

Cutadapt removes adapter sequences from high-throughput sequencing data

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Citation Report

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1	The draft genome and transcriptome of <i>Cannabis sativa</i> . <i>Genome Biology</i> , 2011, 12, R102.	13.9	479
2	Regulatory Impact of RNA Secondary Structure across the <i>Arabidopsis</i> Transcriptome. <i>Plant Cell</i> , 2012, 24, 4346-4359.	3.1	124
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4	miRGator v3.0: a microRNA portal for deep sequencing, expression profiling and mRNA targeting. <i>Nucleic Acids Research</i> , 2012, 41, D252-D257.	6.5	140
5	SAAP-RRBS: streamlined analysis and annotation pipeline for reduced representation bisulfite sequencing. <i>Bioinformatics</i> , 2012, 28, 2180-2181.	1.8	49
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1198	FUS affects circular RNA expression in murine embryonic stem cell-derived motor neurons. <i>Nature Communications</i> , 2017, 8, 14741.	5.8	403
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1340	Robust Identification of Developmentally Active Endothelial Enhancers in Zebrafish Using FANS-Assisted ATAC-Seq. <i>Cell Reports</i> , 2017, 20, 709-720.	2.9	62
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1342	Evaluating hybridization capture with <i>sc</i> RAD probes as a tool for museum genomics with historical bird specimens. <i>Ecology and Evolution</i> , 2017, 7, 4755-4767.	0.8	34
1343	Improved methane production from sugarcane vinasse with filter cake in thermophilic UASB reactors, with predominance of <i>Methanothermobacter</i> and <i>Methanosarcina</i> archaea and <i>Thermotogae</i> bacteria. <i>Bioresource Technology</i> , 2017, 244, 371-381.	4.8	63
1344	Accumulation of Charantin and Expression of Triterpenoid Biosynthesis Genes in Bitter Melon (<i>Momordica charantia</i>). <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 7240-7249.	2.4	18
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1346	The SmAP1/2 proteins of the crenarchaeon <i>Sulfolobus solfataricus</i> interact with the exosome and stimulate A-rich tailing of transcripts. <i>Nucleic Acids Research</i> , 2017, 45, 7938-7949.	6.5	24
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1349	Modeling the evolution of SIV sooty mangabey progenitor virus towards HIV-2 using humanized mice. <i>Virology</i> , 2017, 510, 175-184.	1.1	16
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1363	Developing aptasensors for forensic analysis. <i>TrAC - Trends in Analytical Chemistry</i> , 2017, 94, 150-160.	5.8	34
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1775	Nuclear receptor NR2F6 inhibition potentiates responses to PD-L1/PD-1 cancer immune checkpoint blockade. <i>Nature Communications</i> , 2018, 9, 1538.	5.8	49
1776	Consequences of Asexuality in Natural Populations: Insights from Stick Insects. <i>Molecular Biology and Evolution</i> , 2018, 35, 1668-1677.	3.5	63
1777	Multi-omics analysis of thermal stress response in a zooxanthellate cnidarian reveals the importance of associating with thermotolerant symbionts. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20172654.	1.2	61
1778	An Integrated Genome-wide CRISPRa Approach to Functionalize lncRNAs in Drug Resistance. <i>Cell</i> , 2018, 173, 649-664.e20.	13.5	238
1779	Effects of triclosan in breast milk on the infant fecal microbiome. <i>Chemosphere</i> , 2018, 203, 467-473.	4.2	64
1780	KLRG1+ Effector CD8+ T Cells Lose KLRG1, Differentiate into All Memory T Cell Lineages, and Convey Enhanced Protective Immunity. <i>Immunity</i> , 2018, 48, 716-729.e8.	6.6	300
1781	Multiple nuclear-replicating viruses require the stress-induced protein ZC3H11A for efficient growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3808-E3816.	3.3	35
1782	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
1783	Identification of Hub Genes and Pathways in Zika Virus Infection Using RNA-Seq Data: A Network-Based Computational Approach. <i>Viral Immunology</i> , 2018, 31, 321-332.	0.6	10
1784	Standing genetic diversity and selection at functional gene loci are associated with differential invasion success in two non-native fish species. <i>Molecular Ecology</i> , 2018, 27, 1572-1585.	2.0	13
1785	Rapid divergence of mussel populations despite incomplete barriers to dispersal. <i>Molecular Ecology</i> , 2018, 27, 1556-1571.	2.0	29
1786	Landscape of long non-coding RNAs in <i>Trichophyton mentagrophytes</i> -induced rabbit dermatophytosis lesional skin and normal skin. <i>Functional and Integrative Genomics</i> , 2018, 18, 401-410.	1.4	3
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1789	Genome-wide analysis of the regulation of Cu metabolism in <i>Cryptococcus neoformans</i> . <i>Molecular Microbiology</i> , 2018, 108, 473-494.	1.2	34
1790	Increasing the utility of barcode databases through high-throughput sequencing of amplicons from dried museum specimens, an example on parasitic hymenoptera (Braconidae). <i>Biological Control</i> , 2018, 122, 93-100.	1.4	10
1791	Highly parallel genome variant engineering with CRISPR-Cas9. <i>Nature Genetics</i> , 2018, 50, 510-514.	9.4	73
1792	The role of epistatic interactions underpinning resistance to parasitic <i>Varroa</i> mites in haploid honey bee (<i>Apis mellifera</i>) drones. <i>Journal of Evolutionary Biology</i> , 2018, 31, 801-809.	0.8	21
1793	Gene expression during different periods of the handling-stress response in <i>Pampus argenteus</i> . <i>Journal of Oceanology and Limnology</i> , 2018, 36, 1349-1359.	0.6	3
1794	Microbial activity during a coastal phytoplankton bloom on the Western Antarctic Peninsula in late summer. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	24
1795	Effect of <i>Lactobacillus rhamnosus</i> GG Supplementation on Intestinal Inflammation Assessed by PET/MRI Scans and Gut Microbiota Composition in HIV-Infected Individuals. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2018, 78, 450-457.	0.9	26
1796	Genomic analysis reveals secondary glioblastoma after radiotherapy in a subset of recurrent medulloblastomas. <i>Acta Neuropathologica</i> , 2018, 135, 939-953.	3.9	32
1797	HiMAP: Robust phylogenomics from highly multiplexed amplicon sequencing. <i>Molecular Ecology Resources</i> , 2018, 18, 1000-1019.	2.2	30
1798	The reduced genome of <i>Candidatus</i> Kinetoplastibacterium sorsogonicus, the endosymbiont of <i>Kentomonas sorsogonicus</i> (Trypanosomatidae): loss of the haem-synthesis pathway. <i>Parasitology</i> , 2018, 145, 1287-1293.	0.7	20
1799	Srf destabilizes cellular identity by suppressing cell-type-specific gene expression programs. <i>Nature Communications</i> , 2018, 9, 1387.	5.8	35
1800	Drosha drives the formation of DNA:RNA hybrids around DNA break sites to facilitate DNA repair. <i>Nature Communications</i> , 2018, 9, 532.	5.8	164
1801	Host genetic variation strongly influences the microbiome structure and function in fungal fruiting bodies. <i>Environmental Microbiology</i> , 2018, 20, 1641-1650.	1.8	23
1802	Tissue- and strain-specific effects of a genotoxic carcinogen 1,3-butadiene on chromatin and transcription. <i>Mammalian Genome</i> , 2018, 29, 153-167.	1.0	21
1803	Amphibian chytridiomycosis outbreak dynamics are linked with host skin bacterial community structure. <i>Nature Communications</i> , 2018, 9, 693.	5.8	126
1804	A High-Throughput Approach for Identification of Nontuberculous Mycobacteria in Drinking Water Reveals Relationship between Water Age and <i>Mycobacterium avium</i> . <i>MBio</i> , 2018, 9, .	1.8	54
1805	Interrelations between the rumen microbiota and production, behavioral, rumen fermentation, metabolic, and immunological attributes of dairy cows. <i>Journal of Dairy Science</i> , 2018, 101, 4615-4637.	1.4	90

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1807	Scikit-ribo Enables Accurate Estimation and Robust Modeling of Translation Dynamics at Codon Resolution. <i>Cell Systems</i> , 2018, 6, 180-191.e4.	2.9	41
1808	Expression of homing endonuclease gene and insertion-like element in sea anemone mitochondrial genomes: Lesson learned from <i>Anemonia viridis</i> . <i>Gene</i> , 2018, 652, 78-86.	1.0	15
1809	Dual Strategies for Argonaute2-Mediated Biogenesis of Erythroid miRNAs Underlie Conserved Requirements for Slicing in Mammals. <i>Molecular Cell</i> , 2018, 69, 265-278.e6.	4.5	56
1810	Biochar affects community composition of nitrous oxide reducers in a field experiment. <i>Soil Biology and Biochemistry</i> , 2018, 119, 143-151.	4.2	46
1811	Replication stress induces accumulation of FANCD2 at central region of large fragile genes. <i>Nucleic Acids Research</i> , 2018, 46, 2932-2944.	6.5	70
1812	Systems Analysis of the Liver Transcriptome in Adult Male Zebrafish Exposed to the Plasticizer (2-Ethylhexyl) Phthalate (DEHP). <i>Scientific Reports</i> , 2018, 8, 2118.	1.6	48
1813	Chromatin Modification and Global Transcriptional Silencing in the Oocyte Mediated by the mRNA Decay Activator ZFP36L2. <i>Developmental Cell</i> , 2018, 44, 392-402.e7.	3.1	65
1814	Optimal extraction methods for the simultaneous analysis of <scp>DNA</scp> from diverse organisms and sample types. <i>Molecular Ecology Resources</i> , 2018, 18, 557-569.	2.2	65
1815	Genome sequence of M6, a diploid inbred clone of the high-glycoalkaloid-producing tuber-bearing potato species <i>Solanum chacoense</i> , reveals residual heterozygosity. <i>Plant Journal</i> , 2018, 94, 562-570.	2.8	112
1816	Sensitive detection of mitochondrial DNA variants for analysis of mitochondrial DNA-enriched extracts from frozen tumor tissue. <i>Scientific Reports</i> , 2018, 8, 2261.	1.6	12
1817	Comparative analysis of the transcriptome of injured nerve segments reveals spatiotemporal responses to neural damage in mice. <i>Journal of Comparative Neurology</i> , 2018, 526, 1195-1208.	0.9	17
1818	StructureFold2: Bringing chemical probing data into the computational fold of RNA structural analysis. <i>Methods</i> , 2018, 143, 12-15.	1.9	26
1819	Statistical modeling of RNA structure profiling experiments enables parsimonious reconstruction of structure landscapes. <i>Nature Communications</i> , 2018, 9, 606.	5.8	46
1820	Combined aptamer and transcriptome sequencing of single cells. <i>Scientific Reports</i> , 2018, 8, 2919.	1.6	23
1821	Melanization of mycorrhizal fungal necromass structures microbial decomposer communities. <i>Journal of Ecology</i> , 2018, 106, 468-479.	1.9	66
1822	Increased socially mediated plasticity in gene expression accompanies rapid adaptive evolution. <i>Ecology Letters</i> , 2018, 21, 546-556.	3.0	21
1823	Maize chlorotic mottle virus exhibits low divergence between differentiated regional sub-populations. <i>Scientific Reports</i> , 2018, 8, 1173.	1.6	36

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1825	Genetic and morphological support for possible sympatric origin of fish from subterranean habitats. <i>Scientific Reports</i> , 2018, 8, 2909.	1.6	16
1826	Optimized methods of chromatin immunoprecipitation for profiling histone modifications in industrial microalgae <i>Nannochloropsis</i> spp.. <i>Journal of Phycology</i> , 2018, 54, 358-367.	1.0	14
1827	The Unstructured Paramyxovirus Nucleocapsid Protein Tail Domain Modulates Viral Pathogenesis through Regulation of Transcriptase Activity. <i>Journal of Virology</i> , 2018, 92, .	1.5	23
1828	Circulating Tumor DNA Genomics Correlate with Resistance to Abiraterone and Enzalutamide in Prostate Cancer. <i>Cancer Discovery</i> , 2018, 8, 444-457.	7.7	376
1829	Transcriptome-Wide Characterization of the MADS-Box Family in Pinesap <i>Monotropa hypopitys</i> Reveals Flowering Conservation in Non-photosynthetic Myco-Heterotrophs. <i>Journal of Plant Growth Regulation</i> , 2018, 37, 768-783.	2.8	3
1830	Different milk diets have substantial effects on the jejunal mucosal immune system of pre-weaning calves, as demonstrated by whole transcriptome sequencing. <i>Scientific Reports</i> , 2018, 8, 1693.	1.6	17
1831	Modulation of oncogenic miRNA biogenesis using functionalized polyamines. <i>Scientific Reports</i> , 2018, 8, 1667.	1.6	39
1832	NGS-based methylation profiling differentiates TCF3-HLF and TCF3-PBX1 positive B-cell acute lymphoblastic leukemia. <i>Epigenomics</i> , 2018, 10, 133-147.	1.0	10
1833	Dynamic evolution of regulatory element ensembles in primate CD4+ T cells. <i>Nature Ecology and Evolution</i> , 2018, 2, 537-548.	3.4	65
1834	Low-pass single-chromosome sequencing of human small supernumerary marker chromosomes (sSMCs) and Apodemus B chromosomes. <i>Chromosoma</i> , 2018, 127, 301-311.	1.0	18
1835	Tbx5a lineage tracing shows cardiomyocyte plasticity during zebrafish heart regeneration. <i>Nature Communications</i> , 2018, 9, 428.	5.8	62
1836	PlasFlow: predicting plasmid sequences in metagenomic data using genome signatures. <i>Nucleic Acids Research</i> , 2018, 46, e35-e35.	6.5	389
1837	Down-expression of <i>P2RX2</i> , <i>KCNQ5</i> , <i>ERBB3</i> and <i>SOCS3</i> through DNA hypermethylation in elderly women with presbycusis. <i>Biomarkers</i> , 2018, 23, 347-356.	0.9	31
1838	Progesterone effects on extracellular vesicles in the sheep uterus. <i>Biology of Reproduction</i> , 2018, 98, 612-622.	1.2	56
1839	Incomplete Co-cladogenesis Between <i>Zootermopsis</i> Termites and Their Associated Protists. <i>Environmental Entomology</i> , 2018, 47, 184-195.	0.7	19
1840	Association of <i>IGFN1</i> variant with polypoidal choroidal vasculopathy. <i>Journal of Gene Medicine</i> , 2018, 20, e3007.	1.4	8
1841	Antimicrobial and stress responses to increased temperature and bacterial pathogen challenge in the holobiont of a reef-building coral. <i>Molecular Ecology</i> , 2018, 27, 1065-1080.	2.0	53

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1843	Ultraconserved Enhancers Are Required for Normal Development. <i>Cell</i> , 2018, 172, 491-499.e15.	13.5	169
1844	Identifying metabolic pathways for production of extracellular polymeric substances by the diatom <i>Fragilariopsis cylindrus</i> inhabiting sea ice. <i>ISME Journal</i> , 2018, 12, 1237-1251.	4.4	43
1845	Experimental infection of cattle with <i>Mycobacterium tuberculosis</i> isolates shows the attenuation of the human tubercle bacillus for cattle. <i>Scientific Reports</i> , 2018, 8, 894.	1.6	52
1846	Asparagine bioavailability governs metastasis in a model of breast cancer. <i>Nature</i> , 2018, 554, 378-381.	13.7	362
1847	Phylogenetic clustering of small low nucleic acid-content bacteria across diverse freshwater ecosystems. <i>ISME Journal</i> , 2018, 12, 1344-1359.	4.4	84
1848	Drylands soil bacterial community is affected by land use change and different irrigation practices in the Mezquital Valley, Mexico. <i>Scientific Reports</i> , 2018, 8, 1413.	1.6	58
1849	Nitrogen Cycle Evaluation (NiCE) Chip for Simultaneous Analysis of Multiple N Cycle-Associated Genes. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	23
1850	Pancreatic gene expression during recovery after pancreatitis reveals unique transcriptome profiles. <i>Scientific Reports</i> , 2018, 8, 1406.	1.6	14
1851	miR-145 overexpression triggers alteration of the whole transcriptome and inhibits breast cancer development. <i>Biomedicine and Pharmacotherapy</i> , 2018, 100, 72-82.	2.5	34
1852	Analysis of rat cardiac myocytes and fibroblasts identifies combinatorial enhancer organization and transcription factor families. <i>Journal of Molecular and Cellular Cardiology</i> , 2018, 116, 91-105.	0.9	13
1853	Homeolog expression analysis in an allotriploid non-model crop via integration of transcriptomics and proteomics. <i>Scientific Reports</i> , 2018, 8, 1353.	1.6	34
1854	<i>De novo</i> assembly and characterization of the <i>Hucho taimen</i> transcriptome. <i>Ecology and Evolution</i> , 2018, 8, 1271-1285.	0.8	8
1855	High-resolution transcription maps reveal the widespread impact of roadblock termination in yeast. <i>EMBO Journal</i> , 2018, 37, .	3.5	60
1856	Cropping practices manipulate abundance patterns of root and soil microbiome members paving the way to smart farming. <i>Microbiome</i> , 2018, 6, 14.	4.9	399
1857	Diff-seq: A high throughput sequencing-based mismatch detection assay for DNA variant enrichment and discovery. <i>Nucleic Acids Research</i> , 2018, 46, e42-e42.	6.5	7
1858	TimeLapse-seq: adding a temporal dimension to RNA sequencing through nucleoside recoding. <i>Nature Methods</i> , 2018, 15, 221-225.	9.0	185
1859	Plasma levels of hsa-miR-152-3p are associated with diabetic nephropathy in patients with type 2 diabetes. <i>Nephrology Dialysis Transplantation</i> , 2018, 33, 2201-2207.	0.4	20

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1861	The Evolutionary History of Nebraska Deer Mice: Local Adaptation in the Face of Strong Gene Flow. <i>Molecular Biology and Evolution</i> , 2018, 35, 792-806.	3.5	76
1862	Evaluation of marine zooplankton community structure through environmental DNA metabarcoding. <i>Limnology and Oceanography: Methods</i> , 2018, 16, 209-221.	1.0	108
1863	Assessing the utility of metabarcoding for diet analyses of the omnivorous wild pig (<i>Sus</i>). <i>Journal of Animal Ecology</i> , 2018, 87, 107-115.	6.8	63
1864	The unique epigenetic features of Pack-MULEs and their impact on chromosomal base composition and expression spectrum. <i>Nucleic Acids Research</i> , 2018, 46, 2380-2397.	6.5	14
1865	microRNA regulation in an ancient obligate endosymbiosis. <i>Molecular Ecology</i> , 2018, 27, 1777-1793.	2.0	25
1866	Female reproductive impacts of dietary methylmercury in yellow perch (<i>Perca flavescens</i>) and zebrafish (<i>Danio rerio</i>). <i>Chemosphere</i> , 2018, 195, 301-311.	4.2	8
1867	piRNA analysis framework from small RNA-Seq data by a novel cluster prediction tool - PILFER. <i>Genomics</i> , 2018, 110, 355-365.	1.3	26
1868	Enhancer transcription reveals subtype-specific gene expression programs controlling breast cancer pathogenesis. <i>Genome Research</i> , 2018, 28, 159-170.	2.4	137
1869	De novo transcriptome analyses reveals putative pathway genes involved in biosynthesis and regulation of camptothecin in <i>Nothapodytes nimmoniana</i> (Graham) Mabb.. <i>Plant Molecular Biology</i> , 2018, 96, 197-215.	2.0	41
1870	Transcriptome data of <i>Epinephelus fuscoguttatus</i> infected by <i>Vibrio vulnificus</i> . <i>Data in Brief</i> , 2018, 16, 466-469.	0.5	6
1871	Endocrine disruption and differential gene expression in sentinel fish on St. Lawrence Island, Alaska: Health implications for indigenous residents. <i>Environmental Pollution</i> , 2018, 234, 279-287.	3.7	17
1872	Transcriptional landscapes of Axolotl (<i>Ambystoma mexicanum</i>). <i>Developmental Biology</i> , 2018, 433, 227-239.	0.9	31
1873	MMTV does not encode viral microRNAs but alters the levels of cancer-associated host microRNAs. <i>Virology</i> , 2018, 513, 180-187.	1.1	8
1874	Angiogenic factor imbalance precedes complement deposition in placentae of the BPH/5 model of preeclampsia. <i>FASEB Journal</i> , 2018, 32, 2574-2586.	0.2	41
1875	Individual- and Species-Specific Skin Microbiomes in Three Different Estrildid Finch Species Revealed by 16S Amplicon Sequencing. <i>Microbial Ecology</i> , 2018, 76, 518-529.	1.4	29
1876	MicroRNAs in CSF as prodromal biomarkers for Huntington disease in the PREDICT-HD study. <i>Neurology</i> , 2018, 90, e264-e272.	1.5	65
1877	Comparative transcriptome analysis of two citrus germplasm with contrasting susceptibility to <i>Phytophthora nicotianae</i> provides new insights into tolerance mechanisms. <i>Plant Cell Reports</i> , 2018, 37, 483-499.	2.8	8

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1879	Retrieval of a million high-quality, full-length microbial 16S and 18S rRNA gene sequences without primer bias. <i>Nature Biotechnology</i> , 2018, 36, 190-195.	9.4	165
1880	Geometagenomics illuminates the impact of agriculture on the distribution and prevalence of plant viruses at the ecosystem scale. <i>ISME Journal</i> , 2018, 12, 173-184.	4.4	132
1881	Differential effects of chronic stress in young-adult and old female mice: cognitive-behavioral manifestations and neurobiological correlates. <i>Molecular Psychiatry</i> , 2018, 23, 1432-1445.	4.1	28
1882	Ultradeep mapping of neuronal mitochondrial deletions in Parkinson's disease. <i>Neurobiology of Aging</i> , 2018, 63, 120-127.	1.5	47
1883	Ecological plasticity in the gastrointestinal microbiomes of Ethiopian <i>Chlorocebus</i> monkeys. <i>Scientific Reports</i> , 2018, 8, 20.	1.6	37
1884	Comparative Genomics Highlights Symbiotic Capacities and High Metabolic Flexibility of the Marine Genus <i>Pseudovibrio</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 125-142.	1.1	26
1885	Dengue Virus Selectively Annexes Endoplasmic Reticulum-Associated Translation Machinery as a Strategy for Co-opting Host Cell Protein Synthesis. <i>Journal of Virology</i> , 2018, 92, .	1.5	59
1886	Genome re-annotation of the wild strawberry <i>Fragaria vesca</i> using extensive Illumina- and SMRT-based RNA-seq datasets. <i>DNA Research</i> , 2018, 25, 61-70.	1.5	67
1887	Blow flies as urban wildlife sensors. <i>Molecular Ecology Resources</i> , 2018, 18, 502-510.	2.2	10
1888	Discovering circRNA-microRNA Interactions from CLIP-Seq Data. <i>Methods in Molecular Biology</i> , 2018, 1724, 193-207.	0.4	23
1889	Co-Emergence of Specialized Endothelial Cells from Embryonic Stem Cells. <i>Stem Cells and Development</i> , 2018, 27, 326-335.	1.1	8
1890	Novel Transcriptional Activity and Extensive Allelic Imbalance in the Human MHC Region. <i>Journal of Immunology</i> , 2018, 200, 1496-1503.	0.4	20
1891	Draft genome sequences of the oomycete <i>Pythium insidiosum</i> strain CBS 573.85 from a horse with pythiosis and strain CR02 from the environment. <i>Data in Brief</i> , 2018, 16, 47-50.	0.5	17
1892	Perturbation-response genes reveal signaling footprints in cancer gene expression. <i>Nature Communications</i> , 2018, 9, 20.	5.8	436
1893	Emergence of Double- and Triple-Gene Reassortant G1P[8] Rotaviruses Possessing a DS-1-Like Backbone after Rotavirus Vaccine Introduction in Malawi. <i>Journal of Virology</i> , 2018, 92, .	1.5	61
1894	SOAPnuke: a MapReduce acceleration-supported software for integrated quality control and preprocessing of high-throughput sequencing data. <i>GigaScience</i> , 2018, 7, 1-6.	3.3	1,265
1895	Growth is required for perception of water availability to pattern root branches in plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E822-E831.	3.3	72

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1897	Genome-Wide circRNA Profiling from RNA-seq Data. <i>Methods in Molecular Biology</i> , 2018, 1724, 27-41.	0.4	32
1898	<i>Geobacteraceae</i> are important members of mercury-methylating microbial communities of sediments impacted by waste water releases. <i>ISME Journal</i> , 2018, 12, 802-812.	4.4	96
1899	Positive diversity-functioning relationships in model communities of methanotrophic bacteria. <i>Ecology</i> , 2018, 99, 714-723.	1.5	30
1900	Transcriptome-based identification and characterization of genes commonly responding to five different insecticides in the diamondback moth, <i>Plutella xylostella</i> . <i>Pesticide Biochemistry and Physiology</i> , 2018, 144, 1-9.	1.6	49
1901	Impact of cycling cells and cell cycle regulation on Hydra regeneration. <i>Developmental Biology</i> , 2018, 433, 240-253.	0.9	28
1902	Human-mediated introduction of introgressed deer across Wallace's line: Historical biogeography of <i>Rusa unicolor</i> and <i>R. timorensis</i> . <i>Ecology and Evolution</i> , 2018, 8, 1465-1479.	0.8	21
1903	MicroRNAs from the parasitic plant <i>Cuscuta campestris</i> target host messenger RNAs. <i>Nature</i> , 2018, 553, 82-85.	13.7	303
1904	Oxidative stress damages rRNA inside the ribosome and differentially affects the catalytic center. <i>Nucleic Acids Research</i> , 2018, 46, 1945-1957.	6.5	101
1905	Demographic analysis of cyanobacteria based on the mutation rates estimated from an ancient ice core. <i>Heredity</i> , 2018, 120, 562-573.	1.2	19
1906	Interplay between the catabolite repression control protein Crc, Hfq and RNA in Hfq-dependent translational regulation in <i>Pseudomonas aeruginosa</i> . <i>Nucleic Acids Research</i> , 2018, 46, 1470-1485.	6.5	85
1907	Trio, a novel high fecundity allele: I. Transcriptome analysis of granulosa cells from carriers and noncarriers of a major gene for bovine ovulation rate. <i>Biology of Reproduction</i> , 2018, 98, 323-334.	1.2	17
1908	Spliceosome Profiling Visualizes Operations of a Dynamic RNP at Nucleotide Resolution. <i>Cell</i> , 2018, 173, 1014-1030.e17.	13.5	39
1909	Transcriptome-wide Interrogation of the Functional Intronome by Spliceosome Profiling. <i>Cell</i> , 2018, 173, 1031-1044.e13.	13.5	26
1910	Unbiased quantification of immunoglobulin diversity at the DNA level with VDJ-seq. <i>Nature Protocols</i> , 2018, 13, 1232-1252.	5.5	21
1911	Cryptic species in a well-known habitat: applying taxonomics to the amphipod genus <i>Epimeria</i> (Crustacea, Peracarida). <i>Scientific Reports</i> , 2018, 8, 6893.	1.6	15
1912	Metagenome Sequences of Sediment from a Recovering Industrialized Appalachian River in West Virginia. <i>Genome Announcements</i> , 2018, 6, .	0.8	10
1913	Extensive mitochondrial gene rearrangements in Ctenophora: insights from benthic <i>Platyctenida</i> . <i>BMC Evolutionary Biology</i> , 2018, 18, 65.	3.2	15

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1915	RNA-Seq reveals the existence of a CDKN1C-E2F1-TP53 axis that is altered in human T-cell lymphoblastic lymphomas. <i>BMC Cancer</i> , 2018, 18, 430.	1.1	8
1916	Madagascar ground gecko genome analysis characterizes asymmetric fates of duplicated genes. <i>BMC Biology</i> , 2018, 16, 40.	1.7	49
1917	SGLT2 inhibition via dapagliflozin improves generalized vascular dysfunction and alters the gut microbiota in type 2 diabetic mice. <i>Cardiovascular Diabetology</i> , 2018, 17, 62.	2.7	178
1918	Evaluating the breast cancer predisposition role of rare variants in genes associated with low-penetrance breast cancer risk SNPs. <i>Breast Cancer Research</i> , 2018, 20, 3.	2.2	19
1919	Epidermal Wnt signalling regulates transcriptome heterogeneity and proliferative fate in neighbouring cells. <i>Genome Biology</i> , 2018, 19, 3.	3.8	17
1920	Reproducible protocols for metagenomic analysis of human faecal phageomes. <i>Microbiome</i> , 2018, 6, 68.	4.9	162
1921	Simultaneous sequencing of coding and noncoding RNA reveals a human transcriptome dominated by a small number of highly expressed noncoding genes. <i>Rna</i> , 2018, 24, 950-965.	1.6	61
1922	Tissue-Specific Transcriptome for <i>Poeciliopsis prolifica</i> Reveals Evidence for Genetic Adaptation Related to the Evolution of a Placental Fish. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2181-2192.	0.8	10
1923	ENHANCED DISEASE SUSCEPTIBILITY 1 (EDS1) affects development, photosynthesis, and hormonal homeostasis in hybrid aspen (<i>Populus tremula</i> L. × <i>P. tremuloides</i>). <i>Journal of Plant Physiology</i> , 2018, 226, 91-102.	1.6	13
1924	GoldCLIP: Gel-omitted Ligation-dependent CLIP. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 136-143.	3.0	21
1925	Genetic analyses of reddish-brown polyoxin-resistant mutants of <i>Bipolaris maydis</i> . <i>Mycoscience</i> , 2018, 59, 236-246.	0.3	0
1926	DUOX2-mediated production of reactive oxygen species induces epithelial mesenchymal transition in 5-fluorouracil resistant human colon cancer cells. <i>Redox Biology</i> , 2018, 17, 224-235.	3.9	44
1927	Saquinone controls hepatic cholesterol homeostasis by the negative regulation of PCSK9 transcriptional network. <i>Scientific Reports</i> , 2018, 8, 6737.	1.6	26
1928	Dominance of <i>Endozoicomonas</i> bacteria throughout coral bleaching and mortality suggests structural inflexibility of the <i>Pocillopora verrucosa</i> microbiome. <i>Ecology and Evolution</i> , 2018, 8, 2240-2252.	0.8	130
1929	A Saturation Mutagenesis Approach to Understanding PTEN Lipid Phosphatase Activity and Genotype-Phenotype Relationships. <i>American Journal of Human Genetics</i> , 2018, 102, 943-955.	2.6	149
1930	A technical assessment of the porcine ejaculated spermatozoa for a sperm-specific RNA-seq analysis. <i>Systems Biology in Reproductive Medicine</i> , 2018, 64, 291-303.	1.0	45
1931	Deep Sequencing of Small RNAs in Blood of Patients with Brain Arteriovenous Malformations. <i>World Neurosurgery</i> , 2018, 115, e570-e579.	0.7	16

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1932	Selective concentration for ciprofloxacin resistance in <i>Escherichia coli</i> grown in complex aquatic bacterial biofilms. <i>Environment International</i> , 2018, 116, 255-268.	4.8	71
1933	<i>Escherichia coli</i> cultures maintain stable subpopulation structure during long-term evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4642-E4650.	3.3	46
1934	Beaver Fever: Whole-Genome Characterization of Waterborne Outbreak and Sporadic Isolates To Study the Zoonotic Transmission of Giardiasis. <i>MSphere</i> , 2018, 3, .	1.3	34
1935	Dust-associated microbiomes from dryland wheat fields differ with tillage practice and biosolids application. <i>Atmospheric Environment</i> , 2018, 185, 29-40.	1.9	5
1936	Biosynthesis of abscisic acid in fungi: identification of a sesquiterpene cyclase as the key enzyme in <i>Botrytis cinerea</i> . <i>Environmental Microbiology</i> , 2018, 20, 2469-2482.	1.8	37
1937	Conservation tillage and organic farming induce minor variations in <i>Pseudomonas</i> abundance, their antimicrobial function and soil disease resistance. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	10
1938	Comprehensive viral enrichment enables sensitive respiratory virus genomic identification and analysis by next generation sequencing. <i>Genome Research</i> , 2018, 28, 869-877.	2.4	74
1939	Hidden genomic MHC disparity between HLA-matched sibling pairs in hematopoietic stem cell transplantation. <i>Scientific Reports</i> , 2018, 8, 5396.	1.6	11
1940	Å— <i>Lindsaeosoria flynnii</i> (Lindsaeaceae), Another Confirmed Example of Deep Hybridization Among the Ferns. <i>American Fern Journal</i> , 2018, 108, 7-18.	0.2	8
1941	Effects of prenatal exposure to triclosan on the liver transcriptome in chicken embryos. <i>Toxicology and Applied Pharmacology</i> , 2018, 347, 23-32.	1.3	23
1942	Hagfish and lamprey Hox genes reveal conservation of temporal colinearity in vertebrates. <i>Nature Ecology and Evolution</i> , 2018, 2, 859-866.	3.4	55
1943	Inflammation-Modulated Metabolic Reprogramming Is Required for DUOX-Dependent Gut Immunity in <i>Drosophila</i> . <i>Cell Host and Microbe</i> , 2018, 23, 338-352.e5.	5.1	79
1944	Systematic Discovery of RNA Binding Proteins that Regulate MicroRNA Levels. <i>Molecular Cell</i> , 2018, 69, 1005-1016.e7.	4.5	107
1945	Targeted genetic analysis in a large cohort of familial and sporadic cases of aneurysm or dissection of the thoracic aorta. <i>Genetics in Medicine</i> , 2018, 20, 1414-1422.	1.1	48
1946	De novo annotation and characterization of the translome with ribosome profiling data. <i>Nucleic Acids Research</i> , 2018, 46, e61-e61.	6.5	104
1947	Abiotic Stresses Shift Belowground <i>Populus</i> -Associated Bacteria Toward a Core Stress Microbiome. <i>MSystems</i> , 2018, 3, .	1.7	89
1948	Ecological responses to forest age, habitat, and host vary by mycorrhizal type in boreal peatlands. <i>Mycorrhiza</i> , 2018, 28, 315-328.	1.3	22
1949	Profiling and identification of pregnancy-associated circulating microRNAs in dairy cattle. <i>Genes and Genomics</i> , 2018, 40, 1111-1117.	0.5	22

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1950	Characterization of S-layer proteins of potential probiotic starter culture <i>Lactobacillus brevis</i> SF9B isolated from sauerkraut. <i>LWT - Food Science and Technology</i> , 2018, 93, 257-267.	2.5	19
1951	Aphid (<i>Myzus persicae</i>) feeding on the parasitic plant dodder (<i>Cuscuta australis</i>) activates defense responses in both the parasite and soybean host. <i>New Phytologist</i> , 2018, 218, 1586-1596.	3.5	39
1952	Ablation of the stress protease OMA1 protects against heart failure in mice. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	66
1953	Next-Generation Sequencing of Hepatitis C Virus (HCV) Mixed-Genotype Infections in Anti-HCV-Negative Blood Donors. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1096, 65-71.	0.8	7
1954	Malignant cells from pleural fluids in malignant mesothelioma patients reveal novel mutations. <i>Lung Cancer</i> , 2018, 119, 64-70.	0.9	23
1955	Genome-wide analysis of replication timing by next-generation sequencing with E/L Repli-seq. <i>Nature Protocols</i> , 2018, 13, 819-839.	5.5	126
1956	A review of somatic single nucleotide variant calling algorithms for next-generation sequencing data. <i>Computational and Structural Biotechnology Journal</i> , 2018, 16, 15-24.	1.9	195
1957	Long- and short-term effects of mercury pollution on the soil microbiome. <i>Soil Biology and Biochemistry</i> , 2018, 120, 191-199.	4.2	84
1958	Variations in methane yield and microbial community profiles in the rumen of dairy cows as they pass through stages of first lactation. <i>Journal of Dairy Science</i> , 2018, 101, 5102-5114.	1.4	22
1959	The Draft Genome Sequence of a Novel High-Efficient Butanol-Producing Bacterium <i>Clostridium Diolis</i> Strain WST. <i>Current Microbiology</i> , 2018, 75, 1011-1015.	1.0	10
1960	Insulin resistance in cavefish as an adaptation to a nutrient-limited environment. <i>Nature</i> , 2018, 555, 647-651.	13.7	196
1961	Expansions, diversification, and interindividual copy number variations of AID/APOBEC family cytidine deaminase genes in lampreys. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3211-E3220.	3.3	23
1962	Identification and rapid mapping of a gene conferring broad-spectrum late blight resistance in the diploid potato species <i>Solanum verrucosum</i> through DNA capture technologies. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1287-1297.	1.8	65
1963	Bacterial communities in mining soils and surrounding areas under regeneration process in a former ore mine. <i>Brazilian Journal of Microbiology</i> , 2018, 49, 489-502.	0.8	30
1964	Cost-effective high-throughput single-haplotype iterative mapping and sequencing for complex genomic structures. <i>Nature Protocols</i> , 2018, 13, 787-809.	5.5	12
1965	<i>In Vitro</i> Culture of the Insect Endosymbiont <i>Spiroplasma poulsonii</i> Highlights Bacterial Genes Involved in Host-Symbiont Interaction. <i>MBio</i> , 2018, 9, .	1.8	51
1966	Inter-replicon Gene Flow Contributes to Transcriptional Integration in the <i>Sinorhizobium meliloti</i> Multipartite Genome. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1711-1720.	0.8	14
1967	Identification of Novel Viruses in <i>Amblyomma americanum</i> , <i>Dermacentor variabilis</i> , and <i>Ixodes scapularis</i> Ticks. <i>MSphere</i> , 2018, 3, .	1.3	88

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1968	Regulation of <i>RNA</i> polymerase processivity by Spt5 is restricted to a narrow window during elongation. <i>EMBO Journal</i> , 2018, 37, .	3.5	64
1969	Rapid Multiplex Small DNA Sequencing on the MinION Nanopore Sequencing Platform. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1649-1657.	0.8	25
1970	Transcriptional Activation of Glycogen Catabolism and the Oxidative Pentose Phosphate Pathway by NrrA Facilitates Cell Survival Under Nitrogen Starvation in the Cyanobacterium <i>Synechococcus</i> sp. Strain PCC 7002. <i>Plant and Cell Physiology</i> , 2018, 59, 1225-1233.	1.5	10
1971	Dynamics of the human gut phageome during antibiotic treatment. <i>Computational Biology and Chemistry</i> , 2018, 74, 420-427.	1.1	15
1972	Tn5Prime, a Tn5 based 5â€² capture method for single cell RNA-seq. <i>Nucleic Acids Research</i> , 2018, 46, e62-e62.	6.5	35
1973	Disrupting the three-dimensional regulatory topology of the <i>Pitx1</i> locus results in overtly normal development. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	14
1974	Circular DNA elements of chromosomal origin are common in healthy human somatic tissue. <i>Nature Communications</i> , 2018, 9, 1069.	5.8	232
1975	Nutritional preferences of human gut bacteria reveal their metabolic idiosyncrasies. <i>Nature Microbiology</i> , 2018, 3, 514-522.	5.9	196
1976	Approaches for the Analysis and Interpretation of Whole Genome Bisulfite Sequencing Data. <i>Methods in Molecular Biology</i> , 2018, 1767, 299-310.	0.4	6
1977	Laboratory evolution reveals regulatory and metabolic trade-offs of glycerol utilization in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2018, 47, 73-82.	3.6	47
1978	Complementarity of assembly-first and mapping-first approaches for alternative splicing annotation and differential analysis from RNAseq data. <i>Scientific Reports</i> , 2018, 8, 4307.	1.6	31
1979	Automated high throughput animal CO1 metabarcoding classification. <i>Scientific Reports</i> , 2018, 8, 4226.	1.6	112
1980	A benzene-degrading nitrate-reducing microbial consortium displays aerobic and anaerobic benzene degradation pathways. <i>Scientific Reports</i> , 2018, 8, 4490.	1.6	74
1981	Transcriptome landscape of a bacterial pathogen under plant immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3055-E3064.	3.3	166
1982	Extended and Continuous Decline in Effective Population Size Results in Low Genomic Diversity in the World's Rarest Hyena Species, the Brown Hyena. <i>Molecular Biology and Evolution</i> , 2018, 35, 1225-1237.	3.5	72
1983	Effective mosquito and arbovirus surveillance using metabarcoding. <i>Molecular Ecology Resources</i> , 2018, 18, 32-40.	2.2	51
1984	Maternal phthalate exposure promotes allergic airway inflammation over 2 generations through epigenetic modifications. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 741-753.	1.5	92
1985	Application of metagenomic methods for selection of an optimal growth medium for bacterial diversity analysis of microbiocenoses on historical stone surfaces. <i>International Biodeterioration and Biodegradation</i> , 2018, 131, 2-10.	1.9	20

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1986	Anxiety-Related Behaviours Associated with microRNA-206-3p and BDNF Expression in Pregnant Female Mice Following Psychological Social Stress. <i>Molecular Neurobiology</i> , 2018, 55, 1097-1111.	1.9	37
1987	Transcriptome analysis of root-knot nematode (<i>Meloidogyne incognita</i>)-infected tomato (<i>Solanum lycopersicum</i>) roots reveals complex gene expression profiles and metabolic networks of both host and nematode during susceptible and resistance responses. <i>Molecular Plant Pathology</i> , 2018, 19, 615-633.	2.0	127
1988	A survey of the approaches for identifying differential methylation using bisulfite sequencing data. <i>Briefings in Bioinformatics</i> , 2018, 19, 737-753.	3.2	51
1989	Isotretinoin and lymecycline treatments modify the skin microbiota in acne. <i>Experimental Dermatology</i> , 2018, 27, 30-36.	1.4	48
1990	Investigation into the nitrate removal efficiency and microbial communities in a sequencing batch reactor treating reverse osmosis concentrate produced by a coking wastewater treatment plant. <i>Environmental Technology (United Kingdom)</i> , 2018, 39, 2203-2214.	1.2	5
1991	Validating novel oligonucleotide primers targeting three classes of bacterial non-specific acid phosphatase genes in grassland soils. <i>Plant and Soil</i> , 2018, 427, 39-51.	1.8	24
1992	Chromatin remodeling factor OsINO80 is involved in regulation of gibberellin biosynthesis and is crucial for rice plant growth and development. <i>Journal of Integrative Plant Biology</i> , 2018, 60, 144-159.	4.1	30
1993	De Novo Identification of sRNA Loci and Non-coding RNAs by High-Throughput Sequencing. <i>Methods in Molecular Biology</i> , 2018, 1675, 297-314.	0.4	3
1994	MATAM: reconstruction of phylogenetic marker genes from short sequencing reads in metagenomes. <i>Bioinformatics</i> , 2018, 34, 585-591.	1.8	50
1995	The Draft Genome Sequence of <i>Clostridium beijerinckii</i> NJP7, a Unique Bacterium Capable of Producing Isopropanol-Butanol from Hemicellulose Through Consolidated Bioprocessing. <i>Current Microbiology</i> , 2018, 75, 305-308.	1.0	13
1996	Characterization of 13 polymorphic microsatellite loci in the Japanese land leech. <i>Parasitology International</i> , 2018, 67, 13-15.	0.6	2
1997	Microbiome and infectivity studies reveal complex polyspecies tree disease in Acute Oak Decline. <i>ISME Journal</i> , 2018, 12, 386-399.	4.4	75
1998	Targeted sequencing of clade-specific markers from skin microbiomes for forensic human identification. <i>Forensic Science International: Genetics</i> , 2018, 32, 50-61.	1.6	69
1999	The impact of endogenous content, replicates and pooling on genome capture from faecal samples. <i>Molecular Ecology Resources</i> , 2018, 18, 319-333.	2.2	33
2000	Microbial community differentiation between active and inactive sulfide chimneys of the Kolumbo submarine volcano, Hellenic Volcanic Arc. <i>Extremophiles</i> , 2018, 22, 13-27.	0.9	21
2001	Gut microbiome in gestational diabetes: a cross-sectional study of mothers and offspring 5 years postpartum. <i>Acta Obstetrica Et Gynecologica Scandinavica</i> , 2018, 97, 38-46.	1.3	51
2002	Small RNA-mediated regulation of DNA dosage in the ciliate <i>Oxytricha</i> . <i>Rna</i> , 2018, 24, 18-29.	1.6	20
2003	Supplementation of pancreatic digestive enzymes alters the composition of intestinal microbiota in mice. <i>Biochemical and Biophysical Research Communications</i> , 2018, 495, 273-279.	1.0	43

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2004	DISARM is a widespread bacterial defence system with broad anti-phage activities. <i>Nature Microbiology</i> , 2018, 3, 90-98.	5.9	225
2005	<i>hace1</i> Influences zebrafish cardiac development via ROS-dependent mechanisms. <i>Developmental Dynamics</i> , 2018, 247, 289-303.	0.8	17
2006	RNA sequencing and SSR marker development for genetic diversity research in <i>Woonyoungia septentrionalis</i> (Magnoliaceae). <i>Conservation Genetics Resources</i> , 2018, 10, 867-872.	0.4	3
2007	Loss of protein phosphatase 2A regulatory subunit B56 \hat{r} promotes spontaneous tumorigenesis in vivo. <i>Oncogene</i> , 2018, 37, 544-552.	2.6	39
2008	Expanding the map of protein-RNA interaction sites via cell fusion followed by PAR-CLIP. <i>RNA Biology</i> , 2018, 15, 359-368.	1.5	7
2009	Profiling Open Chromatin Structure in the Ovarian Somatic Cells Using ATAC-seq. <i>Methods in Molecular Biology</i> , 2018, 1680, 165-177.	0.4	4
2010	Accurate Profiling and Quantification of tRNA Fragments from RNA-Seq Data: A Vade Mecum for MINTmap. <i>Methods in Molecular Biology</i> , 2018, 1680, 237-255.	0.4	21
2011	Tropical soils are a reservoir for fluorescent <i>Pseudomonas</i> spp. biodiversity. <i>Environmental Microbiology</i> , 2018, 20, 62-74.	1.8	28
2012	Arbuscular mycorrhizal fungi promote coexistence and niche divergence of sympatric palm species on a remote oceanic island. <i>New Phytologist</i> , 2018, 217, 1254-1266.	3.5	36
2013	Ribosome Profiling in Maize. <i>Methods in Molecular Biology</i> , 2018, 1676, 165-183.	0.4	20
2014	Identification of a Hypervirulent Pathotype of <i>Rice yellow mottle virus</i> : A Threat to Genetic Resistance Deployment in West-Central Africa. <i>Phytopathology</i> , 2018, 108, 299-307.	1.1	25
2015	The oral microbiota in colorectal cancer is distinctive and predictive. <i>Gut</i> , 2018, 67, 1454-1463.	6.1	425
2016	A randomised trial of the effect of omega-3 polyunsaturated fatty acid supplements on the human intestinal microbiota. <i>Gut</i> , 2018, 67, 1974-1983.	6.1	332
2017	<i>Tremblaya phenacola</i> PPER: an evolutionary beta-gammaproteobacterium collage. <i>ISME Journal</i> , 2018, 12, 124-135.	4.4	14
2018	Genotyping-by-sequencing through transcriptomics: implementation in a range of crop species with varying reproductive habits and ploidy levels. <i>Plant Biotechnology Journal</i> , 2018, 16, 877-889.	4.1	45
2019	Exploring deep-water coral communities using environmental DNA. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2018, 150, 229-241.	0.6	39
2020	Examination of the Bacterial Biodiversity of Coastal Eroded Surface Soils from the Padza de Dapani (Mayotte Island). <i>Geomicrobiology Journal</i> , 2018, 35, 355-365.	1.0	6
2021	Transcriptomics reveals tissue/organ-specific differences in gene expression in the starfish <i>Patiria pectinifera</i> . <i>Marine Genomics</i> , 2018, 37, 92-96.	0.4	8

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2022	Stable association of a <i>Drosophila</i> -derived microbiota with its animal partner and the nutritional environment throughout a fly population's life cycle. <i>Journal of Insect Physiology</i> , 2018, 106, 2-12.	0.9	34
2023	Cold adaptation of tRNA nucleotidyltransferases: A tradeoff in activity, stability and fidelity. <i>RNA Biology</i> , 2018, 15, 144-155.	1.5	24
2024	HbA1c is associated with altered expression in blood of cell cycle- and immune response-related genes. <i>Diabetologia</i> , 2018, 61, 138-146.	2.9	10
2025	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
2026	Next generation sequencing elucidates cacao badnavirus diversity and reveals the existence of more than ten viral species. <i>Virus Research</i> , 2018, 244, 235-251.	1.1	39
2027	Viral unmasking of cellular 5S rRNA pseudogene transcripts induces RIG-I-mediated immunity. <i>Nature Immunology</i> , 2018, 19, 53-62.	7.0	179
2028	A Workflow Guide to RNA-seq Analysis of Chaperone Function and Beyond. <i>Methods in Molecular Biology</i> , 2018, 1709, 233-252.	0.4	3
2029	Identification and Functional Characterization of Phosphorylation Sites of the Human Papillomavirus 31 E8 ^{E2} Protein. <i>Journal of Virology</i> , 2018, 92, .	1.5	11
2030	Using a new RAD-sequencing approach to study the evolution of <i>Micromeria</i> in the Canary islands. <i>Molecular Phylogenetics and Evolution</i> , 2018, 119, 160-169.	1.2	15
2031	Feeding strategy shapes gut metagenomic enrichment and functional specialization in captive lemurs. <i>Gut Microbes</i> , 2018, 9, 202-217.	4.3	21
2032	Evolution in the Amphi-Atlantic tropical genus <i>Guibourtia</i> (Fabaceae, Detarioideae), combining NGS phylogeny and morphology. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 83-93.	1.2	31
2033	Transcriptional memory contributes to drought tolerance in coffee (<i>Coffea canephora</i>) plants. <i>Environmental and Experimental Botany</i> , 2018, 147, 220-233.	2.0	47
2034	Archaeal community changes in Lateglacial lake sediments: Evidence from ancient DNA. <i>Quaternary Science Reviews</i> , 2018, 181, 19-29.	1.4	78
2035	Removal of the cecum affects intestinal fermentation, enteric bacterial community structure, and acute colitis in mice. <i>Gut Microbes</i> , 2018, 9, 218-235.	4.3	63
2036	Data on RNA-seq analysis of <i>Garcinia mangostana</i> L. seed development. <i>Data in Brief</i> , 2018, 16, 90-93.	0.5	5
2037	Rapid allopolyploid radiation of moonwort ferns (<i>Botrychium</i> ; Ophioglossaceae) revealed by PacBio sequencing of homologous and homeologous nuclear regions. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 342-353.	1.2	60
2038	Identifying miRNA Targets Using AGO-RIPseq. <i>Methods in Molecular Biology</i> , 2018, 1720, 131-140.	0.4	12
2039	Ecological selection of siderophore-producing microbial taxa in response to heavy metal contamination. <i>Ecology Letters</i> , 2018, 21, 117-127.	3.0	97

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2040	Genome Assembly and Annotation of the Medicinal Plant <i>Calotropis gigantea</i> , a Producer of Anticancer and Antimalarial Cardenolides. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 385-391.	0.8	38
2041	Discovery of microRNAs associated with the antiviral immune response of Atlantic cod macrophages. <i>Molecular Immunology</i> , 2018, 93, 152-161.	1.0	64
2042	Changes in gut microbiota during development of compulsive checking and locomotor sensitization induced by chronic treatment with the dopamine agonist quinpirole. <i>Behavioural Pharmacology</i> , 2018, 29, 211-224.	0.8	13
2043	Enhanced Wort Fermentation with <i>De Novo</i> Lager Hybrids Adapted to High-Ethanol Environments. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	39
2044	Voluntary exposure to a toxin: the genetic influence on ethanol consumption. <i>Mammalian Genome</i> , 2018, 29, 128-140.	1.0	9
2045	Pan-arthropod analysis reveals somatic piRNAs as an ancestral defence against transposable elements. <i>Nature Ecology and Evolution</i> , 2018, 2, 174-181.	3.4	214
2046	Is <i>Tuber melanosporum</i> colonizing the roots of herbaceous, non-ectomycorrhizal plants?. <i>Fungal Ecology</i> , 2018, 31, 59-68.	0.7	39
2047	RNA polymerases IV and V influence the 3' boundaries of Polymerase II transcription units in <i>Arabidopsis</i> . <i>RNA Biology</i> , 2018, 15, 269-279.	1.5	7
2048	A targeted sequencing panel identifies rare damaging variants in multiple genes in the cranial neural tube defect, anencephaly. <i>Clinical Genetics</i> , 2018, 93, 870-879.	1.0	29
2049	Great tits and the city: Distribution of genomic diversity and gene-environment associations along an urbanization gradient. <i>Evolutionary Applications</i> , 2018, 11, 593-613.	1.5	42
2050	An acetyltable lysine controls CRP function in <i>E. coli</i> . <i>Molecular Microbiology</i> , 2018, 107, 116-131.	1.2	51
2051	Metagenomics for the study of viruses in urban sewage as a tool for public health surveillance. <i>Science of the Total Environment</i> , 2018, 618, 870-880.	3.9	116
2052	Transcriptomic analysis of synovial extracellular RNA following knee trauma: A pilot study. <i>Journal of Orthopaedic Research</i> , 2018, 36, 1659-1665.	1.2	11
2053	(-)-Epicatechin protects the intestinal barrier from high fat diet-induced permeabilization: Implications for steatosis and insulin resistance. <i>Redox Biology</i> , 2018, 14, 588-599.	3.9	109
2054	Predicting the genetic impact of stocking in Brook Charr (<i>Salvelinus fontinalis</i>) by combining RAD sequencing and modeling of explanatory variables. <i>Evolutionary Applications</i> , 2018, 11, 577-592.	1.5	36
2055	The <i>Streptococcus agalactiae</i> Stringent Response Enhances Virulence and Persistence in Human Blood. <i>Infection and Immunity</i> , 2018, 86, .	1.0	31
2056	Thermal acclimation in <i>Arabidopsis lyrata</i> : genotypic costs and transcriptional changes. <i>Journal of Evolutionary Biology</i> , 2018, 31, 123-135.	0.8	12
2057	Contemporary evolution of a Lepidopteran species, <i>Heliopsis virescens</i> , in response to modern agricultural practices. <i>Molecular Ecology</i> , 2018, 27, 167-181.	2.0	28

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2058	A Novel Mechanism of Inactivating Antibacterial Nitro Compounds in the Human Pathogen <i>Staphylococcus aureus</i> by Overexpression of a NADH-Dependent Flavin Nitroreductase. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	10
2059	Differential Content of Proteins, mRNAs, and miRNAs Suggests that MDSC and Their Exosomes May Mediate Distinct Immune Suppressive Functions. <i>Journal of Proteome Research</i> , 2018, 17, 486-498.	1.8	84
2060	<i>Pseudomonas silesiensis</i> sp. nov. strain A3T isolated from a biological pesticide sewage treatment plant and analysis of the complete genome sequence. <i>Systematic and Applied Microbiology</i> , 2018, 41, 13-22.	1.2	23
2061	The limited role of differential fractionation in genome content variation and function in maize (<i>Zea mays</i> L.) inbred lines. <i>Plant Journal</i> , 2018, 93, 131-141.	2.8	42
2062	<i>Brachypodium distachyon</i> Long Noncoding RNAs: Genome-Wide Identification and Expression Analysis. <i>Methods in Molecular Biology</i> , 2018, 1667, 31-42.	0.4	15
2063	Lost but not forgotten: MHC genotypes predict overwinter survival despite depauperate MHC diversity in a declining frog. <i>Conservation Genetics</i> , 2018, 19, 309-322.	0.8	24
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2065	Microbiomes of the Arctic carnivorous sponges <i>Chondrocladia grandis</i> and <i>Cladorhiza oxeata</i> suggest a specific, but differential involvement of bacterial associates. <i>Arctic Science</i> , 2018, 4, 186-204.	0.9	14
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2068	Additives in Plasticised Polyvinyl Chloride Fuel Microbial Nitrate Reduction at High pH: Implications for Nuclear Waste Disposal. <i>Frontiers in Environmental Science</i> , 2018, 6, .	1.5	12
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2072	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
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2210	DNA G-quadruplex structures mold the DNA methylome. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 951-957.	3.6	185
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2229	Accurate annotation of accessible chromatin in mouse and human primordial germ cells. <i>Cell Research</i> , 2018, 28, 1077-1089.	5.7	17
2230	Complement receptor CD46 co-stimulates optimal human CD8+ T cell effector function via fatty acid metabolism. <i>Nature Communications</i> , 2018, 9, 4186.	5.8	75
2231	Comparative RNA-Seq Analysis of High- and Low-Oil Yellow Horn During Embryonic Development. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3071.	1.8	19
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2240	Determinants of promoter and enhancer transcription directionality in metazoans. <i>Nature Communications</i> , 2018, 9, 4472.	5.8	22
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2266	Exosomes from normal and diabetic human corneolimbal keratocytes differentially regulate migration, proliferation and marker expression of limbal epithelial cells. <i>Scientific Reports</i> , 2018, 8, 15173.	1.6	48
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2271	High-quality genome sequences of uncultured microbes by assembly of read clouds. <i>Nature Biotechnology</i> , 2018, 36, 1067-1075.	9.4	103
2272	Immune-suppression by OsHV-1 viral infection causes fatal bacteraemia in Pacific oysters. <i>Nature Communications</i> , 2018, 9, 4215.	5.8	217
2273	Transcription-factor-mediated supervision of global genome architecture maintains B cell identity. <i>Nature Immunology</i> , 2018, 19, 1257-1264.	7.0	83
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2291	Delimitation of <i>Alosa</i> species (Teleostei: Clupeiformes) from the Sea of Azov: integrating morphological and molecular approaches. <i>Journal of Fish Biology</i> , 2018, 93, 1216-1228.	0.7	2
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2294	N6-Methyladenosine Inhibits Local Ribonucleolytic Cleavage to Stabilize mRNAs in <i>Arabidopsis</i> . <i>Cell Reports</i> , 2018, 25, 1146-1157.e3.	2.9	175
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2309	The Atlantic salmon (<i>Salmo salar</i>) antimicrobial peptide cathelicidin-2 is a molecular host-associated cue for the salmon louse (<i>Lepeophtheirus salmonis</i>). <i>Scientific Reports</i> , 2018, 8, 13738.	1.6	13
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2339	Transcriptional landscape changes during human embryonic stem cell derivation. <i>Molecular Human Reproduction</i> , 2018, 24, 543-555.	1.3	5
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2350	Molecular variability and genetic structure of white spot syndrome virus strains from northwest Mexico based on the analysis of genomes. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	11
2351	A Comparative Study on the Faecal Bacterial Community and Potential Zoonotic Bacteria of Muskoxen (<i>Ovibos moschatus</i>) in Northeast Greenland, Northwest Greenland and Norway. <i>Microorganisms</i> , 2018, 6, 76.	1.6	10
2352	From Short Reads to Chromosome-Scale Genome Assemblies. <i>Methods in Molecular Biology</i> , 2018, 1848, 151-197.	0.4	7
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2777	High temperature utilization of PAM and HPAM by microbial communities enriched from oilfield produced water and activated sludge. <i>AMB Express</i> , 2019, 9, 46.	1.4	9
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2787	The pause-initiation limit restricts transcription activation in human cells. <i>Nature Communications</i> , 2019, 10, 3603.	5.8	60
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2789	Dickkopf-related protein 1 is a progesterone acting on the bovine embryo during the morula-to-blastocyst transition to program trophoblast elongation. <i>Scientific Reports</i> , 2019, 9, 11816.	1.6	14
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2803	Multiplexed genome engineering by Cas12a and CRISPR arrays encoded on single transcripts. <i>Nature Methods</i> , 2019, 16, 887-893.	9.0	187
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2904	De novo phased assembly of the <i>Vitis riparia</i> grape genome. <i>Scientific Data</i> , 2019, 6, 127.	2.4	71

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2917	Open chromatin landscape of rat microglia upon proinvasive or inflammatory polarization. <i>Glia</i> , 2019, 67, 2312-2328.	2.5	8
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2931	First Insights Into Bacterial Gastrointestinal Tract Communities of the Eurasian Beaver (<i>Castor fiber</i>). <i>Frontiers in Microbiology</i> , 2019, 10, 1646.	1.5	4
2932	The effects of benzo[a]pyrene on the composition of gut microbiota and the gut health of the juvenile sea cucumber <i>Apostichopus japonicus</i> Selenka. <i>Fish and Shellfish Immunology</i> , 2019, 93, 369-379.	1.6	32
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3642	Metagenomic analysis reveals distinct patterns of denitrification gene abundance across soil moisture, nitrate gradients. <i>Environmental Microbiology</i> , 2019, 21, 1255-1266.	1.8	49
3643	No differences in microbiome changes between anti-adhesive and antibacterial ingredients in toothpastes during periodontal therapy. <i>Journal of Periodontal Research</i> , 2019, 54, 435-443.	1.4	25
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4021	MicroRNA fingerprints in serum and whole blood of sarcoid-affected horses as potential non-invasive diagnostic biomarkers. <i>Veterinary and Comparative Oncology</i> , 2019, 17, 107-117.	0.8	11
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4064	MicroRNA signature changes during induction of neural stem cells from human mesenchymal stem cells. <i>Nanomedicine: Nanotechnology, Biology, and Medicine</i> , 2019, 17, 94-105.	1.7	8
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4066	The embryonic transcriptome of <i>Arabidopsis thaliana</i> . <i>Plant Reproduction</i> , 2019, 32, 77-91.	1.3	82
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4077	Identification and validation of plant miRNA from NGS data—an experimental approach. <i>Briefings in Functional Genomics</i> , 2019, 18, 13-22.	1.3	7
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4477	Seasonal Variations in Soil Microbiota Profile of Termite (<i>Syntermes wheeleri</i>) Mounds in the Brazilian Tropical Savanna. <i>Microorganisms</i> , 2020, 8, 1482.	1.6	10
4478	Metabolic Response of <i>Faecalibacterium prausnitzii</i> to Cell-Free Supernatants from Lactic Acid Bacteria. <i>Microorganisms</i> , 2020, 8, 1528.	1.6	16
4479	Nematodes as bioindicators of polluted sediments using metabarcoding and microscopic taxonomy. <i>Environment International</i> , 2020, 143, 105922.	4.8	25
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4481	Bacterial microbiota associated with insect vectors of grapevine Bois noir disease in relation to phytoplasma infection. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	4
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4488	Comparison of culture-independent and dependent approaches for identification of native arsenic-resistant bacteria and their potential use for arsenic bioremediation. <i>Ecotoxicology and Environmental Safety</i> , 2020, 205, 111267.	2.9	29
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4494	A comparative analysis of chromatin accessibility in cattle, pig, and mouse tissues. <i>BMC Genomics</i> , 2020, 21, 698.	1.2	43
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4498	Assessing the Variation within the Oral Microbiome of Healthy Adults. <i>MSphere</i> , 2020, 5, .	1.3	49
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4504	Pan-European regional marine benthic cryptobiome biodiversity patterns revealed by metabarcoding Autonomous Reef Monitoring Structures. <i>Molecular Ecology</i> , 2020, 29, 4882-4897.	2.0	19
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4506	Sequencing and Analysis of the Complete Organellar Genomes of <i>Prototheca wickerhamii</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 1296.	1.7	5
4507	Transcriptome and Gene Fusion Analysis of Synchronous Lesions Reveals IncMRPS31P5 as a Novel Transcript Involved in Colorectal Cancer. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7120.	1.8	3
4508	Combinatorial Action of Temporally Segregated Transcription Factors. <i>Developmental Cell</i> , 2020, 55, 483-499.e7.	3.1	36
4509	Maternal oxycodone treatment causes pathophysiological changes in the mouse placenta. <i>Placenta</i> , 2020, 100, 96-110.	0.7	16
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4513	Placental microRNA expression associates with birthweight through control of adipokines: results from two independent cohorts. <i>Epigenetics</i> , 2021, 16, 770-782.	1.3	12
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4519	The longevity-associated variant of BPIFB4 improves a CXCR4-mediated striatum-microglia crosstalk preventing disease progression in a mouse model of Huntington's disease. <i>Cell Death and Disease</i> , 2020, 11, 546.	2.7	15
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4523	Construction of high-resolution genetic linkage map in pear pseudo-BC1 (<i>Pyrus pyrifolia</i> P.) Tj ETQq0 0 0 rgBT /Overlock 161, 745-753.	0.7	7
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4525	Computational Methods for Analysis of Large-Scale CRISPR Screens. <i>Annual Review of Biomedical Data Science</i> , 2020, 3, 137-162.	2.8	4
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4527	Targeted Cell Sorting Combined With Single Cell Genomics Captures Low Abundant Microbial Dark Matter With Higher Sensitivity Than Metagenomics. <i>Frontiers in Microbiology</i> , 2020, 11, 1377.	1.5	25
4528	Meta-Transcriptomic Analysis of RNAseq Data Reveals Pacu and Loach Fish with Unusually High Levels of Myoglobin Expression in Skeletal Muscles. <i>Animals</i> , 2020, 10, 1130.	1.0	2

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4530	Epigenetic landscape links upper airway microbiota in infancy with allergic rhinitis at 6 years of age. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 146, 1358-1366.	1.5	31
4531	The complete mitochondrial genome of Indian gaur, <i>Bos gaurus</i> and its phylogenetic implications. <i>Scientific Reports</i> , 2020, 10, 11936.	1.6	15
4532	Adenovirus-mediated ubiquitination alters protein-RNA binding and aids viral RNA processing. <i>Nature Microbiology</i> , 2020, 5, 1217-1231.	5.9	22
4533	DNA methylation reprogramming during seed development and its functional relevance in seed size/weight determination in chickpea. <i>Communications Biology</i> , 2020, 3, 340.	2.0	44
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4536	Gene Loss Predictably Drives Evolutionary Adaptation. <i>Molecular Biology and Evolution</i> , 2020, 37, 2989-3002.	3.5	55
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4540	CAFRI-Rice: CRISPR applicable functional redundancy inspector to accelerate functional genomics in rice. <i>Plant Journal</i> , 2020, 104, 532-545.	2.8	26
4541	MethylStar: A fast and robust pre-processing pipeline for bulk or single-cell whole-genome bisulfite sequencing data. <i>BMC Genomics</i> , 2020, 21, 479.	1.2	11
4542	Syntrophic acetate oxidation replaces acetoclastic methanogenesis during thermophilic digestion of biowaste. <i>Microbiome</i> , 2020, 8, 105.	4.9	118
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4545	Glyceroglycolipid Metabolism Regulations under Phosphate Starvation Revealed by Transcriptome Analysis in <i>Synechococcus elongatus</i> PCC 7942. <i>Marine Drugs</i> , 2020, 18, 360.	2.2	5
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4549	Diverse Microbial Composition of Sourdoughs From Different Origins. <i>Frontiers in Microbiology</i> , 2020, 11, 1212.	1.5	56
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4551	Interstitial Cell Remodeling Promotes Aberrant Adipogenesis in Dystrophic Muscles. <i>Cell Reports</i> , 2020, 31, 107597.	2.9	64
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4553	Transcriptomic dataset reveals the molecular basis of genotypic variation in hexaploid wheat (<i>T. turgidum</i> L. var. <i>Hereward</i>). <i>PLoS Genetics</i> , 2020, 16, e1008033.	0.5	3
4554	Extracellular vesicles from <i>Heligmosomoides bakeri</i> and <i>Trichuris muris</i> contain distinct microRNA families and small RNAs that could underpin different functions in the host. <i>International Journal for Parasitology</i> , 2020, 50, 719-729.	1.3	16
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4557	Ocean currents promote rare species diversity in protists. <i>Science Advances</i> , 2020, 6, eaaz9037.	4.7	13
4558	CeMbio - The <i>Caenorhabditis elegans</i> Microbiome Resource. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3025-3039.	0.8	96
4559	Co-Expression Networks for Causal Gene Identification Based on RNA-Seq Data of <i>Corynebacterium pseudotuberculosis</i> . <i>Genes</i> , 2020, 11, 794.	1.0	3
4560	Distinct Microbiota Dysbiosis in Patients with Non-Erosive Reflux Disease and Esophageal Adenocarcinoma. <i>Journal of Clinical Medicine</i> , 2020, 9, 2162.	1.0	26
4561	Metabarcoding Analyses of Gut Microbiota of Nile Tilapia (<i>Oreochromis niloticus</i>) from Lake Awassa and Lake Chamo, Ethiopia. <i>Microorganisms</i> , 2020, 8, 1040.	1.6	37
4562	High-Resolution Whole-Genome Analysis of Sister-Chromatid Contacts. <i>Molecular Cell</i> , 2020, 79, 857-869.e3.	4.5	19
4563	The yeast exoribonuclease Xrn1 and associated factors modulate RNA polymerase II processivity in 5' and 3' gene regions. <i>Journal of Biological Chemistry</i> , 2020, 295, 11435-11454.	1.6	25
4564	TCR-Seq Identifies Distinct Repertoires of Distant-Metastatic and Nondistant-Metastatic Thyroid Tumors. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, 3036-3045.	1.8	4

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4570	Reconstructing marine plankton food web interactions using DNA metabarcoding. <i>Molecular Ecology</i> , 2020, 29, 3380-3395.	2.0	46
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4576	The chromatin remodeling enzyme Chd4 regulates genome architecture in the mouse brain. <i>Nature Communications</i> , 2020, 11, 3419.	5.8	33
4577	Body-size Scaling is Related to Gut Microbial Diversity, Metabolism and Dietary Niche of Arboreal Folivorous Flying Squirrels. <i>Scientific Reports</i> , 2020, 10, 7809.	1.6	9
4578	Roles of Elm1 in antifungal susceptibility and virulence in <i>Candida glabrata</i> . <i>Scientific Reports</i> , 2020, 10, 9789.	1.6	4
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4585	Draft Genome Sequences of Three <i>Bacillus</i> Species Isolated from Biofouled Reverse-Osmosis Membranes. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
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4588	Random epigenetic modulation of CHO cells by repeated knockdown of DNA methyltransferases increases population diversity and enables sorting of cells with higher production capacities. <i>Biotechnology and Bioengineering</i> , 2020, 117, 3435-3447.	1.7	15
4589	The Transition From Stochastic to Deterministic Bacterial Community Assembly During Permafrost Thaw Succession. <i>Frontiers in Microbiology</i> , 2020, 11, 596589.	1.5	29
4590	Microbial Species–Area Relationships in Antarctic Cryoconite Holes Depend on Productivity. <i>Microorganisms</i> , 2020, 8, 1747.	1.6	8
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4592	Biogeography and Diversity of Multi-Trophic Root Zone Microbiomes in Michigan Apple Orchards: Analysis of Rootstock, Scion, and Local Growing Region. <i>Phytobiomes Journal</i> , 2020, 4, 122-132.	1.4	8
4593	Environmental DNA metabarcoding of cow dung reveals taxonomic and functional diversity of invertebrate assemblages. <i>Molecular Ecology</i> , 2021, 30, 3374-3389.	2.0	19
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4596	Disease Diagnostics and Potential Coinfections by <i>Vibrio coralliilyticus</i> During an Ongoing Coral Disease Outbreak in Florida. <i>Frontiers in Microbiology</i> , 2020, 11, 569354.	1.5	55
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4602	Disease-associated gut microbiome and metabolome changes in patients with chronic obstructive pulmonary disease. <i>Nature Communications</i> , 2020, 11, 5886.	5.8	194
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4606	First report of Plum bark necrosis stem pitting-associated virus infecting grapevine in China. <i>Virology Journal</i> , 2020, 17, 181.	1.4	3
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4616	Heritable Variation in Pea for Resistance Against a Root Rot Complex and Its Characterization by Amplicon Sequencing. <i>Frontiers in Plant Science</i> , 2020, 11, 542153.	1.7	11
4617	Community State Types of Vaginal Microbiota and Four Types of Abnormal Vaginal Microbiota in Pregnant Korean Women. <i>Frontiers in Public Health</i> , 2020, 8, 507024.	1.3	11
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4621	Monitoring of spatiotemporal occupancy patterns of fish and amphibian species in a lentic aquatic system using environmental DNA. <i>Molecular Ecology</i> , 2021, 30, 3097-3110.	2.0	41
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4627	Transcriptional Remodeling Patterns in Murine Dendritic Cells Infected with <i>Paracoccidioides brasiliensis</i> : More Is Not Necessarily Better. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 311.	1.5	2
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4640	I-KCKT allows dissection-free RNA profiling of adult <i>Drosophila</i> intestinal progenitor cells. <i>Development (Cambridge)</i> , 2020, 148, .	1.2	9
4641	ASH2L drives proliferation and sensitivity to bleomycin and other genotoxins in Hodgkin's lymphoma and testicular cancer cells. <i>Cell Death and Disease</i> , 2020, 11, 1019.	2.7	10
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4791	Draft Genome Sequences of <i>Micrococcus luteus</i> MFP06 and MFP07, Isolated from the Skin of Healthy Volunteers. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
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4874	Comprehensive Identification and Expression Profiling of Circular RNAs During Nodule Development in <i>Phaseolus vulgaris</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 587185.	1.7	10
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4877	Association between Aquatic Micropollutant Dissipation and River Sediment Bacterial Communities. <i>Environmental Science & Technology</i> , 2020, 54, 14380-14392.	4.6	37
4878	A genomic and historical synthesis of plague in 18th century Eurasia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28328-28335.	3.3	31
4879	LncRBase V.2: an updated resource for multispecies lncRNAs and ClinixLSNP hosting genetic variants in lncRNAs for cancer patients. <i>RNA Biology</i> , 2021, 18, 1136-1151.	1.5	14
4880	Incomplete removal of ribosomal RNA can affect chromatin RNA-seq data analysis. <i>Transcription</i> , 2020, 11, 230-235.	1.7	7
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4889	Biogeographic parallels in thermal tolerance and gene expression variation under temperature stress in a widespread bumble bee. <i>Scientific Reports</i> , 2020, 10, 17063.	1.6	42
4890	Host-symbiont coevolution, cryptic structure, and bleaching susceptibility, in a coral species complex (<i>Scleractinia</i> ; <i>Poritidae</i>). <i>Scientific Reports</i> , 2020, 10, 16995.	1.6	33
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4894	Focal adhesion ribonucleoprotein complex proteins are major humoral cancer antigens and targets in autoimmune diseases. <i>Communications Biology</i> , 2020, 3, 588.	2.0	4
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4897	Molecular insights into information processing and developmental and immune regulation of <i>Eriocheir sinensis megalopa</i> under hyposaline stress. <i>Genomics</i> , 2020, 112, 4647-4656.	1.3	3
4898	Inoculation of arbuscular mycorrhizal fungi increases lettuce yield without altering natural soil communities. <i>Archives of Agronomy and Soil Science</i> , 2022, 68, 413-430.	1.3	6
4899	Chromosome reciprocal translocations have accompanied subspecies evolution in bananas. <i>Plant Journal</i> , 2020, 104, 1698-1711.	2.8	35
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4905	The Potential of HTS Approaches for Accurate Genotyping in Grapevine (<i>Vitis vinifera</i> L.). <i>Genes</i> , 2020, 11, 917.	1.0	4
4906	Transcriptome-Wide N6-Methyladenosine (m6A) Methylome Profiling of Heat Stress in Pak-choi (<i>Brassica rapa</i> ssp. <i>chinensis</i>). <i>Plants</i> , 2020, 9, 1080.	1.6	33
4907	Targeted isolation based on metagenome-assembled genomes reveals a phylogenetically distinct group of thermophilic spirochetes from deep biosphere. <i>Environmental Microbiology</i> , 2021, 23, 3585-3598.	1.8	23
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4911	Beneficial rhizobacteria <i>Pseudomonas simiae</i> WCS417 induce major transcriptional changes in plant sugar transport. <i>Journal of Experimental Botany</i> , 2020, 71, 7301-7315.	2.4	35
4912	Evolutionarily conserved sequence motif analysis guides development of chemically defined hydrogels for therapeutic vascularization. <i>Science Advances</i> , 2020, 6, eaaz5894.	4.7	17
4913	A novel antiviral lncRNA, EDAL, shields a T309 O-GlcNAcylation site to promote EZH2 lysosomal degradation. <i>Genome Biology</i> , 2020, 21, 228.	3.8	38
4914	Systemic spreading of exogenous applied RNA biopesticides in the crop plant <i>Hordeum vulgare</i> . <i>ExRNA</i> , 2020, 2, .	1.0	37
4915	The genomic landscape of Mongolian hepatocellular carcinoma. <i>Nature Communications</i> , 2020, 11, 4383.	5.8	55
4916	Expression Profiles of CircRNA and mRNA in Lacrimal Glands of AQP5 ^{-/-} Mice With Primary Dry Eye. <i>Frontiers in Physiology</i> , 2020, 11, 1010.	1.3	20
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4923	Clinical benefit of remdesivir in rhesus macaques infected with SARS-CoV-2. <i>Nature</i> , 2020, 585, 273-276.	13.7	592
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4925	Differential processing and localization of human Nocturnin controls metabolism of mRNA and nicotinamide adenine dinucleotide cofactors. <i>Journal of Biological Chemistry</i> , 2020, 295, 15112-15133.	1.6	6
4926	Distinct Effects of Milk-Derived and Fermented Dairy Protein on Gut Microbiota and Cardiometabolic Markers in Diet-Induced Obese Mice. <i>Journal of Nutrition</i> , 2020, 150, 2673-2686.	1.3	13
4927	The microbiome of captive hamadryas baboons. <i>Animal Microbiome</i> , 2020, 2, 25.	1.5	5

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4929	The Microbial Community Associated with <i>Rhizostoma pulmo</i> : Ecological Significance and Potential Consequences for Marine Organisms and Human Health. <i>Marine Drugs</i> , 2020, 18, 437.	2.2	16
4930	Association between the microbiomes of tonsil and saliva samples isolated from pediatric patients subjected to tonsillectomy for the treatment of tonsillar hyperplasia. <i>Experimental and Molecular Medicine</i> , 2020, 52, 1564-1573.	3.2	10
4931	Thermal stratification and fish thermal preference explain vertical eDNA distributions in lakes. <i>Molecular Ecology</i> , 2021, 30, 3083-3096.	2.0	55
4932	Are Antisense Proteins in Prokaryotes Functional?. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 187.	1.6	19
4933	Manganese Ions Individually Alter the Reverse Transcription Signature of Modified Ribonucleosides. <i>Genes</i> , 2020, 11, 950.	1.0	15
4934	Metagenomic Insights into the Sewage RNA Virosphere of a Large City. <i>Viruses</i> , 2020, 12, 1050.	1.5	22
4935	Poorly known microbial taxa dominate the microbiome of hypersaline Sambhar Lake salterns in India. <i>Extremophiles</i> , 2020, 24, 875-885.	0.9	15
4936	The conserved elongation factor Spn1 is required for normal transcription, histone modifications, and splicing in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2020, 48, 10241-10258.	6.5	21
4937	Multi-omics profiling reveals microRNA-mediated insulin signaling networks. <i>BMC Bioinformatics</i> , 2020, 21, 389.	1.2	3
4938	16S Metagenomics Reveals Dysbiosis of Nasal Core Microbiota in Children With Chronic Nasal Inflammation: Role of Adenoid Hypertrophy and Allergic Rhinitis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 458.	1.8	21
4939	Decrease of oral microbial diversity might correlate with radiation esophagitis in patients with esophageal cancer undergoing chemoradiation: A pilot study. <i>Precision Radiation Oncology</i> , 2020, 4, 81-88.	0.4	4
4940	Transcriptome profiling analysis of caeca in chicks challenged with <i>Salmonella Typhimurium</i> reveals differential expression of genes involved in host mucosal immune response. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 9327-9342.	1.7	16
4941	<i>Mcdadea</i> : A New Genus of Acanthaceae Endemic to the Namib Desert of Southwestern Angola. <i>Systematic Botany</i> , 2020, 45, 200-211.	0.2	7
4942	The transcriptomic response of a wine strain of <i>Lachancea thermotolerans</i> to oxygen deprivation. <i>FEMS Yeast Research</i> , 2020, 20, .	1.1	5
4943	<i>Arabidopsis</i> exoribonuclease USB1 interacts with the PPR-domain protein SOAR1 to negatively regulate abscisic acid signaling. <i>Journal of Experimental Botany</i> , 2020, 71, 5837-5851.	2.4	12
4944	Genomic signatures of convergent adaptation to Alpine environments in three Brassicaceae species. <i>Molecular Ecology</i> , 2020, 29, 4350-4365.	2.0	17
4945	Export of Rgg Quorum Sensing Peptides is Mediated by the PptAB ABC Transporter in <i>Streptococcus Thermophilus</i> Strain LMD-9. <i>Genes</i> , 2020, 11, 1096.	1.0	7

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4947	The complete chloroplast genome of the rare species <i>Epimedium tianmenshanensis</i> and comparative analysis with related species. <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 2075-2083.	1.4	11
4948	Multispecies models reveal that eDNA metabarcoding is more sensitive than backpack electrofishing for conducting fish surveys in freshwater streams. <i>Molecular Ecology</i> , 2021, 30, 3111-3126.	2.0	29
4949	Generation of Comprehensive Ecosystem-Specific Reference Databases with Species-Level Resolution by High-Throughput Full-Length 16S rRNA Gene Sequencing and Automated Taxonomy Assignment (AutoTax). <i>MBio</i> , 2020, 11, .	1.8	66
4950	circUSP42 Is Downregulated in Triple-Negative Breast Cancer and Associated With Poor Prognosis. <i>Technology in Cancer Research and Treatment</i> , 2020, 19, 153303382095082.	0.8	13
4951	Tracing key genes associated with the <i>Pinctada margaritifera</i> albino phenotype from juvenile to cultured pearl harvest stages using multiple whole transcriptome sequencing. <i>BMC Genomics</i> , 2020, 21, 662.	1.2	8
4952	B chromosomes of multiple species have intense evolutionary dynamics and accumulated genes related to important biological processes. <i>BMC Genomics</i> , 2020, 21, 656.	1.2	22
4953	Persistence of Suspected Probiotic Organisms in Preterm Infant Gut Microbiota Weeks After Probiotic Supplementation in the NICU. <i>Frontiers in Microbiology</i> , 2020, 11, 574137.	1.5	20
4954	Targeting Mitochondria-Located circRNA SCAR Alleviates NASH via Reducing mROS Output. <i>Cell</i> , 2020, 183, 76-93.e22.	13.5	237
4955	Zeb2 regulates the balance between retinal interneurons and Müller glia by inhibition of BMP/Smad signaling. <i>Developmental Biology</i> , 2020, 468, 80-92.	0.9	5
4956	Multiple capsid protein binding sites mediate selective packaging of the alphavirus genomic RNA. <i>Nature Communications</i> , 2020, 11, 4693.	5.8	23
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4958	Removing reference bias and improving indel calling in ancient DNA data analysis by mapping to a sequence variation graph. <i>Genome Biology</i> , 2020, 21, 250.	3.8	44
4959	Chromatin regulates expression of small RNAs to help maintain transposon methylome homeostasis in <i>Arabidopsis</i> . <i>Genome Biology</i> , 2020, 21, 251.	3.8	61
4960	The Gut Microbial Community Structure of the North American River Otter (<i>Lontra canadensis</i>) in the Alberta Oil Sands Region in Canada: Relationship with Local Environmental Variables and Metal Body Burden. <i>Environmental Toxicology and Chemistry</i> , 2020, 39, 2516-2526.	2.2	5
4961	SUPER STARCHY1/ONAC025 participates in rice grain filling. <i>Plant Direct</i> , 2020, 4, e00249.	0.8	11
4962	DENR promotes translation reinitiation via ribosome recycling to drive expression of oncogenes including ATF4. <i>Nature Communications</i> , 2020, 11, 4676.	5.8	58
4963	Therapeutic vaccination of koalas harbouring endogenous koala retrovirus (KoRV) improves antibody responses and reduces circulating viral load. <i>Npj Vaccines</i> , 2020, 5, 60.	2.9	10

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4965	Aquatic suspended particulate matter as source of eDNA for fish metabarcoding. <i>Scientific Reports</i> , 2020, 10, 14352.	1.6	10
4966	Transcription factor expression defines subclasses of developing projection neurons highly similar to single-cell RNA-seq subtypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25074-25084.	3.3	23
4967	Detection of SARS-CoV-2 in a cat owned by a COVID-19â€‘affected patient in Spain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 24790-24793.	3.3	154
4968	Readthrough of stop codons under limiting ABCE1 concentration involves frameshifting and inhibits nonsense-mediated mRNA decay. <i>Nucleic Acids Research</i> , 2020, 48, 10259-10279.	6.5	28
4969	Ultrasensitive deletion detection links mitochondrial DNA replication, disease, and aging. <i>Genome Biology</i> , 2020, 21, 248.	3.8	48
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4971	Transcriptome of the Southern Muriqui <i>Brachyteles arachnoides</i> (Primates:Platyrrhini), a Critically Endangered New World Monkey: Evidence of Adaptive Evolution. <i>Frontiers in Genetics</i> , 2020, 11, 831.	1.1	1
4972	Alleleâ€‘specific proximal promoter hypomethylation of the telomerase reverse transcriptase gene (<i>TERT</i>) associates with <i>TERT</i> expression in multiple cancers. <i>Molecular Oncology</i> , 2020, 14, 2358-2374.	2.1	23
4973	RNA-Seq profiling of microdissected glomeruli identifies potential biomarkers for human IgA nephropathy. <i>American Journal of Physiology - Renal Physiology</i> , 2020, 319, F809-F821.	1.3	15
4974	Long-read individual-molecule sequencing reveals CRISPR-induced genetic heterogeneity in human ESCs. <i>Genome Biology</i> , 2020, 21, 213.	3.8	20
4975	High-resolution analysis of Merkel Cell Polyomavirus in Merkel Cell Carcinoma reveals distinct integration patterns and suggests NHEJ and MMBIR as underlying mechanisms. <i>PLoS Pathogens</i> , 2020, 16, e1008562.	2.1	24
4976	Rumen Microbiome Composition Is Altered in Sheep Divergent in Feed Efficiency. <i>Frontiers in Microbiology</i> , 2020, 11, 1981.	1.5	72
4977	Modulation of Gut Microbiota in Korean Navy Trainees following a Healthy Lifestyle Change. <i>Microorganisms</i> , 2020, 8, 1265.	1.6	11
4978	Influenza virus repurposes the antiviral protein IFIT2 to promote translation of viral mRNAs. <i>Nature Microbiology</i> , 2020, 5, 1490-1503.	5.9	45
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4980	Comparative Genomics Underlines Multiple Roles of <i>Proffotella</i> , an Obligate Symbiont of Psyllids: Providing Toxins, Vitamins, and Carotenoids. <i>Genome Biology and Evolution</i> , 2020, 12, 1975-1987.	1.1	39
4981	Size reductions and genomic changes within two generations in wild walleye populations: associated with harvest?. <i>Evolutionary Applications</i> , 2020, 13, 1128-1144.	1.5	25

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4983	Genotyping by Sequencing Reads of 20 <i>Vicia faba</i> Lines with High and Low Vicine and Convicine Content. <i>Data</i> , 2020, 5, 63.	1.2	0
4984	Development of Chromosome Segment Substitution Lines (CSSLs) Derived from Guangxi Wild Rice (<i>Oryza rufipogon</i> Griff.) under Rice (<i>Oryza sativa</i> L.) Background and the Identification of QTLs for Plant Architecture, Agronomic Traits and Cold Tolerance. <i>Genes</i> , 2020, 11, 980.	1.0	20
4985	Microbiome Diversity and Community-Level Change Points within Manure-Based Small Biogas Plants. <i>Microorganisms</i> , 2020, 8, 1169.	1.6	12
4986	Persistent BK Polyomavirus Viruria Is Associated with Accumulation of VP1 Mutations and Neutralization Escape. <i>Viruses</i> , 2020, 12, 824.	1.5	18
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4988	Analysis of the human breast milk microbiome and bacterial extracellular vesicles in healthy mothers. <i>Experimental and Molecular Medicine</i> , 2020, 52, 1288-1297.	3.2	42
4989	ATAC-seq footprinting unravels kinetics of transcription factor binding during zygotic genome activation. <i>Nature Communications</i> , 2020, 11, 4267.	5.8	318
4990	Temporal changes in gene expression and genotype frequency of the ornithine decarboxylase gene in native silverside <i>Basilichthys microlepidotus</i> : Impact of wastewater reduction due to implementation of public policies. <i>Evolutionary Applications</i> , 2020, 13, 1183-1194.	1.5	5
4991	Gene flow and climate-associated genetic variation in a vagile habitat specialist. <i>Molecular Ecology</i> , 2020, 29, 3889-3906.	2.0	19
4992	Complete Genome Sequence of an Alphacoronavirus from Common Vampire Bats in Peru. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	14
4993	Does Fibre-fix provided to people with irritable bowel syndrome who are consuming a low FODMAP diet improve their gut health, gut microbiome, sleep and mental health? A double-blinded, randomised controlled trial. <i>BMJ Open Gastroenterology</i> , 2020, 7, e000448.	1.1	2
4994	Sperm DNA Hypomethylation Proximal to Reproduction Pathway Genes in Maturing Elite Norwegian Red Bulls. <i>Frontiers in Genetics</i> , 2020, 11, 922.	1.1	9
4995	Cross-Species Transmission and Evolution of SIV Chimpanzee Progenitor Viruses Toward HIV-1 in Humanized Mice. <i>Frontiers in Microbiology</i> , 2020, 11, 1889.	1.5	7
4996	miR-452 Reverses Abnormal Glycosylation Modification of ER α and Estrogen Resistance in TNBC (Triple-Negative Breast Cancer) Through Targeting UGT1A1. <i>Frontiers in Oncology</i> , 2020, 10, 1509.	1.3	10
4997	Transcriptome Analysis and Metabolic Profiling of Green and Red Mizuna (<i>Brassica rapa</i> L. var.) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.95	18
4998	Plastome phylogenomics and phylogenetic diversity of endangered and threatened grassland species (Poaceae) in a North American tallgrass prairie. <i>Ecology and Evolution</i> , 2020, 10, 7602-7615.	0.8	3
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5001	Antibacterial and Antivirulence Activity of Manuka Honey against Genetically Diverse <i>Staphylococcus pseudintermedius</i> Strains. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	8
5002	TRADES: Targeted RNA Demethylation by SunTag System. <i>Advanced Science</i> , 2020, 7, 2001402.	5.6	27
5003	Resource quality determines the evolution of resistance and its genetic basis. <i>Molecular Ecology</i> , 2020, 29, 4128-4142.	2.0	8
5004	Genome-wide identification of genes regulating DNA methylation using genetic anchors for causal inference. <i>Genome Biology</i> , 2020, 21, 220.	3.8	27
5005	Classification of <i>Takifugu rubripes</i> , <i>T. chinensis</i> and <i>T. pseudommus</i> by genotyping-by-sequencing. <i>PLoS ONE</i> , 2020, 15, e0236483.	1.1	4
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5007	Improved Reference Genome Uncovers Novel Sex-Linked Regions in the Guppy (<i>Poecilia reticulata</i>). <i>Genome Biology and Evolution</i> , 2020, 12, 1789-1805.	1.1	36
5008	The SDHB Arg230His mutation causing familial paraganglioma alters glycolysis in a new <i>Caenorhabditis elegans</i> model. <i>DMM Disease Models and Mechanisms</i> , 2020, 13, .	1.2	7
5009	Epimutations driven by small RNAs arise frequently but most have limited duration in <i>Caenorhabditis elegans</i> . <i>Nature Ecology and Evolution</i> , 2020, 4, 1539-1548.	3.4	33
5010	Alteration of genome folding via contact domain boundary insertion. <i>Nature Genetics</i> , 2020, 52, 1076-1087.	9.4	35
5011	ddRAD Sequencing-Based Identification of Genomic Boundaries and Permeability in <i>Quercus ilex</i> and <i>Q. suber</i> Hybrids. <i>Frontiers in Plant Science</i> , 2020, 11, 564414.	1.7	19
5012	Multi-Omics Investigation of Innate Navitoclax Resistance in Triple-Negative Breast Cancer Cells. <i>Cancers</i> , 2020, 12, 2551.	1.7	12
5013	NSD1-deposited H3K36me2 directs de novo methylation in the mouse male germline and counteracts Polycomb-associated silencing. <i>Nature Genetics</i> , 2020, 52, 1088-1098.	9.4	96
5014	Kinship analysis on single cells after whole genome amplification. <i>Scientific Reports</i> , 2020, 10, 14647.	1.6	6
5015	Interactions between genetics and environment shape <i>Camelina</i> seed oil composition. <i>BMC Plant Biology</i> , 2020, 20, 423.	1.6	22
5016	Characterization of Differentially Expressed miRNAs and Their Predicted Target Transcripts during Smoltification and Adaptation to Seawater in Head Kidney of Atlantic Salmon. <i>Genes</i> , 2020, 11, 1059.	1.0	12
5017	Sox17 Controls Emergence and Remodeling of Nestin-Expressing Coronary Vessels. <i>Circulation Research</i> , 2020, 127, e252-e270.	2.0	19

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5020	The impact of anthelmintic treatment on gut bacterial and fungal communities in diagnosed parasite-free sika deer <i>Cervus nippon</i> . <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 9239-9250.	1.7	11
5021	Marine Sediments Hold an Untapped Potential for Novel Taxonomic and Bioactive Bacterial Diversity. <i>MSystems</i> , 2020, 5, .	1.7	24
5022	Reprogramming roadmap reveals route to human induced trophoblast stem cells. <i>Nature</i> , 2020, 586, 101-107.	13.7	131
5023	Metagenome analysis using serum extracellular vesicles identified distinct microbiota in asthmatics. <i>Scientific Reports</i> , 2020, 10, 15125.	1.6	20
5024	Grad-seq shines light on unrecognized RNA and protein complexes in the model bacterium <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2020, 48, 9301-9319.	6.5	30
5025	Overproduction of the AlgT Sigma Factor Is Lethal to Mucoid <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2020, 202, .	1.0	4
5026	Chromatin remodeling in bovine embryos indicates species-specific regulation of genome activation. <i>Nature Communications</i> , 2020, 11, 4654.	5.8	53
5027	Integration of absolute multi-omics reveals dynamic protein-to-RNA ratios and metabolic interplay within mixed-domain microbiomes. <i>Nature Communications</i> , 2020, 11, 4708.	5.8	28
5028	Epigenetic silencing of clustered tRNA genes in <i>Arabidopsis</i> . <i>Nucleic Acids Research</i> , 2020, 48, 10297-10312.	6.5	12
5029	RELATe enables genome-scale engineering in fungal genomics. <i>Science Advances</i> , 2020, 6, .	4.7	6
5030	Transcriptome profiling at osmotic and ionic phases of salt stress response in bread wheat uncovers trait-specific candidate genes. <i>BMC Plant Biology</i> , 2020, 20, 428.	1.6	16
5031	A total crapshoot? Evaluating bioinformatic decisions in animal diet metabarcoding analyses. <i>Ecology and Evolution</i> , 2020, 10, 9721-9739.	0.8	40
5032	Bacterial Diversity in the Rhizosphere of <i>Anabasis aphylla</i> in the Gurbantunggut Desert, China. <i>Current Microbiology</i> , 2020, 77, 3750-3759.	1.0	7
5033	Insufficiently complex unique-molecular identifiers (UMIs) distort small RNA sequencing. <i>Scientific Reports</i> , 2020, 10, 14593.	1.6	9
5034	Comparative study of preimplantation development following distinct assisted oocyte activation protocols in a PLC-zeta knockout mouse model. <i>Molecular Human Reproduction</i> , 2020, 26, 801-815.	1.3	11
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5037	Digging into the Genomic Past of Swiss Honey Bees by Whole-Genome Sequencing Museum Specimens. <i>Genome Biology and Evolution</i> , 2020, 12, 2535-2551.	1.1	26
5038	Hi-C chromosome conformation capture sequencing of avian genomes using the BGISEQ-500 platform. <i>GigaScience</i> , 2020, 9, .	3.3	6
5039	Transcriptome Dynamics of the Inflorescence in Reciprocally Formed Allopolyploid <i>Tragopogon miscellus</i> (Asteraceae). <i>Frontiers in Genetics</i> , 2020, 11, 888.	1.1	26
5040	Discovering the indigenous microbial communities associated with the natural fermentation of sap from the cider gum <i>Eucalyptus gunnii</i> . <i>Scientific Reports</i> , 2020, 10, 14716.	1.6	13
5041	Human norovirus exhibits strain-specific sensitivity to host interferon pathways in human intestinal enteroids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23782-23793.	3.3	63
5042	Prebiotics and Community Composition Influence Gas Production of the Human Gut Microbiota. <i>MBio</i> , 2020, 11, .	1.8	23
5043	First Cryo-Scanning Electron Microscopy Images and X-Ray Microanalyses of Mucoromycotinian Fine Root Endophytes in Vascular Plants. <i>Frontiers in Microbiology</i> , 2020, 11, 2018.	1.5	16
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5045	Transgenerational inheritance of impaired larval T cell development in zebrafish. <i>Nature Communications</i> , 2020, 11, 4505.	5.8	15
5046	Microbiome Patterns in Matched Bile, Duodenal, Pancreatic Tumor Tissue, Drainage, and Stool Samples: Association with Preoperative Stenting and Postoperative Pancreatic Fistula Development. <i>Journal of Clinical Medicine</i> , 2020, 9, 2785.	1.0	16
5047	Soil potassium is correlated with root secondary metabolites and root-associated core bacteria in licorice of different ages. <i>Plant and Soil</i> , 2020, 456, 61-79.	1.8	33
5048	Parallel analysis of miRNAs and mRNAs suggests distinct regulatory networks in <i>Crassostrea gigas</i> infected by <i>Ostreid herpesvirus 1</i> . <i>BMC Genomics</i> , 2020, 21, 620.	1.2	12
5049	A genomeâ€scale CRISPR knockâ€out screen in chronic myeloid leukemia identifies novel drug resistance mechanisms along with intrinsic apoptosis and MAPK signaling. <i>Cancer Medicine</i> , 2020, 9, 6739-6751.	1.3	6
5050	910 metagenome-assembled genomes from the phytobiomes of three urban-farmed leafy Asian greens. <i>Scientific Data</i> , 2020, 7, 278.	2.4	17
5051	Generation of a chromosome-scale genome assembly of the insect-repellent terpenoid-producing Lamiaceae species, <i>Callicarpa americana</i> . <i>GigaScience</i> , 2020, 9, .	3.3	21
5052	Alterations of Rice (<i>Oryza sativa</i> L.) DNA Methylation Patterns Associated with Gene Expression in Response to Rice Black Streaked Dwarf Virus. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5753.	1.8	6
5053	DNA damage triggers reprogramming of differentiated cells into stem cells in <i>Physcomitrella</i> . <i>Nature Plants</i> , 2020, 6, 1098-1105.	4.7	22

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5055	Assessment of stream macroinvertebrate communities with eDNA is not congruent with tissue-based metabarcoding. <i>Molecular Ecology</i> , 2021, 30, 3239-3251.	2.0	38
5056	3'UTR + RIP defines differential Staufen1 binding to alternative 3'UTR isoforms and reveals structures and sequence motifs influencing binding and polysome association. <i>Rna</i> , 2020, 26, 1621-1636.	1.6	8
5057	Chromosome-Scale Assembly of the Bread Wheat Genome Reveals Thousands of Additional Gene Copies. <i>Genetics</i> , 2020, 216, 599-608.	1.2	34
5058	Alternatively Spliced BnaPAP2.A7 Isoforms Play Opposing Roles in Anthocyanin Biosynthesis of <i>Brassica napus</i> L. <i>Frontiers in Plant Science</i> , 2020, 11, 983.	1.7	23
5059	Caveolin1 and YAP drive mechanically induced mesothelial to mesenchymal transition and fibrosis. <i>Cell Death and Disease</i> , 2020, 11, 647.	2.7	39
5060	SPOCD1 is an essential executor of piRNA-directed de novo DNA methylation. <i>Nature</i> , 2020, 584, 635-639.	13.7	96
5061	Principles of mRNA control by human PUM proteins elucidated from multimodal experiments and integrative data analysis. <i>Rna</i> , 2020, 26, 1680-1703.	1.6	14
5062	Dead cells release a necrosignal that activates antibiotic survival pathways in bacterial swarms. <i>Nature Communications</i> , 2020, 11, 4157.	5.8	48
5063	NusG controls transcription pausing and RNA polymerase translocation throughout the <i>Bacillus subtilis</i> genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21628-21636.	3.3	38
5064	A specific combination of dual index adaptors decreases the sensitivity of amplicon sequencing with the Illumina platform. <i>DNA Research</i> , 2020, 27, .	1.5	0
5065	METTL4 catalyzes m6Am methylation in U2 snRNA to regulate pre-mRNA splicing. <i>Nucleic Acids Research</i> , 2020, 48, 9250-9261.	6.5	60
5066	Distinct oxygen environments shape picoeukaryote assemblages thriving oxygen minimum zone waters off central Chile. <i>Journal of Plankton Research</i> , 2020, 42, 514-529.	0.8	13
5067	Clinical implications of prospective genomic profiling of metastatic breast cancer patients. <i>Breast Cancer Research</i> , 2020, 22, 91.	2.2	32
5068	DiMSum: an error model and pipeline for analyzing deep mutational scanning data and diagnosing common experimental pathologies. <i>Genome Biology</i> , 2020, 21, 207.	3.8	39
5069	Comprehensive Fungal Community Analysis of House Dust Using Next-Generation Sequencing. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 5842.	1.2	8
5070	Lactobacillus Mucosae Strain Promoted by a High-Fiber Diet in Genetic Obese Child Alleviates Lipid Metabolism and Modifies Gut Microbiota in ApoE-/- Mice on a Western Diet. <i>Microorganisms</i> , 2020, 8, 1225.	1.6	22
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5074	Identification of Essential Genes and Fluconazole Susceptibility Genes in <i>Candida glabrata</i> by Profiling Hermes Transposon Insertions. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3859-3870.	0.8	27
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5076	DNA polymerase stalling at structured DNA constrains the expansion of short tandem repeats. <i>Genome Biology</i> , 2020, 21, 209.	3.8	40
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5643	Populations of the Parasitic Plant <i>Phelipanche ramosa</i> Influence Their Seed Microbiota. <i>Frontiers in Plant Science</i> , 2020, 11, 1075.	1.7	25
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5765	Rocaglates Induce Gain-of-Function Alterations to eIF4A and eIF4F. <i>Cell Reports</i> , 2020, 30, 2481-2488.e5.	2.9	48
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5779	Draft genome sequence data of <i>Bacillus subtilis</i> strain 9407, isolated from healthy apples in China. <i>Data in Brief</i> , 2020, 29, 105143.	0.5	1
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6211	Population structure, inbreeding and stripe pattern abnormalities in plains zebras. <i>Molecular Ecology</i> , 2021, 30, 379-390.	2.0	17
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6220	Differential requirement of MED14/17 recruitment for activation of heat inducible genes. <i>New Phytologist</i> , 2021, 229, 3360-3376.	3.5	10
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6324	Cross-resistance of cisplatin selected cells to anti-microtubule agents: Role of general survival mechanisms. <i>Translational Oncology</i> , 2021, 14, 100917.	1.7	8
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6336	Long-term liming promotes drastic changes in the composition of the microbial community in a tropical savanna soil. <i>Biology and Fertility of Soils</i> , 2021, 57, 31-46.	2.3	10
6337	OGRE: Overlap Graph-based metagenomic Read clustEring. <i>Bioinformatics</i> , 2021, 37, 905-912.	1.8	6
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6341	Deconstructing Stepwise Fate Conversion of Human Fibroblasts to Neurons by MicroRNAs. <i>Cell Stem Cell</i> , 2021, 28, 127-140.e9.	5.2	39
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6348	Stochastic processes shape the biogeographic variations in core bacterial communities between aerial and belowground compartments of common bean. <i>Environmental Microbiology</i> , 2021, 23, 949-964.	1.8	25
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6354	Metagenomics Approaches to Investigate the Gut Microbiome of COVID-19 Patients. <i>Bioinformatics and Biology Insights</i> , 2021, 15, 117793222199942.	1.0	8
6355	Loss of <i>XIST</i> Impairs Human Mammary Stem Cell Differentiation and Increases Tumorigenicity Through Enhancer and Mediator Complex Hyperactivation. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
6356	Metagenomic Assembly: Reconstructing Genomes from Metagenomes. <i>Methods in Molecular Biology</i> , 2021, 2242, 139-152.	0.4	1
6357	Whole genome analysis unveils genetic diversity and potential virulence determinants in <i>Vibrio parahaemolyticus</i> associated with disease outbreak among cultured <i>Litopenaeus vannamei</i> (Pacific white shrimp) in India. <i>Virulence</i> , 2021, 12, 1936-1949.	1.8	15
6358	Systemic viral spreading and defective host responses are associated with fatal Lassa fever in macaques. <i>Communications Biology</i> , 2021, 4, 27.	2.0	19
6359	Transcriptional response of <i>Aspergillus fumigatus</i> to copper and the role of the Cu chaperones. <i>Virulence</i> , 2021, 12, 2186-2200.	1.8	6
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7017	The gut microbiota composition of <i>Trichoplusia ni</i> is altered by diet and may influence its polyphagous behavior. <i>Scientific Reports</i> , 2021, 11, 5786.	1.6	19
7019	Disproportionate CH ₄ Sink Strength from an Endemic, Sub-Alpine Australian Soil Microbial Community. <i>Microorganisms</i> , 2021, 9, 606.	1.6	1
7020	RNA-seq and GSEA identifies suppression of ligand-gated chloride efflux channels as the major gene pathway contributing to form deprivation myopia. <i>Scientific Reports</i> , 2021, 11, 5280.	1.6	14
7021	Vegetative cells may perform nitrogen fixation function under nitrogen deprivation in <i>Anabaena</i> sp. strain PCC 7120 based on genome-wide differential expression analysis. <i>PLoS ONE</i> , 2021, 16, e0248155.	1.1	5
7022	Whole-Genome Enrichment and Sequencing of <i>Chlamydia trachomatis</i> Directly from Patient Clinical Vaginal and Rectal Swabs. <i>MSphere</i> , 2021, 6, .	1.3	9
7023	DNA Metabarcoding Reveals Broad Presence of Plant Pathogenic Oomycetes in Soil From Internationally Traded Plants. <i>Frontiers in Microbiology</i> , 2021, 12, 637068.	1.5	11
7026	The <i>Mitragyna speciosa</i> (Kratom) Genome: a resource for data-mining potent pharmaceuticals that impact human health. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	19
7027	Composition and diversity of bacterial communities in the rhizosphere of the Chinese medicinal herb <i>Dendrobium</i> . <i>BMC Plant Biology</i> , 2021, 21, 127.	1.6	36
7028	Allopatric Plant Pathogen Population Divergence following Disease Emergence. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	14
7029	Lake Ecosystem Robustness and Resilience Inferred from a Climate-Stressed Protistan Plankton Network. <i>Microorganisms</i> , 2021, 9, 549.	1.6	17
7030	Wheat Pm4 resistance to powdery mildew is controlled by alternative splice variants encoding chimeric proteins. <i>Nature Plants</i> , 2021, 7, 327-341.	4.7	85
7031	Identification of m6A-Associated RNA Binding Proteins Using an Integrative Computational Framework. <i>Frontiers in Genetics</i> , 2021, 12, 625797.	1.1	4
7032	Regulation of endoplasmic reticulum stress and trophectoderm lineage specification by the mevalonate pathway in the mouse preimplantation embryo. <i>Molecular Human Reproduction</i> , 2021, 27, .	1.3	4
7033	Analysis of a Methanogen and an Actinobacterium Dominating the Thermophilic Microbial Community of an Electromethanogenic Biocathode. <i>Archaea</i> , 2021, 2021, 1-13.	2.3	4
7034	Stress resets ancestral heritable small RNA responses. <i>ELife</i> , 2021, 10, .	2.8	60
7035	Thermal adaptation rather than demographic history drives genetic structure inferred by copy number variants in a marine fish. <i>Molecular Ecology</i> , 2021, 30, 1624-1641.	2.0	19
7036	ODC (Ornithine Decarboxylase)-Dependent Putrescine Synthesis Maintains MerTK (MER) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 <i>Biology</i> , 2021, 41, e144-e159.	1.1	23

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7039	Genomic signatures of divergent selection are associated with social behaviour for spinner dolphin ecotypes. <i>Molecular Ecology</i> , 2021, 30, 1993-2008.	2.0	6
7040	Complete Genome Sequence of <i>Staphylococcus epidermidis</i> PH1-28, Isolated from the Forehead of a Hyperseborrheic Donor. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1
7041	Integrated miRNA-Seq and mRNA-Seq Study to Identify miRNAs Associated With Alzheimer's Disease Using Post-mortem Brain Tissue Samples. <i>Frontiers in Neuroscience</i> , 2021, 15, 620899.	1.4	22
7042	Altered metabolic and inflammatory transcriptomics after cardiac surgery in neonates with congenital heart disease. <i>Scientific Reports</i> , 2021, 11, 4965.	1.6	3
7043	Local prey shortages drive foraging costs and breeding success in a declining seabird, the Atlantic puffin. <i>Journal of Animal Ecology</i> , 2021, 90, 1152-1164.	1.3	30
7044	Hypoxia-inducible factor-dependent induction of myeloid-derived netrin-1 attenuates natural killer cell infiltration during endotoxin-induced lung injury. <i>FASEB Journal</i> , 2021, 35, e21334.	0.2	15
7045	Gene expression for secondary metabolite biosynthesis in hop (<i>Humulus lupulus</i> L.) leaf lupulin glands exposed to heat and low-water stress. <i>Scientific Reports</i> , 2021, 11, 5138.	1.6	16
7046	The TOR-EIN2 axis mediates nuclear signalling to modulate plant growth. <i>Nature</i> , 2021, 591, 288-292.	13.7	70
7047	aniFOUND: analysing the associated proteome and genomic landscape of the repaired nascent non-replicative chromatin. <i>Nucleic Acids Research</i> , 2021, 49, e64-e64.	6.5	5
7049	MEF2 (Myocyte Enhancer Factor 2) Is Essential for Endothelial Homeostasis and the Atheroprotective Gene Expression Program. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2021, 41, 1105-1123.	1.1	27
7050	Lung virome: New potential biomarkers for asthma severity and exacerbation. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 148, 1007-1015.e9.	1.5	30
7051	Leaf-associated fungal and viral communities of wild plant populations differ between cultivated and natural ecosystems. <i>Plant-Environment Interactions</i> , 2021, 2, 87-99.	0.7	14
7052	Molecular characterization of DICER1-mutated pituitary blastoma. <i>Acta Neuropathologica</i> , 2021, 141, 929-944.	3.9	11
7053	Germline inherited small RNAs facilitate the clearance of untranslated maternal mRNAs in <i>C. elegans</i> embryos. <i>Nature Communications</i> , 2021, 12, 1441.	5.8	29
7054	Dbx2 regulation in limbs suggests inter-TAD sharing of enhancers. <i>Developmental Dynamics</i> , 2021, 250, 1280-1299.	0.8	14
7055	Exploring the Use of Environmental DNA (eDNA) to Detect Animal Taxa in the Mesopelagic Zone. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	29
7056	Glacier clear ice bands indicate englacial channel microbial distribution. <i>Journal of Glaciology</i> , 2021, 67, 811-823.	1.1	1

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7057	Allium Extract Implements Weaned Piglet's Productive Parameters by Modulating Distal Gut Microbiota. <i>Antibiotics</i> , 2021, 10, 269.	1.5	14
7058	HOXBLOC long non-coding RNA activation promotes leukemogenesis in NPM1-mutant acute myeloid leukemia. <i>Nature Communications</i> , 2021, 12, 1956.	5.8	28
7059	Connecting structure to function with the recovery of over 1000 high-quality metagenome-assembled genomes from activated sludge using long-read sequencing. <i>Nature Communications</i> , 2021, 12, 2009.	5.8	177
7060	Testing small-scale ecological gradients and intraspecific differentiation for hundreds of kelp forest species using haplotypes from metabarcoding. <i>Molecular Ecology</i> , 2021, 30, 3355-3373.	2.0	19
7061	Improved Microbial Community Characterization of 16S rRNA via Metagenome Hybridization Capture Enrichment. <i>Frontiers in Microbiology</i> , 2021, 12, 644662.	1.5	23
7062	Aureoverticillactam, a potent antifungal macrocyclic lactam from <i>Streptomyces aureoverticillatus</i> NH6, generates calcium dyshomeostasis induced cell apoptosis via the phospholipase C pathway in <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> race 4. <i>Phytopathology</i> , 2021, , PHYTO12200543R.	1.1	2
7063	Hypoxia-Driven HIF-1 α Activation Reprograms Pre-Activated NK Cells towards Highly Potent Effector Phenotypes via ERK/STAT3 Pathways. <i>Cancers</i> , 2021, 13, 1904.	1.7	20
7064	Genomic Resources for <i>Erysimum</i> spp. (Brassicaceae): Transcriptome and Chloroplast Genomes. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	5
7065	The transcriptional landscape of a hepatoma cell line grown on scaffolds of extracellular matrix proteins. <i>BMC Genomics</i> , 2021, 22, 238.	1.2	0
7066	Identification and Characterization of Osmoregulation Related MicroRNAs in Gills of Hybrid Tilapia Under Three Types of Osmotic Stress. <i>Frontiers in Genetics</i> , 2021, 12, 526277.	1.1	2
7068	Succession of endophytic fungi and arbuscular mycorrhizal fungi associated with the growth of plant and their correlation with secondary metabolites in the roots of plants. <i>BMC Plant Biology</i> , 2021, 21, 165.	1.6	26
7069	Small Conductance Ca ²⁺ -Activated K ⁺ (SK) Channel mRNA Expression in Human Atrial and Ventricular Tissue: Comparison Between Donor, Atrial Fibrillation and Heart Failure Tissue. <i>Frontiers in Physiology</i> , 2021, 12, 650964.	1.3	27
7070	Repulsive Guidance Molecule b Deficiency Induces Gut Microbiota Dysbiosis and Increases the Susceptibility to Intestinal Inflammation in Mice. <i>Frontiers in Microbiology</i> , 2021, 12, 648915.	1.5	12
7072	Next-Generation Sequencing Identification and Characterization of MicroRNAs in Dwarfed Citrus Trees Infected With Citrus Dwarfing Viroid in High-Density Plantings. <i>Frontiers in Microbiology</i> , 2021, 12, 646273.	1.5	8
7073	Impact of Chronic Exposure to Sublethal Doses of Glyphosate on Honey Bee Immunity, Gut Microbiota and Infection by Pathogens. <i>Microorganisms</i> , 2021, 9, 845.	1.6	35
7074	Multi-omic analyses in Abyssinian cats with primary renal amyloid deposits. <i>Scientific Reports</i> , 2021, 11, 8339.	1.6	6
7075	Rootstocks Shape Their Microbiome's Bacterial Communities in the Rhizosphere of Different Grapevine Rootstocks. <i>Microorganisms</i> , 2021, 9, 822.	1.6	18
7076	Population genomic evidence of <i>Plasmodium vivax</i> Southeast Asian origin. <i>Science Advances</i> , 2021, 7, .	4.7	21

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7078	Leukemic extracellular vesicles induce chimeric antigen receptor T cell dysfunction in chronic lymphocytic leukemia. <i>Molecular Therapy</i> , 2021, 29, 1529-1540.	3.7	43
7079	Monitoring and contamination incidence of gnotobiotic experiments performed in microisolator cages. <i>International Journal of Medical Microbiology</i> , 2021, 311, 151482.	1.5	8
7081	Selective antisense oligonucleotide inhibition of human IRF4 prevents malignant myeloma regeneration via cell cycle disruption. <i>Cell Stem Cell</i> , 2021, 28, 623-636.e9.	5.2	29
7082	An early cell shape transition drives evolutionary expansion of the human forebrain. <i>Cell</i> , 2021, 184, 2084-2102.e19.	13.5	139
7083	Slow Protein Turnover Explains Limited Protein-Level Response to Diurnal Transcriptional Oscillations in Cyanobacteria. <i>Frontiers in Microbiology</i> , 2021, 12, 657379.	1.5	13
7084	The gut microbiome composition and degradation enzymes activity of black Amur bream (<i>Megalobrama terminalis</i>) in response to breeding migratory behavior. <i>Ecology and Evolution</i> , 2021, 11, 5150-5163.	0.8	11
7085	Disruption of the MSL complex inhibits tumour maintenance by exacerbating chromosomal instability. <i>Nature Cell Biology</i> , 2021, 23, 401-412.	4.6	13
7086	Digging into bivalve miRNomes: between conservation and innovation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200165.	1.8	16
7087	Genome-wide analysis of plant miRNA action clarifies levels of regulatory dynamics across developmental contexts. <i>Genome Research</i> , 2021, 31, 811-822.	2.4	16
7088	Taxonomy of the Apicomplexan Symbionts of Coral, including Coralicolida ord. nov., Reassignment of the Genus <i>Gemmocystis</i> , and Description of New Species <i>Coralicola aquarius</i> gen. nov. sp. nov. and <i>Anthozoaphila gnarlus</i> gen. nov. sp. nov.. <i>Journal of Eukaryotic Microbiology</i> , 2021, 68, e12852.	0.8	9
7090	A step towards the validation of bacteria biotic indices using DNA metabarcoding for benthic monitoring. <i>Molecular Ecology Resources</i> , 2021, 21, 1889-1903.	2.2	15
7091	Skeletal muscle transcriptome in healthy aging. <i>Nature Communications</i> , 2021, 12, 2014.	5.8	56
7092	H2AK119ub1 guides maternal inheritance and zygotic deposition of H3K27me3 in mouse embryos. <i>Nature Genetics</i> , 2021, 53, 539-550.	9.4	77
7093	High-throughput sequencing clarifies the spatial structures of microbial communities in cadmium-polluted rice soils. <i>Environmental Science and Pollution Research</i> , 2021, 28, 47086-47098.	2.7	13
7094	Fast lightweight accurate xenograft sorting. <i>Algorithms for Molecular Biology</i> , 2021, 16, 2.	0.3	9
7095	Evolution of rumen and oral microbiota in calves is influenced by age and time of weaning. <i>Animal Microbiome</i> , 2021, 3, 31.	1.5	20
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7098	Negative elongation factor regulates muscle progenitor expansion for efficient myofiber repair and stem cell pool repopulation. <i>Developmental Cell</i> , 2021, 56, 1014-1029.e7.	3.1	18
7099	The structure, function and evolution of a complete human chromosome 8. <i>Nature</i> , 2021, 593, 101-107.	13.7	221
7100	Glioblastomas acquire myeloid-affiliated transcriptional programs via epigenetic immunoeediting to elicit immune evasion. <i>Cell</i> , 2021, 184, 2454-2470.e26.	13.5	165
7101	Soluble ACE2-mediated cell entry of SARS-CoV-2 via interaction with proteins related to the renin-angiotensin system. <i>Cell</i> , 2021, 184, 2212-2228.e12.	13.5	216
7102	Whole-Genome Sequence of <i>Avian coronavirus</i> from a 15-Year-Old Sample Confirms Evidence of GA08-like Strain Circulation 4 Years Prior to Its First Reported Outbreak. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1
7103	Mouse Retinal Organoid Growth and Maintenance in Longer-Term Culture. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 645704.	1.8	13
7104	The long non-coding RNA MIR31HG regulates the senescence associated secretory phenotype. <i>Nature Communications</i> , 2021, 12, 2459.	5.8	27
7105	Gene Expression Profiling of <i>Pseudomonas aeruginosa</i> Upon Exposure to Colistin and Tobramycin. <i>Frontiers in Microbiology</i> , 2021, 12, 626715.	1.5	16
7106	Draft Genome Sequences of <i>Pseudomonas syringae</i> pv. tomato Strains J4 and J6, Isolated in Florida. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
7107	CaptureSeq: Hybridization-Based Enrichment of cpn60 Gene Fragments Reveals the Community Structures of Synthetic and Natural Microbial Ecosystems. <i>Microorganisms</i> , 2021, 9, 816.	1.6	8
7108	Comparison of Deep-Sea Picoeukaryotic Composition Estimated from the V4 and V9 Regions of 18S rRNA Gene with a Focus on the Hadal Zone of the Mariana Trench. <i>Microbial Ecology</i> , 2022, 83, 34-47.	1.4	5
7109	Dysbiosis and Intestinal Barrier Dysfunction in Pediatric Congenital Heart Disease Is Exacerbated Following Cardiopulmonary Bypass. <i>JACC Basic To Translational Science</i> , 2021, 6, 311-327.	1.9	18
7110	The complete genome sequence of <i>Listeria monocytogenes</i> strain S2542 and expression of selected genes under high-pressure processing. <i>BMC Research Notes</i> , 2021, 14, 137.	0.6	1
7111	The Influence of Diet Change and Oral Metformin on Blood Glucose Regulation and the Fecal Microbiota of Healthy Horses. <i>Animals</i> , 2021, 11, 976.	1.0	5
7112	Beneficial Effect of Alkaloids From <i>Sophora alopecuroides</i> L. on CUMS-Induced Depression Model Mice via Modulating Gut Microbiota. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 665159.	1.8	19
7114	High Dose IFN- β Activates GAF to Enhance Expression of ISGF3 Target Genes in MLE12 Epithelial Cells. <i>Frontiers in Immunology</i> , 2021, 12, 651254.	2.2	5
7115	Translational Attenuation by an Intron Retention in the 5' UTR of ENAM Causes Amelogenesis Imperfecta. <i>Biomedicines</i> , 2021, 9, 456.	1.4	4

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7119	Identification of a Homozygous PEX26 Mutation in a Heimler Syndrome Patient. <i>Genes</i> , 2021, 12, 646.	1.0	5
7120	In vitro Fermentation Reveals Changes in Butyrate Production Dependent on Resistant Starch Source and Microbiome Composition. <i>Frontiers in Microbiology</i> , 2021, 12, 640253.	1.5	27
7122	Cellular mRNA triggers structural transformation of Ebola virus matrix protein VP40 to its essential regulatory form. <i>Cell Reports</i> , 2021, 35, 108986.	2.9	12
7123	Elevated rates of horizontal gene transfer in the industrialized human microbiome. <i>Cell</i> , 2021, 184, 2053-2067.e18.	13.5	167
7124	Bacterial Diversity in <i>Rhipicephalus sanguineus</i> (Acari: Ixodidae) from Two States in Nigeria. <i>Journal of Entomological Science</i> , 2021, 56, 256-271.	0.2	1
7125	<i>Vibrio parahaemolyticus</i> CadC regulates acid tolerance response to enhance bacterial motility and cytotoxicity. <i>Journal of Fish Diseases</i> , 2021, 44, 1155-1168.	0.9	7
7126	Exploring the Diversity of Fungal DyPs in Mangrove Soils to Produce and Characterize Novel Biocatalysts. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 321.	1.5	5
7127	Changes in Gut Microbiota Correlates with Response to Treatment with Probiotics in Patients with Atopic Dermatitis. A Post Hoc Analysis of a Clinical Trial. <i>Microorganisms</i> , 2021, 9, 854.	1.6	20
7128	MicroRNA-29 is an essential regulator of brain maturation through regulation of CH methylation. <i>Cell Reports</i> , 2021, 35, 108946.	2.9	25
7129	BET inhibition blocks inflammation-induced cardiac dysfunction and SARS-CoV-2 infection. <i>Cell</i> , 2021, 184, 2167-2182.e22.	13.5	131
7130	Genome-wide identification and analysis of long non-coding RNAs involved in fatty acid biosynthesis in young soybean pods. <i>Scientific Reports</i> , 2021, 11, 7603.	1.6	11
7131	Interactions Between Commensal Microbiota and Mucosal Immunity in Teleost Fish During Viral Infection With SVCV. <i>Frontiers in Immunology</i> , 2021, 12, 654758.	2.2	22
7132	Composition and temporal dynamics of sand-dwelling dinoflagellate communities from three Mediterranean beaches. <i>Aquatic Microbial Ecology</i> , 2021, 86, 85-98.	0.9	6
7133	Understanding the Shift in the Microbiome of Composts That Are Optimized for a Better Fit-for-Purpose in Growing Media. <i>Frontiers in Microbiology</i> , 2021, 12, 643679.	1.5	16
7134	The National Ecological Observatory Network's soil metagenomes: assembly and basic analysis. <i>F1000Research</i> , 0, 10, 299.	0.8	2
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7138	A compendium and comparative epigenomics analysis of cis-regulatory elements in the pig genome. Nature Communications, 2021, 12, 2217.	5.8	63
7139	The Microbiome of the Reef Macroalga Sargassum ilicifolium in Singapore. Microorganisms, 2021, 9, 898.	1.6	13
7141	OTUs and ASVs Produce Comparable Taxonomic and Diversity from Shrimp Microbiota 16S Profiles Using Tailored Abundance Filters. Genes, 2021, 12, 564.	1.0	23
7142	Genome-Wide Changes of Regulatory Non-Coding RNAs Reveal Pollen Development Initiated at Ecodormancy in Peach. Frontiers in Molecular Biosciences, 2021, 8, 612881.	1.6	10
7143	Massively Parallel Sequencing of 43 Arrhythmia Genes in a Selected SUDI Cohort from Cape Town. Journal of Pediatric Genetics, 2022, 11, 292-297.	0.3	1
7144	Bacterial community composition and functional potential associated with a variety of urban stormwater sources. Urban Ecosystems, 2021, 24, 1379.	1.1	1
7145	Global Analysis of RNA-Dependent RNA Polymerase-Dependent Small RNAs Reveals New Substrates and Functions for These Proteins and SCS3 in Arabidopsis. Non-coding RNA, 2021, 7, 28.	1.3	10
7146	Performance evaluation of pipelines for mapping, variant calling and interval padding, for the analysis of NGS germline panels. BMC Bioinformatics, 2021, 22, 218.	1.2	5
7147	Deep Insight Into Long Non-coding RNA and mRNA Transcriptome Profiling in HepG2 Cells Expressing Genotype IV Swine Hepatitis E Virus ORF3. Frontiers in Veterinary Science, 2021, 8, 625609.	0.9	1
7150	Ocean Acidification Induces Changes in Virus-Host Relationships in Mediterranean Benthic Ecosystems. Microorganisms, 2021, 9, 769.	1.6	10
7151	Transcriptome analysis of the liver of <i>Eospalax fontanierii</i> under hypoxia. PeerJ, 2021, 9, e11166.	0.9	3
7152	Targeting Cancer Stem Cells with Differentiation Agents as an Alternative to Genotoxic Chemotherapy for the Treatment of Malignant Testicular Germ Cell Tumors. Cancers, 2021, 13, 2045.	1.7	5
7153	Effects of Fermented Oat Straw as a Lovastatin Carrier on in vitro Methane Production and Rumen Microbiota. Frontiers in Energy Research, 2021, 9, .	1.2	7
7156	Foliar Aphid Herbivory Alters the Tomato Rhizosphere Microbiome, but Initial Soil Community Determines the Legacy Effects. Frontiers in Sustainable Food Systems, 2021, 5, .	1.8	13
7157	A total of 219 metagenome-assembled genomes of microorganisms from Icelandic marine waters. PeerJ, 2021, 9, e11112.	0.9	11
7158	Divergent Gene Expression Following Duplication of Meiotic Genes in the Stick Insect <i>Clitarchus hookeri</i> . Genome Biology and Evolution, 2021, 13, .	1.1	1

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7160	Chromatin conformation capture (Hi-C) sequencing of patient-derived xenografts: analysis guidelines. <i>GigaScience</i> , 2021, 10, .	3.3	6
7161	PU.1 enforces quiescence and limits hematopoietic stem cell expansion during inflammatory stress. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	49
7162	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
7163	Rare instances of haploid inducer DNA in potato dihaploids and ploidy-dependent genome instability. <i>Plant Cell</i> , 2021, 33, 2149-2163.	3.1	11
7164	Queuine Is a Nutritional Regulator of <i>Entamoeba histolytica</i> Response to Oxidative Stress and a Virulence Attenuator. <i>MBio</i> , 2021, 12, .	1.8	29
7166	ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework. <i>F1000Research</i> , 2021, 10, 103.	0.8	8
7167	Prediction of eye and hair pigmentation phenotypes using the HirisPlex system in a Brazilian admixed population sample. <i>International Journal of Legal Medicine</i> , 2021, 135, 1329-1339.	1.2	8
7168	Whole exome sequencing of a gut-associated lymphoid tissue neoplasm points to precursor or early form of sporadic colon carcinoma. <i>Pathology Research and Practice</i> , 2021, 220, 153406.	1.0	1
7169	Illumina Sequencing and Metabolomics Analysis Reveal Thiamine Modulation of Ruminal Microbiota and Metabolome Characteristics in Goats Fed a High-Concentrate Diet. <i>Frontiers in Microbiology</i> , 2021, 12, 653283.	1.5	16
7170	Transcriptome assembly dataset of anthelmintic response in <i>Fasciola hepatica</i> . <i>Data in Brief</i> , 2021, 35, 106808.	0.5	7
7171	<i>Brassica napus</i> phyllosphere bacterial composition changes with growth stage. <i>Plant and Soil</i> , 2021, 464, 501-516.	1.8	13
7172	Comparative genomics identifies thousands of candidate structured RNAs in human microbiomes. <i>Genome Biology</i> , 2021, 22, 100.	3.8	4
7173	Effects of hypoxia stress on the intestinal microflora of juvenile of cobia (<i>Rachycentron canadum</i>). <i>Aquaculture</i> , 2021, 536, 736419.	1.7	35
7174	High-resolution quantitative profiling of tRNA abundance and modification status in eukaryotes by mim-tRNAseq. <i>Molecular Cell</i> , 2021, 81, 1802-1815.e7.	4.5	115
7175	Targeted degradation of the enhancer lysine acetyltransferases CBP and p300. <i>Cell Chemical Biology</i> , 2021, 28, 503-514.e12.	2.5	80
7176	Comprehensive Analysis of Differential m6A RNA Methylomes in the Hippocampus of Cocaine-Conditioned Mice. <i>Molecular Neurobiology</i> , 2021, 58, 3759-3768.	1.9	8
7177	Targeted sequencing and integrative analysis to prioritize candidate genes in neurodevelopmental disorders. <i>Molecular Neurobiology</i> , 2021, 58, 3863-3873.	1.9	5

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7333	Rapid Parallel Adaptation to Anthropogenic Heavy Metal Pollution. <i>Molecular Biology and Evolution</i> , 2021, 38, 3724-3736.	3.5	19
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7336	Cell-specific transcriptional control of mitochondrial metabolism by TIF1 ^β drives erythropoiesis. <i>Science</i> , 2021, 372, 716-721.	6.0	25
7337	Elevated NK-cell transcriptional signature and dysbalance of resting and activated NK cells in atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 1959-1965.e2.	1.5	17
7338	<i>Nepenthes</i> <i>venetrata</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
7339	Unraveling the dietary diversity of Neotropical top predators using scat DNA metabarcoding: A case study on the elusive Giant Otter. <i>Environmental DNA</i> , 2021, 3, 889-900.	3.1	8
7340	Targeting novel LSD1-dependent ACE2 demethylation domains inhibits SARS-CoV-2 replication. <i>Cell Discovery</i> , 2021, 7, 37.	3.1	11
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7343	MIR-NATs repress MAPT translation and aid proteostasis in neurodegeneration. <i>Nature</i> , 2021, 594, 117-123.	13.7	29
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7347	Fetal meconium does not have a detectable microbiota before birth. <i>Nature Microbiology</i> , 2021, 6, 865-873.	5.9	95
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7354	16S rRNA Gene Amplicon Sequencing of Contaminated Coastal Sediment Collected from the Taehwa River Estuary, South Korea. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
7355	Next-Generation Sequencing to Detect Pathogens in Pediatric Febrile Neutropenia: A Single-Center Retrospective Study of 112 Cases. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofab223.	0.4	11
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7358	Urban wastewater bacterial communities assemble into seasonal steady states. <i>Microbiome</i> , 2021, 9, 116.	4.9	35
7360	Transcriptome Analysis of Tetraploid and Octoploid Common Reed (<i>Phragmites australis</i>). <i>Frontiers in Plant Science</i> , 2021, 12, 653183.	1.7	5
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7365	Early life stress in mice alters gut microbiota independent of maternal microbiota inheritance. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2021, 320, R663-R674.	0.9	17
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7367	Beyond taxonomy: Validating functional inference approaches in the context of fishâ€™farm impact assessments. <i>Molecular Ecology Resources</i> , 2021, 21, 2264-2277.	2.2	8
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7369	Desulfobacterales stimulates nitrate reduction in the mangrove ecosystem of a subtropical gulf. <i>Science of the Total Environment</i> , 2021, 769, 144562.	3.9	33
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7385	Effects of Monochromatic Lighting During Incubation and Vaccination on the Splenic Transcriptome Profiles of Chicken. <i>Frontiers in Genetics</i> , 2021, 12, 628041.	1.1	3
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7428	Transcriptome Profiling of Embryonic Retinal Pigment Epithelium Reprogramming. <i>Genes</i> , 2021, 12, 840.	1.0	9
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7430	The Impact of Intensive Fish Farming on Pond Sediment Microbiome and Antibiotic Resistance Gene Composition. <i>Frontiers in Veterinary Science</i> , 2021, 8, 673756.	0.9	19
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7443	A genetic screen for regulators of muscle morphogenesis in <i>Drosophila</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	3
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7465	Metagenomics: A viable tool for reconstructing herbivore diet. <i>Molecular Ecology Resources</i> , 2021, 21, 2249-2263.	2.2	16
7466	Concurrent X chromosome inactivation and upregulation during non-human primate preimplantation development revealed by single-cell RNA-sequencing. <i>Scientific Reports</i> , 2021, 11, 9624.	1.6	3
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7472	Minimized combinatorial CRISPR screens identify genetic interactions in autophagy. <i>Nucleic Acids Research</i> , 2021, 49, 5684-5704.	6.5	31
7473	Integrated genomic analysis reveals key features of long undecoded transcript isoform-based gene repression. <i>Molecular Cell</i> , 2021, 81, 2231-2245.e11.	4.5	20
7475	Metabarcoding Malaise traps and soil eDNA reveals seasonal and local arthropod diversity shifts. <i>Scientific Reports</i> , 2021, 11, 10498.	1.6	24
7476	Dadaist2: A Toolkit to Automate and Simplify Statistical Analysis and Plotting of Metabarcoding Experiments. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5309.	1.8	12
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7483	Transcriptomic and metabolomic characterization of post-hatch metabolic reprogramming during hepatic development in the chicken. <i>BMC Genomics</i> , 2021, 22, 380.	1.2	7
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7489	A primer on metagenomics and next-generation sequencing in fish gut microbiome research. <i>Aquaculture Research</i> , 2021, 52, 4574-4600.	0.9	12
7490	A chromosome-level genome of a Kordofan melon illuminates the origin of domesticated watermelons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	37
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7493	Gut microbiome contributions to altered metabolism in a pig model of undernutrition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	18
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7495	The tepary bean genome provides insight into evolution and domestication under heat stress. <i>Nature Communications</i> , 2021, 12, 2638.	5.8	43
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7497	Living in a Puddle of Mud: Isolation and Characterization of Two Novel Caulobacteraceae Strains <i>Brevundimonas pondensis</i> sp. nov. and <i>Brevundimonas goettingensis</i> sp. nov.. <i>Applied Microbiology</i> , 2021, 1, 38-59.	0.7	20
7498	Identification and characterization of novel microRNAs in disease-resistant and disease-susceptible <i>Penaeus monodon</i> . <i>Fish and Shellfish Immunology</i> , 2021, 119, 347-372.	1.6	1
7499	Convergence of the turkey gut microbiota following cohabitation under commercial settings. <i>Journal of Animal Science and Biotechnology</i> , 2021, 12, 59.	2.1	2
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7843	Virome comparison of deferred blood donations obtained from different geographic regions in the Sao Paulo State, Brazil. <i>Transfusion and Apheresis Science</i> , 2021, 60, 103106.	0.5	1
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7853	Greater extent of blood-tumor TCR repertoire overlap is associated with favorable clinical responses to PD-1 blockade. <i>Cancer Science</i> , 2021, 112, 2993-3004.	1.7	5
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7930	Changthangi Pashmina Goat Genome: Sequencing, Assembly, and Annotation. <i>Frontiers in Genetics</i> , 2021, 12, 695178.	1.1	0
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7970	Age-Related miRNA-Mediated Regulatory Networks Orchestrating Chronological Development of Meristems in <i>Larix Kaempferi</i> . <i>Journal of Plant Growth Regulation</i> , 2022, 41, 2305-2318.	2.8	2
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7984	Genomic Analysis of <i>Staphylococcus aureus</i> Isolates Associated With Peracute Non-gangrenous or Gangrenous Mastitis and Comparison With Other Mastitis-Associated <i>Staphylococcus aureus</i> Isolates. <i>Frontiers in Microbiology</i> , 2021, 12, 688819.	1.5	8
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7992	Transcriptome sequencing and drought resistance gene annotation in <i>Quercus liaotungensis</i> leaves. <i>Acta Physiologiae Plantarum</i> , 2021, 43, 1.	1.0	1
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7995	Deciphering <i>Trifolium pratense</i> L. holobiont reveals a microbiome resilient to future climate changes. <i>MicrobiologyOpen</i> , 2021, 10, e1217.	1.2	6
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8001	Identification of microRNAs and their target genes related to needle discoloration of evergreen tree Chinese cedar (<i>Cryptomeria fortunei</i>) in cold winters. <i>Planta</i> , 2021, 254, 31.	1.6	10
8002	Isolation and Characterization of Barley (<i>Hordeum vulgare</i>) Extracellular Vesicles to Assess Their Role in RNA Spray-Based Crop Protection. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7212.	1.8	9
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8004	An integrated functional and clinical genomics approach reveals genes driving aggressive metastatic prostate cancer. <i>Nature Communications</i> , 2021, 12, 4601.	5.8	18
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8015	Complete loss of H3K9 methylation dissolves mouse heterochromatin organization. <i>Nature Communications</i> , 2021, 12, 4359.	5.8	41
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8018	Population genomics reveals variable patterns of immune gene evolution in monarch butterflies (<i>Danaus plexippus</i>). <i>Molecular Ecology</i> , 2021, 30, 4381-4391.	2.0	4
8019	RNA demethylation increases the yield and biomass of rice and potato plants in field trials. <i>Nature Biotechnology</i> , 2021, 39, 1581-1588.	9.4	102
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8023	BANP opens chromatin and activates CpG-island-regulated genes. <i>Nature</i> , 2021, 596, 133-137.	13.7	49
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8026	The role of the PZP domain of AF10 in acute leukemia driven by AF10 translocations. <i>Nature Communications</i> , 2021, 12, 4130.	5.8	8
8027	HOME-BIO (sHOTgun METagenomic analysis of BIOlogical entities): a specific and comprehensive pipeline for metagenomic shotgun sequencing data analysis. <i>BMC Bioinformatics</i> , 2021, 22, 106.	1.2	9
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8029	Composition and Functions of the Gut Microbiome in Pediatric Obesity: Relationships with Markers of Insulin Resistance. <i>Microorganisms</i> , 2021, 9, 1490.	1.6	15
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8047	Changes in the transcript and protein profiles of <i>Quercus ilex</i> seedlings in response to drought stress. <i>Journal of Proteomics</i> , 2021, 243, 104263.	1.2	13
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8055	Reciprocal effect of temperature and dietary lipids on metabolic performance and gut microbiota of Yellowtail kingfish (<i>Seriola lalandi</i>) juveniles. <i>Aquaculture Research</i> , 2021, 52, 6189-6204.	0.9	3

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8062	Altered microRNA expression in COVID-19 patients enables identification of SARS-CoV-2 infection. <i>PLoS Pathogens</i> , 2021, 17, e1009759.	2.1	107
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8068	Effects of three probiotic strains (<i>Bacillus coagulans</i> , <i>B. licheniformis</i> and <i>Paenibacillus polymyxa</i>) on growth, immune response, gut morphology and microbiota, and resistance against <i>Vibrio harveyi</i> of northern whittings, <i>Sillago sihama</i> Forsskål (1775). <i>Animal Feed Science and Technology</i> , 2021, 277, 114958.	1.1	16
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8097	Genetic effects on liver chromatin accessibility identify disease regulatory variants. <i>American Journal of Human Genetics</i> , 2021, 108, 1169-1189.	2.6	22
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8114	Feeding sites promoting wildlife-related tourism might highly expose the endangered Yunnan snub-nosed monkey (<i>Rhinopithecus bieti</i>) to parasite transmission. <i>Scientific Reports</i> , 2021, 11, 15817.	1.6	5
8115	Fasting increases microbiome-based colonization resistance and reduces host inflammatory responses during an enteric bacterial infection. <i>PLoS Pathogens</i> , 2021, 17, e1009719.	2.1	14
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8117	Tree diversity and soil chemical properties drive the linkages between soil microbial community and ecosystem functioning. <i>ISME Communications</i> , 2021, 1, .	1.7	28
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8129	Draft Genome Sequence of the Mucin Degradator <i>Clostridium tertium</i> WC0709. <i>Microbiology Resource Announcements</i> , 2021, 10, e0064221.	0.3	1
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8140	Two distinct mechanisms of RNA polymerase II elongation stimulation in vivo. <i>Molecular Cell</i> , 2021, 81, 3096-3109.e8.	4.5	53
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8145	Genome-wide DNA polymorphisms of Citrus unshiu Marc. cv. Miyagawa-wase cultivated in different regions based on whole-genome re-sequencing. <i>Plant Biotechnology Reports</i> , 2021, 15, 551-559.	0.9	3
8146	Complete Genome Sequence of <i>Sphingobium xenophagum</i> PH3-15, Isolated from La Roche-Posay Thermal Water Sources. <i>Microbiology Resource Announcements</i> , 2021, 10, e0070021.	0.3	2
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8151	The human ribosomal DNA array is composed of highly homogenized tandem clusters. <i>Genome Research</i> , 2021, 31, 1971-1982.	2.4	33
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8160	A body map of somatic mutagenesis in morphologically normal human tissues. <i>Nature</i> , 2021, 597, 398-403.	13.7	107
8161	Chromosome-Level Genome Assembly of Chinese Sucker (<i>Myxocyprinus asiaticus</i>) Reveals Strongly Conserved Synteny Following a Catostomid-Specific Whole-Genome Duplication. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	12
8162	Construction of a Genetic Linkage Map Based on SNP Markers, QTL Mapping and Detection of Candidate Genes of Growth-Related Traits in Pacific Abalone Using Genotyping-by-Sequencing. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	5
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8165	Transcriptional epigenetic regulation of <i>Fkbp1/Pax9</i> genes is associated with impaired sensitivity to platinum treatment in ovarian cancer. <i>Clinical Epigenetics</i> , 2021, 13, 167.	1.8	7
8166	Elevated Systemic and Intestinal Inflammatory Response Are Associated With Gut Microbiome Disorder After Cardiovascular Surgery. <i>Frontiers in Microbiology</i> , 2021, 12, 686648.	1.5	9
8167	INFIMA leverages multi-omics model organism data to identify effector genes of human GWAS variants. <i>Genome Biology</i> , 2021, 22, 241.	3.8	3
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8171	Molecular analysis of the 2012 Bundibugyo virus disease outbreak. <i>Cell Reports Medicine</i> , 2021, 2, 100351.	3.3	4
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8177	Prebiotic, Probiotic, and Synbiotic Consumption Alter Behavioral Variables and Intestinal Permeability and Microbiota in BTBR Mice. <i>Microorganisms</i> , 2021, 9, 1833.	1.6	17
8178	<i>Lactobacillus fermentum</i> PS150 promotes non-rapid eye movement sleep in the first night effect of mice. <i>Scientific Reports</i> , 2021, 11, 16313.	1.6	8
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8213	Inhibition of YTHDF2 triggers proteotoxic cell death in MYC-driven breast cancer. <i>Molecular Cell</i> , 2021, 81, 3048-3064.e9.	4.5	86
8214	The MURAL collection of prostate cancer patient-derived xenografts enables discovery through preclinical models of uro-oncology. <i>Nature Communications</i> , 2021, 12, 5049.	5.8	33
8216	A novel mechanism of enhanced transcription activity and fidelity for influenza A viral RNA-dependent RNA polymerase. <i>Nucleic Acids Research</i> , 2021, 49, 8796-8810.	6.5	5
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8254	Gene expression shapes the patterns of parallel evolution of herbicide resistance in the agricultural weed <i>Monochoria vaginalis</i> . <i>New Phytologist</i> , 2021, 232, 928-940.	3.5	11
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8261	Molecular Pathogenesis and Peripheral Monitoring of Adult Fragile X-Associated Syndromes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8368.	1.8	6
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8274	CLAMP regulates zygotic genome activation in <i>Drosophila</i> embryos. <i>Genetics</i> , 2021, 219, .	1.2	10
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8278	Dynamics of Microbial Community During Nitrification Biofilter Acclimation with Low and High Ammonia. <i>Marine Biotechnology</i> , 2021, 23, 671-681.	1.1	4
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8282	Enhanced nitrogen removal and mitigation of nitrous oxide emission potential in a lab-scale rain garden with internal water storage. <i>Journal of Water Process Engineering</i> , 2021, 42, 102147.	2.6	17
8283	Comparative Genomic and Transcriptomic Analysis of <i>Naegleria fowleri</i> Clinical and Environmental Isolates. <i>MSphere</i> , 2021, 6, e0063721.	1.3	8
8284	Stool microbiome dataset of the critically endangered Puerto Rican parrot (<i>Amazona vittata</i>). <i>Data in Brief</i> , 2021, 37, 107175.	0.5	0
8286	The native cisrome and sequence motif families of the maize ear. <i>PLoS Genetics</i> , 2021, 17, e1009689.	1.5	19
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8290	Patrolling human SLE haematopoietic progenitors demonstrate enhanced extramedullary colonisation; implications for peripheral tissue injury. <i>Scientific Reports</i> , 2021, 11, 15759.	1.6	5
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8295	Bioengineered embryoids mimic post-implantation development in vitro. <i>Nature Communications</i> , 2021, 12, 5140.	5.8	35
8296	Spore-forming <i>Bacillus coagulans</i> SNZ 1969 improved intestinal motility and constipation perception mediated by microbial alterations in healthy adults with mild intermittent constipation: A randomized controlled trial. <i>Food Research International</i> , 2021, 146, 110428.	2.9	20
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8306	Analysis of m6A methylation in skin tissues of different sex Liaoning cashmere goats. <i>Animal Biotechnology</i> , 2021, , 1-11.	0.7	2
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8313	The Tomato <i>ddm1b</i> Mutant Shows Decreased Sensitivity to Heat Stress Accompanied by Transcriptional Alterations. <i>Genes</i> , 2021, 12, 1337.	1.0	5
8314	Acquisition of aneuploidy drives mutant p53-associated gain-of-function phenotypes. <i>Nature Communications</i> , 2021, 12, 5184.	5.8	30
8315	Evidence for the genetic similarity rule at an expanding mangrove range limit. <i>American Journal of Botany</i> , 2021, 108, 1331-1342.	0.8	2
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8318	The genetics and evolution of eye color in domestic pigeons (<i>Columba livia</i>). <i>PLoS Genetics</i> , 2021, 17, e1009770.	1.5	6
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8333	Soil arthropod communities are not affected by invasive <i>Solidago gigantea</i> Aiton (Asteraceae), based on morphology and metabarcoding analyses. <i>Soil Biology and Biochemistry</i> , 2021, 159, 108288.	4.2	7
8334	Characterizing parasitic nematode faunas in faeces and soil using DNA metabarcoding. <i>Parasites and Vectors</i> , 2021, 14, 422.	1.0	12
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8346	Genetic and physiological traits conferring tolerance to ocean acidification in mesophotic corals. <i>Global Change Biology</i> , 2021, 27, 5276-5294.	4.2	13
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8791	Draft genome analysis, poly-phasic study and lipid biosynthesis pathway of <i>Scenedesmus</i> sp. SVMIICT1. <i>Bioresource Technology</i> , 2021, 341, 125809.	4.8	4
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9502	Nanopore direct RNA sequencing maps the complexity of Arabidopsis mRNA processing and m6A modification. <i>ELife</i> , 2020, 9, .	2.8	312
9503	Compensatory sequence variation between trans-species small RNAs and their target sites. <i>ELife</i> , 2019, 8, .	2.8	27
9504	Coronary arterial development is regulated by a Dll4-Jag1-EphrinB2 signaling cascade. <i>ELife</i> , 2019, 8, .	2.8	27
9505	A curative combination cancer therapy achieves high fractional cell killing through low cross-resistance and drug additivity. <i>ELife</i> , 2019, 8, .	2.8	78
9506	Imp/IGF2BP levels modulate individual neural stem cell growth and division through myc mRNA stability. <i>ELife</i> , 2020, 9, .	2.8	57
9507	Rarity is a more reliable indicator of land-use impacts on soil invertebrate communities than other diversity metrics. <i>ELife</i> , 2020, 9, .	2.8	20

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9508	A complex regulatory landscape involved in the development of mammalian external genitals. <i>ELife</i> , 2020, 9, .	2.8	26
9509	Spn links RNA-mediated endogenous retrovirus silencing and X chromosome inactivation. <i>ELife</i> , 2020, 9, .	2.8	33
9510	Umbilical cord blood-derived ILC1-like cells constitute a novel precursor for mature KIR+NKG2A- NK cells. <i>ELife</i> , 2020, 9, .	2.8	25
9511	Genomic architecture and evolutionary antagonism drive allelic expression bias in the social supergene of red fire ants. <i>ELife</i> , 2020, 9, .	2.8	16
9512	DAZL mediates a broad translational program regulating expansion and differentiation of spermatogonial progenitors. <i>ELife</i> , 2020, 9, .	2.8	28
9513	A tudor domain protein, SIMR-1, promotes siRNA production at piRNA-targeted mRNAs in <i>C. elegans</i> . <i>ELife</i> , 2020, 9, .	2.8	45
9514	A molecular filter for the cnidarian stinging response. <i>ELife</i> , 2020, 9, .	2.8	18
9515	Isolation and transcriptomic analysis of <i>Anopheles gambiae</i> oenocytes enables the delineation of hydrocarbon biosynthesis. <i>ELife</i> , 2020, 9, .	2.8	20
9516	Mitochondrial fatty acid synthesis coordinates oxidative metabolism in mammalian mitochondria. <i>ELife</i> , 2020, 9, .	2.8	62
9517	Damage-responsive, maturity-silenced enhancers regulate multiple genes that direct regeneration in <i>Drosophila</i> . <i>ELife</i> , 2020, 9, .	2.8	41
9518	Manipulation of the human tRNA pool reveals distinct tRNA sets that act in cellular proliferation or cell cycle arrest. <i>ELife</i> , 2020, 9, .	2.8	21
9519	Gene autoregulation by 3' UTR-derived bacterial small RNAs. <i>ELife</i> , 2020, 9, .	2.8	41
9520	Recurrent evolution of high virulence in isolated populations of a DNA virus. <i>ELife</i> , 2020, 9, .	2.8	11
9521	Cell types and neuronal circuitry underlying female aggression in <i>Drosophila</i> . <i>ELife</i> , 2020, 9, .	2.8	62
9522	A rat epigenetic clock recapitulates phenotypic aging and co-localizes with heterochromatin. <i>ELife</i> , 2020, 9, .	2.8	36
9523	Clusters of polymorphic transmembrane genes control resistance to schistosomes in snail vectors. <i>ELife</i> , 2020, 9, .	2.8	18
9524	Odd-paired is a pioneer-like factor that coordinates with Zelda to control gene expression in embryos. <i>ELife</i> , 2020, 9, .	2.8	30
9525	High neural activity accelerates the decline of cognitive plasticity with age in <i>Caenorhabditis elegans</i> . <i>ELife</i> , 2020, 9, .	2.8	12

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9527	Molecular evidence of hybridization between pig and human <i>Ascaris</i> indicates an interbred species complex infecting humans. <i>ELife</i> , 2020, 9, .	2.8	42
9528	Phylogenomics of white-eyes, a "great speciator"™, reveals Indonesian archipelago as the center of lineage diversity. <i>ELife</i> , 2020, 9, .	2.8	17
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9530	Comparing sediment DNA extraction methods for assessing organic enrichment associated with marine aquaculture. <i>PeerJ</i> , 2020, 8, e10231.	0.9	27
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9534	Testing the potential of a ribosomal 16S marker for DNA metabarcoding of insects. <i>PeerJ</i> , 2016, 4, e1966.	0.9	111
9535	The PARA-suite: PAR-CLIP specific sequence read simulation and processing. <i>PeerJ</i> , 2016, 4, e2619.	0.9	8
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9537	Transcriptome analysis of <i>Polygonum minus</i> reveals candidate genes involved in important secondary metabolic pathways of phenylpropanoids and flavonoids. <i>PeerJ</i> , 2017, 5, e2938.	0.9	37
9538	Metagenomic identification of active methanogens and methanotrophs in serpentinite springs of the Voltri Massif, Italy. <i>PeerJ</i> , 2017, 5, e2945.	0.9	91
9539	Spatial distribution of environmental DNA in a nearshore marine habitat. <i>PeerJ</i> , 2017, 5, e3044.	0.9	138
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9541	Using high-throughput sequencing of ITS2 to describe <i>Symbiodinium</i> metacommunities in St. John, US Virgin Islands. <i>PeerJ</i> , 2017, 5, e3472.	0.9	88
9542	Short reads from honey bee (<i>Apis</i> sp.) sequencing projects reflect microbial associate diversity. <i>PeerJ</i> , 2017, 5, e3529.	0.9	13
9543	Atropos: specific, sensitive, and speedy trimming of sequencing reads. <i>PeerJ</i> , 2017, 5, e3720.	0.9	187

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9548	Viromes of one year old infants reveal the impact of birth mode on microbiome diversity. PeerJ, 2018, 6, e4694.	0.9	103
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10823	The Effects of Silkworm-Derived Polysaccharide (Silkrose) on Ectoparasitic Infestations in Yellowtail (<i>Seriola quinqueradiata</i>) and White Trevally (<i>Pseudocaranx dentex</i>). <i>Fishes</i> , 2022, 7, 14.	0.7	1
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10829	Integrated Population Genomic Analysis and Numerical Simulation to Estimate Larval Dispersal of <i>Acanthaster cf. solaris</i> Between Ogasawara and Other Japanese Regions. <i>Frontiers in Marine Science</i> , 2022, 8, .	1.2	7
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10834	Circular Chromosome Conformation Sequencing (4C-Seq) in. <i>Methods in Molecular Biology</i> , 2022, 2458, 301-320.	0.4	0
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10866	Oxidative pentose phosphate pathway controls vascular mural cell coverage by regulating extracellular matrix composition. <i>Nature Metabolism</i> , 2022, 4, 123-140.	5.1	10
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10869	Phytoplankton diversity and ecology through the lens of high throughput sequencing technologies. , 2022, , 353-413.		8
10870	An inherited night blindness in Wiltshire sheep. <i>Veterinary Pathology</i> , 2022, , 030098582110674.	0.8	0
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10883	Nfe2l2 Regulates Metabolic Rewiring and Epigenetic Reprogramming in Mediating Cancer Protective Effect by Fucoxanthin. <i>AAPS Journal</i> , 2022, 24, 30.	2.2	7
10884	Skin Microbiome in Patients with Hand Eczema and Healthy Controls: A Three-week Prospective Study. <i>Acta Dermato-Venereologica</i> , 2021, 102, adv00633.	0.6	3
10885	Development and validation of a RNAseq signature for prognostic stratification in endometrial cancer. <i>Gynecologic Oncology</i> , 2022, , .	0.6	5
10886	Construction of Aerobic/Anaerobic-Substrate-Induced Gene Expression Procedure for Exploration of Metagenomes From Subseafloor Sediments. <i>Frontiers in Microbiology</i> , 2021, 12, 726024.	1.5	0
10887	Intratumor Microbiome Analysis Identifies Positive Association Between Megasphaera and Survival of Chinese Patients With Pancreatic Ductal Adenocarcinomas. <i>Frontiers in Immunology</i> , 2022, 13, 785422.	2.2	25
10888	Microbiota of the Digestive Glands and Extrapallial Fluids of Clams Evolve Differently Over Time Depending on the Intertidal Position. <i>Microbial Ecology</i> , 2023, 85, 288-297.	1.4	4
10889	Gut microbiome alteration as a diagnostic tool and associated with inflammatory response marker in primary liver cancer. <i>Hepatology International</i> , 2022, 16, 99-111.	1.9	24
10890	DNA Metabarcoding from Microbial Communities Recovered from Stream and Its Potential for Bioremediation Processes. <i>Current Microbiology</i> , 2022, 79, 70.	1.0	3
10891	Draft Genome Sequences of <i>Lacticaseibacillus rhamnosus</i> cek-R1, <i>Lacticaseibacillus paracasei</i> cek-R2, and <i>Lentilactobacillus otakiensis</i> cek-R3, Isolated from a Beetroot Product. <i>Microbiology Resource Announcements</i> , 2022, 11, e0092121.	0.3	1
10892	Effect of Different Initial Fermentation pH on Exopolysaccharides Produced by <i>Pseudoalteromonas agarivorans</i> Hao 2018 and Identification of Key Genes Involved in Exopolysaccharide Synthesis via Transcriptome Analysis. <i>Marine Drugs</i> , 2022, 20, 89.	2.2	12
10893	Analysis and Performance Assessment of the Whole Genome Bisulfite Sequencing Data Workflow: Currently Available Tools and a Practical Guide to Advance DNA Methylation Studies. <i>Small Methods</i> , 2022, 6, e2101251.	4.6	10
10894	Managing human-mediated range shifts: understanding spatial, temporal and genetic variation in marine non-native species. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, 20210025.	1.8	8
10895	Means, motive and opportunity for biological invasions: Genetic introgression in a fungal pathogen. <i>Molecular Ecology</i> , 2023, 32, 2428-2442.	2.0	10
10896	Evaluating Antibody Mediated Protection against Alpha, Beta, and Delta SARS-CoV-2 Variants of Concern in K18-hACE2 Transgenic Mice. <i>Journal of Virology</i> , 2022, 96, jvi0218421.	1.5	14
10897	Multimodal regulatory elements within a hormone-specific super enhancer control a heterogeneous transcriptional response. <i>Molecular Cell</i> , 2022, 82, 803-815.e5.	4.5	14
10898	Role of key-stone microbial taxa in algae amended soil for mediating nitrogen transformation. <i>Science of the Total Environment</i> , 2022, 823, 153547.	3.9	6
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10901	Composition identification and functional verification of bacterial community in disease-suppressive soils by machine learning. <i>Environmental Microbiology</i> , 2022, 24, 3405-3419.	1.8	35
10902	CLASH Analyst: A Web Server to Identify In Vivo RNA-RNA Interactions from CLASH Data. <i>Non-coding RNA</i> , 2022, 8, 6.	1.3	2
10903	Single-cell transcription profiles in Bloom syndrome patients link <i>BLM</i> deficiency with altered condensin complex expression signatures. <i>Human Molecular Genetics</i> , 2022, 31, 2185-2193.	1.4	2
10904	The transcriptional regulator HDP1 controls expansion of the inner membrane complex during early sexual differentiation of malaria parasites. <i>Nature Microbiology</i> , 2022, 7, 289-299.	5.9	15
10905	The METTL5-TRMT112 N6-methyladenosine methyltransferase complex regulates mRNA translation via 18S rRNA methylation. <i>Journal of Biological Chemistry</i> , 2022, 298, 101590.	1.6	26
10906	Primary germinal center-resident T follicular helper cells are a physiologically distinct subset of CXCR5hiPD-1hi T follicular helper cells. <i>Immunity</i> , 2022, 55, 272-289.e7.	6.6	25
10907	An ultra low-input method for global RNA structure probing uncovers Regnase-1-mediated regulation in macrophages. <i>Fundamental Research</i> , 2022, 2, 2-13.	1.6	9
10908	The embryonic node behaves as an instructive stem cell niche for axial elongation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	4
10909	TRACE generates fluorescent human reporter cell lines to characterize epigenetic pathways. <i>Molecular Cell</i> , 2022, 82, 479-491.e7.	4.5	7
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10911	Generating Sequencing-Based DNA Methylation Maps from Low DNA Input Samples. <i>Methods in Molecular Biology</i> , 2022, 2458, 3-21.	0.4	3
10912	ID2 controls differentiation of enteroendocrine cells in mouse small intestine. <i>Acta Physiologica</i> , 2022, 234, e13773.	1.8	3
10915	Detailed Transcriptional Landscape of Peripheral Blood Points to Increased Neutrophil Activation in Treatment-Naïve Inflammatory Bowel Disease. <i>Journal of Crohn's and Colitis</i> , 2022, 16, 1097-1109.	0.6	5
10917	Interaction with mammalian enteric viruses alters outer membrane vesicle production and content by commensal bacteria. <i>Journal of Extracellular Vesicles</i> , 2022, 11, e12172.	5.5	16
10919	Hen raising helps chicks establish gut microbiota in their early life and improve microbiota stability after H9N2 challenge. <i>Microbiome</i> , 2022, 10, 14.	4.9	17
10920	Comparative transcriptomic analysis reveals translationally relevant processes in mouse models of malaria. <i>ELife</i> , 2022, 11, .	2.8	10
10921	Increased expression of pro-inflammatory cytokines at the fetal-maternal interface in bovine pregnancies produced by cloning. <i>American Journal of Reproductive Immunology</i> , 2022, 87, .	1.2	3

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10946	Cell-Wall-Degrading Enzymes-Related Genes Originating from <i>Rhizoctonia solani</i> Increase Sugar Beet Root Damage in the Presence of <i>Leuconostoc mesenteroides</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 1366.	1.8	9
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10949	Stereotyped B cell responses are linked to IgG constant region polymorphisms in multiple sclerosis. <i>European Journal of Immunology</i> , 2022, 52, 550-565.	1.6	10
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10951	Approximate Bayesian Computation Untangles Signatures of Contemporary and Historical Hybridization between Two Endangered Species. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	4
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10956	SARS-CoV-2 nucleocapsid protein binds host mRNAs and attenuates stress granules to impair host stress response. <i>IScience</i> , 2022, 25, 103562.	1.9	68
10957	Mapping the Green-Lipped Mussel (<i>Perna canaliculus</i>) Microbiome: A Multi-Tissue Analysis of Bacterial and Fungal Diversity. <i>Current Microbiology</i> , 2022, 79, 76.	1.0	10
10958	Genomic context sensitivity of insulator function. <i>Genome Research</i> , 2022, 32, 425-436.	2.4	12
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10960	A MicroRNA Next-Generation-Sequencing Discovery Assay (miND) for Genome-Scale Analysis and Absolute Quantitation of Circulating MicroRNA Biomarkers. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1226.	1.8	16

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10962	Niche differentiation of sulfur-oxidizing bacteria (SUP05) in submarine hydrothermal plumes. <i>ISME Journal</i> , 2022, 16, 1479-1490.	4.4	11
10963	Prokaryotic diversity and biogeochemical characteristics of benthic microbial ecosystems from James Ross Archipelago (West Antarctica). <i>Polar Biology</i> , 2022, 45, 405-418.	0.5	7
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10967	Protocol: A Multiplexed Reporter Assay to Study Effects of Chromatin Context on DNA Double-Strand Break Repair. <i>Frontiers in Genetics</i> , 2021, 12, 785947.	1.1	1
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10970	DNA metabarcoding reveals host-specific communities of arthropods residing in fungal fruit bodies. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, 20212622.	1.2	6
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10973	Gene expression plasticity and frontloading promote thermotolerance in <i>Pocillopora</i> corals. , 0, 2, .		9
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10975	Epiphytic fungal communities vary by substrate type and at submetre spatial scales. <i>Molecular Ecology</i> , 2022, 31, 1879-1891.	2.0	7
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10977	Hybridization underlies localized trait evolution in cavefish. <i>IScience</i> , 2022, 25, 103778.	1.9	17
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10981	Multiomic identification of factors associated with progression to cystic kidney disease in mice with nephron lft88 disruption. <i>American Journal of Physiology - Renal Physiology</i> , 2022, 322, F175-F192.	1.3	3
10982	Phylogeography of a canopy-forming kelp, <i>Eisenia bicyclis</i> (Laminariales, Phaeophyceae), based on a genome-wide sequencing analysis. <i>Journal of Phycology</i> , 2022, , .	1.0	1
10985	Circulating miR-320b and miR-483-5p levels are associated with COVID-19 in-hospital mortality. <i>Mechanisms of Ageing and Development</i> , 2022, 202, 111636.	2.2	15
10986	An invasive <i>Haemophilus influenzae</i> serotype b infection in an Anglo-Saxon plague victim. <i>Genome Biology</i> , 2022, 23, 22.	3.8	13
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10989	New Insight Into the Interspecies Shift of Anammox Bacteria <i>Ca. Brocadia</i> and <i>Ca. Jettenia</i> in Reactors Fed With Formate and Folate. <i>Frontiers in Microbiology</i> , 2021, 12, 802201.	1.5	13
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10992	Determinants and Interactions of Oral Bacterial and Fungal Microbiota in Healthy Chinese Adults. <i>Microbiology Spectrum</i> , 2022, 10, e0241021.	1.2	15
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10994	ILF3 represses repeat-derived microRNAs targeting RIG-I mediated type I interferon response. <i>Journal of Molecular Biology</i> , 2022, 434, 167469.	2.0	2
10995	Comparative microbiome analysis reveals bacterial communities associated with <i>Candidatus Liberibacter asiaticus</i> infection in the Huanglongbing insect vector <i>Diaphorina citri</i> . <i>Journal of Asia-Pacific Entomology</i> , 2022, 25, 101884.	0.4	5
10996	Single Circulating-Tumor-Cell-Targeted Sequencing to Identify Somatic Variants in Liquid Biopsies in Non-Small-Cell Lung Cancer Patients. <i>Current Issues in Molecular Biology</i> , 2022, 44, 750-763.	1.0	7
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11000	Pyrazinamide Susceptibility Is Driven by Activation of the SigE-Dependent Cell Envelope Stress Response in <i>Mycobacterium tuberculosis</i> . <i>MBio</i> , 2022, 13, e0043921.	1.8	10

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11003	Assessment of Hydrocarbon Degradation Potential in Microbial Communities in Arctic Sea Ice. <i>Microorganisms</i> , 2022, 10, 328.	1.6	13
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11008	Identification of the rhizosphere microbes that actively consume plant-derived carbon. <i>Soil Biology and Biochemistry</i> , 2022, 166, 108577.	4.2	14
11009	Spatial and temporal distribution of SARS-CoV-2 diversity circulating in wastewater. <i>Water Research</i> , 2022, 211, 118007.	5.3	37
11010	Disentangling the impact of contrasting agricultural management practices on soil microbial communities – Importance of rare bacterial community members. <i>Soil Biology and Biochemistry</i> , 2022, 166, 108573.	4.2	27
11011	Integrative analysis of fecal metabolome and gut microbiota in high-fat diet-induced hyperlipidemic rats treated with <i>Rosa Roxburghii</i> Tratt juice. <i>Journal of Functional Foods</i> , 2022, 90, 104978.	1.6	13
11012	Multi-CUT&Tag to simultaneously profile multiple chromatin factors. <i>STAR Protocols</i> , 2022, 3, 101100.	0.5	3
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11014	Molecular dissemination of emerging antibiotic, biocide, and metal co-resistomes in the Himalayan hot springs. <i>Journal of Environmental Management</i> , 2022, 307, 114569.	3.8	8
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11016	Wanted not, wasted not: Searching for non-target taxa in environmental DNA metabarcoding by-catch. <i>Environmental Advances</i> , 2022, 7, 100169.	2.2	6
11017	Nutrients, temperature, and oxygen mediate microbial antibiotic resistance in sea bass (<i>Lateolabrax</i>) Tj ETQq1 1 0.784314 rgBT /Over	3.9	10
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11023	An improved molecular inversion probe based targeted sequencing approach for low variant allele frequency. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqab125.	1.5	4
11024	Full-Likelihood Genomic Analysis Clarifies a Complex History of Species Divergence and Introgression: The Example of the <i>erato-sara</i> Group of <i>Heliconius</i> Butterflies. <i>Systematic Biology</i> , 2022, 71, 1159-1177.	2.7	16
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11032	Vertical stratification of the air microbiome in the lower troposphere. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	13
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11042	Seasonal airway microbiome and transcriptome interactions promote childhood asthma exacerbations. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 150, 204-213.	1.5	31
11043	Patterns of eukaryotic diversity from the surface to the deep-ocean sediment. <i>Science Advances</i> , 2022, 8, eabj9309.	4.7	52

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11046	METTL16 exerts an m6A-independent function to facilitate translation and tumorigenesis. <i>Nature Cell Biology</i> , 2022, 24, 205-216.	4.6	143
11047	SARS-CoV-2 accessory protein ORF8 is secreted extracellularly as a glycoprotein homodimer. <i>Journal of Biological Chemistry</i> , 2022, 298, 101724.	1.6	28
11048	Phyllosphere-associated microbiota in built environment: Do they have the potential to antagonize human pathogens?. <i>Journal of Advanced Research</i> , 2023, 43, 109-121.	4.4	9
11050	Temporal and spatial microbiome dynamics across natural populations of the social spider <i>Stegodyphus dumicola</i> . <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	7
11052	Complete Genome Sequence of <i>Bacillus</i> sp. Strain NC3, Isolated from <i>Trichonephila</i> Spider Ground Extract. <i>Microbiology Resource Announcements</i> , 2022, , e0111021.	0.3	2
11053	Additional Resistant Starch from One Potato Side Dish per Day Alters the Gut Microbiota but Not Fecal Short-Chain Fatty Acid Concentrations. <i>Nutrients</i> , 2022, 14, 721.	1.7	7
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11055	The landscape of promoter-centred RNA-DNA interactions in rice. <i>Nature Plants</i> , 2022, 8, 157-170.	4.7	15
11056	Spatial, temporal and molecular dynamics of swine influenza virus-specific CD8 tissue resident memory T cells. <i>Mucosal Immunology</i> , 2022, 15, 428-442.	2.7	9
11057	Integration of multiple lineage measurements from the same cell reconstructs parallel tumor evolution. <i>Cell Genomics</i> , 2022, 2, 100096.	3.0	13
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11167	Molecular Profiling of Liquid Biopsies for Precision Oncology. <i>Advances in Experimental Medicine and Biology</i> , 2022, 1361, 235-247.	0.8	6
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11229	Phylogenetic Position of Whitefish <i>Coregonus lavaretus</i> (L.) from Teletskoye Lake (Siberia) Based on Complete Mitochondrial DNA. <i>Russian Journal of Genetics</i> , 2022, 58, 235-240.	0.2	1
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14150	Large-scale genome editing based on high-capacity adenovectors and CRISPR-Cas9 nucleases rescues full-length dystrophin synthesis in DMD muscle cells. <i>Nucleic Acids Research</i> , 2022, 50, 7761-7782.	6.5	9

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14152	Developmental programming: Impact of prenatal bisphenol-A exposure on liver and muscle transcriptome of female sheep. <i>Toxicology and Applied Pharmacology</i> , 2022, 451, 116161.	1.3	8
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14154	Identification and Functional Prediction of Poplar Root circRNAs Involved in Treatment With Different Forms of Nitrogen. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
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14251	Human 5-lipoxygenase regulates transcription by association to euchromatin. <i>Biochemical Pharmacology</i> , 2022, 203, 115187.	2.0	6
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14296	Interaction between Cervical Microbiota and Host Gene Regulation in Caesarean Section Scar Diverticulum. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5
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15018	Variant calling enhances the identification of cancer cells in single-cell RNA sequencing data. <i>PLoS Computational Biology</i> , 2022, 18, e1010576.	1.5	1
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15021	Comparative transcriptome analysis of <i>Citrus macrophylla</i> tree infected with <i>Citrus tristeza virus</i> stem pitting mutants provides new insight into the role of phloem regeneration in stem pitting disease. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
15022	The RNA helicase DDX6 controls early mouse embryogenesis by repressing aberrant inhibition of BMP signaling through miRNA-mediated gene silencing. <i>PLoS Genetics</i> , 2022, 18, e1009967.	1.5	7
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15028	Experimental evidence that group size generates divergent benefits of cooperative breeding for male and female ostriches. <i>ELife</i> , 0, 11, .	2.8	3
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