	1.1	7
2110	Endophytes from African Rice ( <i>Oryza glaberrima</i> L.) Efficiently Colonize Asian Rice ( <i>Oryza sativa</i> L.) Stimulating the Activity of Its Antioxidant Enzymes and Increasing the Content of Nitrogen, Carbon, and Chlorophyll. <i>Microorganisms</i> , 2021, 9, 1714.	1.6	8

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2113	<scp>KEGG</scp> mapping tools for uncovering hidden features in biological data. <i>Protein Science</i> , 2022, 31, 47-53.	3.1	365
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2115	Transitional genomes and nutritional role reversals identified for dual symbionts of adelgids (Aphidoidea: Adelgidae). <i>ISME Journal</i> , 2022, 16, 642-654.	4.4	11
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2123	Molecular adaptations to heat stress in the thermophilic ant genus <i>Cataglyphis</i> . <i>Molecular Ecology</i> , 2021, 30, 5503-5516.	2.0	14
2124	A tetraploidization event shaped the <i>Aquilaria sinensis</i> genome and contributed to the ability of sesquiterpenes synthesis. <i>BMC Genomics</i> , 2021, 22, 647.	1.2	3
2125	Characterization and engineering of <i>Streptomyces griseofuscus</i> DSM 40191 as a potential host for heterologous expression of biosynthetic gene clusters. <i>Scientific Reports</i> , 2021, 11, 18301.	1.6	11
2127	<i>Streptomyces poriferorum</i> sp. nov., a novel marine sponge-derived Actinobacteria species expressing anti-MRSA activity. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126244.	1.2	10
2128	Adaptation of Fig Wasps (Agaodinae) to Their Host Revealed by Large-Scale Transcriptomic Data. <i>Insects</i> , 2021, 12, 815.	1.0	5
2129	Molecular and evolutionary basis for survival, its failure, and virulence factors of the zoonotic nematode <i>Anisakis pegreffii</i> . <i>Genomics</i> , 2021, 113, 2891-2905.	1.3	11

#	ARTICLE	IF	CITATIONS
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2131	Comparative genome analysis of <i>Clostridium beijerinckii</i> strains isolated from pit mud of Chinese strong flavor baijiu ecosystem. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	4
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2133	Sex-Biased Gene Expression and Isoform Profile of Brine Shrimp <i>Artemia franciscana</i> by Transcriptome Analysis. <i>Animals</i> , 2021, 11, 2630.	1.0	4
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2138	Novel genome reveals susceptibility of popular gamebird, the red-legged partridge ( <i>Alectoris rufa</i> ), to <i>Escherichia coli</i> O157:H7. <i>Overlook 10 Tf 50</i>	1.3	6
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2140	Effect of food source availability in the salivary gland transcriptome of the unique burying beetle <i>Nicrophorus pustulatus</i> (Coleoptera: Silphidae). <i>PLoS ONE</i> , 2021, 16, e0255660.	1.1	0
2141	Development of Genome-Wide Functional Markers Using Draft Genome Assembly of Guava ( <i>Psidium</i> ) Tj ETQq1 1 0.784314 rgBT /Overlook 8	1.7	8
2142	Exposure of American lobster ( <i>Homarus americanus</i> ) to the pesticide chlorpyrifos results in changes in gene expression. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 40, 100918.	0.4	0
2143	Inverted microbial community stratification and spatial-temporal stability in hypersaline anaerobic sediments from the Avall solar salterns. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126231.	1.2	5
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2145	Revealing the coexistence of differentiation and communication in an endemic hare, <i>Lepus yarkandensis</i> (Mammalia, Leporidae) using specific-length amplified fragment sequencing. <i>Frontiers in Zoology</i> , 2021, 18, 50.	0.9	2
2146	Co-occurrence of antimicrobial and metal resistance genes in pig feces and agricultural fields fertilized with slurry. <i>Science of the Total Environment</i> , 2021, 792, 148259.	3.9	21
2147	Genomic and biochemical characterization of antifungal compounds produced by <i>Bacillus subtilis</i> PMB102 against <i>Alternaria brassicicola</i> . <i>Microbiological Research</i> , 2021, 251, 126815.	2.5	18

#	ARTICLE	IF	CITATIONS
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2149	Metagenomic insights into the effect of thermal hydrolysis pre-treatment on microbial community of an anaerobic digestion system. <i>Science of the Total Environment</i> , 2021, 791, 148096.	3.9	31
2150	Novel Corneal Protein Biomarker Candidates Reveal Iron Metabolic Disturbance in High Myopia Eyes. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 689917.	1.8	2
2151	Cellular uptake of chitosan and its role in antifungal action against <i>Penicillium expansum</i> . <i>Carbohydrate Polymers</i> , 2021, 269, 118349.	5.1	11
2152	Proteome analysis and thermal-tolerant protein marker screening in the skin mucus of large yellow croaker <i>Larimichthys crocea</i> . <i>Aquaculture Reports</i> , 2021, 21, 100870.	0.7	3
2153	The salmon louse genome: Copepod features and parasitic adaptations. <i>Genomics</i> , 2021, 113, 3666-3680.	1.3	17
2154	Transcriptomics reveals that the caudal neurosecretory system in the olive flounder ( <i>Paralichthys</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2021, 544, 737032.	1.7	7
2155	Prediction of adverse effects of effluents containing phenolic compounds in the Ba River on the ovary of fish ( <i>Hemiculter leucisculus</i> ) using transcriptomic and metabolomic analyses. <i>Science of the Total Environment</i> , 2021, 801, 149554.	3.9	12
2156	Incubation trial indicated the earthworm intestinal bacteria as promising biodigester for mitigating tetracycline resistance risk in anthropogenic disturbed forest soil. <i>Science of the Total Environment</i> , 2021, 798, 149337.	3.9	14
2157	Transcriptome analysis of growth variation in early juvenile stage sandfish <i>Holothuria scabra</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 40, 100904.	0.4	2
2158	The degradation mechanisms of <i>Rhodopseudomonas palustris</i> toward hexabromocyclododecane by time-course transcriptome analysis. <i>Chemical Engineering Journal</i> , 2021, 425, 130489.	6.6	9
2159	Metatranscriptomic insight into the effects of antibiotic exposure on performance during anaerobic co-digestion of food waste and sludge. <i>Journal of Hazardous Materials</i> , 2022, 423, 127163.	6.5	25
2160	Comparison of methane metabolism in the rhizomicrobiomes of wild and related cultivated rice accessions reveals a strong impact of crop domestication. <i>Science of the Total Environment</i> , 2022, 803, 150131.	3.9	8
2161	Harnessing the potential of modern omics approaches to study plant biotic and abiotic stresses. , 2022, , 101-122.		1
2162	Multi-omic approach to evaluate the response of gilt-head sea bream ( <i>Sparus aurata</i> ) exposed to the UV filter sulisobenzone. <i>Science of the Total Environment</i> , 2022, 803, 150080.	3.9	16
2163	Advancement in bioinformatics and microarray-based technologies for genome sequence analysis and its application in bioremediation of soil and water pollutants. , 2021, , 209-225.		0
2164	Transcriptome analysis reveals salinity responses in four Tartary buckwheat cultivars. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2021, 30, 564-578.	0.9	6
2165	<i>Amyntas corticis</i> genome reveals molecular mechanisms behind global distribution. <i>Communications Biology</i> , 2021, 4, 135.	2.0	6

#	ARTICLE	IF	CITATIONS
2166	Genome-wide association study reveals the genes associated with the leaf inclusion contents in Chinese medical tree <i>Eucommia ulmoides</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2021, 85, 233-241.	0.6	3
2167	RNA-Seq in Nonmodel Organisms. <i>Methods in Molecular Biology</i> , 2021, 2243, 143-167.	0.4	4
2168	Integrative multiomics analysis of <i>Premolis semirufa</i> caterpillar venom in the search for molecules leading to a joint disease. <i>Scientific Reports</i> , 2021, 11, 1995.	1.6	2
2169	Analysis of the core genome and pangenome of <i>Clostridium butyricum</i> . <i>Genome</i> , 2021, 64, 51-61.	0.9	10
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#	ARTICLE	IF	CITATIONS
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2558	Transcriptome Responses to Defined Insecticide Selection Pressures in the German Cockroach ( <i>Blattella germanica</i> L.). <i>Frontiers in Physiology</i> , 2021, 12, 816675.	1.3	7
2559	<i>Massilia soli</i> sp. nov., isolated from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	16
2560	Changes in Gene Expression in Leaves of Cacao Genotypes Resistant and Susceptible to <i>Phytophthora palmivora</i> Infection. <i>Frontiers in Plant Science</i> , 2021, 12, 780805.	1.7	6
2561	Intergenerational Effects of Early-Life Starvation on Life History, Consumption, and Transcriptome of a Holometabolous Insect. <i>American Naturalist</i> , 2022, 199, E229-E243.	1.0	4
2562	The gut microbiome and antibiotic resistome of chronic diarrhea rhesus macaques ( <i>Macaca mulatta</i> ) and its similarity to the human gut microbiome. <i>Microbiome</i> , 2022, 10, 29.	4.9	24
2563	Transcriptome signature changes in the liver of a migratory passerine. <i>Genomics</i> , 2022, 114, 110283.	1.3	8
2564	A comprehensive characterization of culturable endophytic bacteria of <i>Paris polyphylla</i> and their potential role in microalgal growth in co-culture. <i>Applied Soil Ecology</i> , 2022, 174, 104410.	2.1	8

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2566	Transcriptome analysis of finger millet ( <i>L. Gaertn.</i> ) reveals unique drought responsive genes. <i>Journal of Genetics</i> , 2019, 98, .	0.4	5
2567	Integrated Analysis of Metabolome and Transcriptome of <i>Bambusa emeiensis</i> Shoots in Response to Bamboo Snout Beetle <i>Cyrtotrachelus buqueti</i> (Coleoptera: Curculionidae). <i>Phyton</i> , 2022, 91, 1227-1244.	0.4	0
2568	Applications of microbial omics in healthcare. , 2022, , 227-248.		0
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2574	The transcription factor complex CmAP3-CmPI-CmUIF1 modulates carotenoid metabolism by directly regulating the carotenogenic gene <i>CmCCD4a-2</i> in chrysanthemum. <i>Horticulture Research</i> , 2022, 9, .	2.9	9
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2580	Comparative transcriptomes of three different skin sites for the Asiatic toad ( <i>Bufo</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 149	0.9	1
2581	Full-length transcriptome analysis of multiple organs and identification of adaptive genes and pathways in <i>Mikania micrantha</i> . <i>Scientific Reports</i> , 2022, 12, 3272.	1.6	0
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2585	Whole-Genome and Transcriptome Sequencing-Based Characterization of <i>Bacillus Cereus</i> NR1 From Subtropical Marine Mangrove and Its Potential Role in Sulfur Metabolism. <i>Frontiers in Microbiology</i> , 2022, 13, 856092.	1.5	8
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2588	Adaptation Potential of Three Psychrotolerant Aquatic Bacteria in the Pan-Okhotsk Region. <i>Water (Switzerland)</i> , 2022, 14, 1107.	1.2	1
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2590	The Space-Exposed Kombucha Microbial Community Member <i>Komagataeibacter oboediens</i> Showed Only Minor Changes in Its Genome After Reactivation on Earth. <i>Frontiers in Microbiology</i> , 2022, 13, 782175.	1.5	5
2591	Metformin improves high-fat diet-induced insulin resistance in mice by downregulating the expression of long noncoding RNA NONMMUT031874.2. <i>Experimental and Therapeutic Medicine</i> , 2022, 23, 332.	0.8	6
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2595	Draft Genome Sequence Resource of <i>Fragaria</i> <i>Ananassa</i> ™ Phyllody Phytoplasma Strain StrPh-CL from Chilean Strawberry. <i>Plant Disease</i> , 2022, 106, 1031-1034.	0.7	1
2596	Distinct N and C Cross-Feeding Networks in a Synthetic Mouse Gut Consortium. <i>MSystems</i> , 2022, 7, e0148421.	1.7	9
2597	Comparative transcriptome profiling of <i>Polianthes tuberosa</i> during a compatible interaction with root-knot nematode <i>Meloidogyne incognita</i> . <i>Molecular Biology Reports</i> , 2022, , 1.	1.0	1
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2599	Transcriptome Profiling and Functional Validation of RING-Type E3 Ligases in Halophyte <i>Sesuvium verrucosum</i> under Salinity Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2821.	1.8	3
2600	RNA-Seq Reveals Differentially Expressed Genes Associated with High Fiber Quality in Abaca ( <i>Musa</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.0	1
2601	Fine Mapping and Functional Analysis of the Gene <i>PcTYR</i> , Involved in Control of Cap Color of <i>Pleurotus cornucopiae</i> . <i>Applied and Environmental Microbiology</i> , 2022, 88, e0217321.	1.4	6



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2604	Isolation of Anaerobic Bromate-Reducing Bacteria Using Different Carbon Sources and Transcriptomic Insights From <i>Klebsiella variicola</i> Glu3. <i>Frontiers in Microbiology</i> , 2022, 13, 851844.	1.5	2
2605	Transcriptome characterization of <i>Larrea tridentata</i> and identification of genes associated with phenylpropanoid metabolic pathways. <i>PLoS ONE</i> , 2022, 17, e0265231.	1.1	1
2606	Comparative Genomics of <i>Fusarium circinatum</i> Isolates Used to Screen Southern Pines for Pitch Canker Resistance. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 477-487.	1.4	1
2607	Proteome-Wide Identification and Functional Analysis of Lysine Crotonylation in <i>Trichophyton rubrum</i> Conidial and Mycelial Stages. <i>Frontiers in Genetics</i> , 2022, 13, 832668.	1.1	1
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2610	Developmental transcriptomics throughout the embryonic developmental process of <i>Rhipicephalus turanicus</i> reveals stage-specific gene expression profiles. <i>Parasites and Vectors</i> , 2022, 15, 89.	1.0	0
2611	Transcriptome alterations of radish shoots exposed to cadmium can be interpreted in the context of leaf senescence. <i>Protoplasma</i> , 2023, 260, 35-62.	1.0	1
2612	Transposon insertions regulate genome-wide allele-specific expression and underpin flower colour variations in apple ( <i>Malus</i> spp.). <i>Plant Biotechnology Journal</i> , 2022, 20, 1285-1297.	4.1	21
2613	Draft Genome Sequence of <i>Paenibacillus sonchi</i> IIRBNF1, a Nitrogen-Fixing and Plant Growth-Promoting Bacterium Isolated from Rice Rhizosphere. <i>Microbiology Resource Announcements</i> , 2022, 11, e0012622.	0.3	1
2615	Transcriptomic insights into the regulatory networks of chilling-induced early flower in tobacco ( <i>Nicotiana tabacum</i> L.). <i>Journal of Plant Interactions</i> , 2022, 17, 496-506.	1.0	1
2617	Brain transcriptome response to <i>Streptococcus agalactiae</i> infection and the heterogeneous regulation of neuropeptides on immune response in tilapia, <i>Oreochromis niloticus</i> . <i>Aquaculture</i> , 2022, 555, 738222.	1.7	4
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2619	Comparative genomics analysis of <i>Acinetobacter baumannii</i> multi-drug resistant and drug sensitive strains in China. <i>Microbial Pathogenesis</i> , 2022, 165, 105492.	1.3	7
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2622	Identification and characterization of genic simple sequence repeats from the leaf and stem transcriptomes of <i>Stevia rebaudiana</i> Bertoni. <i>Scientia Horticulturae</i> , 2022, 300, 111067.	1.7	0

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2624	Transcriptomic and Proteomic Characterizations of the Molecular Response to Blue Light and Salicylic Acid in <i>Haematococcus pluvialis</i> . <i>Marine Drugs</i> , 2022, 20, 1.	2.2	20
2625	Integrative Analyses of Biochemical Properties and Transcriptome Reveal the Dynamic Changes in Leaf Senescence of Tobacco ( <i>Nicotiana tabacum</i> L.). <i>Frontiers in Genetics</i> , 2021, 12, 790167.	1.1	5
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2629	<i>Cryptosporidium felis</i> differs from other <i>Cryptosporidium</i> spp. in codon usage. <i>Microbial Genomics</i> , 2021, 7, .	1.0	3
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2631	Quantitative Trait Loci and Transcriptome Analysis Reveal Genetic Basis of Fiber Quality Traits in CCRI70 RIL Population of <i>Gossypium hirsutum</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 753755.	1.7	5
2632	Prediction of Novel Drug Targets and Vaccine Candidates against Human Lice (Insecta), Acari (Arachnida), and Their Associated Pathogens. <i>Vaccines</i> , 2022, 10, 8.	2.1	8
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2637	Genomic evidence for homoploid hybrid speciation between ancestors of two different genera. <i>Nature Communications</i> , 2022, 13, 1987.	5.8	18
2638	Comparative transcriptome analysis provides insights into the molecular mechanisms of high-frequency hearing differences between the sexes of <i>Odorrana tormota</i> . <i>BMC Genomics</i> , 2022, 23, 296.	1.2	3
2640	Draft Genome Sequence from a Putative New Genus and Species in the Family <i>M1A02</i> within the Phylum <i>Planctomycetes</i> , Isolated from Benthic Pinnacle Mats in Lake Untersee, Antarctica. <i>Microbiology Resource Announcements</i> , 2022, , e0119221.	0.3	0
2641	Synergy of <i>Yiqi</i> and <i>Huoxue</i> components of QishenYiqi formula in ischemic stroke protection via lysosomal/inflammatory mechanisms. <i>Journal of Ethnopharmacology</i> , 2022, 293, 115301.	2.0	10
2881	Leveraging big data bioinformatics approaches to extract knowledge from <i>Staphylococcus aureus</i> public omics data. <i>Critical Reviews in Microbiology</i> , 2022, , 1-23.	2.7	1
2882	<i>Wolbachia</i> endosymbionts in two <i>Anopheles</i> species indicates independent acquisitions and lack of prophage elements. <i>Microbial Genomics</i> , 2022, 8, .	1.0	3

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2884	Qualitative Proteome-Wide Analysis Reveals the Diverse Functions of Lysine Crotonylation in <i>Dendrobium huoshanense</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 822374.	1.7	7
2885	Biochemical profiling, transcriptomic analysis, and biotechnological potential of native microalgae from the Peruvian Amazon. , 2022, , 305-321.		1
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2887	Fuel source shift or cost reduction: Context-dependent adaptation strategies in closely related <i>Neodon fuscus</i> and <i>Lasiopodomys brandtii</i> against hypoxia. <i>Zoological Research</i> , 2022, 43, 497-513.	0.9	0
2888	Basic Characteristics of Flower Transcriptome Data and Derived Novel EST-SSR Markers of <i>Luculia yunnanensis</i> , an Endangered Species Endemic to Yunnan, Southwestern China. <i>Plants</i> , 2022, 11, 1204.	1.6	4
2889	Comprehensive Genomic Analysis of Marine Strain <i>Streptomyces</i> sp. 891, an Excellent Producer of Chrysomycin A with Therapeutic Potential. <i>Marine Drugs</i> , 2022, 20, 287.	2.2	5
2890	Transcriptomic Changes of <i>Bemisia tabaci</i> Asia II 1 Induced by Chilli Leaf Curl Virus Trigger Infection and Circulation in Its Vector. <i>Frontiers in Microbiology</i> , 2022, 13, 890807.	1.5	5
2891	Comparative genomic analysis of <i>Thermus</i> provides insights into the evolutionary history of an incomplete denitrification pathway. , 0, , .		3
2892	Genome evolution of a nonparasitic secondary heterotroph, the diatom <i>Nitzschia putrida</i>. <i>Science Advances</i> , 2022, 8, eabi5075.	4.7	9
2893	Opportunities and challenges of using metagenomic data to bring uncultured microbes into cultivation. <i>Microbiome</i> , 2022, 10, 76.	4.9	59
2894	Dataset of De Novo hybrid berry transcriptome profiling and characterization of <i>Piper</i> species ( <i>Piper</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 0.5 10		
2895	Whole-Genome Sequencing Reveals Lignin-Degrading Capacity of a Ligninolytic Bacterium ( <i>Bacillus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 10		
2896	Transcriptomic profile of the predatory mite <i>Amblyseius swirskii</i> (Acari: Phytoseiidae) on different host plants. <i>Experimental and Applied Acarology</i> , 2022, 86, 479-498.	0.7	3
2897	Identification and bioinformatic characterization of rare variants of <i>Rhododendron canescens</i> architecture genes. <i>Euphytica</i> , 2022, 218, 1.	0.6	0
2898	Study on the mechanism of <i>Mycoplasma gallisepticum</i> infection on chicken tracheal mucosa injury. <i>Avian Pathology</i> , 2022, 51, 361-373.	0.8	2
2899	<i>Hydrogenophilus thiooxidans</i> sp. nov., a moderately thermophilic chemotrophic bacterium unable to grow on hydrogen gas, isolated from hot spring microbial mats. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	6
2900	Nitrogen fixation and other biogeochemically important features of Atacama Desert giant horsetail plant microbiomes inferred from metagenomic contig analysis. <i>Annals of Botany</i> , 2022, , .	1.4	2

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2902	Comparative proteomics reveals biochemical changes in <i>Salvia miltiorrhiza</i> Bunge during sweating processing. <i>Journal of Ethnopharmacology</i> , 2022, 293, 115329.	2.0	0
2903	Proteomics and Co-expression Network Analysis Reveal the Importance of Hub Proteins and Metabolic Pathways in Nicotine Synthesis and Accumulation in Tobacco ( <i>Nicotiana tabacum</i> L.). <i>Frontiers in Plant Science</i> , 2022, 13, 860455.	1.7	5
2904	Comparative transcriptome profiling of high and low oil yielding <i>Santalum album</i> L. <i>PLoS ONE</i> , 2022, 17, e0252173.	1.1	0
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2906	De novo transcriptome analysis of industrially important agarophyte <i>Gracilaria dura</i> (Rhodophyta: <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i> ) <i>Algal Research</i> , 2022, 65, 102712.	2.4	1
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2910	iTRAQ proteomic analysis of the inhibitory effect of 1,6-O,O-diacetylbritannilactone on the plant pathogenic oomycete <i>Phytophthora capsici</i> . <i>Pesticide Biochemistry and Physiology</i> , 2022, 184, 105125.	1.6	6
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2912	Hippocampal proteins discovery of diabetes-induced central neuropathy based on proteomics. <i>NeuroReport</i> , 2022, 33, 354-362.	0.6	3
2913	Genome Assembly and Population Resequencing Reveal the Geographical Divergence of Shanmei ( <i>Rubus</i> ) <i>Tj ETQq0,0,0 rgBT /Overlock 1</i>	3.0	3
2914	Vitamin D Receptor affects male mouse fertility via regulation of lipid metabolism and testosterone biosynthesis in testis. <i>Gene</i> , 2022, 834, 146589.	1.0	10
2915	Comparative transcriptome provides insights into differentially expressed genes between testis and ovary of <i>Onychostoma macrolepis</i> in reproduction period. <i>General and Comparative Endocrinology</i> , 2022, 326, 114066.	0.8	3
2916	Transcriptomics in Plant. , 2022, , 99-127.		1
2917	A chromosome-level genome assembly of the pollinating fig wasp <i>Valisia javana</i> . <i>DNA Research</i> , 2022, 29, .	1.5	3
2918	<i>Ustilago maydis</i> Metabolic Characterization and Growth Quantification with a Genome-Scale Metabolic Model. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 524.	1.5	6

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2920	Transcriptomics and metagenomics of common cutworm ( <i>Spodoptera litura</i> ) and fall armyworm ( <i>Spodoptera frugiperda</i> ) demonstrate differences in detoxification and development. <i>BMC Genomics</i> , 2022, 23, .	1.2	5
2921	Transcriptome analysis revealed hub genes for muscle growth in Indian major carp, <i>Catla catla</i> (Hamilton, 1822). <i>Genomics</i> , 2022, 114, 110393.	1.3	3
2924	Genomes and demographic histories of the endangered <i>Bretschneidera sinensis</i> (Akaniaceae). <i>GigaScience</i> , 2022, 11, .	3.3	6
2925	Denitrification in foraminifera has an ancient origin and is complemented by associated bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	9
2926	Structured Framework and Genome Analysis of <i>Magnaporthe grisea</i> Inciting Pearl Millet Blast Disease Reveals Versatile Metabolic Pathways, Protein Families, and Virulence Factors. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 1078.	0.784314	1
2928	<i>Rhodococcus oxybenzonivorans</i> sp. nov., a benzophenone-3-degrading bacterium, isolated from stream sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	6
2929	Taxonomy, comparative genomics and evolutionary insights of <i>Penicillium ucsense</i> : a novel species in series <i>Oxalica</i> . <i>Antonie Van Leeuwenhoek</i> , 2022, 115, 1009-1029.	0.7	5
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2933	A telomere-to-telomere gap-free reference genome of watermelon and its mutation library provide important resources for gene discovery and breeding. <i>Molecular Plant</i> , 2022, 15, 1268-1284.	3.9	74
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2935	In vivo Trial of <i>Bifidobacterium longum</i> Revealed the Complex Network Correlations Between Gut Microbiota and Health Promotional Effects. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	2
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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3042	Complete genome sequencing and comparison of two nitrogen-metabolizing bacteria isolated from Antarctic deep-sea sediment. <i>BMC Genomics</i> , 2022, 23, .	1.2	4
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3071	Adaptation of winged bean ( <i>Psophocarpus tetragonolobus</i> (L.) DC.) to drought stress is mediated by root-tuber heat-shock proteins and specific metabolites. <i>Current Plant Biology</i> , 2022, 32, 100266.	2.3	2
3073	<i>Idiomarina rhizosphaerae</i> sp. nov. isolated from rhizosphere soil of <i>Kalidium cuspidatum</i> , and reclassification of <i>Idiomarina andamanensis</i> as <i>Pseudidiomarina andamanensis</i> comb. nov., and <i>Idiomarina mangrovi</i> as <i>Pseudidiomarina mangrovi</i> comb. nov. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	3
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3080	A Subtraction Genomics-Based Approach to Identify and Characterize New Drug Targets in <i>Bordetella pertussis</i> : Whooping Cough. <i>Vaccines</i> , 2022, 10, 1915.	2.1	4
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#	ARTICLE	IF	CITATIONS
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3085	Genome sequence analysis of halophilic <i>Luteibacter</i> sp. CQ10 to prospect its dual roles in antioxidants production and lignocellulose degradation. <i>Gene Reports</i> , 2022, 29, 101708.	0.4	0
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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3123	<i>Syringa oblata</i> genome provides new insights into molecular mechanism of flower color differences among individuals and biosynthesis of its flower volatiles. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
3124	High-Quality Draft Genome Sequence and Characterization of ProBC Plus <i>Weizmannia</i> () Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 60	0.3	0
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3164	The chromosome-level genome of double-petal phenotype jasmine provides insights into the biosynthesis of floral scent. <i>Horticultural Plant Journal</i> , 2024, 10, 259-272.	2.3	1
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3168	Microbial species from multiple maternal body sites shape the developing giant panda ( <i>Ailuropoda</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	2.0	0
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3183	Full-length transcriptome from different life stages of cobia ( <i>Rachycentron canadum</i> ,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 702	2.4	1
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3186	Phylotranscriptomics and evolution of key genes for terpene biosynthesis in Pinaceae. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
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3205	Gene Coexpression Analysis Identifies Genes Associated with Chlorophyll Content and Relative Water Content in Pearl Millet. <i>Plants</i> , 2023, 12, 1412.	1.6	0
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3210	Antibiotic resistance in <i>Neisseria gonorrhoeae</i> : broad-spectrum drug target identification using subtractive genomics. <i>Genomics and Informatics</i> , 2023, 21, e5.	0.4	1
3211	FishGET: A fish gene expression and transcriptome database with improved accuracy and visualization. <i>IScience</i> , 2023, 26, 106539.	1.9	1
3212	<i>Tsuneonella litorea</i> sp. nov., a novel carotenoid-producing bacterium isolated from coastal sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	0.8	1
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