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sequence data**

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2232	.		
2231	Birthday Honours. 1899 , 1, 1421-1422		
2230	Encyclopedia of Metagenomics. 2013 , 1-12		1
2229	Uncovering genomic features and maternal origin of korean native chicken by whole genome sequencing. 2014 , 9, e114763		6

2228	IM-TORNADO: a tool for comparison of 16S reads from paired-end libraries. 2014 , 9, e114804	76
2227	Allele Workbench: transcriptome pipeline and interactive graphics for allele-specific expression. 2014 , 9, e115740	8
2226	Genome-wide DNA Methylation Profiles of Small Intestine and Liver in Fast-growing and Slow-growing Weaning Piglets. 2014 , 27, 1532-9	5
2225	The transcriptome of an amphioxus, <i>Asymmetron lucayanum</i> , from the Bahamas: a window into chordate evolution. 2014 , 6, 2681-96	52
2224	Fastq_clean: An optimized pipeline to clean the Illumina sequencing data with quality control. 2014 ,	31
2223	<i>Populus tremula</i> (European aspen) shows no evidence of sexual dimorphism. 2014 , 14, 276	37
2222	Single molecule sequencing and genome assembly of a clinical specimen of <i>Loa loa</i> , the causative agent of loiasis. 2014 , 15, 788	21
2221	Genomic characterization of the LEED..PEEDs, a gene family unique to the medicago lineage. 2014 , 4, 2003-12	10
2220	Complete Genome Sequence of <i>Haemophilus influenzae</i> Strain 375 from the Middle Ear of a Pediatric Patient with Otitis Media. 2014 , 2,	14
2219	Systems biology studies of adult <i>paragonimus</i> lung flukes facilitate the identification of immunodominant parasite antigens. 2014 , 8, e3242	20
2218	AlienTrimmer removes adapter oligonucleotides with high sensitivity in short-insert paired-end reads. Commentary on Turner (2014) Assessment of insert sizes and adapter content in FASTQ data from NexteraXT libraries. 2014 , 5, 130	22
2217	Whole-genome sequences of three symbiotic <i>endozoicomonas</i> strains. 2014 , 2,	45
2216	Draft Genome Sequence of <i>Pseudoalteromonas</i> sp. Strain ND6B, an Oil-Degrading Isolate from Eastern Mediterranean Sea Water Collected at a Depth of 1,210 Meters. 2014 , 2,	1
2215	Draft Genome Sequence of <i>Thalassotalea</i> sp. Strain ND16A Isolated from Eastern Mediterranean Sea Water Collected from a Depth of 1,055 Meters. 2014 , 2,	7
2214	Genome Sequence of <i>Bacillus simplex</i> Strain P558, Isolated from a Human Fecal Sample. 2014 , 2,	6
2213	Seeking the source of <i>Pseudomonas aeruginosa</i> infections in a recently opened hospital: an observational study using whole-genome sequencing. 2014 , 4, e006278	69
2212	CAMDA 2014: Making sense of RNA-Seq data: From low-level processing to functional analysis. 2014 , 2, 31-40	5
2211	Recent advances in candidate-gene and whole-genome approaches to the discovery of anthelmintic resistance markers and the description of drug/receptor interactions. 2014 , 4, 164-84	125

2210	The genome of the sparganosis tapeworm <i>Spirometra erinaceieuropaei</i> isolated from the biopsy of a migrating brain lesion. 2014 , 15, 510	33
2209	Detection of variants of the pRAS3, pAB5S9, and pSN254 plasmids in <i>Aeromonas salmonicida</i> subsp. <i>salmonicida</i> : multidrug resistance, interspecies exchanges, and plasmid reshaping. 2014 , 58, 7367-74	44
2208	Liver transcriptome characterization of the endangered freshwater silverside <i>Basilichthys microlepidotus</i> (Teleostei: Atherinopsidae) using next generation sequencing. 2014 , 18PB, 147-150	3
2207	Hyb-Seq: Combining target enrichment and genome skimming for plant phylogenomics. 2014 , 2, 1400042	227
2206	Intragenic duplication--a novel causative mechanism for SATB2-associated syndrome. 2014 , 164A, 3083-7	26
2205	Draft genome sequence of <i>Sphingobium</i> sp. strain ba1, resistant to kanamycin and nickel ions. 2014 , 361, 8-9	11
2204	The mitochondrial genome of <i>Parascaris univalens</i> --implications for a "forgotten" parasite. 2014 , 7, 428	23
2203	The transcriptome of <i>Nacobbus aberrans</i> reveals insights into the evolution of sedentary endoparasitism in plant-parasitic nematodes. 2014 , 6, 2181-94	35
2202	European sea bass genome and its variation provide insights into adaptation to euryhalinity and speciation. 2014 , 5, 5770	281
2201	RNA-Seq profile of flavescence doré phytoplasma in grapevine. 2014 , 15, 1088	27
2200	The draft genome of the pest tephritid fruit fly <i>Bactrocera tryoni</i> : resources for the genomic analysis of hybridising species. 2014 , 15, 1153	28
2199	A transcriptome resource for the koala (<i>Phascolarctos cinereus</i>): insights into koala retrovirus transcription and sequence diversity. 2014 , 15, 786	42
2198	Lassa and Marburg viruses elicit distinct host transcriptional responses early after infection. 2014 , 15, 960	25
2197	Reagent and laboratory contamination can critically impact sequence-based microbiome analyses. 2014 , 12, 87	1745
2196	Hoyeraal-Hreidarsson syndrome caused by a germline mutation in the TEL patch of the telomere protein TPP1. 2014 , 28, 2090-102	86
2195	Global MEF2 target gene analysis in cardiac and skeletal muscle reveals novel regulation of DUSP6 by p38MAPK-MEF2 signaling. 2014 , 42, 11349-62	55
2194	Single-base resolution analysis of active DNA demethylation using methylase-assisted bisulfite sequencing. 2014 , 32, 1231-40	107
2193	Allelic expression mapping across cellular lineages to establish impact of non-coding SNPs. 2014 , 10, 754	16

2192	Bulk de novo mitogenome assembly from pooled total DNA elucidates the phylogeny of weevils (Coleoptera: Curculionoidea). 2014 , 31, 2223-37		157
2191	Pertussis outbreak, southeastern Minnesota, 2012. 2014 , 89, 1378-88		17
2190	Protocols for metagenomic DNA extraction and Illumina amplicon library preparation for faecal and swab samples. 2014 , 14, 1183-97		45
2189	Draft Genome Sequencing of <i>Vibrio cholerae</i> O1 El Tor Isolates Collected in the Russian Federation from Imported Cholera Cases. 2014 , 2,		3
2188	SLaP mapper: a webserver for identifying and quantifying spliced-leader addition and polyadenylation site usage in kinetoplastid genomes. 2014 , 196, 71-4		11
2187	Exploring the stability of long intergenic non-coding RNA in K562 cells by comparative studies of RNA-Seq datasets. 2014 , 9, 15		6
2186	Targeted Chromatin Capture (T2C): a novel high resolution high throughput method to detect genomic interactions and regulatory elements. 2014 , 7, 10		66
2185	The complete mitochondrial genome of Baikalian amphipoda <i>Eulimnogammarus vittatus</i> Dybowski, 1874. 2016 , 27, 1795-7		3
2184	Identification of differentially expressed genes during development of the zebrafish pineal complex using RNA sequencing. 2014 , 395, 144-53		8
2183	Software for pre-processing Illumina next-generation sequencing short read sequences. 2014 , 9, 8		132
2182	Estimates of allele-specific expression in <i>Drosophila</i> with a single genome sequence and RNA-seq data. <i>Bioinformatics</i> , 2014 , 30, 2603-10	7.2	12
2181	eQTL mapping of transposon silencing reveals a position-dependent stable escape from epigenetic silencing and transposition of <i>AtMu1</i> in the <i>Arabidopsis</i> lineage. 2014 , 26, 3261-71		8
2180	Review of current methods, applications, and data management for the bioinformatics analysis of whole exome sequencing. 2014 , 13, 67-82		82
2179	Draft Genome Sequence of <i>Burkholderia pyrrocinia</i> Lyc2, a Biological Control Strain That Can Suppress Multiple Plant Microbial Pathogens. 2014 , 2,		4
2178	Leveraging the new with the old: providing a framework for the integration of historic microarray studies with next generation sequencing. 2014 , 15 Suppl 11, S3		0
2177	Revealing the inherent heterogeneity of human malignancies by variant consensus strategies coupled with cancer clonal analysis. 2014 , 15 Suppl 11, S9		3
2176	Draft Genome Sequence of the Nominated Type Strain of " <i>Ferroplasma myxofaciens</i> ," an Acidophilic, Iron-Oxidizing Betaproteobacterium. 2014 , 2,		22
2175	Genome-wide analysis of <i>Fusarium graminearum</i> field populations reveals hotspots of recombination. 2015 , 16, 996		42

2174	RNA sequencing of the nephron transcriptome: a technical note. 2015 , 34, 219-27	1
2173	Identification of the meiotic toolkit in diatoms and exploration of meiosis-specific SPO11 and RAD51 homologs in the sexual species <i>Pseudo-nitzschia multistriata</i> and <i>Seminais robusta</i> . 2015 , 16, 930	40
2172	Genomic and expression analysis of transition proteins in <i>Drosophila</i> . 2015 , 5, e1178518	3
2171	Two forward genetic screens for vein density mutants in sorghum converge on a cytochrome P450 gene in the brassinosteroid pathway. 2015 , 84, 257-66	24
2170	A metagenetic approach to determine the diversity and distribution of cyst nematodes at the level of the country, the field and the individual. 2015 , 24, 5842-51	17
2169	COLQ variant associated with Devon Rex and Sphynx feline hereditary myopathy. 2015 , 46, 711-5	24
2168	Basil Downy Mildew (<i>Peronospora belbahrii</i>): Discoveries and Challenges Relative to Its Control. 2015 , 105, 885-94	45
2167	Redesigning EHRs and Clinical Decision Support Systems for the Precision Medicine Era. 2015 ,	2
2166	Integrated analysis of DNA methylation and microRNA regulation of the lung adenocarcinoma transcriptome. 2015 , 34, 585-94	18
2165	Gene expression profiling of pre-eclamptic placentae by RNA sequencing. 2015 , 5, 14107	52
2164	Adaptation of the autotrophic acetogen <i>Sporomusa ovata</i> to methanol accelerates the conversion of CO ₂ to organic products. 2015 , 5, 16168	56
2163	Comparative genomics and genome biology of invasive <i>Campylobacter jejuni</i> . 2015 , 5, 17300	14
2162	Genomic expression catalogue of a global collection of BCG vaccine strains show evidence for highly diverged metabolic and cell-wall adaptations. 2015 , 5, 15443	57
2161	Conferring resistance to geminiviruses with the CRISPR-Cas prokaryotic immune system. 2015 , 1,	247
2160	Quantitative and qualitative analysis of small RNAs in human endothelial cells and exosomes provides insights into localized RNA processing, degradation and sorting. 2015 , 4, 26760	180
2159	Mimosoid legume plastome evolution: IR expansion, tandem repeat expansions, and accelerated rate of evolution in <i>clpP</i> . 2015 , 5, 16958	72
2158	Global regulation of heterochromatin spreading by Leo1. 2015 , 5,	31
2157	iSRAP - a one-touch research tool for rapid profiling of small RNA-seq data. 2015 , 4, 29454	14

2156	Transcriptomic variation of hepatopancreas reveals the energy metabolism and biological processes associated with molting in Chinese mitten crab, <i>Eriocheir sinensis</i> . 2015 , 5, 14015	56
2155	The power of single molecule real-time sequencing technology in the de novo assembly of a eukaryotic genome. 2015 , 5, 16780	51
2154	Horizontal functional gene transfer from bacteria to fishes. 2015 , 5, 18676	6
2153	Exploring molecular variation in <i>Schistosoma japonicum</i> in China. 2015 , 5, 17345	19
2152	Phylogenetic and genomic diversity in isolates from the globally distributed <i>Acinetobacter baumannii</i> ST25 lineage. 2015 , 5, 15188	44
2151	Modular approach to customise sample preparation procedures for viral metagenomics: a reproducible protocol for virome analysis. 2015 , 5, 16532	168
2150	Draft genome of the most devastating insect pest of coffee worldwide: the coffee berry borer, <i>Hypothenemus hampei</i> . 2015 , 5, 12525	44
2149	Genome-wide expression analysis offers new insights into the origin and evolution of <i>Physcomitrella patens</i> stress response. 2015 , 5, 17434	33
2148	Defining the <i>Schistosoma haematobium</i> kinome enables the prediction of essential kinases as anti-schistosome drug targets. 2015 , 5, 17759	32
2147	Chloroplast microsatellite markers for <i>Artocarpus</i> (Moraceae) developed from transcriptome sequences. 2015 , 3, 1500049	7
2146	TRIM32 modulates pluripotency entry and exit by directly regulating Oct4 stability. 2015 , 5, 13456	13
2145	De novo transcriptome profiling of highly purified human lymphocytes primary cells. 2015 , 2, 150051	25
2144	Hybrid male sterility and genome-wide misexpression of male reproductive proteases. 2015 , 5, 11976	25
2143	Transcriptomes of parents identify parenting strategies and sexual conflict in a subsocial beetle. 2015 , 6, 8449	61
2142	Genomic Sequence of <i>Burkholderia multivorans</i> NK1379, a Soil Bacterium That Inhibits the Growth of <i>Burkholderia pseudomallei</i> . 2015 , 3,	4
2141	Transcriptome Analysis in Domesticated Species: Challenges and Strategies. 2015 , 9, 21-31	8
2140	Advanced Applications of RNA Sequencing and Challenges. 2015 , 9, 29-46	126
2139	Back to Basics--The Influence of DNA Extraction and Primer Choice on Phylogenetic Analysis of Activated Sludge Communities. 2015 , 10, e0132783	294

2138	Detrimental effects of duplicate reads and low complexity regions on RNA- and ChIP-seq data. 2015 , 16 Suppl 13, S10	14
2137	Enhancing cancer clonality analysis with integrative genomics. 2015 , 16 Suppl 13, S7	3
2136	A genetic linkage map of black raspberry (<i>Rubus occidentalis</i>) and the mapping of Ag(4) conferring resistance to the aphid <i>Amphorophora agathonica</i> . 2015 , 128, 1631-46	25
2135	Enhanced reduced representation bisulfite sequencing for assessment of DNA methylation at base pair resolution. 2015 , e52246	65
2134	Imbalance between the expression dosages of X-chromosome and autosomal genes in mammalian oocytes. 2015 , 5, 14101	10
2133	Environmental marine pathogen isolation using mesocosm culture of sharpsnout seabream: striking genomic and morphological features of novel <i>Endozoicomonas</i> sp. 2015 , 5, 17609	38
2132	Characterization and expression analysis of adipokinetic hormone and its receptor in eusocial aphid <i>Pseudoregma bambucicola</i> . 2015 , 223, 38-46	11
2131	A novel splice variant of the decapentaplegic (<i>dpp</i>) gene in the wild silkworm, <i>Bombyx mandarina</i> . 2015 , 466, 295-9	3
2130	The assessment of inter-individual variation of whole-genome DNA sequence in 32 cows. 2015 , 26, 658-65	7
2129	Phylogenomic methods outperform traditional multi-locus approaches in resolving deep evolutionary history: a case study of formicine ants. 2015 , 15, 271	118
2128	Genome analyses of the sunflower pathogen <i>Plasmopara halstedii</i> provide insights into effector evolution in downy mildews and <i>Phytophthora</i> . 2015 , 16, 741	78
2127	A high-density genetic map for anchoring genome sequences and identifying QTLs associated with dwarf vine in pumpkin (<i>Cucurbita maxima</i> Duch.). 2015 , 16, 1101	42
2126	The estrous cycle surpasses sex differences in regulating the transcriptome in the rat medial prefrontal cortex and reveals an underlying role of early growth response 1. 2015 , 16, 256	34
2125	An integrative analysis of post-translational histone modifications in the marine diatom <i>Phaeodactylum tricornutum</i> . 2015 , 16, 102	52
2124	The <i>Haemonchus contortus</i> kinome—a resource for fundamental molecular investigations and drug discovery. 2015 , 8, 623	12
2123	IMA Genome-F 4: Draft genome sequences of <i>Chrysoporthe austroafricana</i> , <i>Diplodia scrobiculata</i> , <i>Fusarium nygamai</i> , <i>Leptographium lundbergii</i> , <i>Limonomyces culmigenus</i> , <i>Stagonosporopsis tanacetii</i> , and <i>Thielaviopsis punctulata</i> . 2015 , 6, 233-48	40
2122	Widespread alternative and aberrant splicing revealed by lariat sequencing. 2015 , 43, 8488-501	36
2121	Substantial genome synteny preservation among woody angiosperm species: comparative genomics of Chinese chestnut (<i>Castanea mollissima</i>) and plant reference genomes. 2015 , 16, 744	25

2120	Simultaneous transcriptional profiling of <i>Leishmania major</i> and its murine macrophage host cell reveals insights into host-pathogen interactions. 2015 , 16, 1108	53
2119	Conservation and modification of genetic and physiological toolkits underpinning diapause in bumble bee queens. 2015 , 24, 5596-615	62
2118	A unique ecological niche fosters hybridization of oak-tree and vineyard isolates of <i>Saccharomyces cerevisiae</i> . 2015 , 24, 5886-98	6
2117	Genome Sequence of the Deep-Sea Bacterium <i>Idiomarina abyssalis</i> KMM 227T. 2015 , 3,	
2116	Evaluation of shotgun metagenomics sequence classification methods using in silico and in vitro simulated communities. 2015 , 16, 363	85
2115	Transcriptome analysis of the white pine blister rust pathogen <i>Cronartium ribicola</i> : de novo assembly, expression profiling, and identification of candidate effectors. 2015 , 16, 678	34
2114	Transcriptome-enabled marker discovery and mapping of plastochron-related genes in <i>Petunia</i> spp. 2015 , 16, 726	22
2113	A transcriptome approach towards understanding the development of ripening capacity in 'Bartlett' pears (<i>Pyrus communis</i> L.). 2015 , 16, 762	17
2112	Gene expression underlying enhanced, steroid-dependent auditory sensitivity of hair cell epithelium in a vocal fish. 2015 , 16, 782	5
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2110	Age and prior blood feeding of <i>Anopheles gambiae</i> influences their susceptibility and gene expression patterns to ivermectin-containing blood meals. 2015 , 16, 797	22
2109	Whole genome sequencing reveals genomic heterogeneity and antibiotic purification in <i>Mycobacterium tuberculosis</i> isolates. 2015 , 16, 857	48
2108	Identification of sensory hair-cell transcripts by thiouracil-tagging in zebrafish. 2015 , 16, 842	31
2107	A genomic approach to understand interactions between <i>Streptococcus pneumoniae</i> and its bacteriophages. 2015 , 16, 972	14
2106	High transcript abundance, RNA editing, and small RNAs in intergenic regions within the massive mitochondrial genome of the angiosperm <i>Silene noctiflora</i> . 2015 , 16, 938	27
2105	Analysis of the FnrL regulon in <i>Rhodobacter capsulatus</i> reveals limited regulon overlap with orthologues from <i>Rhodobacter sphaeroides</i> and <i>Escherichia coli</i> . 2015 , 16, 895	15
2104	The direction of cross affects [corrected] obesity after puberty in male but not female offspring. 2015 , 16, 904	4
2103	Transcriptome profiling of differentially expressed genes in floral buds and flowers of male sterile and fertile lines in watermelon. 2015 , 16, 914	43

2102	Transcriptomics of diapause in an isogenic self-fertilizing vertebrate. 2015 , 16, 989	9
2101	Transcriptomes of post-mitotic neurons identify the usage of alternative pathways during adult and embryonic neuronal differentiation. 2015 , 16, 1100	10
2100	Daily transcriptome changes reveal the role of nitrogen in controlling microcystin synthesis and nutrient transport in the toxic cyanobacterium, <i>Microcystis aeruginosa</i> . 2015 , 16, 1068	45
2099	Physiological and transcriptional analyses of developmental stages along sugarcane leaf. 2015 , 15, 300	30
2098	Horizontal gene transfer in bdelloid rotifers is ancient, ongoing and more frequent in species from desiccating habitats. 2015 , 13, 90	47
2097	RNA-seq analysis of <i>Pichia anomala</i> reveals important mechanisms required for survival at low pH. 2015 , 14, 143	17
2096	Phylogenetically typing bacterial strains from partial SNP genotypes observed from direct sequencing of clinical specimen metagenomic data. 2015 , 7, 52	32
2095	Virulence characteristics of hcp (+) <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> isolates from retail chicken. 2015 , 7, 20	28
2094	Deeply sequenced metagenome and metatranscriptome of a biogas-producing microbial community from an agricultural production-scale biogas plant. 2015 , 4, 33	53
2093	De novo assembly of <i>Dekkera bruxellensis</i> : a multi technology approach using short and long-read sequencing and optical mapping. 2015 , 4, 56	20
2092	Genome sequence of <i>Anoxybacillus ayderensis</i> AB04(T) isolated from the Ayder hot spring in Turkey. 2015 , 10, 70	13
2091	Genome sequence of <i>Pedobacter glucosidilyticus</i> DD6b, isolated from zooplankton <i>Daphnia magna</i> . 2015 , 10, 100	8
2090	Towards next generation CHO cell biology: Bioinformatics methods for RNA-Seq-based expression profiling. 2015 , 10, 950-66	12
2089	Complete Genome Sequence of the Acetogenic Bacterium <i>Moorella thermoacetica</i> DSM 2955T. 2015 , 3,	12
2088	Discovering All Transcriptome Single-Nucleotide Polymorphisms and Scanning for Selection Signatures in Ducks (<i>Anas platyrhynchos</i>). 2015 , 11, 67-76	3
2087	B-Cell and Monocyte Contribution to Systemic Lupus Erythematosus Identified by Cell-Type-Specific Differential Expression Analysis in RNA-Seq Data. 2015 , 9, 11-9	28
2086	Protein and small non-coding RNA-enriched extracellular vesicles are released by the pathogenic blood fluke <i>Schistosoma mansoni</i> . 2015 , 4, 28665	101
2085	Enzymatic Degradation of Phenazines Can Generate Energy and Protect Sensitive Organisms from Toxicity. 2015 , 6, e01520-15	29

2084	Unique evolutionary trajectories in repeated adaptation to hydrogen sulphide-toxic habitats of a neotropical fish (<i>Poecilia mexicana</i>). 2015 , 24, 5446-59	41
2083	Draft Genome Sequence of Purine-Degrading <i>Gottschalkia purinilyticum</i> (Formerly <i>Clostridium purinilyticum</i>) WA1 (DSM 1384). 2015 , 3,	3
2082	Draft Genome Sequence of the Strict Anaerobe <i>Clostridium homopropionicum</i> LuHBu1 (DSM 5847). 2015 , 3,	3
2081	Complete Genome Sequence of a New Member of the <i>Marseilleviridae</i> Recovered from the Brackish Submarine Spring in the Cassis Port-Miou Calanque, France. 2015 , 3,	16
2080	Complete Genome Sequence of the Type Strain of the Acetogenic Bacterium <i>Moorella thermoacetica</i> DSM 521T. 2015 , 3,	14
2079	Draft Genome Sequence of Cellulolytic and Xylanolytic <i>Paenibacillus</i> sp. A59, Isolated from Decaying Forest Soil from Patagonia, Argentina. 2015 , 3,	5
2078	Patterns of Wnt signaling in the life cycle of <i>Podocoryna carnea</i> and its implications for medusae evolution in Hydrozoa (Cnidaria). 2015 , 17, 325-36	16
2077	Draft Genome Sequence of a Diarrheagenic <i>Morganella morganii</i> Isolate. 2015 , 3,	2
2076	Draft Genome Sequence of <i>Komagataeibacter intermedius</i> Strain AF2, a Producer of Cellulose, Isolated from Kombucha Tea. 2015 , 3,	7
2075	Genome Sequence of the Acetogenic Bacterium <i>Oxobacter pfennigii</i> DSM 3222T. 2015 , 3,	12
2074	Draft Genome of Australian Environmental Strain WM 09.24 of the Opportunistic Human Pathogen <i>Scedosporium aurantiacum</i> . 2015 , 3,	18
2073	Differential Susceptibility of Human Pleural and Peritoneal Mesothelial Cells to Asbestos Exposure. 2015 , 116, 1540-52	22
2072	Draft Genome Sequence of <i>Phomopsis longicolla</i> Type Strain TWH P74, a Fungus Causing <i>Phomopsis</i> Seed Decay in Soybean. 2015 , 3,	7
2071	Draft Whole-Genome Sequence of the Marine Bacterium <i>Idiomarina zobellii</i> KMM 231T. 2015 , 3,	1
2070	Draft Genome Sequence and Assembly of <i>Photorhabdus heterorhabditis</i> Strain VMG, a Bacterial Symbiont Associated with the Entomopathogenic Nematode <i>Heterorhabditis zealandica</i> . 2015 , 3,	
2069	Complete Genome Sequences of an <i>Escherichia coli</i> Laboratory Strain and Trimethoprim-Resistant (TMP32XR) Mutant Strains. 2015 , 3,	3
2068	Multiple displacement amplification of the DNA from single flow-sorted plant chromosome. 2015 , 84, 838-44	17
2067	Molecular Differentiation of Gender in Buffalograss. 2015 , 55, 1827-1833	0

2066	Optimizing Transcriptome Assemblies for <i>Eleusine indica</i> Leaf and Seedling by Combining Multiple Assemblies from Three De Novo Assemblers. 2015 , 8, eplantgenome2014.10.0064	15
2065	Epigenetics Potential for Programming Fish for Aquaculture?. 2015 , 3, 175-192	29
2064	Prediction of multi-drug resistance transporters using a novel sequence analysis method. 2015 , 4, 60	3
2063	Development of microsatellite markers for the endangered <i>Pedicularis ishidoyana</i> (Orobanchaceae) using next-generation sequencing. 2015 , 3, 1500083	8
2062	A survey of polymorphisms detected from sequences of popular beef breeds. 2015 , 93, 5128-43	12
2061	A DNA extraction protocol for improved DNA yield from individual mosquitoes. 2015 , 4, 1314	20
2060	Menadione-Induced Oxidative Stress Re-Shapes the Oxylipin Profile of <i>Aspergillus flavus</i> and Its Lifestyle. 2015 , 7, 4315-29	21
2059	Differentially-Expressed Pseudogenes in HIV-1 Infection. 2015 , 7, 5191-205	8
2058	On Accounting for Sequence-Specific Bias in Genome-Wide Chromatin Accessibility Experiments: Recent Advances and Contradictions. 2015 , 3, 144	14
2057	Characterization of enteropathogenic and Shiga toxin-producing <i>Escherichia coli</i> in cattle and deer in a shared agroecosystem. 2015 , 5, 29	36
2056	Secretory Gene Recruitments in Vampire Bat Salivary Adaptation and Potential Convergences With Sanguivorous Leeches. 2015 , 3,	8
2055	Of monkeys and men: immunomic profiling of sera from humans and non-human primates resistant to schistosomiasis reveals novel potential vaccine candidates. 2015 , 6, 213	32
2054	Metatranscriptome analysis of the reef-building coral <i>Orbicella faveolata</i> indicates holobiont response to coral disease. 2015 , 2,	44
2053	Combining genomic sequencing methods to explore viral diversity and reveal potential virus-host interactions. 2015 , 6, 265	47
2052	Microbial community structure and function on sinking particles in the North Pacific Subtropical Gyre. 2015 , 6, 469	96
2051	Phylogenomics of <i>Xanthomonas</i> field strains infecting pepper and tomato reveals diversity in effector repertoires and identifies determinants of host specificity. 2015 , 6, 535	94
2050	The reduced genomes of <i>Parcubacteria</i> (OD1) contain signatures of a symbiotic lifestyle. 2015 , 6, 713	176
2049	<i>Coxiella burnetii</i> and <i>Leishmania mexicana</i> residing within similar parasitophorous vacuoles elicit disparate host responses. 2015 , 6, 794	2

2048	The green impact: bacterioplankton response toward a phytoplankton spring bloom in the southern North Sea assessed by comparative metagenomic and metatranscriptomic approaches. 2015 , 6, 805	52
2047	Metabolic diversity and ecological niches of <i>Achromatium</i> populations revealed with single-cell genomic sequencing. 2015 , 6, 822	17
2046	Strand-specific community RNA-seq reveals prevalent and dynamic antisense transcription in human gut microbiota. 2015 , 6, 896	20
2045	Co-occurrence of <i>Methanosarcina mazei</i> and <i>Geobacteraceae</i> in an iron (III)-reducing enrichment culture. 2015 , 6, 941	29
2044	Metabolomic and high-throughput sequencing analysis-modern approach for the assessment of biodeterioration of materials from historic buildings. 2015 , 6, 979	67
2043	Diversity and Homogeneity among Small Plasmids of <i>Aeromonas salmonicida</i> subsp. <i>salmonicida</i> Linked with Geographical Origin. 2015 , 6, 1274	18
2042	Genomic and Functional Characterization of <i>qnr</i> -Encoding Plasmids from Municipal Wastewater Biosolid <i>Klebsiella pneumoniae</i> Isolates. 2015 , 6, 1354	19
2041	Year-Long Metagenomic Study of River Microbiomes Across Land Use and Water Quality. 2015 , 6, 1405	39
2040	Gene Expression Associated with Early and Late Chronotypes in <i>Drosophila melanogaster</i> . 2015 , 6, 100	11
2039	A New Splicing Isoform of <i>Cacna2d4</i> Mimicking the Effects of <i>c.2451insC</i> Mutation in the Retina: Novel Molecular and Electrophysiological Insights. 2015 , 56, 4846-56	8
2038	Identification of new genomospecies in the <i>Mycobacterium terrae</i> complex. 2015 , 10, e0120789	6
2037	Small RNA sequencing for profiling microRNAs in long-term preserved formalin-fixed and paraffin-embedded non-small cell lung cancer tumor specimens. 2015 , 10, e0121521	14
2036	Informatics for RNA Sequencing: A Web Resource for Analysis on the Cloud. 2015 , 11, e1004393	50
2035	Multifactorial Competition and Resistance in a Two-Species Bacterial System. 2015 , 11, e1005715	32
2034	De novo Assembly, Characterization of Immature Seed Transcriptome and Development of Genic-SSR Markers in Black Gram [<i>Vigna mungo</i> (L.) Hepper]. 2015 , 10, e0128748	35
2033	Next Generation Sequencing and Transcriptome Analysis Predicts Biosynthetic Pathway of Sennosides from <i>Senna</i> (<i>Cassia angustifolia</i> Vahl.), a Non-Model Plant with Potent Laxative Properties. 2015 , 10, e0129422	34
2032	Comparative Transcriptome Analysis of Cultivated and Wild Watermelon during Fruit Development. 2015 , 10, e0130267	61
2031	Identification of Candidate Adherent-Invasive <i>E. coli</i> Signature Transcripts by Genomic/Transcriptomic Analysis. 2015 , 10, e0130902	17

2030	Comparative Transcriptomes Analysis of Red- and White-Fleshed Apples in an F1 Population of <i>Malus sieversii</i> f. <i>niedzetzkyana</i> Crossed with <i>M. domestica</i> 'Fuji'. 2015 , 10, e0133468	22
2029	Genomic Analysis of the Emergence and Rapid Global Dissemination of the Clonal Group 258 <i>Klebsiella pneumoniae</i> Pandemic. 2015 , 10, e0133727	125
2028	Vitamin D Modulates Expression of the Airway Smooth Muscle Transcriptome in Fatal Asthma. 2015 , 10, e0134057	26
2027	Transcriptome Analysis of the Emerald Ash Borer (EAB), <i>Agrilus planipennis</i> : De Novo Assembly, Functional Annotation and Comparative Analysis. 2015 , 10, e0134824	8
2026	Virulence Characterization of <i>Salmonella enterica</i> by a New Microarray: Detection and Evaluation of the Cytolethal Distending Toxin Gene Activity in the Unusual Host <i>S. Typhimurium</i> . 2015 , 10, e0135010	29
2025	De Novo Transcriptome Analysis of <i>Allium cepa</i> L. (Onion) Bulb to Identify Allergens and Epitopes. 2015 , 10, e0135387	15
2024	Identification of Distinct Tumor Subpopulations in Lung Adenocarcinoma via Single-Cell RNA-seq. 2015 , 10, e0135817	45
2023	Genetic Adaptation of <i>Achromobacter</i> sp. during Persistence in the Lungs of Cystic Fibrosis Patients. 2015 , 10, e0136790	26
2022	Comparison of a Real-Time Multiplex PCR and Sequotyping Assay for Pneumococcal Serotyping. 2015 , 10, e0137349	14
2021	The Oral Microbiome of Denture Wearers Is Influenced by Levels of Natural Dentition. 2015 , 10, e0137717	60
2020	Comprehensive Identification of Sexual Dimorphism-Associated Differentially Expressed Genes in Two-Way Factorial Designed RNA-Seq Data on Japanese Quail (<i>Coturnix coturnix japonica</i>). 2015 , 10, e0139324	9
2019	The Effects of Synthetic Estrogen Exposure on the Sexually Dimorphic Liver Transcriptome of the Sex-Role-Reversed Gulf Pipefish. 2015 , 10, e0139401	8
2018	Deciphering Mineral Homeostasis in Barley Seed Transfer Cells at Transcriptional Level. 2015 , 10, e0141398	8
2017	Identification of Putative Nuclear Receptors and Steroidogenic Enzymes in Murray-Darling Rainbowfish (<i>Melanotaenia fluviatilis</i>) Using RNA-Seq and De Novo Transcriptome Assembly. 2015 , 10, e0142636	2
2016	Investigation of a Quadruplex-Forming Repeat Sequence Highly Enriched in <i>Xanthomonas</i> and <i>Nostoc</i> sp. 2015 , 10, e0144275	11
2015	Utilization of Benchtop Next Generation Sequencing Platforms Ion Torrent PGM and MiSeq in Noninvasive Prenatal Testing for Chromosome 21 Trisomy and Testing of Impact of In Silico and Physical Size Selection on Its Analytical Performance. 2015 , 10, e0144811	31
2014	The White-Nose Syndrome Transcriptome: Activation of Anti-fungal Host Responses in Wing Tissue of Hibernating Little Brown Myotis. 2015 , 11, e1005168	69
2013	TAL effectors and activation of predicted host targets distinguish Asian from African strains of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> while strict conservation suggests universal importance of five TAL effectors. 2015 , 6, 536	59

2012	Using targeted enrichment of nuclear genes to increase phylogenetic resolution in the neotropical rain forest genus <i>Inga</i> (Leguminosae: Mimosoideae). 2015 , 6, 710	76
2011	A novel workflow correlating RNA-seq data to <i>Phytophthora infestans</i> resistance levels in wild <i>Solanum</i> species and potato clones. 2015 , 6, 718	15
2010	Challenges of the Unknown: Clinical Application of Microbial Metagenomics. 2015 , 2015, 292950	12
2009	Cross-talk between PRMT1-mediated methylation and ubiquitylation on RBM15 controls RNA splicing. 2015 , 4,	69
2008	Whole-genome sequencing of a <i>Plasmodium vivax</i> isolate from the China-Myanmar border area. 2015 , 110, 814-6	7
2007	Base-resolution methylation patterns accurately predict transcription factor bindings in vivo. 2015 , 43, 2757-66	33
2006	Complete Genome Sequence of <i>Mycobacterium</i> sp. Strain VKM Ac-1817D, Capable of Producing 9 β -Hydroxy-androst-4-ene-3,17-dione from Phytosterol. 2015 , 3,	8
2005	Deep developmental transcriptome sequencing uncovers numerous new genes and enhances gene annotation in the sponge <i>Amphimedon queenslandica</i> . 2015 , 16, 387	68
2004	Effort versus Reward: Preparing Samples for Fungal Community Characterization in High-Throughput Sequencing Surveys of Soils. 2015 , 10, e0127234	23
2003	Primer to Analysis of Genomic Data Using R. 2015 ,	6
2002	Complete genome sequence of a porcine epidemic diarrhea s gene indel strain isolated in france in december 2014. 2015 , 3,	55
2001	Draft genomes of <i>Shigella</i> strains used by the STOPENTERICS consortium. 2015 , 7, 14	6
2000	Gene Expression Analysis. 2015 , 163-200	
1999	The generation of macrophages with anti-inflammatory activity in the absence of STAT6 signaling. 2015 , 98, 395-407	33
1998	An ancient protein-DNA interaction underlying metazoan sex determination. 2015 , 22, 442-51	70
1997	Phylogenomics of phrynosomatid lizards: conflicting signals from sequence capture versus restriction site associated DNA sequencing. 2015 , 7, 706-19	120
1996	Impact of traumatic brain injury on sleep structure, electrocorticographic activity and transcriptome in mice. 2015 , 47, 118-30	27
1995	FCMM: A comparative metagenomic approach for functional characterization of multiple metagenome samples. 2015 , 115, 121-8	2

1994	Massively parallel sequencing (MPS) assays for sequencing mitochondrial genomes: the phylogenomic implications for <i>Acropora</i> staghorn corals (Scleractinia; Acroporidae). 2015 , 162, 1383-1392	5
1993	Defining bacterial regulons using ChIP-seq. 2015 , 86, 80-8	17
1992	Dynamic and Widespread lncRNA Expression in a Sponge and the Origin of Animal Complexity. 2015 , 32, 2367-82	48
1991	The Challenges of Resolving a Rapid, Recent Radiation: Empirical and Simulated Phylogenomics of Philippine Shrews. 2015 , 64, 727-40	97
1990	Determinants of nucleosome positioning and their influence on plant gene expression. 2015 , 25, 1182-95	40
1989	Spectral sensitivity of cone photoreceptors and opsin expression in two colour-divergent lineages of the lizard <i>Ctenophorus decresii</i> . 2015 , 218, 1556-63	24
1988	Early transcriptional events linked to induction of diapause revealed by RNAseq in larvae of drosophilid fly, <i>Chymomyza costata</i> . 2015 , 16, 720	60
1987	Rank-based characterization of pollen assemblages collected by honey bees using a multi-locus metabarcoding approach. 2015 , 3, 1500043	69
1986	Whole-Genome Sequencing of Kaposi's Sarcoma-Associated Herpesvirus from Zambian Kaposi's Sarcoma Biopsy Specimens Reveals Unique Viral Diversity. 2015 , 89, 12299-308	31
1985	Improvement of barley genome annotations by deciphering the Haruna Nijo genome. 2016 , 23, 21-8	22
1984	Next-generation sequencing reveals the biological significance of the N(2),3-ethenoguanine lesion in vivo. 2015 , 43, 5489-500	28
1983	Neural transcriptome reveals molecular mechanisms for temporal control of vocalization across multiple timescales. 2015 , 16, 408	21
1982	Complex and extensive post-transcriptional regulation revealed by integrative proteomic and transcriptomic analysis of metabolite stress response in <i>Clostridium acetobutylicum</i> . 2015 , 8, 81	27
1981	Multiple Conserved Heteroplasmic Sites in tRNA Genes in the Mitochondrial Genomes of Terrestrial Isopods (Oniscidea). 2015 , 5, 1317-22	11
1980	Fecal Bacterial Composition of the Endangered Yangtze Finless Porpoises Living Under Captive and Semi-natural Conditions. 2016 , 72, 306-14	14
1979	Unique transposon landscapes are pervasive across <i>Drosophila melanogaster</i> genomes. 2015 , 43, 10655-72	70
1978	A single chromosome assembly of <i>Bacteroides fragilis</i> strain BE1 from Illumina and MinION nanopore sequencing data. 2015 , 4, 60	55
1977	Distinctive Genome Reduction Rates Revealed by Genomic Analyses of Two <i>Coxiella</i> -Like Endosymbionts in Ticks. 2015 , 7, 1779-96	98

1976	Population Genomics of Infectious and Integrated Wolbachia pipientis Genomes in Drosophila ananassae. 2015 , 7, 2362-82	21
1975	A Feedback-Insensitive Isopropylmalate Synthase Affects Acylsugar Composition in Cultivated and Wild Tomato. 2015 , 169, 1821-35	50
1974	Photosynthetic Genes and Genes Associated with the C4 Trait in Maize Are Characterized by a Unique Class of Highly Regulated Histone Acetylation Peaks on Upstream Promoters. 2015 , 168, 1378-88	13
1973	Population genomic structure and adaptation in the zoonotic malaria parasite Plasmodium knowlesi. 2015 , 112, 13027-32	62
1972	In Vitro and In Vivo Modulation of Alternative Splicing by the Biguanide Metformin. 2015 , 4, e262	44
1971	Functional Genomics Analysis of Big Data Identifies Novel Peroxisome Proliferator-Activated Receptor Target Single Nucleotide Polymorphisms Showing Association With Cardiometabolic Outcomes. 2015 , 8, 842-51	1
1970	Same Exposure but Two Radically Different Responses to Antibiotics: Resilience of the Salivary Microbiome versus Long-Term Microbial Shifts in Feces. 2015 , 6, e01693-15	253
1969	Accuracy of the high-throughput amplicon sequencing to identify species within the genus Aspergillus. 2015 , 119, 1311-1321	7
1968	Capture Hi-C reveals novel candidate genes and complex long-range interactions with related autoimmune risk loci. 2015 , 6, 10069	121
1967	Evaluation of preprocessing, mapping and postprocessing algorithms for analyzing whole genome bisulfite sequencing data. 2016 , 17, 938-952	15
1966	Large-scale transcriptome sequencing reveals novel expression patterns for key sex-related genes in a sex-changing fish. 2015 , 6, 26	58
1965	De novo assembly and functional annotation of Myrciaria dubia fruit transcriptome reveals multiple metabolic pathways for L-ascorbic acid biosynthesis. 2015 , 16, 997	16
1964	Genome Sequences of 11 Shiga Toxin-Producing Escherichia coli Strains. 2015 , 3,	4
1963	Draft Genome Sequence of the Thermophile Thermus filiformis ATCC 43280, Producer of Carotenoid-(Di)glucoside-Branched Fatty Acid (Di)esters and Source of Hyperthermostable Enzymes of Biotechnological Interest. 2015 , 3,	3
1962	Genome Sequence of Anoxybacillus thermarum AF/04T, Isolated from the Euganean Hot Springs in Abano Terme, Italy. 2015 , 3,	8
1961	Complete genome sequence of a porcine epidemic diarrhea virus from a novel outbreak in Belgium, January 2015. 2015 , 3,	60
1960	Complete Genome Sequence of Listeria monocytogenes Strain DPC6895, a Serotype 1/2b Isolate from Bovine Raw Milk. 2015 , 3,	3
1959	Draft Genome Sequence of Gerbil-Adapted Carcinogenic Helicobacter pylori Strain 7.13. 2015 , 3,	8

1958	Draft Genome Sequence of <i>Delftia tsuruhatensis</i> MTQ3, a Strain of Plant Growth-Promoting Rhizobacterium with Antimicrobial Activity. 2015 , 3,	12
1957	Complete Genome Sequence of <i>Enterobacter cloacae</i> UW5, a Rhizobacterium Capable of High Levels of Indole-3-Acetic Acid Production. 2015 , 3,	9
1956	The Genotoxin Colibactin Is a Determinant of Virulence in <i>Escherichia coli</i> K1 Experimental Neonatal Systemic Infection. 2015 , 83, 3704-11	47
1955	Single-molecule sequencing of the desiccation-tolerant grass <i>Oropetium thomaeum</i> . 2015 , 527, 508-11	208
1954	Structure, phylogeny, and expression of the frizzled-related gene family in the lophotrochozoan annelid <i>Platynereis dumerilii</i> . 2015 , 6, 37	13
1953	IMA Genome-F 5: Draft genome sequences of <i>Ceratocystis eucalypticola</i> , <i>Chrysosporthe cubensis</i> , <i>C. deuterocubensis</i> , <i>Davidsoniella virescens</i> , <i>Fusarium temperatum</i> , <i>Graphilbum fragrans</i> , <i>Penicillium nordicum</i> , and <i>Thielaviopsis musarum</i> . 2015 , 6, 493-506	42
1952	Draft genome sequences of three chemically rich actinomycetes isolated from Mediterranean sponges. 2015 , 24 Pt 3, 285-7	7
1951	Draft Genome Sequences of Three <i>Mycobacterium chimaera</i> Respiratory Isolates. 2015 , 3,	11
1950	Telomere maintenance through recruitment of internal genomic regions. 2015 , 6, 8189	17
1949	Elucidating the phylodynamics of endemic rabies virus in eastern Africa using whole-genome sequencing. 2015 , 1, vev011	41
1948	Draft Genome Sequence of <i>Exiguobacterium</i> sp. Strain BMC-KP, an Environmental Isolate from Bryn Mawr, Pennsylvania. 2015 , 3,	4
1947	The microbiome quality control project: baseline study design and future directions. 2015 , 16, 276	140
1946	MALBACsim: A Multiple Annealing and Looping Based Amplification Cycles simulator. 2015 ,	
1945	Understanding the biochemical basis of temperature-induced lipid pathway adjustments in plants. 2015 , 27, 86-103	94
1944	Roquin binds microRNA-146a and Argonaute2 to regulate microRNA homeostasis. 2015 , 6, 6253	48
1943	Target enrichment of ultraconserved elements from arthropods provides a genomic perspective on relationships among Hymenoptera. 2015 , 15, 489-501	175
1942	Comparison of sister species identifies factors underpinning plastid compatibility in green sea slugs. 2015 , 282,	29
1941	Molecular characterization of canine kobuvirus in wild carnivores and the domestic dog in Africa. 2015 , 477, 89-97	29

1940	Promiscuous mRNA splicing under the control of AIRE in medullary thymic epithelial cells. <i>Bioinformatics</i> , 2015 , 31, 986-90	7.2	17
1939	Multiplex metabolic pathway engineering using CRISPR/Cas9 in <i>Saccharomyces cerevisiae</i> . 2015 , 28, 213-222		292
1938	Transcriptome analysis of response to drought in poplar interspecific hybrids. 2015 , 3, 143-5		15
1937	dev1 is an evolutionarily young negative regulator of <i>Myxococcus xanthus</i> development. 2015 , 197, 1249-62		17
1936	Brain tumor mutations detected in cerebral spinal fluid. 2015 , 61, 514-22		176
1935	Analyses of germline, chromosomally integrated human herpesvirus 6A and B genomes indicate emergent infection and new inflammatory mediators. 2015 , 96, 370-389		22
1934	Rapid identification of major <i>Escherichia coli</i> sequence types causing urinary tract and bloodstream infections. 2015 , 53, 160-6		83
1933	Complete Genome Sequence of Steroid-Transforming <i>Nocardioides simplex</i> VKM Ac-2033D. 2015 , 3,		12
1932	HTSeq—a Python framework to work with high-throughput sequencing data. <i>Bioinformatics</i> , 2015 , 31, 166-9	7.2	10519
1931	RNA-Rocket: an RNA-Seq analysis resource for infectious disease research. <i>Bioinformatics</i> , 2015 , 31, 1496-8		9
1930	Prevalence of Type VI Secretion System in Spanish <i>Campylobacter jejuni</i> Isolates. 2015 , 62, 497-500		19
1929	Single-cell DNA methylome sequencing and bioinformatic inference of epigenomic cell-state dynamics. 2015 , 10, 1386-97		290
1928	An evidence-based approach to identify aging-related genes in <i>Caenorhabditis elegans</i> . 2015 , 16, 40		7
1927	Promoter hypermethylation of TERT is associated with hepatocellular carcinoma in the Han Chinese population. 2015 , 39, 600-9		26
1926	Gene loss in the fungal canola pathogen <i>Leptosphaeria maculans</i> . 2015 , 15, 189-96		30
1925	A proportion of mutations fixed in the genomes of in vitro selected isogenic drug-resistant <i>Mycobacterium tuberculosis</i> mutants can be detected as minority variants in the parent culture. 2015 , 362, 1-7		5
1924	The utility and public health implications of PCR and whole genome sequencing for the detection and investigation of an outbreak of Shiga toxin-producing <i>Escherichia coli</i> serogroup O26:H11. 2015 , 143, 1672-80		32
1923	Evolutionary Advantage Conferred by an Eukaryote-to-Eukaryote Gene Transfer Event in Wine Yeasts. 2015 , 32, 1695-707		96

1922	Genetics and genotype-phenotype correlations in Finnish patients with dilated cardiomyopathy. 2015 , 36, 2327-37	101
1921	Impact of ceftiofur injection on gut microbiota and Escherichia coli resistance in pigs. 2015 , 59, 5171-80	14
1920	Growth dynamics of gut microbiota in health and disease inferred from single metagenomic samples. 2015 , 349, 1101-1106	245
1919	Comparative transcriptome analysis reveals that the extracellular matrix receptor interaction contributes to the venous metastases of hepatocellular carcinoma. 2015 , 208, 482-91	39
1918	PGPR enhanced phytoremediation of petroleum contaminated soil and rhizosphere microbial community response. 2015 , 138, 592-8	132
1917	Cyberinfrastructure resources enabling creation of the loblolly pine reference transcriptome. 2015 ,	
1916	FastQFS DA tool for evaluating and filtering paired-end sequencing data generated from high throughput sequencing. 2015 , 14, 1	8
1915	Characterization of the secretome of Plasmopara viticola by de novo transcriptome analysis. 2015 , 91, 1-10	28
1914	The DNA methylation landscape of Chinese hamster ovary (CHO) DP-12 cells. 2015 , 199, 38-46	29
1913	A first insight into the spleen transcriptome of the nototheniid fish Lepidonotothen nudifrons: Resource description and functional overview. 2015 , 24 Pt 3, 237-9	11
1912	Transcriptomic profiling of gene expression and RNA processing during Leishmania major differentiation. 2015 , 43, 6799-813	55
1911	Bacterial Community Profiling of Plastic Litter in the Belgian Part of the North Sea. 2015 , 49, 9629-38	205
1910	Development of a Multilocus Sequence Typing Scheme for Molecular Typing of Mycoplasma pneumoniae. 2015 , 53, 3195-203	28
1909	The Methylome of Soybean Roots during the Compatible Interaction with the Soybean Cyst Nematode. 2015 , 168, 1364-77	43
1908	Genome Sequence of Vibrio VPAP30, Isolated from an Episode of Massive Mortality of Reared Larvae of the Scallop Argopecten purpuratus. 2015 , 3,	4
1907	Evolution of genome size and complexity in the rhabdoviridae. 2015 , 11, e1004664	103
1906	Complete Dosage Compensation in Anopheles stephensi and the Evolution of Sex-Biased Genes in Mosquitoes. 2015 , 7, 1914-24	30
1905	Identification of Prognostic Groups in High-Grade Serous Ovarian Cancer Treated with Platinum-Taxane Chemotherapy. 2015 , 75, 2987-98	27

1904	Duplication and Adaptive Evolution of a Key Centromeric Protein in <i>Mimulus</i> , a Genus with Female Meiotic Drive. 2015 , 32, 2694-706	38
1903	Differential expression of HERV-K (HML-2) proviruses in cells and virions of the teratocarcinoma cell line Tera-1. 2015 , 7, 939-68	43
1902	PPLine: An Automated Pipeline for SNP, SAP, and Splice Variant Detection in the Context of Proteogenomics. 2015 , 14, 3729-37	46
1901	Rapid draft sequencing and real-time nanopore sequencing in a hospital outbreak of <i>Salmonella</i> . 2015 , 16, 114	211
1900	The genetic architecture of the genome-wide transcriptional response to ER stress in the mouse. 2015 , 11, e1004924	20
1899	Reconstructing SALMFamide Neuropeptide Precursor Evolution in the Phylum Echinodermata: Ophiuroid and Crinoid Sequence Data Provide New Insights. 2015 , 6, 2	18
1898	Detecting rare structural variation in evolving microbial populations from new sequence junctions using breseq. 2014 , 5, 468	38
1897	Microbes & neurodevelopment--Absence of microbiota during early life increases activity-related transcriptional pathways in the amygdala. 2015 , 50, 209-220	160
1896	A CASQ1 founder mutation in three Italian families with protein aggregate myopathy and hyperCKaemia. 2015 , 52, 617-26	9
1895	Root precursors of microRNAs in wild emmer and modern wheats show major differences in response to drought stress. 2015 , 15, 587-98	88
1894	Comparative Phylodynamics of Rabbit Hemorrhagic Disease Virus in Australia and New Zealand. 2015 , 89, 9548-58	27
1893	Complete Genome Sequences of vB_LmoS_188 and vB_LmoS_293, Two Bacteriophages with Specificity for <i>Listeria monocytogenes</i> Strains of Serotypes 4b and 4e. 2015 , 3,	6
1892	Emergence of a virulent porcine reproductive and respiratory syndrome virus in vaccinated herds in the United States. 2015 , 210, 34-41	37
1891	Induced tigecycline resistance in <i>Streptococcus pneumoniae</i> mutants reveals mutations in ribosomal proteins and rRNA. 2015 , 70, 2973-80	31
1890	Improving small RNA-seq by using a synthetic spike-in set for size-range quality control together with a set for data normalization. 2015 , 43, e89	26
1889	High-Resolution Analysis by Whole-Genome Sequencing of an International Lineage (Sequence Type 111) of <i>Pseudomonas aeruginosa</i> Associated with Metallo-Carbapenemases in the United Kingdom. 2015 , 53, 2622-31	39
1888	Exploring the limits for reduction of plastid genomes: a case study of the mycoheterotrophic orchids <i>Epipogium aphyllum</i> and <i>Epipogium roseum</i> . 2015 , 7, 1179-91	85
1887	Multiple mutations and increased RNA expression in tetracycline-resistant <i>Streptococcus pneumoniae</i> as determined by genome-wide DNA and mRNA sequencing. 2015 , 70, 1946-59	17

1886	The Impact of the Branched-Chain Ketoacid Dehydrogenase Complex on Amino Acid Homeostasis in Arabidopsis. 2015 , 169, 1807-20	59
1885	Comparative transcriptome analysis reveals defense-related genes and pathways against downy mildew in <i>Vitis amurensis</i> grapevine. 2015 , 95, 1-14	54
1884	Examining the evolution of the regulatory circuit controlling secondary metabolism and development in the fungal genus <i>Aspergillus</i> . 2015 , 11, e1005096	48
1883	Computational prediction of molecular pathogen-host interactions based on dual transcriptome data. 2015 , 6, 65	43
1882	Diversity of thermophiles in a Malaysian hot spring determined using 16S rRNA and shotgun metagenome sequencing. 2015 , 6, 177	104
1881	A new method for studying population genetics of cyst nematodes based on Pool-Seq and genomewide allele frequency analysis. 2015 , 15, 1356-65	21
1880	The histone deacetylase SIRT6 controls embryonic stem cell fate via TET-mediated production of 5-hydroxymethylcytosine. 2015 , 17, 545-57	111
1879	Isolation of a significant fraction of non-phototroph diversity from a desert Biological Soil Crust. 2015 , 6, 277	37
1878	Subpopulations in aMPV vaccines are unlikely to be the only cause of reversion to virulence. 2015 , 33, 2438-41	9
1877	Genome-wide analysis of human global and transcription-coupled excision repair of UV damage at single-nucleotide resolution. 2015 , 29, 948-60	147
1876	The microbiome of uncontacted Amerindians. 2015 , 1,	517
1875	Antiviral gene expression in psoriasis. 2015 , 29, 1951-7	24
1874	Pyruvate metabolism: A therapeutic opportunity in radiation-induced skin injury. 2015 , 460, 504-10	10
1873	PEAT: an intelligent and efficient paired-end sequencing adapter trimming algorithm. 2015 , 16 Suppl 1, S2	35
1872	TagDust2: a generic method to extract reads from sequencing data. 2015 , 16, 24	44
1871	GBSX: a toolkit for experimental design and demultiplexing genotyping by sequencing experiments. 2015 , 16, 73	58
1870	Transcriptome analysis of northern elephant seal (<i>Mirounga angustirostris</i>) muscle tissue provides a novel molecular resource and physiological insights. 2015 , 16, 64	20
1869	The genome of the basal agaricomycete <i>Xanthophyllomyces dendrorhous</i> provides insights into the organization of its acetyl-CoA derived pathways and the evolution of Agaricomycotina. 2015 , 16, 233	33

1868	Genome diversification within a clonal population of pandemic <i>Vibrio parahaemolyticus</i> seems to depend on the life circumstances of each individual bacteria. 2015 , 16, 176		11
1867	Transcriptome characterization of three wild Chinese <i>Vitis</i> uncovers a large number of distinct disease related genes. 2015 , 16, 223		15
1866	Comparative genomic analysis of <i>Ralstonia solanacearum</i> reveals candidate genes for host specificity. 2015 , 16, 270		56
1865	<i>Lactobacillus ruminis</i> strains cluster according to their mammalian gut source. 2015 , 15, 80		22
1864	Establishment of <i>Anthoceros agrestis</i> as a model species for studying the biology of hornworts. 2015 , 15, 98		40
1863	Functional analysis of <i>Girardia tigrina</i> transcriptome seeds pipeline for anthelmintic target discovery. 2015 , 8, 34		7
1862	DNA methylation and chromatin organization in insects: insights from the Ant <i>Camponotus floridanus</i> . 2015 , 7, 931-42		21
1861	Dissection of the style's response to pollination using transcriptome profiling in self-compatible (<i>Solanum pimpinellifolium</i>) and self-incompatible (<i>Solanum chilense</i>) tomato species. 2015 , 15, 119		14
1860	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. 2015 , 15, 62		49
1859	A MAT1-2 wild-type strain from <i>Penicillium chrysogenum</i> : functional mating-type locus characterization, genome sequencing and mating with an industrial penicillin-producing strain. 2015 , 95, 859-74		21
1858	Dynamics of gene expression patterns during early development of the European seabass (<i>Dicentrarchus labrax</i>). 2015 , 47, 158-69		14
1857	Dissecting meiotic recombination based on tetrad analysis by single-microspore sequencing in maize. 2015 , 6, 6648		71
1856	IVA: accurate de novo assembly of RNA virus genomes. <i>Bioinformatics</i> , 2015 , 31, 2374-6	7.2	123
1855	Complete Genome Sequences of T4-Like Bacteriophages RB3, RB5, RB6, RB7, RB9, RB10, RB27, RB33, RB55, RB59, and RB68. 2015 , 3,		8
1854	Structural imprints in vivo decode RNA regulatory mechanisms. 2015 , 519, 486-90		454
1853	RNA sequencing of laser-capture microdissected compartments of the maize kernel identifies regulatory modules associated with endosperm cell differentiation. 2015 , 27, 513-31		141
1852	Regulation of histone methylation and reprogramming of gene expression in the rice inflorescence meristem. 2015 , 27, 1428-44		56
1851	Multiplex single cell profiling of chromatin accessibility by combinatorial cellular indexing. 2015 , 348, 910-4		668

1850	Bioinformatics analysis of circulating cell-free DNA sequencing data. 2015 , 48, 962-75	14
1849	Comparison of nuclear, plastid, and mitochondrial phylogenies and the origin of wild octoploid strawberry species. 2015 , 102, 544-54	34
1848	Systematic Identification of a Panel of Strong Constitutive Promoters from <i>Streptomyces albus</i> . 2015 , 4, 1001-10	101
1847	A <i>Coxiella</i> -like endosymbiont is a potential vitamin source for the Lone Star tick. 2015 , 7, 831-8	144
1846	Complex archaea that bridge the gap between prokaryotes and eukaryotes. 2015 , 521, 173-179	726
1845	Polar freshwater cyanophage S-EIV1 represents a new widespread evolutionary lineage of phages. 2015 , 9, 2046-58	39
1844	Comparative analysis of gill transcriptomes of two freshwater crayfish, <i>Cherax cainii</i> and <i>C. destructor</i> . 2015 , 22, 11-3	13
1843	Draft genome sequence of <i>Acinetobacter</i> sp. neg1 capable of degrading ochratoxin A. 2015 , 362,	6
1842	Development of a large set of SNP markers for assessing phylogenetic relationships between the olive cultivars composing the Israeli olive germplasm collection. 2015 , 35, 1	34
1841	Biogas Upgrading via Hydrogenotrophic Methanogenesis in Two-Stage Continuous Stirred Tank Reactors at Mesophilic and Thermophilic Conditions. 2015 , 49, 12585-93	211
1840	Low-cost ddRAD method of SNP discovery and genotyping applied to the periwinkle <i>Littorina saxatilis</i> . 2015 , eyv042	7
1839	The Impact of Recombination Hotspots on Genome Evolution of a Fungal Plant Pathogen. 2015 , 201, 1213-28	84
1838	Functionally Structured Genomes in <i>Lactobacillus kunkeei</i> Colonizing the Honey Crop and Food Products of Honeybees and Stingless Bees. 2015 , 7, 1455-73	32
1837	High throughput profiling of the cotton bollworm <i>Helicoverpa armigera</i> immunotranscriptome during the fungal and bacterial infections. 2015 , 16, 321	67
1836	Transcriptome and venom proteome of the box jellyfish <i>Chironex fleckeri</i> . 2015 , 16, 407	73
1835	Culture-independent genome sequencing of clinical samples reveals an unexpected heterogeneity of infections by <i>Chlamydia pecorum</i> . 2015 , 53, 1573-81	35
1834	The <i>Lingula</i> genome provides insights into brachiopod evolution and the origin of phosphate biomineralization. 2015 , 6, 8301	105
1833	Two cytochromes P450 catalyze S-heterocyclizations in cabbage phytoalexin biosynthesis. 2015 , 11, 837-9	32

1832 DNA-Protein Interactions. **2015,**

1831 Probing the Missing Human Proteome: A Computational Perspective. **2015, 14, 4949-58**

5

1830 An Arabidopsis PWI and RRM motif-containing protein is critical for pre-mRNA splicing and ABA responses. **2015, 6, 8139**

62

1829 Microscale insights into pneumococcal antibiotic mutant selection windows. **2015, 6, 8773**

16

1828 High-throughput linkage mapping of Australian white cypress pine (*Callitris glaucophylla*) and map transferability to related species. **2015, 11, 1**

52

1827 GO2TR: a gene ontology-based workflow to generate target regions for target enrichment experiments. **2015, 7, 851-857**

4

1826 UrQt: an efficient software for the Unsupervised Quality trimming of NGS data. **2015, 16, 137**

38

1825 Noninvasive monitoring of infection and rejection after lung transplantation. **2015, 112, 13336-41**

206

1824 Methanobacterium enables high rate electricity-driven autotrophic sulfate reduction. **2015, 5, 89368-89374**

31

1823 Heterologous expression and transcript analysis of gibberellin biosynthetic genes of grasses reveals novel functionality in the GA3ox family. **2015, 15, 130**

85

1822 RNA-sequencing elucidates the regulation of behavioural transitions associated with the mating process in honey bee queens. **2015, 16, 563**

25

1821 Genomic Epidemiology of a Protracted Hospital Outbreak Caused by a Toxin A-Negative *Clostridium difficile* Sublineage PCR Ribotype 017 Strain in London, England. **2015, 53, 3141-7**

37

1820 Ecological and Genetic Barriers Differentiate Natural Populations of *Saccharomyces cerevisiae*. **2015, 32, 2317-27**

22

1819 Genome and physiology of the ascomycete filamentous fungus *Xeromyces bisporus*, the most xerophilic organism isolated to date. **2015, 17, 496-513**

29

1818 Conserved Gene Expression Programs in Developing Roots from Diverse Plants. **2015, 27, 2119-32**

48

1817 . **2015,**

1816 Draft Genome Sequence of *Sporidiobolus salmonicolor* CBS 6832, a Red-Pigmented Basidiomycetous Yeast. **2015, 3,**

6

1815 *Caenorhabditis elegans* is a useful model for anthelmintic discovery. **2015, 6, 7485**

103

1814	Genome-wide identification of CCA1 targets uncovers an expanded clock network in Arabidopsis. 2015 , 112, E4802-10	156
1813	Poly(A)-specific ribonuclease (PARN) mediates 3'-end maturation of the telomerase RNA component. 2015 , 47, 1482-8	117
1812	Genome Sequencing of Multiple Isolates Highlights Subtelomeric Genomic Diversity within <i>Fusarium fujikuroi</i> . 2015 , 7, 3062-9	32
1811	Complete Genome Sequences of a <i>Mycobacterium smegmatis</i> Laboratory Strain (MC2 155) and Isoniazid-Resistant (4XR1/R2) Mutant Strains. 2015 , 3,	30
1810	Aggregate and Heatmap Representations of Genome-Wide Localization Data Using VAP, a Versatile Aggregate Profiler. 2015 , 1334, 273-98	11
1809	Complex genome evolution in <i>Anopheles coluzzii</i> associated with increased insecticide usage in Mali. 2015 , 24, 5145-57	32
1808	Characterization of 13 microsatellite markers for <i>Calochortus gunnisonii</i> (Liliaceae) from Illumina MiSeq sequencing. 2015 , 3, 1500051	1
1807	Snake venoms are integrated systems, but abundant venom proteins evolve more rapidly. 2015 , 16, 647	51
1806	Molecular and phenotypic distinction of the very recently evolved insular subspecies <i>Mus musculus helgolandicus</i> ZIMMERMANN, 1953. 2015 , 15, 160	12
1805	Mining Genomes of Three Marine Sponge-Associated Actinobacterial Isolates for Secondary Metabolism. 2015 , 3,	8
1804	Draft Genome Sequences of Nine <i>Pseudomonas aeruginosa</i> Strains, Including Eight Clinical Isolates. 2015 , 3,	2
1803	The ferrous iron-responsive BqsRS two-component system activates genes that promote cationic stress tolerance. 2015 , 6, e02549	26
1802	Exploring evidence of positive selection reveals genetic basis of meat quality traits in Berkshire pigs through whole genome sequencing. 2015 , 16, 104	22
1801	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Cercoosporium bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes. 2015 , 7, 2781-98	14
1800	Candidate gene selection and detailed morphological evaluations of fs8.1, a quantitative trait locus controlling tomato fruit shape. 2015 , 66, 6471-82	16
1799	Histone reader BRWD1 targets and restricts recombination to the Igk locus. 2015 , 16, 1094-103	24
1798	Draft Genome Sequences of 10 <i>Microbacterium</i> spp., with Emphasis on Heavy Metal-Contaminated Environments. 2015 , 3,	13
1797	Genome expansion via lineage splitting and genome reduction in the cicada endosymbiont <i>Hodgkinia</i> . 2015 , 112, 10192-9	56

1796	Identifying genomic changes associated with insecticide resistance in the dengue mosquito <i>Aedes aegypti</i> by deep targeted sequencing. 2015 , 25, 1347-59	110
1795	Single-Cell RNA-Seq with Waterfall Reveals Molecular Cascades underlying Adult Neurogenesis. 2015 , 17, 360-72	507
1794	Comparison of variations detection between whole-genome amplification methods used in single-cell resequencing. 2015 , 4, 37	107
1793	A protocol for targeted enrichment of intron-containing sequence markers for recent radiations: A phylogenomic example from <i>Heuchera</i> (Saxifragaceae). 2015 , 3, 1500039	53
1792	Complete Genome Sequencing of a Multidrug-Resistant and Human-Invasive <i>Salmonella enterica</i> Serovar Typhimurium Strain of the Emerging Sequence Type 213 Genotype. 2015 , 3,	11
1791	Transposon Mutagenesis Paired with Deep Sequencing of <i>Caulobacter crescentus</i> under Uranium Stress Reveals Genes Essential for Detoxification and Stress Tolerance. 2015 , 197, 3160-72	24
1790	Phylogenomics of Horned Lizards (Genus: <i>Phrynosoma</i>) Using Targeted Sequence Capture Data. 2015 , 103, 586-594	14
1789	Evolution of Mating Systems in Basidiomycetes and the Genetic Architecture Underlying Mating-Type Determination in the Yeast <i>Leucosporidium scottii</i> . 2015 , 201, 75-89	25
1788	Metronidazole- and carbapenem-resistant bacteroides thetaiotaomicron isolated in Rochester, Minnesota, in 2014. 2015 , 59, 4157-61	24
1787	Genome Sequence of <i>Jannaschia aquimarina</i> GSW-M26, a Member of the Roseobacter Clade. 2015 , 3,	
1786	First Insights into the Genome of the N-Methylhydantoin-Degrading <i>Clostridium</i> sp. Strain FS41 (DSM 6877). 2015 , 3,	
1785	Whole-Genome Sequence and Annotation of Octopine-Utilizing <i>Pseudomonas kilonensis</i> (Previously <i>P. fluorescens</i>) Strain 1855-344. 2015 , 3,	5
1784	The use of transcriptomic next-generation sequencing data to assemble mitochondrial genomes of <i>Ancistrus</i> spp. (Loricariidae). 2015 , 573, 171-5	13
1783	Genome-wide RNA sequencing analysis of quorum sensing-controlled regulons in the plant-associated <i>Burkholderia glumae</i> PG1 strain. 2015 , 81, 7993-8007	32
1782	Chromosomal Copy Number Variation in <i>Saccharomyces pastorianus</i> Is Evidence for Extensive Genome Dynamics in Industrial Lager Brewing Strains. 2015 , 81, 6253-67	50
1781	Properties of short double-stranded RNAs carrying randomized base pairs: toward better controls for RNAi experiments. 2015 , 21, 2132-42	8
1780	Functional overlap of the <i>Arabidopsis</i> leaf and root microbiota. 2015 , 528, 364-9	612
1779	Draft Genome Sequences of <i>Clostridium tyrobutyricum</i> Strains FAM22552 and FAM22553, Isolated from Swiss Semihard Red-Smear Cheese. 2015 , 3,	7

1778	High-frequency, precise modification of the tomato genome. 2015 , 16, 232	378
1777	Fully reversible current driven by a dual marine photosynthetic microbial community. 2015 , 195, 248-53	10
1776	Analysis of the repetitive component and retrotransposon population in the genome of a marine angiosperm, <i>Posidonia oceanica</i> (L.) Delile. 2015 , 24 Pt 3, 397-404	14
1775	A mechanism for expansion of regulatory T-cell repertoire and its role in self-tolerance. 2015 , 528, 132-136	96
1774	Dietary Fiber-Induced Improvement in Glucose Metabolism Is Associated with Increased Abundance of <i>Prevotella</i> . 2015 , 22, 971-82	748
1773	Characterization of a second secologanin synthase isoform producing both secologanin and secoxyloganin allows enhanced de novo assembly of a <i>Catharanthus roseus</i> transcriptome. 2015 , 16, 619	35
1772	Evaluating whole transcriptome amplification for gene profiling experiments using RNA-Seq. 2015 , 15, 65	18
1771	Genomic Analysis Through High-Throughput Sequencing. 2015 , 297-311	
1770	Prokaryotic Metatranscriptomics. 2015 , 69-98	1
1769	Genome-wide analysis of the ATP-binding cassette (ABC) transporter gene family in sea lamprey and Japanese lamprey. 2015 , 16, 436	17
1768	Population Genomics Analysis of Legume Host Preference for Specific Rhizobial Genotypes in the <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> Symbioses. 2015 , 28, 310-8	15
1767	Mosquito genomics. Extensive introgression in a malaria vector species complex revealed by phylogenomics. 2015 , 347, 1258524	378
1766	<i>Listeria booriae</i> sp. nov. and <i>Listeria newyorkensis</i> sp. nov., from food processing environments in the USA. 2015 , 65, 286-292	71
1765	The major cystic fibrosis causing mutation exhibits defective propensity for phosphorylation. 2015 , 15, 447-61	21
1764	Mutations in the voltage-gated potassium channel gene <i>KCNH1</i> cause Temple-Baraitser syndrome and epilepsy. 2015 , 47, 73-7	91
1763	Methodological aspects of whole-genome bisulfite sequencing analysis. 2015 , 16, 369-79	54
1762	A phylogenomic analysis of turtles. 2015 , 83, 250-7	189
1761	Investigating flavour characteristics of British ale yeasts: techniques, resources and opportunities for innovation. 2015 , 32, 281-7	2

1760	Mycobacterium celeriflavum sp. nov., a rapidly growing scotochromogenic bacterium isolated from clinical specimens. 2015 , 65, 510-515	17
1759	De novo sequencing and analysis of the lily pollen transcriptome: an open access data source for an orphan plant species. 2015 , 87, 69-80	20
1758	Adaptation of an abundant Roseobacter RCA organism to pelagic systems revealed by genomic and transcriptomic analyses. 2015 , 9, 371-84	69
1757	Comparative Genomics of Domesticated and Wild Sunflower: Complete Chloroplast and Mitochondrial Genomes. 2016 , 16, 71-75	9
1756	Draft Genome Sequence of the Commensal Escherichia coli Strain F-18. 2016 , 4,	3
1755	Genome Sequence of the Facultative Anaerobe Oerskovia enterophila DFA-19 (DSM 43852T). 2016 , 4,	1
1754	Two Linked Enteroinvasive Escherichia coli Outbreaks, Nottingham, UK, June 2014. 2016 , 22, 1178-84	25
1753	Genome Sequence of the Acetogenic Bacterium Butyribacterium methylotrophicum DSM 3468T. 2016 , 4,	10
1752	Draft Genome Sequence of Corynebacterium amycolatum Strain ICIS 53 Isolated from a Female Urogenital Tract. 2016 , 4,	2
1751	Evaluation of Next Generation Sequencing Platforms for Whole Exome Variant Analysis. 2016 , 2,	
1750	Transcriptome Profiling Identifies Multiplexin as a Target of SAGA Deubiquitinase Activity in Glia Required for Precise Axon Guidance During Drosophila Visual Development. 2016 , 6, 2435-45	7
1749	Characterization of a Single Genomic Locus Encoding the Clustered Protocadherin Receptor Diversity in Xenopus tropicalis. 2016 , 6, 2309-18	5
1748	SNHG8 is identified as a key regulator of epstein-barr virus(EBV)-associated gastric cancer by an integrative analysis of lncRNA and mRNA expression. 2016 , 7, 80990-81002	36
1747	Genome of Rhizobium leucaenae strains CFN 299(T) and CPAO 29.8: searching for genes related to a successful symbiotic performance under stressful conditions. 2016 , 17, 534	10
1746	Transcriptomics of liver and muscle in Holstein cows genetically divergent for fertility highlight differences in nutrient partitioning and inflammation processes. 2016 , 17, 603	9
1745	Dynamic transcriptome profiling of Bean Common Mosaic Virus (BCMV) infection in Common Bean (Phaseolus vulgaris L.). 2016 , 17, 613	21
1744	Culture-independent genomic characterisation of Candidatus Chlamydia sanzinia, a novel uncultivated bacterium infecting snakes. 2016 , 17, 710	38
1743	Evaluation of 16S rRNA Gene Primer Pairs for Monitoring Microbial Community Structures Showed High Reproducibility within and Low Comparability between Datasets Generated with Multiple Archaeal and Bacterial Primer Pairs. 2016 , 7, 1297	49

1742	Bioinformatics Identification of Drug Resistance-Associated Gene Pairs in Mycobacterium tuberculosis. 2016 , 17,	17
1741	Molecular Diagnosis of Inherited Retinal Diseases in Indigenous African Populations by Whole-Exome Sequencing. 2016 , 57, 6374-6381	11
1740	Proximal and distal regulation of the HYAL1 gene cluster by the estrogen receptor β in breast cancer cells. 2016 , 7, 77276-77290	11
1739	Whole-genome characterization in pedigreed non-human primates using genotyping-by-sequencing (GBS) and imputation. 2016 , 17, 676	6
1738	Evolution of Dosage Compensation in <i>Anolis carolinensis</i> , a Reptile with XX/XY Chromosomal Sex Determination. 2017 , 9, 231-240	21
1737	De novo assembly and analysis of changes in the protein-coding transcriptome of the freshwater shrimp <i>Paratya australiensis</i> (Decapoda: Atyidae) in response to acid sulfate drainage water. 2016 , 17, 890	6
1736	Mutational profiling of non-small-cell lung cancer patients resistant to first-generation EGFR tyrosine kinase inhibitors using next generation sequencing. 2016 , 7, 61755-61763	25
1735	The green ash transcriptome and identification of genes responding to abiotic and biotic stresses. 2016 , 17, 702	20
1734	Web-based bioinformatics workflows for end-to-end RNA-seq data computation and analysis in agricultural animal species. 2016 , 17, 761	5
1733	Similar Mutation Rates but Highly Diverse Mutation Spectra in Ascomycete and Basidiomycete Yeasts. 2016 , 8, 3815-3821	26
1732	Diurnal Transcriptional Regulation of Endosymbiotically Derived Genes in the Chlorarachniophyte <i>Bigeloviella natans</i> . 2016 , 8, 2672-82	21
1731	IMA Genome-F 6: Draft genome sequences of <i>Armillaria fuscipes</i> , <i>Ceratocystiopsis minuta</i> , <i>Ceratocystis adiposa</i> , <i>Endoconidiophora laricicola</i> , <i>E. polonica</i> and <i>Penicillium frei</i> DAOMC 242723. 2016 , 7, 217-27	28
1730	The complete mitochondrial genome of <i>Corydoras nattereri</i> (Callichthyidae: Corydoradinae). 2016 , 14,	7
1729	Detection and molecular characterization of Slovak tomato isolates belonging to two recombinant strains of potato virus Y. 2016 , 60, 347-353	7
1728	Genealogy of the Genome Components in the Highly Homogeneous Pandemic <i>Vibrio parahaemolyticus</i> Population. 2016 , 04,	3
1727	Draft genome of the <i>Leptospira interrogans</i> strains, Acegua, RCA, Prea, and Capivara, obtained from wildlife maintenance hosts and infected domestic animals. 2016 , 111, 280-3	13
1726	IMA Genome-F 7: Draft genome sequences for and. 2016 , 7, 317-323	25
1725	Proteolysis-a characteristic of tumor-initiating cells in murine metastatic breast cancer. 2016 , 7, 58244-58260	9

1724	Bacillus wiedmannii sp. nov., a psychrotolerant and cytotoxic Bacillus cereus group species isolated from dairy foods and dairy environments. 2016 , 66, 4744-4753	82
1723	From reads to genes to pathways: differential expression analysis of RNA-Seq experiments using Rsubread and the edgeR quasi-likelihood pipeline. 2016 , 5, 1438	184
1722	Draft Genome Sequences of Methanobrevibacter curvatus DSM11111, Methanobrevibacter cuticularis DSM11139, Methanobrevibacter filiformis DSM11501, and Methanobrevibacter oralis DSM7256. 2016 , 4,	2
1721	Next Generation Sequencing Identifies Five Major Classes of Potentially Therapeutic Enzymes Secreted by Lucilia sericata Medical Maggots. 2016 , 2016, 8285428	16
1720	Workflow for Genome-Wide Determination of Pre-mRNA Splicing Efficiency from Yeast RNA-seq Data. 2016 , 2016, 4783841	8
1719	On-Chip Reconfigurable Hardware Accelerators for Popcount Computations. 2016 , 2016, 1-11	5
1718	The Vertical Distribution of Sediment Archaeal Community in the "Black Bloom" Disturbing Zhushan Bay of Lake Taihu. 2016 , 2016, 8232135	24
1717	Digital gene expression analysis with sample multiplexing and PCR duplicate detection: A straightforward protocol. 2016 , 61, 26-32	4
1716	Tentacle Transcriptome and Venom Proteome of the Pacific Sea Nettle, Chrysaora fuscescens (Cnidaria: Scyphozoa). 2016 , 8, 102	54
1715	Transcriptomic Profiling Using Next Generation Sequencing - Advances, Advantages, and Challenges. 2016 ,	4
1714	RNA-Seq following PCR-based sorting reveals rare cell transcriptional signatures. 2016 , 17, 361	15
1713	RNA-Seq analysis of seasonal and individual variation in blood transcriptomes of healthy managed bottlenose dolphins. 2016 , 17, 720	20
1712	A transcriptional blueprint for a spiral-cleaving embryo. 2016 , 17, 552	12
1711	Microbial Community Structure of Activated Sludge in Treatment Plants with Different Wastewater Compositions. 2016 , 7, 90	113
1710	From Mollusks to Medicine: A Venomics Approach for the Discovery and Characterization of Therapeutics from Terebridae Peptide Toxins. 2016 , 8, 117	29
1709	Evolution of the Cytolytic Pore-Forming Proteins (Actinoporins) in Sea Anemones. 2016 , 8,	24
1708	Complete Genome Sequence of Germline Chromosomally Integrated Human Herpesvirus 6A and Analyses Integration Sites Define a New Human Endogenous Virus with Potential to Reactivate as an Emerging Infection. 2016 , 8,	36
1707	Resistome diversity in cattle and the environment decreases during beef production. 2016 , 5, e13195	68

1706	Microbiome Analysis Across a Natural Copper Gradient at a Proposed Northern Canadian Mine Site. 2016, 3,	6
1705	<i>Colwellia psychrerythraea</i> Strains from Distant Deep Sea Basins Show Adaptation to Local Conditions. 2016, 4,	16
1704	Comparative Epigenomic Profiling of the DNA Methylome in Mouse and Zebrafish Uncovers High Interspecies Divergence. 2016, 7, 110	21
1703	Single-Cell Transcriptomics Bioinformatics and Computational Challenges. 2016, 7, 163	80
1702	Evolutionary and Functional Features of Copy Number Variation in the Cattle Genome. 2016, 7, 207	24
1701	Benchmarking DNA Metabarcoding for Biodiversity-Based Monitoring and Assessment. 2016, 3,	98
1700	Distribution of <i>Prochlorococcus</i> Ecotypes in the Red Sea Basin Based on Analyses of <i>rpoC1</i> Sequences. 2016, 3,	14
1699	Draft Genomes Shed Light on the Dual Bacterial Symbiosis that Dominates the Microbiome of the Coral Reef Sponge <i>Amphimedon queenslandica</i> . 2016, 3,	35
1698	Expanding our Understanding of the Seaweed Holobiont: RNA Viruses of the Red Alga <i>Delisea pulchra</i> . 2015, 6, 1489	27
1697	Metagenomic Analysis Reveals Symbiotic Relationship among Bacteria in <i>Microcystis</i> -Dominated Community. 2016, 7, 56	31
1696	Genetic Evidence for O-Specific Antigen as Receptor of <i>Pseudomonas aeruginosa</i> Phage K8 and Its Genomic Analysis. 2016, 7, 252	13
1695	How to Predict Molecular Interactions between Species?. 2016, 7, 442	22
1694	Chitin Mixed in Potting Soil Alters Lettuce Growth, the Survival of Zoonotic Bacteria on the Leaves and Associated Rhizosphere Microbiology. 2016, 7, 565	44
1693	Genomic and Secondary Metabolite Analyses of <i>Streptomyces</i> sp. 2AW Provide Insight into the Evolution of the Cycloheximide Pathway. 2016, 7, 573	11
1692	Antimicrobial Susceptibility Profiles of Human <i>Campylobacter jejuni</i> Isolates and Association with Phylogenetic Lineages. 2016, 7, 589	25
1691	Transcriptome Analysis of <i>Scrippsiella trochoidea</i> CCMP 3099 Reveals Physiological Changes Related to Nitrate Depletion. 2016, 7, 639	26
1690	Capturing One of the Human Gut Microbiome's Most Wanted: Reconstructing the Genome of a Novel Butyrate-Producing, Clostridial Scavenger from Metagenomic Sequence Data. 2016, 7, 783	20
1689	Gene Loss and Horizontal Gene Transfer Contributed to the Genome Evolution of the Extreme Acidophile "Ferrovum". 2016, 7, 797	26

1688	Fungal and Prokaryotic Activities in the Marine Subsurface Biosphere at Peru Margin and Canterbury Basin Inferred from RNA-Based Analyses and Microscopy. 2016, 7, 846	34
1687	Phylogenomic Study of Burkholderia glathei-like Organisms, Proposal of 13 Novel Burkholderia Species and Emended Descriptions of Burkholderia sordidicola, Burkholderia zhejiangensis, and Burkholderia grimmiae. 2016, 7, 877	40
1686	Microbiomes of Muricea californica and M. fruticosa: Comparative Analyses of Two Co-occurring Eastern Pacific Octocorals. 2016, 7, 917	26
1685	Whole-Metagenome-Sequencing-Based Community Profiles of Vitis vinifera L. cv. Corvina Berries Withered in Two Post-harvest Conditions. 2016, 7, 937	33
1684	Taxonomic Assessment of Rumen Microbiota Using Total RNA and Targeted Amplicon Sequencing Approaches. 2016, 7, 987	42
1683	Industrial Acetogenic Biocatalysts: A Comparative Metabolic and Genomic Analysis. 2016, 7, 1036	59
1682	Lichen-Associated Fungal Community in Hypogymnia hypotrypea (Parmeliaceae, Ascomycota) Affected by Geographic Distribution and Altitude. 2016, 7, 1231	17
1681	New Genomic Insights into "Entotheonella" Symbionts in Theonella swinhoei: Mixotrophy, Anaerobic Adaptation, Resilience, and Interaction. 2016, 7, 1333	17
1680	Microbiome Dynamics of a Polychlorobiphenyl (PCB) Historically Contaminated Marine Sediment under Conditions Promoting Reductive Dechlorination. 2016, 7, 1502	27
1679	Differences in the Composition of Archaeal Communities in Sediments from Contrasting Zones of Lake Taihu. 2016, 7, 1510	21
1678	Transparent DNA/RNA Co-extraction Workflow Protocol Suitable for Inhibitor-Rich Environmental Samples That Focuses on Complete DNA Removal for Transcriptomic Analyses. 2016, 7, 1588	11
1677	Genome Sequencing of Four Multidrug-Resistant Isolates from Hospitalized Patients in Brazil. 2016, 7, 1649	7
1676	Molecular Characterization of Serovars Anatum and Ealing Associated with Two Historical Outbreaks, Linked to Contaminated Powdered Infant Formula. 2016, 7, 1664	1
1675	Molecular Keys to the and spp. Interaction with the Plant Pathogen. 2016, 7, 1668	45
1674	An Enrichment of CRISPR and Other Defense-Related Features in Marine Sponge-Associated Microbial Metagenomes. 2016, 7, 1751	53
1673	Comparative Genomics of the ST204 Subgroup. 2016, 7, 2057	25
1672	Dynamics in the Strawberry Rhizosphere Microbiome in Response to Biochar and Leaf Infection. 2016, 7, 2062	31
1671	Reconstruction of the Metabolic Potential of Acidophilic Strains from the Metagenome of an Microaerophilic Enrichment Culture of Acidophilic Iron-Oxidizing Bacteria from a Pilot Plant for the Treatment of Acid Mine Drainage Reveals Metabolic Versatility and Adaptation to Life at Low pH. 2016, 7, 2088	15

1670	Early Recovery of from Food Using a 6-Hour Non-selective Pre-enrichment and Reformulation of Tetrathionate Broth. 2016 , 7, 2103	24
1669	Bidirectional Expression of Metabolic, Structural, and Immune Pathways in Early Myopia and Hyperopia. 2016 , 10, 390	22
1668	Identification of Novel Equine (<i>Equus caballus</i>) Tendon Markers Using RNA Sequencing. 2016 , 7,	5
1667	Transcriptome and Gene Ontology (GO) Enrichment Analysis Reveals Genes Involved in Biotin Metabolism That Affect L-Lysine Production in <i>Corynebacterium glutamicum</i> . 2016 , 17, 353	11
1666	Genes Expressed Differentially in Hessian Fly Larvae Feeding in Resistant and Susceptible Plants. 2016 , 17,	4
1665	De novo assembly of Sockeye salmon kidney transcriptomes reveal a limited early response to piscine reovirus with or without infectious hematopoietic necrosis virus superinfection. 2016 , 17, 848	25
1664	Genetic mapping of <i>Pinus flexilis</i> major gene (Cr4) for resistance to white pine blister rust using transcriptome-based SNP genotyping. 2016 , 17, 753	24
1663	Surprisingly rich repertoire of Wnt genes in the demosponge <i>Halisarca dujardini</i> . 2016 , 16, 123	32
1662	Capture Hi-C identifies a novel causal gene, IL20RA, in the pan-autoimmune genetic susceptibility region 6q23. 2016 , 17, 212	62
1661	RNAseq reveals hydrophobins that are involved in the adaptation of <i>Aspergillus nidulans</i> to lignocellulose. 2016 , 9, 145	20
1660	An RNAi-Based Control of <i>Fusarium graminearum</i> Infections Through Spraying of Long dsRNAs Involves a Plant Passage and Is Controlled by the Fungal Silencing Machinery. 2016 , 12, e1005901	255
1659	Novel Structural and Functional Motifs in cellulose synthase (<i>CesA</i>) Genes of Bread Wheat (<i>Triticum aestivum</i> , L.). 2016 , 11, e0147046	21
1658	A Comprehensive Genomic Analysis Reveals the Genetic Landscape of Mitochondrial Respiratory Chain Complex Deficiencies. 2016 , 12, e1005679	163
1657	Uncovering the Ancestry of B Chromosomes in <i>Moenkhausia sanctaefilomenae</i> (Teleostei, Characidae). 2016 , 11, e0150573	36
1656	Proteinaceous Pheromone Homologs Identified from the Cloacal Gland Transcriptome of a Male Axolotl, <i>Ambystoma mexicanum</i> . 2016 , 11, e0146851	5
1655	The Complete Plastid Genome of <i>Lagerstroemia fauriei</i> and Loss of <i>rpl2</i> Intron from <i>Lagerstroemia</i> (Lythraceae). 2016 , 11, e0150752	27
1654	Aptamer-Assisted Detection of the Altered Expression of Estrogen Receptor Alpha in Human Breast Cancer. 2016 , 11, e0153001	19
1653	Mitochondrial Genomes of Kinorhyncha: <i>trnM</i> Duplication and New Gene Orders within Animals. 2016 , 11, e0165072	7

1652	Context Specific and Differential Gene Co-expression Networks via Bayesian Biclustering. 2016 , 12, e1004791	32
1651	Metagenome and Metatranscriptome Analyses Using Protein Family Profiles. 2016 , 12, e1004991	13
1650	Histone H3 Variant Regulates RNA Polymerase II Transcription Termination and Dual Strand Transcription of siRNA Loci in <i>Trypanosoma brucei</i> . 2016 , 12, e1005758	32
1649	Continuous Influx of Genetic Material from Host to Virus Populations. 2016 , 12, e1005838	48
1648	Selection on Coding and Regulatory Variation Maintains Individuality in Major Urinary Protein Scent Marks in Wild Mice. 2016 , 12, e1005891	28
1647	Allelic Imbalance in Regulation of ANRIL through Chromatin Interaction at 9p21 Endometriosis Risk Locus. 2016 , 12, e1005893	34
1646	BRR2a Affects Flowering Time via FLC Splicing. 2016 , 12, e1005924	35
1645	<i>Drosophila</i> Adaptation to Viral Infection through Defensive Symbiont Evolution. 2016 , 12, e1006297	17
1644	The Genetic Basis of Host Preference and Resting Behavior in the Major African Malaria Vector, <i>Anopheles arabiensis</i> . 2016 , 12, e1006303	55
1643	Genome-Wide Analyses of Individual <i>Strongyloides stercoralis</i> (Nematoda: Rhabditoidea) Provide Insights into Population Structure and Reproductive Life Cycles. 2016 , 10, e0005253	21
1642	Genome Analysis of the Biotechnologically Relevant Acidophilic Iron Oxidising Strain JA12 Indicates Phylogenetic and Metabolic Diversity within the Novel Genus "Ferrovum". 2016 , 11, e0146832	29
1641	Correlative Gene Expression to Protective Seroconversion in Rift Valley Fever Vaccinates. 2016 , 11, e0147027	4
1640	Systematic Identification and Characterization of Long Non-Coding RNAs in the Silkworm, <i>Bombyx mori</i> . 2016 , 11, e0147147	72
1639	Digital Droplet Multiple Displacement Amplification (ddMDA) for Whole Genome Sequencing of Limited DNA Samples. 2016 , 11, e0153699	34
1638	Massive Shift in Gene Expression during Transitions between Developmental Stages of the Gall Midge, <i>Mayetiola Destructor</i> . 2016 , 11, e0155616	5
1637	Differential RNA-seq, Multi-Network Analysis and Metabolic Regulation Analysis of <i>Kluyveromyces marxianus</i> Reveals a Compartmentalised Response to Xylose. 2016 , 11, e0156242	23
1636	The Microbiome and Metabolites in Fermented Pu-erh Tea as Revealed by High-Throughput Sequencing and Quantitative Multiplex Metabolite Analysis. 2016 , 11, e0157847	39
1635	Development of Molecular Markers for Determining Continental Origin of Wood from White Oaks (<i>Quercus L. sect. Quercus</i>). 2016 , 11, e0158221	24

1634	The De Novo Transcriptome and Its Functional Annotation in the Seed Beetle <i>Callosobruchus maculatus</i> . 2016 , 11, e0158565	30
1633	RNAseq Analyses Identify Tumor Necrosis Factor-Mediated Inflammation as a Major Abnormality in ALS Spinal Cord. 2016 , 11, e0160520	38
1632	Genomic and Evolutionary Analysis of Two <i>Salmonella enterica</i> Serovar Kentucky Sequence Types Isolated from Bovine and Poultry Sources in North America. 2016 , 11, e0161225	24
1631	Sequence Capture and Phylogenetic Utility of Genomic Ultraconserved Elements Obtained from Pinned Insect Specimens. 2016 , 11, e0161531	97
1630	MetaStorm: A Public Resource for Customizable Metagenomics Annotation. 2016 , 11, e0162442	42
1629	Transcriptome Profile of the Chicken Thrombocyte: New Implications as an Advanced Immune Effector Cell. 2016 , 11, e0163890	18
1628	Deciphering Transcriptional Programming during Pod and Seed Development Using RNA-Seq in <i>Pigeonpea</i> (<i>Cajanus cajan</i>). 2016 , 11, e0164959	10
1627	Gene Expression Dynamics Accompanying the Sponge Thermal Stress Response. 2016 , 11, e0165368	25
1626	Identification of the Core Set of Carbon-Associated Genes in a Bioenergy Grassland Soil. 2016 , 11, e0166578	11
1625	Pathoadaptive Mutations of <i>Escherichia coli</i> K1 in Experimental Neonatal Systemic Infection. 2016 , 11, e0166793	6
1624	Brain Transcriptional Profiles of Male Alternative Reproductive Tactics and Females in Bluegill Sunfish. 2016 , 11, e0167509	20
1623	Genome and Proteome Analysis of <i>Rhodococcus erythropolis</i> MI2: Elucidation of the 4,4'-Dithiodibutyric Acid Catabolism. 2016 , 11, e0167539	7
1622	Transformed Recombinant Enrichment Profiling Rapidly Identifies HMW1 as an Intracellular Invasion Locus in <i>Haemophilus influenzae</i> . 2016 , 12, e1005576	10
1621	Integrative Transcriptome, Genome and Quantitative Trait Loci Resources Identify Single Nucleotide Polymorphisms in Candidate Genes for Growth Traits in Turbot. 2016 , 17, 243	25
1620	Insights into the innate immunome of actinarians using a comparative genomic approach. 2016 , 17, 850	36
1619	Mitochondrial DNA Sequence and Lack of Response to Anoxia in the Annual Killifish <i>Austrofundulus limnaeus</i> . 2016 , 7, 379	5
1618	RNA-seq Analysis of <i>Nepenthes ampullaria</i> . 2015 , 6, 1229	10
1617	The Pokeweed Leaf mRNA Transcriptome and Its Regulation by Jasmonic Acid. 2016 , 7, 283	9

1616	Comprehensive Transcriptome Profiling Reveals Long Noncoding RNA Expression and Alternative Splicing Regulation during Fruit Development and Ripening in Kiwifruit (<i>Actinidia chinensis</i>). 2016 , 7, 335	54
1615	RNA-seq Transcriptome Analysis of <i>Panax japonicus</i> , and Its Comparison with Other <i>Panax</i> Species to Identify Potential Genes Involved in the Saponins Biosynthesis. 2016 , 7, 481	44
1614	Transcriptome Profiling of Buffalograss Challenged with the Leaf Spot Pathogen <i>Curvularia inaequalis</i> . 2016 , 7, 715	5
1613	Identification of Circular RNAs from the Parental Genes Involved in Multiple Aspects of Cellular Metabolism in Barley. 2016 , 7, 776	64
1612	Natural Allelic Variations in Highly Polyploidy <i>Saccharum</i> Complex. 2016 , 7, 804	28
1611	A De Novo-Assembly Based Data Analysis Pipeline for Plant Obligate Parasite Metatranscriptomic Studies. 2016 , 7, 925	9
1610	Transcriptome Profiling of Petal Abscission Zone and Functional Analysis of an Aux/IAA Family Gene Involved in Petal Shedding in Rose. 2016 , 7, 1375	24
1609	Transcriptome Dynamics in Mango Fruit Peel Reveals Mechanisms of Chilling Stress. 2016 , 7, 1579	44
1608	Identification of a Chromosome 4 Fruit Flavor and Nutritional Quality-Associated Metabolite QTL. 2016 , 7, 1671	19
1607	Insights into the Sesquiterpenoid Pathway by Metabolic Profiling and Transcriptome Assembly of Stem-Chicory (Cultigroup "Catalogna"). 2016 , 7, 1676	15
1606	Transcriptomic Effects of the Cell Cycle Regulator LGO in Sepals. 2016 , 7, 1744	11
1605	Comparative Transcriptomic Analysis of Virulence Factors in during Compatible and Incompatible Interactions with Canola. 2016 , 7, 1784	30
1604	Identification and Expression Analysis of Candidate Genes Involved in Carotenoid Biosynthesis in Chickpea Seeds. 2016 , 7, 1867	22
1603	Glutathione S-transferases and UDP-glycosyltransferases Are Involved in Response to Aluminum Stress in Flax. 2016 , 7, 1920	37
1602	Duplication and Divergence of Leucine-Rich Repeat Receptor-Like Protein Kinase () Genes in Basal Angiosperm. 2016 , 7, 1952	13
1601	Bioinformatics for RNA-Seq Data Analysis. 2016 ,	4
1600	Eighteenth century <i>Yersinia pestis</i> genomes reveal the long-term persistence of an historical plague focus. 2016 , 5, e12994	101
1599	A <i>Ralstonia solanacearum</i> Strain from Guatemala Infects Diverse Flower Crops, Including New Asymptomatic Hosts <i>Vinca</i> and <i>Sutera</i> , and Causes Symptoms in <i>Geranium</i> , <i>Mandevilla</i> Vine, and New Host African Daisy (<i>Osteospermum ecklonis</i>). 2016 , 17, 114-121	15

1598	Exon capture optimization in amphibians with large genomes. 2016 , 16, 1084-94	40
1597	An evaluation of transcriptome-based exon capture for frog phylogenomics across multiple scales of divergence (Class: Amphibia, Order: Anura). 2016 , 16, 1069-83	65
1596	Para-allopatry in hybridizing fire-bellied toads (<i>Bombina bombina</i> and <i>B. variegata</i>): Inference from transcriptome-wide coalescence analyses. 2016 , 70, 1803-18	17
1595	Transcriptome analysis provides insight into venom evolution in a seed-parasitic wasp, <i>Megastigmus spermotrophus</i> . 2016 , 25, 604-16	7
1594	Endogenous Gibbon Ape Leukemia Virus Identified in a Rodent (<i>Melomys burtoni</i> subsp.) from Wallacea (Indonesia). 2016 , 90, 8169-80	18
1593	The evolution of silicon transporters in diatoms. 2016 , 52, 716-731	27
1592	The importance of replicating genomic analyses to verify phylogenetic signal for recently evolved lineages. 2016 , 25, 3683-95	19
1591	Comparative transcriptomic analyses of <i>Zyloseptoria tritici</i> strains show complex lifestyle transitions and intraspecific variability in transcription profiles. 2016 , 17, 845-59	58
1590	NODULES WITH ACTIVATED DEFENSE 1 is required for maintenance of rhizobial endosymbiosis in <i>Medicago truncatula</i> . 2016 , 212, 176-91	55
1589	Diversity and Activity of Communities Inhabiting Plastic Debris in the North Pacific Gyre. 2016 , 1,	191
1588	Elucidation of Taste- and Odor-Producing Bacteria and Toxigenic Cyanobacteria in a Midwestern Drinking Water Supply Reservoir by Shotgun Metagenomic Analysis. 2016 , 82, 5410-20	32
1587	Genomic characterization of the uncultured Bacteroidales family S24-7 inhabiting the guts of homeothermic animals. 2016 , 4, 36	322
1586	Transcriptomic analysis of the hippocampus from six inbred strains of mice suggests a basis for sex-specific susceptibility and severity of neurological disorders. 2016 , 524, 2696-710	15
1585	Lessons from genome skimming of arthropod-preserving ethanol. 2016 , 16, 1365-1377	42
1584	Fungal compositions and diversities on indoor surfaces with visible mold growths in residential buildings in the Seoul Capital Area of South Korea. 2016 , 26, 714-23	19
1583	Primary and Secondary Sequence Structure Requirements for Recognition and Discrimination of Target RNAs by <i>Pseudomonas aeruginosa</i> RsmA and RsmF. 2016 , 198, 2458-69	17
1582	Draft Genome Sequence of <i>Vibrio toranzoniae</i> Strain CECT 7225T. 2016 , 4,	1
1581	Genome Sequence of the Endophytic Bacterium <i>Bacillus thuringiensis</i> Strain KB1, a Potential Biocontrol Agent against Phytopathogens. 2016 , 4,	10

1580	Strongly asymmetric hybridization barriers shape the origin of a new polyploid species and its hybrid ancestor. 2016 , 103, 1272-88	33
1579	Alkaline phosphatases are involved in the response of <i>Aedes aegypti</i> larvae to intoxication with <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i> Cry toxins. 2016 , 18, 1022-36	14
1578	Response of bacterial communities from California coastal waters to alginate particles and an alginolytic <i>Alteromonas macleodii</i> strain. 2016 , 18, 4369-4377	23
1577	Identification and characterization of parasitism genes from the pinewood nematode <i>Bursaphelenchus xylophilus</i> reveals a multilayered detoxification strategy. 2016 , 17, 286-95	69
1576	Homomorphic ZW chromosomes in a wild strawberry show distinctive recombination heterogeneity but a small sex-determining region. 2016 , 211, 1412-23	29
1575	Functional network analysis of genes differentially expressed during xylogenesis in social woody <i>Arabidopsis</i> plants. 2016 , 86, 376-90	22
1574	High-throughput sequencing and de novo transcriptome assembly of <i>Swertia japonica</i> to identify genes involved in the biosynthesis of therapeutic metabolites. 2016 , 35, 2091-111	26
1573	Type IV pili promote early biofilm formation by <i>Clostridium difficile</i> . 2016 , 74,	39
1572	Rickettsial endosymbiont in the "early-diverging" streptophyte green alga <i>Mesostigma viride</i> . 2016 , 52, 219-29	11
1571	Revisiting a classic case of introgression: hybridization and gene flow in Californian sunflowers. 2016 , 25, 2630-43	30
1570	The genome of black raspberry (<i>Rubus occidentalis</i>). 2016 , 87, 535-47	78
1569	Genome Sequence of <i>Pseudomonas aeruginosa</i> Strain DK1-NH57388A, a Stable Muroid Cystic Fibrosis Isolate. 2016 , 4,	10
1568	Draft Genome Sequences of 63 <i>Pseudomonas aeruginosa</i> Isolates Recovered from Cystic Fibrosis Sputum. 2016 , 4,	4
1567	First Insights into the Draft Genome of <i>Clostridium colicanis</i> DSM 13634, Isolated from Canine Feces. 2016 , 4,	3
1566	Draft Genome Sequence of an Oxalate-Degrading Strain of <i>Clostridium sporogenes</i> from the Gastrointestinal Tract of the White-Throated Woodrat (<i>Neotoma albigula</i>). 2016 , 4,	2
1565	Genome Sequence of <i>Listeria monocytogenes</i> Strain F6540 (Sequence Type 360) Collected from Food Samples in Ontario, Canada. 2016 , 4,	
1564	Draft Genome Sequences of the Turfgrass Pathogen <i>Sclerotinia homoeocarpa</i> . 2016 , 4,	9
1563	Rapid Capture Next-Generation Sequencing in Clinical Diagnostics of Kinase Pathway Aberrations in B-Cell Precursor ALL. 2016 , 63, 1283-6	9

1562	Status of dosage compensation of X chromosome in bovine genome. 2016 , 144, 435-44	3
1561	An Examination of Dynamic Gene Expression Changes in the Mouse Brain During Pregnancy and the Postpartum Period. 2015 , 6, 221-33	27
1560	Massive Amplification at an Unselected Locus Accompanies Complex Chromosomal Rearrangements in Yeast. 2016 , 6, 1201-15	3
1559	Combined Chlorophyll Fluorescence and Transcriptomic Analysis Identifies the P3/P4 Transition as a Key Stage in Rice Leaf Photosynthetic Development. 2016 , 170, 1655-74	9
1558	Spatial disturbances in altered mucosal and luminal gut viromes of diet-induced obese mice. 2016 , 18, 1498-510	45
1557	Methanogenic paraffin degradation proceeds via alkane addition to fumarate by 'Smithella' spp. mediated by a syntrophic coupling with hydrogenotrophic methanogens. 2016 , 18, 2604-19	61
1556	Phylogenetic marker development for target enrichment from transcriptome and genome skim data: the pipeline and its application in southern African Oxalis (Oxalidaceae). 2016 , 16, 1124-35	53
1555	FASTmC: A Suite of Predictive Models for Nonreference-Based Estimations of DNA Methylation. 2015 , 6, 447-52	13
1554	Biologically Induced Hydrogen Production Drives High Rate/High Efficiency Microbial Electrosynthesis of Acetate from Carbon Dioxide. 2016 , 3, 581-591	94
1553	Detection and screening of chromosomal rearrangements in uterine leiomyomas by long-distance inverse PCR. 2016 , 55, 215-26	5
1552	Exposure to soil, house dust and decaying plants increases gut microbial diversity and decreases serum immunoglobulin E levels in BALB/c mice. 2016 , 18, 1326-37	34
1551	Draft Genome Sequence of Toluene-Resistant Staphylococcus epidermidis SNUT. 2016 , 4,	
1550	Draft Genome Sequences of Seven Multidrug-Resistant Acinetobacter baumannii Strains, Isolated from Respiratory Samples in Spain. 2016 , 4,	1
1549	Draft Genome Sequences of Four Plant Probiotic Bacillus Strains. 2016 , 4,	2
1548	Draft Genome Sequence of an Invasive Streptococcus agalactiae Isolate Lacking Pigmentation. 2016 , 4,	8
1547	Complete Genome Sequence of Mycobacterium abscessus subsp. bolletii. 2016 , 4,	4
1546	Elevated IgA Plasmablast Levels in Subjects at Risk of Developing Rheumatoid Arthritis. 2016 , 68, 2372-83	60
1545	Estimating species richness using environmental DNA. 2016 , 6, 4214-26	108

1544	Identification and qualification of 500 nuclear, single-copy, orthologous genes for the Eupulmonata (Gastropoda) using transcriptome sequencing and exon capture. 2016 , 16, 1107-23	34
1543	Exon capture phylogenomics: efficacy across scales of divergence. 2016 , 16, 1059-68	91
1542	Protein Sialylation Regulates a Gene Expression Signature that Promotes Breast Cancer Cell Pathogenicity. 2016 , 11, 2131-9	23
1541	Hierarchy within the mammary STAT5-driven Wap super-enhancer. 2016 , 48, 904-911	147
1540	Identification and characterization of toxins in the venom gland of the Chinese bird spider, <i>Haplopelma hainanum</i> , by transcriptomic analysis. 2016 , 23, 487-99	9
1539	Simultaneous identification of host, ectoparasite and pathogen DNA via in-solution capture. 2016 , 16, 1224-39	23
1538	Diverse phenotypic and genetic responses to short-term selection in evolving <i>Escherichia coli</i> populations. 2016 , 70, 586-99	17
1537	Whole Genome Comparison Reveals High Levels of Inbreeding and Strain Redundancy Across the Spectrum of Commercial Wine Strains of <i>Saccharomyces cerevisiae</i> . 2016 , 6, 957-71	81
1536	Increasing Genome Sampling and Improving SNP Genotyping for Genotyping-by-Sequencing with New Combinations of Restriction Enzymes. 2016 , 6, 845-56	18
1535	First High-Quality Draft Genome Sequence of <i>Pasteurella multocida</i> Sequence Type 128 Isolated from Infected Bone. 2016 , 4,	2
1534	Chloroplast Genome Sequence of <i>Lagerstroemia guilinensis</i> (Lythraceae, Myrtales), a Species Endemic to the Guilin Limestone Area in Guangxi Province, China. 2016 , 4,	2
1533	Draft Genome Sequence of <i>Lampenflora Chlorobium limicola</i> Strain Frasassi in a Sulfidic Cave System. 2016 , 4,	3
1532	Draft Genome Sequence of a 94-Year-Old <i>Listeria monocytogenes</i> Isolate, SLCC208. 2016 , 4,	6
1531	Draft Genome Sequence of <i>Janthinobacterium</i> sp. Ant5-2-1, Isolated from Proglacial Lake Podprudnoye in the Schirmacher Oasis of East Antarctica. 2016 , 4,	15
1530	High throughput genomic sequencing of bioaerosols in broiler chicken production facilities. 2016 , 9, 782-791	14
1529	The complete mitochondrial genome of the Endangered European brown frog through RNAseq. 2016 , 1, 394-396	3
1528	Genome Sequence of <i>Fusarium</i> Isolate MYA-4552 from the Midgut of <i>Anoplophora glabripennis</i> , an Invasive, Wood-Boring Beetle. 2016 , 4,	9
1527	Transcriptomic profile of tobacco in response to <i>Alternaria longipes</i> and <i>Alternaria alternata</i> infections. 2016 , 6, 25635	15

1526	Transcriptome analysis of interactions between silkworm and cytoplasmic polyhedrosis virus. 2016 , 6, 24894	22
1525	Maize pan-transcriptome provides novel insights into genome complexity and quantitative trait variation. 2016 , 6, 18936	41
1524	Mucosal adherent bacterial dysbiosis in patients with colorectal adenomas. 2016 , 6, 26337	101
1523	The caste- and sex-specific DNA methylome of the termite <i>Zootermopsis nevadensis</i> . 2016 , 6, 37110	76
1522	Genome-Wide Association Study Identifies Novel Candidate Genes for Aggressiveness, Deoxynivalenol Production, and Azole Sensitivity in Natural Field Populations of <i>Fusarium graminearum</i> . 2016 , 29, 417-30	48
1521	Next-generation sequencing reveals broad down-regulation of microRNAs in secondary progressive multiple sclerosis CD4+ T cells. 2016 , 8, 87	33
1520	Whole-Genome Sequencing of Two <i>Bartonella bacilliformis</i> Strains. 2016 , 4,	4
1519	Disorders of sex development: insights from targeted gene sequencing of a large international patient cohort. 2016 , 17, 243	166
1518	Recurrence of Chromosome Rearrangements and Reuse of DNA Breakpoints in the Evolution of the Triticeae Genomes. 2016 , 6, 3837-3847	17
1517	Metagenomic investigation of the microbial diversity in a chrysotile asbestos mine pit pond, Lowell, Vermont, USA. 2016 , 10, 158-164	4
1516	Transcriptome analyses of seed development in grape hybrids reveals a possible mechanism influencing seed size. 2016 , 17, 898	23
1515	Utilising polymorphisms to achieve allele-specific genome editing in zebrafish. 2017 , 6, 125-131	12
1514	Microbiota Diurnal Rhythmicity Programs Host Transcriptome Oscillations. 2016 , 167, 1495-1510.e12	410
1513	Development of SSR markers for a Tibetan medicinal plant, (Phrymaceae), based on RAD sequencing. 2016 , 4, 1600076	9
1512	A Consensus Genome-scale Reconstruction of Chinese Hamster Ovary Cell Metabolism. 2016 , 3, 434-443.e8	145
1511	Conserved Noncoding Elements in the Most Distant Genera of Cephalochordates: The Goldilocks Principle. 2016 , 8, 2387-405	18
1510	Draft Genome Sequence of the Thermotolerant Cyanobacterium <i>Desertifilum</i> sp. IPPAS B-1220. 2016 , 4,	4
1509	SeqMaker: A next generation sequencing simulator with variations, sequencing errors and amplification bias integrated. 2016 ,	

1508	Assessing genotype-phenotype associations in three dorsal colour morphs in the meadow spittlebug <i>Philaenus spumarius</i> (L.) (Hemiptera: Aphrophoridae) using genomic and transcriptomic resources. 2016 , 17, 144	9
1507	New insights into the <i>Plasmodium vivax</i> transcriptome using RNA-Seq. 2016 , 6, 20498	46
1506	De novo and comparative transcriptome analysis of cultivated and wild spinach. 2015 , 5, 17706	34
1505	Draft Genome Sequence of a Novel Mucilaginibacter Member Isolated from Brazilian Amazon Soil. 2016 , 4,	2
1504	The Evolution of the FT/TFL1 Genes in Amaranthaceae and Their Expression Patterns in the Course of Vegetative Growth and Flowering in <i>Chenopodium rubrum</i> . 2016 , 6, 3065-3076	9
1503	Venom gland transcriptome analyses of two freshwater stingrays (Myliobatiformes: Potamotrygonidae) from Brazil. 2016 , 6, 21935	16
1502	Computational workflow for the fine-grained analysis of metagenomic samples. 2016 , 17, 802	5
1501	A comprehensive method for amplicon-based and metagenomic characterization of viruses, bacteria, and eukaryotes in freshwater samples. 2016 , 4, 20	52
1500	Long Terminal Repeat Retrotransposon Content in Eight Diploid Sunflower Species Inferred from Next-Generation Sequence Data. 2016 , 6, 2299-308	9
1499	Sex bias in CNS autoimmune disease mediated by androgen control of autoimmune regulator. 2016 , 7, 11350	72
1498	Do novel genes drive morphological novelty? An investigation of the nematosomes in the sea anemone <i>Nematostella vectensis</i> . 2016 , 16, 114	38
1497	Large Deletions at the SHOX Locus in the Pseudoautosomal Region Are Associated with Skeletal Atavism in Shetland Ponies. 2016 , 6, 2213-23	21
1496	Low-coverage, whole-genome sequencing of <i>Artocarpus camansi</i> (Moraceae) for phylogenetic marker development and gene discovery. 2016 , 4, 1600017	24
1495	Genomic and Chemical Diversity in Cannabis. 2016 , 35, 349-363	73
1494	Induction of Germ Cell-like Cells from Porcine Induced Pluripotent Stem Cells. 2016 , 6, 27256	24
1493	Draft Genome Sequence of <i>Planomonospora sphaerica</i> JCM9374, a Rare Actinomycete. 2016 , 4,	5
1492	The Genetic Basis of Natural Variation in <i>Caenorhabditis elegans</i> Telomere Length. 2016 , 204, 371-83	64
1491	Comparative transcriptomics enlarges the toolkit of known developmental genes in mollusks. 2016 , 17, 905	26

1490	Whole genome sequencing of Gyeongbuk Araucana, a newly developed blue-egg laying chicken breed, reveals its origin and genetic characteristics. 2016 , 6, 26484		4
1489	An IFIH1 gene polymorphism associated with risk for autoimmunity regulates canonical antiviral defence pathways in Coxsackievirus infected human pancreatic islets. 2016 , 6, 39378		34
1488	A new method for decontamination of de novo transcriptomes using a hierarchical clustering algorithm. <i>Bioinformatics</i> , 2017 , 33, 1293-1300	7.2	12
1487	The chemosensory receptors of codling moth <i>Cydia pomonella</i> -expression in larvae and adults. 2016 , 6, 23518		35
1486	Limb patterning genes and heterochronic development of the emu wing bud. 2016 , 7, 26		9
1485	The genomic landscape of rapid repeated evolutionary adaptation to toxic pollution in wild fish. 2016 , 354, 1305-1308		250
1484	Ultra-dense SNP genetic map construction and identification of SiDt gene controlling the determinate growth habit in <i>Sesamum indicum</i> L. 2016 , 6, 31556		41
1483	Analysis of Annotation and Differential Expression Methods used in RNA-seq Studies in Crustacean Systems. 2016 , 56, 1067-1079		15
1482	Transcriptome profiling reveals differential gene expression of detoxification enzymes in a hemimetabolous tobacco pest after feeding on jasmonate-silenced <i>Nicotiana attenuata</i> plants. 2016 , 17, 1005		26
1481	Genetic linkage of distinct adaptive traits in sympatrically speciating crater lake cichlid fish. 2016 , 7, 12736		37
1480	Differential morphology and transcriptome profile between the incompletely fused carpels ovary and its wild-type in maize. 2016 , 6, 32652		3
1479	Genome maintenance and bioenergetics of the long-lived hypoxia-tolerant and cancer-resistant blind mole rat, <i>Spalax</i> : a cross-species analysis of brain transcriptome. 2016 , 6, 38624		19
1478	The PAS Domain-Containing Protein HeuR Regulates Heme Uptake in <i>Campylobacter jejuni</i> . 2016 , 7,		8
1477	Enrichment dynamics of <i>Listeria monocytogenes</i> and the associated microbiome from naturally contaminated ice cream linked to a listeriosis outbreak. 2016 , 16, 275		83
1476	Genome sequence, population history, and pelage genetics of the endangered African wild dog (<i>Lycaon pictus</i>). 2016 , 17, 1013		17
1475	Characterization of <i>Pseudomonas aeruginosa</i> Phage C11 and Identification of Host Genes Required for Virion Maturation. 2016 , 6, 39130		11
1474	Whole-Genome Sequences of 26 <i>Vibrio cholerae</i> Isolates. 2016 , 4,		5
1473	Co-expression network analysis of duplicate genes in maize (<i>Zea mays</i> L.) reveals no subgenome bias. 2016 , 17, 875		20

1472	Complete Genome Sequence of <i>Dehalococcoides mccartyi</i> Strain WBC-2, Capable of Anaerobic Reductive Dechlorination of Vinyl Chloride. 2016 , 4,	2
1471	Genome Sequence of the Acetogenic Bacterium <i>Acetobacterium wieringae</i> DSM 1911T. 2016 , 4,	9
1470	Genomes of coral dinoflagellate symbionts highlight evolutionary adaptations conducive to a symbiotic lifestyle. 2016 , 6, 39734	210
1469	Comparing genome versus proteome-based identification of clinical bacterial isolates. 2018 , 19, 495-505	6
1468	Exploring the methanogen and bacterial communities of rumen environments: solid adherent, fluid and epimural. 2017 , 93,	34
1467	The human milk oligosaccharide 2'-fucosyllactose attenuates the severity of experimental necrotising enterocolitis by enhancing mesenteric perfusion in the neonatal intestine. 2016 , 116, 1175-1187	106
1466	Genome-wide genotyping-by-sequencing data provide a high-resolution view of wild <i>Helianthus</i> diversity, genetic structure, and interspecies gene flow. 2016 , 103, 2170-2177	31
1465	Cell Proliferation Pattern and Twist Expression in an Aplousobranch Mollusk Argue Against Segmented Ancestry of Mollusca. 2016 , 326, 422-436	9
1464	Ionic Liquids Impact the Bioenergy Feedstock-Degrading Microbiome and Transcription of Enzymes Relevant to Polysaccharide Hydrolysis. 2016 , 1,	8
1463	Sequential Turnovers of Sex Chromosomes in African Clawed Frogs (<i>Xenopus laevis</i>) Suggest Some Genomic Regions Are Good at Sex Determination. 2016 , 6, 3625-3633	30
1462	The deepest mitochondrial genome sequenced from Mariana Trench (Amphipoda). 2016 , 1, 802-803	11
1461	Synthetic spike-in standards for high-throughput 16S rRNA gene amplicon sequencing. 2017 , 45, e23	66
1460	Differential gene expression in <i>Varroa jacobsoni</i> mites following a host shift to European honey bees (<i>Apis mellifera</i>). 2016 , 17, 926	9
1459	IMP: a pipeline for reproducible reference-independent integrated metagenomic and metatranscriptomic analyses. 2016 , 17, 260	81
1458	Genome Sequence and Analysis of a Stress-Tolerant, Wild-Derived Strain of <i>Saccharomyces cerevisiae</i> Used in Biofuels Research. 2016 , 6, 1757-66	35
1457	A Population of Deletion Mutants and an Integrated Mapping and Exome-seq Pipeline for Gene Discovery in Maize. 2016 , 6, 2385-95	11
1456	The Composite Regulatory Basis of the Large X-Effect in Mouse Speciation. 2017 , 34, 282-295	29
1455	<i>Cercospora zeina</i> from Maize in South Africa Exhibits High Genetic Diversity and Lack of Regional Population Differentiation. 2016 , 106, 1194-1205	8

1454	Transcriptomic characterization and curation of candidate neuropeptides regulating reproduction in the eyestalk ganglia of the Australian crayfish, <i>Cherax quadricarinatus</i> . 2016 , 6, 38658	39
1453	Draft Genome Sequence of <i>Agrobacterium rhizogenes</i> Strain NCPPB2659. 2016 , 4,	8
1452	Spotted phenotypes in horses lost attractiveness in the Middle Ages. 2016 , 6, 38548	21
1451	High-resolution transcript profiling reveals shoot abscission process of spruce dwarf mistletoe <i>Arceuthobium sichuanense</i> in response to ethephon. 2016 , 6, 38889	2
1450	Exogenous Abscisic Acid and Gibberellic Acid Elicit Opposing Effects on <i>Fusarium graminearum</i> Infection in Wheat. 2016 , 106, 986-96	33
1449	The draft genome of whitefly <i>Bemisia tabaci</i> MEAM1, a global crop pest, provides novel insights into virus transmission, host adaptation, and insecticide resistance. 2016 , 14, 110	178
1448	Oxidative stress and carbon metabolism influence <i>Aspergillus flavus</i> transcriptome composition and secondary metabolite production. 2016 , 6, 38747	47
1447	Production of hemolysin BL by <i>Bacillus cereus</i> group isolates of dairy origin is associated with whole-genome phylogenetic clade. 2016 , 17, 581	36
1446	Draft Genome Sequence of Antarctic Methanogen Enriched from Dry Valley Permafrost. 2016 , 4,	2
1445	SePIA: RNA and small RNA sequence processing, integration, and analysis. 2016 , 9, 20	20
1444	Molecular characterization of firefly nuptial gifts: a multi-omics approach sheds light on postcopulatory sexual selection. 2016 , 6, 38556	9
1443	Exploiting the great potential of Sequence Capture data by a new tool, SUPER-CAP. 2017 , 24, 81-91	6
1442	Draft Genome Sequence of <i>Microcystis aeruginosa</i> NIES-98, a Non-Microcystin-Producing Cyanobacterium from Lake Kasumigaura, Japan. 2016 , 4,	6
1441	Digital detection of endonuclease mediated gene disruption in the HIV provirus. 2016 , 6, 20064	18
1440	Identification of Tissue-Specific Protein-Coding and Noncoding Transcripts across 14 Human Tissues Using RNA-seq. 2016 , 6, 28400	28
1439	Having a BLAST: Searchable transcriptome resources for the gilthead sea bream and the European sea bass. 2016 , 30, 67-71	10
1438	Metagenomic profiling of historic Colorado Front Range flood impact on distribution of riverine antibiotic resistance genes. 2016 , 6, 38432	41
1437	Host genome integration and giant virus-induced reactivation of the virophage mavirus. 2016 , 540, 288-291	76

1436	Draft Genome Sequence of the Yeast <i>Saccharomyces cerevisiae</i> GUJ105 From Gujarat, India. 2016 , 4,	1
1435	Single-cell sequencing maps gene expression to mutational phylogenies in PDGF- and EGF-driven gliomas. 2016 , 12, 889	67
1434	Draft Genome Sequences of 15 Isolates of <i>Listeria monocytogenes</i> Serotype 1/2a, Subgroup ST204. 2016 , 4,	7
1433	Somatic retrotransposition is infrequent in glioblastomas. 2016 , 7, 22	12
1432	Transcriptional network in ovarian cancer cell line SKOV3 treated with <i>Pinellia pedatisecta</i> Schott extract. 2016 , 36, 462-70	6
1431	Transcriptome sequencing wide functional analysis of human mesenchymal stem cells in response to TLR4 ligand. 2016 , 6, 30311	19
1430	KDM5 lysine demethylases are involved in maintenance of 3'UTR length. 2016 , 2, e1501662	16
1429	Global transcriptional analysis suggests <i>Lasiodiplodia theobromae</i> pathogenicity factors involved in modulation of grapevine defensive response. 2016 , 17, 615	33
1428	Transcriptome sequencing and simple sequence repeat marker development for three Macaronesian endemic plant species. 2016 , 4, 1600050	13
1427	Exploring genomic databases for in silico discovery of Pht1 genes in high syntenic close related grass species with focus in sugarcane (<i>Saccharum</i> spp.). 2016 , 6, 11-18	1
1426	Transcriptome profiling of equine vitamin E deficient neuroaxonal dystrophy identifies upregulation of liver X receptor target genes. 2016 , 101, 261-271	23
1425	Draft Genome Sequence of the Anaerobic Ammonium-Oxidizing Bacterium " <i>Candidatus Brocadia</i> sp. 40". 2016 , 4,	16
1424	Dataset for a de novo transcriptome assembly, utilized for defining the voltage-gated like ion channel superfamily. 2016 , 9, 1044-1047	9
1423	Two novel viruses associated with the <i>Apis mellifera</i> pathogenic mite <i>Varroa destructor</i> . 2016 , 6, 37710	30
1422	Global Analysis and Comparison of the Transcriptomes and Proteomes of Group A Biofilms. 2016 , 1,	20
1421	Development of microsatellite genetic markers in Siberian stone pine (<i>Pinus sibirica</i> Du Tour) based on the de novo whole genome sequencing. 2016 , 52, 1263-1271	6
1420	Draft Genome Sequence of <i>Hydrotalea flava</i> Strain CCUG 51397T. 2016 , 4,	4
1419	Heterotypic mouse models of canine osteosarcoma recapitulate tumor heterogeneity and biological behavior. 2016 , 9, 1435-1444	10

1418	MetaDP: a comprehensive web server for disease prediction of 16S rRNA metagenomic datasets. 2016 , 2, 106-115	6
1417	Expansion and diversification of the MSDIN family of cyclic peptide genes in the poisonous agarics <i>Amanita phalloides</i> and <i>A. bisporigera</i> . 2016 , 17, 1038	28
1416	Gene Family Evolution Reflects Adaptation to Soil Environmental Stressors in the Genome of the Collembolan <i>Orchesella cincta</i> . 2016 , 8, 2106-17	43
1415	Evolution of mitochondrial genomes in Baikalian amphipods. 2016 , 17, 1016	24
1414	Construction and Annotation of a High Density SNP Linkage Map of the Atlantic Salmon (<i>Salmo salar</i>) Genome. 2016 , 6, 2173-9	33
1413	Live single-cell laser tag. 2016 , 7, 11636	14
1412	Transcriptomic evidence for modulation of host inflammatory responses during febrile <i>Plasmodium falciparum</i> malaria. 2016 , 6, 31291	43
1411	Localisation and origin of the bacteriochlorophyll-derived photosensitizer in the retina of the deep-sea dragon fish <i>Malacosteus niger</i> . 2016 , 6, 39395	9
1410	Draft Genome Sequence of <i>Clostridium</i> sp. Strain W14A Isolated from a Cellulose-Degrading Biofilm in a Landfill Leachate Microcosm. 2016 , 4,	3
1409	Expansion of the molecular and morphological diversity of Acanthamoebidae (Centramoebida, Amoebozoa) and identification of a novel life cycle type within the group. 2016 , 11, 69	41
1408	Somatic genomic alterations in retinoblastoma beyond RB1 are rare and limited to copy number changes. 2016 , 6, 25264	49
1407	Gene expression profiling of flax (<i>Linum usitatissimum</i> L.) under edaphic stress. 2016 , 16, 237	31
1406	High-throughput analysis of the satellitome illuminates satellite DNA evolution. 2016 , 6, 28333	114
1405	Whole genome sequencing in cats, identifies new models for blindness in <i>AiPL1</i> and somite segmentation in <i>HES7</i> . 2016 , 17, 265	31
1404	The Next Generation Sequencing and Applications in Clinical Research. 2016 , 83-113	
1403	Animal Coronaviruses. 2016 ,	3
1402	A comprehensive study of the genetic impact of rare variants in <i>SORL1</i> in European early-onset Alzheimer's disease. 2016 , 132, 213-224	62
1401	Microbial activity in forest soil reflects the changes in ecosystem properties between summer and winter. 2016 , 18, 288-301	231

1400	Cytokinin-induced promotion of root meristem size in the fern <i>Azolla</i> supports a shoot-like origin of euphyllophyte roots. 2016 , 209, 705-20	39
1399	Genome-wide SNP discovery in the annual herb, <i>Lasthenia fremontii</i> (Asteraceae): genetic resources for the conservation and restoration of a California vernal pool endemic. 2016 , 8, 145-158	7
1398	Sorting out relationships among the grouse and ptarmigan using intron, mitochondrial, and ultra-conserved element sequences. 2016 , 98, 123-32	27
1397	Substrate preference, uptake kinetics and bioenergetics in a facultatively autotrophic, thermoacidophilic crenarchaeote. 2016 , 92, fiw069	5
1396	Assessing models of speciation under different biogeographic scenarios; an empirical study using multi-locus and RNA-seq analyses. 2016 , 6, 379-96	5
1395	Transcriptomic and epigenomic characterization of the developing bat wing. 2016 , 48, 528-36	45
1394	Plastid genomes reveal support for deep phylogenetic relationships and extensive rate variation among palms and other commelinid monocots. 2016 , 209, 855-70	124
1393	Paratransgenesis to control malaria vectors: a semi-field pilot study. 2016 , 9, 140	46
1392	Static and Dynamic Factors Limit Chromosomal Replication Complexity in <i>Escherichia coli</i> , Avoiding Dangers of Runaway Overreplication. 2016 , 202, 945-60	17
1391	Biological, physicochemical and plant health responses in lettuce and strawberry in soil or peat amended with biochar. 2016 , 107, 1-12	87
1390	Draft genome sequence of the docosahexaenoic acid producing thraustochytrid <i>Aurantiochytrium</i> sp. T66. 2016 , 8, 115-6	27
1389	Comparison of microbial DNA enrichment tools for metagenomic whole genome sequencing. 2016 , 127, 141-145	78
1388	DIANA-mirExTra v2.0: Uncovering microRNAs and transcription factors with crucial roles in NGS expression data. 2016 , 44, W128-34	35
1387	Deeper insight into the structure of the anaerobic digestion microbial community; the biogas microbiome database is expanded with 157 new genomes. 2016 , 216, 260-6	93
1386	Identification of lymphocytic choriomeningitis mammarenavirus in house mouse (<i>Mus musculus</i> , Rodentia) in French Guiana. 2016 , 37, 225-30	7
1385	Differential expression of photosynthesis-related genes and quantification of gas exchange in rice plants under abiotic stress. 2016 , 38, 1	9
1384	Whole-organism lineage tracing by combinatorial and cumulative genome editing. 2016 , 353, aaf7907	409
1383	Low temperature treatment of domestic wastewater by purple phototrophic bacteria: Performance, activity, and community. 2016 , 100, 537-545	64

1382	Morphological Convergence Between an Allopolyploid and One of its Parental Species Correlates with Biased Gene Expression and DNA Loss. 2016 , 107, 445-54	6
1381	First Insights into the Genome Sequence of the Halophilic Archaeon <i>Halalkalicoccus paucihalophilus</i> (DSM 24557). 2016 , 4,	0
1380	Metagenomic analysis between free-living and cultured <i>Epinephelus fuscoguttatus</i> under different environmental conditions in Indonesian waters. 2016 , 110, 726-34	10
1379	Phylogeographic and population genetic analyses reveal multiple species of <i>Boa</i> and independent origins of insular dwarfism. 2016 , 102, 104-16	32
1378	Rapid Drug Susceptibility Testing of Drug-Resistant <i>Mycobacterium tuberculosis</i> Isolates Directly from Clinical Samples by Use of Amplicon Sequencing: a Proof-of-Concept Study. 2016 , 54, 2058-67	55
1377	The transcriptional regulator <i>c2h2</i> accelerates mushroom formation in <i>Agaricus bisporus</i> . 2016 , 100, 7151-9	29
1376	Characterization of the complete mitochondrial genome of the Yunnan endemic grasshopper <i>Yunnanacris yunnaneus</i> (Insecta: Orthoptera: Acrididae). 2016 , 8, 267-270	1
1375	Genetic distance of inbred lines of Chinese cabbage and its relationship to heterosis. 2016 , 5, 1-7	36
1374	Phylogenomics, biogeography and diversification of obligate mealybug-tending ants in the genus <i>Acropyga</i> . 2016 , 102, 20-9	46
1373	Gene expression changes in damaged osteoarthritic cartilage identify a signature of non-chondrogenic and mechanical responses. 2016 , 24, 1431-40	64
1372	A transcriptome resource for the Antarctic pteropod <i>Limacina helicina antarctica</i> . 2016 , 28, 25-28	16
1371	Advances in DNA metabarcoding for food and wildlife forensic species identification. 2016 , 408, 4615-30	111
1370	Genomic insights into members of the candidate phylum Hyd24-12 common in mesophilic anaerobic digesters. 2016 , 10, 2352-64	31
1369	Untangling the Effect of Fatty Acid Addition at Species Level Revealed Different Transcriptional Responses of the Biogas Microbial Community Members. 2016 , 50, 6079-90	54
1368	Evaluation of Molecular Methods for Serotyping <i>Shigella flexneri</i> . 2016 , 54, 1456-1461	26
1367	Data set for transcriptional response to depletion of the <i>Shoc2</i> scaffolding protein. 2016 , 7, 770-8	4
1366	Susceptibility to chlorhexidine amongst multidrug-resistant clinical isolates of <i>Staphylococcus epidermidis</i> from bloodstream infections. 2016 , 48, 86-90	30
1365	Regulation of Meristem Morphogenesis by Cell Wall Synthases in <i>Arabidopsis</i> . 2016 , 26, 1404-15	61

1364	Targeted virus detection in next-generation sequencing data using an automated e-probe based approach. 2016 , 495, 122-8	18
1363	Domestic wastewater treatment with purple phototrophic bacteria using a novel continuous photo anaerobic membrane bioreactor. 2016 , 100, 486-495	125
1362	The Proteasome Stress Regulon Is Controlled by a Pair of NAC Transcription Factors in Arabidopsis. 2016 , 28, 1279-96	47
1361	Measurements of Intrahost Viral Diversity Are Extremely Sensitive to Systematic Errors in Variant Calling. 2016 , 90, 6884-95	74
1360	Transcriptomic and proteomic analyses provide new insights into the regulation mechanism of low-temperature-induced leafy head formation in Chinese cabbage. 2016 , 144, 1-10	20
1359	Transcriptomics provides insight into <i>Mytilus galloprovincialis</i> (Mollusca: Bivalvia) mantle function and its role in biomineralisation. 2016 , 27, 37-45	31
1358	Next-Generation Sequencing for Porcine Coronaviruses. 2016 , 209-216	1
1357	Transcriptomic features associated with energy production in the muscles of Pacific bluefin tuna and Pacific cod. 2016 , 80, 1114-24	5
1356	Chromosome-scale shotgun assembly using an in vitro method for long-range linkage. 2016 , 26, 342-50	415
1355	Characterization of the complete mitochondrial genome of the myrmicine ant <i>Vollenhovia emeryi</i> (Insecta: Hymenoptera: Formicidae). 2016 , 8, 211-214	7
1354	Draft Genome Sequences of <i>Streptococcus pneumoniae</i> with High-Level Resistance to Respiratory Fluoroquinolones. 2016 , 4,	0
1353	Bivalve-specific gene expansion in the pearl oyster genome: implications of adaptation to a sessile lifestyle. 2016 , 2, 3	95
1352	Genome sequencing of <i>Metrosideros polymorpha</i> (Myrtaceae), a dominant species in various habitats in the Hawaiian Islands with remarkable phenotypic variations. 2016 , 129, 727-736	10
1351	Phylogenomic analyses reveal novel relationships among snake families. 2016 , 100, 160-169	40
1350	Differential DNA repair underlies mutation hotspots at active promoters in cancer genomes. 2016 , 532, 259-63	138
1349	Complete Genome Sequence of a Human Cytomegalovirus Strain AD169 Bacterial Artificial Chromosome Clone. 2016 , 4,	6
1348	<i>Mycobacterium tuberculosis</i> whole genome sequencing and protein structure modelling provides insights into anti-tuberculosis drug resistance. 2016 , 14, 31	77
1347	Gut microbiome remodeling induces depressive-like behaviors through a pathway mediated by the host's metabolism. 2016 , 21, 786-96	888

1346	Dosage Compensation in the African Malaria Mosquito <i>Anopheles gambiae</i> . 2016 , 8, 411-25	25
1345	Ochratoxin A production by <i>Penicillium thymicola</i> . 2016 , 120, 1041-1049	13
1344	Microbiome analysis and detection of pathogenic bacteria of <i>Penaeus monodon</i> from Jakarta Bay and Bali. 2016 , 110, 718-25	13
1343	Transcriptome profiling in fast versus slow-growing rainbow trout across seasonal gradients. 2016 , 17, 60	29
1342	Does Choice Matter? Reference-Based Alignment for Molecular Epidemiology of Tuberculosis. 2016 , 54, 1891-1895	20
1341	The Genome and Methylome of a Subsocial Small Carpenter Bee, <i>Ceratina calcarata</i> . 2016 , 8, 1401-10	45
1340	The Atlantic salmon genome provides insights into rediploidization. 2016 , 533, 200-5	606
1339	Benefit of transferred mutations is better predicted by the fitness of recipients than by their ecological or genetic relatedness. 2016 , 113, 5047-52	24
1338	Antibiotic treatment enhances the genome-wide mutation rate of target cells. 2016 , 113, E2498-505	104
1337	Detection of the plasmid-mediated <i>mcr-1</i> gene conferring colistin resistance in human and food isolates of <i>Salmonella enterica</i> and <i>Escherichia coli</i> in England and Wales. 2016 , 71, 2300-5	197
1336	RNA-seq analysis in forest tree species: bioinformatic problems and solutions. 2016 , 12, 1	20
1335	CRISPR/Cas9-Derived Mutations Both Inhibit HIV-1 Replication and Accelerate Viral Escape. 2016 , 15, 481-489	171
1334	Comparing human and macaque placental transcriptomes to disentangle preterm birth pathology from gestational age effects. 2016 , 41, 74-82	14
1333	Genome Sequence of <i>Bacillus subtilis</i> Strain HUK15, Isolated from Hexachlorocyclohexane-Contaminated Soil. 2016 , 4,	3
1332	Genome Sequence of <i>Pseudomonas</i> sp. HUK17, Isolated from Hexachlorocyclohexane-Contaminated Soil. 2016 , 4,	1
1331	Genome analysis of the sugar beet pathogen <i>Rhizoctonia solani</i> AG2-2IIIB revealed high numbers in secreted proteins and cell wall degrading enzymes. 2016 , 17, 245	52
1330	Gene expression profiling of microbial activities and interactions in sediments under haloclines of E. Mediterranean deep hypersaline anoxic basins. 2016 , 10, 2643-2657	24
1329	Post-weaning blood transcriptomic differences between Yorkshire pigs divergently selected for residual feed intake. 2016 , 17, 73	18

1328	Accurate Profiling of Gene Expression and Alternative Polyadenylation with Whole Transcriptome Termini Site Sequencing (WTTS-Seq). 2016 , 203, 683-97	20
1327	Genome-wide analysis of superoxide dismutase gene family in <i>Gossypium raimondii</i> and <i>G. arboreum</i> . 2016 , 6, 18-29	34
1326	<i>Vibrio</i> elicits targeted transcriptional responses from copepod hosts. 2016 , 92, fiw072	16
1325	Multi-omics maps of cotton fibre reveal epigenetic basis for staged single-cell differentiation. 2016 , 44, 4067-79	33
1324	Genomic analysis and D-xylose fermentation of three novel <i>Spathaspora</i> species: <i>Spathaspora girioi</i> sp. nov., <i>Spathaspora hagerdaliae</i> f. a., sp. nov. and <i>Spathaspora gorwiae</i> f. a., sp. nov. 2016 , 16,	31
1323	Integrated analysis of miRNA and mRNA expression profiles in tilapia gonads at an early stage of sex differentiation. 2016 , 17, 328	56
1322	Colistin resistance in <i>Salmonella</i> and <i>Escherichia coli</i> isolates from a pig farm in Great Britain. 2016 , 71, 2306-13	97
1321	RNA-seq analysis of early enteromyxosis in turbot (<i>Scophthalmus maximus</i>): new insights into parasite invasion and immune evasion strategies. 2016 , 46, 507-17	36
1320	Genome-wide identification of novel genetic markers from RNA sequencing assembly of diverse <i>Aegilops tauschii</i> accessions. 2016 , 291, 1681-94	16
1319	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. 2016 , 352, 565-9	929
1318	Ultra-deep and quantitative saliva proteome reveals dynamics of the oral microbiome. 2016 , 8, 44	122
1317	Genotype imputation in the domestic dog. 2016 , 27, 485-94	30
1316	Comparative transcriptome analysis of <i>Gastrodia elata</i> (Orchidaceae) in response to fungus symbiosis to identify gastrodin biosynthesis-related genes. 2016 , 17, 212	26
1315	Complete genome sequence of nucleoside producing strain <i>Corynebacterium stationis</i> ATCC 6872. 2016 , 225, 57-8	1
1314	CRISPR-directed mitotic recombination enables genetic mapping without crosses. 2016 , 352, 1113-6	62
1313	Proyl-4 Hydroxylase 2 (PHD2) Deficiency in Endothelial Cells and Hematopoietic Cells Induces Obliterative Vascular Remodeling and Severe Pulmonary Arterial Hypertension in Mice and Humans Through Hypoxia-Inducible Factor-2. 2016 , 133, 2447-58	122
1312	Comparative Transcriptomics Indicates a Role for SHORT VEGETATIVE PHASE (SVP) Genes in <i>Mimulus guttatus</i> Vernalization Response. 2016 , 6, 1239-49	4
1311	AtWRKY22 promotes susceptibility to aphids and modulates salicylic acid and jasmonic acid signalling. 2016 , 67, 3383-96	62

1310	Independent and Parallel Evolution of New Genes by Gene Duplication in Two Origins of C4 Photosynthesis Provides New Insight into the Mechanism of Phloem Loading in C4 Species. 2016 , 33, 1796-806	38
1309	Regulatory Differences in Natal Down Development between Altricial Zebra Finch and Precocial Chicken. 2016 , 33, 2030-43	10
1308	Microsatellite markers for the notothenioid fish <i>Lepidonotothen nudifrons</i> and two congeneric species. 2016 , 9, 238	3
1307	Activation of Plasmacytoid Dendritic Cells in Colon-Draining Lymph Nodes during <i>Citrobacter rodentium</i> Infection Involves Pathogen-Sensing and Inflammatory Pathways Distinct from Conventional Dendritic Cells. 2016 , 196, 4750-9	7
1306	Associations between transcriptional changes and protein phenotypes provide insights into immune regulation in corals. 2016 , 62, 17-28	24
1305	Metagenomic analysis of rapid gravity sand filter microbial communities suggests novel physiology of <i>Nitrospira</i> spp. 2016 , 10, 2569-2581	137
1304	Complete Genome Sequence of Porcine Epidemic Diarrhea Virus Strain COL/Cundinamarca/2014 from Colombia. 2016 , 4,	6
1303	Non contiguous-finished genome sequence and description of <i>Microbacterium gorillae</i> sp. nov. 2016 , 11, 32	12
1302	Another look at the phylogenetic position of the grape order Vitales: Chloroplast phylogenomics with an expanded sampling of key lineages. 2016 , 101, 216-223	22
1301	miR-135b, a key regulator of malignancy, is linked to poor prognosis in human myxoid liposarcoma. 2016 , 35, 6177-6188	32
1300	Candidate gene networks and blood biomarkers of methamphetamine-associated psychosis: an integrative RNA-sequencing report. 2016 , 6, e802	22
1299	High-throughput cis-regulatory element discovery in the vector mosquito <i>Aedes aegypti</i> . 2016 , 17, 341	18
1298	An automated approach for global identification of sRNA-encoding regions in RNA-Seq data from <i>Mycobacterium tuberculosis</i> . 2016 , 48, 544-53	11
1297	SeqPurge: highly-sensitive adapter trimming for paired-end NGS data. 2016 , 17, 208	71
1296	Genetic engineering in <i>Actinoplanes</i> sp. SE50/110 - development of an intergeneric conjugation system for the introduction of actinophage-based integrative vectors. 2016 , 232, 79-88	13
1295	Characterization of the mantle transcriptome in bivalves: <i>Pecten maximus</i> , <i>Mytilus edulis</i> and <i>Crassostrea gigas</i> . 2016 , 27, 9-15	34
1294	No evidence for mitochondrial genetic variability in the largest population of critically endangered Tonkin snub-nosed monkeys in Vietnam. 2016 , 57, 449-53	3
1293	Syllidae mitochondrial gene order is unusually variable for Annelida. 2016 , 594, 89-96	13

1292	Epithelial Expression of Human ABO Blood Group Genes Is Dependent upon a Downstream Regulatory Element Functioning through an Epithelial Cell-specific Transcription Factor, Elf5. 2016 , 291, 22594-22606	9
1291	The influence of trematode parasite burden on gene expression in a mammalian host. 2016 , 17, 600	4
1290	De novo transcriptome assembly and identification of the gene conferring a "pandan-like" aroma in coconut (<i>Cocos nucifera</i> L.). 2016 , 252, 324-334	29
1289	An essential role for the IL-2 receptor in T cell function. 2016 , 17, 1322-1333	379
1288	Oligotrophic lagoons of the South Pacific Ocean are home to a surprising number of novel eukaryotic microorganisms. 2016 , 18, 4549-4563	15
1287	Distinctive gut microbial community structure in both the wild and farmed Swan goose (<i>Anser cygnoides</i>). 2016 , 56, 1299-1307	25
1286	Up-regulation of carbon metabolism-related glyoxylate cycle and toxin production in <i>Beauveria bassiana</i> JEF-007 during infection of bean bug, <i>Riptortus pedestris</i> (Hemiptera: Alydidae). 2016 , 120, 1236-48	14
1285	Truncation of Gal4p explains the inactivation of the GAL/MEL regulon in both <i>Saccharomyces bayanus</i> and some <i>Saccharomyces cerevisiae</i> wine strains. 2016 , 16,	3
1284	Stronger sink demand for metabolites supports dominance of the apical bud in etiolated growth. 2016 , 67, 5495-5508	10
1283	From FASTQ to Function: In Silico Methods for Processing Next-Generation Sequencing Data. 2016 , 1476, 23-33	1
1282	Complete Sequencing of Plasmids Containing blaOXA-163 and blaOXA-48 in <i>Escherichia coli</i> Sequence Type 131. 2016 , 60, 6948-6951	14
1281	A Primer on Infectious Disease Bacterial Genomics. 2016 , 29, 881-913	26
1280	Structure of an N276-Dependent HIV-1 Neutralizing Antibody Targeting a Rare V5 Glycan Hole Adjacent to the CD4 Binding Site. 2016 , 90, 10220-10235	21
1279	The photomorphogenic factors UV-B RECEPTOR 1, ELONGATED HYPOCOTYL 5, and HY5 HOMOLOGUE are part of the UV-B signalling pathway in grapevine and mediate flavonol accumulation in response to the environment. 2016 , 67, 5429-5445	64
1278	Multi-locus Analyses Reveal Four Giraffe Species Instead of One. 2016 , 26, 2543-2549	125
1277	Genomic Landscape of Intrahost Variation in Group A <i>Streptococcus</i> : Repeated and Abundant Mutational Inactivation of the fabT Gene Encoding a Regulator of Fatty Acid Synthesis. 2016 , 84, 3268-3281	13
1276	Domestication and Divergence of <i>Saccharomyces cerevisiae</i> Beer Yeasts. 2016 , 166, 1397-1410.e16	332
1275	In vitro analysis of partially hydrolyzed guar gum fermentation on identified gut microbiota. 2016 , 42, 60-66	14

1274	Complementary feature selection from alternative splicing events and gene expression for phenotype prediction. <i>Bioinformatics</i> , 2016 , 32, i421-i429	7.2	8
1273	Complete genome sequencing and comparative analyses of broad-spectrum antimicrobial-producing <i>Micromonospora</i> sp. HK10. 2016 , 594, 97-107		7
1272	Identifying Centromeric RNAs Involved in Histone Dynamics In Vivo. 2016 , 573, 445-66		3
1271	A Single-Cell Transcriptomic Map of the Human and Mouse Pancreas Reveals Inter- and Intra-cell Population Structure. 2016 , 3, 346-360.e4		614
1270	West African <i>Anopheles gambiae</i> mosquitoes harbor a taxonomically diverse virome including new insect-specific flaviviruses, mononegaviruses, and totiviruses. 2016 , 498, 288-299		79
1269	Causes and consequences of large clonal assemblies in a poplar hybrid zone. 2016 , 25, 5330-5344		6
1268	Deep metagenome and metatranscriptome analyses of microbial communities affiliated with an industrial biogas fermenter, a cow rumen, and elephant feces reveal major differences in carbohydrate hydrolysis strategies. 2016 , 9, 121		82
1267	A timecourse analysis of systemic and gonadal effects of temperature on sexual development of the red-eared slider turtle <i>Trachemys scripta elegans</i> . 2016 , 420, 166-177		56
1266	Noninvasive chromosome screening of human embryos by genome sequencing of embryo culture medium for in vitro fertilization. 2016 , 113, 11907-11912		107
1265	Aerobic glycolysis promotes T helper 1 cell differentiation through an epigenetic mechanism. 2016 , 354, 481-484		367
1264	De-novo transcriptome assembly for gene identification, analysis, annotation, and molecular marker discovery in <i>Onobrychis viciifolia</i> . 2016 , 17, 756		28
1263	Repression of p63 and induction of EMT by mutant Ras in mammary epithelial cells. 2016 , 113, E6107-E6116		33
1262	Draft genome sequence of an inbred line of <i>Chenopodium quinoa</i> , an allotetraploid crop with great environmental adaptability and outstanding nutritional properties. 2016 , 23, 535-546		58
1261	Design of the MCAW compute service for food safety bioinformatics. 2016 , 60, 2:1-2:12		4
1260	SAMSA: a comprehensive metatranscriptome analysis pipeline. 2016 , 17, 399		39
1259	Proteogenomics. 2016 ,		
1258	The effect of host genetics on the gut microbiome. 2016 , 48, 1407-1412		434
1257	Comprehensive evaluation of de novo transcriptome assembly programs and their effects on differential gene expression analysis. <i>Bioinformatics</i> , 2017 , 33, 327-333	7.2	41

1256	EpiRADseq: scalable analysis of genomewide patterns of methylation using next-generation sequencing. 2016 , 7, 60-69	50
1255	Proteogenomics: Key Driver for Clinical Discovery and Personalized Medicine. 2016 , 926, 21-47	13
1254	Differential cytokine sensitivities of STAT5-dependent enhancers rely on Stat5 autoregulation. 2016 , 44, 10277-10291	19
1253	First Draft Genome Sequence of a Mycobacterium gordonae Clinical Isolate. 2016 , 4,	3
1252	Genetic basis for high population diversity in Protea-associated Knoxdaviesia. 2016 , 96, 47-57	11
1251	16S rRNA gene profiling of planktonic and biofilm microbial populations in the Gulf of Guinea using Illumina NGS. 2016 , 122, 105-112	28
1250	A Bacillus anthracis Genome Sequence from the Sverdlovsk 1979 Autopsy Specimens. 2016 , 7,	35
1249	The draft genome sequence and annotation of the desert woodrat Neotoma lepida. 2016 , 9, 58-9	5
1248	Accumulation of transposable elements in Hox gene clusters during adaptive radiation of Anolis lizards. 2016 , 283,	19
1247	Genome Sequence of a Novel Multiple-Antibiotic-Resistant Member of the Erysipelotrichaceae Family Isolated from a Swine Manure Storage Pit. 2016 , 4,	3
1246	Accounting for Uncertainty in Gene Tree Estimation: Summary-Coalescent Species Tree Inference in a Challenging Radiation of Australian Lizards. 2017 , 66, 352-366	40
1245	De Novo Truncating Variants in ASXL2 Are Associated with a Unique and Recognizable Clinical Phenotype. 2016 , 99, 991-999	42
1244	Cyanotoxin degradation activity and mlr gene expression profiles of a Sphingopyxis sp. isolated from Lake Champlain, Canada. 2016 , 18, 1417-1426	18
1243	Genomic imprinting, disrupted placental expression, and speciation. 2016 , 70, 2690-2703	17
1242	De novo assembly and transcriptome characterization of spruce dwarf mistletoe Arceuthobium sichuanense uncovers gene expression profiling associated with plant development. 2016 , 17, 771	15
1241	Picodroplet partitioned whole genome amplification of low biomass samples preserves genomic diversity for metagenomic analysis. 2016 , 4, 52	13
1240	Genome-wide association analysis identifies variation in vitamin D receptor and other host factors influencing the gut microbiota. 2016 , 48, 1396-1406	369
1239	NOD2-RIP2-Mediated Signaling Helps Shape Adaptive Immunity in Visceral Leishmaniasis. 2016 , 214, 1647-1657	14

1238	Ionizing Radiation Potentiates High-Fat Diet-Induced Insulin Resistance and Reprograms Skeletal Muscle and Adipose Progenitor Cells. 2016 , 65, 3573-3584	25
1237	Characterization of <i>Pseudomonas aeruginosa</i> phage K5 genome and identification of its receptor related genes. 2016 , 56, 1344-1353	10
1236	<i>Vibrio barjaei</i> sp. nov., a new species of the Mediterranei clade isolated in a shellfish hatchery. 2016 , 39, 553-556	3
1235	KlebSeq, a Diagnostic Tool for Surveillance, Detection, and Monitoring of <i>Klebsiella pneumoniae</i> . 2016 , 54, 2582-96	26
1234	Analysis RNA-seq and Noncoding RNA. 2016 , 1480, 125-35	14
1233	Complete Genome Sequences of 17 Rapidly Growing Nontuberculous Mycobacterial Strains. 2016 , 4,	2
1232	ChIP-seq Data Processing for PcG Proteins and Associated Histone Modifications. 2016 , 1480, 37-53	1
1231	Insertion sequence-caused large-scale rearrangements in the genome of <i>Escherichia coli</i> . 2016 , 44, 7109-19	49
1230	Nuclear Innate Immune DNA Sensor IFI16 Is Degraded during Lytic Reactivation of Kaposi's Sarcoma-Associated Herpesvirus (KSHV): Role of IFI16 in Maintenance of KSHV Latency. 2016 , 90, 8822-41	43
1229	Contrasting Levels of Molecular Evolution on the Mouse X Chromosome. 2016 , 203, 1841-57	16
1228	Recurrent selection explains parallel evolution of genomic regions of high relative but low absolute differentiation in a ring species. 2016 , 25, 4488-507	55
1227	Rare Spontaneous Loss of Multiresistance Gene Carrying IncI/ST12 Plasmid in <i>Escherichia coli</i> in Pig Microbiota. 2016 , 60, 6046-9	4
1226	Genome sequence analysis of two South African isolates of Moroccan watermelon mosaic virus infecting cucurbits. 2016 , 52, 896-899	6
1225	On the study of microbial transcriptomes using second- and third-generation sequencing technologies. 2016 , 54, 527-36	9
1224	Alternative haplotypes of antigen processing genes in zebrafish diverged early in vertebrate evolution. 2016 , 113, E5014-23	31
1223	Does adaptive radiation of a host lineage promote ecological diversity of its bacterial communities? A test using gut microbiota of <i>Anolis</i> lizards. 2016 , 25, 4793-804	34
1222	Sequence capture using RAD probes clarifies phylogenetic relationships and species boundaries in <i>Primula</i> sect. <i>Auricula</i> . 2016 , 104, 60-72	20
1221	Pharmacological properties of microneurotrophin drugs developed for treatment of amyotrophic lateral sclerosis. 2016 , 117, 68-77	18

1220	A Phylogenomic Framework to Study the Diversity and Evolution of Stramenopiles (=Heterokonts). 2016 , 33, 2890-2898	85
1219	Specific alleles at immune genes, rather than genome-wide heterozygosity, are related to immunity and survival in the critically endangered Attwater's prairie-chicken. 2016 , 25, 4730-44	42
1218	The developmental transcriptome atlas of the biofuel crop <i>Camelina sativa</i> . 2016 , 88, 879-894	42
1217	Evaluation of artificial selection in Standard Poodles using whole-genome sequencing. 2016 , 27, 599-609	10
1216	Characterization of Acr2, an H-NS-like protein encoded on A/C2-type plasmids. 2016 , 87-88, 17-27	14
1215	High-Throughput Sequencing of Complete Mitochondrial Genomes. 2016 , 1452, 45-64	8
1214	Phylogenomics Using Transcriptome Data. 2016 , 1452, 65-80	1
1213	Capture-based next-generation sequencing reveals multiple actionable mutations in cancer patients failed in traditional testing. 2016 , 4, 262-72	9
1212	Tales from the crypt: genome mining from fungarium specimens improves resolution of the mushroom tree of life. 2016 , 117, 11-32	52
1211	Herbarium genomics: plastome sequence assembly from a range of herbarium specimens using an Iterative Organelle Genome Assembly pipeline. 2016 , 117, 33-43	85
1210	Transgenerational effects persist down the maternal line in marine sticklebacks: gene expression matches physiology in a warming ocean. 2016 , 9, 1096-1111	59
1209	Evolutionary conservation of candidate osmoregulation genes in plant phloem sap-feeding insects. 2016 , 25, 251-8	14
1208	Moleculo Long-Read Sequencing Facilitates Assembly and Genomic Binning from Complex Soil Metagenomes. 2016 , 1,	51
1207	Raman spectroscopy detects phenotypic differences among <i>Escherichia coli</i> enriched for 1-butanol tolerance using a metagenomic DNA library. 2016 , 11, 877-89	9
1206	Transcriptome response to infraorbital nerve transection in the gonadally intact male rat barrel cortex: RNA-seq. 2016 , 524, 152-9	1
1205	Elucidating and mining the <i>Tulipa</i> and <i>Lilium</i> transcriptomes. 2016 , 92, 249-61	15
1204	Ecological speciation in sympatric palms: 1. Gene expression, selection and pleiotropy. 2016 , 29, 1472-87	19
1203	Analysis of Illumina MiSeq Metabarcoding Data: Application to Benthic Indices for Environmental Monitoring. 2016 , 1452, 237-49	10

1202	Characterization of circular RNAs landscape in multiple system atrophy brain. 2016 , 139, 485-496	62
1201	Comparative transcriptomics of rice plants under cold, iron, and salt stresses. 2016 , 16, 567-79	28
1200	Transmission of Drug-Resistant Leprosy in Guinea-Conakry Detected Using Molecular Epidemiological Approaches. 2016 , 63, 1482-1484	20
1199	Living apart together: crosstalk between the core and supernumerary genomes in a fungal plant pathogen. 2016 , 17, 670	41
1198	Healthy human gut phageome. 2016 , 113, 10400-5	316
1197	Repeated replacement of an intrabacterial symbiont in the tripartite nested mealybug symbiosis. 2016 , 113, E5416-24	133
1196	β Integrin Expression and Activation of TGF- β by Intestinal Dendritic Cells Are Determined by Both Tissue Microenvironment and Cell Lineage. 2016 , 197, 1968-78	40
1195	Role of Wax Ester Synthase/Acyl Coenzyme A:Diacylglycerol Acyltransferase in Oleaginous <i>Streptomyces</i> sp. Strain G25. 2016 , 82, 5969-81	12
1194	The Tumor Microenvironment. 2016 ,	3
1193	Conserved but Attenuated Parental Gene Expression in Allopolyploids: Constitutive Zinc Hyperaccumulation in the Allotetraploid <i>Arabidopsis kamchatica</i> . 2016 , 33, 2781-2800	24
1192	First Report of blaIMP-14 on a Plasmid Harboring Multiple Drug Resistance Genes in <i>Escherichia coli</i> Sequence Type 131. 2016 , 60, 5068-71	12
1191	RNA-Seq as a Tool to Study the Tumor Microenvironment. 2016 , 1458, 311-37	6
1190	Bacterial dynamics and functional analysis of microbial metagenomes during ripening of Dutch-type cheese. 2016 , 61, 182-188	27
1189	Hidden histories of gene flow in highland birds revealed with genomic markers. 2016 , 25, 5144-5157	49
1188	Rapid proliferation and nucleolar organizer targeting centromeric retrotransposons in cotton. 2016 , 88, 992-1005	24
1187	The <i>Aspergillus fumigatus</i> SchA kinase modulates Saka MAP kinase activity and it is essential for virulence. 2016 , 102, 642-671	24
1186	Minor intron splicing is regulated by FUS and affected by ALS-associated FUS mutants. 2016 , 35, 1504-21	69
1185	Phylogenetics and biogeography of the dung beetle genus <i>Onthophagus</i> inferred from mitochondrial genomes. 2016 , 105, 86-95	37

1184	RNA-Seq reveals virus-virus and virus-plant interactions in nature. 2016 , 92,	51
1183	Transcriptomic changes in relation to early-life events in the gilthead sea bream (<i>Sparus aurata</i>). 2016 , 17, 506	13
1182	Selecting Hypomethylated Genomic Regions Using MRE-Seq. 2016 , 1482, 83-102	5
1181	Genetic Convergence in the Evolution of Male-Specific Color Patterns in <i>Drosophila</i> . 2016 , 26, 2423-2433	18
1180	First high quality draft genome sequence of a plant growth promoting and cold active enzyme producing psychrotrophic <i>Arthrobacter agilis</i> strain L77. 2016 , 11, 54	68
1179	Gld2-catalyzed 3' monoadenylation of miRNAs in the hippocampus has no detectable effect on their stability or on animal behavior. 2016 , 22, 1492-9	18
1178	Characterization of the complete mitochondrial genome of the Asian planthopper <i>Ricania speculum</i> (Hemiptera: Fulgoroidea: Ricanidae). 2016 , 8, 463-466	12
1177	Genomic Methods Take the Plunge: Recent Advances in High-Throughput Sequencing of Marine Mammals. 2016 , 107, 481-95	40
1176	Regulatory Divergence among Beta-Keratin Genes during Bird Evolution. 2016 , 33, 2769-2780	8
1175	A Galaxy-based bioinformatics pipeline for optimised, streamlined microsatellite development from Illumina next-generation sequencing data. 2016 , 8, 481-486	18
1174	A draft genome of the brown alga, <i>Cladosiphon okamuranus</i> , S-strain: a platform for future studies of 'mozuku' biology. 2016 , 23, 561-570	50
1173	Cooperation between the H3K27me3 Chromatin Mark and Non-CG Methylation in Epigenetic Regulation. 2016 , 172, 1131-1141	28
1172	Dynamic chromatin changes associated with de novo centromere formation in maize euchromatin. 2016 , 88, 854-866	15
1171	Transcriptome comparison reveals a genetic network regulating the lower temperature limit in fish. 2016 , 6, 28952	27
1170	Phytopathogen Genome Announcement: Draft Genome Sequences of 62 <i>Pseudomonas syringae</i> Type and Pathotype Strains. 2016 , 29, 243-6	27
1169	Transcript, protein and metabolite temporal dynamics in the CAM plant Agave. 2016 , 2, 16178	84
1168	Single-stranded DNA library preparation uncovers the origin and diversity of ultrashort cell-free DNA in plasma. 2016 , 6, 27859	105
1167	Gene Expression Profiling in the Hibernating Primate, <i>Cheirogaleus Medius</i> . 2016 , 8, 2413-26	20

1166	Transcriptional Categorization of the Etiology of Pneumonia Syndrome in Pediatric Patients in Malaria-Endemic Areas. 2017 , 215, 312-320	3
1165	Candidate egg case silk genes for the spider <i>Argiope argentata</i> from differential gene expression analyses. 2016 , 25, 757-768	9
1164	Identifying Genetic Signatures of Natural Selection Using Pooled Population Sequencing in <i>Picea abies</i> . 2016 , 6, 1979-89	19
1163	A novel picorna-like virus, <i>Riptortus pedestris</i> virus-1 (RiPV-1), found in the bean bug, <i>R. pedestris</i> , after fungal infection. 2016 , 141, 57-65	8
1162	Toward a new paradigm of DNA writing using a massively parallel sequencing platform and degenerate oligonucleotide. 2016 , 6, 37176	4
1161	Transcriptomic analysis of instinctive and learned reward-related behaviors in honey bees. 2016 , 219, 3554-3561	14
1160	A Comprehensive Characterization of the Function of LincRNAs in Transcriptional Regulation Through Long-Range Chromatin Interactions. 2016 , 6, 36572	16
1159	Doxycycline, metronidazole and isotretinoin: Do they modify microRNA/mRNA expression profiles and function in murine T-cells?. 2016 , 6, 37082	13
1158	Draft Genome Sequence of <i>Robinsoniella peoriensis</i> 6600698, a Confounder of <i>Clostridium difficile</i> Diagnosis. 2016 , 4,	1
1157	Genome Sequences of Two <i>Salmonella enterica</i> Serovar Kentucky Isolates Recovered from Poultry Carcasses in the United States. 2016 , 4,	1
1156	Persistent microbiome alterations modulate the rate of post-dieting weight regain. 2016 , 540, 544-551	269
1155	In-depth comparison of somatic point mutation callers based on different tumor next-generation sequencing depth data. 2016 , 6, 36540	64
1154	Pathogen Infection and MORC Proteins Affect Chromatin Accessibility of Transposable Elements and Expression of Their Proximal Genes in <i>Arabidopsis</i> . 2016 , 29, 674-687	9
1153	HDR: a statistical two-step approach successfully identifies disease genes in autosomal recessive families. 2016 , 61, 959-963	10
1152	<i>Streptomyces thermoautotrophicus</i> does not fix nitrogen. 2016 , 6, 20086	20
1151	The microRNA toolkit of insects. 2016 , 6, 37736	32
1150	Broad histone H3K4me3 domains in mouse oocytes modulate maternal-to-zygotic transition. 2016 , 537, 548-552	311
1149	Transcriptomic Resources for the Rocky Intertidal Blue Mussel <i>Mytilus edulis</i> from the Gulf of Maine. 2016 , 35, 435-465	5

1148	Contrasting elevational diversity patterns for soil bacteria between two ecosystems divided by the treeline. 2016 , 59, 1177-1186	12
1147	Metagenomics as a preliminary screen for antimicrobial bioprospecting. 2016 , 594, 248-258	21
1146	Geographic Population Structure in Epstein-Barr Virus Revealed by Comparative Genomics. 2016 , 8, 3284-3291	23
1145	Ancestral Gene Flow and Parallel Organellar Genome Capture Result in Extreme Phylogenomic Discord in a Lineage of Angiosperms. 2017 , 66, 320-337	65
1144	Near complete genome sequence of the animal feed probiotic, <i>Bacillus amyloliquefaciens</i> H57. 2016 , 11, 60	7
1143	Lost crops of the Incas: Origins of domestication of the Andean pulse crop tarwi, <i>Lupinus mutabilis</i> . 2016 , 103, 1592-606	32
1142	The Deep Origin and Recent Loss of Venom Toxin Genes in Rattlesnakes. 2016 , 26, 2434-2445	83
1141	<i>Xanthomonas campestris attenuates virulence by sensing light through a bacteriophytochrome photoreceptor.</i> 2016 , 17, 1565-1577	41
1140	Complete Mitochondrial Genome Sequence of Sunflower (<i>Helianthus annuus</i> L.). 2016 , 4,	11
1139	Laser capture microdissection microscopy and genome sequencing of the avian malaria parasite, <i>Plasmodium relictum</i> . 2016 , 115, 4503-4510	14
1138	Analysis of <i>C. elegans</i> muscle transcriptome using trans-splicing-based RNA tagging (SRT). 2016 , 44, e156	12
1137	Comprehensive Genome Scale Phylogenetic Study Provides New Insights on the Global Expansion of Chikungunya Virus. 2016 , 90, 10600-10611	59
1136	De Novo Transcriptome Assembly and Sex-Biased Gene Expression in the Cyclical Parthenogenetic <i>Daphnia galeata</i> . 2016 , 8, 3120-3139	25
1135	Proceedings of the 15th Annual UT-KBRIN Bioinformatics Summit 2016 : Cadiz, KY, USA. 8-10 April 2016. 2016 , 17, 297	
1134	Outbreak of Zika Virus Infection, Chiapas State, Mexico, 2015, and First Confirmed Transmission by <i>Aedes aegypti</i> Mosquitoes in the Americas. 2016 , 214, 1349-1356	146
1133	Cortisol-treated zebrafish embryos develop into pro-inflammatory adults with aberrant immune gene regulation. 2016 , 5, 1134-41	38
1132	Marine Genomics. 2016 ,	2
1131	Systematic improvement of amplicon marker gene methods for increased accuracy in microbiome studies. 2016 , 34, 942-9	347

1130	On the origin and evolutionary consequences of gene body DNA methylation. 2016 , 113, 9111-6	189
1129	Rice Varieties in Archaic East Asia: Reduction of Its Diversity from Past to Present Times. 2016 , 33, 2496-505	6
1128	Certified DNA Reference Materials to Compare HER2 Gene Amplification Measurements Using Next-Generation Sequencing Methods. 2016 , 18, 753-761	13
1127	Rapid Evolution of Genomic Imprinting in Two Species of the Brassicaceae. 2016 , 28, 1815-27	53
1126	Metatranscriptomes of oil-contaminated marine coastal sediment affected by oil addition and/or by the bioturbating activity of the marine polychaete <i>Hediste diversicolor</i> : Who are the microbial players?. 2016 , 29, 55-59	3
1125	Phytohormone sensing in the biotrophic fungus <i>Ustilago maydis</i> - the dual role of the transcription factor <i>Rss1</i> . 2016 , 102, 290-305	12
1124	HybPiper: Extracting coding sequence and introns for phylogenetics from high-throughput sequencing reads using target enrichment. 2016 , 4, 1600016	204
1123	Inhibition of spleen tyrosine kinase attenuates IgE-mediated airway contraction and mediator release in human precision cut lung slices. 2016 , 173, 3080-3087	13
1122	MetaG: a graph-based metagenomic gene analysis for big DNA data. 2016 , 5, 1	6
1121	Dietary breadth is positively correlated with venom complexity in cone snails. 2016 , 17, 401	60
1120	Genomic survey sequencing for development and validation of single-locus SSR markers in peanut (<i>Arachis hypogaea</i> L.). 2016 , 17, 420	25
1119	Elucidating and Regulating the Acetoin Production Role of Microbial Functional Groups in Multispecies Acetic Acid Fermentation. 2016 , 82, 5860-8	30
1118	Leveraging Genetic-Background Effects in <i>Saccharomyces cerevisiae</i> To Improve Lignocellulosic Hydrolysate Tolerance. 2016 , 82, 5838-49	16
1117	High-throughput SNP genotyping of historical and modern samples of five bird species via sequence capture of ultraconserved elements. 2016 , 16, 1204-23	23
1116	Transcriptional analysis and adaptive evolution of <i>Escherichia coli</i> strains growing on acetate. 2016 , 100, 7777-85	22
1115	Transcriptome sequencing reveals that LPS-triggered transcriptional responses in established microglia BV2 cell lines are poorly representative of primary microglia. 2016 , 13, 182	68
1114	Here We Are, But Where Do We Go? A Systematic Review of Crustacean Transcriptomic Studies from 2014-2015. 2016 , 56, 1055-1066	16
1113	Climate-mediated adaptation after mainland colonization of an ancestrally subtropical island lizard, <i>Anolis carolinensis</i> . 2016 , 29, 2168-2180	24

1112	The genetics of extreme microgeographic adaptation: an integrated approach identifies a major gene underlying leaf trichome divergence in Yellowstone <i>Mimulus guttatus</i> . 2016 , 25, 5647-5662	25
1111	Osmoadaptative Strategy and Its Molecular Signature in Obligately Halophilic Heterotrophic Protists. 2016 , 8, 2241-58	43
1110	Zucchini shoestring virus: a distinct potyvirus in the papaya ringspot virus cluster. 2016 , 161, 2321-3	5
1109	Receptors are affected by selection with each <i>Bacillus thuringiensis israelensis</i> Cry toxin but not with the full Bti mixture in <i>Aedes aegypti</i> . 2016 , 44, 218-227	12
1108	Rescue of neural crest-derived phenotypes in a zebrafish CHARGE model by Sox10 downregulation. 2016 , 25, 3539-3554	20
1107	Comparison of a Modern and Fossil Pithovirus Reveals Its Genetic Conservation and Evolution. 2016 , 8, 2333-9	24
1106	Genomic Characteristics Behind the Spread of Bacteremic Group A Streptococcus Type emm89 in Finland, 2004-2014. 2016 , 214, 1987-1995	16
1105	Complete Genome Sequences of <i>Bordetella flabilis</i> , <i>Bordetella bronchialis</i> , and " <i>Bordetella pseudohinzii</i> ". 2016 , 4,	6
1104	De Novo Deep Transcriptome Analysis of Medicinal Plants for Gene Discovery in Biosynthesis of Plant Natural Products. 2016 , 576, 19-45	20
1103	ALKBH1-Mediated tRNA Demethylation Regulates Translation. 2016 , 167, 816-828.e16	197
1102	Genome-scale comparison of expanded gene families in <i>Plasmodium ovale wallikeri</i> and <i>Plasmodium ovale curtisi</i> with <i>Plasmodium malariae</i> and with other <i>Plasmodium</i> species. 2016 , 46, 685-96	43
1101	Differentiation of human embryonic stem cells to HOXA hemogenic vasculature that resembles the aorta-gonad-mesonephros. 2016 , 34, 1168-1179	96
1100	Identifying lineage effects when controlling for population structure improves power in bacterial association studies. 2016 , 1, 16041	143
1099	Evolutionary patterns of genic DNA methylation vary across land plants. 2016 , 2, 15222	133
1098	Ancestral light and chloroplast regulation form the foundations for C gene expression. 2016 , 2, 16161	15
1097	Geogenetic patterns in mouse lemurs (genus <i>Microcebus</i>) reveal the ghosts of Madagascar's forests past. 2016 , 113, 8049-56	62
1096	Comparative population genomics reveals genetic basis underlying body size of domestic chickens. 2016 , 8, 542-552	15
1095	The pangenome of an agronomically important crop plant <i>Brassica oleracea</i> . 2016 , 7, 13390	240

1094	An evaluation of the accuracy and speed of metagenome analysis tools. 2016 , 6, 19233	209
1093	Emergence of human G2P[4] rotaviruses containing animal derived gene segments in the post-vaccine era. 2016 , 6, 36841	8
1092	Genome-Wide Divergence in the West-African Malaria Vector <i>Anopheles melas</i> . 2016 , 6, 2867-79	8
1091	Impact of donor-recipient phylogenetic distance on bacterial genome transplantation. 2016 , 44, 8501-11	27
1090	Chromatin accessibility maps of chronic lymphocytic leukaemia identify subtype-specific epigenome signatures and transcription regulatory networks. 2016 , 7, 11938	95
1089	High-fat diet disrupts metabolism in two generations of rats in a parent-of-origin specific manner. 2016 , 6, 31857	27
1088	Sequence capture and next-generation sequencing of ultraconserved elements in a large-genome salamander. 2016 , 25, 6162-6174	18
1087	Multilocus resistance evolution to azole fungicides in fungal plant pathogen populations. 2016 , 25, 6124-6142	35
1086	In vivo Ebola virus infection leads to a strong innate response in circulating immune cells. 2016 , 17, 707	40
1085	Genomic resources for a unique, low-virulence <i>Babesia</i> taxon from China. 2016 , 9, 564	10
1084	<i>Daphnia magna</i> transcriptome by RNA-Seq across 12 environmental stressors. 2016 , 3, 160030	62
1083	Characterization of the resistome in manure, soil and wastewater from dairy and beef production systems. 2016 , 6, 24645	63
1082	GATA1-Deficient Dendritic Cells Display Impaired CCL21-Dependent Migration toward Lymph Nodes Due to Reduced Levels of Polysialic Acid. 2016 , 197, 4312-4324	7
1081	Hybridization-Based Enrichment and Next Generation Sequencing to Explore Genetic Diversity in Plants. 2016 , 117-136	2
1080	DecontaMiner: A Pipeline for the Detection and Analysis of Contaminating Sequences in Human NGS Sequencing Data. 2016 , 137-148	2
1079	Genome sequence and analysis of the Japanese morning glory <i>Ipomoea nil</i> . 2016 , 7, 13295	91
1078	Resolving evolutionary relationships in lichen-forming fungi using diverse phylogenomic datasets and analytical approaches. 2016 , 6, 22262	34
1077	Toward a Reference Gene Catalog of Human Primary Monocytes. 2016 , 20, 627-634	9

1076	Red squirrels in the British Isles are infected with leprosy bacilli. 2016 , 354, 744-747	97
1075	Mutation allele burden remains unchanged in chronic myelomonocytic leukaemia responding to hypomethylating agents. 2016 , 7, 10767	140
1074	Complete Genome Sequence of Human Adenovirus 7 Associated with Fatal Adult Pneumonia. 2016 , 4,	2
1073	Detection of a novel circovirus PCV3 in pigs with cardiac and multi-systemic inflammation. 2016 , 13, 184	227
1072	Genome-Wide Analysis and Functional Characterization of the Polyadenylation Site in Pigs Using RNAseq Data. 2016 , 6, 36388	4
1071	Finding neoepitopes in mouse models of personalized cancer immunotherapy. 2016 , 11, 366-375	
1070	Akkermansia muciniphila mediates negative effects of IFN γ on glucose metabolism. 2016 , 7, 13329	144
1069	Diversity of antibiotic-resistance genes in Canadian isolates of <i>Aeromonas salmonicida</i> subsp. <i>salmonicida</i> : dominance of pSN254b and discovery of pAsa8. 2016 , 6, 35617	38
1068	Transcriptome analysis uncovers key regulatory and metabolic aspects of soybean embryonic axes during germination. 2016 , 6, 36009	49
1067	Population genomic analysis uncovers environmental stress-driven selection and adaptation of <i>Lentinula edodes</i> population in China. 2016 , 6, 36789	14
1066	Synergistically acting agonists and antagonists of G protein-coupled receptors prevent photoreceptor cell degeneration. 2016 , 9, ra74	22
1065	Comprehensive Identification of Meningococcal Genes and Small Noncoding RNAs Required for Host Cell Colonization. 2016 , 7,	21
1064	The Evolution of Orphan Regions in Genomes of a Fungal Pathogen of Wheat. 2016 , 7,	85
1063	An assemblage of Frankia Cluster II strains from California contains the canonical nod genes and also the sulfotransferase gene nodH. 2016 , 17, 796	41
1062	Antiviral CD8 T Cells Restricted by Human Leukocyte Antigen Class II Exist during Natural HIV Infection and Exhibit Clonal Expansion. 2016 , 45, 917-930	43
1061	Control of embryonic stem cell self-renewal and differentiation via coordinated alternative splicing and translation of YY2. 2016 , 113, 12360-12367	37
1060	Metagenomic analysis and functional characterization of the biogas microbiome using high throughput shotgun sequencing and a novel binning strategy. 2016 , 9, 26	164
1059	A new primer set for DNA metabarcoding of soil Metazoa. 2016 , 77, 53-59	11

1058	Evaluation of a membrane bioreactor system as post-treatment in waste water treatment for better removal of micropollutants. 2016 , 107, 37-46	32
1057	Endemic hydrothermal vent species identified in the open ocean seed bank. 2016 , 1, 16086	32
1056	HIPSTR and thousands of lncRNAs are heterogeneously expressed in human embryos, primordial germ cells and stable cell lines. 2016 , 6, 32753	26
1055	Increased GVHD-related mortality with broad-spectrum antibiotic use after allogeneic hematopoietic stem cell transplantation in human patients and mice. 2016 , 8, 339ra71	284
1054	Molecular Epidemiology of Colonizing and Infecting Isolates of. 2016 , 1,	114
1053	The cnidarian <i>Hydractinia echinata</i> employs canonical and highly adapted histones to pack its DNA. 2016 , 9, 36	19
1052	Characterization of microsatellite loci in the lichen-forming fungus <i>Cetraria aculeata</i> (Parmeliaceae, Ascomycota). 2016 , 4, 1600047	7
1051	Consistent responses of the microbial community structure to organic farming along the middle and lower reaches of the Yangtze River. 2016 , 6, 35046	49
1050	Sequence and gene expression evolution of paralogous genes in willows. 2015 , 5, 18662	10
1049	The induction and identification of novel Colistin resistance mutations in <i>Acinetobacter baumannii</i> and their implications. 2016 , 6, 28291	54
1048	Very Short Mitochondrial DNA Fragments and Heteroplasmy in Human Plasma. 2016 , 6, 36097	37
1047	RNA Sequencing Applied to Livestock Production. 2016 , 63-94	
1046	Comparative transcriptomic profiling of hydrogen peroxide signaling networks in zebrafish and human keratinocytes: Implications toward conservation, migration and wound healing. 2016 , 6, 20328	39
1045	<i>Schizophyllum commune</i> has an extensive and functional alternative splicing repertoire. 2016 , 6, 33640	13
1044	Transcriptomic comparison of invasive bigheaded carps (and) and their hybrids. 2016 , 6, 8452-8459	6
1043	Dynamics of Mathematical Models in Biology. 2016 ,	1
1042	Translational Biomedical Informatics. 2016 ,	1
1041	Widespread adaptive evolution during repeated evolutionary radiations in New World lupins. 2016 , 7, 12384	52

1040	Speciation with Gene Flow in North American Myotis Bats. 2017 , 66, 440-452	40
1039	NGS for Sequence Variants. 2016 , 939, 1-20	2
1038	BAC-pool sequencing and analysis confirms growth-associated QTLs in the Asian seabass genome. 2016 , 6, 36647	2
1037	Small RNAs from a Big Genome: The piRNA Pathway and Transposable Elements in the Salamander Species <i>Desmognathus fuscus</i> . 2016 , 83, 126-136	10
1036	Dynamic functional characterization and phylogenetic changes due to Long Chain Fatty Acids pulses in biogas reactors. 2016 , 6, 28810	44
1035	Genome-wide Identification and Structural, Functional and Evolutionary Analysis of WRKY Components of Mulberry. 2016 , 6, 30794	28
1034	A robust ambient temperature collection and stabilization strategy: Enabling worldwide functional studies of the human microbiome. 2016 , 6, 31731	41
1033	<i>Aiptasia</i> sp. larvae as a model to reveal mechanisms of symbiont selection in cnidarians. 2016 , 6, 32366	51
1032	Gut microbiota Modulated by Probiotics and <i>Garcinia cambogia</i> Extract Correlate with Weight Gain and Adipocyte Sizes in High Fat-Fed Mice. 2016 , 6, 33566	32
1031	Tissue-Specific Venom Composition and Differential Gene Expression in Sea Anemones. 2016 , 8, 2358-75	51
1030	Complete Chloroplast Genome Sequence and Annotation of the <i>Saccharum</i> Hybrid Cultivar RB867515. 2016 , 4,	3
1029	Transcriptome analysis of human brain tissue identifies reduced expression of complement complex C1Q Genes in Rett syndrome. 2016 , 17, 427	26
1028	Time-resolved dual RNA-seq reveals extensive rewiring of lung epithelial and pneumococcal transcriptomes during early infection. 2016 , 17, 198	72
1027	Developmental dynamics of the preterm infant gut microbiota and antibiotic resistome. 2016 , 1, 16024	229
1026	TCF7L1 Modulates Colorectal Cancer Growth by Inhibiting Expression of the Tumor-Suppressor Gene EPHB3. 2016 , 6, 28299	28
1025	Genomic Survey of a Hyperparasitic Microsporidian <i>Amphiamblys</i> sp. (Metchnikovellidae). 2017 , 9, 454-467	33
1024	Genomic resources for wild populations of the house mouse, <i>Mus musculus</i> and its close relative <i>Mus spretus</i> . 2016 , 3, 160075	67
1023	Transcriptomic analysis of submergence-tolerant and sensitive <i>Brachypodium distachyon</i> ecotypes reveals oxidative stress as a major tolerance factor. 2016 , 6, 27686	24

1022	Novel compound heterozygous mutations in CNGA1 in a Chinese family affected with autosomal recessive retinitis pigmentosa by targeted sequencing. 2016 , 16, 101	4
1021	Multi-omics integration accurately predicts cellular state in unexplored conditions for <i>Escherichia coli</i> . 2016 , 7, 13090	90
1020	<i>Mycobacterium tuberculosis</i> lineage 4 comprises globally distributed and geographically restricted sublineages. 2016 , 48, 1535-1543	208
1019	Comparative analysis of plastid genomes of non-photosynthetic Ericaceae and their photosynthetic relatives. 2016 , 6, 30042	35
1018	microRNA-132/212 deficiency enhances A β production and senile plaque deposition in Alzheimer's disease triple transgenic mice. 2016 , 6, 30953	66
1017	Physiological basis for low-temperature survival and storage of quiescent larvae of the fruit fly <i>Drosophila melanogaster</i> . 2016 , 6, 32346	27
1016	Authentication and characterisation of a new oesophageal adenocarcinoma cell line: MFD-1. 2016 , 6, 32417	15
1015	Novel highly divergent reassortant bat rotaviruses in Cameroon, without evidence of zoonosis. 2016 , 6, 34209	34
1014	Independent Domestication of Two Old World Cotton Species. 2016 , 8, 1940-7	23
1013	Transcriptomic responses of a simplified soil microcosm to a plant pathogen and its biocontrol agent reveal a complex reaction to harsh habitat. 2016 , 17, 838	10
1012	The draft genome of the C panicoid grass species <i>Dichanthelium oligosanthes</i> . 2016 , 17, 223	26
1011	Comparative transcriptome analysis reveals insights into the streamlined genomes of haplosclerid demosponges. 2016 , 6, 18774	20
1010	Australian human and parrot <i>Chlamydia psittaci</i> strains cluster within the highly virulent 6BC clade of this important zoonotic pathogen. 2016 , 6, 30019	39
1009	Genome Sequence of the Poly-3-Hydroxybutyrate Producer <i>Clostridium acetireducens</i> DSM 10703. 2016 , 4,	2
1008	Metabarcoding-based Assessment of Community Structures of Stream Invertebrates in Rivers Fragmented by Dams with Sediment Bypass Tunnels. 2016 , 72, III_559-III_566	1
1007	Draft Genome Sequence for a Clinical Isolate of Vancomycin-Resistant <i>Enterococcus faecalis</i> . 2016 , 4,	2
1006	Biological Pathway Analysis for De Novo Transcriptomes through Multiple Reference Species Selections. 2016 ,	3
1005	Genome-Wide Analysis of NBS-LRR Genes in Sorghum Genome Revealed Several Events Contributing to NBS-LRR Gene Evolution in Grass Species. 2016 , 12, 9-21	22

1004	Platelet functional and transcriptional changes induced by intralipid infusion. 2016 , 115, 1147-56	5
1003	Draft Genome Sequence of Cellulolytic and Xylanolytic Cellulomonas sp. Strain B6 Isolated from Subtropical Forest Soil. 2016 , 4,	2
1002	Assembling the <i>Setaria italica</i> L. Beauv. genome into nine chromosomes and insights into regions affecting growth and drought tolerance. 2016 , 6, 35076	6
1001	Assessing the feasibility of fly based surveillance of wildlife infectious diseases. 2016 , 6, 37952	11
1000	Comparing three complete mitochondrial genomes of the moss genus Hedw. 2016 , 1, 168-170	6
999	Draft Genome Sequence of <i>Yarrowia lipolytica</i> Strain A-101 Isolated from Polluted Soil in Poland. 2016 , 4,	15
998	Analysis of differential gene expression by RNA-seq data in brain areas of laboratory animals. 2016 , 13, 1-15	2
997	Genome-wide <i>Escherichia coli</i> stress response and improved tolerance towards industrially relevant chemicals. 2016 , 15, 176	32
996	Genome Sequence of the Autotrophic Acetogen <i>Clostridium magnum</i> DSM 2767. 2016 , 4,	4
995	Combining independent de novo assemblies optimizes the coding transcriptome for nonconventional model eukaryotic organisms. 2016 , 17, 525	34
994	Differential variation patterns between hubs and bottlenecks in human protein-protein interaction networks. 2016 , 16, 260	11
993	RNA-Sequencing for profiling goat milk transcriptome in colostrum and mature milk. 2016 , 12, 264	38
992	Extremely low nucleotide diversity in the X-linked region of papaya caused by a strong selective sweep. 2016 , 17, 230	13
991	Streaming algorithms for identification of pathogens and antibiotic resistance potential from real-time MinION(TM) sequencing. 2016 , 5, 32	58
990	Quantitative trait variation is revealed in a novel hypomethylated population of woodland strawberry (<i>Fragaria vesca</i>). 2016 , 16, 240	13
989	Immunoseq: the identification of functionally relevant variants through targeted capture and sequencing of active regulatory regions in human immune cells. 2016 , 9, 59	16
988	Dual leucine zipper kinase regulates expression of axon guidance genes in mouse neuronal cells. 2016 , 11, 13	4
987	Molecular analysis of the Sydney rock oyster (<i>Saccostrea glomerata</i>) CO ₂ stress response. 2016 , 3,	7

986	Draft genome sequence of the marine strain O3.65, cultivated from oil-polluted seawater of the Deepwater Horizon oil spill. 2016 , 11, 81	9
985	Draft genome of CCAP 1490/1 (CALU1027), the chlorophyll containing filamentous cyanobacterium. 2016 , 11, 82	
984	Limited Antigenic Diversity in Contemporary H7 Avian-Origin Influenza A Viruses from North America. 2016 , 6, 20688	17
983	The complete chloroplast genome of queen's crape-myrtle(). 2016 , 1, 408-409	2
982	The complete mitochondrial genome of barley. 2016 , 1, 430-431	1
981	Draft Genome Sequence of a <i>Cardiobacterium hominis</i> Strain Isolated from Blood Cultures of a Patient with Infective Endocarditis. 2016 , 4,	1
980	Microsatellite markers for (<i>Nymphaeaceae</i>), an aquatic plant in the agricultural ecosystem of Japan. 2016 , 4, 1600082	2
979	Depletion of Mouse Cells from Human Tumor Xenografts Significantly Improves Downstream Analysis of Target Cells. 2016 ,	3
978	Use of Metatranscriptomics in Microbiome Research. 2016 , 10, 19-25	217
977	Epigenetic Reprogramming in Naive CD4+ T Cells Favoring T Cell Activation and Non-Th1 Effector T Cell Immune Response as an Early Event in Lupus Flares. 2016 , 68, 2200-9	63
976	Utilizing Gene Tree Variation to Identify Candidate Effector Genes in <i>Zymoseptoria tritici</i> . 2016 , 6, 779-91	20
975	Two adjacent inversions maintain genomic differentiation between migratory and stationary ecotypes of Atlantic cod. 2016 , 25, 2130-43	109
974	Reproductive isolation and introgression between sympatric <i>Mimulus</i> species. 2016 , 25, 2499-517	44
973	Integration host factor and LuxR synergistically bind DNA to coactivate quorum-sensing genes in <i>Vibrio harveyi</i> . 2016 , 101, 823-40	28
972	Resistance to <i>Streptomyces turgidiscabies</i> in potato involves an early and sustained transcriptional reprogramming at initial stages of tuber formation. 2016 , 17, 703-13	9
971	Complete Genome Sequence of Bluetongue Virus Serotype 8, Which Reemerged in France in August 2015. 2016 , 4,	21
970	Draft Genome Sequence of the Strict Anaerobe <i>Clostridium neopropionicum</i> X4 (DSM 3847T). 2016 , 4,	2
969	First Insights into the Genome of the Moderately Thermophilic Bacterium <i>Clostridium tepidiprofundii</i> SG 508T. 2016 , 4,	0

968	Complete Genome Sequences of the Obligate Symbionts "Candidatus Sulcia muelleri" and "Ca. Nasuia deltocephalinicola" from the Pestiferous Leafhopper <i>Macrosteles quadripunctulatus</i> (Hemiptera: Cicadellidae). 2016 , 4,	22
967	Draft Genome Sequence of the Syntrophic Lactate-Degrading Bacterium <i>Tepidanaerobacter syntrophicus</i> JLT. 2016 , 4,	3
966	Identification of interleukin genes in <i>Pogona vitticeps</i> using a de novo transcriptome assembly from RNA-seq data. 2016 , 68, 719-31	1
965	Trimming of sequence reads alters RNA-Seq gene expression estimates. 2016 , 17, 103	89
964	Shared and divergent pathways for flower abscission are triggered by gibberellic acid and carbon starvation in seedless <i>Vitis vinifera</i> L. 2016 , 16, 38	22
963	Insights into the transcriptional and translational mechanisms of linear organellar chromosomes in the box jellyfish <i>Alatina alata</i> (Cnidaria: Medusozoa: Cubozoa). 2016 , 13, 799-809	3
962	Draft Genome Sequence of <i>Marinobacter</i> sp. Strain P4B1, an Electrogenic Perchlorate-Reducing Strain Isolated from a Long-Term Mixed Enrichment Culture of Marine Bacteria. 2016 , 4,	7
961	Whole-Genome Sequencing Recommendations. 2016 , 13-41	1
960	Transcriptome Profiling Strategies. 2016 , 69-104	
959	Analysis of Long Noncoding RNAs in RNA-Seq Data. 2016 , 143-174	
958	Transcriptome analysis of immune response genes induced by pathogen agonists in the Antarctic bullhead notothen <i>Notothenia coriiceps</i> . 2016 , 55, 315-22	9
957	Draft Genome Sequence of <i>Megasphaera</i> sp. Strain DJF_B143, an Isolate from Pig Hindgut Unable to Produce Skatole. 2016 , 4,	1
956	Draft Genome Sequence of "Candidatus Methanomethylophilus" sp. 1R26, Enriched from Bovine Rumen, a Methanogenic Archaeon Belonging to the Methanomassiliicoccales Order. 2016 , 4,	9
955	Transcriptome analysis of human cumulus cells reveals hypoxia as the main determinant of follicular senescence. 2016 , 22, 866-76	25
954	Draft Genome Sequences of <i>Listeria monocytogenes</i> Serotype 4b Strains 944 and 2993 and Serotype 1/2c Strains 198 and 2932. 2016 , 4,	1
953	Comparative genomic analyses reveal broad diversity in botulinum-toxin-producing <i>Clostridia</i> . 2016 , 17, 180	56
952	Xylan degradation by the human gut <i>Bacteroides xylanisolvens</i> XB1A(T) involves two distinct gene clusters that are linked at the transcriptional level. 2016 , 17, 326	44
951	The complete mitochondrial genomes of two globally invasive ants, the Argentine ant <i>Linepithema humile</i> and the little fire ant <i>Wasmannia auropunctata</i> . 2016 , 8, 275-277	8

950	Assembly of the draft genome of buckwheat and its applications in identifying agronomically useful genes. 2016 , 23, 215-24	80
949	Evidence of Natural Hybridization in Brazilian Wild Lineages of <i>Saccharomyces cerevisiae</i> . 2016 , 8, 317-29	45
948	Genus-Wide Comparative Genome Analyses of <i>Colletotrichum</i> Species Reveal Specific Gene Family Losses and Gains during Adaptation to Specific Infection Lifestyles. 2016 , 8, 1467-81	50
947	The Role of microRNAs in the Repeated Parallel Diversification of Lineages of Midas Cichlid Fish from Nicaragua. 2016 , 8, 1543-55	27
946	Host-Associated Genomic Features of the Novel Uncultured Intracellular Pathogen <i>Ca. Ichthyocystis</i> Revealed by Direct Sequencing of Epitheliocysts. 2016 , 8, 1672-89	9
945	Evolution of Vertebrate Phototransduction: Cascade Activation. 2016 , 33, 2064-87	33
944	Shotgun Metagenomic Profiles Have a High Capacity To Discriminate Samples of Activated Sludge According to Wastewater Type. 2016 , 82, 5186-96	31
943	Characterization of Somatically-Eliminated Genes During Development of the Sea Lamprey (<i>Petromyzon marinus</i>). 2016 , 33, 2337-44	25
942	Dietary Fiber and Bacterial SCFA Enhance Oral Tolerance and Protect against Food Allergy through Diverse Cellular Pathways. 2016 , 15, 2809-24	323
941	Mitochondrial genomes of the South American electric knifefishes (Order Gymnotiformes). 2016 , 1, 401-403	6
940	Characterization of frataxin gene network in Friedreich's ataxia fibroblasts using the RNA-Seq technique. 2016 , 30, 59-66	9
939	Culture-independent bacterial community profiling of carbon dioxide treated raw milk. 2016 , 233, 81-89	13
938	Amplification of WHSC1L1 regulates expression and estrogen-independent activation of ER α in SUM-44 breast cancer cells and is associated with ER α over-expression in breast cancer. 2016 , 10, 850-65	28
937	Epigenetics and energetics in ventral hippocampus mediate rapid antidepressant action: Implications for treatment resistance. 2016 , 113, 7906-11	61
936	Sex, Scavengers, and Chaperones: Transcriptome Secrets of Divergent <i>Symbiodinium</i> Thermal Tolerances. 2016 , 33, 2201-15	88
935	First Genome Sequence of <i>Leptospira interrogans</i> Serovar Pomona, Isolated from a Bovine Abortion. 2016 , 4,	7
934	Transcriptome sequences spanning key developmental states as a resource for the study of the cestode <i>Schistocephalus solidus</i> , a threespine stickleback parasite. 2016 , 5, 24	32
933	Microbial community structure of two freshwater sponges using Illumina MiSeq sequencing revealed high microbial diversity. 2016 , 6, 40	15

932	Transcriptional Profiling of Banana Shrimp <i>Fenneropenaeus merguensis</i> with Differing Levels of Viral Load. 2016 , 56, 1131-1143	11
931	Genome Sequence of <i>Staphylococcus aureus</i> Strain HUK16, Isolated from Hexachlorocyclohexane-Contaminated Soil. 2016 , 4,	
930	Targeted genome editing in the rare actinomycete <i>Actinoplanes</i> sp. SE50/110 by using the CRISPR/Cas9 System. 2016 , 231, 122-128	31
929	The gene <i>cortex</i> controls mimicry and crypsis in butterflies and moths. 2016 , 534, 106-10	137
928	Characterization of a genetically heterogeneous porcine rotavirus C, and other viruses present in the fecal virome of a non-diarrheic Belgian piglet. 2016 , 43, 135-45	15
927	Gene expression profiling in melanised sites of Atlantic salmon fillets. 2016 , 55, 56-63	10
926	Transcriptome adaptation of the bovine mammary gland to diets rich in unsaturated fatty acids shows greater impact of linseed oil over safflower oil on gene expression and metabolic pathways. 2016 , 17, 104	35
925	Comparative transcriptome analysis of three color variants of the sea cucumber <i>Apostichopus japonicus</i> . 2016 , 28, 21-24	10
924	Exploring the virome of cattle with non-suppurative encephalitis of unknown etiology by metagenomics. 2016 , 493, 22-30	32
923	High resolution mapping of traits related to whole-plant transpiration under increasing evaporative demand in wheat. 2016 , 67, 2847-60	38
922	Effects of <i>Mecp2</i> loss of function in embryonic cortical neurons: a bioinformatics strategy to sort out non-neuronal cells variability from transcriptome profiling. 2016 , 17 Suppl 2, 14	9
921	GBS-SNP-CROP: a reference-optional pipeline for SNP discovery and plant germplasm characterization using variable length, paired-end genotyping-by-sequencing data. 2016 , 17, 29	67
920	SPARTA: Simple Program for Automated reference-based bacterial RNA-seq Transcriptome Analysis. 2016 , 17, 66	27
919	Phylogenomics of a rapid radiation: is chromosomal evolution linked to increased diversification in north american spiny lizards (Genus <i>Sceloporus</i>)?. 2016 , 16, 63	53
918	Increasing genomic diversity and evidence of constrained lifestyle evolution due to insertion sequences in <i>Aeromonas salmonicida</i> . 2016 , 17, 44	32
917	Transcriptome analysis reveals differentially expressed genes associated with germ cell and gonad development in the Southern bluefin tuna (<i>Thunnus maccoyii</i>). 2016 , 17, 217	30
916	Comprehensive identification of sexually dimorphic genes in diverse cattle tissues using RNA-seq. 2016 , 17, 81	18
915	Transcriptome wide analyses reveal a sustained cellular stress response in the gill tissue of <i>Trematomus bernacchii</i> after acclimation to multiple stressors. 2016 , 17, 127	60

914	Unraveling the pectinolytic function of <i>Bacteroides xyloisolvans</i> using a RNA-seq approach and mutagenesis. 2016 , 17, 147	26
913	Rapid gene identification in sugar beet using deep sequencing of DNA from phenotypic pools selected from breeding panels. 2016 , 17, 236	17
912	Genome-wide analysis of ionotropic receptors provides insight into their evolution in <i>Heliconius</i> butterflies. 2016 , 17, 254	23
911	Fecal metagenomics for the simultaneous assessment of diet, parasites, and population genetics of an understudied primate. 2016 , 13, 17	59
910	Diagnosis of late-onset Pompe disease and other muscle disorders by next-generation sequencing. 2016 , 11, 8	33
909	RISC-mediated control of selected chromatin regulators stabilizes ground state pluripotency of mouse embryonic stem cells. 2016 , 17, 94	8
908	Farewell to GBM-O: Genomic and transcriptomic profiling of glioblastoma with oligodendroglioma component reveals distinct molecular subgroups. 2016 , 4, 4	22
907	Draft genome of the <i>Arabidopsis thaliana</i> phyllosphere bacterium, <i>Williamsia</i> sp. ARP1. 2016 , 11, 8	8
906	Genome sequence of <i>Shimia</i> str. SK013, a representative of the <i>Roseobacter</i> group isolated from marine sediment. 2016 , 11, 25	4
905	Contribution of Vegetation to the Microbial Composition of Nearby Outdoor Air. 2016 , 82, 3822-33	88
904	Elevated paternal glucocorticoid exposure alters the small noncoding RNA profile in sperm and modifies anxiety and depressive phenotypes in the offspring. 2016 , 6, e837	109
903	Annual Killifish Transcriptomics and Candidate Genes for Metazoan Diapause. 2016 , 33, 2391-5	13
902	Consumption of <i>Ulva clathrata</i> as a dietary supplement stimulates immune and lipid metabolism genes in Pacific white shrimp <i>Litopenaeus vannamei</i> . 2016 , 28, 3667-3677	13
901	Pooled Enrichment Sequencing Identifies Diversity and Evolutionary Pressures at NLR Resistance Genes within a Wild Tomato Population. 2016 , 8, 1501-15	38
900	Antibiotic Resistance, Core-Genome and Protein Expression in IncHI1 Plasmids in <i>Salmonella</i> Typhimurium. 2016 , 8, 1661-71	16
899	The Draft Genome Sequence of <i>Paenibacillus polymyxa</i> Strain CCI-25 Encompasses High Potential for Secondary Metabolite Production. 2016 , 4,	2
898	Description of <i>Endozoicomonas ascidiicola</i> sp. nov., isolated from Scandinavian ascidians. 2016 , 39, 313-8	12
897	Genome Sequence of the Acetogenic Bacterium <i>Moorella mulderi</i> DSM 14980T. 2016 , 4,	7

896	Dual Transcriptome Profiling of Leishmania-Infected Human Macrophages Reveals Distinct Reprogramming Signatures. 2016 , 7,	59
895	The genome of the yellow potato cyst nematode, <i>Globodera rostochiensis</i> , reveals insights into the basis of parasitism and virulence. 2016 , 17, 124	95
894	AdapterRemoval v2: rapid adapter trimming, identification, and read merging. 2016 , 9, 88	658
893	Genome sequence of <i>Shinella</i> sp. strain DD12, isolated from homogenized guts of starved <i>Daphnia magna</i> . 2016 , 11, 14	3
892	Substantial molecular evolution and mutation rates in prolonged latent <i>Mycobacterium tuberculosis</i> infection in humans. 2016 , 306, 580-585	28
891	Next generation sequencing technology and genomewide data analysis: Perspectives for retinal research. 2016 , 55, 1-31	39
890	Genomewide ancestry and divergence patterns from low-coverage sequencing data reveal a complex history of admixture in wild baboons. 2016 , 25, 3469-83	54
889	Scale-dependent variation in nitrogen cycling and soil fungal communities along gradients of forest composition and age in regenerating tropical dry forests. 2016 , 209, 845-54	70
888	Complete Genome Sequence of <i>Mycobacterium tuberculosis</i> Clinical Isolate Spoligotype SIT745/EAI1-MYS. 2016 , 4,	1
887	Draft Whole-Genome Sequence of <i>Haemophilus ducreyi</i> Strain AUSPNG1, Isolated from a Cutaneous Ulcer of a Child from Papua New Guinea. 2016 , 4,	6
886	Complete Chloroplast Genome Sequence of Phagomixotrophic Green Alga <i>Cymbomonas tetramitiformis</i> . 2016 , 4,	6
885	Phylogenomic analysis supports a recent change in nitrate assimilation in the White-nose Syndrome pathogen, <i>Pseudogymnoascus destructans</i> . 2016 , 23, 20-29	5
884	Regulation of Gene Expression in <i>Shewanella oneidensis</i> MR-1 during Electron Acceptor Limitation and Bacterial Nanowire Formation. 2016 , 82, 5428-43	32
883	Illumina-based RiboMethSeq approach for mapping of 2'-O-Me residues in RNA. 2016 , 44, e135	116
882	The mitochondrial genomes of twelve <i>Anopheles</i> mosquitoes (Diptera: Culicidae) and their phylogenetic implications. 2016 , 8, 387-390	5
881	Development and characterization of polymorphic microsatellite markers for <i>Neolitsea sericea</i> using Illumina paired-end draft sequencing data. 2016 , 31, 163-166	3
880	An introduction to plant phylogenomics with a focus on palms. 2016 , 182, 234-255	27
879	The complete mitochondrial genome of a Chinese rufous horseshoe bat subspecies, <i>Rhinolophus sinicus sinicus</i> (Chiroptera: Rhinolophidae). 2016 , 27, 3301-2	4

878	The complete mitochondrial genome of a deep-water Baikalian amphipoda <i>Brachyuropus grewingkii</i> (Dybowsky, 1874). 2016 , 27, 4158-4159	4
877	A primer on precision medicine informatics. 2016 , 17, 145-53	30
876	A phylotranscriptomic analysis of gene family expansion and evolution in the largest order of pleurocarpous mosses (Hypnales, Bryophyta). 2016 , 98, 29-40	24
875	Root Type-Specific Reprogramming of Maize Pericycle Transcriptomes by Local High Nitrate Results in Disparate Lateral Root Branching Patterns. 2016 , 170, 1783-98	39
874	Non-coding RNA profiling of the developing murine lens. 2016 , 145, 347-351	13
873	Integration of ATAC-seq and RNA-seq identifies human alpha cell and beta cell signature genes. 2016 , 5, 233-244	139
872	The fruRBA Operon Is Necessary for Group A Streptococcal Growth in Fructose and for Resistance to Neutrophil Killing during Growth in Whole Human Blood. 2016 , 84, 1016-1031	18
871	Molecular candidates for early-stage flower-to-fruit transition in stenospermocarpic table grape (<i>Vitis vinifera</i> L.) inflorescences ascribed by differential transcriptome and metabolome profiles. 2016 , 244, 40-56	16
870	SutA is a bacterial transcription factor expressed during slow growth in <i>Pseudomonas aeruginosa</i> . 2016 , 113, E597-605	32
869	RNA sequencing-based analysis of the spleen transcriptome following infectious bronchitis virus infection of chickens selected for different mannose-binding lectin serum concentrations. 2016 , 17, 82	16
868	Microbial Environmental Genomics (MEG). 2016 ,	3
867	Evaluation of a DLA-79 allele associated with multiple immune-mediated diseases in dogs. 2016 , 68, 205-17	9
866	RNA-seq of human reference RNA samples using a thermostable group II intron reverse transcriptase. 2016 , 22, 597-613	53
865	RNA-seq analysis for secondary metabolite pathway gene discovery in <i>Polygonum minus</i> . 2016 , 7, 12-3	16
864	Transcriptional, translational, and physiological signatures of undernourished honey bees (<i>Apis mellifera</i>) suggest a role for hormonal factors in hypopharyngeal gland degradation. 2016 , 85, 65-75	23
863	Enhancer Turnover Is Associated with a Divergent Transcriptional Response to Glucocorticoid in Mouse and Human Macrophages. 2016 , 196, 813-822	45
862	Bacteria increase arid-land soil surface temperature through the production of sunscreens. 2016 , 7, 10373	107
861	Analyzing MiRNA-LncRNA Interactions. 2016 , 1402, 271-286	485

860	Repression of p53-target gene Bbc3/PUMA by MYSM1 is essential for the survival of hematopoietic multipotent progenitors and contributes to stem cell maintenance. 2016 , 23, 759-75	40
859	Quantitative developmental transcriptomes of the Mediterranean sea urchin <i>Paracentrotus lividus</i> . 2016 , 25, 89-94	20
858	Directing an artificial zinc finger protein to new targets by fusion to a non-DNA-binding domain. 2016 , 44, 3118-30	4
857	Episodic Diversifying Selection Shaped the Genomes of Gibbon Ape Leukemia Virus and Related Gammaretroviruses. 2016 , 90, 1757-72	7
856	RiboFR-Seq: a novel approach to linking 16S rRNA amplicon profiles to metagenomes. 2016 , 44, e99	20
855	De Novo assembly and annotation of the freshwater crayfish <i>Astacus astacus</i> transcriptome. 2016 , 28, 7-10	36
854	Draft Genome Sequence of <i>Thermodesulfovibrio aggregans</i> TGE-P1T, an Obligately Anaerobic, Thermophilic, Sulfate-Reducing Bacterium in the Phylum Nitrospirae. 2016 , 4,	2
853	Discovery and functional characterization of novel miRNAs in the marine medaka <i>Oryzias melastigma</i> . 2016 , 175, 106-16	8
852	RNA-seq reveals a diminished acclimation response to the combined effects of ocean acidification and elevated seawater temperature in <i>Pagothenia borchgrevinki</i> . 2016 , 28, 87-97	23
851	De novo assembly and annotation of the European abalone <i>Haliotis tuberculata</i> transcriptome. 2016 , 28, 11-16	27
850	BaitFisher: A Software Package for Multispecies Target DNA Enrichment Probe Design. 2016 , 33, 1875-86	49
849	High-throughput sequencing reveals the core gut microbiome of Bar-headed goose (<i>Anser indicus</i>) in different wintering areas in Tibet. 2016 , 5, 287-95	29
848	Transcriptome analysis of phycocyanin inhibitory effects on SKOV-3 cell proliferation. 2016 , 585, 58-64	19
847	Phylogenomics of 'Discosea': A new molecular phylogenetic perspective on Amoebozoa with flat body forms. 2016 , 99, 144-154	22
846	A Comparative Analysis of Mitochondrial Genomes in Eustigmatophyte Algae. 2016 , 8, 705-22	22
845	Whole-Genome Sequencing Reveals a New Genospecies of <i>Methylobacterium</i> sp. GXS13, Isolated from <i>Vitis vinifera</i> L. Xylem Sap. 2016 , 4,	2
844	The Eurasian invasion: phylogenomic data reveal multiple Southeast Asian origins for Indian Dragon Lizards. 2016 , 16, 43	31
843	Transcriptome analyses of insect cells to facilitate baculovirus-insect expression. 2016 , 7, 373-82	10

842	MEGAHIT v1.0: A fast and scalable metagenome assembler driven by advanced methodologies and community practices. 2016 , 102, 3-11	529
841	Genome-wide kinetics of DNA excision repair in relation to chromatin state and mutagenesis. 2016 , 113, E2124-33	100
840	Carbapenem- and Colistin-Resistant <i>Enterobacter cloacae</i> from Delta, Colorado, in 2015. 2016 , 60, 3141-4	23
839	Draft genome sequence of <i>Diaporthe aspalathi</i> isolate MS-SSC91, a fungus causing stem canker in soybean. 2016 , 7, 262-3	10
838	Evolutionary Relationships among Extinct and Extant Sloths: The Evidence of Mitogenomes and Retroviruses. 2016 , 8, 607-21	31
837	Sediments and Soils Act as Reservoirs for Taxonomic and Functional Bacterial Diversity in the Upper Mississippi River. 2016 , 71, 814-24	20
836	Using single nuclei for RNA-seq to capture the transcriptome of postmortem neurons. 2016 , 11, 499-524	199
835	Ecological Genomics of the Uncultivated Marine <i>Roseobacter</i> Lineage CHAB-I-5. 2016 , 82, 2100-2111	29
834	Metagenomic analysis of viruses associated with field-grown and retail lettuce identifies human and animal viruses. 2016 , 223, 50-6	41
833	Highly Accurate Sequencing of Full-Length Immune Repertoire Amplicons Using Tn5-Enabled and Molecular Identifier-Guided Amplicon Assembly. 2016 , 196, 2902-7	24
832	Use of Metagenomic Shotgun Sequencing Technology To Detect Foodborne Pathogens within the Microbiome of the Beef Production Chain. 2016 , 82, 2433-2443	80
831	An Untranslated <i>cis</i> -Element Regulates the Accumulation of Multiple C4 Enzymes in <i>Gynandropsis gynandra</i> Mesophyll Cells. 2016 , 28, 454-65	38
830	Gene Expression Variation Resolves Species and Individual Strains among Coral-Associated Dinoflagellates within the Genus <i>Symbiodinium</i> . 2016 , 8, 665-80	73
829	Clinical Isolates of <i>Pseudomonas aeruginosa</i> from Chronically Infected Cystic Fibrosis Patients Fail To Activate the Inflammasome during Both Stable Infection and Pulmonary Exacerbation. 2016 , 196, 3097-108	20
828	Effects of the biocides on the culturable house dust-borne bacterial compositions and diversities. 2016 , 22, 1133-1146	2
827	Quantification of the effects of ocean acidification on sediment microbial communities in the environment: the importance of ecosystem approaches. 2016 , 92, fiw027	30
826	circTAIL-seq, a targeted method for deep analysis of RNA 3' tails, reveals transcript-specific differences by multiple metrics. 2016 , 22, 477-86	10
825	Ultra-Deep Sequencing of Bisulfite-Modified DNA. 2016 , 47-72	

824	Recovering complete mitochondrial genome sequences from RNA-Seq: A case study of <i>Polytomella</i> non-photosynthetic green algae. 2016 , 98, 57-62	27
823	Linking the T cell receptor to the single cell transcriptome in antigen-specific human T cells. 2016 , 94, 604-11	91
822	A gene associated with social immunity in the burying beetle <i>Nicrophorus vespilloides</i> . 2016 , 283,	33
821	Development of microsatellite markers and a preliminary assessment of population structuring in the rice weevil, <i>Sitophilus oryzae</i> (L.). 2016 , 66, 12-17	9
820	PHYLUCE is a software package for the analysis of conserved genomic loci. <i>Bioinformatics</i> , 2016 , 32, 786-82	352
819	First multigene analysis of Archamoebae (Amoebozoa: Conosa) robustly reveals its phylogeny and shows that Entamoebidae represents a deep lineage of the group. 2016 , 98, 41-51	19
818	Emerging pathogens of gilthead seabream: characterisation and genomic analysis of novel intracellular ϵ proteobacteria. 2016 , 10, 1791-803	21
817	Meta-omics in Inflammatory Bowel Disease Research: Applications, Challenges, and Guidelines. 2016 , 10, 735-46	23
816	Detection of SNPs based on transcriptome sequencing in Norway spruce (<i>Picea abies</i> (L.) Karst). 2016 , 8, 105-107	9
815	De novo transcriptome assembly of <i>Perkinsus olseni</i> trophozoite stimulated in vitro with Manila clam (<i>Ruditapes philippinarum</i>) plasma. 2016 , 135, 22-33	11
814	Hydroxymethyl cytosine marks in the human mitochondrial genome are dynamic in nature. 2016 , 27, 25-31	18
813	A survey of best practices for RNA-seq data analysis. 2016 , 17, 13	1203
812	Retrospective diagnosis of two rabies cases in humans by high throughput sequencing. 2016 , 78, 74-81	8
811	Rapid detection of germline mutations for hereditary gastrointestinal polyposis/cancers using HaloPlex target enrichment and high-throughput sequencing technologies. 2016 , 15, 553-62	16
810	Mitogenomics of 'Old World <i>Acraea</i> ' butterflies reveals a highly divergent 'Bematistes'. 2016 , 97, 233-241	12
809	Functional Dissection of an Alternatively Spliced Herpesvirus Gene by Splice Site Mutagenesis. 2016 , 90, 4626-4636	8
808	Molecular analysis of DNA in blastocoele fluid using next-generation sequencing. 2016 , 33, 637-645	28
807	Differential RNA-seq analysis comparing APC-defective and APC-restored SW480 colorectal cancer cells. 2016 , 7, 293-6	6

806	Into the deep: Evaluation of SourceTracker for assessment of faecal contamination of coastal waters. 2016 , 93, 242-253	78
805	Most microRNAs in the single-cell alga <i>Chlamydomonas reinhardtii</i> are produced by Dicer-like 3-mediated cleavage of introns and untranslated regions of coding RNAs. 2016 , 26, 519-29	32
804	Dichloroacetate Prevents Cisplatin-Induced Nephrotoxicity without Compromising Cisplatin Anticancer Properties. 2016 , 27, 3331-3344	35
803	Molecular characterization of Capim and Enseada orthobunyaviruses. 2016 , 40, 47-53	12
802	Sequence Diversity, Intersubgroup Relationships, and Origins of the Mouse Leukemia Gammaretroviruses of Laboratory and Wild Mice. 2016 , 90, 4186-98	11
801	Shoc2-transduced ERK1/2 motility signals--Novel insights from functional genomics. 2016 , 28, 448-459	10
800	Characterisation of 12 microsatellite loci in the Vietnamese commercial clam <i>Lutraria rhynchaena</i> Jonas 1844 (Heterodonta: Bivalvia: Mactridae) through next-generation sequencing. 2016 , 43, 391-6	5
799	Genome-wide analysis, expression dynamics and varietal comparison of NAC gene family at various developmental stages in <i>Morus notabilis</i> . 2016 , 291, 1305-17	12
798	Making sense of genomes of parasitic worms: Tackling bioinformatic challenges. 2016 , 34, 663-686	27
797	Impact of the administration of a third-generation cephalosporin (3GC) to one-day-old chicks on the persistence of 3GC-resistant <i>Escherichia coli</i> in intestinal flora: An in vivo experiment. 2016 , 185, 29-33	12
796	Chasing the elusive Euryarchaeota class WSA2: genomes reveal a uniquely fastidious methyl-reducing methanogen. 2016 , 10, 2478-87	146
795	Developmental Progression in the Coral <i>Acropora digitifera</i> Is Controlled by Differential Expression of Distinct Regulatory Gene Networks. 2016 , 8, 851-70	15
794	Heat stress yields a unique MADS box transcription factor in determining seed size and thermal sensitivity. 2016 , 171, 606-22	70
793	Molecular detection of bovine Noroviruses in Argentinean dairy calves: Circulation of a tentative new genotype. 2016 , 40, 144-150	19
792	Cerebellar Transcriptome Profiles of ATXN1 Transgenic Mice Reveal SCA1 Disease Progression and Protection Pathways. 2016 , 89, 1194-1207	60
791	Multilocus phylogeny and phylogenomics of <i>Eriochrysis</i> P. Beauv. (Poaceae-Andropogoneae): Taxonomic implications and evidence of interspecific hybridization. 2016 , 99, 155-167	16
790	A Global Genomic Characterization of Nairoviruses Identifies Nine Discrete Genogroups with Distinctive Structural Characteristics and Host-Vector Associations. 2016 , 94, 1107-1122	32
789	Prevention of SHIV transmission by topical IFN- β treatment. 2016 , 9, 1528-1536	36

788	Tumor DNA in cerebral spinal fluid reflects clinical course in a patient with melanoma leptomeningeal brain metastases. 2016 , 128, 93-100	64
787	Long Non-Coding RNAs. 2016 ,	3
786	Adaptation to Parasites and Costs of Parasite Resistance in Mutator and Nonmutator Bacteria. 2016 , 33, 770-82	16
785	The Vigna Genome Server, 'VigGS': A Genomic Knowledge Base of the Genus Vigna Based on High-Quality, Annotated Genome Sequence of the Azuki Bean, <i>Vigna angularis</i> (Willd.) Ohwi & Ohashi. 2016 , 57, e2	29
784	DNA-seq analysis of <i>Garcinia mangostana</i> . 2016 , 7, 62-3	8
783	Loss of PPAR α in endothelial cells leads to impaired angiogenesis. 2016 , 129, 693-705	28
782	Effects of DNA Methylation and Chromatin State on Rates of Molecular Evolution in Insects. 2015 , 6, 357-63	10
781	Testing the kinship theory of intragenomic conflict in honey bees (<i>Apis mellifera</i>). 2016 , 113, 1020-5	51
780	Genomic analysis of 38 <i>Legionella</i> species identifies large and diverse effector repertoires. 2016 , 48, 167-75	156
779	No Accumulation of Transposable Elements in Asexual Arthropods. 2016 , 33, 697-706	44
778	Detecting the Anomaly Zone in Species Trees and Evidence for a Misleading Signal in Higher-Level Skink Phylogeny (Squamata: Scincidae). 2016 , 65, 465-77	57
777	High concentrations of bioavailable heavy metals impact freshwater sediment microbial communities. 2016 , 66, 1003-1012	32
776	Identification of important long non-coding RNAs and highly recurrent aberrant alternative splicing events in hepatocellular carcinoma through integrative analysis of multiple RNA-Seq datasets. 2016 , 291, 1035-51	26
775	HPMCD: the database of human microbial communities from metagenomic datasets and microbial reference genomes. 2016 , 44, D604-9	50
774	Precision methylome characterization of <i>Mycobacterium tuberculosis</i> complex (MTBC) using PacBio single-molecule real-time (SMRT) technology. 2016 , 44, 730-43	62
773	Assessment throughout a whole fishing year of the dominant microbiota of peeled brown shrimp (<i>Crangon crangon</i>) stored for 7 days under modified atmosphere packaging at 4°C without preservatives. 2016 , 54, 60-71	18
772	Assessing similarity to primary tissue and cortical layer identity in induced pluripotent stem cell-derived cortical neurons through single-cell transcriptomics. 2016 , 25, 989-1000	64
771	Identification of an Immunogenic Subset of Metastatic Uveal Melanoma. 2016 , 22, 2237-49	60

770	Analysis of Genotyping-by-Sequencing (GBS) Data. 2016 , 1374, 269-84	4
769	DIANA-LncBase v2: indexing microRNA targets on non-coding transcripts. 2016 , 44, D231-8	431
768	Epidemiologic and Genotypic Review of Carbapenemase-Producing Organisms in British Columbia, Canada, between 2008 and 2014. 2016 , 54, 317-27	13
767	RNA-seq analysis for plant carnivory gene discovery in <i>Nepenthes ventrata</i> . 2016 , 7, 18-9	16
766	Integrated Transcriptomic-Proteomic Analysis Using a Proteogenomic Workflow Refines Rat Genome Annotation. 2016 , 15, 329-39	25
765	DIANA-miRGen v3.0: accurate characterization of microRNA promoters and their regulators. 2016 , 44, D190-5	39
764	Seeking the driver in tumours with apparent normal molecular profile on comparative genomic hybridization and targeted gene panel sequencing: what is the added value of whole exome sequencing?. 2016 , 27, 344-52	6
763	A FISH-based chromosome map for the European corn borer yields insights into ancient chromosomal fusions in the silkworm. 2016 , 116, 75-83	19
762	First comprehensive multi-tissue transcriptome of <i>Cherax quadricarinatus</i> (Decapoda: Parastacidae) reveals unexpected diversity of endogenous cellulase. 2016 , 16, 185-200	16
761	Whole transcriptome profiling of adult and infective stages of the trematode <i>Opisthorchis felinus</i> . 2016 , 65, 12-19	20
760	Multiple Origins of Eukaryotic <i>cox15</i> Suggest Horizontal Gene Transfer from Bacteria to Jakobid Mitochondrial DNA. 2016 , 33, 122-33	15
759	Transcriptome analysis of <i>Solanum melongena</i> L. (eggplant) fruit to identify putative allergens and their epitopes. 2016 , 576, 64-71	13
758	Comparative analysis of the gastrointestinal microbial communities of bar-headed goose (<i>Anser indicus</i>) in different breeding patterns by high-throughput sequencing. 2016 , 182, 59-67	49
757	Identification and Resolution of Microdiversity through Metagenomic Sequencing of Parallel Consortia. 2016 , 82, 255-67	34
756	How Should Genes and Taxa be Sampled for Phylogenomic Analyses with Missing Data? An Empirical Study in Iguanian Lizards. 2016 , 65, 128-45	116
755	Mapping the non-standardized biases of ribosome profiling. 2016 , 397, 23-35	40
754	Functional analysis of NtMPK2 uncovers its positive role in response to <i>Pseudomonas syringae</i> pv. tomato DC3000 in tobacco. 2016 , 90, 19-31	4
753	High-sensitivity sequencing reveals multi-organ somatic mosaicism causing DICER1 syndrome. 2016 , 53, 43-52	51

752	Nucleotide-Level Profiling of m ⁶ A RNA Methylation. 2016 , 1358, 269-84	9
751	Multiple Genetic Mechanisms Contribute to Visual Sensitivity Variation in the Labridae. 2016 , 33, 201-15	30
750	Sequence capture of ultraconserved elements from bird museum specimens. 2016 , 16, 1189-203	146
749	Preface. 2016 , 1358, v-viii	2
748	Relationship Between Microbiota of the Colonic Mucosa vs Feces and Symptoms, Colonic Transit, and Methane Production in Female Patients With Chronic Constipation. 2016 , 150, 367-79.e1	173
747	The complete chloroplast genome of Tibetan hulless barley. 2017 , 28, 324-325	4
746	Phylogenetic relationships within <i>Lactuca</i> L. (Asteraceae), including African species, based on chloroplast DNA sequence comparisons. 2017 , 64, 55-71	19
745	Phenylalanine Ammonia-Lyase: A Key Gene for Color Discrimination of Edible Mushroom <i>Flammulina velutipes</i> . 2023 , 9, 339	0
744	Genomic and Transcriptomic Characterization of <i>Alternaria alternata</i> during Infection. 2023 , 13, 809	0
743	Quantitative 16S rRNA Gene Amplicon Sequencing for Comprehensive Pathogenic Bacterial Tracking in a Municipal Wastewater Treatment Plant. 2023 , 3, 923-933	0
742	Chromosome-level genome of the three-spot damselfish, <i>Dascyllus trimaculatus</i> . 2023 , 13,	0
741	Changes in community structures and functions of the gut microbiomes of deep-sea cold seep mussels during in situ transplantation experiment. 2023 , 5,	0
740	Characterization of methanotrophic community and activity in landfill cover soils under dimethyl sulfide stress. 2023 , 161, 263-274	0
739	Characterization and complete genome sequence analysis of the novel phage RPZH3 infecting <i>Ralstonia solanacearum</i> . 2023 , 168,	0
738	Differential universal ortholog composition of <i>Coffea arabica</i> L. sub-genomes and its contribution to regulatory networks governing essential biological processes.	0
737	Genomic characterization of a novel torradovirus infecting <i>Arctium lappa</i> L. in China. 2023 , 168,	0
736	MYC-driven U2SURP regulates alternative splicing of SAT1 to promote triple-negative breast cancer progression. 2023 , 560, 216124	0
735	Comammox <i>Nitrospira</i> and Ammonia-Oxidizing Archaea Are Dominant Ammonia Oxidizers in Sediments of an Acid Mine Lake Containing High Ammonium Concentrations. 2023 , 89,	0

- 734 Genomic clines across the species boundary between a hybrid pine and its progenitor in the eastern Tibetan Plateau. **2023**, 100574 ○
- 733 Loss of daylength sensitivity by splice site mutation in Cannabis. ○
- 732 A learning experience elicits sex-dependent neurogenomic responses in *Bicyclus anynana* butterflies. ○
- 731 Abiotic selection of microbial genome size in the global ocean. **2023**, 14, ○
- 730 Leukemic stem cells hijack lineage inappropriate signalling pathways to promote their growth. ○
- 729 Comparative Genomic Analysis of Enterococci across Sectors of the One Health Continuum. **2023**, 11, 727 ○
- 728 A phylogenomic analysis of *Limosilactobacillus reuteri* reveals ancient and stable evolutionary relationships with rodents and birds and zoonotic transmission to humans. **2023**, 21, ○
- 727 RNA-seq data science: From raw data to effective interpretation. 14, ○
- 726 Testing and using complete plastomes for authentication of medicinal *Polygonatum* species (*Asparagaceae*). **2023**, 197, 116557 ○
- 725 MangoBase: A Genomics Portal and Gene Expression Atlas for *Mangifera indica*. **2023**, 12, 1273 ○
- 724 Distinctive origin and evolution of endemic thistle of Korean volcanic island: Structural organization and phylogenetic relationships with complete chloroplast genome. **2023**, 18, e0277471 ○
- 723 Genome-Wide Analysis of MIKCC-Type MADS-Box Genes Reveals Their Involvement in Flower Development in *Malus* Lineage. **2023**, 9, 373 ○
- 722 The Complete Genome Sequence of *Verbascum thapsus* (*Scrophulariaceae*, *Lamiales*), the Common Mullein. ○
- 721 The phylogeny and evolutionary ecology of hoverflies (Diptera: *Syrphidae*) inferred from mitochondrial genomes. **2023**, 184, 107759 ○
- 720 Vitamin B12 attenuates leukocyte inflammatory signature in COVID-19 via methyl-dependent changes in epigenetic markings. 14, ○
- 719 Vaccination against swine influenza in pigs causes different drift evolutionary patterns upon swine influenza virus experimental infection and reduces the likelihood of genomic reassortments. 13, ○
- 718 Lipid extract derived from newly isolated *Rhodotorula toruloides* LAB-07 for cosmetic applications. **2023**, 21, 2009-2017 ○
- 717 Integrative Analyses Reveal the Anticancer Mechanisms and Sensitivity Markers of the Next-Generation Hypomethylating Agent NTX-301. **2023**, 15, 1737 ○

- 716 Draft Genome Sequence of *Granulicatella* sp. Strain S8, Isolated from a Marine Fish, *Seriola quinqueradiata*. **2023**, 12,
- 715 Homoeologous non-reciprocal translocation explains a major QTL for seed lignin content in oilseed rape (*Brassica napus*L.).
- 714 C-Type Natriuretic Peptide Acts as a Microorganism-Activated Regulator of the Skin Commensals *Staphylococcus epidermidis* and *Cutibacterium acnes* in Dual-Species Biofilms. **2023**, 12, 436
- 713 A Genome-Scale Atlas Reveals Complex Interplay of Transcription and Translation in an Archaeon.
- 712 *Aspergillus fumigatus* Can Display Persistence to the Fungicidal Drug Voriconazole. **2023**, 11,
- 711 Single-cell analyses reveal distinct expression patterns and roles of long non-coding RNAs during hESC differentiation into pancreatic progenitors. **2023**, 14,
- 710 Genome-wide identification and comparative analyses of key genes involved in C4 photosynthesis in five main gramineous crops. 14,
- 709 Triap1 upregulation promotes escape from mitotic-slippage-induced G1 arrest. **2023**, 42, 112215
- 708 Draft Genome Sequence of *Bacillus anthracis* N1, Isolated from a Recreational Freshwater Kettle Lake in Ontario, Canada. **2023**, 12,
- 707 *Kengiochloa*, a new bamboo genus to accommodate the morphologically unique species, *Pseudosasa pubiflora* (Poaceae). 221, 131-145
- 706 Analysis of blood and nasal epithelial transcriptomes to identify mechanisms associated with control of SARS-CoV-2 viral load in the upper respiratory tract.
- 705 Phylogenomics of novel ploetid taxa contribute to the backbone of the euglenid tree.
- 704 Fragment length profiles of cancer mutations enhance detection of circulating tumor DNA in patients with early-stage hepatocellular carcinoma. **2023**, 23,
- 703 The proposed role of MSL-lncRNAs in causing sex lability of female poplars.
- 702 Time-Series Transcriptome Analysis Reveals the Molecular Mechanism of Ethylene Reducing Cold Sensitivity of Postharvest Huangguan Pear. **2023**, 24, 5326
- 701 Comprehensive Genome-Wide Analyses of Poplar R2R3-MYB Transcription Factors and Tissue-Specific Expression Patterns under Drought Stress. **2023**, 24, 5389
- 700 The tropical cookbook: Termite diet and phylogenetics Drive the microbiome and functional genetic structure of nests. 14,
- 699 Transmission of stimulus-induced epigenetic changes through cell division is coupled to continuous transcription factor activity. 14,

- 698 Global Long Noncoding RNA Expression Profiling of MSTN and FGF5 Double-Knockout Sheep Reveals the Key Gatekeepers of Skeletal Muscle Development. **2023**, 42, 163-175 ○
- 697 An ancient gene regulatory network sets the position of the forebrain in chordates. ○
- 696 Site-specific analysis reveals candidate cross-kingdom small RNAs, tRNA and rRNA fragments, and signs of fungal RNA phasing in the barley powdery mildew interaction. ○
- 695 Stability in gene expression and body-plan development leads to evolutionary conservation. **2023**, 14, ○
- 694 Hybrid inferiority and genetic incompatibilities drive divergence of fungal pathogens infecting the same host. ○
- 693 Changes in the gut microbiota composition of healthy young volunteers after administration of *Lactobacillus rhamnosus* LRA05: A placebo-controlled study. 10, ○
- 692 Brevicillin, a novel lanthipeptide from the genus *Brevibacillus* with antimicrobial, antifungal, and antiviral activity. **2023**, 134, ○
- 691 The first complete mitochondrial genomes of three dobsonfly species (Megaloptera: Corydalidae) from Pakistan with phylogenetic implications. **2022**, 66, ○
- 690 Analysis of the chloroplast genome and phylogenetic evolution of *Bidens pilosa*. **2023**, 24, ○
- 689 Osmopriming with selenium: physical and physiological quality of tomato seeds in response to water deficit. 45, ○
- 688 First complete mitochondrial genome of the endemic goby, *Rhinogobius davidi* (Gobiiformes: Gobiidae: Gobionellinae), in China. **2023**, 8, 410-413 ○
- 687 Designing Effective Multi-Target Drugs and Identifying Biomarkers in Recurrent Pregnancy Loss (RPL) Using In Vivo, In Vitro, and In Silico Approaches. **2023**, 11, 879 ○
- 686 Peptidome and Transcriptome Analysis of Plant Peptides Involved in *Bipolaris maydis* Infection of Maize. **2023**, 12, 1307 ○
- 685 Clonal isolates of *Treponema pallidum* subsp. *pallidum* Nichols provide evidence for the occurrence of microevolution during experimental rabbit infection and in vitro culture. **2023**, 18, e0281187 ○
- 684 Metabolic Versatility of the Family Halieaceae Revealed by the Genomics of Novel Cultured Isolates. **2023**, 11, ○
- 683 *Arabidopsis* cell suspension culture and RNA sequencing reveal regulatory networks underlying plant programmed cell death. ○
- 682 Conservation and divergence of canonical and non-canonical imprinting in murids. **2023**, 24, ○
- 681 Mycobacterial RNase E cleaves with a distinct sequence preference and controls the degradation rates of most *Mycobacterium smegmatis* RNAs. ○

- 680 Molecular signature of domestication in the arboviral vector *Aedes aegypti*. ○
- 679 Endophyte genomes support greater metabolic gene cluster diversity compared with non-endophytes in *Trichoderma*. ○
- 678 The mobile gene cassette carrying tetracycline resistance genes in *Aeromonas veronii* strain Ah5S-24 isolated from catfish pond sediments shows similarity with a cassette found in other environmental and foodborne bacteria. 14, ○
- 677 Congruent downy mildew-associated microbiomes reduce plant disease and function as transferable resistobiomes. ○
- 676 RSV infection does not induce EMT. ○
- 675 Orpinolide disrupts a leukemic dependency on cholesterol transport by inhibiting the oxysterol-binding protein OSBP. ○
- 674 Perturbomics of tumor-infiltrating NK cells. ○
- 673 Molecular Profile of MSH6-Associated Colorectal Carcinomas Shows Distinct Features From Other Lynch Syndrome-Associated Colorectal Carcinomas. **2023**, ○
- 672 MatrIn3 regulates mitotic spindle dynamics by controlling alternative splicing of CDC14B. **2023**, 42, 112260 ○
- 671 Evaluation of the Oral Bacterial Genome and Metabolites in Patients with Wolfram Syndrome. **2023**, 24, 5596 ○
- 670 Whole-Genome Sequence of Endophytic Bacteria Associated with Poison Ivy Vine (*Toxicodendron radicans*). **2023**, 12, ○
- 669 Population genetics and geographic origins of mallards harvested in northwestern Ohio. **2023**, 18, e0282874 ○
- 668 Comparative transcriptome analysis reveals the molecular mechanism of heat-tolerance in *Neopyropia yezoensis* induced by *Sargassum horneri* extract. 10, ○
- 667 Integration of pharmacoproteomic and computational approaches reveals the cellular signal transduction pathways affected by apatinib in gastric cancer cell lines. **2023**, 21, 2172-2187 ○
- 666 The tissue-specific chromatin accessibility landscape of *Papaver somniferum*. 14, ○
- 665 The gut microbiota diversity of five Orthoptera (Insecta, Polyneoptera) insects determined by DNA metabarcoding. 11, ○
- 664 Elements of divergence in germline determination in closely related species. **2023**, 26, 106402 ○
- 663 Whole-Genome Sequence and Assembly of Eight Africa Horse Sickness Virus Strains Collected in Namibia and South Africa. **2023**, 12, ○

- 662 Revealing evolution of tropane alkaloid biosynthesis by analyzing two genomes in the Solanaceae family. **2023**, 14, ○
- 661 Human pluripotent stem cell-derived kidney organoids reveal tubular epithelial pathobiology of heterozygous HNF1B-associated dysplastic kidney malformations. ○
- 660 Identification of asthma-related genes using asthmatic blood eQTLs of Korean patients. ○
- 659 Downregulation of Hsp90 and the antimicrobial peptide Mtk suppresses poly(GR)-induced neurotoxicity in C9ORF72-ALS/FTD. **2023**, ○
- 658 Disease-induced multifaceted variations in community assembly and functions of plant-associated microbiomes. 14, ○
- 657 *Ligilactobacillus ubinensis* sp. nov., a novel species isolated from the wild ferment of a durian fruit (*Durio zibethinus*). **2023**, 73, ○
- 656 Biological and molecular characterization of chrysanthemum stem necrosis orthotospovirus infecting sweet pepper in Brazil. **2023**, 171, 217-221 ○
- 655 Genome-wide identification and characterization of tissue-specific non-coding RNAs in black pepper (*Piper nigrum* L.). 14, ○
- 654 Hybrid zone or hybrid lineage: a genomic reevaluation of Sibley's classic species conundrum in *Pipilo* towhees. **2023**, 77, 852-869 1
- 653 Single substitution in H3.3G34 alters DNMT3A recruitment to cause progressive neurodegeneration. **2023**, 186, 1162-1178.e20 ○
- 652 Differentiation trajectories of the hydranervous system reveal transcriptional regulators of neuronal fate. ○
- 651 Bioinformatic and Statistical Analysis of Microbiome Data. **2023**, 183-229 ○
- 650 Integration of Human and Viral miRNAs in Epstein-Barr Virus-Associated Tumors and Implications for Drug Repurposing. **2023**, 27, 93-108 ○
- 649 Complete Genome Sequence of *Klebsiella oxytoca* Strain AHC-6, Isolated from a Patient during Acute Antibiotic-Associated Hemorrhagic Colitis. **2023**, 12, ○
- 648 The association between the composition of the early-life intestinal microbiome and eczema in the first year of life. 2, ○
- 647 Using a whole genome co-expression network to inform the functional characterisation of predicted genomic elements from *Mycobacterium tuberculosis* transcriptomic data. **2023**, 119, 381-400 ○
- 646 Reproducible chemostat cultures to eliminate eukaryotic viruses from fecal transplant material. ○
- 645 Synthetic regulatory genomics uncovers enhancer context dependence at the *Sox2* locus. **2023**, 83, 1140-1152.e7

- 644 Cervicovaginal Human Papillomavirus Genomes, Microbiota Composition and Cytokine Concentrations in South African Adolescents. **2023**, 15, 758 ○
- 643 Electrokinetic-Enhanced Bioremediation of Trichloroethylene-Contaminated Low-Permeability Soils: Mechanistic Insight from Spatio-Temporal Variations of Indigenous Microbial Community and Biodehalogenation Activity. **2023**, 57, 5046-5055 ○
- 642 Comparative Gut Microbiome Differences between High and Low Aortic Arch Calcification Score in Patients with Chronic Diseases. **2023**, 24, 5673 ○
- 641 Unlocking the genome of perch [From genes to ecology and back again. ○
- 640 Complete Mitochondrial Genome and Phylogenetic Position of *Chirolophis wui* (Perciformes: Stichaeidae). **2023**, 8, 165 ○
- 639 The genetic basis of plumage coloration and elevation adaptation in a clade of recently diverged alpine and arctic songbirds. **2023**, 77, 705-717 ○
- 638 Comparative mitogenomics of native European and alien Ponto-Caspian amphipods. ○
- 637 Genomic discovery and functional validation of MRP1 as a novel fetal hemoglobin modulator and potential therapeutic target in sickle cell disease. ○
- 636 Virome diversity of *Hyalomma dromedarii* ticks collected from camels in the United Arab Emirates. **2023**, 439-448 ○
- 635 Antiviral immune response reveals host-specific virus infections in natural ant populations. 14, ○
- 634 Hypothalamic thyroid hormone deficiency underlies reversible anorexia in a mammalian hibernator. ○
- 633 Pharmacogenomic and Statistical Analysis. **2023**, 305-330 ○
- 632 Asexual male production by ZW recombination in *Artemia parthenogenetica*. **2023**, 77, 1-12 ○
- 631 Exploring the Inhibitory Activity of Selected Lactic Acid Bacteria against Bread Rope Spoilage Agents. **2023**, 9, 290 ○
- 630 Hematopoietic/erythroid enhancers activate nearby target genes by extending histone H3K27ac and transcribing intergenic RNA. **2023**, 37, ○
- 629 Association of Fungi in the Intestine of Black Carp and Grass Carp Compared with their Cultured Water. **2023**, 2023, 1-10 ○
- 628 Assembly of novel microbial genomes from gut metagenomes of rhesus macaque (*Macaca mulatta*). **2023**, 15, ○
- 627 Genome-wide characterization of the MBF1 gene family and its expression pattern in different tissues and stresses in *Medicago*. ○

- 626 Analyzing CRISPR screens in non-conventional microbes. **2023**, 50, ○
- 625 Exploring the sorghum race level diversity utilizing 272 sorghum accessions genomic resources. 14, ○
- 624 The genomic characteristics affect phenotypic diversity from the perspective of genetic improvement of economic traits. **2023**, 26, 106426 ○
- 623 Assessment of bacterial and viral gut communities in healthy and tumoral colorectal tissue using RNA and DNA deep-sequencing. ○
- 622 The prophage-encoded transcriptional regulator AppY has pleiotropic effects on E. coli physiology. **2023**, 19, e1010672 ○
- 621 Analysis of Genome Structure and Its Variations in Potato Cultivars Grown in Russia. **2023**, 24, 5713 ○
- 620 Functional and Proteomic Insights into Aculeata Venoms. **2023**, 15, 224 ○
- 619 Transcriptome sequencing of sesame (*Sesamum indicum*) using Illumina Platform. **2018**, 88, 442-446 ○
- 618 Genetics of destemming in pepper: A step towards mechanical harvesting. 14, ○
- 617 mRNAs encoding IL-12 and a decoy-resistant variant of IL-18 synergize to engineer T cells for efficacious intratumoral adoptive immunotherapy. **2023**, 4, 100978 ○
- 616 Assessing the potential use of environmental DNA for multifaceted genetic monitoring of cetaceans: Example of a wandering whale in a highly disturbed bay area. **2023**, 148, 110125 ○
- 615 Using Next-Generation Sequencing to Disentangle the Diet and Incidence of Intestinal Parasites of Falkland Flightless Steamer Duck *Tachyeres brachypterus* and Patagonian Crested Duck *Lophonetta specularioides* Sharing a South Atlantic Island. **2023**, 14, 731 ○
- 614 The vascular gene *Apold1* is dispensable for normal development but controls angiogenesis under pathological conditions. ○
- 613 Integrated transcriptome and metabonomic analysis of key metabolic pathways in response to cadmium stress in novel buckwheat and cultivated species. 14, ○
- 612 Evolutionary history and patterns of divergence in three tropical east Asian squirrels across the Isthmus of Kra. ○
- 611 Transcription regulation by CarD in mycobacteria is guided by basal promoter kinetics. ○
- 610 Evolution of chemosensory and detoxification gene families across herbivorous Drosophilidae. ○
- 609 Widespread gene flow following range expansion in Anna's Hummingbird. ○

- 608 Depletion of LONP2 unmasks differential requirements for peroxisomal function between cell types and in cholesterol metabolism. ○
- 607 DNA virus BdDV-1 of the amphibian pathogen *Batrachochytrium dendrobatidis* associated with hypervirulence. ○
- 606 Diverse and Abundant Viruses Exploit Conjugative Plasmids. ○
- 605 Identification of mammalian transcription factors that bind to inaccessible chromatin. ○
- 604 Novel in-silico predicted matrikines are differential mediators of in vitro and in vivo cellular metabolism. ○
- 603 Analysis of spike protein variants evolved in a novel mouse model of persistent SARS-CoV-2 infection. ○
- 602 *Treponema pallidum* subsp. *pallidum* with an Artificially impaired TprK antigenic variation system is attenuated in the Rabbit model of syphilis. **2023**, 19, e1011259 ○
- 601 Comprehensive transcriptomic analysis to identify biological and clinical differences in cholangiocarcinoma. ○
- 600 Long-read single-cell sequencing reveals expressions of hypermutation clusters of isoforms in human liver cancer cells. ○
- 599 The gut microbiome in social anxiety disorder: evidence of altered composition and function. **2023**, 13, ○
- 598 Rapid evolution of pre-zygotic reproductive barriers in allopatric populations. ○
- 597 Genic-SSR-based genetic diversity and population structure analysis in a global germplasm collection highlights the African origin of winged bean (*Psophocarpus tetragonolobus* L.). ○
- 596 Transcriptional Regulation of Female and Male Flower Bud Initiation and Development in Pecan (*Carya illinoensis*). **2023**, 12, 1378 ○
- 595 Propagated Circulating Tumor Cells Uncover the Potential Role of NF κ B, EMT, and TGF β Signaling Pathways and COP1 in Metastasis. **2023**, 15, 1831 ○
- 594 Complete mitochondrial genome sequence and annotation of *Rhinogobius lentiginis* (Gobiiformes: Gobiidae: Gobionellinae). **2023**, 8, 418-421 ○
- 593 Non-catalytic regulation of 18S rRNA methyltransferase DIMT1 in acute myeloid leukemia. ○
- 592 An efficient diazotroph-derived nitrogen transfer pathway in coral reef system. **2023**, 68, 963-981 ○
- 591 Highly efficient and rapid generation of human pluripotent stem cells by chemical reprogramming. **2023**, 30, 450-459.e9 ○

- 590 Stepwise activities of mSWI/SNF family chromatin remodeling complexes direct T cell activation and exhaustion. **2023**, 83, 1216-1236.e12 ○
- 589 Selective whole-genome amplification reveals population genetics of *Leishmania braziliensis* directly from patient skin biopsies. **2023**, 19, e1011230 ○
- 588 Biocatalytic potential of Pseudolycoxia CAZymes (Sciarioidea, Diptera) in degrading plant and fungal cell wall polysaccharides. **2023**, 26, 106449 ○
- 587 Parthenocarpy-related genes induced by naphthalene acetic acid in oil palm interspecific *O. [Elaeis oleifera (Kunth) Cort. [Elaeis guineensis Jacq.]* hybrids. 14, ○
- 586 Genotypic Characterization of Infectious Spleen and Kidney Necrosis Virus (ISKNV) in Southeast Asian Aquaculture. **2023**, 2023, 1-16 ○
- 585 *Brevundimonas* and *Serratia* as host systems for assessing associated environmental viromes and phage diversity by complementary approaches. 14, ○
- 584 A reproducible enteric phage community improves blood glucose regulation in an obesity mouse model. ○
- 583 Genomic Analysis of the Deep-Sea Bacterium *Shewanella* sp. MTB7 Reveals Backgrounds Related to Its Deep-Sea Environment Adaptation. **2023**, 11, 798 ○
- 582 Analysis of Small Non-coding RNAs as Signaling Intermediates of Environmentally Integrated Responses to Abiotic Stress. **2023**, 403-427 ○
- 581 Genome-Wide Identification of Expansin Gene Family and Their Response under Hormone Exposure in *Ginkgo biloba* L.. **2023**, 24, 5901 ○
- 580 An integrated RNA-proteomic landscape of drug induced senescence in a cancer cell line. ○
- 579 The characteristics of soil microbial co-occurrence networks across a high-latitude forested wetland ecotone in China. 14, ○
- 578 Genomic adaptation underlies nutrient-driven reprogramming in the malaria-causing parasite. ○
- 577 Bacterial c-di-GMP plays a key role in the evolution of host-association. ○
- 576 Whole genome characterization of thermophilic *Campylobacter* species isolated from dairy manure in small specialty crop farms of Northeast Ohio. 14, ○
- 575 Classification of Tumor Immune Microenvironment According to Programmed Death-Ligand 1 Expression and Immune Infiltration Predicts Response to Immunotherapy Plus Chemotherapy in Advanced Patients With NSCLC. **2023**, ○
- 574 Metabarcoding the zooplankton species of the Saudi Arabian Gulf: A study employing mock communities and two gene markers. **2023**, ○
- 573 Different waves of postglacial recolonisation and genomic structure of bank vole populations in NE Poland. ○

- 572 Rapid survey of de novo mutations in naturally growing tree species following the March 2011 disaster in Fukushima: The effect of low-dose-rate radiation. **2023**, 174, 107893 ○
- 571 Discovery of Brassica Yellow Virus and Porcine Reproductive and Respiratory Syndrome Virus in *Diaphorina citri* and Changes in Virome Due to Infection with *Ca. L. asiaticus* **2023**, 11, ○
- 570 Transcriptome sequencing identifies prognostic genes involved in gastric adenocarcinoma. ○
- 569 Genetic sequencing of a 1944 Rocky Mountain spotted fever vaccine. **2023**, 13, ○
- 568 Characteristics of the rumen virome in Japanese cattle. ○
- 567 The Complete Genome Sequence of *Curcuma longa* (Zingiberaceae, Zingiberales), Turmeric. ○
- 566 Plastome characterization of *Musa indandamanensis*, an endemic banana in Andaman and Nicobar Islands, India. ○
- 565 Isolation and characterisation of novel *Methanocorpusculum* species indicates the genus is ancestrally host-associated. **2023**, 21, ○
- 564 Genome-resolved metagenomics of milk microbiomes reveals the influence of maternal dietary fiber on neonatal inheritance of immunoregulatory traits. ○
- 563 Combing fecal microbial community data to identify consistent obesity-specific microbial signatures and shared metabolic pathways. **2023**, 26, 106476 ○
- 562 Co-segregation of recombinant chromatids maintains genome-wide heterozygosity in an asexual nematode. ○
- 561 Native solitary bee reproductive success depends on early season precipitation and host plant richness. **2023**, 201, 965-978 ○
- 560 Genomic-wide analysis approach revealed genomic similarity for environmental Mexican *S. Oranienburg* genomes. 1-12 ○
- 559 Comparative genomics of *Mycoplasma feriruminatoris*, a fast-growing pathogen of wild *Caprinae*. ○
- 558 Multi-faceted metagenomic analysis of spacecraft associated surfaces reveal planetary protection relevant microbial composition. **2023**, 18, e0282428 ○
- 557 Conditional Forest Models Built Using Metagenomic Data Accurately Predicted *Salmonella* Contamination in Northeastern Streams. **2023**, 11, ○
- 556 Complete Genome Sequence of *Streptococcus gallolyticus* Strain XH2168. **2023**, 12, ○
- 555 Adaptation of the Porcine Pituitary Transcriptome, Spliceosome and Editome during Early Pregnancy. **2023**, 24, 5946 ○

- 554 Gene Coexpression Analysis Identifies Genes Associated with Chlorophyll Content and Relative Water Content in Pearl Millet. **2023**, 12, 1412 ○
- 553 Genome assembly of the ectoparasitoid wasp *Theocolax elegans*. **2023**, 10, ○
- 552 Characterizing Cellular Differentiation Potency and Waddington Landscape via Energy Indicator. **2023**, 6, ○
- 551 Response of intestinal microbiota to saline-alkaline water in mud crab (*Scylla paramamosain*) based on multiple low salinity culture modes. 10, ○
- 550 Capture RIC-seq reveals positional rules of PTBP1-associated RNA loops in splicing regulation. **2023**, 83, 1311-1327.e7 ○
- 549 Sida chlorotic leaf virus: a new recombinant begomovirus found in non-cultivated plants and *Cucumis sativus* L. 11, e15047 ○
- 548 Analysis of metatranscriptomic methods to enable wastewater-based biosurveillance of all infectious diseases. 11, ○
- 547 The phylogeny and metabolic potentials of an n-alkane-degrading *Venatorbacter* bacterium isolated from deep-sea sediment of the Mariana Trench. 14, ○
- 546 Potential Auxiliary Metabolic Capabilities and Activities Reveal Biochemical Impacts of Viruses in Municipal Wastewater Treatment Plants. **2023**, 57, 5485-5498 ○
- 545 SARS-CoV-2 infection alters the gut microbiome in diabetes patients: A cross-sectional study from Bangladesh. **2023**, 95, ○
- 544 Discovering the Repeatome of Five Species Belonging to the Asteraceae Family: A Computational Study. **2023**, 12, 1405 ○
- 543 Evolutionary differences in gene loss and pseudogenization among mycoheterotrophic orchids in the tribe Vanilleae (subfamily Vanilloideae). 14, ○
- 542 High nucleotide diversity accompanies differential DNA methylation in naturally diverging populations. ○
- 541 Upper respiratory tract mycobiome alterations in different kinds of pulmonary disease. 14, ○
- 540 The genome of medicinal plant *Sophora flavescens* has undergone significant expansion of both transposons and genes. ○
- 539 Hybrid De Novo Whole-Genome Assembly, Annotation, and Identification of Secondary Metabolite Gene Clusters in the Ex-Type Strain of *Chrysosporium keratinophilum*. **2023**, 9, 389 ○
- 538 Transcriptional Control of *hgcAB* by an ArsR-Like Regulator in *Pseudodesulfovibrio mercurii* ND132. ○
- 537 The evolution of white-tailed jackrabbit camouflage in response to past and future seasonal climates. **2023**, 379, 1238-1242 ○

- 536 High performance *Legionella pneumophila* source attribution using genomics-based machine learning classification. ○
- 535 Establishing a Generalizable Framework for Generating Cost-Aware Training Data and Building Unique Context-Aware Walltime Prediction Regression Models. **2022**, ○
- 534 Elucidation of the pathway for biosynthesis of saponin adjuvants from the soapbark tree. **2023**, 379, 1252-1264 1
- 533 Strong Positive Selection in *Aedes aegypti* and the Rapid Evolution of Insecticide Resistance. **2023**, 40, ○
- 532 Unmasking the tissue-resident eukaryotic DNA virome in humans. ○
- 531 Discovery of a novel bacterial class with the capacity to drive sulfur cycling and microbiome structure in a paleo-ocean analog. ○
- 530 Metagenomics reveals the diversity and role of surface-water microbes in biogeochemical cycles in lakes at different terrain ladders. 11, ○
- 529 Multiple gene co-options underlie the rapid evolution of sexually deceptive flowers in *Gorteria diffusa*. **2023**, ○
- 528 Fever-like temperature impacts on *Staphylococcus aureus* and *Pseudomonas aeruginosa* interaction, physiology, and virulence both in vitro and in vivo. ○
- 527 Identification of a stable major sucrose-related QTL and diagnostic marker for flavor improvement in peanut. **2023**, 136, ○
- 526 Eubiotic effect of rifaximin is associated with decreasing abdominal pain in symptomatic uncomplicated diverticular disease: results from an observational cohort study. **2023**, 23, ○
- 525 Flexible parsing and preprocessing of technical sequences with splitcode. ○
- 524 Comparative transcriptomic and metabolite profiling reveals genotype-specific responses to Fe starvation in chickpea. **2023**, 175, ○
- 523 A role for heritable transcriptomic variation in maize adaptation to temperate environments. **2023**, 24, ○
- 522 High-Resolution Genomic Profiling of Liver Cancer Links Etiology With Mutation and Epigenetic Signatures. **2023**, ○
- 521 Vaginal microbiota of adolescents and their mothers: A preliminary study of vertical transmission and persistence. 2, ○
- 520 Effects of Starvation on the Physiology and Liver Transcriptome of Yellowcheek (*Elopichthys bambusa*). **2023**, 8, 175 ○
- 519 Investigating the Function of Predicted Proteins from RNA-Seq Data in Holstein and Cholistani Cattle Breeds. **2020**, 11, 121-135 ○

- 518 Photobiomodulation Reduces the Cytokine Storm Syndrome Associated with COVID-19 in the Zebrafish Model. **2023**, 24, 6104 ○
- 517 Metabarcoding and Metabolomics Reveal the Effect of the Invasive Alien Tree *Miconia calvescens* DC. on Soil Diversity on the Tropical Island of Moorea (French Polynesia). **2023**, 11, 832 ○
- 516 Phylogenomic investigation of an outbreak of fluoroquinolone-resistant *Salmonella enterica* subsp. *enterica* serovar Paratyphi A in Phnom Penh, Cambodia. **2023**, 9, ○
- 515 *Rhizohabitans arisaemae* gen. nov., sp. nov., a novel actinomycete of the family Streptosporangiaceae. **2023**, 73, ○
- 514 Characterization of Antimicrobial Resistance Genes and Virulence Factors in the Genomes of *Escherichia coli* ST69 Isolates from Preweaned Dairy Calves and Their Phylogenetic Relationship with Poultry and Human Clinical Strains. ○
- 513 Global scenario of the RmtE pan-aminoglycoside-resistance mechanism: emergence of the rmtE4 gene in South America associated with a hospital-related IncL plasmid. **2023**, 9, ○
- 512 Patterns of Chromosomal Variation, Homoeologous Exchange, and Their Relationship with Genomic Features in Early Generations of a Synthetic Rice Segmental Allotetraploid. **2023**, 24, 6065 ○
- 511 Detection of Selection Signatures on the X Chromosome in Iranian Dromedary Camels using Whole Genome Sequencing Data. **2022**, 13, 155-161 ○
- 510 A comprehensive map of hotspots of de novo telomere addition in *Saccharomyces cerevisiae*. ○
- 509 The Single Nucleotide Polymorphisms (SNP) Discovery on Transcriptome of Pure Sistani and Cross-Breeding of Sistani and Holstein, Simmental and Monte Billiard Bulls. **2022**, 13, 149-157 ○
- 508 Differential Genes Expression of Blood Tissue Related to Pre-Calving Ketosis in Holstein cow using Transcriptomics Data. **2022**, 13, 147-153 ○
- 507 THE RHODOEXPLORER PLATFORM FOR RED ALGAL GENOMICS AND WHOLE GENOME ASSEMBLIES FOR SEVERAL GRACILARIA SPECIES. ○
- 506 Transcriptomic Analyses of Exercise Training in Alzheimer's Disease Cerebral Cortex. **2023**, 1-15 ○
- 505 Chromosome-aware phylogenomics of Assassin Bugs (Hemiptera: Reduviidae) elucidates ancient gene conflict. ○
- 504 A genome sequence for *Biomphalaria pfeifferi*, the major vector snail for the human-infecting parasite *Schistosoma mansoni*. **2023**, 17, e0011208 ○
- 503 An explainable deep learning classifier of bovine mastitis based on whole genome sequence data - circumventing the p>>>n problem. ○
- 502 Nuclease genes occupy boundaries of genetic exchange between bacteriophages. ○
- 501 Gene conversion limits the cost of asexuality in immortal worms. ○

- 500 Convergent deployment of ancestral functions during the evolution of mammalian flight membranes. **2023**, 9, ○
- 499 The complete chloroplast genome of *Nymphaea atrans* (Surrey Wilfrid Laurance Jacobs, 1992: Nymphaeaceae). **2023**, 8, 430-433 ○
- 498 Comparative transcriptome analysis reveals the phosphate starvation alleviation mechanism of phosphate accumulating *Pseudomonas putida* in *Arabidopsis thaliana*. **2023**, 13, ○
- 497 High-resolution functional description of vaginal microbiomes in health and disease. ○
- 496 Seasonal variation of population and individual dietary niche in the avivorous bat, *la io*. **2023**, 201, 733-747 ○
- 495 Spatiotemporal transcriptomics and metabolic profiling provide insights into gene regulatory networks during lentil seed development. ○
- 494 Extensive variation in germlinede novomutations in *Poecilia reticulata*. ○
- 493 Large-scale epidemiological study on feline autosomal dominant polycystic kidney disease and identification of novel PKD1 gene variants. ○
- 492 Comprehensive genomic analyses of *Vigna unguiculata* provide insights into population differentiation and the genetic basis of key agricultural traits. ○
- 491 Transcriptome analysis of gene expression profiles reveals wood formation mechanisms in Chinese fir at different stand ages. **2023**, 9, e14861 ○
- 490 Genome-wide analysis of pathogenesis-related protein-1 (PR-1) genes from Qingke (*Hordeum vulgare* L. var. *nudum*) reveals their roles in stress responses. **2023**, 9, e14899 ○
- 489 Poly(A) tail length regulation by mRNA deadenylases is critical for suppression of transposable elements. ○
- 488 Generation of functional oocytes from male mice in vitro. **2023**, 615, 900-906 ○
- 487 Genome-Wide Effects on Gene Expression Between Parental and Filial Generations of Trisomy 11 and 12 of Rice. **2023**, 16, ○
- 486 Endogenous viral elements constitute a complementary source of antigens for personalized cancer immunotherapy. ○
- 485 Beyond the reference: gene expression variation and transcriptional response to RNAi in *C. elegans*. ○
- 484 An improved reference of the grapevine genome reasserts the origin of the PN40024 highly homozygous genotype. ○
- 483 On the Multiple Pattern String Matching in DNA Databases. **2023**, 4, ○

- 482 A male-killing gene encoded by a symbiotic virus of *Drosophila*. **2023**, 14, ○
- 481 Genomic diversity of non-diarrheagenic fecal *Escherichia coli* from children in sub-Saharan Africa and south Asia and their relatedness to diarrheagenic *E. coli*. **2023**, 14, ○
- 480 ISL1 controls pancreatic alpha cell fate and beta cell maturation. **2023**, 13, ○
- 479 Altered infective competence of the human gut microbiome in COVID-19. **2023**, 11, ○
- 478 ElasticBLAST: accelerating sequence search via cloud computing. **2023**, 24, ○
- 477 Large-scale analysis of putative Euphorbiaceae R2R3-MYB transcription factors identifies a MYB involved in seed oil biosynthesis. **2023**, 23, ○
- 476 A multi-organoid platform identifies CIART as a key factor for SARS-CoV-2 infection. **2023**, 25, 381-389 ○
- 475 Comparative analysis of complete *Artemisia* subgenus *Seriphidium* (Asteraceae: Anthemideae) chloroplast genomes: insights into structural divergence and phylogenetic relationships. **2023**, 23, ○
- 474 High-throughput time series expression profiling of *Plasmopara halstedii* infecting *Helianthus annuus* reveals conserved sequence motifs upstream of co-expressed genes. **2023**, 24, ○
- 473 Expression of down-regulated ERV LTR elements associates with immune activation in human small-cell lung cancers. **2023**, 14, ○
- 472 Transcriptomic profiles of the ruminal wall in Italian Mediterranean dairy buffaloes fed green forage. **2023**, 24, ○
- 471 Genetic architecture of a pollinator shift and its fate in secondary hybrid zones of two *Petunia* species. **2023**, 21, ○
- 470 DELLA functions evolved by rewiring of associated transcriptional networks. **2023**, 9, 535-543 ○
- 469 Fine mapping and candidate gene analysis of CaFCD1 affecting cuticle biosynthesis in *Capsicum annuum* L.. **2023**, 136, ○
- 468 Evidence for ancient selective sweeps followed by differentiation among three species of *Sphyrapicus* sapsuckers. ○
- 467 Targeting oxepitosis-mediated tumor suppression: a novel approach to treat colorectal cancers by sanguinarine. **2023**, 9, ○
- 466 The *Torreya grandis* genome illuminates the origin and evolution of gymnosperm-specific sciadonic acid biosynthesis. **2023**, 14, ○
- 465 QTL mapping and transcriptome analysis identify novel QTLs and candidate genes in *Brassica villosa* for quantitative resistance against *Sclerotinia sclerotiorum*. **2023**, 136, ○

- 464 Relationship between tumor microbiota transcriptional activity and gene expression in breast cancer. **2023**, 23, ○
- 463 *srdA* mutations suppress the *rseA/cpsA* deletion mutant conidiation defect in *Aspergillus nidulans*. **2023**, 13, ○
- 462 Weak gene-gene interaction facilitates the evolution of gene expression plasticity. **2023**, 21, ○
- 461 Dynamics of histone acetylation during human early embryogenesis. **2023**, 9, ○
- 460 The genomic epidemiology of *Escherichia albertii* infecting humans and birds in Great Britain. **2023**, 14, ○
- 459 Complete Genome Sequences of Two *Pasteurella multocida* Isolates from Seabirds. **2023**, 12, ○
- 458 Characterization of centromeric DNA of *Gossypium anomalum* reveals sequence-independent enrichment dynamics of centromeric repeats. **2023**, 31, ○
- 457 Genome-wide identification of tandem repeats associated with splicing variation across 49 tissues in humans. **2023**, 33, 435-447 ○
- 456 Meta-analyses of host metagenomes from colorectal cancer patients reveal strong relationship between colorectal cancer-associated species. ○
- 455 Genomic dissection of endemic carbapenem resistance: metallo-beta-lactamase gene dissemination through clonal, plasmid and integron transfer pathways. ○
- 454 Whole-mitochondrial genomes of *Nannizziopsis* provide insights in evolution and detection. **2023**, 13, ○
- 453 The characteristics of extrachromosomal circular DNA in patients with end-stage renal disease. **2023**, 28, ○
- 452 Conserved transcription factors promote cell fate stability and restrict reprogramming potential in differentiated cells. **2023**, 14, ○
- 451 Mapping pQTLs of circulating inflammatory proteins identifies drivers of immune-related disease risk and novel therapeutic targets. ○
- 450 MetaInvert: A new soil invertebrate genome resource provides insights into below-ground biodiversity and evolution. ○
- 449 Epidemiological and genomic analyses of human isolates of *Streptococcus suis* between 2005 and 2021 in Shenzhen, China. 14, ○
- 448 Metagenomic Sequencing Identified Specific Bacteriophage Signature Discriminating between Healthy and Diarrheal Neonatal Piglets. **2023**, 15, 1616 ○
- 447 Transcriptomic Analysis of Acetaminophen Biodegradation by *Penicillium chrysogenum* var. *halophenicum* and Insights into Energy and Stress Response Pathways. **2023**, 9, 408 ○

- 446 Transposable elements in the transcriptome of the velvetbean caterpillar *Anticarsia gemmatalis* Hübner, 1818 (Lepidoptera: Erebididae). ○
- 445 RNA-Seq Profiling between Commercial and Indigenous Iranian Chickens Highlights Differences in Innate Immune Gene Expression. **2023**, 14, 793 ○
- 444 Preadapted to adapt: underpinnings of adaptive plasticity revealed by the downy brome genome. **2023**, 6, ○
- 443 A Novel Dependoparvovirus Identified in Cloacal Swabs of Monk Parakeet (*Myiopsitta monachus*) from Urban Areas of Spain. **2023**, 15, 850 ○
- 442 Beyond the spore, the exosporium sugar anthrose impacts vegetative *Bacillus anthracis* gene regulation in cis and trans. **2023**, 13, ○
- 441 SO₂ and copper tolerance exhibit an evolutionary trade-off in *Saccharomyces cerevisiae*. **2023**, 19, e1010692 ○
- 440 Genetic diversity and within-breed variation in three indigenous Ethiopian sheep based on whole-genome analysis. **2023**, 9, e14863 ○
- 439 Aneuploidy Is Associated with Azole Resistance in *Aspergillus fumigatus*. **2023**, 67, ○
- 438 The Complete Genome Sequences of 9 Species of Swallowtail Butterflies (Papilionidae, Lepidoptera). ○
- 437 Nitrogen Fixation and Ammonium Assimilation Pathway Expression of *Geobacter sulfurreducens* Changes in Response to the Anode Potential in Microbial Electrochemical Cells. ○
- 436 Draft genome sequence of the apple pathogen *Colletotrichum chrysophilum* strain M932. ○
- 435 MORF2-mediated plastidial retrograde signaling is involved in stress response and skotomorphogenesis beyond RNA editing. 14, ○
- 434 Next Generation of Ovarian Cancer Detection Using Aptamers. **2023**, 24, 6315 ○
- 433 Discovery of an Abundant Viral Genus in Polar Regions through the Isolation and Genomic Characterization of a New Virus against Oceanospirillaceae. ○
- 432 An ancient testis-specific IQ motif-containing H gene regulates specific transcript isoform expression during spermatogenesis. **2023**, 150, ○
- 431 A phylogenomic approach to resolving interrelationships of polyclad flatworms, with implications for life-history evolution. **2023**, 10, ○
- 430 Comparative analysis of soybean transcriptional profiles reveals defense mechanisms involved in resistance against *Diaporthe caulivora*. ○
- 429 Characterization of microRNAs and Target Genes in *Musa acuminata* subsp. *burmannicoides*, var. Calcutta 4 during Interaction with *Pseudocercospora musae*. **2023**, 12, 1473 ○

- 428 Sensing the rainbow: genetic and physiological responses to light quality in *Ostreococcus*, an ecologically important photosynthetic picoeukaryote. ○
- 427 Genomics of Invasive *Cutibacterium acnes* Isolates from Deep-Seated Infections. **2023**, 11, ○
- 426 NGS Reads Dataset of Sunflower Interspecific Hybrids. **2023**, 8, 67 ○
- 425 Organellar genomes of giant kelp from the southern hemisphere. **2023**, 4, 78-86 ○
- 424 Metagenomics Provides a Deeper Assessment of the Diversity of Bacterial Communities in Polar Soils Than Metabarcoding. **2023**, 14, 812 ○
- 423 Real-Time Nanopore Q20+ Sequencing Enables Extremely Fast and Accurate Core Genome MLST Typing and Democratizes Access to High-Resolution Bacterial Pathogen Surveillance. **2023**, 61, ○
- 422 Draft Genome Sequence of *Oenococcus kitaharae* CRBO2176, Isolated from Homemade Water Kefir. **2023**, 12, ○
- 421 Loss of Ezh2 function remodels the DNA replication initiation landscape. **2023**, 42, 112280 ○
- 420 Risk of relapse of ANCA-associated vasculitis among patients homozygous for the proteinase 3 gene Val119Ile polymorphism. **2023**, 9, e002935 ○
- 419 Comparative genomic analysis of Colistin resistant *Escherichia coli* isolated from pigs, a human and wastewater on colistin withdrawn pig farm. **2023**, 13, ○
- 418 The complete chloroplast genome of *Ligusticopsis acaulis* (Shan et Sheh) Pimenov (Apiaceae), an endemic species from China. **2023**, 8, 451-456 ○
- 417 A role for N6-methyldeoxyadenosine in *C. elegans* mitochondrial genome regulation. ○
- 416 Isolation and Characterization of the Genes Involved in the Berberine Synthesis Pathway in Asian Blue Cohosh, *Caulophyllum robustum*. **2023**, 12, 1483 ○
- 415 Evaluation of reference genes for transcript analyses in *Komagataella phaffii* (*Pichia pastoris*). **2023**, 10, ○
- 414 Dynamic changes in gut microbiota during pregnancy among Chinese women and influencing factors: A prospective cohort study. 14, ○
- 413 Bacterial Communities Associated with the Rhizosphere of Transgenic Chrysanthemum. ○
- 412 De novo assembly of the black flounder genome. Why do pleuronectiformes have such a small genome size?. ○
- 411 Comparative Transcriptome of Isonuclear Alloplasmic Strain Revealed the Important Role of Mitochondrial Genome in Regulating *Flammulina filiformis*. **2023**, 13, 998 ○

- 410 Integrative multi-omic sequencing reveals the MMTV-Myc mouse model mimics human breast cancer heterogeneity. ○
- 409 Two haplotype-resolved genomes of highly heterozygous AAB allotriploid bananas provide insights into subgenome asymmetric evolution and banana wilt control. ○
- 408 Comprehensive characterization of FBXW7 mutational and clinicopathological profiles in human colorectal cancers. 13, ○
- 407 *Streptomonospora mangrovi* sp. nov., isolated from mangrove soil showing similar metabolic capabilities, but distinct secondary metabolites profiles. **2023**, 205, ○
- 406 A PvrAP-1Mmp1 signaling pathway is activated in astrocytes upon traumatic brain injury. ○
- 405 Spatiotemporal transcriptomic map of ischemic brain injury. ○
- 404 RNA-Seq Study on the Longissimus thoracis Muscle of Italian Large White Pigs Fed Extruded Linseed with or without Antioxidants and Polyphenols. **2023**, 13, 1187 ○
- 403 Nightmare or delight: taxonomic circumscription meets reticulate evolution in the phylogenomic era. ○
- 402 High level of novelty under the hood of convergent evolution. **2023**, 379, 1043-1049 ○
- 401 The structure of the tetraploid sour cherry *Schattenmorelle* (*Prunus cerasus*L.) genome reveals insights into its segmental allopolyploid nature. ○
- 400 Exploiting a targeted resistome sequencing approach in assessing antimicrobial resistance in retail foods. **2023**, 18, ○
- 399 Temperature-dependent regulation of *Arabidopsis thaliana* growth and development by LSM7. ○
- 398 A parasitoid serpin gene that disrupts host immunity shows adaptive evolution of alternative splicing. ○
- 397 Blood transcriptome of *Rasa Aragonesa* rams with different sexual behavior phenotype reveals CRYL1 and SORCS2 as genes associated with this trait. **2023**, 101, ○
- 396 Complete Genome Sequence of New Cronobacter-Specific Bacteriophage Dev_CS701. **2023**, 12, ○
- 395 Temperate bacteriophages infecting the mucin-degrading bacterium *Ruminococcus gnavus* from the human gut. **2023**, 15, ○
- 394 The Impact of Phase-Specific Macrophage Depletion on Intestinal Anastomotic Healing. **2023**, 12, 1039 ○
- 393 Phylogenetic position and low genomic diversity of *Candidatus Rickettsia kotlanii* inferred by complete genome sequences of two Japanese isolates. ○

- 392 Regulatory Networks of lncRNAs, miRNAs, and mRNAs in Response to Heat Stress in Wheat (*Triticum Aestivum* L.): An Integrated Analysis. **2023**, 2023, 1-17 ○
- 391 Molecular Characterization of *Glaesserella parasuis* Strains Circulating in North American Swine Production Systems. ○
- 390 Top-Down Genomic Surveillance Approach To Investigate the Genomic Epidemiology and Antibiotic Resistance Patterns of *Enterococcus faecium* Detected in Cancer Patients in Arkansas. ○
- 389 Population-level transposable element expression dynamics influence trait evolution in a fungal crop pathogen. ○
- 388 Genomic Characterization and Genetic Profiles of *Salmonella Gallinarum* Strains Isolated from Layers with Fowl Typhoid in Colombia. **2023**, 14, 823 ○
- 387 Genome-wide analysis emancipates genomic diversity and signature of selection in Altay white-headed cattle of Xinjiang, China. 14, ○
- 386 Enrichment Culture but Not Metagenomic Sequencing Identified a Highly Prevalent Phage Infecting *Lactiplantibacillus plantarum* in Human Feces. ○
- 385 Cytosine base editors induce off-target mutations and adverse phenotypic effects in transgenic mice. **2023**, 14, ○
- 384 Assay for Transposase-Accessible Chromatin Using Sequencing of Freshly Isolated Muscle Stem Cells. **2023**, 397-412 ○
- 383 Baicalein-corrected gut microbiota may underlie the amelioration of memory and cognitive deficits in APP/PS1 mice. 14, ○
- 382 Gene expression variability in long-term survivors of childhood cancer and cancer-free controls in response to ionizing irradiation. **2023**, 29, ○
- 381 Epitranscriptome Mapping of N6-Methyladenosine Using m6A Immunoprecipitation with High Throughput Sequencing in Skeletal Muscle Stem Cells. **2023**, 431-443 ○
- 380 Effect of Methionine on Gene Expression in *Komagataella phaffii* Cells. **2023**, 11, 877 ○
- 379 A zebrafish model of growth hormone insensitivity syndrome with immune dysregulation 1 (GHISID1). **2023**, 80, ○
- 378 *Saccharopolyspora* sp. NFXS83 in Marine Biotechnological Applications: From Microalgae Growth Promotion to the Production of Secondary Metabolites. **2023**, 11, 902 ○
- 377 Phenotypic drought stress prediction of European beech (*Fagus sylvatica*) by genomic prediction and remote sensing. ○
- 376 Chromosome-Scale Genome Assembly and Triterpenoid Saponin Biosynthesis in Korean Bellflower (*Platycodon grandiflorum*). **2023**, 24, 6534 ○
- 375 GeNeo: A Bioinformatics Toolbox for Genomics-Guided Neopeptide Prediction. ○

- 374 Maternal diet modulates the infant microbiome and intestinal Flt3L necessary for dendritic cell development and immunity to respiratory infection. **2023**, ○
- 373 Experience of *Klebsiella pneumoniae* genome sequencing using the short read method on the Illumina platform. **2023**, 20, 152-159 ○
- 372 Systemic Lupus Erythematosus Patients with DNASE1L3 Deficiency Have a Distinctive and Specific Genic Circular DNA Profile in Plasma. **2023**, 12, 1061 ○
- 371 Pathogenic genomic alterations in Chinese pancreatic cancer patients and their therapeutical implications. ○
- 370 *Stenotrophomonas maltophilia* natural history and evolution in the airways of adults with cystic fibrosis. ○
- 369 Partial reuse of circadian clock genes along parallel clines of diapause in two moth species. ○
- 368 Effects of different sizes of polystyrene micro(nano)plastics on soil microbial communities. **2023**, 30, 100460 ○
- 367 *Lolliginicoccus levis* gen. nov., sp. nov., a novel bacterium isolated from the brain of the *Chiroteuthis picteti* squid, and reclassification of two *Hoyosella* species as *Lolliginicoccus suaedae* comb. nov. and *Lolliginicoccus lacisalsi* comb. nov.. **2023**, 73, ○
- 366 Executable Network Models of Integrated Multiomics Data. ○
- 365 FishGET: A fish gene expression and transcriptome database with improved accuracy and visualization. **2023**, 26, 106539 ○
- 364 Comprehensive investigation of the expression profiles of common long noncoding RNAs during microglial activation. **2023**, 21, e2 ○
- 363 Statistical mining of triple-negative breast cancer-specific nanobodies among huge libraries from immunized alpacas. ○
- 362 Genotyping of *Haliotis discus hannai* and machine learning models to predict the heat resistant phenotype based on genotype. 14, ○
- 361 Integrated transcriptome and metabolome analysis revealed that flavonoids enhanced the resistance of *Oryza sativa* against *Meloidogyne graminicola*. 14, ○
- 360 Genome-Scale Analysis of the Grapevine KCS Genes Reveals Its Potential Role in Male Sterility. **2023**, 24, 6510 ○
- 359 C 4 gene induction during de-etiolation evolved through changes in cis to allow integration with ancestral C 3 gene regulatory networks. **2023**, 9, ○
- 358 Whole Genome Sequencing Provides Information on the Genomic Architecture and Diversity of Cultivated Gilthead Seabream (*Sparus aurata*) Broodstock Nuclei. **2023**, 14, 839 ○
- 357 Temporal colonization of the gut microbiome in neonatal *Bos taurus* at single nucleotide resolution. ○

- 356 PAK1-dependant mechanotransduction enables myofibroblast nuclear adaptation and chromatin organisation during fibrosis. ○
- 355 Rhytidome- and cork-type barks of holm oak, cork oak and their hybrids highlight processes leading to cork formation. ○
- 354 Non-canonical RNA substrates of Drosha lack many of the conserved features found in primary microRNA stem-loops. ○
- 353 Metagenomic analysis of plant viruses in tropical fresh and wastewater. ○
- 352 Characterization of the Root-Associated Microbiome Provides Insights into Endemism of *Thymus* Species Growing in the Kazdagi National Park. ○
- 351 Distinct mesenchymal cell states mediate prostate cancer progression. ○
- 350 Inflammation and bacteriophages affect DNA inversion states and functionality of the gut microbiota. ○
- 349 Characterization of regeneration initiating cells during *Xenopus laevis* tail regeneration. ○
- 348 Species diversity of arbuscular mycorrhizal but not ectomycorrhizal plants decreases with habitat loss due to environmental filtering. ○
- 347 Clinical usefulness of metagenomic next-generation sequencing for *Rickettsia* and *Coxiella burnetii* diagnosis. ○
- 346 Genomic profiling and characteristics of a C1 degrading heterotrophic fresh-water bacterium *Paracoccus* sp. strain DMF. ○
- 345 Vaginal Microbiome Dysbiosis is Associated with the Different Cervical Disease Status. ○
- 344 De Novo Whole-Genome Sequencing of Two Pathogenic *Pasteurella multocida* Type D:6 Strains Isolated from Pigs. ○
- 343 Modeling *Braf*-induced thyroid cancer development and drug screening using pluripotent stem cell-derived organoids. ○
- 342 Insight into the genomes of dominant yeast symbionts of European spruce bark beetle, *Ips typographus*. 14, ○
- 341 Is Autologous Fecal Microbiota Transfer after Exclusive Enteral Nutrition in Pediatric Crohn's Disease Patients Rational and Feasible? Data from a Feasibility Test. 2023, 15, 1742 ○
- 340 Isolation by resistance explains genetic diversity in the Arremon brushfinches of northern Mesoamerica. ○
- 339 Composition and function of the Galapagos penguin gut microbiome vary with age, location, and a putative bacterial pathogen. 2023, 13, ○

- 338 Genomic characteristics and selection signals of Zhongshan ducks. **2023**, 100797 ○
- 337 Skeletal muscle gene expression dysregulation in long-term spaceflights and aging is clock-dependent. **2023**, 9, ○
- 336 Geographical subdivision of Alviniconcha snail populations in the Indian Ocean hydrothermal vent regions. 10, ○
- 335 Phylogeographic and demographic patterns reveal congruent histories in seven Amazonian White-Sand ecosystems birds. ○
- 334 Molecular identity crisis: environmental DNA metabarcoding meets traditional taxonomy—Assessing biodiversity and freshwater mussel populations (Unionidae) in Alabama. 11, e15127 ○
- 333 Comprehensive Functional Annotation of Metagenomes and Microbial Genomes Using a Deep Learning-Based Method. ○
- 332 Genome-Wide Analysis of the Odorant Receptor Gene Family in *Solenopsis invicta*, *Ooceraea biroi*, and *Monomorium pharaonis* (Hymenoptera: Formicidae). **2023**, 24, 6624 ○
- 331 Comparative transcriptomics of aphid species that diverged >22 MYA reveals genes that are important for the maintenance of their symbiosis. **2023**, 13, ○
- 330 What is *Salvinia molesta* (Salviniaceae)? Determining the maternal progenitor and genetic diversity of the clonal invasive fern giant salvinia. ○
- 329 The impact of culture systems on the gut microbiota and gut metabolome of bighead carp (*Hypophthalmichthys nobilis*). **2023**, 5, ○
- 328 Targeting the NF- κ B pathway enhances responsiveness of mammary tumors to JAK inhibitors. **2023**, 13, ○
- 327 Major proliferation of transposable elements shaped the genome of the soybean rust pathogen *Phakopsora pachyrhizi*. **2023**, 14, ○
- 326 β -THC Protects against Amyloid Beta Toxicity Modulating ER Stress In Vitro: A Transcriptomic Analysis. **2023**, 24, 6598 ○
- 325 First Detection of *mcr-9* in a Multidrug-Resistant *Escherichia coli* of Animal Origin in Italy Is Not Related to Colistin Usage on a Pig Farm. **2023**, 12, 689 ○
- 324 The complete chloroplast genome of *Pseudostellaria davidii* (franch.) Pax, 1934. **2023**, 8, 471-474 ○
- 323 A New Phenotype in *Candida* -Epithelial Cell Interaction Distinguishes Colonization- versus Vulvovaginal Candidiasis-Associated Strains. ○
- 322 Identification and genetic characterization of MERS-related coronavirus isolated from *Nathusius pipistrelle* (*Pipistrellus nathusii*) near Zvenigorod (Moscow region, Russia). ○
- 321 A Novel Bacterial Speciation Process Observed in a Symbiotic Marine Population. ○

- 320 Cell type-specific responses to fungal infection in plants revealed by single-cell transcriptomics. ○
- 319 Low-temperature and circadian signals are integrated by the sigma factor SIG5. **2023**, 9, 661-672 ○
- 318 A complete gap-free diploid genome in *Saccharum* complex and the genomic footprints of evolution in the highly polyploid *Saccharum* genus. **2023**, 9, 554-571 ○
- 317 Back-to-Africa introductions of *Mycobacterium tuberculosis* as the main cause of tuberculosis in Dar es Salaam, Tanzania. **2023**, 19, e1010893 ○
- 316 Metagenome-Assembled Genomes from Appalachian Acid Mine Drainage Sites. ○
- 315 NSD2 E1099K drives relapse in pediatric acute lymphoblastic leukemia by disrupting 3D chromatin organization. **2023**, 24, ○
- 314 Comprehensive genomic analysis of hypocholesterolemic probiotic *Enterococcus faecium* LR13 reveals unique proteins involved in cholesterol-assimilation. 10, ○
- 313 Transcriptomic analyses reveal regional signatures in lung allograft recipients. ○
- 312 In defense of Apocynaceae: inference on evolution of pyrrolizidine alkaloids from evolution of an enzyme in their biosynthetic pathway, homospermidine synthase. ○
- 311 Complete Genome Sequence of the First Colistin-Resistant *Raoultella electrica* Strain. ○
- 310 Gut microbiota alterations in critically ill patients with carbapenem-resistant Enterobacteriaceae colonization: A clinical analysis. 14, ○
- 309 Hypoxia-mediated regulation of DDX5 through decreased chromatin accessibility and post-translational targeting restricts R-loop accumulation. ○
- 308 transXpress: a Snakemake pipeline for streamlined de novo transcriptome assembly and annotation. **2023**, 24, ○
- 307 Alphafold-multimer predicts cross-kingdom interactions at the plant-pathogen interface. ○
- 306 The genomic architecture of a continuous color polymorphism in the European barn owl (*Tyto alba*). ○
- 305 The transcription regulator ATF4 is a mediator of skeletal muscle aging. ○
- 304 Piezo1 activation augments sickling propensity and the adhesive properties of sickle red blood cells in a calcium-dependent manner. ○
- 303 Spurious intragenic transcription is a feature of mammalian cellular senescence and tissue aging. **2023**, 3, 402-417 ○

- 302 Methylglyoxal: a novel upstream regulator of DNA methylation. **2023**, 42, ○
- 301 Multi-omics analysis reveals a crucial role for Retinoic Acid in promoting epigenetic and transcriptional competence of an in vitro model of human Pharyngeal Endoderm. ○
- 300 Transcriptomic insights into archaeal nitrification in the Amundsen Sea Polynya, Antarctica. ○
- 299 Activation of lineage competence in hemogenic endothelium precedes the formation of hematopoietic stem cell heterogeneity. ○
- 298 Lint percentage and boll weight QTLs in three excellent upland cotton (*Gossypium hirsutum*): ZR014121, CCRI60, and EZ60. **2023**, 23, ○
- 297 Direct and indirect viral associations predict coexistence in wild plant virus communities. **2023**, ○
- 296 Hypoxia-inducible factor stabilisation-related lncRNAs in retinopathy of prematurity. **2023**, 43, ○
- 295 A Potential Draft Sequence Analysis of *Enterobacter asburiae* Strain B6_18 of an Endophytic Bacterium. ○
- 294 Molecular characterization and comparative genomic analysis of *Acinetobacter baumannii* isolated from the community and the hospital: an epidemiological study in Segamat, Malaysia. **2023**, 9, ○
- 293 Unveiling the role of emerging metagenomics for the examination of hypersaline environments. 1-39 ○
- 292 Chronosequence of invasion reveals minimal losses of population genomic diversity, niche expansion, and trait divergence in the polyploid, leafy spurge. ○
- 291 A comparison of five Illumina, Ion Torrent, and nanopore sequencing technology-based approaches for whole genome sequencing of SARS-CoV-2. ○
- 290 Abnormal Chromatin Remodeling Caused by ARID1A Deletion Leads to Malformation of the Dentate Gyrus. ○
- 289 Three-dimensional chromatin organization promotes genome evolution in a fungal plant pathogen. ○
- 288 The m6A reader YTHDC1 and the RNA helicase DDX5 control the production of rhabdomyosarcoma-enriched circRNAs. **2023**, 14, ○
- 287 Condensed but liquid-like domain organization of active chromatin regions in living human cells. **2023**, 9, ○
- 286 Extensive MHC class II diversity across multiple loci in the small-spotted catshark (*Scyliorhinus canicula*). **2023**, 13, ○
- 285 WAX INDUCER 1 Regulates β -Ketone Biosynthesis by Mediating Expression of the Cer-cqu Gene Cluster in Barley. **2023**, 24, 6762 ○

- 284 Sampling strategies for sugarcane using either clonal replicates or diverse genotypes can bias the conclusions of RNA-Seq studies. **2023**, 46, ○
- 283 Spontaneously Produced Lysogenic Phages Are an Important Component of the Soybean *Bradyrhizobium Mobilo*me. ○
- 282 The presence of *Enterococcus faecalis* in saliva as a risk factor for endodontic infection. 13, ○
- 281 m6A epitranscriptomic regulation of tissue homeostasis during primate aging. ○
- 280 Genomic adaptation to extreme climate conditions in beef cattle as a consequence of cross-breeding program. **2023**, 24, ○
- 279 Transcriptional investigation of the toxic mechanisms of perfluorooctane sulfonate in rats based on an RNA-Seq approach. **2023**, 329, 138629 ○
- 278 Reading and writing of mRNA m6A modification orchestrate maternal-to-zygotic transition in mice. **2023**, 24, ○
- 277 Plastid phylogenomics and species discrimination in the Chinese clade of *Roscoea* (Zingiberaceae). **2023**, ○
- 276 Adventitial macrophage accumulation impairs perivascular nerve function in mesenteric arteries with inflammatory bowel disease. ○
- 275 Land use modification causes slow, but predictable, change in soil microbial community composition and functional potential. **2023**, 18, ○
- 274 Transcriptomic analysis of the adaptation to prolonged starvation of the insect-dwelling *Trypanosoma cruzi* epimastigotes. 13, ○
- 273 A Longitudinal Study on the Dynamics of *Salmonella enterica* Prevalence and Serovar Composition in Beef Cattle Feces and Lymph Nodes and Potential Contributing Sources from the Feedlot Environment. ○
- 272 Gonadal transcriptomes reveal sex-biased expression genes associated with sex determination and differentiation in red-tail catfish (*Hemibagrus wyckioides*). **2023**, 24, ○
- 271 Intracellular metabolomics and microRNAomics unveil new insight into the regulatory network for potential biocontrol mechanism of stress-tolerant *Trichofusants* interacting with phytopathogen *Sclerotium rolfsii* Sacc. ○
- 270 *Thermococcus argininiproducens* sp. nov., an arginine biosynthesis archaeal species isolated from the Central Indian Ocean ridge. **2023**, 73, ○
- 269 *Vibrio aestuarianus* Clade A and Clade B isolates are associated with Pacific oyster (*Crassostrea gigas*) disease outbreaks across Ireland. ○
- 268 TGF- β induces matrisome pathological alterations and EMT in patient-derived prostate cancer tumoroids. ○
- 267 Transcriptomic Profile of *Penicillium digitatum* Reveals Novel Aspects of the Mode of Action of the Antifungal Protein AfpB. ○

- 266 Deep learning-based polygenic risk analysis for Alzheimer's disease prediction. **2023**, 3, ○
- 265 Study of pathogenic genes in a pedigree with familial dilated cardiomyopathy. 11, 2412-2422 ○
- 264 3D architecture and a bi-cellular mechanism of touch detection in mechanosensory corpuscle. ○
- 263 Genomic diversity and metabolic potential of marine Pseudomonadaceae. 14, ○
- 262 First Report of OXA-181-Producing Enterobacterales Isolates in Latin America. ○
- 261 Differential gene expression underlying the biosynthesis of Dufour's gland signals in *Bombus impatiens*. **2023**, 3, 100056 ○
- 260 Analysis of the *P. lividus* sea urchin genome highlights contrasting trends of genomic and regulatory evolution in deuterostomes. **2023**, 3, 100295 ○
- 259 Tell me if you prefer bovine or poultry sectors and I'll tell you who you are: Characterization of *Salmonella enterica* subsp. *enterica* serovar Mbandaka in France. 14, ○
- 258 Composition of the maternal gastrointestinal microbiome as a predictor of neonatal birth weight. ○
- 257 Functional characterization of five triterpene synthases through De-novo assembly and transcriptome analysis of *Euphorbia grantii* and *Euphorbia tirucalli*. ○
- 256 THAPBI PICT - a fast, cautious, and accurate metabarcoding analysis pipeline. ○
- 255 Histone Deacetylases (HDACs) maintain expression of the pluripotent gene network via recruitment of RNA polymerase II to coding and non-coding loci. ○
- 254 Circulation of SARS-CoV-2 Related Coronaviruses and Alphacoronaviruses in Bats from Croatia. **2023**, 11, 959 ○
- 253 Phylotype resolved spatial variation and association patterns of planktonic Thaumarchaeota in eastern Chinese marginal seas. ○
- 252 KMT2D preferentially binds mRNAs of the genes it regulates, suggesting a role in RNA processing. ○
- 251 Tumor-Naïve Circulating Tumor DNA as an Early Response Biomarker for Patients Treated With Immunotherapy in Early Phase Clinical Trials. **2023**, ○
- 250 Longitudinal study of humoral immunity against SARS-CoV-2 of health professionals in Brazil: the impact of booster dose and reinfection on antibody dynamics. ○
- 249 The methylation landscape of giga-genome and the epigenetic timer of age in Chinese pine. **2023**, 14, ○

- 248 The mitochondrial genome of *Dendrobaena tellermanica*; Perel, 1966 (Annelida: Lumbricidae) and its phylogenetic position. **2023**, 27, 146-152 ○
- 247 Genomics of adaptive evolution in the woolly mammoth. **2023**, ○
- 246 Transposable elements are associated with the variable response to influenza infection. **2023**, 100292 ○
- 245 Testing species relationships and delimitation in the Amazonian hyperdominant *Astrocaryum* section *Huicungo* (Arecaceae) using chloroplast data from genome skimming. ○
- 244 Mesophilic and thermophilic viruses are associated with nutrient cycling during hyperthermophilic composting. ○
- 243 The relative transmission fitness of multidrug-resistant *Mycobacterium tuberculosis* in a drug resistance hotspot. **2023**, 14, ○
- 242 Collateral sensitivity profiling in drug-resistant *Escherichia coli* identifies natural products suppressing cephalosporin resistance. **2023**, 14, ○
- 241 Maturases and Group II Introns in the Mitochondrial Genomes of the Deepest Jakobid Branch. ○
- 240 Standardization and Interpretation of RNA-sequencing for Transplantation. Publish Ahead of Print, ○
- 239 Intracellular Cytomatrix, Immobilized Biocatalysis, Matrix Micromechanics and The Warburg Effect: Entanglement of Two Age-Old Mysteries of the Normal and Malignant Cell. ○
- 238 The evolution and international spread of extensively drug resistant *Shigella sonnei*. **2023**, 14, ○
- 237 Evidence for a Parabasalian Gut Symbiote in Egg-Feeding Poison Frog Tadpoles in Peru. ○
- 236 Metagenomic analysis reveals the short-term influences on conjugation of bla_{NDM-1} and microbiome in hospital wastewater by silver nanoparticles at environmental-related concentration. **2023**, 228, 115866 ○
- 235 Detailed Social Network Interactions and Gut Microbiome Strain-Sharing Within Isolated Honduras Villages. ○
- 234 Genome-wide chromatin accessibility and gene expression profiling during flatfish metamorphosis. **2023**, 10, ○
- 233 Effects of high-grain diet feeding on fatty acid profiles in milk, blood, muscle, and adipose tissue, and transcriptional expression of lipid-related genes in muscle and adipose tissue of dairy cows. **2023**, 14, ○
- 232 Phylogenomics revealed migration routes and adaptive radiation timing of Holarctic malaria mosquito species of the *Maculipennis* Group. **2023**, 21, ○
- 231 Mitochondrial genome of *Artemisia argyi* L. suggested conserved mitochondrial protein-coding genes among genera *Artemisia*, *Tanacetum* and *Chrysanthemum*. **2023**, 147427 ○

- 230 Mechanism of Metabolic Response to Hepatectomy by Integrated Analysis of Gut Microbiota, Metabolomics, and Proteomics. ○
- 229 DT-109 ameliorates nonalcoholic steatohepatitis in nonhuman primates. **2023**, ○
- 228 Phylogenomic evolutionary insights in the fern family Gleicheniaceae. **2023**, 184, 107782 ○
- 227 Genome-Wide Identification and Transcriptome-Based Expression Profile of Cuticular Protein Genes in *Antheraea pernyi*. **2023**, 24, 6991 ○
- 226 Differential Hsp90-dependent gene expression is strain-specific and common among yeast strains. **2023**, 106635 ○
- 225 Metagenomic analysis reveals indole signaling effect on microbial community in sequencing batch reactors: Quorum sensing inhibition and antibiotic resistance enrichment. **2023**, 115897 ○
- 224 The Intestinal Clock Regulates Host Metabolism through the Fiber-Dependent Microbiome and Macronutrient Transcriptome. ○
- 223 Genomic, transcriptomic, and metabolic characterization of 2-Phenylethanol-resistant *Saccharomyces cerevisiae* obtained by evolutionary engineering. 14, ○
- 222 Genomic resources for population analyses of an invasive insect pest *Oryctes rhinoceros*. **2023**, 10, ○
- 221 UltraSEQ, a Universal Bioinformatic Platform for Information-Based Clinical Metagenomics and Beyond. ○
- 220 Identification of breed-specific genomic variants in Colombian Creole pig breeds by whole-genome sequencing. **2023**, 55, ○
- 219 Highly sensitive quantitative phase microscopy and deep learning aided with whole genome sequencing for rapid detection of infection and antimicrobial resistance. 14, 1
- 218 Environmental, Socioeconomic, and Health Factors Associated with Gut Microbiome Species and Strains in Isolated Honduras Villages. ○
- 217 First description of the mitochondrial genomes of the Central American brocket deer *Mazama temama* (Kerr, 1792) and the Yucatán Peninsula brocket deer *Odocoileus pandora* Merriam, 1901. ○
- 216 Thermotolerance improvement of engineered *Saccharomyces cerevisiae* ERG5 Delta ERG4 Delta ERG3 Delta, molecular mechanism, and its application in corn ethanol production. **2023**, 16, ○
- 215 Population genetic structure of the maize weevil, *Sitophilus zeamais*, in southern Mexico. **2023**, 18, e0264469 ○
- 214 Identification of a putative novel cholivirus in the transcriptome of *Gymnema sylvestre* R. Br. **2023**, 205, ○
- 213 Splicing complexity as a pivotal feature of alternative exons in mammalian species. **2023**, 24, ○

- 212 Metabolomics and transcriptomics strategies to reveal the mechanism of diversity of maize kernel color and quality. **2023**, 24, ○
- 211 TEAD1 regulates ITGA1 and ITGA2 to control prostate cancer progression. ○
- 210 Unraveling multifunction of low-temperature Daqu in simultaneous saccharification and fermentation of Chinese light aroma type liquor. **2023**, 397, 110202 ○
- 209 Ageing-associated changes in transcriptional elongation influence longevity. ○
- 208 Complete genome sequence of zoysia mosaic virus, a novel member of the genus Poacevirus. **2023**, 168, ○
- 207 De-novo genome assembly of the invasive mosquito species *Aedes japonicus* and *Aedes koreicus*. ○
- 206 Dengue and chikungunya virus loads in the mosquito *Aedes aegypti* are determined by distinct genetic architectures. **2023**, 19, e1011307 ○
- 205 Metabolomic and Transcriptomic Analysis Reveals the Mechanisms Underlying the Difference in Anthocyanin Accumulation in Apple Fruits at Different Altitudes. **2023**, 9, 475 ○
- 204 A Diverse Virome Is Identified in Parasitic Flatworms of Domestic Animals in Xinjiang, China. ○
- 203 Whole-Genome Sequencing of *Lactobacillus johnsonii* MT4, a Novel Strain Isolated from the Oral Cavity of C57BL/6 Mice. ○
- 202 Long-Term Transcriptomic Changes and Cardiomyocyte Hyperpolyploidy after Lactose Intolerance in Neonatal Rats. **2023**, 24, 7063 ○
- 201 Comparing genomic variant identification protocols for *Candida auris*. **2023**, 9, ○
- 200 CRISPR detection in metagenome-assembled genomes (MAGs) of coal mine. **2023**, 23, ○
- 199 Transcriptomic analysis provides insight into the regulation mechanism of silver ions (Ag⁺) and jasmonic acid methyl ester (MeJA) on secondary metabolism in the hairy roots of *Salvia miltiorrhiza* Bunge (Lamiaceae). **2023**, 0-0 ○
- 198 Draft Genome Sequence Resource of *Erwinia* sp. Strain INIA01, a Phytopathogen Isolated from a Diseased Stalk of Peruvian Maize. ○
- 197 G-quadruplex as a structural modulator of Intron Retention upon viral infection. ○
- 196 Sponge diversification in marine lakes: Implications for phylogeography and population genomic studies on sponges. **2023**, 13, ○
- 195 Dissemination of antibiotic resistance genes from the Pearl River Estuary to adjacent coastal areas. **2023**, 188, 105978 ○

- 194 The origins and functional effects of postzygotic mutations throughout the human life span. **2023**, 380, ○
- 193 New insights into the genome and transmission of the microsporidian pathogen *Nosema muscidifuracis*. 14, ○
- 192 Comparative gene expression analysis of differentiated terminal and lateral haustoria of the obligate root parasitic plant *Phelipanche ramosa* (Orobanchaceae). ○
- 191 Gut microbiota response to sucralose or rebaudioside A in rats under two dietary conditions. ○
- 190 Complete Genome Sequence of *Desulfomicrobium* sp. Strain ZS1 from Zodletone Spring in Oklahoma, USA. ○
- 189 Fine-scale adaptive divergence of *Aedes aegypti* in heterogeneous landscapes and among climatic conditions in Metropolitan Manila, Philippines. ○
- 188 Transcriptional Mechanisms of Thermal Acclimation in *Prochlorococcus*. ○
- 187 Ovule Transcriptome Analysis Discloses Deregulation of Genes and Pathways in Sexual and Apomictic *Limonium* Species (Plumbaginaceae). **2023**, 14, 901 ○
- 186 Dynamic chromatin architectures provide insights into the genetics of cattle myogenesis. **2023**, 14, ○
- 185 Mosaic results after preimplantation genetic testing for aneuploidy may be accompanied by changes in global gene expression. 10, ○
- 184 The Prevalence of Undiagnosed *Salmonella enterica* Serovar Typhi in Healthy School-Aged Children in Osun State, Nigeria. **2023**, 12, 594 ○
- 183 Children with autism show differences in the gut DNA virome compared to non-autistic children: a case control study. **2023**, 23, ○
- 182 Transcriptome analysis of Indian freshwater pearl mussel *Lamellidens marginalis* to unravel the genes associated with biomineralization. ○
- 181 The Complete Mitochondrial Genome of *Mytilisepta virgata* (Mollusca: Bivalvia), Novel Gene Rearrangements, and the Phylogenetic Relationships of Mytilidae. **2023**, 14, 910 ○
- 180 Feeding ecology of the obligate urchin symbiont *Dactylopleustes yoshimurai* (Crustacea: Amphipoda: Pleustidae) revealed by DNA metabarcoding analysis.. ○
- 179 Transcriptome Analysis of Roots from Wheat (*Triticum aestivum* L.) Varieties in Response to Drought Stress. **2023**, 24, 7245 ○
- 178 SOX2 downregulation of PML increases HCMV gene expression and growth of glioma cells. **2023**, 19, e1011316 ○
- 177 Afro-TB dataset as a large scale genomic data of *Mycobacterium tuberculosis* in Africa. **2023**, 10, ○

- 176 An Efficient 2D Protocol for Differentiation of iPSCs into Mature Postmitotic Dopaminergic Neurons: Application for Modeling Parkinson's Disease. **2023**, 24, 7297
- 175 Moderate Salinity Stress Increases the Seedling Biomass in Oilseed Rape (*Brassica napus* L.). **2023**, 12, 1650
- 174 TEAD1 trapping by the Q353R β -amin A/C causes dilated cardiomyopathy. **2023**, 9,
- 173 Validation of the Labcorp Plasma Focus Test to Facilitate Precision Oncology Through Cell-free DNA Genomic Profiling of Solid Tumors. **2023**,
- 172 The complete mitochondrial genome of *Pardosa pusiola* (Araneae, Lycosidae) and its phylogenetic implications.
- 171 Maximal interferon induction by influenza lacking NS1 is infrequent owing to requirements for replication and export. **2023**, 19, e1010943
- 170 Genomic and Transcriptomic Approaches Provide a Predictive Framework for Sesquiterpenes Biosynthesis in *Desarmillaria tabescens* CICC 401429. **2023**, 9, 481
- 169 Species-Level Taxonomic Characterization of Uncultured Core Gut Microbiota of Plateau Pika.
- 168 Haplotype-resolved genomes of two buckwheat crops provide insights into their contrasted rutin concentrations and reproductive systems. **2023**, 21,
- 167 Core-Genome Multilocus Sequence Typing for Epidemiological and Evolutionary Analyses of Phytopathogenic *Xanthomonas citri*.
- 166 Transcriptomic identification of differentially expressed genes in Levonorgestrel resistant endometrial cancer cell lines.
- 165 Draft Genome Sequence and Annotation of the Halotolerant Carotenoid-Producing Strain *Paracoccus bogoriensis* BOG6 T.
- 164 Reassessing the origins of pathogenicity in *Candida auris* and relatives through phylogenomic analysis
- 163 Dynamic changes in P300 enhancers and enhancer-promoter contacts control mouse cardiomyocyte maturation. **2023**,
- 162 Identification of multiple transcription factor genes potentially involved in the development of electrosensory versus mechanosensory lateral line organs.
- 161 Heterogeneity in the immune microenvironment of bone metastasis in driver-positive non-small cell lung cancer.
- 160 Gallium maltolate shows synergism with cisplatin and activates nucleolar stress and ferroptosis in human breast carcinoma cells.
- 159 A novel mouse allele of the DNA/RNA helicase senataxin (*Setxspcar3*) causing meiotic arrest of spermatocytes and male infertility.

- 158 Benzo[a]pyrene stress impacts adaptive strategies and ecological functions of earthworm intestinal viromes. ○
- 157 Using RNA-seq to identify suitable housekeeping genes for hypoxia studies in human adipose-derived stem cells. **2023**, 24, ○
- 156 Domesticating *Vigna stipulacea*: Chromosome-Level genome assembly reveals VsPSAT1 as a candidate gene decreasing hard-seededness. 14, ○
- 155 The detailed population genetic structure of the rare endangered latid fish akame *Lates japonicus* with extremely low genetic diversity revealed from single-nucleotide polymorphisms. ○
- 154 The initiation and maintenance of CHH methylation and its effects on gene expression are unique in maize. ○
- 153 Analysis of endophytic bacterial flora of mulberry cultivars susceptible and resistant to bacterial wilt using metagenomic sequencing and culture-dependent approach. **2023**, 39, ○
- 152 Host phylogeny and environment shape the diversity of the salamander skin microbiome. ○
- 151 Induction of the CtsR regulon improves Xylanase production in *Bacillus subtilis*. ○
- 150 Identification and characterization of miRNAs in spleens of sheep subjected to repetitive vaccination. **2023**, 13, ○
- 149 Haplotype mapping of H3K27me3-associated chromatin interactions defines topological regulation of gene silencing in rice. **2023**, 42, 112350 ○
- 148 De novo genome assembly resolving repetitive structures enables genomic analysis of 35 European *Mycoplasma bovis* strains. ○
- 147 Global transcriptome analysis of allopolyploidization reveals large-scale repression of the D-subgenome in synthetic hexaploid wheat. **2023**, 6, ○
- 146 Transcriptome Analysis of *Solanum Virginianum* and in Silico Prediction of Antimicrobial Peptides. **2023**, 14, 1-10 ○
- 145 Variant-specific introduction and dispersal dynamics of SARS-CoV-2 in New York City from Alpha to Omicron. **2023**, 19, e1011348 ○
- 144 Extracellular Vesicles Secreted by Pre-Hatching Bovine Embryos Produced In Vitro and In Vivo Alter the Expression of IFN τ -Stimulated Genes in Bovine Endometrial Cells. **2023**, 24, 7438 ○
- 143 Analysis of the Complete Mitochondrial Genome of the Bitter Melon (*Momordica charantia*). **2023**, 12, 1686 ○
- 142 Dysregulation of hypoxia-inducible factor 1 α in the sympathetic nervous system accelerates diabetic cardiomyopathy. **2023**, 22, ○
- 141 Environmental viromes reveal the global distribution signatures of deep-sea DNA viruses. **2023**, ○

- 140 Whole-genome selective scans detect genes associated with important phenotypic traits in goat (*Capra hircus*). 14,
- 139 Identification of gut dysbiosis in axial spondyloarthritis patients and improvement of experimental ankylosing spondyloarthritis by microbiome-derived butyrate with immune-modulating function. 14,
- 138 Single worm long read sequencing reveals genome diversity in free-living nematodes.
- 137 KaryoCreate: A CRISPR-based technology to study chromosome-specific aneuploidy by targeting human centromeres. 2023,
- 136 Expression of AtNF-YB1 in rice leading to early flowering shows potential in rice breeding.
- 135 Complete variable domain sequences of monoclonal antibody light chains identified from untargeted RNA sequencing data. 14,
- 134 Genomic Insights into Bacterial Resistance to Proline-Rich Antimicrobial Peptide Bac7. 2023, 13, 438
- 133 Bladder cancer organoids as a functional system to model different disease stages and therapy response. 2023, 14,
- 132 Synthesizing historic and current evidence for anadromy in a northern pike (*Esox lucius* L.) meta-population inhabiting brackish lagoons of the southern Baltic Sea, with implications for management. 2023, 263, 106670
- 131 Metabarcoding of soil environmental DNA to estimate plant diversity globally. 14,
- 130 Analyzing the effect of heparin on in vitro capacitation and spermatozoal RNA population in goats. 2023, 124502
- 129 First mitogenome phylogeny of the sun bear *Helarctos malayanus* reveals a deep split between Indochinese and Sundaic lineages. 2023, 13,
- 128 Unique Salt-Tolerance-Related QTLs, Evolved in *Vigna riukiensis* (Na⁺ Includer) and *V. nakashimae* (Na⁺ Excluder), Shed Light on the Development of Super-Salt-Tolerant Azuki Bean (*V. angularis*) Cultivars. 2023, 12, 1680
- 127 Metabolome and transcriptome signatures shed light on the anti-obesity effect of *Polygonatum sibiricum*. 14,
- 126 DNMT1 mutant ants develop normally but have disrupted oogenesis. 2023, 14,
- 125 Population dynamics and drug resistance mutations in *Plasmodium falciparum* on the Bijagõ Archipelago, Guinea-Bissau. 2023, 13,
- 124 State-of-the-art of data analyses in environmental DNA approaches towards its applicability to sustainable fisheries management. 10,
- 123 The evolutionary history of rice azaleas (*Rhododendron tschonoskii* alliance) involved niche evolution to a montane environment.

- 122 Genomic insight of sulfate reducing bacterial genus *Desulfofabia* reveals their metabolic versatility in biogeochemical cycling. **2023**, 24, ○
- 121 Gene regulatory changes underlie developmental plasticity in respiration and aerobic performance in highland deer mice. ○
- 120 Clinical Diagnostics of Bacterial Infections and Their Resistance to Antibiotics: Current State and Whole Genome Sequencing Implementation Perspectives. **2023**, 12, 781 ○
- 119 Transcriptomics and Metabolomics Reveal Tomato Consumption Alters Hepatic Xenobiotic Metabolism and Induces Steroidal Alkaloid Metabolite Accumulation in Mice. ○
- 118 Novel QTL for Lateral Root Density and Length improve Phosphorus Uptake in Rice (*Oryza sativa* L.). ○
- 117 Transcriptome profiling, physiological, and biochemical analyses provide new insights towards drought stress response in sugar maple (*Acer saccharum* Marshall) saplings. 14, ○
- 116 IKK1 aggravates ischemia/reperfusion kidney injury by promoting the differentiation of effector T cells. **2023**, 80, ○
- 115 Metagenomic and metatranscriptomic exploration of the Egyptian Red Sea sponge *Theonella* sp. associated microbial community. **2023**, 70, 101032 ○
- 114 Integrating Genomics into the Genetic Management of the Endangered Mountain Yellow-Legged Frog. ○
- 113 RWP-RK Domain 3 (*OsRKD3*) induces somatic embryogenesis in black rice. **2023**, 23, ○
- 112 Macrophages from naked mole-rat possess distinct immunometabolic signatures upon polarization. 14, ○
- 111 Genome-environment associations along elevation gradients in two snowbed species of the North-Eastern Calcareous Alps. **2023**, 23, ○
- 110 Microbial functional genes within soil aggregates drive organic carbon mineralization under contrasting tillage practices. ○
- 109 A nuclear NKRF interacting long noncoding RNA controls EBV eradication and suppresses tumor progression in natural killer/T-cell lymphoma. **2023**, 166722 ○
- 108 Description of four new *Medeopteryx* Ballantyne (Coleoptera, Lampyridae, Luciolinae) species from Thailand and their phylogenetic placements based on mitochondrial DNA. **2023**, 102084 ○
- 107 De novo transcriptome sequencing and gene co-expression reveal a genomic basis for drought sensitivity and evidence of a rapid local adaptation on Atlas cedar (*Cedrus atlantica*). 14, ○
- 106 Control of white mold (*Sclerotinia sclerotiorum*) through plant-mediated RNA interference. **2023**, 13, ○
- 105 Complete genome sequence of *Aeromonas* phage GomatiRiver_11, a novel T4-like bacteriophage that infects *Aeromonas hydrophila*. ○

- 104 Analytical Performance of a Highly Sensitive System to Detect Gene Variants Using Next-Generation Sequencing for Lung Cancer Companion Diagnostics. **2023**, 13, 1476 ○
- 103 Gene Losses and Homology of the Chloroplast Genomes of *Taxillus* and *Phacellaria* Species. **2023**, 14, 943 ○
- 102 Metagenome and metabolome insights into the energy compensation and exogenous toxin degradation of gut microbiota in high-altitude rhesus macaques (*Macaca mulatta*). **2023**, 9, ○
- 101 Genomic analysis of the population structure of *Paenibacillus* larvae in New Zealand. 14, ○
- 100 Closed aerobic biodegradation kinetics test with activated sludge and low concentration chemical mixtures. **2023**, 138752 ○
- 99 Complete Genome Sequence of *Rhodospseudomonas palustris* CGA0092 and Corrections to the *R. palustris* CGA009 Genome Sequence. ○
- 98 Enhanced toxicity of entomopathogenic fungi *Beauveria bassiana* with bacteria expressing immune suppressive dsRNA in a leaf beetle. **2023**, 105431 ○
- 97 Targeted DNA methylation analysis and prediction of smoking habits in blood based on massively parallel sequencing. **2023**, 102878 ○
- 96 Dissecting the genotypic features of a fluoroquinolone-resistant *Pseudomonas aeruginosa* ST316 sublineage causing ear infections in Shanghai, China. **2023**, 9, ○
- 95 In Vitro Activity of Cefiderocol on Multiresistant Bacterial Strains and Genomic Analysis of Two Cefiderocol Resistant Strains. **2023**, 12, 785 ○
- 94 Ultraconserved elements improve resolution of marmot phylogeny and offer insights into biogeographic history. **2023**, 107785 ○
- 93 Human immune and gut microbial parameters associated with inter-individual variations in COVID-19 mRNA vaccine-induced immunity. **2023**, 6, ○
- 92 Ecological interactions and the underlying mechanism of anammox and denitrification across the anammox enrichment with eutrophic lake sediments. **2023**, 11, ○
- 91 TRPA1 rare variants in chronic neuropathic and nociplastic pain patients. **2023**, Publish Ahead of Print, ○
- 90 Meta-Analysis of RNA-Seq Data Identifies Potent Biomarkers for Intellectual Disability Disorder (IDD). ○
- 89 Epidemiological and genomic investigation of chikungunya virus in Rio de Janeiro state, Brazil, between 2015 and 2018. ○
- 88 Disruption of peritrophic matrix chitin metabolism and gut immune by chlorantraniliprole results in pathogenic bacterial infection in *Bombyx mori*. **2023**, 105430 ○
- 87 Integrated computational approaches to aid precision medicine for cancer therapy: Present scenario and future prospects. **2023**, 403-424 ○

- 86 Diet suppresses glioblastoma initiation in mice by maintaining quiescence of mutation-bearing neural stem cells. **2023**, ○
- 85 Exploring small RNA in food crops: techniques and approaches. **2023**, 109-127 ○
- 84 Gut Microbiota and Serum Metabolites in Individuals with Class III Obesity Without Type 2 Diabetes Mellitus: Pilot Analysis. ○
- 83 A scoping review on deep learning for next-generation RNA-Seq. data analysis. **2023**, 23, ○
- 82 Influenza virus mRNAs encode determinants for nuclear export via the cellular TREX-2 complex. **2023**, 14, ○
- 81 Overexpression of plastid lipid-associated protein in marine diatom enhances the xanthophyll synthesis and storage. 14, ○
- 80 Cuticle supplementation and nitrogen recycling by a dual bacterial symbiosis in a family of xylophagous beetles. ○
- 79 Soil fertility determines whether ectomycorrhizal fungi accelerate or decelerate decomposition in a temperate forest. ○
- 78 Epidemiological Surveillance Reveals the Rise and Establishment of the Omicron SARS-CoV-2 Variant in Brazil. **2023**, 15, 1017 ○
- 77 m⁶A promotes planarian regeneration. ○
- 76 BH3 mimetics and azacitidine show synergistic effects on juvenile myelomonocytic leukemia. ○
- 75 Metapangenomics of wild and cultivated banana microbiome reveals a plethora of host-associated protective functions. **2023**, 18, ○
- 74 Soil microbial gene expression in an agricultural ecosystem varies with time and neonicotinoid seed treatments. **2023**, 169, ○
- 73 Genomic Sequencing Profiles of Mycobacterium tuberculosis in Mandalay Region, Myanmar. **2023**, 8, 239 ○
- 72 Origin and diversification of a Himalayan orchid genus Pleione. **2023**, 107797 ○
- 71 Gauge your phage: benchmarking of bacteriophage identification tools in metagenomic sequencing data. **2023**, 11, ○
- 70 Extracellular enzyme activity in the coastal upwelling system off Peru: a mesocosm experiment. **2023**, 20, 1605-1619 ○
- 69 NF- κ B/p53 augments ETS1 binding genome-wide to promote glioma progression. **2023**, 6, ○

- 68 Excessive disinfection aggravated the environmental prevalence of antimicrobial resistance during COVID-19 pandemic. **2023**, 163598 ○
- 67 Identification of novel *Carnobacterium maltaromaticum* strains in bone marrow samples of patients with acute myeloid leukemia using a metagenomic binning approach. ○
- 66 Identification and analysis of the DNA content of small extracellular vesicles isolated from *Leishmania* parasites. **2023**, 4, 102248 ○
- 65 Cytochrome P450 superfamily in spotted sea bass: Genome-wide identification and expression profiles under trichlorfon and environmental stresses. **2023**, 101078 ○
- 64 Genomic analysis of *Paenibacillus macerans* strain I6, which can effectively saccharify oil palm empty fruit bunches under nutrient-free conditions. **2023**, ○
- 63 Cardiac performance and heart gene network provide dynamic responses of bay scallop *Argopecten irradians irradians* exposure to marine heatwaves. **2023**, 163594 ○
- 62 The mitochondrial genome of the diploid oat *Avena longiglumis*. **2023**, 23, ○
- 61 Phenotypic variation in milk fatty acid composition and its association with stearoyl-CoA desaturase 1 (SCD1) gene polymorphisms in Gir cows. ○
- 60 The evolutionary patterns, expression profiles, and genetic diversity of expanded genes in barley. 14, ○
- 59 Metagenomic and Genomic Sequences from a Methanogenic Benzene-Degrading Consortium. **2023**, 12, ○
- 58 *Enterobacter pseudoroggenkampii* sp. nov. carrying quinolone-resistant gene *qnrE* recovered from clinical samples in China. ○
- 57 Profiling Plant Proteome and Transcriptome Changes during Grapevine Fanleaf Virus Infection. ○
- 56 Genome-wide analyses of Glutathione S-transferase gene family and expression profiling under deltamethrin exposure in non-biting midge *Propislocerus akamusi*. **2023**, 46, 101081 ○
- 55 Draft Genome Sequences of 27 Rhizogenic *Agrobacterium* Biovar 1 Strains, the Causative Agent of Hairy Root Disease. **2023**, 12, ○
- 54 Early expression onset of tissue-specific effector genes during the specification process in sea urchin embryos. **2023**, 14, ○
- 53 Evolution of stridulatory mechanisms: vibroacoustic communication may be common in leaf-footed bugs and allies (Heteroptera: Coreoidea). **2023**, 10, ○
- 52 Jawless vertebrates do not escape retrovirus infection. **2023**, 583, 52-55 ○
- 51 Complete mitochondrial genomes of the *Acmaeidae* limpets provide new insights into the internal phylogeny of the Patellogastropoda (Mollusca: Gastropoda). 10, ○

- 50 Molecular characterization of sub-frontal recurrent medulloblastomas reveals potential clinical relevance. 14, ○
- 49 Investigating the cecal microbiota of broilers raised in extensive and intensive production systems. ○
- 48 Physiological and biochemical responses of *Limonium tetragonum* to NaCl concentrations in hydroponic solution. 14, ○
- 47 Genome structure and population genomics of the canine heartworm *Dirofilaria immitis*. ○
- 46 Exploring Microbial Diversity and Functional Potential along the Bay of Bengal Coastline in Bangladesh: Insights from Amplicon Sequencing and Shotgun Metagenomics. ○
- 45 Diverse Molecular Mechanisms Underlying Microbe-Inducing Male Killing in the Moth *Homona magnanima*. ○
- 44 Effects of monsoons and storms on the structuring and diversity of picoeukaryotic microbial communities in a tropical coastal environment. **2023**, 209, 105294 ○
- 43 Genomic Analyses of a Fungemia Outbreak Caused by *Lodderomyces elongisporus* in a Neonatal Intensive Care Unit in Delhi, India. ○
- 42 Identification of lncRNAs involved in response to ionizing radiation in fibroblasts of long-term survivors of childhood cancer and cancer-free controls. 13, ○
- 41 *Pseudomonas petrae* sp. nov. isolated from regolith samples in Antarctica. **2023**, 46, 126424 ○
- 40 Draft Genome Sequence of *Citrobacter freundii* AYS58, a Potential Plant Growth-Promoting Endophyte. **2023**, 12, ○
- 39 Phylogenomics and Biogeography of North American Trechine Cave Beetles (Coleoptera: Carabidae). ○
- 38 *Apostasia* Mitochondrial Genome Analysis and Monocot Mitochondria Phylogenomics. **2023**, 24, 7837 ○
- 37 Identification of sequence mutations in *Phytophthora cactorum* genome associated with mefenoxam resistance and development of a molecular assay for the mutant detection in strawberry (*F. ~~lananassa~~*). **2023**, 13, ○
- 36 A new species of the genus *Catillopecten* (Bivalvia: Pectinoidea: Propeamussiidae): morphology, mitochondrial genome, and phylogenetic relationship. 10, ○
- 35 Comparative analysis of dioecious *Amaranthus* plastomes and phylogenomic implications within *Amaranthaceae* s.s.. **2023**, 23, ○
- 34 A Novel Assessment of Metabolic Pathways in Peritoneal Metastases from Low-Grade Appendiceal Mucinous Neoplasms. ○
- 33 Target sequence capture data shed light on the deeper evolutionary relationships of subgenus *Chamaecerasus* in *Lonicera* (Caprifoliaceae). **2023**, 184, 107808 ○

- 32 Detection of long terminal repeat loci derived from endogenous retrovirus in junglefowl using whole-genome sequencing. **2023**, 13,
- 31 Human macroH2A1 drives nucleosome dephasing and genome instability in histone-humanized yeast.
- 30 Inferring secretory and metabolic pathway activity from omic data with secCellFie.
- 29 Transcriptomic analysis of cave, surface, and hybrid samples of the isopod *Asellus aquaticus* and identification of chromosomal location of candidate genes for cave phenotype evolution. **2023**, 14,
- 28 Comparative transcriptome profiling reveals the multiple levels of crosstalk in phytohormone networks in *Brassica napus*.
- 27 Phylogeography of the temperate grassland plant *Tephrosia kirilowii* (Asteraceae) inferred from multiplexed inter-simple sequence repeat genotyping by sequencing (MIG-seq) data.
- 26 Phage-display immunoprecipitation sequencing of the antibody epitope repertoire in inflammatory bowel disease reveals distinct antibody signatures. **2023**,
- 25 Fertility decline in female mosquitoes is regulated by the orco olfactory co-receptor. **2023**, 106883
- 24 NON-TARGET-SITE RESISTANCE DUE TO RAPID PHYSIOLOGICAL RESPONSE IN 2, 4-D RESISTANT *Conyza sumatrensis* : REDUCED 2, 4-D TRANSLOCATION AND AUXIN-INDUCED GENE EXPRESSION.
- 23 Comparison of the chloroplast genomes and phylogenomic analysis of Elaeocarpaceae. 11, e15322
- 22 Enhanced freeze-thaw cycles facilitate the antibiotic resistance proliferation and dissemination risk under global climate change. **2023**, 175, 119-128
- 21 Dissimilar gene repertoires of *Dickeya solani* involved in the colonization of lesions and roots of *Solanum tuberosum*. 14,
- 20 Integrated microbiome-metabolome-genome axis data of Laiwu and Lulai pigs. **2023**, 10,
- 19 The role of oceanic currents in the dispersal and connectivity of the mangrove *Rhizophora mangle* on the Southwest Atlantic region.
- 18 Phylogenomics reveals widespread hybridization and polyploidization in *Henckelia* (Gesneriaceae).
- 17 The complete chloroplast genome sequence of *Eugenia klotzschiana* O. Berg unveils the evolutionary dynamics in plastomes of Myrteae DC. tribe (Myrtaceae). **2023**, 147488
- 16 LncRNA analysis of mAb producing CHO clones reveals marker and engineering potential. **2023**, 78, 26-40
- 15 Using Genomics To Investigate an Outbreak of Vancomycin-Resistant *Enterococcus faecium* ST78 at a Large Tertiary Hospital in Queensland.

- 14 A progesterone derivative linked to a stable phospholipid activates breast cancer cell response without leaving the cell membrane. ○
- 13 Characterization of Early and Late Damage in a Mouse Model of Pelvic Radiation Disease. **2023**, 24, 8800 ○
- 12 Whole Genome Analysis and Assessment of the Metabolic Potential of *Gordonia rubripertincta* Strain 112, a Degradator of Aromatic and Aliphatic Compounds. **2023**, 12, 721 ○
- 11 A Yap-dependent mechanoregulatory program sustains cell migration for embryo axis assembly. **2023**, 14, ○
- 10 Carbapenemase-producing Gram-negative bacteria in hospital wastewater, wastewater treatment plants and surface waters in a metropolitan area in Germany, 2020. **2023**, 164179 ○
- 9 Complete genome analysis of Tequatrovirus *ufvareg1*, a Tequatrovirus species inhibiting *Escherichia coli* O157:H7. 13, ○
- 8 Identification of mRNA and lncRNA profiles and potential targeted agents for fibrolamellar carcinoma based on RNA-sequencing data. ○
- 7 Geography, not lifestyle, explains the population structure of free-living and host-associated deep-sea hydrothermal vent snail symbionts. **2023**, 11, ○
- 6 N/S element transformation modulating lithospheric microbial communities by single-species manipulation. **2023**, 11, ○
- 5 Immunization with Recombinant Accessory Protein-Deficient SARS-CoV-2 Protects against Lethal Challenge and Viral Transmission. ○
- 4 Genome Sequence Resource of the Avocado Scab Pathogen *Elsinoe perseae*. ○
- 3 Acid tolerance of lactate-utilizing bacteria of the order Bacteroidales contributes to prevention of ruminal acidosis in goats adapted to a high-concentrate diet. **2023**, ○
- 2 Domestication of different varieties in the cheese-making fungus *Geotrichum candidum*. 3, ○
- 1 Characterizing sediment functional traits and ecological consequences respond to increasing antibiotic pollution. ○