

Fast gapped-read alignment with Bowtie 2

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Citation Report

#	ARTICLE	IF	CITATIONS
11	Nonketotic hyperosmolar hyperglycemia during glycerol therapy for cerebral edema. <i>Neurology</i> , 1976, 26, 89-89.	1.5	29
12	Benchmarking Short Sequence Mapping Tools. , 2011, , .		5
13	Chapter 6: Structural Variation and Medical Genomics. <i>PLoS Computational Biology</i> , 2012, 8, e1002821.	1.5	26
14	Identification, Characterization, and <i>In Vitro</i> Culture of Highly Divergent Arenaviruses from Boa Constrictors and Annulated Tree Boas: Candidate Etiological Agents for Snake Inclusion Body Disease. <i>MBio</i> , 2012, 3, e00180-12.	1.8	170
15	Tools for mapping high-throughput sequencing data. <i>Bioinformatics</i> , 2012, 28, 3169-3177.	1.8	269
16	nFuse: Discovery of complex genomic rearrangements in cancer using high-throughput sequencing. <i>Genome Research</i> , 2012, 22, 2250-2261.	2.4	67
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18	Ben Langmead. <i>Nature Methods</i> , 2012, 9, 313-313.	9.0	2
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21	From specific to global analysis of posttranscriptional regulation in eukaryotes: posttranscriptional regulatory networks. <i>Briefings in Functional Genomics</i> , 2012, 11, 505-521.	1.3	16
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25	Silencing of Germline-Expressed Genes by DNA Elimination in Somatic Cells. <i>Developmental Cell</i> , 2012, 23, 1072-1080.	3.1	101
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32	Next-Generation Digital Information Storage in DNA. <i>Science</i> , 2012, 337, 1628-1628.	6.0	902
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37	The effect of strand bias in Illumina short-read sequencing data. <i>BMC Genomics</i> , 2012, 13, 666.	1.2	102
38	Genomic basis of broad host range and environmental adaptability of <i>Rhizobium tropici</i> CIAT 899 and <i>Rhizobium</i> sp. PRF 81 which are used in inoculants for common bean (<i>Phaseolus vulgaris</i> L.). <i>BMC Genomics</i> , 2012, 13, 735.	1.2	118
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1691	Genome assembly using Nanopore-guided long and error-free DNA reads. <i>BMC Genomics</i> , 2015, 16, 327.	1.2	177
1692	Integrative epigenomic and genomic filtering for methylation markers in hepatocellular carcinomas. <i>BMC Medical Genomics</i> , 2015, 8, 28.	0.7	24
1693	ConPADE: Genome Assembly Ploidy Estimation from Next-Generation Sequencing Data. <i>PLoS Computational Biology</i> , 2015, 11, e1004229.	1.5	41
1694	Transcriptome Profiling and Genetic Study Reveal Amplified Carboxylesterase Genes Implicated in Temephos Resistance, in the Asian Tiger Mosquito <i>Aedes albopictus</i> . <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003771.	1.3	49
1695	Respiratory Syncytial Virus Utilizes a tRNA Fragment to Suppress Antiviral Responses Through a Novel Targeting Mechanism. <i>Molecular Therapy</i> , 2015, 23, 1622-1629.	3.7	138
1696	Pharmacological targeting of the Wdr5-MLL interaction in C/EBP β N-terminal leukemia. <i>Nature Chemical Biology</i> , 2015, 11, 571-578.	3.9	227
1697	Genomic landscape of carcinogen-induced and genetically induced mouse skin squamous cell carcinoma. <i>Nature Medicine</i> , 2015, 21, 946-954.	15.2	179
1698	Exceptional reduction of the plastid genome of saguaro cactus (<i>Carnegiea gigantea</i>): Loss of the <i>ndh</i> gene suite and inverted repeat. <i>American Journal of Botany</i> , 2015, 102, 1115-1127.	0.8	137
1699	Pharmacoethnicity in Paclitaxel-Induced Sensory Peripheral Neuropathy. <i>Clinical Cancer Research</i> , 2015, 21, 4337-4346.	3.2	39
1700	The mitochondrial genome of a Texas outbreak strain of the cattle tick, <i>Rhipicephalus (Boophilus) microplus</i> , derived from whole genome sequencing Pacific Biosciences and Illumina reads. <i>Gene</i> , 2015, 571, 135-141.	1.0	37
1701	DNA methylation of oestrogen-regulated enhancers defines endocrine sensitivity in breast cancer. <i>Nature Communications</i> , 2015, 6, 7758.	5.8	105
1702	Integrative genomic analysis reveals widespread enhancer regulation by p53 in response to DNA damage. <i>Nucleic Acids Research</i> , 2015, 43, 4447-4462.	6.5	84
1703	Dietary Modulation of Gut Microbiota Contributes to Alleviation of Both Genetic and Simple Obesity in Children. <i>EBioMedicine</i> , 2015, 2, 968-984.	2.7	306
1704	Adaptive Evolution of <i>Thermotoga maritima</i> Reveals Plasticity of the ABC Transporter Network. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5477-5485.	1.4	16
1705	Exome Sequencing Reveals <i>AMER1</i> as a Frequently Mutated Gene in Colorectal Cancer. <i>Clinical Cancer Research</i> , 2015, 21, 4709-4718.	3.2	52
1706	Spectrum of gene mutations detected by next generation exome sequencing in brain metastases of lung adenocarcinoma. <i>European Journal of Cancer</i> , 2015, 51, 1803-1811.	1.3	36
1707	Vacuolar ATPase depletion affects mitochondrial ATPase function, kinetoplast dependency, and drug sensitivity in trypanosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9112-9117.	3.3	39

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1709	An Interactive Database for the Assessment of Histone Antibody Specificity. <i>Molecular Cell</i> , 2015, 59, 502-511.	4.5	139
1710	Next generation sequencing of sex-specific genes in the livers of obese ZSF1 rats. <i>Genomics</i> , 2015, 106, 204-213.	1.3	15
1711	Cellular phenotype database: a repository for systems microscopy data. <i>Bioinformatics</i> , 2015, 31, 2736-2740.	1.8	10
1712	All-or-(N)One “an epistemological characterization of the human tumorigenic neuronal paralogous FAM72 gene loci. <i>Genomics</i> , 2015, 106, 278-285.	1.3	24
1713	Histone H3.3 maintains genome integrity during mammalian development. <i>Genes and Development</i> , 2015, 29, 1377-1392.	2.7	163
1714	Development and Validation of Two Screening Assays for the Hepatitis C Virus NS3 Q80K Polymorphism Associated with Reduced Response to Combination Treatment Regimens Containing Simeprevir. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2942-2950.	1.8	11
1715	Emergence of a virulent porcine reproductive and respiratory syndrome virus in vaccinated herds in the United States. <i>Virus Research</i> , 2015, 210, 34-41.	1.1	47
1716	A genome-wide analysis of Cas9 binding specificity using ChIP-seq and targeted sequence capture. <i>Nucleic Acids Research</i> , 2015, 43, 3389-3404.	6.5	193
1717	Improving small RNA-seq by using a synthetic spike-in set for size-range quality control together with a set for data normalization. <i>Nucleic Acids Research</i> , 2015, 43, e89-e89.	6.5	35
1718	Ramethy. , 2015, , .		15
1719	Experimental Swap of <i>Anopheles gambiae</i> 's Assortative Mating Preferences Demonstrates Key Role of X-Chromosome Divergence Island in Incipient Sympatric Speciation. <i>PLoS Genetics</i> , 2015, 11, e1005141.	1.5	34
1720	Unusual biology across a group comprising more than 15% of domain Bacteria. <i>Nature</i> , 2015, 523, 208-211.	13.7	1,050
1721	Temporal and spatial analysis of the 2014–2015 Ebola virus outbreak in West Africa. <i>Nature</i> , 2015, 524, 97-101.	13.7	272
1722	Quantitative assessment of single-cell whole genome amplification methods for detecting copy number variation using hippocampal neurons. <i>Scientific Reports</i> , 2015, 5, 11415.	1.6	51
1723	Transcriptional Control of an Essential Ribozyme in <i>Drosophila</i> Reveals an Ancient Evolutionary Divide in Animals. <i>PLoS Genetics</i> , 2015, 11, e1004893.	1.5	5
1724	Integrated Genomic Analysis Suggests <i>MLL3</i> Is a Novel Candidate Susceptibility Gene for Familial Nasopharyngeal Carcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1222-1228.	1.1	17
1725	Genome-Wide Association Mapping for Yield and Other Agronomic Traits in an Elite Breeding Population of Tropical Rice (<i>Oryza sativa</i>). <i>PLoS ONE</i> , 2015, 10, e0119873.	1.1	157

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1727	Transcriptional Profiling of Resistant and Susceptible Buffalograsses in Response to <i>Blissus occiduus</i> (Hemiptera: Blissidae) Feeding. <i>Journal of Economic Entomology</i> , 2015, 108, 1354-1362.	0.8	12
1728	Massively parallel quantification of the regulatory effects of noncoding genetic variation in a human cohort. <i>Genome Research</i> , 2015, 25, 1206-1214.	2.4	100
1729	Transcriptome Sequencing Reveals Potential Mechanism of Cryptic 3â€™ Splice Site Selection in SF3B1-mutated Cancers. <i>PLoS Computational Biology</i> , 2015, 11, e1004105.	1.5	177
1730	Benchmarking Transcriptome Quantification Methods for Duplicated Genes in <i>Xenopus laevis</i> . <i>Cytogenetic and Genome Research</i> , 2015, 145, 253-264.	0.6	6
1731	Numerous Transitions of Sex Chromosomes in Diptera. <i>PLoS Biology</i> , 2015, 13, e1002078.	2.6	279
1732	Transcriptome analysis of acetic-acid-treated yeast cells identifies a large set of genes whose overexpression or deletion enhances acetic acid tolerance. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 6391-6403.	1.7	31
1733	The complete mitochondrial genome of <i>Papilio glaucus</i> and its phylogenetic implications. <i>Meta Gene</i> , 2015, 5, 68-83.	0.3	20
1734	Metagenomic Investigation of Viral Communities in Ballast Water. <i>Environmental Science & Technology</i> , 2015, 49, 8396-8407.	4.6	68
1735	Do Bacterial Symbionts Govern Aphid's Dropping Behavior?. <i>Environmental Entomology</i> , 2015, 44, 588-592.	0.7	4
1736	Discovery of Transcription Factors and Regulatory Regions Driving In Vivo Tumor Development by ATAC-seq and FAIRE-seq Open Chromatin Profiling. <i>PLoS Genetics</i> , 2015, 11, e1004994.	1.5	155
1737	Widespread Recombination, Reassortment, and Transmission of Unbalanced Compound Viral Genotypes in Natural Arenavirus Infections. <i>PLoS Pathogens</i> , 2015, 11, e1004900.	2.1	72
1738	Century-scale Methylome Stability in a Recently Diverged <i>Arabidopsis thaliana</i> Lineage. <i>PLoS Genetics</i> , 2015, 11, e1004920.	1.5	148
1739	Next-generation re-sequencing as a tool for rapid bioinformatic screening of presence and absence of genes and accessory chromosomes across isolates of <i>Zymoseptoria tritici</i> . <i>Fungal Genetics and Biology</i> , 2015, 79, 71-75.	0.9	7
1740	Transcriptome-wide measurement of ribosomal occupancy by ribosome profiling. <i>Methods</i> , 2015, 85, 75-89.	1.9	35
1741	A Genome-Wide Hybrid Incompatibility Landscape between <i>Caenorhabditis briggsae</i> and <i>C. nigoni</i> . <i>PLoS Genetics</i> , 2015, 11, e1004993.	1.5	40
1742	Genomic determinants of coral heat tolerance across latitudes. <i>Science</i> , 2015, 348, 1460-1462.	6.0	473
1743	Genomic sequencing and microsatellite marker development for <i>Boswellia papyrifera</i> , an economically important but threatened tree native to dry tropical forests. <i>AoB PLANTS</i> , 2015, 7, .	1.2	20

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1745	<i>Neurospora</i> Importin $\hat{\pm}$ Is Required for Normal Heterochromatic Formation and DNA Methylation. <i>PLoS Genetics</i> , 2015, 11, e1005083.	1.5	25
1746	The Fun30 Chromatin Remodeler Fft3 Controls Nuclear Organization and Chromatin Structure of Insulators and Subtelomeres in Fission Yeast. <i>PLoS Genetics</i> , 2015, 11, e1005101.	1.5	52
1747	Deep Sequencing of the <i>Trypanosoma cruzi</i> GP63 Surface Proteases Reveals Diversity and Diversifying Selection among Chronic and Congenital Chagas Disease Patients. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003458.	1.3	50
1748	Epithelial Cadherin Determines Resistance to Infectious Pancreatic Necrosis Virus in Atlantic Salmon. <i>Genetics</i> , 2015, 200, 1313-1326.	1.2	170
1749	Unexpected evolutionary diversity in a recently extinct Caribbean mammal radiation. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20142371.	1.2	50
1750	Eighteenth-century genomes show that mixed infections were common at time of peak tuberculosis in Europe. <i>Nature Communications</i> , 2015, 6, 6717.	5.8	165
1751	Whole genome sequence analysis of multidrug-resistant <i>Mycobacterium tuberculosis</i> Beijing isolates from an outbreak in Thailand. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1933-1941.	1.0	20
1752	Nanoparticles that deliver triplex-forming peptide nucleic acid molecules correct F508del CFTR in airway epithelium. <i>Nature Communications</i> , 2015, 6, 6952.	5.8	114
1753	A new method for studying population genetics of cyst nematodes based on Poolâ€šeq and genomewide allele frequency analysis. <i>Molecular Ecology Resources</i> , 2015, 15, 1356-1365.	2.2	31
1754	Population genomic analysis uncovers African and European admixture in <i>Drosophila melanogaster</i> populations from the southâ€šeastern United States and Caribbean Islands. <i>Molecular Ecology</i> , 2015, 24, 1499-1509.	2.0	75
1755	Destabilization of pluripotency in the absence of Mad2l2. <i>Cell Cycle</i> , 2015, 14, 1596-1610.	1.3	13
1756	Limited specificity of IRF3 and ISGF3 in the transcriptional innate-immune response to double-stranded RNA. <i>Journal of Leukocyte Biology</i> , 2015, 98, 119-128.	1.5	28
1757	The lncRNA MIR31HG regulates p16INK4A expression to modulate senescence. <i>Nature Communications</i> , 2015, 6, 6967.	5.8	161
1758	A neural basis for melanocortin-4 receptorâ€šregulated appetite. <i>Nature Neuroscience</i> , 2015, 18, 863-871.	7.1	324
1759	Genomic single-nucleotide polymorphisms confirm that Gunnison and Greater sage-grouse are genetically well differentiated and that the Bi-State population is distinct. <i>Condor</i> , 2015, 117, 217-227.	0.7	20
1760	Immunoglobulin transcript sequence and somatic hypermutation computation from unselected RNA-seq reads in chronic lymphocytic leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4322-4327.	3.3	38
1761	Direct multiplexed whole genome sequencing of respiratory tract samples reveals full viral genomic information. <i>Journal of Clinical Virology</i> , 2015, 66, 6-11.	1.6	30

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1763	Subpopulations in aMPV vaccines are unlikely to be the only cause of reversion to virulence. <i>Vaccine</i> , 2015, 33, 2438-2441.	1.7	15
1764	Application of next-generation sequencing to study ascitic microbiome in cirrhotic patients with or without spontaneous bacterial peritonitis. <i>Journal of Microbiology, Immunology and Infection</i> , 2015, 48, 504-509.	1.5	18
1765	Development of Genetic Markers in Eucalyptus Species by Target Enrichment and Exome Sequencing. <i>PLoS ONE</i> , 2015, 10, e0116528.	1.1	29
1766	RNA Polymerase Slippage as a Mechanism for the Production of Frameshift Gene Products in Plant Viruses of the Potyviridae Family. <i>Journal of Virology</i> , 2015, 89, 6965-6967.	1.5	136
1767	Targeted-bisulfite sequence analysis of the methylation of CpG islands in genes encoding PNPLA3, SAMM50, and PARVB of patients with non-alcoholic fatty liver disease. <i>Journal of Hepatology</i> , 2015, 63, 494-502.	1.8	71
1768	Systems Biology Tools for Methylotrophs. <i>Springer Protocols</i> , 2015, , 97-118.	0.1	4
1769	The microbiome of uncontacted Amerindians. <i>Science Advances</i> , 2015, 1, .	4.7	721
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1771	Method Optimization for Fecal Sample Collection and Fecal DNA Extraction. <i>Biopreservation and Biobanking</i> , 2015, 13, 79-93.	0.5	48
1772	Dispersal of H9N2 influenza A viruses between East Asia and North America by wild birds. <i>Virology</i> , 2015, 482, 79-83.	1.1	47
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1774	Rapid and reliable identification of tomato fruit weight and locule number loci by QTL-seq. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1329-1342.	1.8	153
1775	Diversity and evolution of centromere repeats in the maize genome. <i>Chromosoma</i> , 2015, 124, 57-65.	1.0	21
1776	Switchgrass (<i>Panicum virgatum</i> L) flag leaf transcriptomes reveal molecular signatures of leaf development, senescence, and mineral dynamics. <i>Functional and Integrative Genomics</i> , 2015, 15, 1-16.	1.4	52
1777	Two PALB2 germline mutations found in both BRCA1+ and BRCAx familial breast cancer. <i>Breast Cancer Research and Treatment</i> , 2015, 151, 219-224.	1.1	2
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1779	Genome-wide discovery of gene-related SNPs in Barramundi <i>Lates calcarifer</i> . <i>Conservation Genetics Resources</i> , 2015, 7, 605-608.	0.4	33

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1781	Origin, evolution, and population genetics of the selfish <i>Segregation Distorter</i> gene duplication in European and African populations of <i>Drosophila melanogaster</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1271-1283.	1.1	36
1782	Metatranscriptome analyses indicate resource partitioning between diatoms in the field. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2182-90.	3.3	166
1783	A new insight into the role of intracellular nickel levels for the stress response, surface properties and twitching motility by <i>Haemophilus influenzae</i> . <i>Metallomics</i> , 2015, 7, 650-661.	1.0	3
1784	Widespread Macromolecular Interaction Perturbations in Human Genetic Disorders. <i>Cell</i> , 2015, 161, 647-660.	13.5	482
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1786	ScaffMatch: scaffolding algorithm based on maximum weight matching. <i>Bioinformatics</i> , 2015, 31, 2632-2638.	1.8	41
1787	PEAT: an intelligent and efficient paired-end sequencing adapter trimming algorithm. <i>BMC Bioinformatics</i> , 2015, 16, S2.	1.2	49
1788	Fast inexact mapping using advanced tree exploration on backward search methods. <i>BMC Bioinformatics</i> , 2015, 16, 18.	1.2	2
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1791	Integrated transcriptome catalogue and organ-specific profiling of gene expression in fertile garlic (<i>Allium sativum</i> L.). <i>BMC Genomics</i> , 2015, 16, 12.	1.2	85
1792	Cetaceans evolution: insights from the genome sequences of common minke whales. <i>BMC Genomics</i> , 2015, 16, 13.	1.2	28
1793	Re-annotation of the woodland strawberry (<i>Fragaria vesca</i>) genome. <i>BMC Genomics</i> , 2015, 16, 29.	1.2	60
1794	Global transcriptomic profiling demonstrates induction of oxidative stress and of compensatory cellular stress responses in brown trout exposed to glyphosate and Roundup. <i>BMC Genomics</i> , 2015, 16, 32.	1.2	90
1795	Small RNAs derived from tRNAs and rRNAs are highly enriched in exosomes from both old and new world <i>Leishmania</i> providing evidence for conserved exosomal RNA Packaging. <i>BMC Genomics</i> , 2015, 16, 151.	1.2	136
1796	GASS: genome structural annotation for Eukaryotes based on species similarity. <i>BMC Genomics</i> , 2015, 16, 150.	1.2	7
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1801	NexGenEx-Tom: a gene expression platform to investigate the functionalities of the tomato genome. <i>BMC Plant Biology</i> , 2015, 15, 48.	1.6	16
1802	Establishment of <i>Anthoceros agrestis</i> as a model species for studying the biology of hornworts. <i>BMC Plant Biology</i> , 2015, 15, 98.	1.6	53
1803	Genetic diversity of the 2013–14 human isolates of influenza H7N9 in China. <i>BMC Infectious Diseases</i> , 2015, 15, 109.	1.3	8
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1806	A haplotype map of allohexaploid wheat reveals distinct patterns of selection on homoeologous genomes. <i>Genome Biology</i> , 2015, 16, 48.	3.8	216
1807	Transcriptome analysis of ageing in uninjured human Achilles tendon. <i>Arthritis Research and Therapy</i> , 2015, 17, 33.	1.6	68
1808	Replicative senescence is associated with nuclear reorganization and with DNA methylation at specific transcription factor binding sites. <i>Clinical Epigenetics</i> , 2015, 7, 19.	1.8	51
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1811	Genetics, structure, and prevalence of FP967 (CDC Triffid) T-DNA in flax. <i>SpringerPlus</i> , 2015, 4, 146.	1.2	12
1812	High-resolution genetic mapping of maize pan-genome sequence anchors. <i>Nature Communications</i> , 2015, 6, 6914.	5.8	213
1813	Assessing the gene regulatory properties of Argonaute-bound small RNAs of diverse genomic origin. <i>Nucleic Acids Research</i> , 2015, 43, 470-481.	6.5	142
1814	Transcriptome Dynamics of the Stomatal Lineage: Birth, Amplification, and Termination of a Self-Renewing Population. <i>Developmental Cell</i> , 2015, 33, 107-118.	3.1	142
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1819	RNA Nanotechnology and Therapeutics. <i>Methods in Molecular Biology</i> , 2015, , .	0.4	3
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1822	Evaluating the performance of anchored hybrid enrichment at the tips of the tree of life: a phylogenetic analysis of Australian <i>Eugongylus</i> group scincid lizards. <i>BMC Evolutionary Biology</i> , 2015, 15, 62.	3.2	57
1823	Common binding by redundant group B Sox proteins is evolutionarily conserved in <i>Drosophila</i> . <i>BMC Genomics</i> , 2015, 16, 292.	1.2	14
1824	Small mosquitoes, large implications: crowding and starvation affects gene expression and nutrient accumulation in <i>Aedes aegypti</i> . <i>Parasites and Vectors</i> , 2015, 8, 252.	1.0	62
1825	Whole-genome analysis of <i>Fusarium graminearum</i> insertional mutants identifies virulence associated genes and unmasking untagged chromosomal deletions. <i>BMC Genomics</i> , 2015, 16, 261.	1.2	18
1826	Age and sun exposure-related widespread genomic blocks of hypomethylation in nonmalignant skin. <i>Genome Biology</i> , 2015, 16, 80.	3.8	111
1827	A novel sigma factor reveals a unique regulon controlling cell-specific recombination in <i>Mycoplasma genitalium</i> . <i>Nucleic Acids Research</i> , 2015, 43, 4923-4936.	6.5	30
1828	Determination of DNA Methylation Levels Using Illumina HumanMethylation450 BeadChips. <i>Methods in Molecular Biology</i> , 2015, 1288, 143-192.	0.4	13
1829	Parallel and Divergent Evolutionary Solutions for the Optimization of an Engineered Central Metabolism in <i>Methylobacterium extorquens</i> AM1. <i>Microorganisms</i> , 2015, 3, 152-174.	1.6	16
1830	A <i>MAT1-2</i> wild-type strain from <i>Penicillium chrysogenum</i> : functional mating locus characterization, genome sequencing and mating with an industrial penicillin-producing strain. <i>Molecular Microbiology</i> , 2015, 95, 859-874.	1.2	26
1831	Dynamics of gene expression patterns during early development of the European seabass (<i>Dicentrarchus labrax</i>). <i>Physiological Genomics</i> , 2015, 47, 158-169.	1.0	23
1832	<i>Giardia</i> spp. Are Commonly Found in Mixed Assemblages in Surface Water, as Revealed by Molecular and Whole-Genome Characterization. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4827-4834.	1.4	38
1833	The transcription factor GABP selectively binds and activates the mutant TERT promoter in cancer. <i>Science</i> , 2015, 348, 1036-1039.	6.0	451
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1993	StarScan: a web server for scanning small RNA targets from degradome sequencing data. Nucleic Acids Research, 2015, 43, W480-W486.	6.5	36
1994	Complete hematologic response of early T-cell progenitor acute lymphoblastic leukemia to the β -secretase inhibitor BMS-906024: genetic and epigenetic findings in an outlier case. Journal of Physical Education and Sports Management, 2015, 1, a000539.	0.5	47
1995	Complete Genome Sequences of a <i>Mycobacterium smegmatis</i> Laboratory Strain (MC ² 155) and Isoniazid-Resistant (4XR1/R2) Mutant Strains. Genome Announcements, 2015, 3, .	0.8	54
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1997	Transcriptome profiling reveals mechanisms for the evolution of insect seasonality. Journal of Experimental Biology, 2015, 218, 3611-22.	0.8	39

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1999	Limited dissemination of the wastewater treatment plant core resistome. <i>Nature Communications</i> , 2015, 6, 8452.	5.8	173
2000	A dietary phytochemical alters caste-associated gene expression in honey bees. <i>Science Advances</i> , 2015, 1, e1500795.	4.7	81
2001	Read count-based method for high-throughput allelic genotyping of transposable elements and structural variants. <i>BMC Genomics</i> , 2015, 16, 508.	1.2	0
2002	Generation and analysis of expressed sequence tags (ESTs) of <i>Camelina sativa</i> to mine drought stress-responsive genes. <i>Biochemical and Biophysical Research Communications</i> , 2015, 467, 83-93.	1.0	17
2003	Experimental Design and Bioinformatics Analysis for the Application of Metagenomics in Environmental Sciences and Biotechnology. <i>Environmental Science & Technology</i> , 2015, 49, 12628-12640.	4.6	72
2004	Peptidoglycan synthesis in <i>Mycobacterium tuberculosis</i> is organized into networks with varying drug susceptibility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13087-13092.	3.3	82
2005	Transcriptomic changes in the plant pathogenic fungus <i>Rhizoctonia solani</i> AG-3 in response to the antagonistic bacteria <i>Serratia proteamaculans</i> and <i>Serratia plymuthica</i> . <i>BMC Genomics</i> , 2015, 16, 630.	1.2	97
2006	Panoramix enforces piRNA-dependent cotranscriptional silencing. <i>Science</i> , 2015, 350, 339-342.	6.0	162
2007	Opposing intrinsic temporal gradients guide neural stem cell production of varied neuronal fates. <i>Science</i> , 2015, 350, 317-320.	6.0	130
2008	ContextMap 2: fast and accurate context-based RNA-seq mapping. <i>BMC Bioinformatics</i> , 2015, 16, 122.	1.2	54
2009	InteMAP: Integrated metagenomic assembly pipeline for NGS short reads. <i>BMC Bioinformatics</i> , 2015, 16, 244.	1.2	25
2010	Identifying and characterising key alternative splicing events in <i>Drosophila</i> development. <i>BMC Genomics</i> , 2015, 16, 608.	1.2	9
2011	GSWABE: faster GPU-accelerated sequence alignment with optimal alignment retrieval for short DNA sequences. <i>Concurrency Computation Practice and Experience</i> , 2015, 27, 958-972.	1.4	25
2012	A Genome-Wide Landscape of Retrocopies in Primate Genomes. <i>Genome Biology and Evolution</i> , 2015, 7, 2265-2275.	1.1	46
2013	Caste-biases in gene expression are specific to developmental stage in the ant <i>Formica exsecta</i> . <i>Journal of Evolutionary Biology</i> , 2015, 28, 1705-1718.	0.8	28
2014	Distinguishing low frequency mutations from RT-PCR and sequence errors in viral deep sequencing data. <i>BMC Genomics</i> , 2015, 16, 229.	1.2	44
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2020	Integrating microbial and host transcriptomics to characterize asthma-associated microbial communities. BMC Medical Genomics, 2015, 8, 50.	0.7	63
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2025	Recessive mutations in POLR1C cause a leukodystrophy by impairing biogenesis of RNA polymerase III. Nature Communications, 2015, 6, 7623.	5.8	127
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2031	Bioinformatic prediction of upstream microRNAs of PPO and novel microRNAs in potato. Canadian Journal of Plant Science, 2015, 95, 871-877.	0.3	14
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2041	Buying in to bioinformatics: an introduction to commercial sequence analysis software. <i>Briefings in Bioinformatics</i> , 2015, 16, 700-709.	3.2	36
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2056	ChIPmentation: fast, robust, low-input ChIP-seq for histones and transcription factors. <i>Nature Methods</i> , 2015, 12, 963-965.	9.0	417
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2063	Genome-Wide RNA Sequencing Analysis of Quorum Sensing-Controlled Regulons in the Plant-Associated <i>Burkholderia glumae</i> PG1 Strain. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7993-8007.	1.4	43
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2074	Under-detection of endospore-forming Firmicutes in metagenomic data. Computational and Structural Biotechnology Journal, 2015, 13, 299-306.	1.9	88
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2081	Gain-of-function p53 mutants co-opt chromatin pathways to drive cancer growth. Nature, 2015, 525, 206-211.	13.7	386
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2084	Effects of dietary fiber on cecal short-chain fatty acid and cecal microbiota of broiler and laying-hen chicks. Poultry Science, 2015, 94, 2351-2359.	1.5	100
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2086	Tracking Distinct RNA Populations Using Efficient and Reversible Covalent Chemistry. Molecular Cell, 2015, 59, 858-866.	4.5	179
2088	A new approach for annotation of transposable elements using small RNA mapping. Nucleic Acids Research, 2015, 43, e84-e84.	6.5	28
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2093	Blocking of targeted microRNAs from next-generation sequencing libraries. <i>Nucleic Acids Research</i> , 2015, 43, gkv724.	6.5	18
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2581	FBW7 suppression leads to SOX9 stabilization and increased malignancy in medulloblastoma. <i>EMBO Journal</i> , 2016, 35, 2192-2212.	3.5	58
2582	<scp>LIMT</scp> is a novel metastasis inhibiting lnc<scp>RNA</scp> suppressed by <scp>EGF</scp> and downregulated in aggressive breast cancer. <i>EMBO Molecular Medicine</i> , 2016, 8, 1052-1064.	3.3	77
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2586	TEtools facilitates big data expression analysis of transposable elements and reveals an antagonism between their activity and that of piRNA genes. <i>Nucleic Acids Research</i> , 2017, 45, gkw953.	6.5	86
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2597	Oscillating primary transcripts harbor miRNAs with circadian functions. <i>Scientific Reports</i> , 2016, 6, 21598.	1.6	29
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2603	Genome-wide DNA methylation profiles changes associated with constant heat stress in pigs as measured by bisulfite sequencing. <i>Scientific Reports</i> , 2016, 6, 27507.	1.6	80
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2607	Incidental mutations occur frequently during transposon mutagenesis. <i>FEMS Microbiology Letters</i> , 2016, 364, fnw293.	0.7	0
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2609	Genomes of coral dinoflagellate symbionts highlight evolutionary adaptations conducive to a symbiotic lifestyle. <i>Scientific Reports</i> , 2016, 6, 39734.	1.6	303
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2616	Gene network analysis identifies rumen epithelial cell proliferation, differentiation and metabolic pathways perturbed by diet and correlated with methane production. <i>Scientific Reports</i> , 2016, 6, 39022.	1.6	68

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2633	Disease Model of GATA4 Mutation Reveals Transcription Factor Cooperativity in Human Cardiogenesis. <i>Cell</i> , 2016, 167, 1734-1749.e22.	13.5	195
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4952	ASCL1 Reorganizes Chromatin to Direct Neuronal Fate and Suppress Tumorigenicity of Glioblastoma Stem Cells. <i>Cell Stem Cell</i> , 2017, 21, 209-224.e7.	5.2	150
4953	The Bile Acid Nuclear Receptor FXR \pm Is a Critical Regulator of Mouse Germ Cell Fate. <i>Stem Cell Reports</i> , 2017, 9, 315-328.	2.3	19
4954	Infection and Colonization of <i>Nicotiana benthamiana</i> by Grapevine leafroll-associated virus 3. <i>Virology</i> , 2017, 510, 60-66.	1.1	13
4955	Simian varicella virus causes robust transcriptional changes in T cells that support viral replication. <i>Virus Research</i> , 2017, 238, 226-235.	1.1	6
4956	Fusion of Regionally Specified hPSC-Derived Organoids Models Human Brain Development and Interneuron Migration. <i>Cell Stem Cell</i> , 2017, 21, 383-398.e7.	5.2	508
4957	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
4958	Range instability leads to cytonuclear discordance in a morphologically cryptic ground squirrel species complex. <i>Molecular Ecology</i> , 2017, 26, 4743-4755.	2.0	23
4959	Papain-like cysteine protease encoding genes in rubber (<i>Hevea brasiliensis</i>): comparative genomics, phylogenetic, and transcriptional profiling analysis. <i>Planta</i> , 2017, 246, 999-1018.	1.6	41
4960	Methyltransferase SETD2-Mediated Methylation of STAT1 Is Critical for Interferon Antiviral Activity. <i>Cell</i> , 2017, 170, 492-506.e14.	13.5	215
4961	Sequence intrinsic somatic mutation mechanisms contribute to affinity maturation of VRC01-class HIV-1 broadly neutralizing antibodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8614-8619.	3.3	42
4962	Tuning DNA binding affinity and cleavage specificity of an engineered gene-targeting nuclease via surface display, flow cytometry and cellular analyses. <i>Protein Engineering, Design and Selection</i> , 2017, 30, 503-522.	1.0	2
4963	Whole-genome sequencing approaches for conservation biology: Advantages, limitations and practical recommendations. <i>Molecular Ecology</i> , 2017, 26, 5369-5406.	2.0	249
4964	Germ line-inherited H3K27me3 restricts enhancer function during maternal-to-zygotic transition. <i>Science</i> , 2017, 357, 212-216.	6.0	159
4965	Multi-omics Analysis of Periodontal Pocket Microbial Communities Pre- and Posttreatment. <i>MSystems</i> , 2017, 2, .	1.7	47
4966	Sequence-Based Mapping and Genome Editing Reveal Mutations in Stickleback <i>Hps5</i> Cause Oculocutaneous Albinism and the <i>casper</i> Phenotype. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3123-3131.	0.8	15
4967	Whole-Genome Sequencing and Concordance Between Antimicrobial Susceptibility Genotypes and Phenotypes of Bacterial Isolates Associated with Bovine Respiratory Disease. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3059-3071.	0.8	19
4968	Improvement of biomass and lipid yield under stress conditions by using diploid strains of <i>Chlamydomonas reinhardtii</i> . <i>Algal Research</i> , 2017, 26, 180-189.	2.4	41

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4970	Novel metrics to measure coverage in whole exome sequencing datasets reveal local and global non-uniformity. <i>Scientific Reports</i> , 2017, 7, 885.	1.6	43
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4973	Local epigenetic reprogramming induced by G-quadruplex ligands. <i>Nature Chemistry</i> , 2017, 9, 1110-1117.	6.6	88
4974	MLL4 prepares the enhancer landscape for Foxp3 induction via chromatin looping. <i>Nature Immunology</i> , 2017, 18, 1035-1045.	7.0	63
4975	The eukaryotic gut virome in hematopoietic stem cell transplantation: new clues in enteric graft-versus-host disease. <i>Nature Medicine</i> , 2017, 23, 1080-1085.	15.2	109
4976	A hybrid cloud read aligner based on MinHash and kmer voting that preserves privacy. <i>Nature Communications</i> , 2017, 8, 15311.	5.8	24
4977	An intrinsic mechanism controls reactivation of neural stem cells by spindle matrix proteins. <i>Nature Communications</i> , 2017, 8, 122.	5.8	25
4978	Regulation of cancer epigenomes with a histone-binding synthetic transcription factor. <i>Npj Genomic Medicine</i> , 2017, 2, .	1.7	24
4979	Multiple viral infections in <i>Agaricus bisporus</i> - Characterisation of 18 unique RNA viruses and 8 ORFans identified by deep sequencing. <i>Scientific Reports</i> , 2017, 7, 2469.	1.6	59
4980	The invasive <i>Neisseria meningitidis</i> MenC CC103 from Brazil is characterized by an accessory gene repertoire. <i>Scientific Reports</i> , 2017, 7, 1617.	1.6	5
4981	FastGT: an alignment-free method for calling common SNVs directly from raw sequencing reads. <i>Scientific Reports</i> , 2017, 7, 2537.	1.6	42
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4983	Origin and evolutionary history of freshwater Rhodophyta: further insights based on phylogenomic evidence. <i>Scientific Reports</i> , 2017, 7, 2934.	1.6	25
4984	Spatiotemporal expression patterns of wheat amino acid transporters reveal their putative roles in nitrogen transport and responses to abiotic stress. <i>Scientific Reports</i> , 2017, 7, 5461.	1.6	44
4985	Genome-wide mapping of DNase I hypersensitive sites reveals chromatin accessibility changes in <i>Arabidopsis</i> euchromatin and heterochromatin regions under extended darkness. <i>Scientific Reports</i> , 2017, 7, 4093.	1.6	19
4986	Pathogen recognition in compatible plant-microbe interactions. <i>Scientific Reports</i> , 2017, 7, 6383.	1.6	34

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4989	Liquid-phase sequence capture and targeted re-sequencing revealed novel polymorphisms in tomato genes belonging to the MEP carotenoid pathway. <i>Scientific Reports</i> , 2017, 7, 5616.	1.6	12
4990	Deficient glutamate biosynthesis triggers a concerted upregulation of ribosomal protein genes in <i>Arabidopsis</i> . <i>Scientific Reports</i> , 2017, 7, 6164.	1.6	9
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4992	Efficiency of ddRAD target enriched sequencing across spiny rock lobster species (<i>Palinuridae: Jasus</i>). <i>Scientific Reports</i> , 2017, 7, 6781.	1.6	13
4993	Using RNA sequencing to identify putative competing endogenous RNAs (ceRNAs) potentially regulating fat metabolism in bovine liver. <i>Scientific Reports</i> , 2017, 7, 6396.	1.6	65
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4996	Whole genome detection of signature of positive selection in African cattle reveals selection for thermotolerance. <i>Animal Science Journal</i> , 2017, 88, 1889-1901.	0.6	91
4997	The Sortase-Dependent Fimbriome of the Genus <i>Bifidobacterium</i> : Extracellular Structures with Potential To Modulate Microbe-Host Dialogue. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	31
4998	Genome-Wide SNP Discovery and Analysis of Genetic Diversity in Farmed Sika Deer (<i>Cervus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Genes, Genomes, Genetics, 2017, 7, 3169-3176.	0.8	32
4999	Analyses of a Mutant <i>Foxp3</i> Allele Reveal BATF as a Critical Transcription Factor in the Differentiation and Accumulation of Tissue Regulatory T Cells. <i>Immunity</i> , 2017, 47, 268-283.e9.	6.6	126
5000	Elevated auxin biosynthesis and transport underlie high vein density in <i>C₄</i> leaves. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E6884-E6891.	3.3	34
5001	Circulating Tumor DNA Reveals Clinically Actionable Somatic Genome of Metastatic Bladder Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 6487-6497.	3.2	121
5002	Evidence of microbial rhodopsins in Antarctic dry valley edaphic systems. <i>Environmental Microbiology</i> , 2017, 19, 3755-3767.	1.8	17
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5008	High-throughput sequencing revealed a novel <i>SETX</i> mutation in a Hungarian patient with amyotrophic lateral sclerosis. <i>Brain and Behavior</i> , 2017, 7, e00669.	1.0	24
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5010	The first complete genomes of Metalmarks and the classification of butterfly families. <i>Genomics</i> , 2017, 109, 485-493.	1.3	20
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5015	Genome Sequences of <i>Brucella melitensis</i> , Isolated from Blood Samples of Brucellosis Patients in Malaysia. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
5016	Clonal Expansion and Interrelatedness of Distinct B-Lineage Compartments in Multiple Myeloma Bone Marrow. <i>Cancer Immunology Research</i> , 2017, 5, 744-754.	1.6	17
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5019	Development of genome- and transcriptome-derived microsatellites in related species of snapping shrimps with highly duplicated genomes. <i>Molecular Ecology Resources</i> , 2017, 17, e160-e173.	2.2	6
5020	Transcriptome sequencing reveals potential mechanisms of diapause preparation in bivoltine silkworm <i>Bombyx mori</i> (Lepidoptera: Bombycidae). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2017, 24, 68-78.	0.4	20
5021	Identification of essential genes for cancer immunotherapy. <i>Nature</i> , 2017, 548, 537-542.	13.7	668
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5024	Transcriptomic Analysis of Ribosome-Bound mRNA in Cortical Neurites <i><i>In Vivo</i></i> . <i>Journal of Neuroscience</i> , 2017, 37, 8688-8705.	1.7	49
5025	Genome-Wide Transcriptional Dynamics in the Companion Bacterial Symbionts of the Glassy-Winged Sharpshooter (Cicadellidae: <i><i>Homalodisca vitripennis</i></i>) Reveal Differential Gene Expression in Bacteria Occupying Multiple Host Organs. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3073-3082.	0.8	9
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5027	Workflow and web application for annotating NCBI BioProject transcriptome data. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	6
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5038	Transcriptional Analysis of an Ammonium-Excreting Strain of <i>Azotobacter vinelandii</i> Deregulated for Nitrogen Fixation. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	27
5039	Mitotic Vulnerability in Triple-Negative Breast Cancer Associated with LIN9 Is Targetable with BET Inhibitors. <i>Cancer Research</i> , 2017, 77, 5395-5408.	0.4	24
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5070	The complete mitochondrial genome of <i>Tringa semipalmata inornata</i> (Charadriiformes). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10</i>	0.2	1
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5544	Genome analysis of <i>E. coli</i> isolated from Crohnâ€™s disease patients. <i>BMC Genomics</i> , 2017, 18, 544.	1.2	37
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6551	Generic accelerated sequence alignment in SeqAn using vectorization and multi-threading. <i>Bioinformatics</i> , 2018, 34, 3437-3445.	1.8	30
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6553	5A is required for autophagy by mediating ATG3 translation. <i>EMBO Reports</i> , 2018, 19, .	2.0	63
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7272	Active Crossfire Between Cyanobacteria and Cyanophages in Phototrophic Mat Communities Within Hot Springs. <i>Frontiers in Microbiology</i> , 2018, 9, 2039.	1.5	29
7273	Single-cell Transcriptomic Analyses of Mouse Pancreatic Endocrine Cells. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	2
7274	Genomic Characterization of Six Virus-Associated Cancers Identifies Changes in the Tumor Immune Microenvironment and Altered Genetic Programs. <i>Cancer Research</i> , 2018, 78, 6413-6423.	0.4	33
7275	Transcriptomic response of female adult moths to host and non-host plants in two closely related species. <i>BMC Evolutionary Biology</i> , 2018, 18, 145.	3.2	4
7276	Similar hybrid composition among different age and sex classes in the Myrtleâ€™Audubon's warbler hybrid zone. <i>Auk</i> , 2018, 135, 1133-1145.	0.7	13
7277	Comparative Genomic Analysis and Characterization of Two <i>Salmonella enterica</i> Serovar Enteritidis Isolates From Poultry With Notably Different Survival Abilities in Egg Whites. <i>Frontiers in Microbiology</i> , 2018, 9, 2111.	1.5	11
7278	An Efficient Algorithm for Sensitive Detecting Circular RNA from RNA-seq Data. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2897.	1.8	7
7279	HOXA9 Reprograms the Enhancer Landscape to Promote Leukemogenesis. <i>Cancer Cell</i> , 2018, 34, 643-658.e5.	7.7	94
7280	RAB11FIP5 Expression and Altered Natural Killer Cell Function Are Associated with Induction of HIV Broadly Neutralizing Antibody Responses. <i>Cell</i> , 2018, 175, 387-399.e17.	13.5	78
7281	BRWD1 orchestrates epigenetic landscape of late B lymphopoiesis. <i>Nature Communications</i> , 2018, 9, 3888.	5.8	24
7282	Dynamic 3D chromatin architecture contributes to enhancer specificity and limb morphogenesis. <i>Nature Genetics</i> , 2018, 50, 1463-1473.	9.4	147
7283	Comparative in depth RNA sequencing of <i>P. tricornutum</i> â€™s morphotypes reveals specific features of the oval morphotype. <i>Scientific Reports</i> , 2018, 8, 14340.	1.6	19
7284	A unique role for DNA (hydroxy)methylation in epigenetic regulation of human inhibitory neurons. <i>Science Advances</i> , 2018, 4, eaau6190.	4.7	92
7285	Widespread Antibiotic, Biocide, and Metal Resistance in Microbial Communities Inhabiting a Municipal Waste Environment and Anthropogenically Impacted River. <i>MSphere</i> , 2018, 3, .	1.3	12
7286	Characterization of novel glycosyl hydrolases discovered by cell wall glycan directed monoclonal antibody screening and metagenome analysis of maize aerial root mucilage. <i>PLoS ONE</i> , 2018, 13, e0204525.	1.1	34
7287	Maintaining Genome Integrity during Seed Development in <i>Phaseolus vulgaris</i> L.: Evidence from a Transcriptomic Profiling Study. <i>Genes</i> , 2018, 9, 463.	1.0	16
7288	RNA sequencing and Prediction Tools for Circular RNAs Analysis. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1087, 17-33.	0.8	87

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7290	Surveying the genome and constructing a high-density genetic map of napiergrass (<i>Cenchrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1071 1.65 32		
7291	Opaque-2 Regulates a Complex Gene Network Associated with Cell Differentiation and Storage Functions of Maize Endosperm. <i>Plant Cell</i> , 2018, 30, 2425-2446.	3.1	83
7292	A novel population of Hopx-dependent basal radial glial cells in the developing mouse neocortex. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	62
7293	<i>Caenorhabditis elegans</i> <sc>DLC</sc> associates with ribonucleoprotein complexes to promote <sc>mRNA</sc> regulation. <i>FEBS Letters</i> , 2018, 592, 3683-3695.	1.3	3
7294	Recent advances in CRISPR/Cas9 mediated genome editing in <i>Bacillus subtilis</i> . <i>World Journal of Microbiology and Biotechnology</i> , 2018, 34, 153.	1.7	29
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7299	Exome scale map of genetic alterations promoting metastasis in colorectal cancer. <i>BMC Genetics</i> , 2018, 19, 85.	2.7	22
7300	Exploring transcription factors reveals crucial members and regulatory networks involved in different abiotic stresses in <i>Brassica napus</i> L.. <i>BMC Plant Biology</i> , 2018, 18, 202.	1.6	53
7301	Waves of chromatin modifications in mouse dendritic cells in response to LPS stimulation. <i>Genome Biology</i> , 2018, 19, 138.	3.8	19
7302	Gene regulation by a glycine riboswitch singlet uses a finely tuned energetic landscape for helical switching. <i>Rna</i> , 2018, 24, 1813-1827.	1.6	18
7303	Transcriptional and epigenomic landscapes of CNS and non-CNS vascular endothelial cells. <i>ELife</i> , 2018, 7, .	2.8	180
7304	Impact of vitamin D depletion during development on mouse sperm DNA methylation. <i>Epigenetics</i> , 2018, 13, 959-974.	1.3	11
7305	Single-cell RNA-seq reveals dynamic transcriptome profiling in human early neural differentiation. <i>GigaScience</i> , 2018, 7, .	3.3	18
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7308	Hierarchical and stage-specific regulation of murine cardiomyocyte maturation by serum response factor. <i>Nature Communications</i> , 2018, 9, 3837.	5.8	63
7309	Essential Nucleoid Associated Protein mIHf (Rv1388) Controls Virulence and Housekeeping Genes in <i>Mycobacterium tuberculosis</i> . <i>Scientific Reports</i> , 2018, 8, 14214.	1.6	19
7310	BrownieAligner: accurate alignment of Illumina sequencing data to de Bruijn graphs. <i>BMC Bioinformatics</i> , 2018, 19, 311.	1.2	22
7311	ChIP-Seq reveals that QsMYB1 directly targets genes involved in lignin and suberin biosynthesis pathways in cork oak (<i>Quercus suber</i>). <i>BMC Plant Biology</i> , 2018, 18, 198.	1.6	50
7312	The mRNA cap methyltransferase gene <i>TbCMT1</i> is not essential in vitro but is a virulence factor in vivo for bloodstream form <i>Trypanosoma brucei</i> . <i>PLoS ONE</i> , 2018, 13, e0201263.	1.1	2
7313	A mosaic intragenic microduplication of <i>LAMA1</i> and a constitutional 18p11.32 microduplication in a patient with <i>keratosis pilaris</i> and intellectual disability. <i>American Journal of Medical Genetics, Part A</i> , 2018, 176, 2395-2403.	0.7	9
7314	Integrated Proteogenomic Approach for Identifying Degradation Motifs in Eukaryotic Cells. <i>Methods in Molecular Biology</i> , 2018, 1844, 121-136.	0.4	1
7315	Association between possession of <i>ExoU</i> and antibiotic resistance in <i>Pseudomonas aeruginosa</i> . <i>PLoS ONE</i> , 2018, 13, e0204936.	1.1	40
7316	Metagenomic Insights into the Degradation of Resistant Starch by Human Gut Microbiota. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	63
7317	A comprehensive analysis of 195 DNA methylomes reveals shared and cell-specific features of partially methylated domains. <i>Genome Biology</i> , 2018, 19, 150.	3.8	71
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7319	<i>Tripsacum</i> De novo Transcriptome Assemblies Reveal Parallel Gene Evolution with Maize after Ancient Polyploidy. <i>Plant Genome</i> , 2018, 11, 180012.	1.6	9
7320	Transcriptomics and co-expression networks reveal tissue-specific responses and regulatory hubs under mild and severe drought in papaya (<i>Carica papaya</i> L.). <i>Scientific Reports</i> , 2018, 8, 14539.	1.6	39
7321	Binning enables efficient host genome reconstruction in cnidarian holobionts. <i>GigaScience</i> , 2018, 7, .	3.3	16
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7323	HSRA: Hadoop-based spliced read aligner for RNA sequencing data. <i>PLoS ONE</i> , 2018, 13, e0201483.	1.1	12
7324	Considerations for Optimization of High-Throughput Sequencing Bioinformatics Pipelines for Virus Detection. <i>Viruses</i> , 2018, 10, 528.	1.5	21

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7325	Genotypic response of pollen germination in Dura, Pisifera and Tenera oil palm (<i>Elaeis guineensis</i>) Tj ETQq0 0 0 rgBT JOverlock 10 Tf 50	0.6	1
7326	Population genomics of <i>Fundulus grandis</i> exposed to oil from Deepwater Horizon. <i>Journal of Experimental Marine Biology and Ecology</i> , 2018, 509, 82-90.	0.7	3
7327	Transcriptome Analysis of Rainbow Trout (<i>Oncorhynchus mykiss</i>) Eggs Subjected to the High Hydrostatic Pressure Treatment. <i>International Journal of Genomics</i> , 2018, 2018, 1-7.	0.8	4
7328	Single Nucleotide Polymorphism Analysis Indicates Genetic Distinction and Reduced Diversity of Swine-Associated Methicillin Resistant <i>Staphylococcus aureus</i> (MRSA) ST5 Isolates Compared to Clinical MRSA ST5 Isolates. <i>Frontiers in Microbiology</i> , 2018, 9, 2078.	1.5	28
7329	In silico "fishing" using known small regulatory RNA (sRNA) candidates as the decoy from <i>Escherichia coli</i> , <i>Salmonella typhi</i> and <i>Salmonella typhimurium</i> manifested 14 novel sRNA candidates in the orthologous region of <i>Proteus mirabilis</i> . <i>Molecular Biology Reports</i> , 2018, 45, 2333-2343.	1.0	4
7330	Transcriptional recording by CRISPR spacer acquisition from RNA. <i>Nature</i> , 2018, 562, 380-385.	13.7	117
7331	Elongation/Termination Factor Exchange Mediated by PP1 Phosphatase Orchestrates Transcription Termination. <i>Cell Reports</i> , 2018, 25, 259-269.e5.	2.9	58
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7333	Soil Viruses Are Underexplored Players in Ecosystem Carbon Processing. <i>MSystems</i> , 2018, 3, .	1.7	189
7334	Licochalcone A attenuates acne symptoms mediated by suppression of NLRP3 inflammasome. <i>Phytotherapy Research</i> , 2018, 32, 2551-2559.	2.8	45
7335	Direct-to-consumer DNA testing of 6,000 dogs reveals 98.6-kb duplication associated with blue eyes and heterochromia in Siberian Huskies. <i>PLoS Genetics</i> , 2018, 14, e1007648.	1.5	21
7336	Maternal gut and breast milk microbiota affect infant gut antibiotic resistome and mobile genetic elements. <i>Nature Communications</i> , 2018, 9, 3891.	5.8	313
7337	Strain-level diversity drives alternative community types in millimetre-scale granular biofilms. <i>Nature Microbiology</i> , 2018, 3, 1295-1303.	5.9	93
7338	Metagenomic analyses highlight the symbiotic association between the glacier stonefly <i>Andiperla willinki</i> and its bacterial gut community. <i>Environmental Microbiology</i> , 2018, 20, 4170-4183.	1.8	25
7339	Structural features of two major nucleolar organizer regions (NORs), <i>NorA1</i> and <i>NorB2</i> , and chromosome-specific rRNA gene expression in wheat. <i>Plant Journal</i> , 2018, 96, 1148-1159.	2.8	17
7340	Heterogeneous combinatorial expression of <i>Hoxd</i> genes in single cells during limb development. <i>BMC Biology</i> , 2018, 16, 101.	1.7	21
7341	A metagenomics roadmap to the uncultured genome diversity in hypersaline soda lake sediments. <i>Microbiome</i> , 2018, 6, 168.	4.9	120
7342	Comprehensive Transcriptome Profiling and Identification of Potential Genes Responsible for Salt Tolerance in Tall Fescue Leaves under Salinity Stress. <i>Genes</i> , 2018, 9, 466.	1.0	5

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7344	DNA methylation of the promoter region of <i>bnip3</i> and <i>bnip3l</i> genes induced by metabolic programming. <i>BMC Genomics</i> , 2018, 19, 677.	1.2	27
7345	The genomic basis of environmental adaptation in house mice. <i>PLoS Genetics</i> , 2018, 14, e1007672.	1.5	65
7346	Genomic evolution of <i>Staphylococcus aureus</i> isolates colonizing the nares and progressing to bacteremia. <i>PLoS ONE</i> , 2018, 13, e0195860.	1.1	17
7347	Core non-coding RNAs of <i>Piscirickettsia salmonis</i> . <i>PLoS ONE</i> , 2018, 13, e0197206.	1.1	7
7348	4C-seq characterization of <i>Drosophila</i> BEAF binding regions provides evidence for highly variable long-distance interactions between active chromatin. <i>PLoS ONE</i> , 2018, 13, e0203843.	1.1	11
7349	<i>Arabidopsis</i> RNA processing factor <i>SERRATE</i> regulates the transcription of intronless genes. <i>ELife</i> , 2018, 7, .	2.8	32
7350	Whole genome resequencing of tobacco (<i>Nicotiana tabacum</i> L.) genotypes and high-throughput SNP discovery. <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	8
7351	Characterisation of pathogen-specific regions and novel effector candidates in <i>Fusarium oxysporum</i> f. sp. <i>cepae</i> . <i>Scientific Reports</i> , 2018, 8, 13530.	1.6	77
7352	SWI/SNF catalytic subunitsâ€™ switch drives resistance to EZH2 inhibitors in ARID1A-mutated cells. <i>Nature Communications</i> , 2018, 9, 4116.	5.8	38
7353	Impact of energy restriction during late gestation on the muscle and blood transcriptome of beef calves after preconditioning. <i>BMC Genomics</i> , 2018, 19, 702.	1.2	20
7354	The methylome of the marbled crayfish links gene body methylation to stable expression of poorly accessible genes. <i>Epigenetics and Chromatin</i> , 2018, 11, 57.	1.8	56
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7356	Subsampled Assemblies and Hybrid Nucleotide Composition/Differential Coverage Binning for Genome-Resolved Metagenomics. <i>Methods in Molecular Biology</i> , 2018, 1849, 215-225.	0.4	2
7357	Transcriptomic and metabolic response to chronic and acute thermal exposure of juvenile geoduck clams <i>Panopea globosa</i> . <i>Marine Genomics</i> , 2018, 42, 1-13.	0.4	21
7358	Crosstalk between BPA and FXRâ€™ Signaling Pathways Lead to Alterations of Undifferentiated Germ Cell Homeostasis and Male Fertility Disorders. <i>Stem Cell Reports</i> , 2018, 11, 944-958.	2.3	17
7359	Divergent wiring of repressive and active chromatin interactions between mouse embryonic and trophoblast lineages. <i>Nature Communications</i> , 2018, 9, 4189.	5.8	51
7360	Arylvinylpiperazine Amides, a New Class of Potent Inhibitors Targeting QcrB of <i>Mycobacterium tuberculosis</i> . <i>MBio</i> , 2018, 9, .	1.8	52

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7362	<i>Copaifera langsdorffii</i> Novel Putative Long Non-Coding RNAs: Interspecies Conservation Analysis in Adaptive Response to Different Biomes. <i>Non-coding RNA</i> , 2018, 4, 27.	1.3	4
7363	Potential for phenol biodegradation in cloud waters. <i>Biogeosciences</i> , 2018, 15, 5733-5744.	1.3	11
7364	NaOH low salt method for chloroplast isolation and highly pure cpDNA preparation from <i>Aeluropus littoralis</i> . <i>Applications in Plant Sciences</i> , 2018, 6, e01183.	0.8	0
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7367	Spt6 Is Required for the Fidelity of Promoter Selection. <i>Molecular Cell</i> , 2018, 72, 687-699.e6.	4.5	58
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7369	Frequent mutation of the FOXA1 untranslated region in prostate cancer. <i>Communications Biology</i> , 2018, 1, 122.	2.0	21
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7371	Intestinal toxicity of deoxynivalenol is limited by supplementation with <i>Lactobacillus plantarum</i> JM113 and consequentially altered gut microbiota in broiler chickens. <i>Journal of Animal Science and Biotechnology</i> , 2018, 9, 74.	2.1	65
7372	Genomic characterization reveals significant divergence within <i>Chlorella sorokiniana</i> (<i>Chlorellales</i>). <i>Tj ETQq1 1 0.784314 rgBT/Overlook</i>	2.4	27
7373	De Novo assembly and comparative transcriptome analyses of purple and green morphs of <i>Apostichopus japonicus</i> during body wall pigmentation process. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2018, 28, 151-161.	0.4	11
7374	Transcriptome analysis of differentially expressed genes involved in innate immunity following <i>Bacillus thuringiensis</i> challenge in <i>Bombyx mori</i> larvae. <i>Molecular Immunology</i> , 2018, 103, 220-228.	1.0	16
7375	Transcriptome analysis provides novel insights into high-soil-moisture-elevated susceptibility to <i>Ralstonia solanacearum</i> infection in ginger (<i>Zingiber officinale</i> Roscoe cv. Southwest). <i>Plant Physiology and Biochemistry</i> , 2018, 132, 547-556.	2.8	15
7376	Virome Analysis Reveals No Association of Head and Neck Vascular Anomalies with an Active Viral Infection. <i>In Vivo</i> , 2018, 32, 1323-1331.	0.6	3
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7378	Intrinsic Nucleotide Preference of Diversifying Base Editors Guides Antibody Ex Vivo Affinity Maturation. <i>Cell Reports</i> , 2018, 25, 884-892.e3.	2.9	28

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7380	Assortment of Flowering Time and Immunity Alleles in Natural <i>Arabidopsis thaliana</i> Populations Suggests Immunity and Vegetative Lifespan Strategies Coevolve. <i>Genome Biology and Evolution</i> , 2018, 10, 2278-2291.	1.1	14
7381	Enhancer, transcriptional, and cell fate plasticity precedes intestinal determination during endoderm development. <i>Genes and Development</i> , 2018, 32, 1430-1442.	2.7	34
7382	Using transcriptomics to enable a plethodontid salamander (<i>Bolitoglossa ramosi</i>) for limb regeneration research. <i>BMC Genomics</i> , 2018, 19, 704.	1.2	20
7383	Bacterial endosymbiont <i>Cardinium</i> cSfur genome sequence provides insights for understanding the symbiotic relationship in <i>Sogatella furcifera</i> host. <i>BMC Genomics</i> , 2018, 19, 688.	1.2	32
7384	Occurrence and characterization of methicillin-resistant <i>Staphylococcus pseudintermedius</i> in successive parturitions of bitches and their puppies in two kennels in Italy. <i>BMC Veterinary Research</i> , 2018, 14, 308.	0.7	11
7385	Elucidating Gene-by-Environment Interactions Associated with Differential Susceptibility to Chemical Exposure. <i>Environmental Health Perspectives</i> , 2018, 126, 067010.	2.8	21
7386	Genomic heterogeneity differentiates clinical and environmental subgroups of <i>Legionella pneumophila</i> sequence type 1. <i>PLoS ONE</i> , 2018, 13, e0206110.	1.1	9
7387	Aristaless Controls Butterfly Wing Color Variation Used in Mimicry and Mate Choice. <i>Current Biology</i> , 2018, 28, 3469-3474.e4.	1.8	79
7388	Contribution of epigenetic variation to adaptation in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2018, 9, 4446.	5.8	118
7389	Determinants of promoter and enhancer transcription directionality in metazoans. <i>Nature Communications</i> , 2018, 9, 4472.	5.8	22
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7392	HJURP antagonizes CENP-A mislocalization driven by the H3.3 chaperones HIRA and DAXX. <i>PLoS ONE</i> , 2018, 13, e0205948.	1.1	37
7393	In silico identification of conserved miRNAs and their selective target gene prediction in indicine (<i>Bos Tj</i> ETQq0 0 0,rgBT /Overlock 10 Tf	1.1	15
7394	Comparative Genomics of <i>Aspergillus flavus</i> S and L Morphotypes Yield Insights into Niche Adaptation. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3915-3930.	0.8	23
7395	Cytogenetic and Transcriptomic Analysis of Human Endometrial MSC Retaining Proliferative Activity after Sublethal Heat Shock. <i>Cells</i> , 2018, 7, 184.	1.8	10
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7398	CircMarker: a fast and accurate algorithm for circular RNA detection. <i>BMC Genomics</i> , 2018, 19, 572.	1.2	25
7399	The comparison of four mitochondrial genomes reveals cytoplasmic male sterility candidate genes in cotton. <i>BMC Genomics</i> , 2018, 19, 775.	1.2	28
7400	Prediction of smoking by multiplex bisulfite PCR with long amplicons considering allele-specific effects on DNA methylation. <i>Clinical Epigenetics</i> , 2018, 10, 130.	1.8	11
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7402	Molecular bases for the constitutive photomorphogenic phenotypes in <i>Arabidopsis</i> . <i>Development (Cambridge)</i> , 2018, 145, .	1.2	51
7403	Limited Correlation of Shotgun Metagenomics Following Host Depletion and Routine Diagnostics for Viruses and Bacteria in Low Concentrated Surrogate and Clinical Samples. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 375.	1.8	40
7404	Comparative genomics of clinical strains of <i>Pseudomonas aeruginosa</i> strains isolated from different geographic sites. <i>Scientific Reports</i> , 2018, 8, 15668.	1.6	61
7405	The complete chloroplast genome of <i>Notholition macrophyllum</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1102-1103.	0.2	1
7406	Transcriptomic analysis of sweet potato under dehydration stress identifies candidate genes for drought tolerance. <i>Plant Direct</i> , 2018, 2, e00092.	0.8	21
7407	<i>Bacillus megaterium</i> adapts to acid stress condition through a network of genes: Insight from a genome-wide transcriptome analysis. <i>Scientific Reports</i> , 2018, 8, 16105.	1.6	30
7408	Conversion of Methionine to Cysteine in <i>Lactobacillus paracasei</i> Depends on the Highly Mobile <i>cysK-ctl-cysE</i> Gene Cluster. <i>Frontiers in Microbiology</i> , 2018, 9, 2415.	1.5	10
7409	A planarian nidovirus expands the limits of RNA genome size. <i>PLoS Pathogens</i> , 2018, 14, e1007314.	2.1	108
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7419	Transcriptome evidence reveals enhanced autophagy-lysosomal function in centenarians. <i>Genome Research</i> , 2018, 28, 1601-1610.	2.4	36
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7422	Methylation of the Reelin Gene Promoter in Peripheral Blood and Its Relationship with the Cognitive Function of Schizophrenia Patients. <i>Molecular Biology</i> , 2018, 52, 676-685.	0.4	14
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7429	Gene expression variability across cells and species shapes innate immunity. <i>Nature</i> , 2018, 563, 197-202.	13.7	165
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7438	Regulation of Neuroregeneration by Long Noncoding RNAs. <i>Molecular Cell</i> , 2018, 72, 553-567.e5.	4.5	83
7439	SUMO Safeguards Somatic and Pluripotent Cell Identities by Enforcing Distinct Chromatin States. <i>Cell Stem Cell</i> , 2018, 23, 742-757.e8.	5.2	105
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8006	<i>Panax notoginseng</i> Root Cell Death Caused by the Autotoxic Ginsenoside Rg1 Is Due to Over-Accumulation of ROS, as Revealed by Transcriptomic and Cellular Approaches. <i>Frontiers in Plant Science</i> , 2018, 9, 264.	1.7	34
8007	Association Study Reveals Novel Genes Related to Yield and Quality of Fruit in Cape Gooseberry (<i>Physalis peruviana</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 362.	1.7	12
8008	Fine Mapping of CsVYL, Conferring Virescent Leaf Through the Regulation of Chloroplast Development in Cucumber. <i>Frontiers in Plant Science</i> , 2018, 9, 432.	1.7	38
8009	Massive Loss of DNA Methylation in Nitrogen-, but Not in Phosphorus-Deficient Zea mays Roots Is Poorly Correlated With Gene Expression Differences. <i>Frontiers in Plant Science</i> , 2018, 9, 497.	1.7	33

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8012	Identification of Putative Precursor Genes for the Biosynthesis of Cannabinoid-Like Compound in <i>Radula marginata</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 537.	1.7	28
8013	Comparative Chloroplast Genomics of Dipsacales Species: Insights Into Sequence Variation, Adaptive Evolution, and Phylogenetic Relationships. <i>Frontiers in Plant Science</i> , 2018, 9, 689.	1.7	110
8014	Molecular Profiling of Pierce's Disease Outlines the Response Circuitry of <i>Vitis vinifera</i> to <i>Xylella fastidiosa</i> Infection. <i>Frontiers in Plant Science</i> , 2018, 9, 771.	1.7	35
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8016	Functional Microbial Features Driving Community Assembly During Seed Germination and Emergence. <i>Frontiers in Plant Science</i> , 2018, 9, 902.	1.7	92
8017	Dual RNA-Seq Analysis of <i>Trichophyton rubrum</i> and HaCat Keratinocyte Co-Culture Highlights Important Genes for Fungal-Host Interaction. <i>Genes</i> , 2018, 9, 362.	1.0	38
8018	Oncogenic hijacking of the stress response machinery in T cell acute lymphoblastic leukemia. <i>Nature Medicine</i> , 2018, 24, 1157-1166.	15.2	63
8019	Size Distribution of Small Interfering RNAs in Various Organs at Different Developmental Stages is Primarily Determined by the Dicing Activity of Dicer-Like Proteins in Plants. <i>Plant and Cell Physiology</i> , 2018, 59, 2228-2238.	1.5	11
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8021	Viromic Analysis of Wastewater Input to a River Catchment Reveals a Diverse Assemblage of RNA Viruses. <i>MSystems</i> , 2018, 3, .	1.7	59
8022	Evaluation of bias induced by viral enrichment and random amplification protocols in metagenomic surveys of saliva DNA viruses. <i>Microbiome</i> , 2018, 6, 119.	4.9	81
8023	Integration of RNAi and RNA-seq Reveals the Immune Responses of <i>Epinephelus coioides</i> to sigX Gene of <i>Pseudomonas plecoglossicida</i> . <i>Frontiers in Immunology</i> , 2018, 9, 1624.	2.2	67
8024	UGbS-Flex, a novel bioinformatics pipeline for imputation-free SNP discovery in polyploids without a reference genome: finger millet as a case study. <i>BMC Plant Biology</i> , 2018, 18, 117.	1.6	54
8025	Early Transcriptomic Response to Phosphate Deprivation in Soybean Leaves as Revealed by RNA-Sequencing. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2145.	1.8	19
8026	Dissection of progenitor compartments resolves developmental trajectories in B-lymphopoiesis. <i>Journal of Experimental Medicine</i> , 2018, 215, 1947-1963.	4.2	20
8027	The plant compound rosmarinic acid induces a broad quorum sensing response in <i>Pseudomonas aeruginosa</i> PAO1. <i>Environmental Microbiology</i> , 2018, 20, 4230-4244.	1.8	17

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8031	Genomic and Transcriptomic Analysis Identified Gene Clusters and Candidate Genes for Oil Content in Peanut (<i>Arachis hypogaea</i> L.). <i>Plant Molecular Biology Reporter</i> , 2018, 36, 518-529.	1.0	18
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8033	Determination of system level alterations in host transcriptome due to Zika virus (ZIKV) Infection in retinal pigment epithelium. <i>Scientific Reports</i> , 2018, 8, 11209.	1.6	37
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8036	A Diverse Range of Human Gut Bacteria Have the Potential To Metabolize the Dietary Component Gallic Acid. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	20
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8038	Loci under selection and markers associated with host plant and host-related strains shape the genetic structure of Brazilian populations of <i>Spodoptera frugiperda</i> (Lepidoptera, Noctuidae). <i>PLoS ONE</i> , 2018, 13, e0197378.	1.1	15
8039	Different murine-derived feeder cells alter the definitive endoderm differentiation of human induced pluripotent stem cells. <i>PLoS ONE</i> , 2018, 13, e0201239.	1.1	3
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8041	Long Non-coding MIR205HG Depletes Hsa-miR-590-3p Leading to Unrestrained Proliferation in Head and Neck Squamous Cell Carcinoma. <i>Theranostics</i> , 2018, 8, 1850-1868.	4.6	65
8042	Transcriptome analysis for identification of candidate genes related to sex determination and growth in <i>Charybdis japonica</i> . <i>Gene</i> , 2018, 677, 10-16.	1.0	18
8043	Transcriptome analysis reveals the effects of grafting on sugar and \pm -linolenic acid metabolisms in fruits of cucumber with two different rootstocks. <i>Plant Physiology and Biochemistry</i> , 2018, 130, 289-302.	2.8	17
8044	Genes differentially expressed in broccoli as an early and late response to wounding stress. <i>Postharvest Biology and Technology</i> , 2018, 145, 172-182.	2.9	36
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8047	Divergent gene expression among phytoplankton taxa in response to upwelling. <i>Environmental Microbiology</i> , 2018, 20, 3069-3082.	1.8	34
8048	Physiological and genomic signatures of evolutionary thermal adaptation in redband trout from extreme climates. <i>Evolutionary Applications</i> , 2018, 11, 1686-1699.	1.5	38
8049	Whole genome SNP analysis suggests unique virulence factor differences of the Beijing and Manila families of <i>Mycobacterium tuberculosis</i> found in Hawaii. <i>PLoS ONE</i> , 2018, 13, e0201146.	1.1	9
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8051	Application of Transcriptomics to Compare the Carbohydrate Active Enzymes That Are Expressed by Diverse Genera of Anaerobic Fungi to Degrade Plant Cell Wall Carbohydrates. <i>Frontiers in Microbiology</i> , 2018, 9, 1581.	1.5	58
8053	How does normalization impact RNA-seq disease diagnosis?. <i>Journal of Biomedical Informatics</i> , 2018, 85, 80-92.	2.5	20
8054	A comparison of next-generation sequencing analysis methods for cancer xenograft samples. <i>Journal of Genetics and Genomics</i> , 2018, 45, 345-350.	1.7	5
8055	Endosymbiont genomes yield clues of tubeworm success. <i>ISME Journal</i> , 2018, 12, 2785-2795.	4.4	33
8056	Mitochondrial double-stranded RNA triggers antiviral signalling in humans. <i>Nature</i> , 2018, 560, 238-242.	13.7	397
8057	Functional profiles of coronal and dentin caries in children. <i>Journal of Oral Microbiology</i> , 2018, 10, 1495976.	1.2	33
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8059	No detectable effect of <i>Wolbachia w</i> Mel on the prevalence and abundance of the RNA virome of <i>Drosophila melanogaster</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20181165.	1.2	53
8060	Evidence for involvement of a transformer paralogue in sex determination of the wasp <i>Leptopilina clavipes</i> . <i>Insect Molecular Biology</i> , 2018, 27, 780-795.	1.0	12
8061	Genome Reduction in <i>Psychromonas</i> Species within the Gut of an Amphipod from the Ocean's Deepest Point. <i>MSystems</i> , 2018, 3, .	1.7	21
8062	Genome-wide analysis of differentially expressed profiles of mRNAs, lncRNAs and circRNAs during <i>Cryptosporidium baileyi</i> infection. <i>BMC Genomics</i> , 2018, 19, 356.	1.2	26
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8069	Immune-Related Functional Differential Gene Expression in Koi Carp (<i>Cyprinus carpio</i>) after Challenge with <i>Aeromonas sobria</i> . International Journal of Molecular Sciences, 2018, 19, 2107.	1.8	19
8070	Co-Infection Patterns in Individual <i>Ixodes scapularis</i> Ticks Reveal Associations between Viral, Eukaryotic and Bacterial Microorganisms. Viruses, 2018, 10, 388.	1.5	44
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8098	miR-MaGiC improves quantification accuracy for small RNA-seq. <i>BMC Research Notes</i> , 2018, 11, 296.	0.6	9
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8103	A Novel Eukaryotic Denitrification Pathway in Foraminifera. <i>Current Biology</i> , 2018, 28, 2536-2543.e5.	1.8	75
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8107	Transcriptomic comparison reveals genetic variation potentially underlying seed developmental evolution of soybeans. <i>Journal of Experimental Botany</i> , 2018, 69, 5089-5104.	2.4	46
8108	Novel insights on colonization routes and evolutionary potential of <i>Colletotrichum kahawae</i> , a severe pathogen of <i>Coffea arabica</i> . <i>Molecular Plant Pathology</i> , 2018, 19, 2488-2501.	2.0	22
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8114	Current Strategies and Applications for Precision Drug Design. <i>Frontiers in Pharmacology</i> , 2018, 9, 787.	1.6	32
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8125	Genome-Wide Identification of Destruxin A-Responsive Immunity-Related MicroRNAs in Diamondback Moth, <i>Plutella xylostella</i> . <i>Frontiers in Immunology</i> , 2018, 9, 185.	2.2	24
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9866	Enterobacteriaceae dominate the core microbiome and contribute to the resistome of arugula (<i>Eruca</i>) Tj ETQq1 1 0.784314 rgBT /Over 4.9 84		
9867	The Genetics of Mating Song Evolution Underlying Rapid Speciation: Linking Quantitative Variation to Candidate Genes for Behavioral Isolation. <i>Genetics</i> , 2019, 211, 1089-1104.	1.2	26
9868	Identification of Loci and Candidate Genes Responsible for Fiber Length in Upland Cotton (<i>Gossypium</i>) Tj ETQq1 1 0.784314 rgBT /Over 1.7 26		
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9873	Combining CDK4/6 inhibition with taxanes enhances anti-tumor efficacy by sustained impairment of pRB-E2F pathways in squamous cell lung cancer. <i>Oncogene</i> , 2019, 38, 4125-4141.	2.6	34
9874	Marine biofilms constitute a bank of hidden microbial diversity and functional potential. <i>Nature Communications</i> , 2019, 10, 517.	5.8	100
9875	The Virulence Function and Regulation of the Metalloprotease Gene <i>prtA</i> in the Plant-Pathogenic Bacterium <i>Burkholderia glumae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 841-852.	1.4	16
9876	Plant Extracellular Vesicles Contain Diverse Small RNA Species and Are Enriched in 10- to 17-Nucleotide ϵ -Tiny-RNAs. <i>Plant Cell</i> , 2019, 31, 315-324.	3.1	171

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9878	Draft Genome Sequence of <i>Streptococcus halitosis</i> sp. nov., Isolated from the Dorsal Surface of the Tongue of a Patient with Halitosis. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
9879	Host microRNA analysis in cyprinid Herpesvirus-3 (CyHV-3) infected common carp. <i>BMC Genomics</i> , 2019, 20, 46.	1.2	10
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9884	Dynamic Interactions Between the Genome and an Endogenous Retrovirus: Tirant in <i>Drosophila simulans</i> Wild-Type Strains. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 855-865.	0.8	5
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9886	Transcriptome, enzyme activity and histopathology analysis reveal the effects of dietary carbohydrate on glycometabolism in juvenile largemouth bass, <i>Micropterus salmoides</i> . <i>Aquaculture</i> , 2019, 504, 39-51.	1.7	39
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9889	Genomic Analyses of Acute Flaccid Myelitis Cases among a Cluster in Arizona Provide Further Evidence of Enterovirus D68 Role. <i>MBio</i> , 2019, 10, .	1.8	15
9890	Genomic and metagenomic insights into the microbial community of a thermal spring. <i>Microbiome</i> , 2019, 7, 8.	4.9	40
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9902	Metatranscriptomic Analysis of the Bacterial Symbiont <i>Dactylopiibacterium carminicum</i> from the Carmine Cochineal <i>Dactylopius coccus</i> (Hemiptera: Coccoidea: Dactylopiidae). <i>Life</i> , 2019, 9, 4.	1.1	13
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9908	Gut Virome Analysis of Cameroonians Reveals High Diversity of Enteric Viruses, Including Potential Interspecies Transmitted Viruses. <i>MSphere</i> , 2019, 4, .	1.3	57
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9920	Integrative omics analysis in <i>Pandanus odorifer</i> (Forssk.) Kuntze reveals the role of Asparagine synthetase in salinity tolerance. <i>Scientific Reports</i> , 2019, 9, 932.	1.6	24
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9926	Dual RNA-seq reveals the effect of the <i>flgM</i> gene of <i>Pseudomonas plecoglossicida</i> on the immune response of <i>Epinephelus coioides</i> . <i>Fish and Shellfish Immunology</i> , 2019, 87, 515-523.	1.6	39
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9930	Nascent-protein ubiquitination is required for heat shock-induced gene downregulation in human cells. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 137-146.	3.6	42

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9951	Epigenome-wide effects of vitamin D on asthma bronchial epithelial cells. <i>Epigenetics</i> , 2019, 14, 844-849.	1.3	3
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9988	Genomic Resources for <i>Goniozus legneri</i> , <i>Aleochara bilineata</i> and <i>Paykullia maculata</i> , Representing Three Independent Origins of the Parasitoid Lifestyle in Insects. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 987-991.	0.8	10
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10126	Histone demethylase <i>Kdm2a</i> regulates germ cell genes and endogenous retroviruses in embryonic stem cells. <i>Epigenomics</i> , 2019, 11, 751-766.	1.0	11
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10147	Transcriptome and differentially expressed genes of <i>Busseola fusca</i> (Lepidoptera: Noctuidae) larvae challenged with Cry1Ab toxin. <i>Gene</i> , 2019, 710, 387-398.	1.0	7
10148	Genome-wide cell-free DNA fragmentation in patients with cancer. <i>Nature</i> , 2019, 570, 385-389.	13.7	764
10149	Acute depletion of CTCF directly affects MYC regulation through loss of enhancer-promoter looping. <i>Nucleic Acids Research</i> , 2019, 47, 6699-6713.	6.5	98
10150	Crunch: integrated processing and modeling of ChIP-seq data in terms of regulatory motifs. <i>Genome Research</i> , 2019, 29, 1164-1177.	2.4	7
10151	Draft Genome Sequence of Phocine Herpesvirus 1 Isolated from the Brain of a Harbor Seal. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
10152	Differential expression of innate and adaptive immune genes in the survivors of three gibel carp gynogenetic clones after herpesvirus challenge. <i>BMC Genomics</i> , 2019, 20, 432.	1.2	27
10153	Comprehensive analysis of genes contributing to euryhalinity in the bull shark, <i>Carcharhinus leucas</i> ; Na ⁺ -Cl ⁻ co-transporter is one of the key renal factors up-regulated in acclimation to low-salinity environment in bull sharks, but not in houndsharks, <i>Triakis scyllium</i> . <i>Journal of Experimental Biology</i> , 2019, 222, .	0.8	14
10154	Dissecting the genetic control of root and leaf tissue-specific anthocyanin pigmentation in carrot (<i>Daucus carota</i> L.). <i>Theoretical and Applied Genetics</i> , 2019, 132, 2485-2507.	1.8	27
10155	Human Gut Microbiota from Autism Spectrum Disorder Promote Behavioral Symptoms in Mice. <i>Cell</i> , 2019, 177, 1600-1618.e17.	13.5	701
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10158	Guidelines for SHAPE Reagent Choice and Detection Strategy for RNA Structure Probing Studies. <i>Biochemistry</i> , 2019, 58, 2655-2664.	1.2	91
10159	Interspecies conservation of organisation and function between nonhomologous regional centromeres. <i>Nature Communications</i> , 2019, 10, 2343.	5.8	36
10160	RNA-seq analysis and fluorescence imaging of melon powdery mildew disease reveal an orchestrated reprogramming of host physiology. <i>Scientific Reports</i> , 2019, 9, 7978.	1.6	36
10161	Preformed chromatin topology assists transcriptional robustness of <i>Shh</i> during limb development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12390-12399.	3.3	131
10162	High bacterial diversity in nearshore and oceanic biofilms and their influence on larval settlement by <i>Hydroides elegans</i> (Polychaeta). <i>Environmental Microbiology</i> , 2019, 21, 3472-3488.	1.8	22
10163	Rapid molecular evolution of pain insensitivity in multiple African rodents. <i>Science</i> , 2019, 364, 852-859.	6.0	57
10164	Comparative transcriptomic analysis of dermal wound healing reveals de novo skeletal muscle regeneration in <i>Acomys cahirinus</i> . <i>PLoS ONE</i> , 2019, 14, e0216228.	1.1	27

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10166	Systematic Analysis of Non-coding RNAs Involved in the Angora Rabbit (<i>Oryctolagus cuniculus</i>) Hair Follicle Cycle by RNA Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 407.	1.1	57
10167	Cholesterol-25-hydroxylase Is a Chicken ISG That Restricts ALV-J Infection by Producing 25-hydroxycholesterol. <i>Viruses</i> , 2019, 11, 498.	1.5	28
10168	Development of a cost-effective single nucleotide polymorphism genotyping array for management of greater yam germplasm collections. <i>Ecology and Evolution</i> , 2019, 9, 5617-5636.	0.8	8
10169	Kdm1a promotes SCLC progression by transcriptionally silencing the tumor suppressor Rest. <i>Biochemical and Biophysical Research Communications</i> , 2019, 515, 214-221.	1.0	14
10170	Gut microbiome differences between wild and captive black rhinoceros – implications for rhino health. <i>Scientific Reports</i> , 2019, 9, 7570.	1.6	97
10171	Sperm epimutation biomarkers of obesity and pathologies following DDT induced epigenetic transgenerational inheritance of disease. <i>Environmental Epigenetics</i> , 2019, 5, dvz008.	0.9	46
10172	APER0: a genome-wide approach for identifying bacterial small RNAs from RNA-Seq data. <i>Nucleic Acids Research</i> , 2019, 47, e88-e88.	6.5	21
10173	Anacapa Toolkit: An environmental DNA toolkit for processing multilocus metabarcode datasets. <i>Methods in Ecology and Evolution</i> , 2019, 10, 1469-1475.	2.2	88
10174	RB1 Deletion in Retinoblastoma Protein Pathway-Disrupted Cells Results in DNA Damage and Cancer Progression. <i>Molecular and Cellular Biology</i> , 2019, 39, .	1.1	34
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10178	Mitochondrial genome diversity and evolution in Branchiopoda (Crustacea). <i>Zoological Letters</i> , 2019, 5, 15.	0.7	16
10179	Effects of Predator-Prey Interactions on Predator Traits: Differentiation of Diets and Venoms of a Marine Snail. <i>Toxins</i> , 2019, 11, 299.	1.5	9
10180	Evaluation of Sequencing Library Preparation Protocols for Viral Metagenomic Analysis from Pristine Aquifer Groundwaters. <i>Viruses</i> , 2019, 11, 484.	1.5	27
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10184	Induced androgenetic development in rainbow trout and transcriptome analysis of irradiated eggs. <i>Scientific Reports</i> , 2019, 9, 8084.	1.6	7
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10186	Decoding the Inversion Symmetry Underlying Transcription Factor DNA-Binding Specificity and Functionality in the Genome. <i>IScience</i> , 2019, 15, 552-591.	1.9	2
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10189	Structural basis for selective stalling of human ribosome nascent chain complexes by a drug-like molecule. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 501-509.	3.6	67
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10191	Critical role of the fibroblast growth factor signalling pathway in Ewing's sarcoma octamer-binding transcription factor 4-mediated cell proliferation and tumorigenesis. <i>FEBS Journal</i> , 2019, 286, 4443-4472.	2.2	7
10192	Application of high-throughput amplicon sequencing-based SSR genotyping in genetic background screening. <i>BMC Genomics</i> , 2019, 20, 444.	1.2	10
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10195	A defined cultivation medium for <i>Sulfolobus acidocaldarius</i> . <i>Journal of Biotechnology</i> , 2019, 301, 56-67.	1.9	15
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10202	Endodermal Maternal Transcription Factors Establish Super-Enhancers during Zygotic Genome Activation. <i>Cell Reports</i> , 2019, 27, 2962-2977.e5.	2.9	31
10203	DNA methylome profiling in identical twin pairs discordant for body mass index. <i>International Journal of Obesity</i> , 2019, 43, 2491-2499.	1.6	16
10204	Transcriptional activation of elephant shark mineralocorticoid receptor by corticosteroids, progesterone, and spironolactone. <i>Science Signaling</i> , 2019, 12, .	1.6	30
10205	Uncovering anthocyanin biosynthesis related microRNAs and their target genes by small RNA and degradome sequencing in tuberous roots of sweetpotato. <i>BMC Plant Biology</i> , 2019, 19, 232.	1.6	43
10206	<i>De Novo</i> Genome Sequence Assembly of Dwarf Coconut (<i>Cocos nucifera</i> L. 'Catigan Green') Tj ETQq1 1 0.784314 rgB Genes, Genomes, Genetics, 2019, 9, 2377-2393.	0.8	55
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10210	Rapid identification of unknown pathogens in environmental samples using a high-throughput sequencing-based approach. <i>Heliyon</i> , 2019, 5, e01793.	1.4	5
10211	Genomic analysis of human invasive <i>Salmonella enterica</i> serovar Typhimurium ST313 isolate B3589 from India. <i>Infection, Genetics and Evolution</i> , 2019, 73, 416-424.	1.0	7
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10213	Habitat preference modulates trans-oceanic dispersal in a terrestrial vertebrate. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182575.	1.2	21
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10220	Identification of <i>De Novo</i> Enhancers Activated by TGF β 2 to Drive Expression of <i>CDKN2A</i> and <i>B</i> in HeLa Cells. <i>Molecular Cancer Research</i> , 2019, 17, 1854-1866.	1.5	6
10221	Analysis of metabolic pathways related to fertility restoration and identification of fertility candidate genes associated with <i>Aegilops kotschy</i> cytoplasm in wheat (<i>Triticum aestivum</i> L.). <i>BMC Plant Biology</i> , 2019, 19, 252.	1.6	9
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10223	Effect of ethanol supplementation on the transcriptional landscape of bionanocellulose producer <i>Komagataeibacter xylinus</i> E25. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 6673-6688.	1.7	35
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10229	Cell Cycle-Dependent Regulation and Function of ARGONAUTE1 in Plants. <i>Plant Cell</i> , 2019, 31, 1734-1750.	3.1	24
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10233	Genomic erosion and extensive horizontal gene transfer in gut-associated Acetobacteraceae. <i>BMC Genomics</i> , 2019, 20, 472.	1.2	32
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10238	Reverse geneâ€‘environment interaction approach to identify variants influencing body-mass index in humans. <i>Nature Metabolism</i> , 2019, 1, 630-642.	5.1	14
10239	Chickspress: a resource for chicken gene expression. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	17
10240	Coding palindromes in mitochondrial genes of Nematomorpha. <i>Nucleic Acids Research</i> , 2019, 47, 6858-6870.	6.5	8
10241	Global population genomics of the forest pathogen <i>Dothistroma septosporum</i> reveal chromosome duplications in high dothistrominâ€‘producing strains. <i>Molecular Plant Pathology</i> , 2019, 20, 784-799.	2.0	19
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10249	The application of high-throughput sequencing for taxonomy: The case of <i>Plantago</i> subg. <i>Plantago</i> (<i>Plantaginaceae</i>). <i>Molecular Phylogenetics and Evolution</i> , 2019, 138, 156-173.	1.2	27
10250	Mediterranean grassland soil Câ€‘N compound turnover is dependent on rainfall and depth, and is mediated by genomically divergent microorganisms. <i>Nature Microbiology</i> , 2019, 4, 1356-1367.	5.9	170
10251	LanceletDB: an integrated genome database for lancelet, comparing domain types and combination in orthologues among lancelet and other species. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	7
10252	Circular RNA expression profile of knee condyle in osteoarthritis by illumina HiSeq platform. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 17500-17511.	1.2	31
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10256	Uncultured <i>Nitrospina</i> -like species are major nitrite oxidizing bacteria in oxygen minimum zones. <i>ISME Journal</i> , 2019, 13, 2391-2402.	4.4	67
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10259	Mitochondrial Oxidative Phosphorylation defect in the Heart of Subjects with Coronary Artery Disease. <i>Scientific Reports</i> , 2019, 9, 7623.	1.6	59
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10261	The dynamics of mito-nuclear coevolution: A perspective from bivalve species with two different mechanisms of mitochondrial inheritance. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2019, 57, 534-547.	0.6	4
10262	ARID1A spatially partitions interphase chromosomes. <i>Science Advances</i> , 2019, 5, eaaw5294.	4.7	35
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10268	Neuron-Astrocyte Metabolic Coupling Protects against Activity-Induced Fatty Acid Toxicity. <i>Cell</i> , 2019, 177, 1522-1535.e14.	13.5	350
10269	Hand2 Selectively Reorganizes Chromatin Accessibility to Induce Pacemaker-like Transcriptional Reprogramming. <i>Cell Reports</i> , 2019, 27, 2354-2369.e7.	2.9	23
10270	Nutrient Sensing in CD11c Cells Alters the Gut Microbiota to Regulate Food Intake and Body Mass. <i>Cell Metabolism</i> , 2019, 30, 364-373.e7.	7.2	31
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10272	FLASH: a next-generation CRISPR diagnostic for multiplexed detection of antimicrobial resistance sequences. <i>Nucleic Acids Research</i> , 2019, 47, e83-e83.	6.5	168

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10274	Accurate sequence variant genotyping in cattle using variation-aware genome graphs. <i>Genetics Selection Evolution</i> , 2019, 51, 21.	1.2	26
10275	Aberrant activation of CYR61 enhancers in colorectal cancer development. <i>Journal of Experimental and Clinical Cancer Research</i> , 2019, 38, 213.	3.5	34
10276	DNA methylome of human neonatal umbilical cord: Enrichment of differentially methylated regions compared to umbilical cord blood DNA at transcription factor genes involved in body patterning and effects of maternal folate deficiency or children's sex. <i>PLoS ONE</i> , 2019, 14, e0214307.	1.1	11
10277	Physiological and transcriptomic analyses reveal the molecular networks of responses induced by exogenous trehalose in plant. <i>PLoS ONE</i> , 2019, 14, e0217204.	1.1	28
10278	Quantitative Genetic Mapping and Genome Assembly in the Lesser Wax Moth <i>Achroia grisella</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2349-2361.	0.8	3
10279	The Functional and Molecular Effects of Doxycycline Treatment on <i>Borrelia burgdorferi</i> Phenotype. <i>Frontiers in Microbiology</i> , 2019, 10, 690.	1.5	13
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10282	Molecular basis underlying the successful invasion of hexaploid cytotypes of <i>Solidago canadensis</i> L.: Insights from integrated gene and miRNA expression profiling. <i>Ecology and Evolution</i> , 2019, 9, 4820-4852.	0.8	14
10283	The harmful algae, <i>Cochlodinium polykrikoides</i> and <i>Aureococcus anophagefferens</i> , elicit stronger transcriptomic and mortality response in larval bivalves (<i>Argopecten irradians</i>) than climate change stressors. <i>Ecology and Evolution</i> , 2019, 9, 4931-4948.	0.8	6
10284	Zfp281 Shapes the Transcriptome of Trophoblast Stem Cells and Is Essential for Placental Development. <i>Cell Reports</i> , 2019, 27, 1742-1754.e6.	2.9	34
10285	Redondoviridae, a Family of Small, Circular DNA Viruses of the Human Oro-Respiratory Tract Associated with Periodontitis and Critical Illness. <i>Cell Host and Microbe</i> , 2019, 25, 719-729.e4.	5.1	83
10286	Transcriptome and histone epigenome of <i>Plasmodium vivax</i> salivary-gland sporozoites point to tight regulatory control and mechanisms for liver-stage differentiation in relapsing malaria. <i>International Journal for Parasitology</i> , 2019, 49, 501-513.	1.3	42
10287	The RNA-Binding ATPase, Armitage, Couples piRNA Amplification in Nuage to Phased piRNA Production on Mitochondria. <i>Molecular Cell</i> , 2019, 74, 982-995.e6.	4.5	65
10288	T929I and K1774N mutation pair and M918L single mutation identified in the voltage-gated sodium channel gene of pyrethroid-resistant Thrips <i>tabaci</i> (Thysanoptera: Thripidae) in Japan. <i>Pesticide Biochemistry and Physiology</i> , 2019, 158, 77-87.	1.6	7
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10562	Transcriptomic analysis of small intestinal mucosa from porcine epidemic diarrhea virus infected piglets. <i>Microbial Pathogenesis</i> , 2019, 132, 73-79.	1.3	26
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10564	Comparative Transcriptomic Profiling of <i>Yersinia enterocolitica</i> O:3 and O:8 Reveals Major Expression Differences of Fitness- and Virulence-Relevant Genes Indicating Ecological Separation. <i>MSystems</i> , 2019, 4, .	1.7	8
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11885	Computational aspects underlying genome to phenome analysis in plants. <i>Plant Journal</i> , 2019, 97, 182-198.	2.8	50
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11904	Usage Guide of Web-based ncRNA Resources. , 2019, , 267-274.		0
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#	ARTICLE	IF	CITATIONS
12030	Predominantly Antibiotic-resistant Intestinal Microbiome Persists in Patients With Pouchitis Who Respond to Antibiotic Therapy. <i>Gastroenterology</i> , 2020, 158, 610-624.e13.	0.6	53
12031	Inherited variants at 3q13.33 and 3p24.1 are associated with risk of diffuse large B-cell lymphoma and implicate immune pathways. <i>Human Molecular Genetics</i> , 2020, 29, 70-79.	1.4	17
12032	Complex microbial nitrogen-cycling networks in three distinct anammox-inoculated wastewater treatment systems. <i>Water Research</i> , 2020, 168, 115142.	5.3	109
12033	Comparative metagenomics of two distinct biological soil crusts in the Tengger Desert, China. <i>Soil Biology and Biochemistry</i> , 2020, 140, 107637.	4.2	48
12034	The first complete mitochondrial genome of the sand dollar <i>Sinaechinocyamus mai</i> (Echinoidea: Tj ETQq0 0 0 rgBT, /Overlock, 10 Tf 50 5	1.3	16
12035	<tt>neopiscope</tt> improves neopeptide prediction with multivariant phasing. <i>Bioinformatics</i> , 2020, 36, 713-720.	1.8	23
12036	CFEA: a cell-free epigenome atlas in human diseases. <i>Nucleic Acids Research</i> , 2020, 48, D40-D44.	6.5	32
12037	Dense SNP panels resolve closely related Chinook salmon populations. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2020, 77, 451-461.	0.7	33
12038	Enhanced reductive dechlorination of trichloroethene with immobilized <i>Clostridium butyricum</i> in silica gel. <i>Chemosphere</i> , 2020, 238, 124596.	4.2	18
12039	Whole-genome sequencing and analysis of the Chinese herbal plant <i>Gelsemium elegans</i> . <i>Acta Pharmaceutica Sinica B</i> , 2020, 10, 374-382.	5.7	29
12040	A role of age-dependent DNA methylation reprogramming in regulating the regeneration capacity of <i>Boea hygrometrica</i> leaves. <i>Functional and Integrative Genomics</i> , 2020, 20, 133-149.	1.4	13
12041	Location deviations of DNA functional elements affected SNP mapping in the published databases and references. <i>Briefings in Bioinformatics</i> , 2020, 21, 1293-1301.	3.2	7
12042	Translation of TNFAIP2 is tightly controlled by upstream open reading frames. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 2017-2027.	2.4	6
12043	Comparative de novo assembly and annotation of mantle tissue transcriptomes from the <i>Mytilus edulis</i> species complex (<i>M. edulis</i> , <i>M. galloprovincialis</i> , <i>M. trossulus</i>). <i>Marine Genomics</i> , 2020, 51, 100700.	0.4	11
12044	Identification and characterization of miRNAs and lncRNAs of coho salmon (<i>Oncorhynchus kisutch</i>) in normal immune organs. <i>Genomics</i> , 2020, 112, 45-54.	1.3	20
12045	Reconstruction of transcriptional regulatory networks of Fis and H-NS in <i>Escherichia coli</i> from genome-wide data analysis. <i>Genomics</i> , 2020, 112, 1264-1272.	1.3	11
12046	Sclecting epithelioid mesenchymal neoplasm of the pancreas—A proposed new entity. <i>Modern Pathology</i> , 2020, 33, 456-467.	2.9	10
12047	Genomic adaptation of marine phytoplankton populations regulates phosphate uptake. <i>Limnology and Oceanography</i> , 2020, 65, S340.	1.6	13

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12048	Identification of rumen microbial biomarkers linked to methane emission in Holstein dairy cows. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 49-59.	0.8	51
12049	Single-base methylome profiling of the giant kelp <i>Saccharina japonica</i> reveals significant differences in DNA methylation to microalgae and plants. <i>New Phytologist</i> , 2020, 225, 234-249.	3.5	38
12050	Genome-Wide Analysis Reveals Zinc Transporter ZIP9 Regulated by DNA Methylation Promotes Radiation-Induced Skin Fibrosis via the TGF- β 2 Signaling Pathway. <i>Journal of Investigative Dermatology</i> , 2020, 140, 94-102.e7.	0.3	22
12051	Experimental support for multidrug resistance transfer potential in the preterm infant gut microbiota. <i>Pediatric Research</i> , 2020, 88, 57-65.	1.1	21
12052	The draft genome of a wild barley genotype reveals its enrichment in genes related to biotic and abiotic stresses compared to cultivated barley. <i>Plant Biotechnology Journal</i> , 2020, 18, 443-456.	4.1	45
12053	Vitamin D differentially regulates colon stem cells in patient-derived normal and tumor organoids. <i>FEBS Journal</i> , 2020, 287, 53-72.	2.2	67
12054	A high-throughput BAC end analysis protocol (BAC-anchor) for profiling genome assembly and physical mapping. <i>Plant Biotechnology Journal</i> , 2020, 18, 364-372.	4.1	6
12055	Massive postglacial gene flow between European white oaks uncovered genes underlying species barriers. <i>New Phytologist</i> , 2020, 226, 1183-1197.	3.5	46
12056	Global changes in chromatin accessibility and transcription following <i>ATR-X</i> inactivation in human cancer cells. <i>FEBS Letters</i> , 2020, 594, 67-78.	1.3	15
12057	Viral metagenomic analysis of the cheese surface: A comparative study of rapid procedures for extracting viral particles. <i>Food Microbiology</i> , 2020, 85, 103278.	2.1	31
12058	Gene expression during genital morphogenesis in the ground beetle <i>Carabus maiyasanus</i> . <i>Insect Science</i> , 2020, 27, 975-986.	1.5	4
12059	Exploring the potential of nuclear and mitochondrial sequencing data generated through genome-skimming for plant phylogenetics: A case study from a clade of neotropical lianas. <i>Journal of Systematics and Evolution</i> , 2020, 58, 18-32.	1.6	24
12060	4C-seq from beginning to end: A detailed protocol for sample preparation and data analysis. <i>Methods</i> , 2020, 170, 17-32.	1.9	107
12061	Methods for detection and study of virus-derived small RNAs produced from the intramolecular base-pairing region of the picornavirus genome. <i>Methods</i> , 2020, 183, 4-12.	1.9	7
12062	Identifying hidden biocomplexity and genomic diversity in Chinook salmon, an imperiled species with a history of anthropogenic influence. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2020, 77, 534-547.	0.7	4
12063	Age-related DNA hydroxymethylation is enriched for gene expression and immune system processes in human peripheral blood. <i>Epigenetics</i> , 2020, 15, 294-306.	1.3	8
12064	Molecular Evolution of Auxin-Mediated Root Initiation in Plants. <i>Molecular Biology and Evolution</i> , 2020, 37, 1387-1393.	3.5	28
12065	Regulation of signal transduction in <i>Coilia nasus</i> during migration. <i>Genomics</i> , 2020, 112, 55-64.	1.3	9

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12066	Mechanism of <i>S. aureus</i> ATCC 25923 in response to heat stress under different water activity and heating rates. <i>Food Control</i> , 2020, 108, 106837.	2.8	16
12067	Reactivation of super-enhancers by KLF4 in human Head and Neck Squamous Cell Carcinoma. <i>Oncogene</i> , 2020, 39, 262-277.	2.6	15
12068	<i>Burkholderia multivorans</i> Exhibits Antibiotic Collateral Sensitivity. <i>Microbial Drug Resistance</i> , 2020, 26, 1-8.	0.9	7
12069	Genomic analyses reveal three independent introductions of the invasive brown rat (<i>Rattus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	1.2	12
12070	Mapping RNA-seq reads to transcriptomes efficiently based on learning to hash method. <i>Computers in Biology and Medicine</i> , 2020, 116, 103539.	3.9	8
12071	Transcriptome analysis reveals new insights into immune response to hypoxia challenge of large yellow croaker (<i>Larimichthys crocea</i>). <i>Fish and Shellfish Immunology</i> , 2020, 98, 738-747.	1.6	29
12072	Epigenetic Regulator CoREST Controls Social Behavior in Ants. <i>Molecular Cell</i> , 2020, 77, 338-351.e6.	4.5	33
12073	Life-long epigenetic programming of cortical architecture by maternal "Western" diet during pregnancy. <i>Molecular Psychiatry</i> , 2020, 25, 22-36.	4.1	28
12074	Transcriptome-level effects of the model organic pollutant phenanthrene and its solvent acetone in three amphipod species. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 33, 100630.	0.4	2
12075	Comparative metagenomic analysis of microbial taxonomic and functional variations in untreated surface and reclaimed waters used in irrigation applications. <i>Water Research</i> , 2020, 169, 115250.	5.3	21
12076	Variations in genome size between wild and domesticated lineages of fowls belonging to the <i>Gallus gallus</i> species. <i>Genomics</i> , 2020, 112, 1660-1673.	1.3	18
12077	Evidences of aromatic degradation dominantly via the phenylacetic acid pathway in marine benthic Thermoprofundales. <i>Environmental Microbiology</i> , 2020, 22, 329-342.	1.8	12
12078	Museum epigenomics: Characterizing cytosine methylation in historic museum specimens. <i>Molecular Ecology Resources</i> , 2020, 20, 1161-1170.	2.2	24
12079	Genetic evidence of a northward range expansion in the eastern Bering Sea stock of Pacific cod. <i>Evolutionary Applications</i> , 2020, 13, 362-375.	1.5	55
12080	Advances in methods and software for RNA cytosine methylation analysis. <i>Genomics</i> , 2020, 112, 1840-1846.	1.3	5
12081	Analysis of terpenoid biosynthesis pathways in German chamomile (<i>Matricaria recutita</i>) and Roman chamomile (<i>Chamaemelum nobile</i>) based on co-expression networks. <i>Genomics</i> , 2020, 112, 1055-1064.	1.3	23
12082	Nucleic Acid Detection and Structural Investigations. <i>Methods in Molecular Biology</i> , 2020, , .	0.4	1
12083	The Dynamic Chromatin Architecture of the Regenerating Liver. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2020, 9, 121-143.	2.3	37

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12084	Protein Structural Information and Evolutionary Landscape by In Vitro Evolution. <i>Molecular Biology and Evolution</i> , 2020, 37, 1179-1192.	3.5	24
12085	The Nuclear Matrix Protein SAFB Cooperates with Major Satellite RNAs to Stabilize Heterochromatin Architecture Partially through Phase Separation. <i>Molecular Cell</i> , 2020, 77, 368-383.e7.	4.5	104
12086	Genomic Resources for Darters (Percidae: Etheostominae) Provide Insight into Postzygotic Barriers Implicated in Speciation. <i>Molecular Biology and Evolution</i> , 2020, 37, 711-729.	3.5	22
12087	Genomic and transcriptional analyses of novel parvoviruses identified from dead peafowl. <i>Virology</i> , 2020, 539, 80-91.	1.1	25
12088	Genotyping and De Novo Discovery of Allelic Variants at the Brassicaceae Self-Incompatibility Locus from Short-Read Sequencing Data. <i>Molecular Biology and Evolution</i> , 2020, 37, 1193-1201.	3.5	19
12089	Genome-wide epigenetic isolation by environment in a widespread <i>Anolis</i> lizard. <i>Molecular Ecology</i> , 2020, 29, 40-55.	2.0	25
12090	Molecular profiling of TOX-deficient neoplastic cells in cutaneous T cell lymphoma. <i>Archives of Dermatological Research</i> , 2020, 312, 513-525.	1.1	5
12091	RNA-Seq comparative analysis reveals the response of <i>Enterococcus faecalis</i> TV4 under fluoride exposure. <i>Gene</i> , 2020, 726, 144197.	1.0	13
12092	Antibiotic resistance in <i>Vibrio cholerae</i> El Tor strains isolated during cholera complications in Siberia and the Far East of Russia. <i>Infection, Genetics and Evolution</i> , 2020, 78, 104096.	1.0	16
12093	Mycovirus-Induced Hypervirulence of <i>Leptosphaeria biglobosa</i> Enhances Systemic Acquired Resistance to <i>Leptosphaeria maculans</i> in <i>Brassica napus</i> . <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 98-107.	1.4	29
12094	Epigenetic signatures of stress adaptation and flowering regulation in response to extended drought and recovery in <i>Zea mays</i> . <i>Plant, Cell and Environment</i> , 2020, 43, 55-75.	2.8	51
12095	Shotgun metagenomics reveals an enrichment of potentially cross-reactive bacterial epitopes in ankylosing spondylitis patients, as well as the effects of TNFi therapy upon microbiome composition. <i>Annals of the Rheumatic Diseases</i> , 2020, 79, 132-140.	0.5	82
12096	Long solids retention times and attached growth phase favor prevalence of comammox bacteria in nitrogen removal systems. <i>Water Research</i> , 2020, 169, 115268.	5.3	98
12097	Selective whole genome amplification and sequencing of <i>Coxiella burnetii</i> directly from environmental samples. <i>Genomics</i> , 2020, 112, 1872-1878.	1.3	9
12098	A beginner's guide for FMDV quasispecies analysis: sub-consensus variant detection and haplotype reconstruction using next-generation sequencing. <i>Briefings in Bioinformatics</i> , 2020, 21, 1766-1775.	3.2	9
12099	Impact of narrow-spectrum penicillin V on the oral and faecal resistome in a young child treated for otitis media. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 20, 290-297.	0.9	8
12100	In situ metabolic activities of uncultivated <i>Ferroplasma</i> sp. CARN8 evidenced by metatranscriptomic analysis. <i>Research in Microbiology</i> , 2020, 171, 37-43.	1.0	7
12101	The subgingival microbiome associated with periodontitis in type 2 diabetes mellitus. <i>ISME Journal</i> , 2020, 14, 519-530.	4.4	65

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12102	Circulating Tumor Cells Exhibit Metastatic Tropism and Reveal Brain Metastasis Drivers. <i>Cancer Discovery</i> , 2020, 10, 86-103.	7.7	100
12103	Comparative analysis of dsRNA-induced lncRNAs in three kinds of insect species. <i>Archives of Insect Biochemistry and Physiology</i> , 2020, 103, e21640.	0.6	13
12104	A 50K SNP array reveals genetic structure for bald eagles (<i>Haliaeetus leucocephalus</i>). <i>Conservation Genetics</i> , 2020, 21, 65-76.	0.8	8
12105	Microaerobic conditions caused the overwhelming dominance of <i>Acinetobacter</i> spp. and the marginalization of <i>Rhodococcus</i> spp. in diesel fuel/crude oil mixture-amended enrichment cultures. <i>Archives of Microbiology</i> , 2020, 202, 329-342.	1.0	33
12106	Dietary l-serine confers a competitive fitness advantage to Enterobacteriaceae in the inflamed gut. <i>Nature Microbiology</i> , 2020, 5, 116-125.	5.9	93
12107	Genetic basis for the cooperative bioactivation of plant lignans by <i>Eggerthella lenta</i> and other human gut bacteria. <i>Nature Microbiology</i> , 2020, 5, 56-66.	5.9	63
12108	Influenza Vaccine Effectiveness in the Inpatient Setting: Evaluation of Potential Bias in the Test-Negative Design by Use of Alternate Control Groups. <i>American Journal of Epidemiology</i> , 2020, 189, 250-260.	1.6	7
12109	<i>Populus euphratica</i> WRKY1 binds the promoter of H ⁺ -ATPase gene to enhance gene expression and salt tolerance. <i>Journal of Experimental Botany</i> , 2020, 71, 1527-1539.	2.4	47
12110	Individual Responsibilities in Partial Compliance: Skilled Health Worker Emigration from Under-Served Regions. <i>Public Health Ethics</i> , 2020, 13, 89-98.	0.4	0
12111	Mutations in the miR396 binding site of the growth-regulating factor gene <i>VvGRF4</i> modulate inflorescence architecture in grapevine. <i>Plant Journal</i> , 2020, 101, 1234-1248.	2.8	19
12112	Characterizing the genetic structure of introduced Nile tilapia (<i>Oreochromis niloticus</i>) strains in Tanzania using double digest RAD sequencing. <i>Aquaculture International</i> , 2020, 28, 477-492.	1.1	16
12113	Cell Type-Specific Methylome-wide Association Studies Implicate Neurotrophin and Innate Immune Signaling in Major Depressive Disorder. <i>Biological Psychiatry</i> , 2020, 87, 431-442.	0.7	35
12114	Epigenetic transgenerational inheritance of parent-of-origin allelic transmission of outcross pathology and sperm epimutations. <i>Developmental Biology</i> , 2020, 458, 106-119.	0.9	32
12115	Further delineation of neuropsychiatric findings in Tatton-Brown-Rahman syndrome due to disease-causing variants in DNMT3A: seven new patients. <i>European Journal of Human Genetics</i> , 2020, 28, 469-479.	1.4	16
12116	A role for <i>Arabidopsis</i> growth-regulating factors 1 and 3 in growth-stress antagonism. <i>Journal of Experimental Botany</i> , 2020, 71, 1402-1417.	2.4	32
12117	Somatic Mutations and Genome Stability Maintenance in Clonal Coral Colonies. <i>Molecular Biology and Evolution</i> , 2020, 37, 828-838.	3.5	16
12118	Characterization of novel primary miRNA transcription units in human cells using Bru-seq nascent RNA sequencing. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqz014.	1.5	10
12119	Comparative transcriptome profiling of tuberous roots of two sweetpotato lines with contrasting low temperature tolerance during storage. <i>Gene</i> , 2020, 727, 144244.	1.0	21

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12120	Complete genome and bimodal genomic structure of the amoebal symbiont <i>Neochlamydia</i> strain S13 revealed by ultra-long reads obtained from MinION. <i>Journal of Human Genetics</i> , 2020, 65, 41-48.	1.1	1
12121	Groundwater cable bacteria conserve energy by sulfur disproportionation. <i>ISME Journal</i> , 2020, 14, 623-634.	4.4	64
12122	The Evening Complex Establishes Repressive Chromatin Domains Via H2A.Z Deposition. <i>Plant Physiology</i> , 2020, 182, 612-625.	2.3	23
12123	The pulmonary virome, bacteriological and histopathological findings in bovine respiratory disease from western Canada. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 924-934.	1.3	27
12124	AP2/ERF Transcription Factors Integrate Age and Wound Signals for Root Regeneration. <i>Plant Cell</i> , 2020, 32, 226-241.	3.1	100
12125	Metatranscriptomics yields new genomic resources and sensitive detection of infections for diverse blood parasites. <i>Molecular Ecology Resources</i> , 2020, 20, 14-28.	2.2	25
12126	Double missense mutations in cardiac myosin-binding protein C and myopalladin genes: A case report with diffuse coronary disease, complete atrioventricular block, and progression to dilated cardiomyopathy. <i>Annals of Noninvasive Electrocardiology</i> , 2020, 25, e12687.	0.5	7
12127	Twin introductions by independent invader mussel lineages are both associated with recent admixture with a native congener in Australia. <i>Evolutionary Applications</i> , 2020, 13, 515-532.	1.5	43
12128	The transcription factor GATA10 regulates fertility conversion of a two-line hybrid mutant rice via the modulation of <i>Ubl40</i> expression. <i>Journal of Integrative Plant Biology</i> , 2020, 62, 1034-1056.	4.1	16
12129	SIVcpz cross-species transmission and viral evolution toward HIV-1 in a humanized mouse model. <i>Journal of Medical Primatology</i> , 2020, 49, 40-43.	0.3	9
12130	<i>tuxnet</i> : a simple interface to process RNA sequencing data and infer gene regulatory networks. <i>Plant Journal</i> , 2020, 101, 716-730.	2.8	20
12131	Changes in Airway Microbiome and Inflammation with Ivacaftor Treatment in Patients with Cystic Fibrosis and the G551D Mutation. <i>Annals of the American Thoracic Society</i> , 2020, 17, 212-220.	1.5	113
12132	Disease Severity Linked to Increase in Autoantibody Diversity in IgG4-Related Disease. <i>Arthritis and Rheumatology</i> , 2020, 72, 687-693.	2.9	38
12133	Differential nucleosome spacing in neurons and glia. <i>Neuroscience Letters</i> , 2020, 714, 134559.	1.0	10
12134	Molecular responses of an estuarine oyster to multiple metal contamination in Southern China revealed by RNA-seq. <i>Science of the Total Environment</i> , 2020, 701, 134648.	3.9	15
12135	The spinal cord-gut-immune axis as a master regulator of health and neurological function after spinal cord injury. <i>Experimental Neurology</i> , 2020, 323, 113085.	2.0	46
12136	Discovery of hyperstable carbohydrate-active enzymes through metagenomics of extreme environments. <i>FEBS Journal</i> , 2020, 287, 1116-1137.	2.2	32
12137	Natural variation in HsfA2 pre-mRNA splicing is associated with changes in thermotolerance during tomato domestication. <i>New Phytologist</i> , 2020, 225, 1297-1310.	3.5	55

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12138	CG hypomethylation leads to complex changes in DNA methylation and transpositional burst of diverse transposable elements in callus cultures of rice. <i>Plant Journal</i> , 2020, 101, 188-203.	2.8	19
12139	Surfactant plus budesonide decreases lung and systemic responses to injurious ventilation in preterm sheep. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2020, 318, L41-L48.	1.3	19
12140	Metagenomic analysis of sludge and early-stage biofilm communities of a submerged membrane bioreactor. <i>Science of the Total Environment</i> , 2020, 701, 134682.	3.9	43
12141	Cannabis glandular trichomes alter morphology and metabolite content during flower maturation. <i>Plant Journal</i> , 2020, 101, 37-56.	2.8	158
12142	Topologies of N ⁶ -adenosine methylation (m ⁶ A) in land plant mitochondria and their putative effects on organellar gene expression. <i>Plant Journal</i> , 2020, 101, 1269-1286.	2.8	26
12143	What a Difference a Gene Makes: Identification of Virulence Factors of Cowpox Virus. <i>Journal of Virology</i> , 2020, 94, .	1.5	6
12144	Ligand dependent gene regulation by transient ER \pm clustered enhancers. <i>PLoS Genetics</i> , 2020, 16, e1008516.	1.5	20
12145	Structural variant identification and characterization. <i>Chromosome Research</i> , 2020, 28, 31-47.	1.0	13
12146	Whole-genome sequencing and comparative transcriptome analysis of <i>Bombyx mori</i> nucleopolyhedrovirus La strain. <i>Virus Genes</i> , 2020, 56, 249-259.	0.7	6
12147	Body lice and bed bug co-infestation in an emergency department patient, Ohio, USA. <i>IDCases</i> , 2020, 19, e00696.	0.4	5
12148	Organohalide-respiring <i>Desulfoluna</i> species isolated from marine environments. <i>ISME Journal</i> , 2020, 14, 815-827.	4.4	24
12149	Recording transcriptional histories using Record-seq. <i>Nature Protocols</i> , 2020, 15, 513-539.	5.5	19
12150	Mapping and engineering the interaction between adiponectin and T-cadherin. <i>Journal of Biological Chemistry</i> , 2020, 295, 2749-2759.	1.6	16
12151	Toward a Dynamic Threshold for Quality Score Distortion in Reference-Based Alignment. <i>Journal of Computational Biology</i> , 2020, 27, 288-300.	0.8	1
12152	BHBA treatment improves cognitive function by targeting pleiotropic mechanisms in transgenic mouse model of Alzheimer's disease. <i>FASEB Journal</i> , 2020, 34, 1412-1429.	0.2	53
12153	The chromatin remodeler Snf2h is essential for oocyte meiotic cell cycle progression. <i>Genes and Development</i> , 2020, 34, 166-178.	2.7	21
12154	High-resolution expression profiling of selected gene sets during plant immune activation. <i>Plant Biotechnology Journal</i> , 2020, 18, 1610-1619.	4.1	21
12155	Disordered chromatin packing regulates phenotypic plasticity. <i>Science Advances</i> , 2020, 6, eaax6232.	4.7	34

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12156	Nonthermal Plasma Induces the Viable-but-Nonculturable State in <i>Staphylococcus aureus</i> via Metabolic Suppression and the Oxidative Stress Response. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	43
12157	The transcriptional correlates of divergent electric organ discharges in <i>Paramormyrops</i> electric fish. <i>BMC Evolutionary Biology</i> , 2020, 20, 6.	3.2	6
12158	Identification of a novel anthocyanin synthesis pathway in the fungus <i>Aspergillus sydowii</i> H-1. <i>BMC Genomics</i> , 2020, 21, 29.	1.2	26
12159	Strains used in whole organism <i>Plasmodium falciparum</i> vaccine trials differ in genome structure, sequence, and immunogenic potential. <i>Genome Medicine</i> , 2020, 12, 6.	3.6	61
12160	DNA methylation and expression analyses reveal epialleles for the foliar disease resistance genes in peanut (<i>Arachis hypogaea</i> L.). <i>BMC Research Notes</i> , 2020, 13, 20.	0.6	9
12161	Molecular characterization and distribution of the voltage-gated sodium channel, Para, in the brain of the grasshopper and vinegar fly. <i>Journal of Comparative Physiology A: Neuroethology, Sensory, Neural, and Behavioral Physiology</i> , 2020, 206, 289-307.	0.7	6
12162	Transcriptome analysis and histopathological observations of <i>Geloina erosa</i> gills upon Cr(VI) exposure. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2020, 231, 108706.	1.3	7
12163	Dual-initiation promoters with intertwined canonical and TCT/TOP transcription start sites diversify transcript processing. <i>Nature Communications</i> , 2020, 11, 168.	5.8	37
12164	Maternal factor NELFA drives a 2C-like state in mouse embryonic stem cells. <i>Nature Cell Biology</i> , 2020, 22, 175-186.	4.6	72
12165	SWAV: a web-based visualization browser for sliding window analysis. <i>Scientific Reports</i> , 2020, 10, 149.	1.6	10
12166	Microbial abundance, composition, and function in nectar are shaped by flower visitor identity. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	46
12167	Disentangling Population History and Character Evolution among Hybridizing Lineages. <i>Molecular Biology and Evolution</i> , 2020, 37, 1295-1305.	3.5	5
12168	Integrative genomics reveal a role for MCPIP1 in adipogenesis and adipocyte metabolism. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 4899-4919.	2.4	13
12169	Contribution of introns to the species diversity associated with the apicomplexan parasite, <i>Neospora caninum</i> . <i>Parasitology Research</i> , 2020, 119, 431-445.	0.6	2
12170	Domestication and breeding changed tomato fruit transcriptome. <i>Journal of Integrative Agriculture</i> , 2020, 19, 120-132.	1.7	18
12171	Comparative transcriptome analysis revealed gamma-irradiation mediated disruption of floral integrator gene(s) leading to prolonged vegetative phase in <i>Stevia rebaudiana</i> Bertoni. <i>Plant Physiology and Biochemistry</i> , 2020, 148, 90-102.	2.8	14
12172	A shared genetic basis of mimicry across swallowtail butterflies points to ancestral co-option of doublesex. <i>Nature Communications</i> , 2020, 11, 6.	5.8	55
12173	Single-cell reconstruction of the adult human heart during heart failure and recovery reveals the cellular landscape underlying cardiac function. <i>Nature Cell Biology</i> , 2020, 22, 108-119.	4.6	270

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12174	Evolutionarily conserved pachytene piRNA loci are highly divergent among modern humans. <i>Nature Ecology and Evolution</i> , 2020, 4, 156-168.	3.4	58
12175	Differential Expression in Testis and Liver Transcriptomes from Four Species of <i>Peromyscus</i> (Rodentia: Tj ETQq1 1 0.784314 rgBT /Over	1.1	2
12176	Genome Sequence Resource of <i>Candidatus</i> <i>Liberibacter asiaticus</i> ™ from Thailand. <i>Plant Disease</i> , 2020, 104, 624-626.	0.7	7
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12266	Computational approaches for effective CRISPR guide RNA design and evaluation. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 35-44.	1.9	119
12267	Global transcriptomic analysis of <i>Lactobacillus plantarum</i> CAUH2 in response to hydrogen peroxide stress. <i>Food Microbiology</i> , 2020, 87, 103389.	2.1	31
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12269	The Impact of High-mobility Group Box Mutation of T-cell Factor 4 on Its Genomic Binding Pattern in Non-small Cell Lung Cancer. <i>Translational Oncology</i> , 2020, 13, 79-85.	1.7	1
12270	Bacterial enrichment in highly-selective acetate-fed bioreactors and its application in rapid biofilm formation. <i>Water Research</i> , 2020, 170, 115359.	5.3	5
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12276	In vitro antifungal activity of dimethyl trisulfide against <i>Colletotrichum gloeosporioides</i> from mango. <i>World Journal of Microbiology and Biotechnology</i> , 2020, 36, 4.	1.7	17
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12279	Translational Landscape of Protein-Coding and Non-Protein-Coding RNAs upon Light Exposure in <i>Arabidopsis</i> . <i>Plant and Cell Physiology</i> , 2020, 61, 536-545.	1.5	15
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12283	Dual RNA-Seq analysis of <i>Medicago truncatula</i> and the pea powdery mildew <i>Erysiphe pisi</i> uncovers distinct host transcriptional signatures during incompatible and compatible interactions and pathogen effector candidates. <i>Genomics</i> , 2020, 112, 2130-2145.	1.3	13
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12286	An intrinsic role of IL-33 in Treg cell-mediated tumor immunoevasion. <i>Nature Immunology</i> , 2020, 21, 75-85.	7.0	82
12287	A DeoR-Type Transcription Regulator Is Required for Sugar-Induced Expression of Type III Secretion-Encoding Genes in <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 509-518.	1.4	17
12288	Ecogenomics of the SAR11 clade. <i>Environmental Microbiology</i> , 2020, 22, 1748-1763.	1.8	66
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12296	The Chaperone FACT and Histone H2B Ubiquitination Maintain <i>S. pombe</i> Genome Architecture through Genic and Subtelomeric Functions. <i>Molecular Cell</i> , 2020, 77, 501-513.e7.	4.5	32
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12301	GCNA Preserves Genome Integrity and Fertility Across Species. <i>Developmental Cell</i> , 2020, 52, 38-52.e10.	3.1	53
12302	The gut microbiota is associated with psychiatric symptom severity and treatment outcome among individuals with serious mental illness. <i>Journal of Affective Disorders</i> , 2020, 264, 98-106.	2.0	50
12303	The Use of Histidine-tryptophan-ketoglutarate Solution as a New Storage Medium for the Avulsed Tooth. <i>Journal of Endodontics</i> , 2020, 46, 74-80.	1.4	0
12304	Multiple-Site Diversification of Regulatory Sequences Enables Interspecies Operability of Genetic Devices. <i>ACS Synthetic Biology</i> , 2020, 9, 104-114.	1.9	15
12305	Mapping RNA-capsid interactions and RNA secondary structure within virus particles using next-generation sequencing. <i>Nucleic Acids Research</i> , 2020, 48, e12-e12.	6.5	17
12306	FLASH: ultra-fast protocol to identify RNA-protein interactions in cells. <i>Nucleic Acids Research</i> , 2020, 48, e15-e15.	6.5	21
12307	Set1/COMPASS repels heterochromatin invasion at euchromatic sites by disrupting Suv39/Clr4 activity and nucleosome stability. <i>Genes and Development</i> , 2020, 34, 99-117.	2.7	26
12308	Dark-Induced Senescence Causes Localized Changes in DNA Methylation. <i>Plant Physiology</i> , 2020, 182, 949-961.	2.3	11
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12752	Liver transcriptome resources of four commercially exploited teleost species. <i>Scientific Data</i> , 2020, 7, 214.	2.4	4
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12763	The Diversity and Distribution of Viruses Associated with <i>Culex annulirostris</i> Mosquitoes from the Kimberley Region of Western Australia. <i>Viruses</i> , 2020, 12, 717.	1.5	17
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12771	Bacterial and archaeal community structure in benthic sediments from glacial lakes at the Mjallágljúkull Glacier, central Iceland. <i>Polar Biology</i> , 2020, 43, 2085-2099.	0.5	1

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12785	Transcriptome dataset from bark and latex tissues of three <i>Hevea brasiliensis</i> clones. <i>Data in Brief</i> , 2020, 32, 106188.	0.5	2
12786	Backcross breeding for improvement of heat tolerance at reproductive phase in Thai rice (<i>Oryza</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.6	5
12787	Proteomic profiling and genome-wide mapping of O-GlcNAc chromatin-associated proteins reveal an O-GlcNAc-regulated genotoxic stress response. <i>Nature Communications</i> , 2020, 11, 5898.	5.8	19
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12803	Rethinking temperature effects on leaf growth, gene expression and metabolism: Diel variation matters. <i>Plant, Cell and Environment</i> , 2021, 44, 2262-2276.	2.8	14
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12823	Chemosensory-Related Gene Family Members of the Horn Fly, <i>Haematobia irritans irritans</i> (Diptera:) Tj ETQq1 1 0.784314 rgBT /Overlap 5	1.0	5
12824	Serpentovirus (Nidovirus) and Orthoreovirus Coinfection in Captive Veiled Chameleons (<i>Chamaeleo</i>) Tj ETQq0 0 0 rgBT /Overlap 10 Tf 5	1.5	13
12825	Genes Contributing to the Unique Biology and Intrinsic Antibiotic Resistance of <i>Enterococcus faecalis</i> . <i>MBio</i> , 2020, 11, .	1.8	19

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12834	Transcription-dependent cohesin repositioning rewires chromatin loops in cellular senescence. <i>Nature Communications</i> , 2020, 11, 6049.	5.8	42
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12839	Evolution of Antibiotic Resistance in Surrogates of <i>Francisella tularensis</i> (LVS and <i>Francisella</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 16	1.5	16
12840	Full-Length Transcriptome from <i>Camellia oleifera</i> Seed Provides Insight into the Transcript Variants Involved in Oil Biosynthesis. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 14670-14683.	2.4	33
12841	Cadmium stress dictates central carbon flux and alters membrane composition in <i>Streptococcus pneumoniae</i> . <i>Communications Biology</i> , 2020, 3, 694.	2.0	19
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12845	Genome-wide identification of <i>Azospirillum brasilense</i> Sp245 small RNAs responsive to nitrogen starvation and likely involvement in plant-microbe interactions. <i>BMC Genomics</i> , 2020, 21, 821.	1.2	2
12846	Combination of T-Cell Bispecific Antibodies With PD-L1 Checkpoint Inhibition Elicits Superior Anti-Tumor Activity. <i>Frontiers in Oncology</i> , 2020, 10, 575737.	1.3	28
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12849	Unique maternal immune and functional microbial profiles during prenatal stress. <i>Scientific Reports</i> , 2020, 10, 20288.	1.6	26
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12860	Feral populations of <i>Brassica oleracea</i> along Atlantic coasts in western Europe. <i>Ecology and Evolution</i> , 2020, 10, 11810-11825.	0.8	11
12861	Transcriptome analysis of genes related to cadmium absorption and transportation in pepper. <i>Israel Journal of Ecology and Evolution</i> , 2020, 67, 29-38.	0.2	0

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12863	Systematic comparison and assessment of RNA-seq procedures for gene expression quantitative analysis. <i>Scientific Reports</i> , 2020, 10, 19737.	1.6	99
12864	Genome-wide mapping of SARS-CoV-2 RNA structures identifies therapeutically-relevant elements. <i>Nucleic Acids Research</i> , 2020, 48, 12436-12452.	6.5	195
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12867	The Lung Microbiome of Three Young Brazilian Patients With Cystic Fibrosis Colonized by Fungi. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 598938.	1.8	8
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14017	Long non-coding RNAs in the alkaline stress response in sugar beet (<i>Beta vulgaris</i> L.). <i>BMC Plant Biology</i> , 2020, 20, 227.	1.6	13
14018	Single-base deletion in <i>GmCHR5</i> increases the genistein-to-daidzein ratio in soybean seed. <i>Breeding Science</i> , 2020, 70, 265-276.	0.9	5
14019	MADS-Box and bHLH Transcription Factors Coordinate Transmitting Tract Development in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 526.	1.7	25
14020	Metagenomic to evaluate norovirus genomic diversity in oysters: Impact on hexamer selection and targeted capture-based enrichment. <i>International Journal of Food Microbiology</i> , 2020, 323, 108588.	2.1	20
14021	Transcriptome analyses provide insights into the effect of temperature change on fiber quality of ramie. <i>Industrial Crops and Products</i> , 2020, 152, 112544.	2.5	6
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14023	Reverse engineering of fatty acid-tolerant <i>Escherichia coli</i> identifies design strategies for robust microbial cell factories. <i>Metabolic Engineering</i> , 2020, 61, 120-130.	3.6	23
14024	Mitogenomics reveals phylogenetic relationships of Arcoida (Mollusca, Bivalvia) and multiple independent expansions and contractions in mitochondrial genome size. <i>Molecular Phylogenetics and Evolution</i> , 2020, 150, 106857.	1.2	32
14025	Genomic prediction applied to multiple traits and environments in second season maize hybrids. <i>Heredity</i> , 2020, 125, 60-72.	1.2	12
14026	Permissive microbiome characterizes human subjects with a neurovascular disease cavernous angioma. <i>Nature Communications</i> , 2020, 11, 2659.	5.8	27
14027	Genetic basis for virulence differences of various <i>Cryptosporidium parvum</i> carcinogenic isolates. <i>Scientific Reports</i> , 2020, 10, 7316.	1.6	10
14028	Adenine DNA methylation, 3D genome organization, and gene expression in the parasite <i>Trichomonas vaginalis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13033-13043.	3.3	15
14029	Metagenomics reveals impact of geography and acute diarrheal disease on the Central Indian human gut microbiome. <i>Gut Microbes</i> , 2020, 12, 1752605.	4.3	22
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14031	First Genome Sequence of the Gunnison's Prairie Dog (<i>Cynomys gunnisoni</i>), a Keystone Species and Player in the Transmission of Sylvatic Plague. <i>Genome Biology and Evolution</i> , 2020, 12, 618-625.	1.1	6
14032	HrrSA orchestrates a systemic response to heme and determines prioritization of terminal cytochrome oxidase expression. <i>Nucleic Acids Research</i> , 2020, 48, 6547-6562.	6.5	10
14033	Gut microbial species and metabolic pathways associated with response to treatment with immune checkpoint inhibitors in metastatic melanoma. <i>Melanoma Research</i> , 2020, 30, 235-246.	0.6	42

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14035	Growth study under combined effects of temperature, pH and salinity and transcriptome analysis revealed adaptations of <i>Aspergillus terreus</i> NT0U4989 to the extreme conditions at Kueishan Island Hydrothermal Vent Field, Taiwan. <i>PLoS ONE</i> , 2020, 15, e0233621.	1.1	21
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14038	The Phylodynamics of Seasonal Influenza A/H1N1pdm Virus in China Between 2009 and 2019. <i>Frontiers in Microbiology</i> , 2020, 11, 735.	1.5	16
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14042	Characterization of the complete chloroplast genome of <i>Paphiopedilum micranthum</i> , an Endangered orchid in China. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 115-116.	0.2	0
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14045	A genetic mechanism for sexual dichromatism in birds. <i>Science</i> , 2020, 368, 1270-1274.	6.0	71
14046	Ahr-Foxp3-ROR γ t axis controls gut homing of CD4 ⁺ T cells by regulating GPR15. <i>Science Immunology</i> , 2020, 5, .	5.6	43
14047	Proteogenomic analysis of Inhibitor of Differentiation 4 (ID4) in basal-like breast cancer. <i>Breast Cancer Research</i> , 2020, 22, 63.	2.2	8
14048	VIBRANT: automated recovery, annotation and curation of microbial viruses, and evaluation of viral community function from genomic sequences. <i>Microbiome</i> , 2020, 8, 90.	4.9	482
14049	Coding and Non-coding RNAs: Molecular Basis of Forest-Insect Outbreaks. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 369.	1.8	9
14050	Application of acidic conditions and inert-gas sparging to achieve high-efficiency nitrous oxide recovery during nitrite denitrification. <i>Water Research</i> , 2020, 182, 116001.	5.3	20
14051	Comparative analysis of <i>Longissimus dorsi</i> tissue from two sheep groups identifies differentially expressed genes related to growth, development and meat quality. <i>Genomics</i> , 2020, 112, 3322-3330.	1.3	13

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14054	In vitro dynamics and mechanisms of resistance development to imipenem and imipenem/relebactam in <i>Pseudomonas aeruginosa</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 2508-2515.	1.3	24
14055	Paternal effects in a wild-type zebrafish implicate a role of sperm-derived small RNAs. <i>Molecular Ecology</i> , 2020, 29, 2722-2735.	2.0	24
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14059	Single-cell ATAC sequencing analysis: From data preprocessing to hypothesis generation. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1429-1439.	1.9	91
14060	Transcriptome analysis reveals molecular strategies in gills and heart of large yellow croaker (<i>Larimichthys crocea</i>) under hypoxia stress. <i>Fish and Shellfish Immunology</i> , 2020, 104, 304-313.	1.6	52
14061	An Erg-driven transcriptional program controls B cell lymphopoiesis. <i>Nature Communications</i> , 2020, 11, 3013.	5.8	29
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14064	Methylation-directed glycosylation of chromatin factors represses retrotransposon promoters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 14292-14298.	3.3	28
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14066	Transcriptome Analysis of Two Flax Varieties at Different Developmental Stages Reveals Significant Differential Expression of Genes Related to Stem Fiber Development. <i>Journal of Natural Fibers</i> , 2020, , 1-15.	1.7	2
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14068	Anaerobic Degradation of Syringic Acid by an Adapted Strain of <i>Rhodopseudomonas palustris</i> . <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	9
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14071	Transcriptome Analysis of the Gene Expression Profiles Associated with Fungal Keratitis in Mice Based on RNA-Seq. , 2020, 61, 32.		15
14072	Comparative Analysis of Sample Extraction and Library Construction for Shotgun Metagenomics. <i>Bioinformatics and Biology Insights</i> , 2020, 14, 117793222091545.	1.0	8
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14074	Whole-Genome Approach to Assessing Human Cytomegalovirus Dynamics in Transplant Patients Undergoing Antiviral Therapy. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 267.	1.8	17
14075	Transcriptome Profiling of <i>Haloxylon persicum</i> (Bunge ex Boiss and Buhse) an Endangered Plant Species under PEG-Induced Drought Stress. <i>Genes</i> , 2020, 11, 640.	1.0	8
14076	miRNA-mRNA Profiling Reveals Prognostic Impact of <i>SMC1A</i> Expression in Acute Myeloid Leukemia. <i>Oncology Research</i> , 2020, 28, 321-330.	0.6	8
14077	Reduced representation approach for identification of genome-wide SNPs and their annotation for economically important traits in Indian Tharparkar cattle. <i>3 Biotech</i> , 2020, 10, 309.	1.1	8
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14084	Detection of renal cell carcinoma using plasma and urine cell-free DNA methylomes. <i>Nature Medicine</i> , 2020, 26, 1041-1043.	15.2	161
14085	Amending microbiota by targeting intestinal inflammation with TNF blockade attenuates development of colorectal cancer. <i>Nature Cancer</i> , 2020, 1, 723-734.	5.7	50
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14089	<scp>ASCL1</scp> regulates neurodevelopmental transcription factors and cell cycle genes in brain tumors of glioma mouse models. <i>Glia</i> , 2020, 68, 2613-2630.	2.5	31
14090	Multi-omics analysis reveals the functional transcription and potential translation of enhancers. <i>International Journal of Cancer</i> , 2020, 147, 2210-2224.	2.3	11
14091	Ustiloxin A is Produced Early in Experimental <i>Ustilaginoidea virens</i> Infection and Affects Transcription in Rice. <i>Current Microbiology</i> , 2020, 77, 2766-2774.	1.0	13
14092	Inducible aging in <i>Hydra oligactis</i> implicates sexual reproduction, loss of stem cells, and genome maintenance as major pathways. <i>GeroScience</i> , 2020, 42, 1119-1132.	2.1	13
14093	OmpA of <i>Klebsiella pneumoniae</i> ATCC 13883 induces pyroptosis in HEp-2 cells, leading to cell-cycle arrest and apoptosis. <i>Microbes and Infection</i> , 2020, 22, 432-440.	1.0	5
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14095	Measuring and interpreting transposable element expression. <i>Nature Reviews Genetics</i> , 2020, 21, 721-736.	7.7	211
14096	The complete chloroplast genome sequence of <i>Pimpinella smithii</i> (Apiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1155-1156.	0.2	2
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14101	Temperature training improves transcriptional homeostasis after heat shock in juvenile Atlantic sturgeon (<i>Acipenser oxyrinchus</i>). <i>Fish Physiology and Biochemistry</i> , 2020, 46, 1653-1664.	0.9	9
14102	Genome-wide DNA methylation analysis of paulownia with phytoplasma infection. <i>Gene</i> , 2020, 755, 144905.	1.0	3
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14105	Widespread transcript shortening through alternative polyadenylation in secretory cell differentiation. <i>Nature Communications</i> , 2020, 11, 3182.	5.8	34

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14108	Genetic Mapping in Autohexaploid Sweet Potato with Low-Coverage NGS-Based Genotyping Data. G3: Genes, Genomes, Genetics, 2020, 10, 2661-2670.	0.8	15
14109	Two Synthetic 18-Way Outcrossed Populations of Diploid Budding Yeast with Utility for Complex Trait Dissection. <i>Genetics</i> , 2020, 215, 323-342.	1.2	17
14110	Impact of DNA Extraction Method on Variation in Human and Built Environment Microbial Community and Functional Profiles Assessed by Shotgun Metagenomics Sequencing. <i>Frontiers in Microbiology</i> , 2020, 11, 953.	1.5	40
14111	CSI NGS Portal: An Online Platform for Automated NGS Data Analysis and Sharing. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3828.	1.8	19
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14114	Metatranscriptomic analysis of modified atmosphere packaged poultry meat enables prediction of <i>Brochothrix thermosphacta</i> and <i>Carnobacterium divergens</i> in situ metabolism. <i>Archives of Microbiology</i> , 2020, 202, 1945-1955.	1.0	17
14115	Proline improves cardiac remodeling following myocardial infarction and attenuates cardiomyocyte apoptosis via redox regulation. <i>Biochemical Pharmacology</i> , 2020, 178, 114065.	2.0	27
14116	Comparative performance of conservation agriculture vis-a-vis organic and conventional farming, in enhancing plant attributes and rhizospheric bacterial diversity in <i>Cajanus cajan</i> : A field study. <i>European Journal of Soil Biology</i> , 2020, 99, 103197.	1.4	36
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14118	Specific fibroblast subpopulations and neuronal structures provide local sources of Vegfc-processing components during zebrafish lymphangiogenesis. <i>Nature Communications</i> , 2020, 11, 2724.	5.8	42
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14126	Universal promoter scanning by Pol II during transcription initiation in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology</i> , 2020, 21, 132.	3.8	35
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14129	Genetic architecture underlying changes in carotenoid accumulation during the evolution of the blind Mexican cavefish, <i>Astyanax mexicanus</i>. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2020, 334, 405-422.	0.6	9
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14135	Genomic predictions improve clonal selection in oil palm (<i>Elaeis guineensis</i> Jacq.) hybrids. <i>Plant Science</i> , 2020, 299, 110547.	1.7	10
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14138	High-resolution epitope mapping of anti-Hu and anti-Yo autoimmunity by programmable phage display. <i>Brain Communications</i> , 2020, 2, fcaa059.	1.5	41
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14145	Specific response mechanism to autotoxicity in melon (<i>Cucumis melo</i> L.) root revealed by physiological analyses combined with transcriptome profiling. <i>Ecotoxicology and Environmental Safety</i> , 2020, 200, 110779.	2.9	26
14146	Integrated analysis of mRNA and miRNA in testis and cauda epididymidis reveals candidate molecular markers associated with reproduction in Dezhou donkey. <i>Livestock Science</i> , 2020, 234, 103885.	0.6	14
14147	The complete mitochondrial genome of <i>Ophiura kinbergi</i> (Ophiuroidea, Ophiurina): genome structure and phylogenetics. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1309-1310.	0.2	0
14148	Transcriptomic plasticity of mesophotic corals among natural populations and transplants of <i>Montastraea cavernosa</i> in the Gulf of Mexico and Belize. <i>Molecular Ecology</i> , 2020, 29, 2399-2415.	2.0	6
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14150	Thaumarchaea Genome Sequences from a High Arctic Active Layer. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
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15582	Climate change driven hyposalinity as a selective agent in the littoral mesoherbivore <i>Idotea balthica</i> . <i>Marine Environmental Research</i> , 2021, 163, 105216.	1.1	3
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15888	Genomic surveillance of Nevada patients revealed prevalence of unique SARS-CoV-2 variants bearing mutations in the RdRp gene. <i>Journal of Genetics and Genomics</i> , 2021, 48, 40-51.	1.7	19
15889	BitmapAligner: Bit-Parallelism String Matching with MapReduce and Hadoop. <i>Computers, Materials and Continua</i> , 2021, 68, 3931-3946.	1.5	7
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15896	Evaluation and measurement of epigenetic modifications in population-based studies. , 2021, , 17-39.		0
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15900	Involvement of phospholipase PLA2 in production of cellulase and xylanase by <i>Penicillium oxalicum</i> . <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 679-694.	1.7	2
15901	A panel of 96 SNPs to identify individuals and differentiate subspecies of elk (<i>Cervus canadensis</i>) for microfluidic and other genotyping platforms. <i>Conservation Genetics Resources</i> , 2021, 13, 111-113.	0.4	2
15903	First detection of a plasmid-encoded New-Delhi metallo-beta-lactamase-1 (NDM-1) producing <i>Acinetobacter baumannii</i> using whole genome sequencing, isolated in a clinical setting in Benin. <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2021, 20, 5.	1.7	6

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15913	De Novo Profiling of Long Non-Coding RNAs Involved in MC-LR-Induced Liver Injury in Whitefish: Discovery and Perspectives. <i>International Journal of Molecular Sciences</i> , 2021, 22, 941.	1.8	2
15915	Identification of Circular RNAs in Hypothalamus of Gilts during the Onset of Puberty. <i>Genes</i> , 2021, 12, 84.	1.0	8
15919	Analysis of Genome DNA Methylation at Inherited Coat Color Dilutions of Rex Rabbits. <i>Frontiers in Genetics</i> , 2020, 11, 603528.	1.1	6
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15930	SARS-CoV-2 infection activates a subset of intrinsic pathways to inhibit type I interferons <i>in vitro</i> and <i>in vivo</i> . <i>International Journal of Medical Sciences</i> , 2021, 18, 2561-2569.	1.1	2
15931	Design and Analysis of RNA Sequencing Data. <i>Learning Materials in Biosciences</i> , 2021, , 143-175.	0.2	0

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15933	Hypothalamic REV-ERB nuclear receptors control diurnal food intake and leptin sensitivity in diet-induced obese mice. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	23
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15935	ZNF143 mediates CTCF-bound promoter-enhancer loops required for murine hematopoietic stem and progenitor cell function. <i>Nature Communications</i> , 2021, 12, 43.	5.8	45
15936	Regulatory roles of Escherichia coli 5' UTR and ORF-internal RNAs detected by 3' end mapping. <i>ELife</i> , 2021, 10, .	2.8	60
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15941	Reference flow: reducing reference bias using multiple population genomes. <i>Genome Biology</i> , 2021, 22, 8.	3.8	44
15942	The MRN complex promotes DNA repair by homologous recombination and restrains antigenic variation in African trypanosomes. <i>Nucleic Acids Research</i> , 2021, 49, 1436-1454.	6.5	11
15943	Robustness of differential gene expression analysis of RNA-seq. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3470-3481.	1.9	39
15944	Genome-resolved metagenomics reveals site-specific diversity of epibiotic CPR bacteria and DPANN archaea in groundwater ecosystems. <i>Nature Microbiology</i> , 2021, 6, 354-365.	5.9	109
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15949	Genetic variability of SARS-CoV-2 in biological samples from patients in Moscow. <i>Zhurnal Mikrobiologii Epidemiologii I Immunologii</i> , 2021, 97, 511-517.	0.3	3
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15955	<i>Culex quinquefasciatus</i> carrying <i>Wolbachia</i> is less susceptible to entomopathogenic bacteria. <i>Scientific Reports</i> , 2021, 11, 1094.	1.6	9
15956	DNA Read Feature Importance Using Machine Learning for Read Alignment Categories. <i>Lecture Notes in Computer Science</i> , 2021, , 3-14.	1.0	0
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15962	Comparisons of oral, intestinal, and pancreatic bacterial microbiomes in patients with pancreatic cancer and other gastrointestinal diseases. <i>Journal of Oral Microbiology</i> , 2021, 13, 1887680.	1.2	17
15963	Association of Microbial Dysbiosis with Gallbladder Diseases Identified by Bile Microbiome Profiling. <i>Journal of Korean Medical Science</i> , 2021, 36, e189.	1.1	13
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15970	Metagenomic Profiling of Viruses Associated with <i>Rhipicephalus microplus</i> Ticks in Yunnan Province, China. <i>Virologica Sinica</i> , 2021, 36, 623-635.	1.2	30

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15972	Genetic pathways underpinning hormonal stress responses in fish exposed to short- and long-term warm ocean temperatures. <i>Ecological Indicators</i> , 2021, 120, 106937.	2.6	38
15973	A computational pipeline to infer alternative poly-adenylation from 3' sequencing data. <i>Methods in Enzymology</i> , 2021, 655, 185-204.	0.4	4
15974	Comparative Analysis of Core and Accessory Genes in Coexpression Network. <i>Methods in Molecular Biology</i> , 2021, 2242, 45-58.	0.4	2
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15984	Polinton-like viruses are abundant in aquatic ecosystems. <i>Microbiome</i> , 2021, 9, 13.	4.9	32
15985	Primer System for Reindeer (<i>Rangifer tarandus</i>) Mitochondrial Genome Sequencing. <i>Russian Journal of Genetics</i> , 2021, 57, 110-113.	0.2	2
15986	PIM-Align: A Processing-in-Memory Architecture for FM-Index Search Algorithm. <i>Journal of Computer Science and Technology</i> , 2021, 36, 56-70.	0.9	11
15987	Efficient Detection of Transposable Element Insertion Polymorphisms Between Genomes Using Short-Read Sequencing Data. <i>Methods in Molecular Biology</i> , 2021, 2250, 157-169.	0.4	10
15988	Alignment. <i>Learning Materials in Biosciences</i> , 2021, , 111-122.	0.2	0
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15990	Computational Analysis of and CircRNAs in. <i>Methods in Molecular Biology</i> , 2021, 2362, 147-172.	0.4	1

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15993	An interpretable bimodal neural network characterizes the sequence and preexisting chromatin predictors of induced transcription factor binding. <i>Genome Biology</i> , 2021, 22, 20.	3.8	9
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15996	A Brief Review of Current 3D Genomics Research. , 2021, , 75-84.		0
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15998	Integration of Transcriptional and Post-transcriptional Analysis Revealed the Early Response Mechanism of Sugarcane to Cold Stress. <i>Frontiers in Genetics</i> , 2020, 11, 581993.	1.1	5
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16002	Evaluation of analytical protocols of alignment mapping tools using high throughput next-generation genome sequencing data. <i>Translational Research in Veterinary Science</i> , 2021, 3, 61.	0.1	1
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16004	Effects of Chinese wolfberry and Astragalus extract on the antioxidant capacity of Tibetan pig liver. <i>PLoS ONE</i> , 2021, 16, e0245749.	1.1	7
16006	Sequencing and comparative analysis of the chloroplast genome of <i>Ribes odoratum</i> provide insights for marker development and phylogenetics in <i>Ribes</i> . <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 81-92.	1.4	7
16009	Transfer of oral bacteria to the fetus during late gestation. <i>Scientific Reports</i> , 2021, 11, 708.	1.6	4
16010	Functional Common and Rare <i>ERBB2</i> Germline Variants Cooperate in Familial and Sporadic Cancer Susceptibility. <i>Cancer Prevention Research</i> , 2021, 14, 441-454.	0.7	0
16012	Adherence Affects Monocyte Innate Immune Function and Metabolic Reprogramming after Lipopolysaccharide Stimulation In Vitro. <i>Journal of Immunology</i> , 2021, 206, 827-838.	0.4	15
16013	A Chromosome-Scale Quinoa Reference Genome Assembly. <i>Compendium of Plant Genomes</i> , 2021, , 65-80.	0.3	0
16014	Global Identification for Targets of Circadian Transcription Factors in <i>Arabidopsis</i> and Rice Using Chromatin Immunoprecipitation Followed by Sequencing (ChIP-seq). <i>Methods in Molecular Biology</i> , 2021, 2297, 61-74.	0.4	2

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16018	The gut virome in Irritable Bowel Syndrome differs from that of controls. <i>Gut Microbes</i> , 2021, 13, 1-15.	4.3	36
16019	Bioinformatics resources for SARS-CoV-2 discovery and surveillance. <i>Briefings in Bioinformatics</i> , 2021, 22, 631-641.	3.2	38
16020	Spontaneous Emergence of Azithromycin Resistance in Independent Lineages of <i>Salmonella</i> Typhi in Northern India. <i>Clinical Infectious Diseases</i> , 2021, 72, e120-e127.	2.9	39
16021	Population genomics of a reindeer lichen species from North American lichen woodlands. <i>American Journal of Botany</i> , 2021, 108, 159-171.	0.8	8
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16023	Genome editing demonstrates that the ~5 kb Nanog enhancer regulates Nanog expression by modulating RNAPII initiation and/or recruitment. <i>Journal of Biological Chemistry</i> , 2021, 296, 100189.	1.6	13
16024	The UFM1 Pathway Impacts HCMV US2-Mediated Degradation of HLA Class I. <i>Molecules</i> , 2021, 26, 287.	1.7	8
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16030	Gut Microbial Structural Variations as Determinants of Human Bile Acid Metabolism. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
16031	Demographic Inferences and Loci Under Selection in a Recently Expanded Coral Population. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
16032	Enteric Phageome Alterations in Patients With Type 2 Diabetes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 575084.	1.8	16
16034	In vitro and in cellula site-directed RNA editing using the Î»NDD-BoxB system. <i>Methods in Enzymology</i> , 2021, 658, 335-358.	0.4	2
16035	Mutation Profile of SARS-CoV-2 Genome Sequences Originating from Eight Israeli Patient Isolates. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	3

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16037	Patient-derived non-small cell lung cancer xenograft mirrors complex tumor heterogeneity. <i>Cancer Biology and Medicine</i> , 2021, 18, 184-198.	1.4	19
16038	Whole genome phylogenies reflect the distributions of recombination rates for many bacterial species. <i>ELife</i> , 2021, 10, .	2.8	42
16039	Subtraction-free and bisulfite-free specific sequencing of 5-methylcytosine and its oxidized derivatives at base resolution. <i>Nature Communications</i> , 2021, 12, 618.	5.8	45
16040	A transposon surveillance mechanism that safeguards plant male fertility during stress. <i>Nature Plants</i> , 2021, 7, 34-41.	4.7	25
16041	Genome sequence and transcriptome profiles of pathogenic fungus <i>Paecilomyces penicillatus</i> reveal its interactions with edible fungus <i>Morchella importuna</i> . <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2607-2617.	1.9	11
16042	A comprehensive epigenome atlas reveals DNA methylation regulating skeletal muscle development. <i>Nucleic Acids Research</i> , 2021, 49, 1313-1329.	6.5	68
16043	Diversification, Introgression, and Rampant Cytonuclear Discordance in Rocky Mountains Chipmunks (<i>Sciuridae</i> : <i>Tamias</i>). <i>Systematic Biology</i> , 2021, 70, 908-921.	2.7	20
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16045	Effect of COVID-19 precautions on the gut microbiota and nosocomial infections. <i>Gut Microbes</i> , 2021, 13, 1-10.	4.3	10
16048	Gene expression of PLAT and ATS3 proteins increases plant resistance to insects. <i>Planta</i> , 2021, 253, 37.	1.6	5
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16051	High-Resolution Mapping of Transcription Initiation in the Asexual Stages of <i>Toxoplasma gondii</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 617998.	1.8	11
16052	Spatial integration of transcription and splicing in a dedicated compartment sustains monogenic antigen expression in African trypanosomes. <i>Nature Microbiology</i> , 2021, 6, 289-300.	5.9	50
16053	Elongin A regulates transcription in vivo through enhanced RNA polymerase processivity. <i>Journal of Biological Chemistry</i> , 2021, 296, 100170.	1.6	7
16054	FOXO1 constrains activation and regulates senescence in CD8 T cells. <i>Cell Reports</i> , 2021, 34, 108674.	2.9	40
16055	Transcriptomic and Network Analysis of Minor Salivary Glands of Patients With Primary Sjögren's Syndrome. <i>Frontiers in Immunology</i> , 2020, 11, 606268.	2.2	21

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16058	EARRINGS: an efficient and accurate adapter trimmer entails no a priori adapter sequences. <i>Bioinformatics</i> , 2021, 37, 1846-1852.	1.8	3
16059	Metagenomic analysis of formalin-fixed paraffin-embedded tumor and normal mucosa reveals differences in the microbiome of colorectal cancer patients. <i>Scientific Reports</i> , 2021, 11, 391.	1.6	21
16060	Deregulation of the Epithelial-to-Mesenchymal Transition Process Underlies Zic2-Linked Holoprosencephaly. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
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16063	Senolysis by glutaminolysis inhibition ameliorates various age-associated disorders. <i>Science</i> , 2021, 371, 265-270.	6.0	222
16064	The androgen receptor is a tumor suppressor in estrogen receptor ⁺ positive breast cancer. <i>Nature Medicine</i> , 2021, 27, 310-320.	15.2	122
16065	Global transcriptomic analysis of functional oligosaccharide metabolism in <i>Pediococcus pentosaceus</i> . <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 1601-1614.	1.7	8
16066	AutoVEM: An automated tool to real-time monitor epidemic trends and key mutations in SARS-CoV-2 evolution. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1976-1985.	1.9	9
16067	Spatial population genomics of a recent mosquito invasion. <i>Molecular Ecology</i> , 2021, 30, 1174-1189.	2.0	31
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16747	Effects of neonatal exposure to methoxychlor on corpus luteum in gilts: A transcriptomic analysis. <i>Molecular Reproduction and Development</i> , 2021, 88, 238-248.	1.0	2
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16808	Epigenomic tensor predicts disease subtypes and reveals constrained tumor evolution. <i>Cell Reports</i> , 2021, 34, 108927.	2.9	12
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18086	Effects of 5-aminolevulinic acid on Anthocyanin synthesis in <i>Vitis Vinifera</i> "Crimson Seedless"™ grapes at the transcriptomics level. <i>Journal of Horticultural Science and Biotechnology</i> , 2021, 96, 797-807.	0.9	10
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18323	Protocol for genome-scale CRISPR screening in engineered lineage reporter hPSCs to study cell fate determination. <i>STAR Protocols</i> , 2021, 2, 100548.	0.5	0
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18364	Transcriptome in combination with experimental validation unveils hub immune-related genes in oriental river prawn <i>Macrobrachium nipponense</i> against <i>Spiroplasma eriocheiris</i> challenge. <i>Aquaculture</i> , 2021, 539, 736625.	1.7	4
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18379	Evolution of fibrinogen domain related proteins in <i>Aedes aegypti</i> : Their expression during Arbovirus infections. <i>Gene Reports</i> , 2021, 23, 101030.	0.4	0
18380	Complete Plastid and Mitochondrial Genomes of <i>Aeginetia indica</i> Reveal Intracellular Gene Transfer (IGT), Horizontal Gene Transfer (HGT), and Cytoplasmic Male Sterility (CMS). <i>International Journal of Molecular Sciences</i> , 2021, 22, 6143.	1.8	28
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18404	Genome-wide mapping of DNA double-strand breaks from eukaryotic cell cultures using Break-seq. <i>STAR Protocols</i> , 2021, 2, 100554.	0.5	3
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18969	Six de novo assemblies from pathogenic and non-pathogenic strains of <i>Fusarium oxysporum</i> f. sp. <i>niveum</i> . <i>PhytoFrontiers</i> , 0, , .	0.8	2

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19086	A simple and robust method for simultaneous dual-omics profiling with limited numbers of cells. <i>Cell Reports Methods</i> , 2021, 1, 100041.	1.4	3
19087	Genetic engineering of <i>Treponema pallidum</i> subsp. <i>pallidum</i> , the Syphilis Spirochete. <i>PLoS Pathogens</i> , 2021, 17, e1009612.	2.1	27
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19473	A clinically applicable integrative molecular classification of meningiomas. <i>Nature</i> , 2021, 597, 119-125.	13.7	180
19474	Life Cycle Stage-Specific Accessibility of <i>Leishmania donovani</i> Chromatin at Transcription Start Regions. <i>MSystems</i> , 2021, 6, e0062821.	1.7	6
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19483	Single-cell Hi-C data analysis: safety in numbers. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	26
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19486	Enrofloxacin induces intestinal disorders of metabolome and microbiome in American shad (<i>Alosa</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.9	5
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19492	Distribution of Holliday junctions and repair forks during <i>Escherichia coli</i> DNA double-strand break repair. <i>PLoS Genetics</i> , 2021, 17, e1009717.	1.5	5
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19500	Spatial and Temporal Dynamics of Prokaryotic and Viral Community Assemblages in a Lotic System (Manatee Springs, Florida). <i>Applied and Environmental Microbiology</i> , 2021, 87, e0064621.	1.4	10
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19682	Elevated murine HB-EGF confers sensitivity to diphtheria toxin in EGFR-mutant lung adenocarcinoma. <i>DMM Disease Models and Mechanisms</i> , 2021, 14, .	1.2	1
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19825	Intragenic Distribution of IS <i>6110</i> in Clinical <i>Mycobacterium tuberculosis</i> Strains: Bioinformatic Evidence for Gene Disruption Leading to Underdiagnosed Antibiotic Resistance. <i>Microbiology Spectrum</i> , 2021, 9, e0001921.	1.2	9
19826	BbWor1, a Regulator of Morphological Transition, Is Involved in <i>Conidium</i> -Hypha Switching, Blastospore Propagation, and Virulence in <i>Beauveria bassiana</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0020321.	1.2	5
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20005	New early phenotypic markers for cucumber green mottle mosaic virus disease in cucumbers exposed to fluctuating extreme temperatures. <i>Scientific Reports</i> , 2021, 11, 19060.	1.6	5
20006	Genomic Differences Between the Sexes in a Fish Species Seen Through Satellite DNAs. <i>Frontiers in Genetics</i> , 2021, 12, 728670.	1.1	7
20007	<i>Aegilops tauschii</i> genome assembly Aet v5.0 features greater sequence contiguity and improved annotation. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	19
20008	Parallel subgenome structure and divergent expression evolution of allo-tetraploid common carp and goldfish. <i>Nature Genetics</i> , 2021, 53, 1493-1503.	9.4	52
20009	Activity and structure of methanogenic microbial communities in sediments of cascade hydropower reservoirs, Southwest China. <i>Science of the Total Environment</i> , 2021, 786, 147515.	3.9	7
20010	Mechanistic insights into the success of xenobiotic degraders resolved from metagenomes of microbial enrichment cultures. <i>Journal of Hazardous Materials</i> , 2021, 418, 126384.	6.5	10
20011	Rambutan genome revealed gene networks for spine formation and aril development. <i>Plant Journal</i> , 2021, 108, 1037-1052.	2.8	7
20012	Sequential actions of EOMES and T-BET promote stepwise maturation of natural killer cells. <i>Nature Communications</i> , 2021, 12, 5446.	5.8	38
20013	Effect of a Wood-Based Carrier of <i>Trichoderma atroviride</i> SC1 on the Microorganisms of the Soil. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 751.	1.5	4
20014	The Thioesterase <i>ACOT1</i> as a Regulator of Lipid Metabolism in Type 2 Diabetes Detected in a Multi-Omics Study of Human Liver. <i>OMICS A Journal of Integrative Biology</i> , 2021, 25, 652-659.	1.0	6
20016	Small extrachromosomal circular DNA (eccDNA): major functions in evolution and cancer. <i>Molecular Cancer</i> , 2021, 20, 113.	7.9	43
20017	Arms race in a cell: genomic, transcriptomic, and proteomic insights into intracellular phage-bacteria interplay in deep-sea snail holobionts. <i>Microbiome</i> , 2021, 9, 182.	4.9	7
20018	INTS11 regulates hematopoiesis by promoting PRC2 function. <i>Science Advances</i> , 2021, 7, eabh1684.	4.7	6
20019	Genomic and Phenotypic Analysis of Heat and Sanitizer Resistance in <i>Escherichia coli</i> from Beef in Relation to the Locus of Heat Resistance. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0157421.	1.4	8
20020	Genomic impact of stress-induced transposable element mobility in <i>Arabidopsis</i> . <i>Nucleic Acids Research</i> , 2021, 49, 10431-10447.	6.5	60
20021	YAP regulates alveolar epithelial cell differentiation and AGER via NFIB/KLF5/NKX2-1. <i>IScience</i> , 2021, 24, 102967.	1.9	24
20022	Genetic and functional analysis reveals TENM4 contributes to schizophrenia. <i>IScience</i> , 2021, 24, 103063.	1.9	10
20023	Integrated transcriptomics and proteomics revealed the distinct toxicological effects of multi-metal contamination on oysters. <i>Environmental Pollution</i> , 2021, 284, 117533.	3.7	5

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20024	Chemical capping improves template switching and enhances sequencing of small RNAs. <i>Nucleic Acids Research</i> , 2022, 50, e2-e2.	6.5	5
20025	RNA-Sequencing (transcriptomic) Data Collected in Liver and Lung of Male and Female B6C3F1 Mice Exposed to Various Dose Levels of 4-Methylimidazole for 2, 5, or 28 days. <i>Data in Brief</i> , 2021, 38, 107420.	0.5	1
20026	Integrative ATAC-seq and RNA-seq Analysis of the Longissimus Muscle of Luchuan and Duroc Pigs. <i>Frontiers in Nutrition</i> , 2021, 8, 742672.	1.6	32
20027	Increasing the power of interpretation for soil metaproteomics data. <i>Microbiome</i> , 2021, 9, 195.	4.9	25
20029	Aberrant activation of m6A demethylase FTO renders HIF2 ^{low} clear cell renal cell carcinoma sensitive to BRD9 inhibitors. <i>Science Translational Medicine</i> , 2021, 13, eabf6045.	5.8	28
20030	piRNA-independent transposon silencing by the Drosophila THO complex. <i>Developmental Cell</i> , 2021, 56, 2623-2635.e5.	3.1	10
20031	Unraveling the functional role of DNA demethylation at specific promoters by targeted steric blockage of DNA methyltransferase with CRISPR/dCas9. <i>Nature Communications</i> , 2021, 12, 5711.	5.8	38
20032	Cochlear Sox2 ⁺ Glial Cells Are Potent Progenitors for Spiral Ganglion Neuron Reprogramming Induced by Small Molecules. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 728352.	1.8	8
20033	Pivotal Roles for Ribonucleases in Streptococcus pneumoniae Pathogenesis. <i>MBio</i> , 2021, 12, e0238521.	1.8	5
20035	Single-cell DNA and RNA sequencing reveals the dynamics of intra-tumor heterogeneity in a colorectal cancer model. <i>BMC Biology</i> , 2021, 19, 207.	1.7	18
20036	Role of Ribosomal RNA Released from Red Cells in Blood Coagulation in Zebrafish and Humans. <i>Blood Advances</i> , 2021, 5, 4634-4647.	2.5	1
20037	<i>Pseudonocardia abyssalis</i> sp. nov. and <i>Pseudonocardia oceani</i> sp. nov., two novel actinomycetes isolated from the deep Southern Ocean. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	11
20040	An integrated pipeline for mammalian genetic screening. <i>Cell Reports Methods</i> , 2021, 1, 100082.	1.4	11
20041	Establishment of a bovine rumen epithelial cell line. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	3
20043	A UVB-responsive common variant at chromosome band 7p21.1 confers tanning response and melanoma risk via regulation of the aryl hydrocarbon receptor, AHR. <i>American Journal of Human Genetics</i> , 2021, 108, 1611-1630.	2.6	7
20044	Position effects at the FGF8 locus are associated with femoral hypoplasia. <i>American Journal of Human Genetics</i> , 2021, 108, 1725-1734.	2.6	4
20045	Genome-centric investigation of anaerobic digestion using sustainable second and third generation substrates. <i>Journal of Biotechnology</i> , 2021, 339, 53-64.	1.9	12
20046	Prospects and challenges of cancer systems medicine: from genes to disease networks. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	7

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20047	A versatile genetic engineering toolkit for <i>E. coli</i> based on CRISPR-prime editing. <i>Nature Communications</i> , 2021, 12, 5206.	5.8	49
20048	Disease-induced changes in plant microbiome assembly and functional adaptation. <i>Microbiome</i> , 2021, 9, 187.	4.9	157
20049	Protocol for using TRIBE to study RNA-protein interactions and nuclear organization in mammalian cells. <i>STAR Protocols</i> , 2021, 2, 100634.	0.5	1
20050	Spatial rearrangement of the <i>Streptomyces venezuelae</i> linear chromosome during sporogenic development. <i>Nature Communications</i> , 2021, 12, 5222.	5.8	23
20053	Gut microbial determinants of clinically important improvement in patients with rheumatoid arthritis. <i>Genome Medicine</i> , 2021, 13, 149.	3.6	41
20054	The time course of molecular acclimation to seawater in a euryhaline fish. <i>Scientific Reports</i> , 2021, 11, 18127.	1.6	9
20056	Association between Chromosome 4 and mercury accumulation in muscle of the three-spined stickleback (<i>Gasterosteus aculeatus</i>). <i>Evolutionary Applications</i> , 2021, 14, 2553-2567.	1.5	6
20057	Transcriptomic Analysis of <i>Pediococcus pentosaceus</i> Reveals Carbohydrate Metabolic Dynamics Under Lactic Acid Stress. <i>Frontiers in Microbiology</i> , 2021, 12, 736411.	1.5	2
20058	Proteogenomic Analysis Provides Novel Insight into Genome Annotation and Nitrogen Metabolism in <i>Nostoc</i> sp. PCC 7120. <i>Microbiology Spectrum</i> , 2021, 9, e0049021.	1.2	5
20059	A population-level invasion by transposable elements triggers genome expansion in a fungal pathogen. <i>ELife</i> , 2021, 10, .	2.8	49
20061	Differences in Acid Stress Response of <i>Lactobacillus paracasei</i> Zhang Cultured from Solid-State Fermentation and Liquid-State Fermentation. <i>Microorganisms</i> , 2021, 9, 1951.	1.6	2
20062	NSG-Pro mouse model for uncovering resistance mechanisms and unique vulnerabilities in human luminal breast cancers. <i>Science Advances</i> , 2021, 7, eabc8145.	4.7	10
20064	The epigenetic role of HTR1A antagonist in facilitating GnRH expression for pubertal initiation control. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 25, 198-206.	2.3	15
20065	Comparative transcriptomic analysis of <i>Macrobrachium nipponense</i> in response to <i>Aeromonas veronii</i> or <i>Staphylococcus aureus</i> infection. <i>Journal of Oceanology and Limnology</i> , 0, , 1.	0.6	0
20066	Integration of metabolomics and transcriptomics revealed the biosynthetic mechanism of anti-parasitic compounds in <i>Salinivibrio proteolyticus</i> strain YCSC6. <i>Journal of Oceanology and Limnology</i> , 0, , 1.	0.6	0
20068	Global gene expression analysis of pigeonpea with male sterility conditioned by A2 cytoplasm. <i>Plant Genome</i> , 2021, 14, e20132.	1.6	7
20069	Comparative physiological, biochemical and transcriptomic analysis of hexaploid wheat (<i>T. aestivum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf and Zn starvation. <i>Genomics</i> , 2021, 113, 3357-3372.	1.3	8
20070	Eight Metagenome-Assembled Genomes Provide Evidence for Microbial Adaptation in 20,000- to 1,000,000-Year-Old Siberian Permafrost. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0097221.	1.4	13

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20075	GRHL3 activates FSCN1 to relax cell-cell adhesions between migrating keratinocytes during wound reepithelialization. <i>JCI Insight</i> , 2021, 6, .	2.3	8
20076	Phylogeographic reconstruction of the marbled crayfish origin. <i>Communications Biology</i> , 2021, 4, 1096.	2.0	8
20077	Recent amplification of microsatellite-associated miniature inverted-repeat transposable elements in the pineapple genome. <i>BMC Plant Biology</i> , 2021, 21, 424.	1.6	1
20079	Butyrate Production Pathway Abundances Are Similar in Human and Nonhuman Primate Gut Microbiomes. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	13
20080	Mechanistic dissection of dominant AIRE mutations in mouse models reveals AIRE autoregulation. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	18
20081	Genome and transcriptome analysis of the beet armyworm <i>Spodoptera exigua</i> reveals targets for pest control. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	9
20082	Using metatranscriptomics to estimate the diversity and composition of zooplankton communities. <i>Molecular Ecology Resources</i> , 2022, 22, 638-652.	2.2	14
20083	Belowground responses of bacterial communities to foliar SA application over four plant generations. <i>Plant and Soil</i> , 2022, 470, 65-79.	1.8	2
20084	Resequencing of 301 ramie accessions identifies genetic loci and breeding selection for fibre yield traits. <i>Plant Biotechnology Journal</i> , 2022, 20, 323-334.	4.1	12
20085	Global chromatin relabeling accompanies spatial inversion of chromatin in rod photoreceptors. <i>Science Advances</i> , 2021, 7, eabj3035.	4.7	16
20086	The CTPase activity of ParB determines the size and dynamics of prokaryotic DNA partition complexes. <i>Molecular Cell</i> , 2021, 81, 3992-4007.e10.	4.5	37
20088	Modeling Ocean Color Niche Selection by <i>Synechococcus</i> Blue-Green Acclimators. <i>Journal of Geophysical Research: Oceans</i> , 2021, 126, e2021JC017434.	1.0	1
20089	Whole-Genome Sequences of SARS-CoV-2 Isolates from Ethiopian Patients. <i>Microbiology Resource Announcements</i> , 2021, 10, e0072121.	0.3	0
20092	Early-life midazolam exposure persistently changes chromatin accessibility to impair adult hippocampal neurogenesis and cognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	10
20093	A novel thermostable prokaryotic fucoidan active sulfatase PsFucS1 with an unusual quaternary hexameric structure. <i>Scientific Reports</i> , 2021, 11, 19523.	1.6	8
20095	A strategy for a high enrichment of insect mitochondrial DNA for mitogenomic analysis. <i>Gene</i> , 2022, 808, 145986.	1.0	3
20097	Multiple introductions of multidrug-resistant typhoid associated with acute infection and asymptomatic carriage, Kenya. <i>ELife</i> , 2021, 10, .	2.8	29

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20099	Oligotyping and metagenomics reveal distinct <i>Candidatus Accumulibacter</i> communities in side-stream versus conventional full-scale enhanced biological phosphorus removal (EBPR) systems. <i>Water Research</i> , 2021, 206, 117725.	5.3	23
20100	The ETS transcription factor ERF controls the exit from the naïve pluripotent state in a MAPK-dependent manner. <i>Science Advances</i> , 2021, 7, eabg8306.	4.7	6
20101	Multi-omic analysis of altered transcriptome and epigenetic signatures in the UV-induced DNA damage response. <i>DNA Repair</i> , 2021, 106, 103172.	1.3	8
20102	Genome-wide analysis of the invertase genes in strawberry (<i>Fragaria</i> — <i>ananassa</i>). <i>Journal of Integrative Agriculture</i> , 2021, 20, 2652-2665.	1.7	7
20103	Fecal Microbiota Transplantation Influences Procarcinogenic <i>Escherichia coli</i> in Recipient Recurrent <i>Clostridioides difficile</i> Patients. <i>Gastroenterology</i> , 2021, 161, 1218-1228.e5.	0.6	18
20104	The n-butanol fraction of the Xiao-Chai-Hu decoction alleviates the endocrine disturbance in the liver of mice exposed to lead. <i>Journal of Ethnopharmacology</i> , 2021, 279, 114381.	2.0	4
20105	Enhancer-associated H3K4 methylation safeguards in vitro germline competence. <i>Nature Communications</i> , 2021, 12, 5771.	5.8	20
20106	Charting oncogenicity of genes and variants across lineages via multiplexed screens in teratomas. <i>IScience</i> , 2021, 24, 103149.	1.9	2
20107	Metagenomic analysis of microbial communities continuously exposed to Bisphenol A in mangrove rhizosphere and non-rhizosphere soils. <i>Science of the Total Environment</i> , 2021, 792, 148486.	3.9	13
20108	Serum Testosterone to Androstenedione Ratio Predicts Metabolic Health in Normal-Weight Polycystic Ovary Syndrome Women. <i>Journal of the Endocrine Society</i> , 2021, 5, bvab158.	0.1	9
20109	Genome-wide transcriptomic analysis of highly virulent African swine fever virus infection reveals complex and unique virus host interaction. <i>Veterinary Microbiology</i> , 2021, 261, 109211.	0.8	22
20110	Monsavirus in monkey rectal swab and throat swab specimens in China: Proposal for Posaliviridae as a new family in Picornvirales. <i>Virus Research</i> , 2021, 303, 198501.	1.1	2
20111	Transcriptome and chromatin landscape changes associated with trastuzumab resistance in HER2+ breast cancer cells. <i>Gene</i> , 2021, 799, 145808.	1.0	12
20112	Differentially methylated gene regions between resistant and susceptible heat-phenotypes of the Pacific oyster <i>Crassostrea gigas</i> . <i>Aquaculture</i> , 2021, 543, 736923.	1.7	5
20113	Isolation of a novel insect-specific flavivirus with immunomodulatory effects in vertebrate systems. <i>Virology</i> , 2021, 562, 50-62.	1.1	14
20114	A resampling strategy for studying robustness in virus detection pipelines. <i>Computational Biology and Chemistry</i> , 2021, 94, 107555.	1.1	0
20115	A single point mutation in the <i>hyaC</i> gene affects <i>Pasteurella multocida</i> serovar A capsule production and virulence. <i>Microbial Pathogenesis</i> , 2021, 159, 105145.	1.3	6

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20116	The genome of the zoonotic malaria parasite <i>Plasmodium simium</i> reveals adaptations to host switching. <i>BMC Biology</i> , 2021, 19, 219.	1.7	21
20117	Transcript responses to drought in Kentucky bluegrass (<i>Poa pratensis</i> L.) germplasm varying in their tolerance to drought stress. <i>Environmental and Experimental Botany</i> , 2021, 190, 104571.	2.0	5
20118	Stachyose inhibits vancomycin-resistant <i>Enterococcus</i> colonization and affects gut microbiota in mice. <i>Microbial Pathogenesis</i> , 2021, 159, 105094.	1.3	5
20119	Genome-wide expression analysis reveal host genes involved in immediate-early infections of different sheeppox virus strains. <i>Gene</i> , 2021, 801, 145850.	1.0	1
20120	Genetic differentiation and selection signatures in two bay scallop (<i>Argopecten irradians</i>) breeds revealed by whole-genome resequencing analysis. <i>Aquaculture</i> , 2021, 543, 736944.	1.7	12
20121	Differences in DNA methylation between slow and fast muscle in <i>Takifugu rubripes</i> . <i>Gene</i> , 2021, 801, 145853.	1.0	4
20122	Genome skims analysis of betel palms (<i>Areca</i> spp., <i>Arecaceae</i>) and development of a profiling method to assess their plastome diversity. <i>Gene</i> , 2021, 800, 145845.	1.0	0
20123	Comparative transcriptome profiling of horseshoe crab <i>Tachypleus gigas</i> hemocytes in response to lipopolysaccharides. <i>Fish and Shellfish Immunology</i> , 2021, 117, 148-156.	1.6	10
20124	Novel Paju Apodemus paramyxovirus 1 and 2, harbored by <i>Apodemus agrarius</i> in the Republic of Korea. <i>Virology</i> , 2021, 562, 40-49.	1.1	10
20126	Genome-wide analysis of the SCPL gene family in grape (<i>Vitis vinifera</i> L.). <i>Journal of Integrative Agriculture</i> , 2021, 20, 2666-2679.	1.7	6
20127	Identifying a genome-wide QTL interval controlling for ammonia-nitrogen tolerance on chrLG1 of Nile tilapia. <i>Aquaculture</i> , 2021, 543, 736946.	1.7	8
20128	Automated library preparation for whole genome sequencing by centrifugal microfluidics. <i>Analytica Chimica Acta</i> , 2021, 1182, 338954.	2.6	6
20129	Direct in vivo observation of the effect of codon usage bias on gene expression in <i>Arabidopsis</i> hybrids. <i>Journal of Plant Physiology</i> , 2021, 265, 153490.	1.6	12
20130	Mechanism of the growth and development of the posterior silk gland and silk secretion revealed by mutation of the fibroin light chain in silkworm. <i>International Journal of Biological Macromolecules</i> , 2021, 188, 375-384.	3.6	9
20131	Hepatopancreas transcriptome analysis reveals the molecular responses to different dietary n-3 PUFA lipid sources in the swimming crab <i>Portunus trituberculatus</i> . <i>Aquaculture</i> , 2021, 543, 737016.	1.7	14
20132	N-acyl-homoserine-lactones signaling as a critical control point for phosphorus entrapment by multi-species microbial aggregates. <i>Water Research</i> , 2021, 204, 117627.	5.3	19
20133	Integrated analysis of blood mRNAs and microRNAs reveals immune changes with age in the Yangtze finless porpoise (<i>Neophocaena asiaeorientalis</i>). <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2021, 256, 110635.	0.7	6
20134	Kefir ameliorates specific microbiota-gut-brain axis impairments in a mouse model relevant to autism spectrum disorder. <i>Brain, Behavior, and Immunity</i> , 2021, 97, 119-134.	2.0	19

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20135	The widespread IS200/IS605 transposon family encodes diverse programmable RNA-guided endonucleases. <i>Science</i> , 2021, 374, 57-65.	6.0	152
20136	<i>Ruminiclostridium 5</i> , <i>Parabacteroides distasonis</i> , and bile acid profile are modulated by prebiotic diet and associate with facilitated sleep/clock realignment after chronic disruption of rhythms. <i>Brain, Behavior, and Immunity</i> , 2021, 97, 150-166.	2.0	34
20137	Genome-Wide Association Mapping of Late Blight Tolerance Trait in Potato (<i>Solanum tuberosum</i> L.). <i>Frontiers in Genetics</i> , 2021, 12, 714575.	1.1	9
20138	Viral Community and Virus-Associated Antibiotic Resistance Genes in Soils Amended with Organic Fertilizers. <i>Environmental Science & Technology</i> , 2021, 55, 13881-13890.	4.6	49
20140	Application and mechanism of benzyl-isothiocyanate, a natural antimicrobial agent from cruciferous vegetables, in controlling postharvest decay of strawberry. <i>Postharvest Biology and Technology</i> , 2021, 180, 111604.	2.9	22
20141	UCE Phylogenomics, detection of a putative hybrid population, and one older mitogenomic node age of <i>Batrachuperus</i> salamanders. <i>Molecular Phylogenetics and Evolution</i> , 2021, 163, 107239.	1.2	0
20142	Comparative transcriptome analysis provides insight into nitric oxide suppressing lignin accumulation of postharvest okra (<i>Abelmoschus esculentus</i> L.) during cold storage. <i>Plant Physiology and Biochemistry</i> , 2021, 167, 49-67.	2.8	27
20143	Genetic Characterization of Seoul Virus in the Seaport of Cotonou, Benin. <i>Emerging Infectious Diseases</i> , 2021, 27, 2704-2706.	2.0	6
20144	Description of four <i>Millepora</i> spp. transcriptomes and their potential to delimit the Caribbean fire coral species. <i>Marine Genomics</i> , 2021, 59, 100863.	0.4	0
20145	Transcriptomic signature of extinction learning in the brain of the fire-bellied toad, <i>Bombina orientalis</i> . <i>Neurobiology of Learning and Memory</i> , 2021, 184, 107502.	1.0	4
20146	<i>Drosophila</i> architectural protein CTCF is not essential for fly survival and is able to function independently of CP190. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194733.	0.9	10
20147	Rett syndrome linked to defects in forming the MeCP2/Rbfox/LASR complex in mouse models. <i>Nature Communications</i> , 2021, 12, 5767.	5.8	16
20148	Baculovirus infection affects caterpillar chemoperception. <i>Insect Biochemistry and Molecular Biology</i> , 2021, 138, 103648.	1.2	10
20149	Conformational Changes of ROR β During Response Element Recognition and Coregulator Engagement. <i>Journal of Molecular Biology</i> , 2021, 433, 167258.	2.0	4
20150	Strain-level multiomics analysis reveals significant variation in cheeses from different regions. <i>LWT - Food Science and Technology</i> , 2021, 151, 112043.	2.5	17
20151	Doxorubicin induces wide-spread transcriptional changes in the myocardium of hearts distinguishing between mice with preserved and impaired cardiac function. <i>Life Sciences</i> , 2021, 284, 119879.	2.0	2
20152	Non-coding Natural Antisense Transcripts: Analysis and Application. <i>Journal of Biotechnology</i> , 2021, 340, 75-101.	1.9	12
20153	Comprehensive analysis of miRNA-mRNA/lncRNA during gonadal development of triploid female rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Genomics</i> , 2021, 113, 3533-3543.	1.3	10

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20154	Large within, and between, species differences in marine cellular responses: Unpredictability in a changing environment. <i>Science of the Total Environment</i> , 2021, 794, 148594.	3.9	10
20155	RNA editing signatures identify melanoma patients who respond to Pembrolizumab or Nivolumab treatment. <i>Translational Oncology</i> , 2021, 14, 101197.	1.7	2
20156	Anthocyanins contribute to fruit defense against postharvest green mold. <i>Postharvest Biology and Technology</i> , 2021, 181, 111661.	2.9	18
20157	The draft genome of the Asian corn borer yields insights into ecological adaptation of a devastating maize pest. <i>Insect Biochemistry and Molecular Biology</i> , 2021, 138, 103638.	1.2	8
20158	Offspring production of ovarian organoids derived from spermatogonial stem cells by defined factors with chromatin reorganization. <i>Journal of Advanced Research</i> , 2021, 33, 81-98.	4.4	17
20159	Transcriptome analysis of immune-related gene expression in Yellow River carp (<i>Cyprinus carpio</i> var.) after challenge with <i>Flavobacterium columnare</i> . <i>Microbial Pathogenesis</i> , 2021, 160, 105148.	1.3	8
20160	Early adaptive chromatin remodeling events precede pathologic phenotypes and are reinforced in the failing heart. <i>Journal of Molecular and Cellular Cardiology</i> , 2021, 160, 73-86.	0.9	17
20161	Genetic contribution of domestic European common carp (<i>Cyprinus carpio carpio</i>) and Amur carp (<i>Cyprinus carpio haematopterus</i>) to the wild Vietnamese carp population as revealed by ddRAD sequencing. <i>Aquaculture</i> , 2021, 544, 737049.	1.7	6
20162	Alteration of the phenylpropanoid pathway by watercore disorder in apple (<i>Malus x domestica</i>). <i>Scientia Horticulturae</i> , 2021, 289, 110438.	1.7	9
20163	Dysfunctional activity of classical DNA end-joining renders acquired resistance to carboplatin in human ovarian cancer cells. <i>Cancer Letters</i> , 2021, 520, 267-280.	3.2	7
20164	Target capture sequencing of SARS-CoV-2 genomes using the ONETest Coronaviruses Plus. <i>Diagnostic Microbiology and Infectious Disease</i> , 2021, 101, 115508.	0.8	4
20165	Long non-coding RNA profile in banana shrimp, <i>Fenneropenaeus merguensis</i> and the potential role of lncPV13 in vitellogenesis. <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2021, 261, 111045.	0.8	6
20166	Compartmentalization of mRNAs in the giant, unicellular green alga <i>Acetabularia acetabulum</i> . <i>Algal Research</i> , 2021, 59, 102440.	2.4	2
20167	Persistent <i>Spodoptera frugiperda</i> rhabdovirus infection in Sf9 cells is not restricted by <i>Wolbachia</i> wMelPop-CLA and wAlbB strains and is targeted by the RNAi machinery. <i>Virology</i> , 2021, 563, 82-87.	1.1	1
20168	MiDSytem: A comprehensive online system for de novo assembly and analysis of microbial genomes. <i>New Biotechnology</i> , 2021, 65, 42-52.	2.4	2
20169	Co-occurring microorganisms regulate the succession of cyanobacterial harmful algal blooms. <i>Environmental Pollution</i> , 2021, 288, 117682.	3.7	39
20170	Novel viruses in hard ticks collected in the Republic of Korea unveiled by metagenomic high-throughput sequencing analysis. <i>Ticks and Tick-borne Diseases</i> , 2021, 12, 101820.	1.1	4
20171	Biological upgrading of pyrolysis-derived wastewater: Engineering <i>Pseudomonas putida</i> for alkylphenol, furfural, and acetone catabolism and (methyl)muconic acid production. <i>Metabolic Engineering</i> , 2021, 68, 14-25.	3.6	20

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20173	Exploring the diversity of coronavirus in sewage during COVID-19 pandemic: Don't miss the forest for the trees. <i>Science of the Total Environment</i> , 2021, 800, 149562.	3.9	14
20174	Reverse transcription recombinase-aided amplification assay for rapid detection of the influenza A(H1N1)pdm09 H275Y mutation that confers oseltamivir resistance. <i>Molecular and Cellular Probes</i> , 2021, 60, 101771.	0.9	0
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20178	Differential gene expression associated with behavioral variation in ecotypes of Lake Superior brook trout (<i>Salvelinus fontinalis</i>). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 40, 100884.	0.4	0
20179	Identifying active rumen epithelial associated bacteria and archaea in beef cattle divergent in feed efficiency using total RNA-seq. <i>Current Research in Microbial Sciences</i> , 2021, 2, 100064.	1.4	10
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20185	First construction of interspecific backcross grouper and genome-wide identification of their genetic variants associated with early growth. <i>Aquaculture</i> , 2021, 545, 737221.	1.7	8
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20189	Transcriptomic and proteomic analyses of venom glands from scorpions <i>Liocheles australasiae</i> , <i>Mesobuthus martensii</i> , and <i>Scorpio maurus palmatus</i> . <i>Peptides</i> , 2021, 146, 170643.	1.2	6

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20206	Non-invasive sex genotyping of paiche <i>Arapaima gigas</i> by qPCR: An applied bioinformatic approach for identifying sex differences. <i>Aquaculture</i> , 2022, 546, 737388.	1.7	1
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20615	SeroBA: rapid high-throughput serotyping of <i>Streptococcus pneumoniae</i> from whole genome sequence data. <i>Microbial Genomics</i> , 2018, 4, .	1.0	68
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22589	Dlk1-Dio3 locus-derived lncRNAs perpetuate postmitotic motor neuron cell fate and subtype identity. <i>ELife</i> , 2018, 7, .	2.8	43
22590	Condensin controls cellular RNA levels through the accurate segregation of chromosomes instead of directly regulating transcription. <i>ELife</i> , 2018, 7, .	2.8	24
22591	Mapping the transcriptional diversity of genetically and anatomically defined cell populations in the mouse brain. <i>ELife</i> , 2019, 8, .	2.8	59

#	ARTICLE	IF	CITATIONS
22592	Single cell functional genomics reveals the importance of mitochondria in cell-to-cell phenotypic variation. <i>ELife</i> , 2019, 8, .	2.8	28
22593	Differing isoforms of the cobalamin binding photoreceptor AerR oppositely regulate photosystem expression. <i>ELife</i> , 2018, 7, .	2.8	13
22594	New insights into the cellular temporal response to proteostatic stress. <i>ELife</i> , 2018, 7, .	2.8	47
22595	Expansion of the fatty acyl reductase gene family shaped pheromone communication in Hymenoptera. <i>ELife</i> , 2019, 8, .	2.8	26
22596	Intergenerational epigenetic inheritance of cancer susceptibility in mammals. <i>ELife</i> , 2019, 8, .	2.8	43
22597	Molecular function limits divergent protein evolution on planetary timescales. <i>ELife</i> , 2019, 8, .	2.8	25
22598	Meiotic drive of female-inherited supernumerary chromosomes in a pathogenic fungus. <i>ELife</i> , 2018, 7, .	2.8	28
22599	H3K9me3 is required for inheritance of small RNAs that target a unique subset of newly evolved genes. <i>ELife</i> , 2019, 8, .	2.8	36
22600	Identification and characterisation of hypomethylated DNA loci controlling quantitative resistance in <i>Arabidopsis</i> . <i>ELife</i> , 2019, 8, .	2.8	73
22601	Targets and genomic constraints of ectopic Dnmt3b expression. <i>ELife</i> , 2018, 7, .	2.8	26
22602	ASH1-catalyzed H3K36 methylation drives gene repression and marks H3K27me2/3-competent chromatin. <i>ELife</i> , 2018, 7, .	2.8	50
22603	Live-cell imaging reveals enhancer-dependent Sox2 transcription in the absence of enhancer proximity. <i>ELife</i> , 2019, 8, .	2.8	220
22604	The novel lncRNA lnc-NR2F1 is pro-neurogenic and mutated in human neurodevelopmental disorders. <i>ELife</i> , 2019, 8, .	2.8	59
22605	Analysis of the genomic architecture of a complex trait locus in hypertensive rat models links <i>Tmem63c</i> to kidney damage. <i>ELife</i> , 2019, 8, .	2.8	25
22606	TRIM28 promotes HIV-1 latency by SUMOylating CDK9 and inhibiting P-TEFb. <i>ELife</i> , 2019, 8, .	2.8	71
22607	Pantonâ€“Valentine leucocidin is the key determinant of <i>Staphylococcus aureus</i> pyomyositis in a bacterial GWAS. <i>ELife</i> , 2019, 8, .	2.8	56
22608	A combination of transcription factors mediates inducible interchromosomal contacts. <i>ELife</i> , 2019, 8, .	2.8	16
22609	The Hox transcription factor Ubx stabilizes lineage commitment by suppressing cellular plasticity in <i>Drosophila</i> . <i>ELife</i> , 2019, 8, .	2.8	22

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22610	The unfolded protein response and endoplasmic reticulum protein targeting machineries converge on the stress sensor IRE1. <i>ELife</i> , 2018, 7, .	2.8	71
22611	Beta-catenin signaling regulates barrier-specific gene expression in circumventricular organ and ocular vasculatures. <i>ELife</i> , 2019, 8, .	2.8	74
22612	Neuroblast-specific open chromatin allows the temporal transcription factor, Hunchback, to bind neuroblast-specific loci. <i>ELife</i> , 2019, 8, .	2.8	46
22613	Dynamic enhancer partitioning instructs activation of a growth-related gene during exit from naïve pluripotency. <i>ELife</i> , 2019, 8, .	2.8	11
22614	Functional evaluation of transposable elements as enhancers in mouse embryonic and trophoblast stem cells. <i>ELife</i> , 2019, 8, .	2.8	108
22615	A de novo evolved gene in the house mouse regulates female pregnancy cycles. <i>ELife</i> , 2019, 8, .	2.8	37
22616	Scc2 counteracts a Wapl-independent mechanism that releases cohesin from chromosomes during G1. <i>ELife</i> , 2019, 8, .	2.8	33
22617	Single-amino acid variants reveal evolutionary processes that shape the biogeography of a global SAR11 subclade. <i>ELife</i> , 2019, 8, .	2.8	89
22618	Genetic interactions of G-quadruplexes in humans. <i>ELife</i> , 2019, 8, .	2.8	91
22619	Evidence for DNA-mediated nuclear compartmentalization distinct from phase separation. <i>ELife</i> , 2019, 8, .	2.8	222
22620	Distinct mechanisms of microRNA sorting into cancer cell-derived extracellular vesicle subtypes. <i>ELife</i> , 2019, 8, .	2.8	164
22621	<i>Toxoplasma gondii</i> infection drives conversion of NK cells into ILC1-like cells. <i>ELife</i> , 2019, 8, .	2.8	91
22622	Free circular introns with an unusual branchpoint in neuronal projections. <i>ELife</i> , 2019, 8, .	2.8	14
22623	Epimutations are associated with CHROMOMETHYLASE 3-induced de novo DNA methylation. <i>ELife</i> , 2019, 8, .	2.8	59
22624	CTCF confers local nucleosome resiliency after DNA replication and during mitosis. <i>ELife</i> , 2019, 8, .	2.8	61
22625	Cardiac neural crest contributes to cardiomyocytes in amniotes and heart regeneration in zebrafish. <i>ELife</i> , 2019, 8, .	2.8	49
22626	Screening identifies small molecules that enhance the maturation of human pluripotent stem cell-derived myotubes. <i>ELife</i> , 2019, 8, .	2.8	45
22627	Controlling gene activation by enhancers through a drug-inducible topological insulator. <i>ELife</i> , 2020, 9, .	2.8	8

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22628	Cis-regulatory basis of sister cell type divergence in the vertebrate retina. <i>ELife</i> , 2019, 8, .	2.8	30
22629	Neutrophils promote CXCR3-dependent itch in the development of atopic dermatitis. <i>ELife</i> , 2019, 8, .	2.8	99
22630	Repressive H3K9me2 protects lifespan against the transgenerational burden of COMPASS activity in <i>C. elegans</i> . <i>ELife</i> , 2019, 8, .	2.8	47
22631	Id4 promotes the elimination of the pro-activation factor <i>Ascl1</i> to maintain quiescence of adult hippocampal stem cells. <i>ELife</i> , 2019, 8, .	2.8	62
22632	Chromatinization of <i>Escherichia coli</i> with archaeal histones. <i>ELife</i> , 2019, 8, .	2.8	23
22633	Genetically diverse uropathogenic <i>Escherichia coli</i> adopt a common transcriptional program in patients with UTIs. <i>ELife</i> , 2019, 8, .	2.8	56
22634	A unicellular relative of animals generates a layer of polarized cells by actomyosin-dependent cellularization. <i>ELife</i> , 2019, 8, .	2.8	41
22635	Combinatorial chromatin dynamics foster accurate cardiopharyngeal fate choices. <i>ELife</i> , 2019, 8, .	2.8	23
22636	Two roles for the yeast transcription coactivator SAGA and a set of genes redundantly regulated by TFIID and SAGA. <i>ELife</i> , 2020, 9, .	2.8	79
22637	Partial loss of <i>CFIm25</i> causes learning deficits and aberrant neuronal alternative polyadenylation. <i>ELife</i> , 2020, 9, .	2.8	25
22638	Herpes simplex viral nucleoprotein creates a competitive transcriptional environment facilitating robust viral transcription and host shut off. <i>ELife</i> , 2019, 8, .	2.8	53
22639	<i>Straightjacket/1±213</i> deregulation is associated with cardiac conduction defects in myotonic dystrophy type 1. <i>ELife</i> , 2019, 8, .	2.8	8
22640	Diversification of the <i>Caenorhabditis</i> heat shock response by Helitron transposable elements. <i>ELife</i> , 2019, 8, .	2.8	21
22641	Robust cullin-RING ligase function is established by a multiplicity of poly-ubiquitylation pathways. <i>ELife</i> , 2019, 8, .	2.8	36
22642	Analysis of zebrafish periderm enhancers facilitates identification of a regulatory variant near human <i>KRT8/18</i> . <i>ELife</i> , 2020, 9, .	2.8	23
22643	Single-cell transcriptome reveals the novel role of T-bet in suppressing the immature NK gene signature. <i>ELife</i> , 2020, 9, .	2.8	19
22644	Epigenetic memory independent of symmetric histone inheritance. <i>ELife</i> , 2019, 8, .	2.8	30
22645	Phenotypic plasticity as a mechanism of cave colonization and adaptation. <i>ELife</i> , 2020, 9, .	2.8	48

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22646	c-Maf restrains T-bet-driven programming of CCR6-negative group 3 innate lymphoid cells. <i>ELife</i> , 2020, 9, .	2.8	22
22647	Cell-type diversity and regionalized gene expression in the planarian intestine. <i>ELife</i> , 2020, 9, .	2.8	35
22648	Whole brain delivery of an instability-prone <i>Mecp2</i> transgene improves behavioral and molecular pathological defects in mouse models of Rett syndrome. <i>ELife</i> , 2020, 9, .	2.8	42
22649	Chromatin accessibility dynamics and single cell RNA-Seq reveal new regulators of regeneration in neural progenitors. <i>ELife</i> , 2020, 9, .	2.8	39
22650	Sphingosine 1-phosphate-regulated transcriptomes in heterogenous arterial and lymphatic endothelium of the aorta. <i>ELife</i> , 2020, 9, .	2.8	34
22651	Hair follicle stem cells regulate retinoid metabolism to maintain the self-renewal niche for melanocyte stem cells. <i>ELife</i> , 2020, 9, .	2.8	25
22652	A complex regulatory landscape involved in the development of mammalian external genitals. <i>ELife</i> , 2020, 9, .	2.8	26
22653	Dual histone methyl reader ZCWPW1 facilitates repair of meiotic double strand breaks in male mice. <i>ELife</i> , 2020, 9, .	2.8	30
22654	Squamous trans-differentiation of pancreatic cancer cells promotes stromal inflammation. <i>ELife</i> , 2020, 9, .	2.8	61
22655	Suppressing proteasome mediated processing of topoisomerase II DNA-protein complexes preserves genome integrity. <i>ELife</i> , 2020, 9, .	2.8	26
22656	The histone modification reader ZCWPW1 links histone methylation to PRDM9-induced double-strand break repair. <i>ELife</i> , 2020, 9, .	2.8	34
22657	RNA-guided retargeting of Sleeping Beauty transposition in human cells. <i>ELife</i> , 2020, 9, .	2.8	44
22658	Zygotic pioneer factor activity of Odd-paired/Zic is necessary for late function of the <i>Drosophila</i> segmentation network. <i>ELife</i> , 2020, 9, .	2.8	36
22659	Spen links RNA-mediated endogenous retrovirus silencing and X chromosome inactivation. <i>ELife</i> , 2020, 9, .	2.8	33
22660	Nuclear receptor Ftz-f1 promotes follicle maturation and ovulation partly via bHLH/PAS transcription factor Sim. <i>ELife</i> , 2020, 9, .	2.8	26
22661	Transposase-assisted tagmentation of RNA/DNA hybrid duplexes. <i>ELife</i> , 2020, 9, .	2.8	40
22662	A highly accurate platform for clone-specific mutation discovery enables the study of active mutational processes. <i>ELife</i> , 2020, 9, .	2.8	5
22663	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

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22664	Smchd1 is a maternal effect gene required for genomic imprinting. <i>ELife</i> , 2020, 9, .	2.8	24
22665	Cardiac endothelial cells maintain open chromatin and expression of cardiomyocyte myofibrillar genes. <i>ELife</i> , 2020, 9, .	2.8	26
22666	<i>Drosophila</i> SWR1 and NuA4 complexes are defined by DOMINO isoforms. <i>ELife</i> , 2020, 9, .	2.8	14
22667	KRAB-zinc finger protein gene expansion in response to active retrotransposons in the murine lineage. <i>ELife</i> , 2020, 9, .	2.8	77
22668	Cohesion is established during DNA replication utilising chromosome associated cohesin rings as well as those loaded de novo onto nascent DNAs. <i>ELife</i> , 2020, 9, .	2.8	36
22669	ODELAM, rapid sequence-independent detection of drug resistance in isolates of <i>Mycobacterium tuberculosis</i> . <i>ELife</i> , 2020, 9, .	2.8	8
22670	Genome streamlining in a minute herbivore that manipulates its host plant. <i>ELife</i> , 2020, 9, .	2.8	33
22671	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
22672	Differentiating <i>Drosophila</i> female germ cells initiate Polycomb silencing by regulating PRC2-interacting proteins. <i>ELife</i> , 2020, 9, .	2.8	25
22673	Repurposing of KLF5 activates a cell cycle signature during the progression from a precursor state to oesophageal adenocarcinoma. <i>ELife</i> , 2020, 9, .	2.8	14
22674	Large domains of heterochromatin direct the formation of short mitotic chromosome loops. <i>ELife</i> , 2020, 9, .	2.8	11
22675	A molecular filter for the cnidarian stinging response. <i>ELife</i> , 2020, 9, .	2.8	18
22676	The testis protein ZNF165 is a SMAD3 cofactor that coordinates oncogenic TGF β 2 signaling in triple-negative breast cancer. <i>ELife</i> , 2020, 9, .	2.8	21
22677	Functional interrogation of HOXA9 regulome in MLLr leukemia via reporter-based CRISPR/Cas9 screen. <i>ELife</i> , 2020, 9, .	2.8	25
22678	Sox17 and β -catenin co-occupy Wnt-responsive enhancers to govern the endoderm gene regulatory network. <i>ELife</i> , 2020, 9, .	2.8	35
22679	IER5, a DNA damage response gene, is required for Notch-mediated induction of squamous cell differentiation. <i>ELife</i> , 2020, 9, .	2.8	13
22680	Mechanisms underlying genome instability mediated by formation of foldback inversions in <i>Saccharomyces cerevisiae</i> . <i>ELife</i> , 2020, 9, .	2.8	10
22681	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

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22682	Spatial inter-centromeric interactions facilitated the emergence of evolutionary new centromeres. <i>ELife</i> , 2020, 9, .	2.8	31
22683	Parallel global profiling of plant TOR dynamics reveals a conserved role for LARP1 in translation. <i>ELife</i> , 2020, 9, .	2.8	61
22684	S-phase-independent silencing establishment in <i>Saccharomyces cerevisiae</i> . <i>ELife</i> , 2020, 9, .	2.8	17
22685	Establishment and maintenance of motor neuron identity via temporal modularity in terminal selector function. <i>ELife</i> , 2020, 9, .	2.8	24
22686	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
22687	Health benefits attributed to 17 β -estradiol, a lifespan-extending compound, are mediated through estrogen receptor α . <i>ELife</i> , 2020, 9, .	2.8	30
22688	Dynamically evolving novel overlapping gene as a factor in the SARS-CoV-2 pandemic. <i>ELife</i> , 2020, 9, .	2.8	74
22689	Cohesin residency determines chromatin loop patterns. <i>ELife</i> , 2020, 9, .	2.8	59
22690	Identification of protein-protected mRNA fragments and structured excised intron RNAs in human plasma by TGIRT-seq peak calling. <i>ELife</i> , 2020, 9, .	2.8	20
22691	Histone deposition pathways determine the chromatin landscapes of H3.1 and H3.3 K27M oncohistones. <i>ELife</i> , 2020, 9, .	2.8	42
22692	Fitness variation across subtle environmental perturbations reveals local modularity and global pleiotropy of adaptation. <i>ELife</i> , 2020, 9, .	2.8	69
22693	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
22694	GTPBP1 resolves paused ribosomes to maintain neuronal homeostasis. <i>ELife</i> , 2020, 9, .	2.8	28
22695	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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22697	CFSAN SNP Pipeline: an automated method for constructing SNP matrices from next-generation sequence data. <i>PeerJ Computer Science</i> , 0, 1, e20.	2.7	254
22698	Biases in genome reconstruction from metagenomic data. <i>PeerJ</i> , 2020, 8, e10119.	0.9	32
22699	The Bacteria Genome Pipeline (BAGEP): an automated, scalable workflow for bacteria genomes with Snakemake. <i>PeerJ</i> , 2020, 8, e10121.	0.9	8

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22701	Transcriptome and gene expression analysis of <i>Rhynchophorus ferrugineus</i> (Coleoptera: Tj ETQq1 1 0.784314 rgBT JOverlock 10 Tf 50	0.9	10
22702	GenomePeek™ an online tool for prokaryotic genome and metagenome analysis. PeerJ, 2015, 3, e1025.	0.9	12
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22710	The complete mitochondrial genome of <i>Lerema accius</i> and its phylogenetic implications. PeerJ, 2016, 4, e1546.	0.9	20
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22714	<i>DChIPRep</i> , an R/Bioconductor package for differential enrichment analysis in chromatin studies. PeerJ, 2016, 4, e1981.	0.9	8
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22719	The PARA-suite: PAR-CLIP specific sequence read simulation and processing. PeerJ, 2016, 4, e2619.	0.9	8
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22722	Brain transcriptomes of harbor seals demonstrate gene expression patterns of animals undergoing a metabolic disease and a viral infection. PeerJ, 2016, 4, e2819.	0.9	6
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22752	Flavonoid biosynthesis controls fiber color in naturally colored cotton. PeerJ, 2018, 6, e4537.	0.9	21
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22930	<i>Lactobacillus rhamnosus</i> ProBio-M9 Improves the Quality of Life in Stressed Adults by Gut Microbiota. <i>Foods</i> , 2021, 10, 2384.	1.9	14
22932	Nuclear-localized human respiratory syncytial virus NS1 protein modulates host gene transcription. <i>Cell Reports</i> , 2021, 37, 109803.	2.9	18
22933	ChAdOx1 nCoV-19 (AZD1222) protects Syrian hamsters against SARS-CoV-2 B.1.351 and B.1.1.7. <i>Nature Communications</i> , 2021, 12, 5868.	5.8	52

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22936	Escape of hair follicle stem cells causes stem cell exhaustion during aging. <i>Nature Aging</i> , 2021, 1, 889-903.	5.3	31
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22952	Multi-tiered analyses of honey bees that resist or succumb to parasitic mites and viruses. <i>BMC Genomics</i> , 2021, 22, 720.	1.2	8
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22958	PRC1 drives Polycomb-mediated gene repression by controlling transcription initiation and burst frequency. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 811-824.	3.6	62
22959	Impact of human gene annotations on RNA-seq differential expression analysis. <i>BMC Genomics</i> , 2021, 22, 730.	1.2	6
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22977	<i>Flavobacterium flabelliforme</i> sp. nov. and <i>Flavobacterium geliluteum</i> sp. nov., Two Multidrug-Resistant Psychrotrophic Species Isolated From Antarctica. <i>Frontiers in Microbiology</i> , 2021, 12, 729977.	1.5	7

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22979	Intraspecific venom variation of Mexican West Coast Rattlesnakes (<i>Crotalus basiliscus</i>) and its implications for antivenom production. <i>Biochimie</i> , 2022, 192, 111-124.	1.3	6
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22993	Genetic landscape of T cells identifies synthetic lethality for T-ALL. <i>Communications Biology</i> , 2021, 4, 1201.	2.0	6
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22995	Intestinal mycobiota composition and changes in children with thalassemia who underwent allogeneic hematopoietic stem cell transplantation. <i>Pediatric Blood and Cancer</i> , 2022, 69, e29411.	0.8	5
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23000	Impact of Bicarbonate- β -Lactam Exposures on Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) Gene Expression in Bicarbonate- β -Lactam-Responsive vs. Non-Responsive Strains. <i>Genes</i> , 2021, 12, 1650.	1.0	7
23001	Heparan sulfate proteoglycans serve as alternative receptors for low affinity LCMV variants. <i>PLoS Pathogens</i> , 2021, 17, e1009996.	2.1	16
23002	The c-Rel transcription factor limits early interferon and neuroinflammatory responses to prevent herpes simplex encephalitis onset in mice. <i>Scientific Reports</i> , 2021, 11, 21171.	1.6	1
23003	Chromatin accessibility and gene expression during adipocyte differentiation identify context-dependent effects at cardiometabolic GWAS loci. <i>PLoS Genetics</i> , 2021, 17, e1009865.	1.5	9
23004	Conserved heterodimeric GTPase Rbg1/Tma46 promotes efficient translation in eukaryotic cells. <i>Cell Reports</i> , 2021, 37, 109877.	2.9	10
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23006	Cell-free DNA 5-hydroxymethylcytosine profiles of long non-coding RNA genes enable early detection and progression monitoring of human cancers. <i>Clinical Epigenetics</i> , 2021, 13, 197.	1.8	6
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23010	Osteoclasts adapt to physioxia perturbation through DNA demethylation. <i>EMBO Reports</i> , 2021, 22, e53035.	2.0	13
23012	Complete Genome Sequence of Bovine Coronavirus in Blood Diarrhea from Adult Cattle That Died from Winter Dysentery in Japan. <i>Microbiology Resource Announcements</i> , 2021, 10, e0080721.	0.3	0
23013	Utilizing the VirIdAI Pipeline to Search for Viruses in the Metagenomic Data of Bat Samples. <i>Viruses</i> , 2021, 13, 2006.	1.5	3
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23019	Comprehensive RNA analysis of CSF reveals a role for CEACAM6 in lung cancer leptomenigeal metastases. <i>Npj Precision Oncology</i> , 2021, 5, 90.	2.3	9
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23021	Frequent germplasm exchanges drive the high genetic diversity of Chinese-cultivated common apricot germplasm. <i>Horticulture Research</i> , 2021, 8, 215.	2.9	16
23022	Tbx5 drives <i>Aldh1a2</i> expression to regulate a RA-Hedgehog-Wnt gene regulatory network coordinating cardiopulmonary development. <i>ELife</i> , 2021, 10, .	2.8	16
23023	Strategy and Performance Evaluation of Low-Frequency Variant Calling for SARS-CoV-2 Using Targeted Deep Illumina Sequencing. <i>Frontiers in Microbiology</i> , 2021, 12, 747458.	1.5	15
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23027	Microbial colonization and resistome dynamics in food processing environments of a newly opened pork cutting industry during 1.5 years of activity. <i>Microbiome</i> , 2021, 9, 204.	4.9	20
23028	Transcriptional changes involved in kumquat (<i>Fortunella</i> spp) defense response to <i>Xanthomonas citri</i> subsp. <i>citri</i> in early stages of infection. <i>Physiological and Molecular Plant Pathology</i> , 2021, 116, 101729.	1.3	4
23031	QTL for seed shattering and threshability in intermediate wheatgrass align closely with well-studied orthologs from wheat, barley, and rice. <i>Plant Genome</i> , 2021, 14, e20145.	1.6	8
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23033	In vivo commensal control of <i>Clostridioides difficile</i> virulence. <i>Cell Host and Microbe</i> , 2021, 29, 1693-1708.e7.	5.1	62
23034	A Polycomb domain found in committed cells impairs differentiation when introduced into PRC1 in pluripotent cells. <i>Molecular Cell</i> , 2021, 81, 4677-4691.e8.	4.5	20
23036	Individual bacteria in structured environments rely on phenotypic resistance to phage. <i>PLoS Biology</i> , 2021, 19, e3001406.	2.6	26
23037	CZON-cutter – a CRISPR-Cas9 system for multiplexed organelle imaging in a simple unicellular alga. <i>Journal of Cell Science</i> , 2021, 134, .	1.2	3
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23039	Differential Transcriptional Regulation of Polymorphic p53 Codon 72 in Metabolic Pathways. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10793.	1.8	3
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23043	Metagenomic investigation of potential abortigenic pathogens in foetal tissues from Australian horses. <i>BMC Genomics</i> , 2021, 22, 713.	1.2	7
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23047	Genetic diversity of <i>Salmonella</i> Paratyphi A isolated from enteric fever patients in Bangladesh from 2008 to 2018. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009748.	1.3	10
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23052	Impact of Gene Flow and Introgression on the Range Wide Genetic Structure of <i>Quercus robur</i> (L.) in Europe. <i>Forests</i> , 2021, 12, 1425.	0.9	13
23053	Novel Candidate Genes Differentially Expressed in Glyphosate-Treated Horseweed (<i>Conyza canadensis</i>). <i>Genes</i> , 2021, 12, 1616.	1.0	1
23056	Characterizing batch effects and binding site-specific variability in ChIP-seq data. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab098.	1.5	3
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23060	Adaptation of <i>Bacillus thuringiensis</i> to Plant Colonization Affects Differentiation and Toxicity. <i>MSystems</i> , 2021, 6, e0086421.	1.7	16
23061	Identification of genes and gene expression associated with dispersal capacity in the mountain pine beetle, <i>Dendroctonus ponderosae</i> Hopkins (Coleoptera: Curculionidae). <i>PeerJ</i> , 2021, 9, e12382.	0.9	1
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23066	Metabolome and Transcriptome Analysis of Liver and Oocytes of <i>Schizothorax oacconnori</i> Raised in Captivity. <i>Frontiers in Genetics</i> , 2021, 12, 677066.	1.1	1
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23072	Prospective study of oral microbiome and gastric cancer risk among Asian, African American and European American populations. <i>International Journal of Cancer</i> , 2022, 150, 916-927.	2.3	17
23073	A Novel Microviridae Phage (CLasMV1) From "Candidatus Liberibacter asiaticus" <i>Frontiers in Microbiology</i> , 2021, 12, 754245.	1.5	9
23074	Developmental Temporal Patterns and Molecular Network Features in the Transcriptome of Rat Spinal Cord. <i>Engineering</i> , 2021, 7, 1592-1602.	3.2	4
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23076	Genome features of common vetch (<i>Vicia sativa</i>) in natural habitats. <i>Plant Direct</i> , 2021, 5, e352.	0.8	12
23078	Endurance exercise training-responsive miR-19b-3p improves skeletal muscle glucose metabolism. <i>Nature Communications</i> , 2021, 12, 5948.	5.8	20
23079	Identification of chromatin states during zebrafish gastrulation using CUT&RUN and CUT&Tag. <i>Developmental Dynamics</i> , 2022, 251, 729-742.	0.8	10
23080	The complete chloroplast genome of <i>Callicarpa rubella</i> Lindl. (Lamiaceae) from Guangxi, China: genome structure and phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 3280-3282.	0.2	3
23082	Severe Stunting Symptoms upon Nepovirus Infection Are Reminiscent of a Chronic Hypersensitive-like Response in a Perennial Woody Fruit Crop. <i>Viruses</i> , 2021, 13, 2138.	1.5	10
23083	Phylogenetic systematics of <i>Butyrivibrio</i> and <i>Pseudobutyrvibrio</i> genomes illustrate vast taxonomic diversity, open genomes and an abundance of carbohydrate-active enzyme family isoforms. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
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23091	ZmCCT regulates photoperiod-dependent flowering and response to stresses in maize. <i>BMC Plant Biology</i> , 2021, 21, 453.	1.6	19
23092	Genome-wide RNA structure changes during human neurogenesis modulate gene regulatory networks. <i>Molecular Cell</i> , 2021, 81, 4942-4953.e8.	4.5	15
23093	Genome, Transcriptome, and Germplasm Sequencing Uncovers Functional Variation in the Warm-Season Grain Legume Horsegram <i>Macrotyloma uniflorum</i> (Lam.) Verdc.. <i>Frontiers in Plant Science</i> , 2021, 12, 758119.	1.7	7
23095	Disrupted circadian oscillations in type 2 diabetes are linked to altered rhythmic mitochondrial metabolism in skeletal muscle. <i>Science Advances</i> , 2021, 7, eabi9654.	4.7	44
23097	Rapid evolutionary turnover of mobile genetic elements drives bacterial resistance to phages. <i>Science</i> , 2021, 374, 488-492.	6.0	96

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23103	<i>CARMN</i> Is an Evolutionarily Conserved Smooth Muscle Cell-Specific LncRNA That Maintains Contractile Phenotype by Binding Myocardin. <i>Circulation</i> , 2021, 144, 1856-1875.	1.6	50
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26086	Domain-adaptive neural networks improve cross-species prediction of transcription factor binding. <i>Genome Research</i> , 2022, 32, 512-523.	2.4	16

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26088	Discovery of a widespread presence bunyavirus that may have symbiont-like relationships with different species of aphids. <i>Insect Science</i> , 2022, 29, 1120-1134.	1.5	10
26090	Construction of Strand-seq libraries in open nanoliter arrays. <i>Cell Reports Methods</i> , 2022, 2, 100150.	1.4	10
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26093	Changes in chemical composition, structural and functional microbiome during alfalfa (<i>Medicago Tj ETQq1 1 0.784314 rgBT /Overlock 2.1 13</i>)	2.1	13
26094	De Novo Assembly and Annotation of the Vaginal Metatranscriptome Associated with Bacterial Vaginosis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1621.	1.8	4
26095	Selective signatures and high genome-wide diversity in traditional Brazilian manioc (<i>Manihot Tj ETQq1 1 0.784314 rgBT /Overlock 1.6 9</i>)	1.6	9
26098	Methionine- and Choline-Deficient Diet Identifies an Essential Role for DNA Methylation in Plasmacytoid Dendritic Cell Biology. <i>Journal of Immunology</i> , 2022, 208, 881-897.	0.4	2
26102	Characterization of the complete mitochondrial genome of <i>Haemadipsa tianmushana</i> Song 1977 (Hirudiniformes, Haemadipsidae) and its phylogenetic analysis. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 103-105.	0.2	0
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26104	A stress-reduced passaging technique improves the viability of human pluripotent cells. <i>Cell Reports Methods</i> , 2022, 2, 100155.	1.4	2
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26127	Gut microbiome alterations and gut barrier dysfunction are associated with host immune homeostasis in COVID-19 patients. <i>BMC Medicine</i> , 2022, 20, 24.	2.3	83
26128	Response of Poplar Leaf Transcriptome to Changed Management and Environmental Conditions in Pure and Mixed with Black Locust Stands. <i>Forests</i> , 2022, 13, 147.	0.9	1
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26135	The plastome of the husk tomato (<i>Physalis philadelphica</i> Lam., Solanaceae): a comparative analysis between wild and cultivated pools. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 1391-1405.	0.8	1
26136	Conservation of magnetite biomineralization genes in all domains of life and implications for magnetic sensing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	20
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26138	SciApps: An Automated Platform for Processing and Distribution of Plant Genomics Data. <i>Methods in Molecular Biology</i> , 2022, 2443, 197-209.	0.4	0
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26172	RNA circles with minimized immunogenicity as potent PKR inhibitors. <i>Molecular Cell</i> , 2022, 82, 420-434.e6.	4.5	52
26173	BAMM (BRAF Autophagy and MEK Inhibition in Melanoma): A Phase I/II Trial of Dabrafenib, Trametinib, and Hydroxychloroquine in Advanced <i>BRAFV600</i> -mutant Melanoma. <i>Clinical Cancer Research</i> , 2022, 28, 1098-1106.	3.2	32
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26181	SETDB1/NSD-dependent H3K9me3/H3K36me3 dual heterochromatin maintains gene expression profiles by bookmarking poised enhancers. <i>Molecular Cell</i> , 2022, 82, 816-832.e12.	4.5	29
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26191	The complete plastid genome of <i>Cheniella didyma</i> (H.Y.Chen) R.Clark & Mackinder (Leguminosae). <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 202-203.	0.2	1
26192	Performance optimization in DNA short-read alignment. <i>Bioinformatics</i> , 2022, 38, 2081-2087.	1.8	5
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26221	The three-dimensional structure of Epstein-Barr virus genome varies by latency type and is regulated by PARP1 enzymatic activity. <i>Nature Communications</i> , 2022, 13, 187.	5.8	30
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26228	Proteomic and Transcriptomic Analyses Indicate Reduced Biofilm-Forming Abilities in Cefiderocol-Resistant <i>Klebsiella pneumoniae</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 778190.	1.5	10
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26244	Differential priority effects impact taxonomy and functionality of host-associated microbiomes. <i>Molecular Ecology</i> , 2023, 32, 6278-6293.	2.0	6
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26437	Spotlight on alternative frame coding: Two long overlapping genes in <i>Pseudomonas aeruginosa</i> are translated and under purifying selection. <i>IScience</i> , 2022, 25, 103844.	1.9	13

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26440	Comparative Physiology and Transcriptome Analysis of Young Spikes in Response to Late Spring Coldness in Wheat (<i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2022, 13, 811884.	1.7	15
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26461	TERT activates endogenous retroviruses to promote an immunosuppressive tumour microenvironment. <i>EMBO Reports</i> , 2022, 23, e52984.	2.0	24
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26774	Fusion Gene Detection Using Whole-Exome Sequencing Data in Cancer Patients. <i>Frontiers in Genetics</i> , 2022, 13, 820493.	1.1	3
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26776	Reduced Virulence and Enhanced Host Adaptation during Antibiotics Therapy: a Story of a Within-Host Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Sequence Type 11 Evolution in a Patient with a Serious Scrotal Abscess. <i>MSystems</i> , 2022, 7, e0134221.	1.7	6
26777	Single-Cell Transcriptome and Network Analyses Unveil Key Transcription Factors Regulating Mesophyll Cell Development in Maize. <i>Genes</i> , 2022, 13, 374.	1.0	13
26779	Gut Virome of the World's Highest-Elevation Lizard Species (<i>Phrynocephalus erythrurus</i> and) Tj ETQq1 10, e0187221.	1.2	12
26781	Isolation and Characterization of Levoglucosan-Metabolizing Bacteria. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0186821.	1.4	6
26782	RNA Virus Diversity in Birds and Small Mammals From Qinghai's Tibet Plateau of China. <i>Frontiers in Microbiology</i> , 2022, 13, 780651.	1.5	7
26783	Methylome and Transcriptome-Based Integration Analysis Identified Molecular Signatures Associated With Meningitis Induced by <i>Glaesserella parasuis</i> . <i>Frontiers in Immunology</i> , 2022, 13, 840399.	2.2	2
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26785	Unraveling Nitrogen, Sulfur, and Carbon Metabolic Pathways and Microbial Community Transcriptional Responses to Substrate Deprivation and Toxicity Stresses in a Bioreactor Mimicking Anoxic Brackish Coastal Sediment Conditions. <i>Frontiers in Microbiology</i> , 2022, 13, 798906.	1.5	2
26788	Static Magnetic Field Inhibits Growth of <i>Escherichia coli</i> Colonies via Restriction of Carbon Source Utilization. <i>Cells</i> , 2022, 11, 827.	1.8	6
26789	Differential Effects on the Translation of Immune-Related Alternatively Polyadenylated mRNAs in Melanoma and T Cells by eIF4A Inhibition. <i>Cancers</i> , 2022, 14, 1177.	1.7	5
26790	Microautophagy Mediates Vacuolar Delivery of Storage Proteins in Maize Aleurone Cells. <i>Frontiers in Plant Science</i> , 2022, 13, 833612.	1.7	11
26791	Circulation, genomic characteristics, and evolutionary dynamics of class I Newcastle disease virus in China. <i>Virulence</i> , 2022, 13, 414-427.	1.8	4
26792	Epigenetic Silencing of Recombinant Adeno-associated Virus Genomes by NP220 and the HUSH Complex. <i>Journal of Virology</i> , 2022, 96, JVI0203921.	1.5	20
26793	Sequence determinants of human gene regulatory elements. <i>Nature Genetics</i> , 2022, 54, 283-294.	9.4	87
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26797	Transcriptome Co-expression Network and Metabolome Analysis Identifies Key Genes and Regulators of Proanthocyanidins Biosynthesis in Brown Cotton. <i>Frontiers in Plant Science</i> , 2021, 12, 822198.	1.7	7
26798	Transcription Analysis for Core Networks of lncRNAs and mRNAs: Implication for Potential Role in Sterility of <i>Crassostrea gigas</i> . <i>Biology</i> , 2022, 11, 378.	1.3	2
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26802	Characterization of the complete chloroplast genome of <i>Brassica oleracea</i> var. <i>italica</i> and phylogenetic relationships in Brassicaceae. <i>PLoS ONE</i> , 2022, 17, e0263310.	1.1	4
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26808	Fragment size-based enrichment of viral sequences in plasma cell-free DNA. <i>Journal of Molecular Diagnostics</i> , 2022, 24, 476-484.	1.2	4
26809	HOTTIP-dependent R-loop formation regulates CTCF boundary activity and TAD integrity in leukemia. <i>Molecular Cell</i> , 2022, 82, 833-851.e11.	4.5	48
26810	Placental methylome reveals a 22q13.33 brain regulatory gene locus associated with autism. <i>Genome Biology</i> , 2022, 23, 46.	3.8	22
26811	TDP-43 loss and ALS-risk SNPs drive mis-splicing and depletion of UINC13A. <i>Nature</i> , 2022, 603, 131-137.	13.7	188
26813	Systematic benchmark of state-of-the-art variant calling pipelines identifies major factors affecting accuracy of coding sequence variant discovery. <i>BMC Genomics</i> , 2022, 23, 155.	1.2	23
26814	A fast Myosin super enhancer dictates muscle fiber phenotype through competitive interactions with Myosin genes. <i>Nature Communications</i> , 2022, 13, 1039.	5.8	26
26816	Metagenomic Geolocation Using Read Signatures. <i>Frontiers in Genetics</i> , 2022, 13, 643592.	1.1	0
26817	Medulloblastoma cerebrospinal fluid reveals metabolites and lipids indicative of hypoxia and cancer-specific RNAs. <i>Acta Neuropathologica Communications</i> , 2022, 10, 25.	2.4	21

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26828	Analyses of human cancer driver genes uncovers evolutionarily conserved RNA structural elements involved in posttranscriptional control. <i>PLoS ONE</i> , 2022, 17, e0264025.	1.1	4
26830	Thymocytes trigger self-antigen-controlling pathways in immature medullary thymic epithelial stages. <i>ELife</i> , 2022, 11, .	2.8	12
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26837	Changes in the Mitochondrial Dynamics and Functions Together with the mRNA/miRNA Network in the Heart Tissue Contribute to Hypoxia Adaptation in Tibetan Sheep. <i>Animals</i> , 2022, 12, 583.	1.0	8
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26839	Rap1 regulates TIP60 function during fate transition between two-cell-like and pluripotent states. <i>Genes and Development</i> , 2022, 36, 313-330.	2.7	6

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26859	SMRT sequencing of full-length transcriptome and gene expression analysis in two chemical types of <i>Pogostemon cablin</i> (Blanco) Benth.. <i>PeerJ</i> , 2022, 10, e12940.	0.9	4

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26864	Enoxacin Shows Broad-Spectrum Antiviral Activity against Diverse Viruses by Enhancing Antiviral RNA Interference in Insects. <i>Journal of Virology</i> , 2022, 96, JV10177821.	1.5	7
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26871	Genome Sequencing and Analysis of <i>Trichoderma</i> (Hypocreaceae) Isolates Exhibiting Antagonistic Activity against the Papaya Dieback Pathogen, <i>Erwinia mallotivora</i> . <i>Journal of Fungi (Basel)</i> , 2022, 8, 1065.	1.0	0
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26876	Simultaneous dimensionality reduction and integration for single-cell ATAC-seq data using deep learning. <i>Nature Machine Intelligence</i> , 2022, 4, 162-168.	8.3	15
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26878	Cross-cohort gut microbiome associations with immune checkpoint inhibitor response in advanced melanoma. <i>Nature Medicine</i> , 2022, 28, 535-544.	15.2	158
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26894	A guanosine tetraphosphate (ppGpp) mediated brake on photosynthesis is required for acclimation to nitrogen limitation in <i>Arabidopsis</i> . <i>ELife</i> , 2022, 11, .	2.8	19
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26933	The Chromosome-Scale Reference Genome of <i>Macadamia tetraphylla</i> Provides Insights Into Fatty Acid Biosynthesis. <i>Frontiers in Genetics</i> , 2022, 13, 835363.	1.1	4
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27072	Uterus-specific transcriptional regulation underlies eggshell pigment production in Japanese quail. <i>PLoS ONE</i> , 2022, 17, e0265008.	1.1	0
27073	Two zinc finger proteins with functions in m6A writing interact with HAKAI. <i>Nature Communications</i> , 2022, 13, 1127.	5.8	32
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27086	Surface Ammonia-Oxidizer Abundance During the Late Summer in the West Antarctic Coastal System. <i>Frontiers in Microbiology</i> , 2022, 13, 821902.	1.5	5
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27089	The Genomics and Population Genomics of the Light Brown Apple Moth, <i>Epiphyas postvittana</i> , an Invasive Tortricid Pest of Horticulture. <i>Insects</i> , 2022, 13, 264.	1.0	5

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27110	De Novo Transcriptome Analysis Reveals Putative Genes Involved in Anthraquinone Biosynthesis in <i>Rubia yunnanensis</i> . <i>Genes</i> , 2022, 13, 521.	1.0	8
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27604	Novel Tyrosine Kinase-Mediated Phosphorylation With Dual Specificity Plays a Key Role in the Modulation of <i>Streptococcus pyogenes</i> Physiology and Virulence. <i>Frontiers in Microbiology</i> , 2021, 12, 689246.	1.5	4
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27607	Hidden biases in germline structural variant detection. <i>Genome Biology</i> , 2021, 22, 347.	3.8	19
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27617	Comparative Transcriptome Analysis of Female and Male Fine-Patterned Puffer: Identification of Candidate Genes Associated with Growth and Sex Differentiation. <i>Fishes</i> , 2021, 6, 79.	0.7	4
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27647	A Chromosome-Level Genome Assembly of Mozambique Tilapia (<i>Oreochromis mossambicus</i>) Reveals the Structure of Sex Determining Regions. Frontiers in Genetics, 2021, 12, 796211.	1.1	5

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27754	Genetic Diversity, Structure, and Selective Sweeps in <i>Spinacia turkestanica</i> Associated With the Domestication of Cultivated Spinach. <i>Frontiers in Genetics</i> , 2021, 12, 740437.	1.1	4
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27769	Quantitative prediction of conditional vulnerabilities in regulatory and metabolic networks using PRIME. <i>Npj Systems Biology and Applications</i> , 2021, 7, 43.	1.4	3
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27786	DNN-Boost: Somatic mutation identification of tumor-only whole-exome sequencing data using deep neural network and XGBoost. <i>Journal of Bioinformatics and Computational Biology</i> , 2021, 19, 2140017.	0.3	4
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27792	Genome-Wide Identification and Expression Profiling of Potassium Transport-Related Genes in <i>Vigna radiata</i> under Abiotic Stresses. <i>Plants</i> , 2022, 11, 2.	1.6	11
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