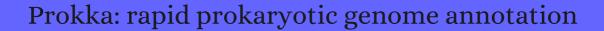
# CITATION REPORT List of articles citing



DOI: 10.1093/bioinformatics/btu153 Bioinformatics, 2014, 30, 2068-9.

Source: https://exaly.com/paper-pdf/58809274/citation-report.pdf

Version: 2024-04-20

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper	IF	Citations
2220	Hydraulically Fractured Natural-Gas Well Microbial Communities Contain Genomic Halogenation and Dehalogenation Potential.		
2219	A trans-Acting Cyclase Offloading Strategy for Nonribosomal Peptide Synthetases.		
2218	Metagenome-Guided Proteomic Quantification of Reductive Dehalogenases in the Dehalococcoides mccartyi-Containing Consortium SDC9.		
2217	Metabolic Traits of Candidatus Accumulibacter clade IIF Strain SCELSE1 Using Amino Acids As Carbon Sources for Enhanced Biological Phosphorus Removal.		
2216	Counting the Homeless: S-Night in New Orleans. <b>1992</b> , 16, 409-417		9
2215	Comparative genome analysis identifies few traits unique to the Escherichia coli ST131 H30Rx clade and extensive mosaicism at the capsule locus. <b>2014</b> , 15, 830		20
2214	Functional phylogenomics analysis of bacteria and archaea using consistent genome annotation with UniFam. <b>2014</b> , 14, 207		14
2213	Use of whole genome sequences to develop a molecular phylogenetic framework for Rhodococcus fascians and the Rhodococcus genus. <b>2014</b> , 5, 406		26
2212	Draft Genome Sequence of a Streptococcus agalactiae Strain Isolated from a Preterm Neonate Blood Sepsis Patient at the Royal Infirmary, Edinburgh, Scotland. <b>2014</b> , 2,		3
2211	Draft Genome Sequence of Lysobacter capsici AZ78, a Bacterium Antagonistic to Plant-Pathogenic Oomycetes. <b>2014</b> , 2,		9
2210	Draft Genome Sequence of Beneficial Rice Rhizosphere Isolate Pseudomonas aeruginosa PUPa3. <b>2014</b> , 2,		1
2209	Draft Genome Sequence of the Bordetella bronchiseptica Swine Isolate KM22. <b>2014</b> , 2,		5
2208	Draft Genome Sequence of Acinetobacter baumannii Strain ABBL099, a Multidrug-Resistant Clinical Outbreak Isolate with a Novel Multilocus Sequence Type. <b>2014</b> , 2,		2
2207	Draft Genome Sequence of a Staphylococcus warneri Strain Isolated from a Preterm Neonate Blood Sepsis Patient at the Royal Infirmary, Edinburgh, Scotland. <b>2014</b> , 2,		1
2206	Draft Genome Sequence of a Pantoea sp. Isolated from a Preterm Neonatal Blood Sepsis Patient. <b>2014</b> , 2,		2
2205	Draft Genome Sequence of a Staphylococcus aureus Isolate Taken from the Blood of a Preterm Neonatal Blood Sepsis Patient. <b>2014</b> , 2,		1
2204	Draft Genome Sequence of an Enterococcus faecalis Strain Isolated from a Neonatal Blood Sepsis Patient. <b>2014</b> , 2,		1

2203	Draft Genome Sequence of a Serratia marcescens Strain Isolated from a Preterm Neonatal Blood Sepsis Patient at the Royal Infirmary, Edinburgh, Scotland, United Kingdom. <b>2014</b> , 2,	1
2202	Complete Genome Sequences of Virulent Mycoplasma capricolum subsp. capripneumoniae Strains F38 and ILRI181. <b>2014</b> , 2,	12
2201	Simplicity Enabling a rapid route to publication. 2014,	
2200	Genome sequencing of an extended series of NDM-producing Klebsiella pneumoniae isolates from neonatal infections in a Nepali hospital characterizes the extent of community- versus hospital-associated transmission in an endemic setting. <b>2014</b> , 58, 7347-57	98
2199	Draft Genome Sequences of the Mycobacterium tuberculosis Clinical Strains A2 and A4, Isolated from a Relapse Patient in Taiwan. <b>2014</b> , 2,	3
2198	Genome Sequence of Maribius sp. Strain MOLA 401, a Marine Roseobacter with a Quorum-Sensing Cell-Dependent Physiology. <b>2014</b> , 2,	2
2197	Draft genome sequence of strain q-1, an iodide-oxidizing alphaproteobacterium isolated from natural gas brine water. <b>2014</b> , 2,	6
2196	The use of genome wide association methods to investigate pathogenicity, population structure and serovar in Haemophilus parasuis. <b>2014</b> , 15, 1179	29
2195	Draft Genome Sequence of Stenotrophomonas maltophilia SeITE02, a Gammaproteobacterium Isolated from Selenite-Contaminated Mining Soil. <b>2014</b> , 2,	4
2194	Complete Genome Sequences of Beijing and Manila Family Strains of Mycobacterium tuberculosis. <b>2014</b> , 2,	4
2193	Gene flow in environmental Legionella pneumophila leads to genetic and pathogenic heterogeneity within a Legionnaires' disease outbreak. <b>2014</b> , 15, 504	30
2192	The extant World War 1 dysentery bacillus NCTC1: a genomic analysis. <b>2014</b> , 384, 1691-7	21
2191	Dissecting vancomycin-intermediate resistance in staphylococcus aureus using genome-wide association. <b>2014</b> , 6, 1174-85	96
2190	Whole-Genome Sequences of Five Oligotrophic Bacteria Isolated from Deep within Lechuguilla Cave, New Mexico. <b>2014</b> , 2,	17
2189	Whole-Genome Sequence of Weissella ceti Strain WS08, Isolated from Diseased Rainbow Trout in Brazil. <b>2014</b> , 2,	2
2188	Complete Genome Sequences of Fish Pathogenic Weissella ceti Strains WS74 and WS105. <b>2014</b> , 2,	4
2187	Genome Sequence of Pectobacterium atrosepticum Strain 21A. <b>2014</b> , 2,	10
2186	blaNDM-5 carried by an IncX3 plasmid in Escherichia coli sequence type 167. <b>2014</b> , 58, 7548-52	69

2185	Draft genome sequences of three Holospora species (Holospora obtusa, Holospora undulata, and Holospora elegans), endonuclear symbiotic bacteria of the ciliate Paramecium caudatum. <b>2014</b> , 359, 16-8	17
2184	Genome and Transcriptome Sequences of Pseudomonas syringae pv. syringae B301D-R. <b>2014</b> , 2,	3
2183	Microbial genomic analysis reveals the essential role of inflammation in bacteria-induced colorectal cancer. <b>2014</b> , 5, 4724	222
2182	In silico prediction of Gallibacterium anatis pan-immunogens. <b>2014</b> , 45, 80	8
2181	Automated ensemble assembly and validation of microbial genomes. <b>2014</b> , 15, 126	45
2180	Community-driven development for computational biology at Sprints, Hackathons and Codefests. <b>2014</b> , 15 Suppl 14, S7	26
2179	Technical and Software Advances in Bacterial Pathogen Typing. <b>2015</b> , 289-327	1
2178	Metagenome-assembled genomes uncover a global brackish microbiome. <b>2015</b> , 16, 279	114
2177	Cyanobacteria and the Great Oxidation Event: evidence from genes and fossils. <b>2015</b> , 58, 769-785	123
2176	A high-resolution genomic analysis of multidrug-resistant hospital outbreaks of Klebsiella pneumoniae. <b>2015</b> , 7, 227-39	67
2175	Transfer of scarlet fever-associated elements into the group A Streptococcus M1T1 clone. <b>2015</b> , 5, 15877	41
2174	RASTtk: a modular and extensible implementation of the RAST algorithm for building custom annotation pipelines and annotating batches of genomes. <b>2015</b> , 5, 8365	1061
2173	The post-vaccine microevolution of invasive Streptococcus pneumoniae. <b>2015</b> , 5, 14952	28
2172	Environmental marine pathogen isolation using mesocosm culture of sharpsnout seabream: striking genomic and morphological features of novel Endozoicomonas sp. <b>2015</b> , 5, 17609	38
2171	The molecular characterisation of Escherichia coli K1 isolated from neonatal nasogastric feeding tubes. <b>2015</b> , 15, 449	13
2170	The pan-genome of Lactobacillus reuteri strains originating from the pig gastrointestinal tract. <b>2015</b> , 16, 1023	28
2169	Draft genome sequence of Methylibium sp. strain T29, a novel fuel oxygenate-degrading bacterial isolate from Hungary. <b>2015</b> , 10, 39	9
2168	Closed Genome Sequence of Octadecabacter temperatus SB1, the First Mesophilic Species of the Genus Octadecabacter. <b>2015</b> , 3,	O

Draft Genome Perspective of Staphylococcus saprophyticus Strain SU8, an N-Acyl Homoserine Lactone-Degrading Bacterium. <b>2015</b> , 3,	3
Complete Genome Sequence of Elizabethkingia sp. BM10, a Symbiotic Bacterium of the Wood-Feeding Termite Reticulitermes speratus KMT1. <b>2015</b> , 3,	5
Genomic dissection of the 1994 Cronobacter sakazakii outbreak in a French neonatal intensive care unit. <b>2015</b> , 16, 750	20
2164 The rumen microbial metagenome associated with high methane production in cattle. <b>2015</b> , 16, 839	186
SMRT sequencing of the Campylobacter coli BfR-CA-9557 genome sequence reveals unique methylation motifs. <b>2015</b> , 16, 1088	17
The Listeria monocytogenes Core-Genome Sequence Typer (LmCGST): a bioinformatic pipeline for molecular characterization with next-generation sequence data. <b>2015</b> , 15, 224	29
2161 Draft Genome Sequence of Turicella otitidis TD1, Isolated from a Patient with Bacteremia. <b>2015</b> , 3,	1
Genome Sequences of Three Pseudoalteromonas Strains (P1-8, P1-11, and P1-30), Isolated from the Marine Hydroid Hydractinia echinata. <b>2015</b> , 3,	4
Draft Genome Sequences of Six Pseudoalteromonas Strains, P1-7a, P1-9, P1-13-1a, P1-16-1b, P1-25, and P1-26, Which Induce Larval Settlement and Metamorphosis in Hydractinia echinata. <b>2015</b> , 3,	7
A transferable plasticity region in Campylobacter coli allows isolates of an otherwise non-glycolytic food-borne pathogen to catabolize glucose. <b>2015</b> , 98, 809-30	23
Whole-Genome Sequence of Listeria monocytogenes Serovar 4b Strain IZSAM_Lm_hs2008, Isolated from a Human Infection in Italy. <b>2015</b> , 3,	2
Complete Genome Sequence of the Novel Temperate Clostridium difficile Phage phiCDIF1296T. <b>21</b> 56 <b>2015</b> , 3,	10
2155 Draft Genome Sequence of a Clinical Isolate of Serratia marcescens, Strain AH0650_Sm1. <b>2015</b> , 3,	5
2154 Genome Sequence Analysis of Mycoplasma sp. HU2014, Isolated from Tissue Culture. <b>2015</b> , 3,	1
Draft Genome Sequence of the Strict Anaerobe Clostridium homopropionicum LuHBu1 (DSM 5847). <b>2015</b> , 3,	3
2152 Draft Genome Sequence of the Pandoraea apista LMG 16407 Type Strain. <b>2015</b> , 3,	4
Draft Genome Sequence of Amantichitinum ursilacus IGB-41, a New Chitin-Degrading Bacterium. <b>21</b> 51 <b>2015</b> , 3,	2
Draft Genome Sequence of Caedibacter varicaedens, a Kappa Killer Endosymbiont Bacterium of the Ciliate Paramecium biaurelia. <b>2015</b> , 3,	2

2149	Complete Genome Sequence of a Human-Invasive Salmonella enterica Serovar Typhimurium Strain of the Emerging Sequence Type 213 Harboring a Multidrug Resistance IncA/C Plasmid and a blaCMY-2-Carrying IncF Plasmid. <b>2015</b> , 3,	8
2148	Draft Genome Sequences of 14 Escherichia coli Phages Isolated from Cattle Slurry. <b>2015</b> , 3,	15
2147	Functional interactions among filamentous Epsilonproteobacteria and Bacteroidetes in a deep-sea hydrothermal vent biofilm. <b>2015</b> , 17, 4063-77	36
2146	Auxotrophy and intrapopulation complementary in the 'interactome' of a cultivated freshwater model community. <b>2015</b> , 24, 4449-59	70
2145	Draft Whole-Genome Sequence of Morganella morganii Serotype O:1ab. <b>2015</b> , 3,	4
2144	Draft Genome Sequence of Kerstersia gyiorum CG1, Isolated from a Leg Ulcer. <b>2015</b> , 3,	2
2143	Draft Genome Sequence of Komagataeibacter intermedius Strain AF2, a Producer of Cellulose, Isolated from Kombucha Tea. <b>2015</b> , 3,	7
2142	Draft Genome Sequence of Paenibacillus Strain P1XP2, a Polysaccharide-Degrading, Thermophilic, Facultative Anaerobic Bacterium Isolated from a Commercial Bioreactor Degrading Food Waste. <b>2015</b> , 3,	1
2141	Draft Genome Sequence of 24570, the Type Strain of Shigella flexneri. <b>2015</b> , 3,	2
2140	Draft Genome Sequence of Roseovarius tolerans EL-164, a Producer of N-Acylated Alanine Methyl Esters and N-Acylhomoserine Lactones. <b>2015</b> , 3,	2
2139	Complete Genome Sequence of the Clostridium difficile Type Strain DSM 1296T. <b>2015</b> , 3,	10
2138	Draft Genome Sequence of Geobacter sp. Strain OR-1, an Arsenate-Respiring Bacterium Isolated from Japanese Paddy Soil. <b>2015</b> , 3,	7
2137	Whole genome sequencing and analysis reveal insights into the genetic structure, diversity and evolutionary relatedness of luxI and luxR homologs in bacteria belonging to the Sphingomonadaceae family. <b>2014</b> , 4, 188	29
2136	Whole genome sequencing of extended-spectrum lactamase producing Klebsiella pneumoniae isolated from a patient in Lebanon. <b>2015</b> , 5, 32	15
2135	Whole-genome comparative analysis of virulence genes unveils similarities and differences between endophytes and other symbiotic bacteria. <b>2015</b> , 6, 419	19
2134	Insights on virulence from the complete genome of Staphylococcus capitis. 2015, 6, 980	29
2133	Physiological and genomic characterization of Arcobacter anaerophilus IR-1 reveals new metabolic features in Epsilonproteobacteria. <b>2015</b> , 6, 987	49
2132	Comparative Genomic Insights into Ecophysiology of Neutrophilic, Microaerophilic Iron Oxidizing Bacteria. <b>2015</b> , 6, 1265	61

2131	Volatile Organic Compounds from Native Potato-associated Pseudomonas as Potential Anti-oomycete Agents. <b>2015</b> , 6, 1295	80
2130	A Metagenomics-Based Metabolic Model of Nitrate-Dependent Anaerobic Oxidation of Methane by Methanoperedens-Like Archaea. <b>2015</b> , 6, 1423	122
2129	Tissue distribution of the Ehrlichia muris-like agent in a tick vector. <b>2015</b> , 10, e0122007	16
2128	Methods for analyzing next-generation sequencing data V. assembly, mapping, and quality control . <b>2015</b> , 26, 193-201	1
2127	Motility defects in Campylobacter jejuni defined gene deletion mutants caused by second-site mutations. <b>2015</b> , 161, 2316-27	18
2126	Vancomycin-resistant Enterococcus faecium harbouring vanN in Canada: a case and complete sequence of pEfm12493 harbouring the vanN operon. <b>2015</b> , 70, 2163-5	5
2125	Analysis of whole genome sequencing for the Escherichia coli O157:H7 typing phages. <b>2015</b> , 16, 271	18
2124	Draft Genome Sequences of Six Different Staphylococcus epidermidis Clones, Isolated Individually from Preterm Neonates Presenting with Sepsis at Edinburgh's Royal Infirmary. <b>2015</b> , 3,	3
2123	Draft genomes of Shigella strains used by the STOPENTERICS consortium. <b>2015</b> , 7, 14	6
2122	Bioinformatics and Biomedical Engineering. 2015,	3
2121	Evolutionary dynamics of methicillin-resistant Staphylococcus aureus within a healthcare system. <b>2015</b> , 16, 81	76
2120	Clostridium sordellii genome analysis reveals plasmid localized toxin genes encoded within pathogenicity loci. <b>2015</b> , 16, 392	32
2119	Draft Genome Sequence of Vibrio owensii Strain SH-14, Which Causes Shrimp Acute Hepatopancreatic Necrosis Disease. <b>2015</b> , 3,	62
2118	Whole Genome Sequencing of the Symbiont Pseudovibrio sp. from the Intertidal Marine Sponge Polymastia penicillus Revealed a Gene Repertoire for Host-Switching Permissive Lifestyle. <b>2015</b> , 7, 3022-32	22
2117	Regulation of plasmid-encoded isoprene metabolism in Rhodococcus, a representative of an important link in the global isoprene cycle. <b>2015</b> , 17, 3314-29	32
2116	BEACON: automated tool for Bacterial GEnome Annotation ComparisON. <b>2015</b> , 16, 616	21
2115	A single chromosome assembly of Bacteroides fragilis strain BE1 from Illumina and MinION nanopore sequencing data. <b>2015</b> , 4, 60	55
2114	RAMPART: a workflow management system for de novo genome assembly. <i>Bioinformatics</i> , <b>2015</b> , 31, 1824-6	20

2113	Roary: rapid large-scale prokaryote pan genome analysis. <i>Bioinformatics</i> , <b>2015</b> , 31, 3691-3	7.2	1949
2112	Extensive Capsule Locus Variation and Large-Scale Genomic Recombination within the Klebsiella pneumoniae Clonal Group 258. <b>2015</b> , 7, 1267-79		73
2111	As Clear as Mud? Determining the Diversity and Prevalence of Prophages in the Draft Genomes of Estuarine Isolates of Clostridium difficile. <b>2015</b> , 7, 1842-55		14
2110	NCBI-compliant genome submissions: tips and tricks to save time and money. <b>2017</b> , 18, 179-182		10
2109	Genome Sequence of Acinetobacter baumannii Strain A1, an Early Example of Antibiotic-Resistant Global Clone 1. <b>2015</b> , 3,		22
2108	Complete Genome Sequence of the Hypervirulent Bacterium Clostridium difficile Strain G46, Ribotype 027. <b>2015</b> , 3,		5
2107	Draft Genome Sequence of Aeromonas caviae Strain L12, a Quorum-Sensing Strain Isolated from a Freshwater Lake in Malaysia. <b>2015</b> , 3,		2
2106	Draft Genome Sequence of a Highly Virulent Strain of the Plant Pathogen Dickeya solani, IFB0099. <b>2015</b> , 3,		12
2105	Draft Genome Sequence of the Phenazine-Producing Pseudomonas fluorescens Strain 2-79. <b>2015</b> , 3,		3
2104	Draft Genome Sequence of Pseudomonas fluorescens SRM1, an Isolate from Spoiled Raw Milk. <b>2015</b> , 3,		3
2103	Whole-Genome Sequencing of Mycoplasma mycoides subsp. mycoides Italian Strain 57/13, the Causative Agent of Contagious Bovine Pleuropneumonia. <b>2015</b> , 3,		4
2102	Draft Genome Sequences of Five Legionella pneumophila Strains Isolated from Environmental Water Samples. <b>2015</b> , 3,		2
2101	Pandoraea sp. Strain E26: Discovery of Its Quorum-Sensing Properties via Whole-Genome Sequence Analysis. <b>2015</b> , 3,		2
2100	Complete Genome Sequence of the Bacterium Aalborg_AAW-1, Representing a Novel Family within the Candidate Phylum SR1. <b>2015</b> , 3,		5
2099	Draft Genome Sequence of Mycobacterium arupense Strain GUC1. <b>2015</b> , 3,		
2098	Complete Genome Sequence of Bordetella pertussis D420. <b>2015</b> , 3,		10
2097	Draft Genome Sequence of "Candidatus Hepatoplasma crinochetorum" Ps, a Bacterial Symbiont in the Hepatopancreas of the Terrestrial Isopod Porcellio scaber. <b>2015</b> , 3,		1
2096	Genome Sequence of the Soil Bacterium Janthinobacterium sp. KBS0711. <b>2015</b> , 3,		20

2095 Draft Genome Sequence of Mycobacterium elephantis Strain Lipa. <b>2015</b> , 3,	1
Complete Genome Sequence of Mycoplasma hominis Strain Sprott (ATCC 33131), Isolated from a Patient with Nongonococcal Urethritis. <b>2015</b> , 3,	6
Draft Genome Sequence of Broad-Spectrum Antifungal Bacterium Burkholderia gladioli Strain NGJ1, Isolated from Healthy Rice Seeds. <b>2015</b> , 3,	9
2092 Draft Genome Sequence of Mycobacterium heraklionense Strain Davo. <b>2015</b> , 3,	3
First Complete Genome Sequence of a Salmonella enterica subsp. enterica Serovar Derby Strain Associated with Pork in France. <b>2015</b> , 3,	8
First Insights into the Genome of Fructobacillus sp. EFB-N1, Isolated from Honey Bee Larva Infected with European Foulbrood. <b>2015</b> , 3,	1
Complete Genome Sequence of Staphylococcus aureus FCFHV36, a Methicillin-Resistant Strain Heterogeneously Resistant to Vancomycin. <b>2015</b> , 3,	5
2088 Draft Genome Sequence of Mycobacterium heckeshornense Strain RLE. <b>2015</b> , 3,	O
Complete Genome Sequence of Achromobacter xylosoxidans MN001, a Cystic Fibrosis Airway Isolate. <b>2015</b> , 3,	6
2086 Complete Genome Sequences of Two Bordetella hinzii Strains Isolated from Humans. <b>2015</b> , 3,	4
Genome Sequence of Borrelia chilensis VA1, a South American Member of the Lyme Borreliosis Group. <b>2015</b> , 3,	6
Draft Genome Sequence of Anoxybacillus Strain BCO1, Isolated from a Thermophilic Microbial Mat Colonizing the Outflow of a Bore Well of the Great Artesian Basin of Australia. <b>2015</b> , 3,	3
Analysis of the Complete Mycoplasma hominis LBD-4 Genome Sequence Reveals Strain-Variable Prophage Insertion and Distinctive Repeat-Containing Surface Protein Arrangements. <b>2015</b> , 3,	9
Finished Annotated Genome Sequence of Burkholderia pseudomallei Strain Bp1651, a Multidrug-Resistant Clinical Isolate. <b>2015</b> , 3,	12
Chlamydiaceae Genomics Reveals Interspecies Admixture and the Recent Evolution of Chlamydia abortus Infecting Lower Mammalian Species and Humans. <b>2015</b> , 7, 3070-84	21
Complete Genome Sequencing of Stenotrophomonas acidaminiphila ZAC14D2_NAIMI4_2, a 2080 Multidrug-Resistant Strain Isolated from Sediments of a Polluted River in Mexico, Uncovers New Antibiotic Resistance Genes and a Novel Class-II Lasso Peptide Biosynthesis Gene Cluster. <b>2015</b> , 3,	6
Accurate Microbial Genome Annotation Using an Integrated and User-Friendly Environment for Community Expertise of Gene Functions: The MicroScope Platform. <b>2015</b> , 141-169	2
Draft Genome Sequence of Bacillus Species from the Rhizosphere of the Desert Plant Rhazya stricta. <b>2015</b> , 3,	3

2077	Complete Genome Sequences of Three Neisseria gonorrhoeae Laboratory Reference Strains, Determined Using PacBio Single-Molecule Real-Time Technology. <b>2015</b> , 3,	11
2076	Genomic sequences of six botulinum neurotoxin-producing strains representing three clostridial species illustrate the mobility and diversity of botulinum neurotoxin genes. <b>2015</b> , 30, 102-113	47
2075	Genomics of Weissella cibaria with an examination of its metabolic traits. 2015, 161, 914-30	28
2074	Dynamics of MDR Enterobacter cloacae outbreaks in a neonatal unit in Nepal: insights using wider sampling frames and next-generation sequencing. <b>2015</b> , 70, 1008-15	31
2073	Multi -omics and metabolic modelling pipelines: challenges and tools for systems microbiology. <b>2015</b> , 171, 52-64	90
2072	Draft Genome Sequence of Anammox Bacterium "Candidatus Scalindua brodae," Obtained Using Differential Coverage Binning of Sequencing Data from Two Reactor Enrichments. <b>2015</b> , 3,	34
2071	Rickettsia buchneri sp. nov., a rickettsial endosymbiont of the blacklegged tick Ixodes scapularis. <b>2015</b> , 65, 965-970	75
2070	Draft Genome Sequence of Erwinia tracheiphila, an Economically Important Bacterial Pathogen of Cucurbits. <b>2015</b> , 3,	11
2069	Two Rapidly Growing Mycobacterial Species Isolated from a Brain Abscess: First Whole-Genome Sequences of Mycobacterium immunogenum and Mycobacterium llatzerense. <b>2015</b> , 53, 2374-7	25
2068	Escherichia coli of sequence type 3835 carrying bla NDM-1, bla CTX-M-15, bla CMY-42 and bla SHV-12. <b>2015</b> , 5, 12275	25
2067	Comparative analysis of the Mycoplasma capricolum subsp. capricolum GM508D genome reveals subrogation of phase-variable contingency genes and a novel integrated genetic element. <b>2015</b> , 73, ftv041	2
2066	Distinct SagA from Hospital-Associated Clade A1 Enterococcus faecium Strains Contributes to Biofilm Formation. <b>2015</b> , 81, 6873-82	17
2065	Draft Genome Sequence of the Beneficial Rhizobacterium Pseudomonas fluorescens DSM 8569, a Natural Isolate of Oilseed Rape (Brassica napus). <b>2015</b> , 3,	2
2064	Genomic Analysis of the Evolution and Global Spread of Hyper-invasive Meningococcal Lineage 5. <b>2015</b> , 2, 234-243	17
2063	Subtyping of the Legionella pneumophila "Ulm" outbreak strain using the CRISPR-Cas system. <b>2015</b> , 305, 828-37	9
2062	Genome Sequence of Vibrio VPAP30, Isolated from an Episode of Massive Mortality of Reared Larvae of the Scallop Argopecten purpuratus. <b>2015</b> , 3,	4
2061	Databases for Microbiologists. <b>2015</b> , 197, 2458-67	21
2060	Metagenomic Sequencing Unravels Gene Fragments with Phylogenetic Signatures of O2-Tolerant NiFe Membrane-Bound Hydrogenases in Lacustrine Sediment. <b>2015</b> , 71, 296-302	1

2059	31, 3406-12	.2	13
2058	A genomic and transcriptomic approach to investigate the blue pigment phenotype in Pseudomonas fluorescens. <b>2015</b> , 213, 88-98		39
2057	The draft genome of Mycobacterium aurum, a potential model organism for investigating drugs against Mycobacterium tuberculosis and Mycobacterium leprae. <b>2015</b> , 4, 207-16		14
2056	Characterization of Three Mycobacterium spp. with Potential Use in Bioremediation by Genome Sequencing and Comparative Genomics. <b>2015</b> , 7, 1871-86		11
2055	First Report of OXA-181-Producing Escherichia coli in China and Characterization of the Isolate Using Whole-Genome Sequencing. <b>2015</b> , 59, 5022-5		63
2054	Draft Genome of the Multidrug-Resistant Acinetobacter baumannii Strain A155 Clinical Isolate. <b>2015</b> , 3,		15
2053	Genomics tools in microbial food safety. <b>2015</b> , 4, 105-110		19
2052	Complete genome sequence of BS49 and draft genome sequence of BS34A, Bacillus subtilis strains carrying Tn916. <b>2015</b> , 362, 1-4		9
2051	High-Resolution Analysis by Whole-Genome Sequencing of an International Lineage (Sequence Type 111) of Pseudomonas aeruginosa Associated with Metallo-Carbapenemases in the United Kingdom. <b>2015</b> , 53, 2622-31		39
2050	A naturally occurring prfA truncation in a Listeria monocytogenes field strain contributes to reduced replication and cell-to-cell spread. <b>2015</b> , 179, 91-101		16
2049	Identification of viruses associated with larvae of the dragonflyLeucorrhinia dubia, and damselflyCoenagrion puellafrom RNA sequencing data. <b>2015</b> , 18, 81-88		2
2048	Complete genome sequence of oxalate-degrading bacterium Pandoraea vervacti DSM 23571(T). <b>2015</b> , 204, 5-6		10
2047	Genome sequencing and comparative genomics provides insights on the evolutionary dynamics and pathogenic potential of different H-serotypes of Shiga toxin-producing Escherichia coli O104. <b>2015</b> , 15, 83		20
2046	MyPro: A seamless pipeline for automated prokaryotic genome assembly and annotation. <b>2015</b> , 113, 72-4		23
2045	Single-molecule sequencing reveals the molecular basis of multidrug-resistance in ST772 methicillin-resistant Staphylococcus aureus. <b>2015</b> , 16, 388		15
2044	Subsistence strategies in traditional societies distinguish gut microbiomes. <b>2015</b> , 6, 6505		304
2043	Phylogeographical analysis of the dominant multidrug-resistant H58 clade of Salmonella Typhi identifies inter- and intracontinental transmission events. <b>2015</b> , 47, 632-9		305
2042	Rethinking the Niche of Upper-Atmosphere Bacteria: Draft Genome Sequences of Bacillus aryabhattai C765 and Bacillus aerophilus C772, Isolated from Rice Fields. <b>2015</b> , 3,		2

2041	IonGAP: integrative bacterial genome analysis for Ion Torrent sequence data. <i>Bioinformatics</i> , <b>2015</b> , 31, 2870-3	9
2040	Complex archaea that bridge the gap between prokaryotes and eukaryotes. <b>2015</b> , 521, 173-179	726
2039	Transmission and microevolution of USA300 MRSA in U.S. households: evidence from whole-genome sequencing. <b>2015</b> , 6, e00054	71
2038	Gene Loss and Lineage-Specific Restriction-Modification Systems Associated with Niche Differentiation in the Campylobacter jejuni Sequence Type 403 Clonal Complex. <b>2015</b> , 81, 3641-7	18
2037	Single-cell genomics of a rare environmental alphaproteobacterium provides unique insights into Rickettsiaceae evolution. <b>2015</b> , 9, 2373-85	33
2036	Use of Whole-Genome Phylogeny and Comparisons for Development of a Multiplex PCR Assay To Identify Sequence Type 36 Vibrio parahaemolyticus. <b>2015</b> , 53, 1864-72	14
2035	Distinct Commensals Induce Interleukin-1 via NLRP3 Inflammasome in Inflammatory Monocytes to Promote Intestinal Inflammation in Response to Injury. <b>2015</b> , 42, 744-55	192
2034	Regulators of gut motility revealed by a gnotobiotic model of diet-microbiome interactions related to travel. <b>2015</b> , 163, 95-107	124
2033	Complete Genome Sequence of a CTX-M-15-Producing Klebsiella pneumoniae Outbreak Strain from Multilocus Sequence Type 514. <b>2015</b> , 3,	7
2032	Comparative Genomics of a Plant-Parasitic Nematode Endosymbiont Suggest a Role in Nutritional Symbiosis. <b>2015</b> , 7, 2727-46	36
2031	Genome Sequence of the Solvent-Producing Clostridium beijerinckii Strain 59B, Isolated from Staffordshire Garden Soil. <b>2015</b> , 3,	3
2030	Complete genome sequence of the heavy metal resistant bacterium Altererythrobacter atlanticus 26DY36(T), isolated from deep-sea sediment of the North Atlantic Mid-ocean ridge. <b>2015</b> , 24 Pt 3, 289-92	9
2029	Draft Genome Sequences of Three Strains of Geobacillus stearothermophilus Isolated from a Milk Powder Manufacturing Plant. <b>2015</b> , 3,	3
2028	Genomic analyses of pneumococci reveal a wide diversity of bacteriocins - including pneumocyclicin, a novel circular bacteriocin. <b>2015</b> , 16, 554	33
2027	Genome Sequence of a Novel Iflavirus from mRNA Sequencing of the Pupa of Bombyx mori Inoculated with Cordyceps militaris. <b>2015</b> , 3,	7
2026	Plant pathogenic anaerobic bacteria use aromatic polyketides to access aerobic territory. <b>2015</b> , 350, 670-4	37
2025	Intercellular wiring enables electron transfer between methanotrophic archaea and bacteria. <b>2015</b> , 526, 587-90	318
2024	Methane metabolism in the archaeal phylum Bathyarchaeota revealed by genome-centric metagenomics. <b>2015</b> , 350, 434-8	45°

2023	2015, 6, 6740	89
2022	Genomic Epidemiology of a Protracted Hospital Outbreak Caused by a Toxin A-Negative Clostridium difficile Sublineage PCR Ribotype 017 Strain in London, England. <b>2015</b> , 53, 3141-7	37
2021	A Genomic View of Lactobacilli and Pediococci Demonstrates that Phylogeny Matches Ecology and Physiology. <b>2015</b> , 81, 7233-43	135
2020	Multiple Genetic Mutations Associated with Polymyxin Resistance in Acinetobacter baumannii. <b>2015</b> , 59, 7899-902	16
2019	Paenibacillus larvae-Directed Bacteriophage HB10c2 and Its Application in American Foulbrood-Affected Honey Bee Larvae. <b>2015</b> , 81, 5411-9	31
2018	Description of a novel pectin-degrading bacterial species Prevotella pectinovora sp. nov., based on its phenotypic and genomic traits. <b>2015</b> , 53, 503-10	12
2017	Polysaccharide utilization locus and CAZYme genome repertoires reveal diverse ecological adaptation of Prevotella species. <b>2015</b> , 38, 453-61	36
2016	Complete Genome Sequences of Escherichia coli Strains 1303 and ECC-1470 Isolated from Bovine Mastitis. <b>2015</b> , 3,	15
2015	Draft Genome Sequences of 10 Microbacterium spp., with Emphasis on Heavy Metal-Contaminated Environments. <b>2015</b> , 3,	13
2014	Acetogenesis from H2 plus CO2 and nitrogen fixation by an endosymbiotic spirochete of a termite-gut cellulolytic protist. <b>2015</b> , 112, 10224-30	65
2013	Complete Genome Sequencing of a Multidrug-Resistant and Human-Invasive Salmonella enterica Serovar Typhimurium Strain of the Emerging Sequence Type 213 Genotype. <b>2015</b> , 3,	11
2012	Complete Genome Sequence of Campylobacter jejuni YH001 from Beef Liver, Which Contains a Novel Plasmid. <b>2015</b> , 3,	4
2011	Genome Sequence of Vibrio campbellii Strain UMTGB204, a Marine Bacterium Isolated from a Green Barrel Tunicate. <b>2015</b> , 3,	
2010	Genome Resequencing of the Virulent and Multidrug-Resistant Reference Strain Clostridium difficile 630. <b>2015</b> , 3,	28
2009	Genome Sequence of Jannaschia aquimarina GSW-M26, a Member of the Roseobacter Clade. <b>2015</b> , 3,	
2008	Draft genome sequence of a novel culturable marine chroococcalean cyanobacterium from the South atlantic ocean. <b>2015</b> , 3,	1
2007	Insights on Quorum-Quenching Properties of Lysinibacillus fusiformis Strain RB21, a Malaysian Municipal Solid-Waste Landfill Soil Isolate, via Complete Genome Sequence Analysis. <b>2015</b> , 3,	1
2006	Draft Genome Sequences of Four NDM-1-Producing Klebsiella pneumoniae Strains from a Health Care Facility in Northern California. <b>2015</b> , 3,	9

Genome Sequence of Rhodococcus sp. Strain PML026, a Trehalolipid Biosurfactant Producer and Biodegrader of Oil and Alkanes. <b>2015</b> , 3,	7
Genome Sequence of Bacillus thuringiensis Strain Btm27, an Egyptian Isolate Highly Toxic to Cotton Leafworm. <b>2015</b> , 3,	2
Draft Genome Sequence of Anaeromyxobacter sp. Strain PSR-1, an Arsenate-Respiring Bacterium Isolated from Arsenic-Contaminated Soil. <b>2015</b> , 3,	12
Draft Genome Sequences of Klebsiella pneumoniae Clinical Type Strain ATCC 13883 and Three Multidrug-Resistant Clinical Isolates. <b>2015</b> , 3,	8
Complete genome sequence of Serratia fonticola DSM 4576 T, a potential plant growth promoting bacterium. <b>2015</b> , 214, 43-4	6
2000 NCBI BLAST+ integrated into Galaxy. <b>2015</b> , 4, 39	100
1999 Functional overlap of the Arabidopsis leaf and root microbiota. <b>2015</b> , 528, 364-9	612
Complete Genome Sequence of Linezolid-Susceptible Staphylococcus haemolyticus Sh29/312/L2, a Clonal Derivative of a Linezolid-Resistant Clinical Strain. <b>2015</b> , 3,	3
Draft Genome Sequence of Mycobacterium obuense Strain UC1, Isolated from Patient Sputum. <b>2015</b> , 3,	3
Complete genome sequence of Serratia multitudinisentens RB-25(T), a novel chitinolytic bacterium <b>2015</b> , 207, 32-3	٦. 6
Whole-genome phylogenomic heterogeneity of Neisseria gonorrhoeae isolates with decreased cephalosporin susceptibility collected in Canada between 1989 and 2013. <b>2015</b> , 53, 191-200	90
The structure of the Morganella morganii lipopolysaccharide core region and identification of its genomic loci. <b>2015</b> , 402, 232-5	1
Complete genome sequence of Bacillus subtilis SG6 antagonistic against Fusarium graminearum. <b>2015</b> , 194, 10-1	10
Emergence of scarlet fever Streptococcus pyogenes emm12 clones in Hong Kong is associated wit toxin acquisition and multidrug resistance. <b>2015</b> , 47, 84-7	h 103
Genome Sequence of the Facultative Anaerobe Oerskovia enterophila DFA-19 (DSM 43852T). <b>2016</b> 4,	5,
Draft Genome Sequences of Pseudomonas aeruginosa Isolates from Wounded Military Personnel. <b>2016</b> , 4,	2
Genome Sequence of the Acetogenic Bacterium Butyribacterium methylotrophicum DSM 3468T. <b>2016</b> , 4,	10
Draft Genome Sequence of Oil-Degrading Bacterium Gallaecimonas pentaromativorans Strain YA_ from the Southwest Indian Ocean. <b>2016</b> , 4,	1 2

1987 Complete Genome Sequence of an African Swine Fever Virus Isolate from Sardinia, Italy. <b>2016</b> , 4,	12
1986 Draft Genome Sequences of Escherichia coli Isolates from Wounded Military Personnel. <b>2016</b> , 4,	
Whole-Genome Characterization and Strain Comparison of VT2f-Producing Escherichia coli Causi Hemolytic Uremic Syndrome. <b>2016</b> , 22, 2078-2086	ng 21
$_{1984}$ Draft Genome Sequence of the Aureocin A53-Producing Strain Staphylococcus aureus A53. <b>2016</b>	, 4,
Genome Sequence of Listeria monocytogenes Plasmid pLM-C-273 Carrying Genes Related to Strong Resistance. <b>2016</b> , 4,	ess 2
1982 Methylome Analysis of Two spp. Using Single-Molecule Real-Time Sequencing. <b>2016</b> , 32, 500-507	12
1981 The diversity of surface polysaccharides. <b>2016</b> , 2, e000073	101
serotyping of from short read data identifies limited novel O-loci but extensive diversity of O:H serotype combinations within and between pathogenic lineages. <b>2016</b> , 2, e000064	69
1979 Identification of capsule synthesis loci from whole genome data. <b>2016</b> , 2, e000102	216
Draft Genome Sequences of Methanobrevibacter curvatus DSM11111, Methanobrevibacter cuticularis DSM11139, Methanobrevibacter filiformis DSM11501, and Methanobrevibacter oralis DSM7256. <b>2016</b> , 4,	2
Draft Genome Assembly of the Bloom-Forming Cyanobacterium Nodularia spumigena Strain CENA596 in Shrimp Production Ponds. <b>2016</b> , 4,	6
1976 DFAST and DAGA: web-based integrated genome annotation tools and resources. <b>2016</b> , 35, 173-	184 117
Phenotypic and Genotypic Characteristics of Shiga Toxin-Producing Escherichia coli Isolated from Surface Waters and Sediments in a Canadian Urban-Agricultural Landscape. <b>2016</b> , 6, 36	11
Selective Pressure of Temperature on Competition and Cross-Feeding within Denitrifying and Fermentative Microbial Communities. <b>2015</b> , 6, 1461	13
1973 A Phylogenomic Analysis of the Bacterial Phylum Fibrobacteres. <b>2015</b> , 6, 1469	48
Complete Genome Sequence Analysis of Pandoraea pnomenusa Type Strain DSM 16536(T) Isolat from a Cystic Fibrosis Patient. <b>2016</b> , 7, 109	ed 6
Why Close a Bacterial Genome? The Plasmid of Alteromonas Macleodii HOT1A3 is a Vector for Inter-Specific Transfer of a Flexible Genomic Island. <b>2016</b> , 7, 248	14
Comparative Genomic Analysis Reveals a Diverse Repertoire of Genes Involved in Prokaryote-Eukaryote Interactions within the Pseudovibrio Genus. <b>2016</b> , 7, 387	13

1969	Deep Subsurface Life from North Pond: Enrichment, Isolation, Characterization and Genomes of Heterotrophic Bacteria. <b>2016</b> , 7, 678	15
1968	Genome-Centric Analysis of Microbial Populations Enriched by Hydraulic Fracture Fluid Additives in a Coal Bed Methane Production Well. <b>2016</b> , 7, 731	38
1967	New Insights into the Genetic Diversity of Clostridium botulinum Group III through Extensive Genome Exploration. <b>2016</b> , 7, 757	16
1966	Comparative Genomics and Proteomic Analysis of Four Non-tuberculous Mycobacterium Species and Mycobacterium tuberculosis Complex: Occurrence of Shared Immunogenic Proteins. <b>2016</b> , 7, 795	13
1965	Phylogenomic Study of Burkholderia glathei-like Organisms, Proposal of 13 Novel Burkholderia Species and Emended Descriptions of Burkholderia sordidicola, Burkholderia zhejiangensis, and Burkholderia grimmiae. <b>2016</b> , 7, 877	40
1964	Identification, Recovery, and Refinement of Hitherto Undescribed Population-Level Genomes from the Human Gastrointestinal Tract. <b>2016</b> , 7, 884	8
1963	From DNA to FBA: How to Build Your Own Genome-Scale Metabolic Model. <b>2016</b> , 7, 907	28
1962	Isolation and Genomic Characterization of 'Desulfuromonas soudanensis WTL', a Metal- and Electrode-Respiring Bacterium from Anoxic Deep Subsurface Brine. <b>2016</b> , 7, 913	34
1961	Whole Genome Sequencing for Genomics-Guided Investigations of Escherichia coli O157:H7 Outbreaks. <b>2016</b> , 7, 985	32
1960	Culture Independent Genomic Comparisons Reveal Environmental Adaptations for Altiarchaeales. <b>2016</b> , 7, 1221	20
1959	Genomic Analysis Reveals Multi-Drug Resistance Clusters in Group B Streptococcus CC17 Hypervirulent Isolates Causing Neonatal Invasive Disease in Southern Mainland China. <b>2016</b> , 7, 1265	31
1958	Demethylase Inhibitor Fungicide Resistance in Pyrenophora teres f. sp. teres Associated with Target Site Modification and Inducible Overexpression of Cyp51. <b>2016</b> , 7, 1279	33
1957	Novel Methyltransferase Recognition Motif Identified in Chania multitudinisentens RB-25(T) gen. nov., sp. nov. <b>2016</b> , 7, 1362	3
1956	Production of the Bioactive Compounds Violacein and Indolmycin Is Conditional in a Mutant of S4054 Lacking the Malic Enzyme. <b>2016</b> , 7, 1461	13
1955	Molecular Characterization of Serovars Anatum and Ealing Associated with Two Historical Outbreaks, Linked to Contaminated Powdered Infant Formula. <b>2016</b> , 7, 1664	1
1954	Molecular Keys to the and spp. Interaction with the Plant Pathogen. <b>2016</b> , 7, 1668	45
1953	Diversity of the Germination Apparatus in Groups I, II, III, and IV. <b>2016</b> , 7, 1702	18
1952	Ultrastructure and Viral Metagenome of Bacteriophages from an Anaerobic Methane Oxidizing Bioreactor Enrichment Culture. <b>2016</b> , 7, 1740	9

1951	Comparative Analysis of Two Strains using Genomics and Mass Spectrometry-Based Proteomics. <b>2016</b> , 7, 1757	10
1950	Complete Genome Sequence of DSM 8809, a Microbe Identified in Spoiled Vacuum Packed Beef. <b>2016</b> , 7, 1764	12
1949	Glucose Metabolism via the Entner-Doudoroff Pathway in : A Rare Trait that Enhances Survival and Promotes Biofilm Formation in Some Isolates. <b>2016</b> , 7, 1877	21
1948	Comprehensive Phylogenetic Analysis of Bovine Non- Staphylococci Species Based on Whole-Genome Sequencing. <b>2016</b> , 7, 1990	32
1947	Construction of a Pan-Genome Allele Database of Serovar Enteritidis for Molecular Subtyping and Disease Cluster Identification. <b>2016</b> , 7, 2010	17
1946	gen. nov., sp. nov., an Unusual Member of the Phylum Planctomycetes from the German Wadden Sea. <b>2016</b> , 7, 2079	34
1945	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.	15
1944	<b>2016</b> , 7, 2082 The Oxidative Stress Regulator RrpB Is Associated with a Genomic Hypervariable Region and Altered Oxidative Stress Resistance. <b>2016</b> , 7, 2117	20
1943	Genomic Recombination Leading to Decreased Virulence of Group B Streptococcus in a Mouse Model of Adult Invasive Disease. <b>2016</b> , 5,	5
1942	Two cases of serotypeable and non-serotypeable variants of Streptococcus pneumoniae detected simultaneously during invasive disease. <b>2016</b> , 16, 126	1
1941	Practical Approaches for Detecting Selection in Microbial Genomes. <b>2016</b> , 12, e1004739	17
1940	Combined Analysis of Variation in Core, Accessory and Regulatory Genome Regions Provides a Super-Resolution View into the Evolution of Bacterial Populations. <b>2016</b> , 12, e1006280	117
1939	Carbapenem-Resistant Bacteria Recovered from Faeces of Dairy Cattle in the High Plains Region of the USA. <b>2016</b> , 11, e0147363	43
1938	Population Structure and Antimicrobial Resistance Profiles of Streptococcus suis Serotype 2 Sequence Type 25 Strains. <b>2016</b> , 11, e0150908	24
1937	De Novo Assembly of Human Herpes Virus Type 1 (HHV-1) Genome, Mining of Non-Canonical Structures and Detection of Novel Drug-Resistance Mutations Using Short- and Long-Read Next Generation Sequencing Technologies. <b>2016</b> , 11, e0157600	37
1936	Comparative Genome Analyses of Streptococcus suis Isolates from Endocarditis Demonstrate Persistence of Dual Phenotypic Clones. <b>2016</b> , 11, e0159558	3
1935	Comparative Genomic and Phenotypic Characterization of Pathogenic and Non-Pathogenic Strains of Xanthomonas arboricola Reveals Insights into the Infection Process of Bacterial Spot Disease of Stone Fruits. <b>2016</b> , 11, e0161977	20
1934	Genomic Epidemiology of Methicillin-Resistant Staphylococcus aureus in a Neonatal Intensive Care Unit. <b>2016</b> , 11, e0164397	16

1933	Real-Time Pathogen Detection in the Era of Whole-Genome Sequencing and Big Data: Comparison of k-mer and Site-Based Methods for Inferring the Genetic Distances among Tens of Thousands of Salmonella Samples. <b>2016</b> , 11, e0166162	6
1932	Genome and Proteome Analysis of Rhodococcus erythropolis MI2: Elucidation of the 4,4I-Dithiodibutyric Acid Catabolism. <b>2016</b> , 11, e0167539	7
1931	Genomic analysis of serotype Paratyphi A during an outbreak in Cambodia, 2013-2015. <b>2016</b> , 2, e000092	16
1930	Genome-centric resolution of microbial diversity, metabolism and interactions in anaerobic digestion. <b>2016</b> , 18, 3144-58	85
1929	Genomic approach to studying nutritional requirements of Clostridium tyrobutyricum and other Clostridia causing late blowing defects. <b>2016</b> , 59, 213-23	4
1928	L-fucose influences chemotaxis and biofilm formation in Campylobacter jejuni. <b>2016</b> , 101, 575-89	43
1927	Elucidation of Taste- and Odor-Producing Bacteria and Toxigenic Cyanobacteria in a Midwestern Drinking Water Supply Reservoir by Shotgun Metagenomic Analysis. <b>2016</b> , 82, 5410-20	32
1926	Genomic characterization of the uncultured Bacteroidales family S24-7 inhabiting the guts of homeothermic animals. <b>2016</b> , 4, 36	322
1925	Draft Genome Sequences of Three Novel Clostridium Isolates from Northern Iraq. 2016, 4,	3
1924	Complete Genome Sequence of Salmonella enterica Serovar Typhimurium Strain SO3 (Sequence Type 302) Isolated from a Baby with Meningitis in Mexico. <b>2016</b> , 4,	5
1923	The deep-sea glass sponge Lophophysema eversa harbours potential symbionts responsible for the nutrient conversions of carbon, nitrogen and sulfur. <b>2016</b> , 18, 2481-94	37
1922	Genome Sequences of Five Clinical Isolates of Klebsiella pneumoniae. <b>2016</b> , 4,	6
1921	Draft Genome Sequence of Syntrophomonas wolfei subsp. methylbutyratica Strain 4J5T (JCM 14075), a Mesophilic Butyrate- and 2-Methylbutyrate-Degrading Syntroph. <b>2016</b> , 4,	4
1920	Draft Genome Sequences of Methanoculleus horonobensis Strain JCM 15517, Methanoculleus thermophilus Strain DSM 2373, and Methanofollis ethanolicus Strain JCM 15103, Hydrogenotrophic Methanogens Belonging to the Family Methanomicrobiaceae. <b>2016</b> , 4,	6
1919	Complete Mitochondrial Genome Sequence of the Pezizomycete Pyronema confluens. 2016, 4,	5
1918	First Insights into the Draft Genome of Clostridium colicanis DSM 13634, Isolated from Canine Feces. <b>2016</b> , 4,	3
1917	Draft Genome Sequence of an Enterobacter Species Associated with Illnesses and Powdered Infant Formula. <b>2016</b> , 4,	1
1916	Genome Sequence of Listeria monocytogenes Strain F6540 (Sequence Type 360) Collected from Food Samples in Ontario, Canada. <b>2016</b> , 4,	

1915	Draft Genome Sequence of Trueperella bernardiae LCDC 89-0504T, Isolated from a Human Blood Culture. <b>2016</b> , 4,	6
1914	Proteogenomics of rare taxonomic phyla: A prospective treasure trove of protein coding genes. <b>2016</b> , 16, 226-40	11
1913	Genome-based Definition of an Inflammatory Bowel Disease-associated Adherent-Invasive Escherichia coli Pathovar. <b>2016</b> , 22, 1-12	33
1912	The microbiome of the leaf surface of Arabidopsis protects against a fungal pathogen. <b>2016</b> , 210, 1033-43	177
1911	Complete Genome Sequence of Salmonella enterica Serovar Typhimurium Strain SO2 (Sequence Type 302) Isolated from an Asymptomatic Child in Mexico. <b>2016</b> , 4,	3
1910	Differential Functional Constraints Cause Strain-Level Endemism in Populations. <b>2016</b> , 1,	11
1909	Draft Genome Sequences of Gluconobacter cerinus CECT 9110 and Gluconobacter japonicus CECT 8443, Acetic Acid Bacteria Isolated from Grape Must. <b>2016</b> , 4,	3
1908	An updated view of plasmid conjugation and mobilization in Staphylococcus. <b>2016</b> , 6, e1208317	58
1907	ConsPred: a rule-based (re-)annotation framework for prokaryotic genomes. <i>Bioinformatics</i> , <b>2016</b> , 32, 3327-3329	7
1906	Bacterial sensing underlies artificial sweetener-induced growth of gut Lactobacillus. <b>2016</b> , 18, 2159-71	21
1905	Draft Genome Sequence of Two Sphingopyxis sp. Strains, Dominant Members of the Bacterial Community Associated with a Drinking Water Distribution System Simulator. <b>2016</b> , 4,	4
1904	Draft Genome Sequence of the Broad-Spectrum Xenobiotic Degrader Achromobacter xylosoxidans ADAF13. <b>2016</b> , 4,	2
1903	Complete Genome Sequence of Salmonella enterica Serovar Typhimurium Strain YU15 (Sequence Type 19) Harboring the Salmonella Genomic Island 1 and Virulence Plasmid pSTV. <b>2016</b> , 4,	3
1902	Complete Genome Sequence of Mycoplasma mycoides subsp. mycoides T1/44, a Vaccine Strain against Contagious Bovine Pleuropneumonia. <b>2016</b> , 4,	3
1901	Complete Genome Sequence of Lactobacillus rhamnosus Strain BPL5 (CECT 8800), a Probiotic for Treatment of Bacterial Vaginosis. <b>2016</b> , 4,	2
1900	Draft Genome Sequences of 37 Salmonella enterica Strains Isolated from Poultry Sources in Nigeria. <b>2016</b> , 4,	4
1899	Draft Genome Sequence of Stenotrophomonas maltophilia CBF10-1, an Organophosphate-Degrading Bacterium Isolated from Ranch Soil in Fairchilds, Texas. <b>2016</b> , 4,	1
1898	Complete Genomic Sequence of an Avian Pathogenic Escherichia coli Strain of Serotype O7:HNT. <b>2016</b> , 4,	6

1897	Draft Genome Sequences of Two Novel Amoeba-Resistant Intranuclear Bacteria, "Candidatus Berkiella cookevillensis" and "Candidatus Berkiella aquae". <b>2016</b> , 4,	3
1896	Draft Genome Sequence of the Bactrocera oleae Symbiont "Candidatus Erwinia dacicola". <b>2016</b> , 4,	15
1895	Draft Genome Sequence of Methylophaga muralis Bur 1, a Haloalkaliphilic (Non-Methane-Utilizing) Methylotroph Isolated from a Soda Lake. <b>2016</b> , 4,	3
1894	Genome analysis of Campylobacter concisus strains from patients with inflammatory bowel disease and gastroenteritis provides new insights into pathogenicity. <b>2016</b> , 6, 38442	24
1893	Complete Genome Sequencing and Comparative Genomic Analysis of the Thermotolerant Acetic Acid Bacterium, Acetobacter pasteurianus SKU1108, Provide a New Insight into Thermotolerance. <b>2016</b> , 31, 395-400	10
1892	First Complete Genome Sequence of a Subdivision 6 Acidobacterium Strain. <b>2016</b> , 4,	12
1891	Genome Sequencing and Transposon Mutagenesis of Burkholderia seminalis TC3.4.2R3 Identify Genes Contributing to Suppression of Orchid Necrosis Caused by B. gladioli. <b>2016</b> , 29, 435-46	12
1890	Draft Genome Sequence of Methyloligella halotolerans 2T, a New Halotolerant Methylotroph, Accumulating Poly-3-Hydroxybutyrate and Ectoine. 2016, 4,	1
1889	Complete genome sequence of P3B5, a candidate for microbial phyllo-remediation of hydrocarbon-contaminated sites. <b>2016</b> , 11, 75	22
1888	Draft Genome Sequences of Microbacterium hominis LCDC-84-0209T Isolated from a Human Lung Aspirate and Microbacterium laevaniformans LCDC 91-0039 Isolated from a Human Blood Culture. <b>2016</b> , 4,	1
1887	Salmonella Degrades the Host Glycocalyx Leading to Altered Infection and Glycan Remodeling. <b>2016</b> , 6, 29525	42
1886	Genomic evidence for plant-parasitic nematodes as the earliest Wolbachia hosts. <b>2016</b> , 6, 34955	38
1885	Complete Genome Sequence of Streptococcus sp. Strain NPS 308. <b>2016</b> , 4,	
1884	Draft Genome Sequence of the Bacteriophage vB_Eco_slurp01. <b>2016</b> , 4,	4
1883	Draft Genome Sequence of a Novel Marinobacter sp. Strain from Honolulu Harbor, Hawai'i. <b>2016</b> , 4,	О
1882	Genomic analysis of nontypeable pneumococci causing invasive pneumococcal disease in South Africa, 2003-2013. <b>2016</b> , 17, 470	10
1881	Complete Genome Sequences of Group III Campylobacter Bacteriophages PC5 and PC14. <b>2016</b> , 4,	3
1880	Delta-proteobacterial SAR324 group in hydrothermal plumes on the South Mid-Atlantic Ridge. <b>2016</b> , 6, 22842	12

1879	Draft Genome Sequence of Planomonospora sphaerica JCM9374, a Rare Actinomycete. <b>2016</b> , 4,	5
1878	Draft Genome Sequence of Arenibacter sp. Strain C-21, an Iodine-Accumulating Bacterium Isolated from Surface Marine Sediment. <b>2016</b> , 4,	4
1877	Comprehensive genomic and phenotypic metal resistance profile of Pseudomonas putida strain S13.1.2 isolated from a vineyard soil. <b>2016</b> , 6, 95	19
1876	Association of Pneumococcal Protein Antigen Serology With Age and Antigenic Profile of Colonizing Isolates. <b>2017</b> , 215, 713-722	17
1875	Diverse mechanisms of metaeffector activity in an intracellular bacterial pathogen, Legionella pneumophila. <b>2016</b> , 12, 893	71
1874	Draft Genome Sequence of Lactococcus garvieae Strain PAQ102015-99, an Outbreak Strain Isolated from a Commercial Trout Farm in the Northwestern United States. <b>2016</b> , 4,	7
1873	Draft Genome Sequence of a Pseudomonas sp. Strain Carrying blaIMP-25 and blaVIM-2 Carbapenemase Genes from Hospital Sewage. <b>2016</b> , 4,	2
1872	Draft Genome Sequence of a Multiresistant Bovine Isolate of Staphylococcus lentus from Tanzania. <b>2016</b> , 4,	1
1871	Rapid scoring of genes in microbial pan-genome-wide association studies with Scoary. <b>2016</b> , 17, 238	229
1870	Comparison of 432 Pseudomonas strains through integration of genomic, functional, metabolic and expression data. <b>2016</b> , 6, 38699	38
1869	Draft Genome Sequences of Nine Clinical Isolates of Vancomycin-Resistant Enterococci. <b>2016</b> , 4,	1
1868	Genome Sequence of the Acetogenic Bacterium Acetobacterium wieringae DSM 1911T. <b>2016</b> , 4,	9
1867	Comparing genome versus proteome-based identification of clinical bacterial isolates. <b>2018</b> , 19, 495-505	6
1866	Draft Whole-Genome Sequence of a Catalase-Negative Staphylococcus aureus subsp. aureus (Sequence Type 25) Strain Isolated from a Patient with Endocarditis and Septic Arthritis. <b>2016</b> , 4,	2
1865	IMP: a pipeline for reproducible reference-independent integrated metagenomic and metatranscriptomic analyses. <b>2016</b> , 17, 260	81
1864	Detection of linezolid resistance due to the optrA gene in Enterococcus faecalis from poultry meat from the American continent (Colombia). <b>2017</b> , 72, 678-683	45
1863	Genome sequence and virulence factors of a group G Streptococcus dysgalactiae subsp. equisimilis strain with a new element carrying erm(B). <b>2016</b> , 6, 20389	5
1862	Occurrence and characterization of mcr-1-harbouring Escherichia coli isolated from pigs in Great Britain from 2013 to 2015. <b>2017</b> , 72, 691-695	30

1861	Use of single molecule sequencing for comparative genomics of an environmental and a clinical isolate of Clostridium difficile ribotype 078. <b>2016</b> , 17, 1020	9
1860	Draft Genome Sequence of Antarctic Methanogen Enriched from Dry Valley Permafrost. <b>2016</b> , 4,	2
1859	Birth of a W sex chromosome by horizontal transfer of Wolbachia bacterial symbiont genome. <b>2016</b> , 113, 15036-15041	62
1858	Host genome integration and giant virus-induced reactivation of the virophage mavirus. <b>2016</b> , 540, 288-291	76
1857	Draft Genome Sequences of Three Clinical Isolates of Tannerella forsythia Isolated from Subgingival Plaque from Periodontitis Patients in the United States. <b>2016</b> , 4,	8
1856	Complete Genome and Plasmid Sequences for Rhodococcus fascians D188 and Draft Sequences for Rhodococcus Isolates PBTS 1 and PBTS 2. <b>2016</b> , 4,	12
1855	Draft Genome Sequence of "Rathayibacter tanaceti" Strain VKM Ac-2596 Isolated from Tanacetum vulgare Infested by a Foliar Nematode. <b>2016</b> , 4,	10
1854	Recent Outbreaks of Shigellosis in California Caused by Two Distinct Populations of with either Increased Virulence or Fluoroquinolone Resistance. <b>2016</b> , 1,	33
1853	Comparative genomics reveals Lysinibacillus sphaericus group comprises a novel species. <b>2016</b> , 17, 709	12
1852	Clonal Complex 17 Group B Streptococcus strains causing invasive disease in neonates and adults originate from the same genetic pool. <b>2016</b> , 6, 20047	29
1851	Draft Genome Sequence of Acetobacter malorum CECT 7742, a Strain Isolated from Strawberry Vinegar. <b>2016</b> , 4,	
1850	Whole genome sequencing identifies a novel species of the genus Capnocytophaga isolated from dog and cat bite wounds in humans. <b>2016</b> , 6, 22919	21
1849	Genome sequence and plasmid transformation of the model high-yield bacterial cellulose producer Gluconacetobacter hansenii ATCC 53582. <b>2016</b> , 6, 23635	42
1848	Genome comparisons provide insights into the role of secondary metabolites in the pathogenic phase of the Photorhabdus life cycle. <b>2016</b> , 17, 537	25
1847	A molecular phylogenetic framework for Bacillus subtilis using genome sequences and its application to Bacillus subtilis subspecies stecoris strain D7XPN1, an isolate from a commercial food-waste degrading bioreactor. <b>2016</b> , 6, 96	4
1846	Draft Genome Sequences of Six Mycobacterium immunogenum Strains Obtained from a Chloraminated Drinking Water Distribution System Simulator. <b>2016</b> , 4,	3
1845	Connectivity to the surface determines diversity patterns in subsurface aquifers of the Fennoscandian shield. <b>2016</b> , 10, 2447-58	50
1844	Draft genome of Leisingera aquaemixtae CECT 8399(T), a member of the Roseobacter clade isolated from a junction of fresh and ocean water in Jeju Island, South Korea. <b>2016</b> , 7, 233-6	1

1843	Whole-Genome Sequence of Staphylococcus epidermidis TB298. <b>2016</b> , 4,	4
1842	The genome and genetics of a high oxidative stress tolerant Serratia sp. LCN16 isolated from the plant parasitic nematode Bursaphelenchus xylophilus. <b>2016</b> , 17, 301	13
1841	First Insights into the Genome Sequence of the Halophilic Archaeon Halalkalicoccus paucihalophilus (DSM 24557). <b>2016</b> , 4,	О
1840	Draft genome sequence of Thalassobius mediterraneus CECT 5383(T), a poly-beta-hydroxybutyrate producer. <b>2016</b> , 7, 237-9	2
1839	Complete Genome Sequence of Streptomyces albus SM254, a Potent Antagonist of Bat White-Nose Syndrome Pathogen Pseudogymnoascus destructans. <b>2016</b> , 4,	8
1838	Genomic Epidemiology and Molecular Resistance Mechanisms of Azithromycin-Resistant Neisseria gonorrhoeae in Canada from 1997 to 2014. <b>2016</b> , 54, 1304-13	98
1837	Phylogenomic analysis of Candidatus 'Izimaplasma' species: free-living representatives from a Tenericutes clade found in methane seeps. <b>2016</b> , 10, 2679-2692	51
1836	Draft Genome Sequences of Streptococcus pneumoniae with High-Level Resistance to Respiratory Fluoroquinolones. <b>2016</b> , 4,	O
1835	Draft Genome Sequence of Caloramator mitchellensis, a Thermoanaerobe Isolated from the Waters of the Great Artesian Basin. <b>2016</b> , 4,	
1834	Population structure and drug resistance patterns of emerging non-PCV-13 Streptococcus pneumoniae serotypes 22F, 15A, and 8 isolated from adults in Ontario, Canada. <b>2016</b> , 42, 1-8	14
1833	Complete genome sequence of Sphingorhabdus sp. M41, a versatile hydrocarbon degrader, isolated from crude oil-contaminated costal sediment. <b>2016</b> , 227, 41-42	11
1832	Colistin resistance in Salmonella and Escherichia coli isolates from a pig farm in Great Britain. <b>2016</b> , 71, 2306-13	97
1831	Draft Genome Sequence of Shewanella sp. Strain P1-14-1, a Bacterial Inducer of Settlement and Morphogenesis in Larvae of the Marine Hydroid Hydractinia echinata. <b>2016</b> , 4,	4
1830	Bacterial Genomic Data Analysis in the Next-Generation Sequencing Era. <b>2016</b> , 1415, 407-22	4
1829	Description of genomic islands associated to the multidrug-resistant Pseudomonas aeruginosa clone ST277. <b>2016</b> , 42, 60-5	22
1828	Companion: a web server for annotation and analysis of parasite genomes. <b>2016</b> , 44, W29-34	68
1827	Draft Genome Sequence of Burkholderia ambifaria RZ2MS16, a Plant Growth-Promoting Rhizobacterium Isolated from Guarana, a Tropical Plant. <b>2016</b> , 4,	3
1826	Draft Genome Sequence of the First Pathogenic Leptospira Isolates from Ecuador. <b>2016</b> , 4,	4

1825	A large conjugative Acinetobacter baumannii plasmid carrying the sul2 sulphonamide and strAB streptomycin resistance genes. <b>2016</b> , 87-88, 43-50	24
1824	Comparative Genomics of Campylobacter fetus from Reptiles and Mammals Reveals Divergent Evolution in Host-Associated Lineages. <b>2016</b> , 8, 2006-19	21
1823	CYP101J2, CYP101J3, and CYP101J4, 1,8-Cineole-Hydroxylating Cytochrome P450 Monooxygenases from Sphingobium yanoikuyae Strain B2. <b>2016</b> , 82, 6507-6517	12
1822	Lack of Overt Genome Reduction in the Bryostatin-Producing Bryozoan Symbiont "Candidatus Endobugula sertula". <b>2016</b> , 82, 6573-6583	33
1821	CRISPRDetect: A flexible algorithm to define CRISPR arrays. <b>2016</b> , 17, 356	154
1820	Transmission of Staphylococcus aureus from Humans to Green Monkeys in The Gambia as Revealed by Whole-Genome Sequencing. <b>2016</b> , 82, 5910-7	22
1819	From FASTQ to Function: In Silico Methods for Processing Next-Generation Sequencing Data. <b>2016</b> , 1476, 23-33	1
1818	Complete Sequencing of Plasmids Containing blaOXA-163 and blaOXA-48 in Escherichia coli Sequence Type 131. <b>2016</b> , 60, 6948-6951	14
1817	A Primer on Infectious Disease Bacterial Genomics. <b>2016</b> , 29, 881-913	26
1816	Genomic Characterization of Colistin Heteroresistance in Klebsiella pneumoniae during a Nosocomial Outbreak. <b>2016</b> , 60, 6837-6843	60
1815	Phage vB_BsuP-Goe1: the smallest identified lytic phage of Bacillus subtilis. <b>2016</b> , 363,	10
1814	Genomic Analysis of Salmonella enterica Serovar Typhimurium from Wild Passerines in England and Wales. <b>2016</b> , 82, 6728-6735	32
1813	Varibaculum anthropi sp. nov. represented by three genetically different genomovars isolated from clinical material and emended description of the genus Varibaculum. <b>2016</b> , 39, 546-552	6
1812	Recent independent emergence of multiple multidrug-resistant Serratia marcescens clones within the United Kingdom and Ireland. <b>2016</b> , 26, 1101-9	47
1811	Genomic Comparison of Campylobacter spp. and Their Potential for Zoonotic Transmission between Birds, Primates, and Livestock. <b>2016</b> , 82, 7165-7175	51
1810	Kluyvera ascorbata Strain from Hospital Sewage Carrying the mcr-1 Colistin Resistance Gene. <b>2016</b> , 60, 7498-7501	39
1809	Draft Genome Sequence of Stenotrophomonas maltophilia SBo1 Isolated from Bactrocera oleae. <b>2016</b> , 4,	8
1808	Draft Genome Sequences for Seven Streptococcus parauberis Isolates from Wild Fish in the Chesapeake Bay. <b>2016</b> , 4,	2

1807	Complete Genome Sequence of a Myoviridae Bacteriophage Infecting Salmonella enterica Serovar Typhimurium. <b>2016</b> , 4,	4
1806	Defining the food microbiome for authentication, safety, and process management. <b>2016</b> , 60, 1:1-1:13	15
1805	Genome sequence of Candidatus Arsenophonus lipopteni, the exclusive symbiont of a blood sucking fly Lipoptena cervi (Diptera: Hippoboscidae). <b>2016</b> , 11, 72	17
1804	Lactobacillus fermentum 90 TC-4 taxonomic status confirmation using whole genome sequencing and MALDI TOF mass spectrum. <b>2016</b> , 52, 907-913	4
1803	Persistence of a dominant bovine lineage of group B Streptococcus reveals genomic signatures of host adaptation. <b>2016</b> , 18, 4216-4229	29
1802	Complete Genome Sequence of a Lytic Siphoviridae Bacteriophage Infecting Several Serovars of Salmonella enterica. <b>2016</b> , 4,	1
1801	Precultivation of Bacillus coagulans DSM2314 in the presence of furfural decreases inhibitory effects of lignocellulosic by-products during L(+)-lactic acid fermentation. <b>2016</b> , 100, 10307-10319	12
1800	Active and adaptive Legionella CRISPR-Cas reveals a recurrent challenge to the pathogen. <b>2016</b> , 18, 1319-38	20
1799	Evidence for an Opportunistic and Endophytic Lifestyle of the Bursaphelenchus xylophilus-Associated Bacteria Serratia marcescens PWN146 Isolated from Wilting Pinus pinaster. <b>2016</b> , 72, 669-81	13
1798	Diversity of the Tetracycline Mobilome within a Chinese Pig Manure Sample. <b>2016</b> , 82, 6454-6462	18
1797	Repeated replacement of an intrabacterial symbiont in the tripartite nested mealybug symbiosis. <b>2016</b> , 113, E5416-24	133
1796	Whole-Genome Sequence of Chlamydia gallinacea Type Strain 08-1274/3. <b>2016</b> , 4,	7
1795	Role of Wax Ester Synthase/Acyl Coenzyme A:Diacylglycerol Acyltransferase in Oleaginous Streptomyces sp. Strain G25. <b>2016</b> , 82, 5969-81	12
1794	Whole-Genome Draft Sequences of Six Commensal Fecal and Six Mastitis-Associated Escherichia coli Strains of Bovine Origin. <b>2016</b> , 4,	6
1793	Draft Genome Sequences of Acinetobacter baumannii Isolates from Wounded Military Personnel. <b>2016</b> , 4,	3
1792	Draft genome sequence of Mameliella alba strain UMTAT08 isolated from clonal culture of toxic dinoflagellate Alexandrium tamiyavanichii. <b>2016</b> , 10, 12-4	4
1791	Tetracycline Selective Pressure and Homologous Recombination Shape the Evolution of Chlamydia suis: A Recently Identified Zoonotic Pathogen. <b>2016</b> , 8, 2613-23	20
1790	First Report of blaIMP-14 on a Plasmid Harboring Multiple Drug Resistance Genes in Escherichia coli Sequence Type 131. <b>2016</b> , 60, 5068-71	12

1789	WGS for surveillance of antimicrobial resistance: a pilot study to detect the prevalence and mechanism of resistance to azithromycin in a UK population of non-typhoidal Salmonella. <b>2016</b> , 71, 3400-3408	3 42
1788	First high quality draft genome sequence of a plant growth promoting and cold active enzyme producing psychrotrophic Arthrobacter agilis strain L77. <b>2016</b> , 11, 54	68
1787	A Phenotypically Silent vanB2 Operon Carried on a Tn1549-Like Element in Clostridium difficile. <b>2016</b> , 1,	17
1786	Comparative Genomics of Syntrophic Branched-Chain Fatty Acid Degrading Bacteria. <b>2016</b> , 31, 288-92	19
1785	Complete Genome Sequence of the Probiotic Strain Lactobacillus salivarius LPM01. <b>2016</b> , 4,	1
1784	Citrobacter freundii carrying blaKPC-2 and blaNDM-1: characterization by whole genome sequencing. <b>2016</b> , 6, 30670	23
1783	A genomic island in Vibrio cholerae with VPI-1 site-specific recombination characteristics contains CRISPR-Cas and type VI secretion modules. <b>2016</b> , 6, 36891	28
1782	Genomic sequencing-based mutational enrichment analysis identifies motility genes in a genetically intractable gut microbe. <b>2016</b> , 113, 14127-14132	8
1781	Effects of a gut pathobiont in a gnotobiotic mouse model of childhood undernutrition. <b>2016</b> , 8, 366ra164	31
1780	Complete Genome Sequence of a Potential Probiotic, Lactobacillus pentosus MP-10, Isolated from Fermented Aloreâ Table Olives. <b>2016</b> , 4,	7
1779	Genomic and phenotypic characterization of the species Acinetobacter venetianus. <b>2016</b> , 6, 21985	15
1778	Complete Genome Sequences of Three Siphoviridae Bacteriophages Infecting Salmonella enterica Serovar Enteritidis. <b>2016</b> , 4,	3
1777	Draft Genome Sequence of Robinsoniella peoriensis 6600698, a Confounder of Clostridium difficile Diagnosis. <b>2016</b> , 4,	1
1776	Draft Genome Sequence of Streptomyces sp. Strain PTY087I2, Isolated from Styela canopus, a Panamanian Tunicate. <b>2016</b> , 4,	1
1775	Near complete genome sequence of the animal feed probiotic, Bacillus amyloliquefaciens H57. <b>2016</b> , 11, 60	7
1774	Support vector machine applied to predict the zoonotic potential of E. coli O157 cattle isolates. <b>2016</b> , 113, 11312-11317	44
1773	The novel 2016 WHO Neisseria gonorrhoeae reference strains for global quality assurance of laboratory investigations: phenotypic, genetic and reference genome characterization. <b>2016</b> , 71, 3096-3108	166
1772	Reclassification of Halomonas caseinilytica Wu et al. 2008 as a later synonym of Halomonas sinaiensis Romano et al. 2007, and emendation of the species description. <b>2016</b> , 109, 1345-52	2

# (2016-2016)

1771	Genome Sequence of Bacillus sp. Strain UMTAT18 Isolated from the Dinoflagellate Alexandrium tamiyavanichii Found in the Straits of Malacca. <b>2016</b> , 4,	1
1770	The dissemination of multidrug-resistant Enterobacter cloacae throughout the UK and Ireland. <b>2016</b> , 1, 16173	16
1769	Complete Genome Sequences of Three Outbreak-Associated Legionella pneumophila Isolates. <b>2016</b> , 4,	
1768	Accurate binning of metagenomic contigs via automated clustering sequences using information of genomic signatures and marker genes. <b>2016</b> , 6, 24175	120
1767	PGAdb-builder: A web service tool for creating pan-genome allele database for molecular fine typing. <b>2016</b> , 6, 36213	29
1766	Genix: a new online automated pipeline for bacterial genome annotation. <b>2016</b> , 363,	13
1765	First Draft Genome Sequences of Neisseria sp. Strain 83E34 and Neisseria sp. Strain 74A18, Previously Identified as CDC Eugonic Fermenter 4b Species. <b>2016</b> , 4,	1
1764	Genome-based microbial ecology of anammox granules in a full-scale wastewater treatment system. <b>2016</b> , 7, 11172	248
1763	Draft Genome Sequence of Piscirickettsia litoralis, Isolated from Seawater. <b>2016</b> , 4,	3
1762	Cytolethal distending toxin producing Escherichia coli O157:H43 strain T22 represents a novel evolutionary lineage within the O157 serogroup. <b>2016</b> , 46, 110-117	1
1761	1,2-Dichloroethane Exposure Alters the Population Structure, Metabolism, and Kinetics of a Trichloroethene-Dechlorinating Dehalococcoides mccartyi Consortium. <b>2016</b> , 50, 12187-12196	12
1760	Large scale analysis of amino acid substitutions in bacterial proteomics. <b>2016</b> , 17, 450	2
1759	Estimation of Gene Insertion/Deletion Rates with Missing Data. <b>2016</b> , 204, 513-529	2
1758	Global phylogeography and evolutionary history of Shigella dysenteriae type 1. <b>2016</b> , 1, 16027	47
1757	Genomic characterization of a fructophilic bee symbiont Lactobacillus kunkeei reveals its niche-specific adaptation. <b>2016</b> , 39, 516-526	30
1756	Evolution of atypical enteropathogenic E. coli by repeated acquisition of LEE pathogenicity island variants. <b>2016</b> , 1, 15010	48
1755	Quorum sensing activity of Citrobacter amalonaticus L8A, a bacterium isolated from dental plaque. <b>2016</b> , 6, 20702	8
1754	Non-toxigenic environmental Vibrio cholerae O1 strain from Haiti provides evidence of pre-pandemic cholera in Hispaniola. <b>2016</b> , 6, 36115	12

1753	The induction and identification of novel Colistin resistance mutations in Acinetobacter baumannii and their implications. <b>2016</b> , 6, 28291	54
1752	Draft Genome Sequences of Four Hospital-Associated Pseudomonas putida Isolates. <b>2016</b> , 4,	4
1751	Methylotrophic methanogenesis discovered in the archaeal phylum Verstraetearchaeota. <b>2016</b> , 1, 16170	276
1750	Draft Genome Sequence of a New Zealand Rickettsia-Like Organism Isolated from Farmed Chinook Salmon. <b>2016</b> , 4,	2
1749	The Mouse Intestinal Bacterial Collection (miBC) provides host-specific insight into cultured diversity and functional potential of the gut microbiota. <b>2016</b> , 1, 16131	222
1748	Biogeography and environmental genomics of the Roseobacter-affiliated pelagic CHAB-I-5 lineage. <b>2016</b> , 1, 16063	22
1747	Dynamics of genome change among Legionella species. <b>2016</b> , 6, 33442	14
1746	Identification of source and sink populations for the emergence and global spread of the East-Asia clone of community-associated MRSA. <b>2016</b> , 17, 160	23
1745	Complete Genome Sequences of Two Marine Vibrio cholerae Strains Isolated from the South Coast of Sweden. <b>2016</b> , 4,	1
1744	Structural and functional analysis of the finished genome of the recently isolated toxic Anabaena sp. WA102. <b>2016</b> , 17, 457	19
1743	Pangenome and Phylogenomic Analysis of the Pathogenic Actinobacterium Rhodococcus equi. <b>2016</b> , 8, 3140-3148	36
1742	Draft Genome Sequence of a Mycobacterium africanum Clinical Isolate from Antioquia, Colombia. <b>2016</b> , 4,	3
1741	Genome Sequence of the Poly-3-Hydroxybutyrate Producer Clostridium acetireducens DSM 10703. <b>2016</b> , 4,	2
1740	Methods for analyzing next-generation sequencing data VIII. Post-assembly analysis. <b>2016</b> , 27, 187-195	
1739	Draft Genome Sequence for a Clinical Isolate of Vancomycin-Resistant Enterococcus faecalis. <b>2016</b> , 4,	2
1738	Draft Genome Sequence of Streptococcus anginosus BVI, a New Vaginal Pathogen Candidate. <b>2016</b> , 4,	2
1737	An emerging zoonotic clone in the Netherlands provides clues to virulence and zoonotic potential of Streptococcus suis. <b>2016</b> , 6, 28984	29
1736	Serotype IV Streptococcus agalactiae ST-452 has arisen from large genomic recombination events between CC23 and the hypervirulent CC17 lineages. <b>2016</b> , 6, 29799	16

1735	Draft Genome Sequence of Altererythrobacter marensis DSM 21428T, Isolated from Seawater. <b>2016</b> , 4,	3
1734	Draft Genome Sequence of Multitrait Plant Growth-Promoting Bacillus sp. Strain RZ2MS9. <b>2016</b> , 4,	11
1733	Draft Genome Sequence of Streptomyces sp. AVP053U2 Isolated from Styela clava, a Tunicate Collected in Long Island Sound. <b>2016</b> , 4,	1
1732	Draft Genome Sequence of Pseudomonas putida CBF10-2, a Soil Isolate with Bioremediation Potential in Agricultural and Industrial Environmental Settings. <b>2016</b> , 4,	3
1731	Draft Genome Sequence of Exiguobacterium sp. KKBO11, Isolated Downstream of a Wastewater Treatment Plant in Houston, Texas. <b>2016</b> , 4,	2
1730	Draft Genome Sequence of Rhizobium sp. GHKF11, Isolated from Farmland Soil in Pecan Grove, Texas. <b>2016</b> , 4,	2
1729	Genome Sequence of the Autotrophic Acetogen Clostridium magnum DSM 2767. <b>2016</b> , 4,	4
1728	Understanding pneumococcal serotype 1 biology through population genomic analysis. <b>2016</b> , 16, 649	17
1727	Complete genome of FORC014 isolated from the toothfish. <b>2016</b> , 8, 59	4
1726	Complete Genome Sequence of the d-Amino Acid Catabolism Bacterium Phaeobacter sp. Strain JL2886, Isolated from Deep Seawater of the South China Sea. <b>2016</b> , 4,	2
1725	Draft Genome Sequence of Alkane-Degrading Acinetobacter venetianus JKSF02, Isolated from Contaminated Sediment of the San Jacinto River in Houston, Texas. <b>2016</b> , 4,	
1724	First Insights into the Genome of the Moderately Thermophilic Bacterium Clostridium tepidiprofundi SG 508T. <b>2016</b> , 4,	О
1723	Complete Genome Sequence of Serratia marcescens SmUNAM836, a Nonpigmented Multidrug-Resistant Strain Isolated from a Mexican Patient with Obstructive Pulmonary Disease. <b>2016</b> , 4,	8
1722	Revised Genome Sequence of the Purple Photosynthetic Bacterium Blastochloris viridis. 2016, 4,	7
1721	Draft Genome Sequence of Megasphaera sp. Strain DJF_B143, an Isolate from Pig Hindgut Unable to Produce Skatole. <b>2016</b> , 4,	1
1720	Draft Genome Sequence of Olsenella scatoligenes SK9K4T, a Producer of 3-Methylindole (Skatole) and 4-Methylphenol (p-Cresol), Isolated from Pig Feces. <b>2016</b> , 4,	1
1719	Draft Genome Sequence of "Candidatus Methanomethylophilus" sp. 1R26, Enriched from Bovine Rumen, a Methanogenic Archaeon Belonging to the Methanomassiliicoccales Order. <b>2016</b> , 4,	9
1718	Comparative genomic analyses reveal broad diversity in botulinum-toxin-producing Clostridia. <b>2016</b> , 17, 180	56

1717	Complete genome sequence of strain Z31. <b>2016</b> , 8, 11	13
1716	Comparative Genomics of Carriage and Disease Isolates of Streptococcus pneumoniae Serotype 22F Reveals Lineage-Specific Divergence and Niche Adaptation. <b>2016</b> , 8, 1243-51	5
1715	Host-Associated Genomic Features of the Novel Uncultured Intracellular Pathogen Ca. Ichthyocystis Revealed by Direct Sequencing of Epitheliocysts. <b>2016</b> , 8, 1672-89	9
1714	Genome Sequences of Two Pseudomonas syringae pv. tomato Race 1 Strains, Isolated from Tomato Fields in California. <b>2016</b> , 4,	6
1713	NCBI prokaryotic genome annotation pipeline. <b>2016</b> , 44, 6614-24	2376
1712	Complete Genome Sequence of a CTX-M-15-Producing Escherichia coli Strain from the H30Rx Subclone of Sequence Type 131 from a Patient with Recurrent Urinary Tract Infections, Closely Related to a Lethal Urosepsis Isolate from the Patient's Sister. <b>2016</b> , 4,	9
1711	A MLST Clade 2 Clostridium difficile strain with a variant TcdB induces severe inflammatory and oxidative response associated with mucosal disruption. <b>2016</b> , 40, 76-84	14
1710	First Genome Sequence of Leptospira interrogans Serovar Pomona, Isolated from a Bovine Abortion. <b>2016</b> , 4,	7
1709	Paradoxical Hypersusceptibility of Drug-resistant Mycobacteriumtuberculosis to 🛭 actam Antibiotics. <b>2016</b> , 9, 170-179	19
1708	Draft Genome Sequences of Six Novel Bacterial Isolates from Chicken Ceca. <b>2016</b> , 4,	4
1707	Resilience of microbial communities in a simulated drinking water distribution system subjected to disturbances: role of conditionally rare taxa and potential implications for antibiotic-resistant bacteria. <b>2016</b> , 2, 645-657	27
1706	Genomic and Phenotypic Analyses Reveal the Emergence of an Atypical Salmonella enterica Serovar Senftenberg Variant in China. <b>2016</b> , 54, 2014-22	12
1705	Engineering control of bacterial cellulose production using a genetic toolkit and a new cellulose-producing strain. <b>2016</b> , 113, E3431-40	114
1704	Peeping into genomic architecture by re-sequencing of Ochrobactrum intermedium M86 strain during laboratory adapted conditions. <b>2016</b> , 8, 72-6	2
1703	Genome Evolution and Nitrogen Fixation in Bacterial Ectosymbionts of a Protist Inhabiting Wood-Feeding Cockroaches. <b>2016</b> , 82, 4682-4695	30
1702	Inducible colistin resistance via a disrupted plasmid-borne mcr-1 gene in a 2008 Vietnamese Shigella sonnei isolate. <b>2016</b> , 71, 2314-7	67
1701	Identification of a Latin American-specific BabA adhesin variant through whole genome sequencing of Helicobacter pylori patient isolates from Nicaragua. <b>2016</b> , 16, 53	16
1700	Draft genome of the Arabidopsis thaliana phyllosphere bacterium, Williamsia sp. ARP1. <b>2016</b> , 11, 8	8

# (2016-2016)

1699	Isolation and complete genome sequence of the thermophilic Geobacillus sp. 12AMOR1 from an Arctic deep-sea hydrothermal vent site. <b>2016</b> , 11, 16	15
1698	Draft genomic sequence of Nereida ignava CECT 5292(T), a marine bacterium of the family Rhodobacteraceae. <b>2016</b> , 11, 21	8
1697	Vibrio anguillarum Is Genetically and Phenotypically Unaffected by Long-Term Continuous Exposure to the Antibacterial Compound Tropodithietic Acid. <b>2016</b> , 82, 4802-4810	18
1696	Horizontal Gene Acquisitions, Mobile Element Proliferation, and Genome Decay in the Host-Restricted Plant Pathogen Erwinia Tracheiphila. <b>2016</b> , 8, 649-64	20
1695	Antibiotic Resistance, Core-Genome and Protein Expression in IncHI1 Plasmids in Salmonella Typhimurium. <b>2016</b> , 8, 1661-71	16
1694	Molecular Evolution of a Klebsiella pneumoniae ST278 Isolate Harboring blaNDM-7 and Involved in Nosocomial Transmission. <b>2016</b> , 214, 798-806	21
1693	Genome Sequence of the Acetogenic Bacterium Moorella mulderi DSM 14980T. <b>2016</b> , 4,	7
1692	Draft genome sequence and overview of the purple non sulfur bacterium Rhodopseudomonas palustris 42OL. <b>2016</b> , 11, 24	10
1691	Characterization of the first cultured representative of Verrucomicrobia subdivision 5 indicates the proposal of a novel phylum. <b>2016</b> , 10, 2801-2816	98
1690	Complete Genome Sequence of emm4 Streptococcus pyogenes MEW427, a Throat Isolate from a Child Meeting Clinical Criteria for Pediatric Autoimmune Neuropsychiatric Disorders Associated with Streptococcus (PANDAS). <b>2016</b> , 4,	7
1689	Complete Genome Sequence of emm28 Type Streptococcus pyogenes MEW123, a Streptomycin-Resistant Derivative of a Clinical Throat Isolate Suitable for Investigation of Pathogenesis. <b>2016</b> , 4,	5
1688	Draft Genome Sequences of 11 Clinical Isolates of Acinetobacter baumannii. <b>2016</b> , 4,	
1687	Draft Genome Sequence of Pseudomonas stutzeri ODKF13, Isolated from Farmland Soil in Alvin, Texas. <b>2016</b> , 4,	3
1686	Draft Genome Sequence of Organophosphate-Degrading Ochrobactrum anthropi FRAF13. <b>2016</b> , 4,	1
1685	Three Genome Sequences of Legionella pneumophila subsp. pascullei Associated with Colonization of a Health Care Facility. <b>2016</b> , 4,	3
1684	Complete Genome Sequence of Algoriphagus sp. Strain M8-2, Isolated from a Brackish Lake. <b>2016</b> , 4,	1
1683	Whole-Genome Sequences of Four Strains Closely Related to Members of the Mycobacterium chelonae Group, Isolated from Biofilms in a Drinking Water Distribution System Simulator. <b>2016</b> , 4,	5
1682	Genome Sequence of Pectobacterium carotovorum Phage PPWS1, Isolated from Japanese Horseradish [Eutrema japonicum (Miq.) Koidz] Showing Soft-Rot Symptoms. <b>2016</b> , 4,	9

1681	Complete Genome Sequences of Two Interactive Moderate Thermophiles, Paenibacillus napthalenovorans 32O-Y and Paenibacillus sp. 32O-W. <b>2016</b> , 4,	4
1680	Complete genome sequence of the potato pathogen Ralstonia solanacearum UY031. <b>2016</b> , 11, 7	20
1679	Complete genome sequence of cyanobacterium Fischerella sp. NIES-3754, providing thermoresistant optogenetic tools. <b>2016</b> , 220, 45-6	17
1678	Analysis of TcdB Proteins within the Hypervirulent Clade 2 Reveals an Impact of RhoA Glucosylation on Clostridium difficile Proinflammatory Activities. <b>2016</b> , 84, 856-65	21
1677	Draft genomes of Nautella italica strains CECT 7645(T) and CECT 7321: Two roseobacters with potential pathogenic and biotechnological traits. <b>2016</b> , 26, 73-80	5
1676	Complete genome sequence of the Variibacter gotjawalensis GJW-30(T) from soil of lava forest, Gotjawal. <b>2016</b> , 218, 64-5	4
1675	Complete genome sequence of cyanobacterium Nostoc sp. NIES-3756, a potentially useful strain for phytochrome-based bioengineering. <b>2016</b> , 218, 51-2	11
1674	Genomic Features of Environmental and Clinical Vibrio parahaemolyticus Isolates Lacking Recognized Virulence Factors Are Dissimilar. <b>2016</b> , 82, 1102-1113	17
1673	Strain-level microbial epidemiology and population genomics from shotgun metagenomics. <b>2016</b> , 13, 435-8	249
1672	Complete genome sequence of a bacterium Pseudomonas fragi P121, a strain with degradation of toxic compounds. <b>2016</b> , 224, 68-9	7
1671	Phylogenetic Analysis of Invasive Serotype 1 Pneumococcus in South Africa, 1989 to 2013. <b>2016</b> , 54, 1326-34	11
1670	MEGAnnotator: a user-friendly pipeline for microbial genomes assembly and annotation. 2016, 363,	73
1669	Complete Genome Sequence of Cyanobacterium Leptolyngbya sp. NIES-3755. <b>2016</b> , 4,	5
1668	Evolutionary History of the Global Emergence of the Escherichia coli Epidemic Clone ST131. <b>2016</b> , 7, e02162	200
1667	Draft Genome of Rhodococcus rhodochrous TRN7, Isolated from the Coast of Trindade Island, Brazil. <b>2016</b> , 4,	2
1666	Characterization of an emergent clone of enteroinvasive Escherichia coli circulating in Europe. <b>2016</b> , 22, 287.e11-9	16
1665	Complete genome of Zhongshania aliphaticivorans SM-2(T), an aliphatic hydrocarbon-degrading bacterium isolated from tidal flat sediment. <b>2016</b> , 226, 22-3	6
1664	Organellar Genomes of White Spruce (Picea glauca): Assembly and Annotation. <b>2015</b> , 8, 29-41	40

# (2016-2016)

1663	Usefulness of High-Quality Core Genome Single-Nucleotide Variant Analysis for Subtyping the Highly Clonal and the Most Prevalent Salmonella enterica Serovar Heidelberg Clone in the Context of Outbreak Investigations. <b>2016</b> , 54, 289-95	60
1662	Gut bacteria that prevent growth impairments transmitted by microbiota from malnourished children. <b>2016</b> , 351,	406
1661	Draft genome sequence of Shimia marina CECT 7688(T). <b>2016</b> , 28, 83-86	4
1660	Complete genome sequence of the Aneurinibacillus soli CB4(T) from soil of mountain. <b>2016</b> , 221, 116-7	1
1659	Complete genome sequence of antibiotic and anticancer agent violacein producing Massilia sp. strain NR 4-1. <b>2016</b> , 223, 36-7	18
1658	Draft Genome Sequence of Neisseria gonorrhoeae Strain NG_869 with Penicillin, Tetracycline and Ciprofloxacin Resistance Determinants Isolated from Malaysia. <b>2016</b> , 56, 225-7	O
1657	Emerging pathogens of gilthead seabream: characterisation and genomic analysis of novel intracellular Eproteobacteria. <b>2016</b> , 10, 1791-803	21
1656	Complete genome sequence of Pandoraea oxalativorans DSM 23570(T), an oxalate metabolizing soil bacterium. <b>2016</b> , 219, 124-5	2
1655	Rare Detection of the Acinetobacter Class D Carbapenemase blaOXA-23 Gene in Proteus mirabilis. <b>2016</b> , 60, 3243-5	19
1654	Rapid Emergence and Evolution of Staphylococcus aureus Clones Harboring fusC-Containing Staphylococcal Cassette Chromosome Elements. <b>2016</b> , 60, 2359-65	34
1653	Chasing the elusive Euryarchaeota class WSA2: genomes reveal a uniquely fastidious methyl-reducing methanogen. <b>2016</b> , 10, 2478-87	146
1652	New Small Plasmid Harboring blaKPC-2 in Pseudomonas aeruginosa. <b>2016</b> , 60, 3211-4	10
1651	Complete Genome Sequence of MIDG2331, a Genetically Tractable Serovar 8 Clinical Isolate of Actinobacillus pleuropneumoniae. <b>2016</b> , 4,	16
1650	Draft Genome Sequences of Streptomyces scabiei S58, Streptomyces turgidiscabies T45, and Streptomyces acidiscabies a10, the Pathogens of Potato Common Scab, Isolated in Japan. <b>2016</b> , 4,	9
1649	Comparative Genomics of Candidate Phylum TM6 Suggests That Parasitism Is Widespread and Ancestral in This Lineage. <b>2016</b> , 33, 915-27	50
1648	Microbial Genomics of a Host-Associated Commensal Bacterium in Fragmented Populations of Endangered Takahe. <b>2016</b> , 71, 1020-9	7
1647	Genetic Diversity of Clostridium sporogenes PA 3679 Isolates Obtained from Different Sources as Resolved by Pulsed-Field Gel Electrophoresis and High-Throughput Sequencing. <b>2016</b> , 82, 384-93	15
1646	Utility of Whole-Genome Sequencing in Characterizing Acinetobacter Epidemiology and Analyzing Hospital Outbreaks. <b>2016</b> , 54, 593-612	60

1645	Prospective Whole-Genome Sequencing Enhances National Surveillance of Listeria monocytogenes. <b>2016</b> , 54, 333-42	152
1644	Complete genome sequence of Pandoraea thiooxydans DSM 25325(T), a thiosulfate-oxidizing bacterium. <b>2016</b> , 217, 51-2	3
1643	Increase in bacteraemia cases in the East Midlands region of the UK due to MDR Escherichia coli ST73: high levels of genomic and plasmid diversity in causative isolates. <b>2016</b> , 71, 339-43	16
1642	Characterization of Acinetobacter johnsonii isolate XBB1 carrying nine plasmids and encoding NDM-1, OXA-58 and PER-1 by genome sequencing. <b>2016</b> , 71, 71-5	46
1641	Comparative Genomics of Community-Associated Methicillin-Resistant Staphylococcus aureus Shows the Emergence of Clone ST8-USA300 in Geneva, Switzerland. <b>2016</b> , 213, 1370-9	29
1640	Microbial bioinformatics for food safety and production. <b>2016</b> , 17, 283-92	39
1639	Next-generation sequencing (NGS) in the microbiological world: How to make the most of your money. <b>2017</b> , 138, 60-71	78
1638	A fibrolytic potential in the human ileum mucosal microbiota revealed by functional metagenomic. <b>2017</b> , 7, 40248	27
1637	Complete Sequence and Organization of pFR260, the Bacillus thuringiensis INTA Fr7-4 Plasmid Harboring Insecticidal Genes. <b>2017</b> , 27, 43-54	3
1636	Impacts of chemical gradients on microbial community structure. <b>2017</b> , 11, 920-931	50
1635	MetaSort untangles metagenome assembly by reducing microbial community complexity. <b>2017</b> , 8, 14306	43
1634	Global and regional dissemination and evolution of Burkholderia pseudomallei. <b>2017</b> , 2, 16263	87
1633	Single nucleotide polymorphisms may explain the contrasting phenotypes of two variants of a multidrug-resistant Mycobacterium tuberculosis strain. <b>2017</b> , 103, 28-36	10
1632	Pyruvic oxime dioxygenase from heterotrophic nitrifier Alcaligenes faecalis is a nonheme Fe-dependent enzyme homologous to class II aldolase. <b>2017</b> , 7, 39991	10
1631	The driving force of prophages and CRISPR-Cas system in the evolution of Cronobacter sakazakii. <b>2017</b> , 7, 40206	22
1630	MicroScope in 2017: an expanding and evolving integrated resource for community expertise of microbial genomes. <b>2017</b> , 45, D517-D528	133
1629	Ecotype diversification of an abundant Roseobacter lineage. <b>2017</b> , 19, 1625-1638	8
1628	A Whole-Genome Sequencing Approach To Study Cefoxitin-Resistant Salmonella enterica Serovar Heidelberg Isolates from Various Sources. <b>2017</b> , 61,	41

,	A Clostridium difficile Lineage Endemic to Costa Rican Hospitals Is Multidrug Resistant by Acquisition of Chromosomal Mutations and Novel Mobile Genetic Elements. <b>2017</b> , 61,	16
1626	Draft Genome of Scalindua rubra, Obtained from the Interface Above the Discovery Deep Brine in the Red Sea, Sheds Light on Potential Salt Adaptation Strategies in Anammox Bacteria. <b>2017</b> , 74, 1-5	53
1625	Genetic Organization of Anabaenopeptin and Spumigin Biosynthetic Gene Clusters in the Cyanobacterium Sphaerospermopsis torques-reginae ITEP-024. <b>2017</b> , 12, 769-778	14
1624	Identification of endoribonuclease specific cleavage positions reveals novel targets of RNase III in Streptococcus pyogenes. <b>2017</b> , 45, 2329-2340	10
1623	Complete genome sequence of the heavy metal resistant bacterium AR33 and comparison with related. <b>2017</b> , 12, 2	11
1622	Whole genome sequencing reveals high-resolution epidemiological links between clinical and environmental Klebsiella pneumoniae. <b>2017</b> , 9, 6	35
1621	A Clostridioides difficile bacteriophage genome encodes functional binary toxin-associated genes. <b>2017</b> , 250, 23-28	27
1620	Physiological and comparative genomic analysis of Acidithiobacillus ferrivorans PQ33 provides psychrotolerant fitness evidence for oxidation at low temperature. <b>2017</b> , 168, 482-492	10
1619	Genome Sequences of Bacillus thuringiensis Serovar kurstaki Strain BP865 and B. thuringiensis Serovar aizawai Strain HD-133. <b>2017</b> , 5,	4
1618	Fallacy of the Unique Genome: Sequence Diversity within Single Strains. 2017, 8,	49
1617	Evolution and Epidemiology of Multidrug-Resistant in the United Kingdom and Ireland. 2017, 8,	59
1616	Scaffolding and completing genome assemblies in real-time with nanopore sequencing. <b>2017</b> , 8, 14515	72
1616 1615	Scaffolding and completing genome assemblies in real-time with nanopore sequencing. <b>2017</b> , 8, 14515  Potential probiotic-associated traits revealed from completed high quality genome sequence of 3872. <b>2017</b> , 12, 19	72 9
	Potential probiotic-associated traits revealed from completed high quality genome sequence of	
1615	Potential probiotic-associated traits revealed from completed high quality genome sequence of 3872. <b>2017</b> , 12, 19  Comparative analysis of Corynebacterium glutamicum genomes: a new perspective for the	9
1615 1614	Potential probiotic-associated traits revealed from completed high quality genome sequence of 3872. <b>2017</b> , 12, 19  Comparative analysis of Corynebacterium glutamicum genomes: a new perspective for the industrial production of amino acids. <b>2017</b> , 18, 940  Culture-independent genomics of a novel chlamydial pathogen of fish provides new insight into	9 27
1615 1614 1613	Potential probiotic-associated traits revealed from completed high quality genome sequence of 3872. <b>2017</b> , 12, 19  Comparative analysis of Corynebacterium glutamicum genomes: a new perspective for the industrial production of amino acids. <b>2017</b> , 18, 940  Culture-independent genomics of a novel chlamydial pathogen of fish provides new insight into host-specific adaptations utilized by these intracellular bacteria. <b>2017</b> , 19, 1899-1913  Draft Genome Sequence of a Colistin-Resistant Clinical Strain Carrying the Carbapenemase Gene.	9 27 14

1609	Novel quorum quenching enzymes identified from draft genome of sp. TAS13. <b>2017</b> , 12, 22-23	0
1608	Comparative Analyses of Selection Operating on Nontranslated Intergenic Regions of Diverse Bacterial Species. <b>2017</b> , 206, 363-376	30
1607	Complete Genome Sequence of Strain SNUV360, a Probiotic for Treatment of Bacterial Vaginosis Isolated from the Vagina of a Healthy Korean Woman. <b>2017</b> , 5,	4
1606	Complete genome sequence of Altererythrobacter dongtanensis KCTC 22672T, isolated from a tidal flat. <b>2017</b> , 34, 11-14	2
1605	Complete Genome Sequence of Type 2 Reference Strain FH Using Single-Molecule Real-Time Sequencing Technology. <b>2017</b> , 5,	2
1604	Advances in the application of high-throughput sequencing in invertebrate virology. <b>2017</b> , 147, 145-156	8
1603	Complete genome sequence of Thermus brockianus GE-1 reveals key enzymes of xylan/xylose metabolism. <b>2017</b> , 12, 22	3
1602	Draft Genome Sequences of Clinical Isolates of Multidrug-Resistant Acinetobacter baumannii. <b>2017</b> , 5,	2
1601	Genomic Epidemiology of Penicillin-Nonsusceptible Pneumococci with Nonvaccine Serotypes Causing Invasive Disease in the United States. <b>2017</b> , 55, 1104-1115	20
1600	Draft Genome Sequence of Pseudonocardia autotrophica Strain DSM 43083, an Efficient Producer of Peroxidases for Lignin Modification. <b>2017</b> , 5,	4
1599	Genome Sequence of the Symbiotic Type Strain Rhizobium tibeticum CCBAU85039T. <b>2017</b> , 5,	1
1598	Towards long-read metagenomics: complete assembly of three novel genomes from bacteria dependent on a diazotrophic cyanobacterium in a freshwater lake co-culture. <b>2017</b> , 12, 9	38
1597	Complete genome sequencing of newly isolated thermotolerant Corynebacterium glutamicum N24 provides a new insights into its thermotolerant phenotype. <b>2017</b> , 247, 29-33	3
1596	Simple discovery of bacterial biocatalysts from environmental samples through functional metaproteomics. <b>2017</b> , 5, 28	16
1595	Ecological and Evolutionary Insights into Xanthomonas citri Pathovar Diversity. 2017, 83,	22
1594	Genome analysis of Acidiplasma sp. MBA-1, a polyextremophilic archaeon predominant in the microbial community of a bioleaching reactor. <b>2017</b> , 86, 89-95	5
1593	Whole genome sequences of three Clade 3 Clostridium difficile strains carrying binary toxin genes in China. <b>2017</b> , 7, 43555	18
1592	Infection control in the new age of genomic epidemiology. <b>2017</b> , 45, 170-179	56

1591	New natural products identified by combined genomics-metabolomics profiling of marine Streptomyces sp. MP131-18. <b>2017</b> , 7, 42382	49
1590	Genome Sequence of Uric Acid-Fermenting Eubacterium angustum DSM 1989T (MK-1). <b>2017</b> , 5,	1
1589	Draft Genome Sequence of a Sequence Type 11 Clinical Strain Carrying a Carbapenemase Gene and an 16S rRNA Methylase Gene. <b>2017</b> , 5,	
1588	Draft Genome Sequences of Two Strains of Serovar Typhimurium Displaying Different Virulence in an Experimental Chicken Model. <b>2017</b> , 5,	4
1587	Investigation of intra-herd spread of Mycobacterium caprae in cattle by generation and use of a whole-genome sequence. <b>2017</b> , 41, 113-128	11
1586	The secondary resistome of multidrug-resistant Klebsiella pneumoniae. <b>2017</b> , 7, 42483	41
1585	Elucidation of quantitative structural diversity of remarkable rearrangement regions, shufflons, in Incl2 plasmids. <b>2017</b> , 7, 928	24
1584	Genome improvement of the acarbose producer Actinoplanes sp. SE50/110 and annotation refinement based on RNA-seq analysis. <b>2017</b> , 251, 112-123	9
1583	Epidemiological and Molecular Characterization of an Invasive Group A Streptococcus 32.2 Outbreak. <b>2017</b> , 55, 1837-1846	9
1582	Whole-Genome Sequence of Strain J31 Isolated from Healthy Human Skin. <b>2017</b> , 5,	2
1581	Fungal volatile compounds induce production of the secondary metabolite Sodorifen in Serratia plymuthica PRI-2C. <b>2017</b> , 7, 862	65
1580	Dissemination of -Carrying Plasmids among Colistin-Resistant Salmonella Strains from Humans and Food-Producing Animals in Taiwan. <b>2017</b> , 61,	42
1579	Draft Genome Sequence of a Biosurfactant-Producing Bacillus subtilis UMX-103 Isolated from Hydrocarbon-Contaminated Soil in Terengganu, Malaysia. <b>2017</b> , 74, 803-805	O
1578	Genome and epigenome of a novel marine Thaumarchaeota strain suggest viral infection, phosphorothioation DNA modification and multiple restriction systems. <b>2017</b> , 19, 2434-2452	44
1577	Pneumococcal prophages are diverse, but not without structure or history. <b>2017</b> , 7, 42976	34
1576	Phylogenomic analysis of the complete sequence of a gastroenteritis-associated cetacean adenovirus (bottlenose dolphin adenovirus 1) reveals a high degree of genetic divergence. <b>2017</b> , 53, 47-55	2
1575	Complete Genome Sequence of the Disinfectant Susceptibility Testing Reference Strain subsp. ATCC 6538. <b>2017</b> , 5,	11
1574	New Macrolide-Lincosamide-Streptogramin B Resistance Gene (48) on the Novel Plasmid pJW2311 in Staphylococcus xylosus. <b>2017</b> , 61,	12

1573	First Whole-Genome Sequences of Two Multidrug-Resistant Strains Isolated from a Moroccan Hospital Floor. <b>2017</b> , 5,	2
1572	Draft Genome Sequence of Multidrug-Resistant Abortive from Northern California. <b>2017</b> , 5,	3
1571	Closing gaps for performing a risk assessment on Listeria monocytogenes in ready-to-eat (RTE) foods: activity 3, the comparison of isolates from different compartments along the food chain, and from humans using whole genome sequencing (WGS) analysis. <b>2017</b> , 14, 1151E	38
1570	Draft Genome Sequence of Strain CBo1 Isolated from. <b>2017</b> , 5,	3
1569	Isolation, Biosynthesis and Chemical Modifications of Rubterolones A-F: Rare Tropolone Alkaloids from Actinomadura sp. 5-2. <b>2017</b> , 23, 9338-9345	24
1568	Characterization of the Polymyxin D Synthetase Biosynthetic Cluster and Product Profile of Paenibacillus polymyxa ATCC 10401. <b>2017</b> , 80, 1264-1274	15
1567	Genomic landscape of extended-spectrum 🛘 actamase resistance in Escherichia coli from an urban African setting. <b>2017</b> , 72, 1602-1609	27
1566	Draft Genome Sequence of Uncultured Upland Soil Cluster Gives Molecular Insights into High-Affinity Methanotrophy. <b>2017</b> , 5,	16
1565	Draft Genome Sequence of a High-Level Colistin-Resistant Clinical Strain of the Complex. <b>2017</b> , 5,	1
1564	Draft Genome Sequence of Campylobacter jejuni 11168H. <b>2017</b> , 5,	1
1563	The metabolic potential of the single cell genomes obtained from the Challenger Deep, Mariana Trench within the candidate superphylum Parcubacteria (OD1). <b>2017</b> , 19, 2769-2784	50
1562	Whole genome sequencing and functional features of UMX-103: a new Bacillus strain with biosurfactant producing capability. <b>2017</b> , 39, 877-886	1
1561	BusyBee Web: metagenomic data analysis by bootstrapped supervised binning and annotation. <b>2017</b> , 45, W171-W179	43
1560	First Complete Genome Sequence of. <b>2017</b> , 5,	1
1559	Draft Genome Sequence of sp. Strain IB2014011-1, Isolated from sp. Larvae of Lake Baikal. <b>2017</b> , 5,	1
1558	IncP Plasmid Carrying Colistin Resistance Gene mcr-1 in Klebsiella pneumoniae from Hospital Sewage. <b>2017</b> , 61,	57
1557	Shotgun Metagenomic Sequencing Analysis of Soft-Rot Enterobacteriaceae in Polymicrobial Communities. <b>2017</b> , 1539, 85-97	2
1556	Development of new methods for the quantitative detection and typing of Lactobacillus parabuchneri in dairy products. <b>2017</b> , 70, 65-71	16

1555	Detection of the florfenicol resistance gene floR in Chryseobacterium isolates from rainbow trout. Exception to the general rule?. <b>2017</b> , 93,	10
1554	Cedratvirus lausannensis - digging into Pithoviridae diversity. <b>2017</b> , 19, 4022-4034	19
1553	Genome Sequences for spp. Isolated from Disease-Suppressive Soils and Long-Term Ecological Research Sites. <b>2017</b> , 5,	3
1552	Draft Genome Sequence of sp. TNHR37B Isolated from a Heated Aquifer Bore Well of the Great Artesian Basin, Australia. <b>2017</b> , 5,	
1551	Draft Genome Sequence of 'subsp.' Strain C161L1 Isolated in Vellore, India. <b>2017</b> , 5,	
1550	Complete Genome Sequence of a Strain Isolated from a Paraplegic Patient with Neurogenic Bladder Using Single-Molecule Real-Time Sequencing Technology. <b>2017</b> , 5,	2
1549	Draft Genome Sequence of Strain ATCC 49145 Associated with Bacterial Vaginosis. 2017, 5,	
1548	Rapid and Consistent Evolution of Colistin Resistance in Extensively Drug-Resistant Pseudomonas aeruginosa during Morbidostat Culture. <b>2017</b> , 61,	34
1547	Insights into enterotoxigenic Escherichia coli diversity in Bangladesh utilizing genomic epidemiology. <b>2017</b> , 7, 3402	20
1546	Prokaryotic Contig Annotation Pipeline Server: Web Application for a Prokaryotic Genome Annotation Pipeline Based on the Shiny App Package. <b>2017</b> , 24, 917-922	4
1545	Genome-wide-analyses of Listeria monocytogenes from food-processing plants reveal clonal diversity and date the emergence of persisting sequence types. <b>2017</b> , 9, 428-440	34
1544	Persistent Listeria monocytogenes strains isolated from mussel production facilities form more biofilm but are not linked to specific genetic markers. <b>2017</b> , 256, 45-53	35
1543	High metabolic versatility of different toxigenic and non-toxigenic Clostridioides difficile isolates. <b>2017</b> , 307, 311-320	24
1542	Crenothrix are major methane consumers in stratified lakes. <b>2017</b> , 11, 2124-2140	87
1541	Complete Genome Sequence of the Plasmid-Bearing Strain SNUV175, a Probiotic for Women's Health Isolated from the Vagina of a Healthy South Korean Woman. <b>2017</b> , 5,	0
1540	Genome Sequence of E28, a Multidrug-Resistant Strain Isolated from a Chicken Carcass, and Its Spontaneously Inducible Prophage. <b>2017</b> , 5,	2
1539	First Insights into the Genome of the Cr(VI)-Reducing Bacterium DSM 23318. <b>2017</b> , 5,	
1538	Whole-Genome Sequence of a Colombian Strain, a Coproducer of OXA-72 and OXA-255-Like Carbapenemases. <b>2017</b> , 5,	4

1537	First Complete Providencia rettgeri Genome Sequence, the NDM-1-Producing Clinical Strain RB151. <b>2017</b> , 5,	9
1536	Complete Genome Sequence of H78, a Plant Growth-Promoting Rhizobacterium. <b>2017</b> , 5,	10
1535	First Insight into the Genome Sequence of DSM 4928, a Butyrate-Producing Moderate Thermophile. <b>2017</b> , 5,	O
1534	Complete Genome Sequence of subsp. Strain OT-51443 Isolated from Yellowtail () in Japan. <b>2017</b> , 5,	4
1533	Discovery of extremely halophilic, methyl-reducing euryarchaea provides insights into the evolutionary origin of methanogenesis. <b>2017</b> , 2, 17081	126
1532	Complete Genome Sequence of the Autotrophic Acetogen DSM 92 Using Nanopore and Illumina Sequencing Data. <b>2017</b> , 5,	4
1531	Exploring bacterial interspecific interactions for discovery of novel antimicrobial compounds. <b>2017</b> , 10, 910-925	37
1530	Evolutionary dynamics and genomic features of the Elizabethkingia anophelis 2015 to 2016 Wisconsin outbreak strain. <b>2017</b> , 8, 15483	79
1529	Isothermal Amplification and Lateral-Flow Assay for Detecting Crown-Gall-Causing Agrobacterium spp. <b>2017</b> , 107, 1062-1068	16
1528	Fine-Scale Structure Analysis Shows Epidemic Patterns of Clonal Complex 95, a Cosmopolitan Lineage Responsible for Extraintestinal Infection. <b>2017</b> , 2,	23
1527	Comparative genomics of free-living Gammaproteobacteria: pathogenesis-related genes or interaction-related genes?. <b>2017</b> , 75,	14
1526	Neisseria genomics: current status and future perspectives. <b>2017</b> , 75,	16
1525	FRI-2 carbapenemase-producing Enterobacter cloacae complex in the UK. <b>2017</b> , 72, 2478-2482	18
1524	Draft Genome Sequences of Strains CAPREx E7 and CAPREx E2-2. <b>2017</b> , 5,	
1523	Draft Genome Sequence of Strain GM3FR, an Endophyte Isolated from Aerial Plant Tissues of L. <b>2017</b> , 5,	5
1522	Characterization and genome comparisons of three Achromobacter phages of the family Siphoviridae. <b>2017</b> , 162, 2191-2201	12
1521	Phenotypic diversity and genotypic flexibility of during long-term chronic infection of cystic fibrosis lungs. <b>2017</b> , 27, 650-662	31
1520	Comparative genomics of Vibrio campbellii strains and core species of the Vibrio Harveyi clade. <b>2017</b> , 7, 41394	25

1519	Decay of the glycolytic pathway and adaptation to intranuclear parasitism within Enterocytozoonidae microsporidia. <b>2017</b> , 19, 2077-2089	43
1518	Genome sequencing and comparative analysis of an NDM-1-producing Klebsiella pneumoniae ST15 isolated from a refugee patient. <b>2017</b> , 111, 166-175	13
1517	Origin and Evolution of the Kiwifruit Canker Pandemic. <b>2017</b> , 9, 932-944	59
1516	Genotypic and Phenotypic Characterization of Streptomyces Species Causing Potato Common Scab in Uruguay. <b>2017</b> , 101, 1362-1372	13
1515	Genomic characterization of Nontuberculous Mycobacteria. <b>2017</b> , 7, 45258	106
1514	Draft Genome Sequence of 'subsp.' ATCC 9621. <b>2017</b> , 5,	
1513	Genomic potential of Marinobacter salinus Hb8T as sulfur oxidizing and aromatic hydrocarbon degrading bacterium. <b>2017</b> , 34, 19-21	4
1512	Comparative genomics analysis of five Psychrobacter strains isolated from world-wide habitats reveal high intra-genus variations. <b>2017</b> , 21, 581-589	6
1511	Draft Genome Sequence of Desulfovibrio BerOc1, a Mercury-Methylating Strain. 2017, 5,	1
1510	Comparative genomics provides a timeframe for Wolbachia evolution and exposes a recent biotin synthesis operon transfer. <b>2016</b> , 2, 16241	72
1509	Use of pan-genome analysis for the identification of lineage-specific genes of Helicobacter pylori. <b>2017</b> , 364,	16
1508	Benzalkonium tolerance genes and outcome in Listeria monocytogenes meningitis. <b>2017</b> , 23, 265.e1-265.e7	59
1507	Comparative Genome Analysis and Global Phylogeny of the Toxin Variant Clostridium difficile PCR Ribotype 017 Reveals the Evolution of Two Independent Sublineages. <b>2017</b> , 55, 865-876	39
1506	Physiological and gene expression responses to nitrogen regimes and temperatures in Mastigocladus sp. strain CHP1, a predominant thermotolerant cyanobacterium of hot springs. <b>2017</b> , 40, 102-113	9
1505	Using bacterial genomes and essential genes for the development of new antibiotics. 2017, 134, 74-86	47
1504	Characterization of the first cultured representative of a Bacteroidetes clade specialized on the scavenging of cyanobacteria. <b>2017</b> , 19, 1134-1148	24
1503	RelA Mutant Enterococcus faecium with Multiantibiotic Tolerance Arising in an Immunocompromised Host. <b>2017</b> , 8,	53
1502	Protracted Regional Dissemination of GIM-1-Producing Serratia marcescens in Western Germany. <b>2017</b> , 61,	5

1501	Emergence of Novel Pathogenic Streptomyces Species by Site-Specific Accretion and cis-Mobilization of Pathogenicity Islands. <b>2017</b> , 30, 72-82	15
1500	Unusual Legionnaires' outbreak in cool, dry Western Canada: an investigation using genomic epidemiology. <b>2017</b> , 145, 254-265	6
1499	Draft Genome Sequence of sp. Strain 66b. <b>2017</b> , 5,	1
1498	Whole-Genome Sequence of the Fruiting Myxobacterium DSM 52655. <b>2017</b> , 5,	1
1497	Complete Genome Sequence and Annotation of the Strain HG001. <b>2017</b> , 5,	9
1496	Genome-Wide Discovery of Genes Required for Capsule Production by Uropathogenic. 2017, 8,	29
1495	Lactobacillus fermentum FTDC 8312 combats hypercholesterolemia via alteration of gut microbiota. <b>2017</b> , 262, 75-83	33
1494	The Biofilm Inhibitor Carolacton Enters Gram-Negative Cells: Studies Using a TolC-Deficient Strain of. <b>2017</b> , 2,	6
1493	First Draft Genome Sequence of a Clinical Strain of. <b>2017</b> , 5,	2
1492	Draft Genome Sequence of NBRC 3561, a Bioactive Peptide-Producing Actinobacterium. <b>2017</b> , 5,	5
1491	Identification and characterization of the novel colonization factor CS30 based on whole genome sequencing in enterotoxigenic Escherichia coli (ETEC). <b>2017</b> , 7, 12514	14
1490	Geographically widespread honeybee-gut symbiont subgroups show locally distinct antibiotic-resistant patterns. <b>2017</b> , 26, 6590-6607	18
1489	Analysis of the CRISPR-Cas system in bacteriophages active on epidemic strains of Vibrio cholerae in Bangladesh. <b>2017</b> , 7, 14880	22
1488	Evolution of Sphingomonad Gene Clusters Related to Pesticide Catabolism Revealed by Genome Sequence and Mobilomics of Sphingobium herbicidovorans MH. <b>2017</b> , 9, 2477-2490	19
1487	Draft genome sequence of Thalassobius gelatinovorus CECT 4357T, a roseobacter with the potential ability to degrade polycyclic aromatic hydrocarbons. <b>2017</b> , 9, 32-36	6
1486	Natural product diversity associated with the nematode symbionts Photorhabdus and Xenorhabdus. <b>2017</b> , 2, 1676-1685	78
1485	The new phylogeny of the genus Mycobacterium: The old and the news. <b>2017</b> , 56, 19-25	82
1484	Complete Genome Sequence of Strain DE2-B, a Bacterium with Broad Inhibitory Activity toward Human and Fish Pathogens. <b>2017</b> , 5,	3

 $_{14}8_{3}$  Conservation and Recombination in the Genome Sequence of Type f WAPHL1. **2017**, 5,

$_{1482}$ Draft Genome Sequence of sp. Strain Rs-Y01, Isolated from the Gut of the Lower Termite. <b>2017</b> , 5,	1
Conjugation-Mediated Horizontal Gene Transfer of Clostridium perfringens Plasmids in the Chicken Gastrointestinal Tract Results in the Formation of New Virulent Strains. <b>2017</b> , 83,	20
Meropenem-Vaborbactam Resistance Selection, Resistance Prevention, and Molecular Mechanisms in Mutants of KPC-Producing Klebsiella pneumoniae. <b>2017</b> , 61,	88
The first characterized phage against a member of the ecologically important sphingomonads reveals high dissimilarity against all other known phages. <b>2017</b> , 7, 13566	7
Draft Genome Sequence of a Novel sp. Strain, MD30, Isolated from a Biofilm in an Air Conditioner Condensate Pipe. <b>2017</b> , 5,	1
Large-scale genomic analyses reveal the population structure and evolutionary trends of Streptococcus agalactiae strains in Brazilian fish farms. <b>2017</b> , 7, 13538	21
Detection of optrA in the African continent (Tunisia) within a mosaic Enterococcus faecalis plasmid from urban wastewaters. <b>2017</b> , 72, 3245-3251	38
1475 Draft Genome Sequence of Bacteriophage vB_Eco_swan01. <b>2017</b> , 5,	3
Draft Genome Sequences of Three Strains Presenting New Candidate Organisms with High Potentials for Specific P450 Cytochromes. <b>2017</b> , 5,	4
Genome Sequence of sp. NBS 11-29, an Antibiotic and Hydrolytic Enzyme Producer, Isolated from River Sediment in Brazil. <b>2017</b> , 5,	2
1472 Complete Genome Sequences of Three Strains from Texas. <b>2017,</b> 5,	4
1471 Complete Genome Sequence of Serotype III Sequence Type 17 Strain 874391. <b>2017</b> , 5,	6
Transient exposure to oxygen or nitrate reveals ecophysiology of fermentative and sulfate-reducing benthic microbial populations. <b>2017</b> , 19, 4866-4881	13
Candidatus Dactylopiibacterium carminicum, a Nitrogen-Fixing Symbiont of Dactylopius Cochineal Insects (Hemiptera: Coccoidea: Dactylopiidae). <b>2017</b> , 9, 2237-2250	11
mcr-1 and mcr-2 variant genes identified in Moraxella species isolated from pigs in Great Britain from 2014 to 2015. <b>2017</b> , 72, 2745-2749	143
Genotype distribution of Chinese Mycoplasma bovis isolates and their evolutionary relationship to strains from other countries. <b>2017</b> , 111, 108-117	14
1466 Molecular epidemiology of Epizootic haematopoietic necrosis virus (EHNV). <b>2017</b> , 511, 320-329	2

1465	Torix group Rickettsia are widespread in Culicoides biting midges (Diptera: Ceratopogonidae), reach high frequency and carry unique genomic features. <b>2017</b> , 19, 4238-4255	27
1464	A Supervised Statistical Learning Approach for Accurate Legionella pneumophila Source Attribution during Outbreaks. <b>2017</b> , 83,	4
1463	Spontaneous Loss of Virulence in Natural Populations of Listeria monocytogenes. 2017, 85,	49
1462	Draft Genome Sequence of sp. Strain 5.13, a Highly Stress-Resistant Bacterium Isolated from the Southwest Indian Ridge. <b>2017</b> , 5,	1
1461	Draft Genome Sequence of sp. Strain A 288, Isolated from an Iron-Precipitating Biofilm. <b>2017</b> , 5,	1
1460	Large-Scale Phylogenomics of the Group Highlights Taxonomic Inconsistencies and Reveals Novel Clade-Associated Features. <b>2017</b> , 2,	56
1459	Whole-Genome Sequencing of Bacterial Pathogens: the Future of Nosocomial Outbreak Analysis. <b>2017</b> , 30, 1015-1063	180
1458	Whole-Genome Sequence of the First Sequence Type 27 Strain Isolated from European Waters. <b>2017</b> , 5,	4
1457	Parallel Evolution of Group B Hypervirulent Clonal Complex 17 Unveils New Pathoadaptive Mutations. <b>2017</b> , 2,	22
1456	Host modification of a bacterial quorum-sensing signal induces a phenotypic switch in bacterial symbionts. <b>2017</b> , 114, E8488-E8497	48
1455	Draft Genome Sequence of sp. Strain EMTCatA1, Reconstructed from the Metagenome of a Thermophilic Electromethanogenesis-Catalyzing Biocathode. <b>2017</b> , 5,	4
1454	Complete genome sequence of the nematicidal Bacillus thuringiensis MYBT18247. <b>2017</b> , 260, 48-52	7
1453	Draft Genome Sequence of C6, an Environmental Isolate Engaging in Interspecific Metabolic Interactions. <b>2017</b> , 5,	5
1452	Community-like genome in single cells of the sulfur bacterium Achromatium oxaliferum. <b>2017</b> , 8, 455	16
1451	Alterations of c-di-GMP turnover proteins modulate semi-constitutive rdar biofilm formation in commensal and uropathogenic Escherichia coli. <b>2017</b> , 6, e00508	16
1450	Clinical metagenomics of bone and joint infections: a proof of concept study. <b>2017</b> , 7, 7718	53
1449	Metagenomic analysis reveals a green sulfur bacterium as a potential coral symbiont. <b>2017</b> , 7, 9320	15
1448	Enabling the democratization of the genomics revolution with a fully integrated web-based bioinformatics platform. <b>2017</b> , 45, 67-80	95

1447	Simultaneous Production of Anabaenopeptins and Namalides by the Cyanobacterium Nostoc sp. CENA543. <b>2017</b> , 12, 2746-2755	21
1446	Genome and Plasmid Sequences of KV7, an Extended-Spectrum Lactamase Isolate Derived from Feces of a Healthy Pig. <b>2017</b> , 5,	1
1445	Insights into the Genome of the Anaerobic Acetogen DSM 10669. <b>2017</b> , 5,	2
1444	Whole-Genome Sequence of the Soil Bacterium sp. KBS0714. <b>2017</b> , 5,	4
1443	Systematic longitudinal survey of invasive in England demonstrates a stable population structure only transiently disturbed by the emergence of ST131. <b>2017</b> ,	122
1442	Multi-drug resistant Klebsiella pneumoniae strains circulating in hospital setting: whole-genome sequencing and Bayesian phylogenetic analysis for outbreak investigations. <b>2017</b> , 7, 3534	15
1441	Draft Genome Sequence of 3T412C, Harboring an Arsenic Resistance Genomic Island, Isolated from Mine Tailings in Peru. <b>2017</b> , 5,	2
1440	Monitoring microevolution of OXA-48-producing Klebsiella pneumoniae ST147 in a hospital setting by SMRT sequencing. <b>2017</b> , 72, 2737-2744	20
1439	Ninety-nine de novo assembled genomes from the moose (Alces alces) rumen microbiome provide new insights into microbial plant biomass degradation. <b>2017</b> , 11, 2538-2551	70
1438	High-Quality Draft Genome Sequence of Strain Z11, Isolated from a Human Adult Intestinal Biopsy Sample. <b>2017</b> , 5,	3
1437	Differentiating Botulinum Neurotoxin-Producing Clostridia with a Simple, Multiplex PCR Assay. <b>2017</b> , 83,	15
1436	Draft Genome Sequence of sp. Strain MY03, a Terrestrial Bacterium Capable of Degrading Multiple Marine-Derived Polysaccharides. <b>2017</b> , 5,	3
1435	soxRS induces colistin hetero-resistance in Enterobacter asburiae and Enterobacter cloacae by regulating the acrAB-tolC efflux pump. <b>2017</b> , 72, 2715-2721	36
1434	Validation and Implementation of Clinical Laboratory Improvements Act-Compliant Whole-Genome Sequencing in the Public Health Microbiology Laboratory. <b>2017</b> , 55, 2502-2520	53
1433	Plasmids of Distinct IncK Lineages Show Compatible Phenotypes. <b>2017</b> , 61,	16
1432	First report of two complete Clostridium chauvoei genome sequences and detailed in silico genome analysis. <b>2017</b> , 54, 287-298	14
1431	Identification of EloR (Spr1851) as a regulator of cell elongation in Streptococcus pneumoniae. <b>2017</b> , 105, 954-967	27
1430	Galleria mellonella is low cost and suitable surrogate host for studying virulence of human pathogenic Vibrio cholerae. <b>2017</b> , 628, 1-7	9

1429	Recombination of Virulence Genes in Divergent Acidovorax avenae Strains That Infect a Common Host. <b>2017</b> , 30, 813-828	8
1428	First Insights into the Genome Sequence of DSM 28571, Isolated from the Soil of a Japanese Rice Field. <b>2017</b> , 5,	1
1427	First Insights into the Genome Sequence of the Strictly Anaerobic Homoacetogenic Strain E (DSM 2875). <b>2017</b> , 5,	6
1426	The invasive Neisseria meningitidis MenC CC103 from Brazil is characterized by an accessory gene repertoire. <b>2017</b> , 7, 1617	3
1425	Genomic epidemiology of global Klebsiella pneumoniae carbapenemase (KPC)-producing Escherichia coli. <b>2017</b> , 7, 5917	68
1424	Metabolic pathway and cell adaptation mechanisms revealed through genomic, proteomic and transcription analysis of a Sphingomonas haloaromaticamans strain degrading ortho-phenylphenol. <b>2017</b> , 7, 6449	12
1423	Complete Genome Sequences of Three Representative Beijing Family Strains Belonging to Distinct Genotype Clusters in Hanoi, Vietnam, during 2007 to 2009. <b>2017</b> , 5,	7
1422	Draft Genome Sequence of sp. SK021, a Representative of the Marine Group, Isolated from North Sea Sediment. <b>2017</b> , 5,	2
1421	Brucella Genetic Variability in Wildlife Marine Mammals Populations Relates to Host Preference and Ocean Distribution. <b>2017</b> , 9, 1901-1912	19
1420	Molecular epidemiology of Klebsiella pneumoniae invasive infections over a decade at Kilifi County Hospital in Kenya. <b>2017</b> , 307, 422-429	33
1419	Draft Genome Sequences of Strain DKU_NT_01 Isolated from Traditional Korean Food Containing Soybean (Chung-gook-jang). <b>2017</b> , 5,	
1418	Whole-Genome Sequencing of Human Clinical Isolates Reveals Misidentification and Misunderstandings of , , and. <b>2017</b> , 2,	78
1417	Metabolic potential and in situ activity of marine Marinimicrobia bacteria in an anoxic water column. <b>2017</b> , 19, 4392-4416	26
1416	Impact of Exposure of Methicillin-Resistant Staphylococcus aureus to Polyhexanide and. <b>2017</b> , 61,	20
1415	Bacteria contribute to pesticide degradation in cryoconite holes in an Alpine glacier. <b>2017</b> , 230, 919-926	21
1414	High potential for temperate viruses to drive carbon cycling in chemoautotrophy-dominated shallow-water hydrothermal vents. <b>2017</b> , 19, 4432-4446	14
1413	From a Natural Product to Its Biosynthetic Gene Cluster: A Demonstration Using Polyketomycin from Streptomyces diastatochromogenes TB028. <b>2017</b> ,	3
1412	Whole-Genome Sequence of subsp. Strain 91-197, Isolated from Hybrid Striped Bass (sp.) in the United States. <b>2017</b> , 5,	4

1411	Pathogenicity Locus, Core Genome, and Accessory Gene Contributions to Virulence. 2017, 8,	36
1410	Comparative Genomics of Reveals a Path to Specialized Exploitation of Multiple Invertebrate Hosts. <b>2017</b> , 8,	31
1409	Genomic epidemiology of methicillin-susceptible Staphylococcus aureus across colonisation and skin and soft tissue infection. <b>2017</b> , 75, 326-335	6
1408	Genomic and clinical evidence uncovers the enterohepatic species Helicobacter valdiviensis as a potential human intestinal pathogen. <b>2017</b> , 22, e12425	6
1407	Evolution of fixNOQP genes encoding cytochrome oxidase with high affinity to oxygen in rhizobia and related bacteria. <b>2017</b> , 53, 766-774	7
1406	Using KBase to Assemble and Annotate Prokaryotic Genomes. <b>2017</b> , 46, 1E.13.1-1E.13.18	9
1405	Genomics of the new species Kingella negevensis: diagnostic issues and identification of a locus encoding a RTX toxin. <b>2017</b> , 19, 546-552	17
1404	Complete Genome Sequence of a Strain Belonging to the East African-Indian Family in the Indo-Oceanic Lineage, Isolated in Hanoi, Vietnam. <b>2017</b> , 5,	6
1403	Complete Genome Sequence of -Encoding Strain H105 of Sequence Type 131 Lineage C1/H30R. <b>2017</b> , 5,	11
1402	Lignocellulose-Degrading Microbial Communities in Landfill Sites Represent a Repository of Unexplored Biomass-Degrading Diversity. <b>2017</b> , 2,	29
1401	Draft Genome Sequence of SGL 03, a Novel Potential Probiotic Strain. <b>2017</b> , 5,	
1400	Comparative genome analysis of the vineyard weed endophyte Pseudomonas viridiflava CDRTc14 showing selective herbicidal activity. <b>2017</b> , 7, 17336	15
1399	Characterization of the Mechanisms of Daptomycin Resistance among Gram-Positive Bacterial Pathogens by Multidimensional Lipidomics. <b>2017</b> , 2,	52
1398	Draft Genome Sequence of Strain GM4FR, an Endophytic Bacterium Isolated from L. <b>2017</b> , 5,	2
1397	Genomic Variation and Evolution of ST36 over the Course of a Transcontinental Epidemic Expansion. <b>2017</b> , 8,	36
1396	Genome Sequence of Strain SMR3, Isolated from a Culture of the Diatom. <b>2017</b> , 5,	5
1395	Atmospheric trace gases support primary production in Antarctic desert surface soil. <b>2017</b> , 552, 400-403	159
1394	Genomic assessment in Lactobacillus plantarum links the butyrogenic pathway with glutamine metabolism. <b>2017</b> , 7, 15975	17

1393	Increased Biosynthetic Gene Dosage in a Genome-Reduced Defensive Bacterial Symbiont. <b>2017</b> , 2,	28
1392	Complete Genome Sequence of Strain a523 Isolated from Urban Raw Sewage. <b>2017</b> , 5,	3
1391	Constraints on lateral gene transfer in promoting fimbrial usher protein diversity and function. <b>2017</b> , 7,	7
1390	First Insight into the Genome Sequences of Two Linezolid-Resistant Strains Isolated from Patients with Cystic Fibrosis. <b>2017</b> , 5,	1
1389	Genomic, Transcriptomic, and Phenotypic Analyses of Isolates from Disease Patients and Their Household Contacts. <b>2017</b> , 2,	2
1388	De novo assembly and annotation of the whole genomic analysis of Vibrio campbellii RT-1 strain, from infected shrimp: Litopenaeus vannamei. <b>2017</b> , 113, 372-377	3
1387	Draft Genome Sequence of the Polysaccharide-Degrading Marine Bacterium sp. Strain A601. <b>2017</b> , 5,	2
1386	Global phylogenetic analysis of Escherichia coli and plasmids carrying the mcr-1 gene indicates bacterial diversity but plasmid restriction. <b>2017</b> , 7, 15364	128
1385	Canonical germinant receptor is dispensable for spore germination in Clostridium botulinum group II strain NCTC 11219. <b>2017</b> , 7, 15426	5
1384	Virioplankton Assemblage Structure in the Lower River and Ocean Continuum of the Amazon. <b>2017</b> , 2,	7
1383	Vitamin and Amino Acid Auxotrophy in Anaerobic Consortia Operating under Methanogenic Conditions. <b>2017</b> , 2,	16
1382	Distinct Campylobacter fetus lineages adapted as livestock pathogens and human pathobionts in the intestinal microbiota. <b>2017</b> , 8, 1367	27
1381	Genomic history of the seventh pandemic of cholera in Africa. 2017, 358, 785-789	157
1380	Integrated view of in the Americas. 2017, 358, 789-793	79
1379	Draft Genome Sequence of VU-DES13, Isolated from (Collembola: Entomobryidae). <b>2017</b> , 5,	3
1378	Evolution and comparative genomics of pAQU-like conjugative plasmids in Vibrio species. <b>2017</b> , 72, 2503-250	67
1377	Complete Genome Sequence of from a Patient with Interstitial Lung Disease Using Single-Molecule Real-Time Sequencing Technology. <b>2017</b> , 5,	1
1376	Reclassification of the Specialized Metabolite Producer Pseudomonas mesoacidophila ATCC 31433 as a Member of the Burkholderia cepacia Complex. <b>2017</b> , 199,	21

1375	Parallel Evolution of Two Clades of an Atlantic-Endemic Pathogenic Lineage of Vibrio parahaemolyticus by Independent Acquisition of Related Pathogenicity Islands. <b>2017</b> , 83,	14
1374	First Insights into the Genome Sequence of the Alkaliphilic Thermotolerant Bacterium JW/YL23-2. <b>2017</b> , 5,	
1373	RCH51, a multiply antibiotic-resistant Acinetobacter baumannii ST103IP isolate, carries resistance genes in three plasmids, including a novel potentially conjugative plasmid carrying oxa235 in transposon Tn6252. <b>2017</b> , 72, 1907-1910	8
1372	Analysis of the Viable Microbiota and Helicobacter pylori Transcriptome in Gastric Infection and Early Stages of Carcinogenesis. <b>2017</b> , 85,	40
1371	Genomic Epidemiology of NDM-1-Encoding Plasmids in Latin American Clinical Isolates Reveals Insights into the Evolution of Multidrug Resistance. <b>2017</b> , 9, 1725-1741	35
1370	Genome analysis of three novel lytic Vibrio coralliilyticus phages isolated from seawater, Okinawa, Japan. <b>2017</b> , 35, 69-75	9
1369	Draft Genome Sequence of a Multidrug-Resistant Sequence Type 231 Outbreak-Associated Clone of , KP41-2015, Producing OXA-232 Carbapenemase. <b>2017</b> , 5,	1
1368	Genomic Analysis of Clavibacter michiganensis Reveals Insight Into Virulence Strategies and Genetic Diversity of a Gram-Positive Bacterial Pathogen. <b>2017</b> , 30, 786-802	31
1367	Complete Genome Sequence of the Livestock-Associated Methicillin-Resistant Strain subsp. 08S00974 (Sequence Type 398). <b>2017</b> , 5,	4
1366	Lebetimonas natsushimae sp. nov., a novel strictly anaerobic, moderately thermophilic chemoautotroph isolated from a deep-sea hydrothermal vent polychaete nest in the Mid-Okinawa Trough. <b>2017</b> , 40, 352-356	10
1365	Marine viruses discovered via metagenomics shed light on viral strategies throughout the oceans. <b>2017</b> , 8, 15955	129
1364	Customized workflow development and data modularization concepts for RNA-Sequencing and metatranscriptome experiments. <b>2017</b> , 261, 85-96	10
1363	Evolution of the ST2250 Clone in Northeastern Thailand Is Linked with the Acquisition of Livestock-Associated Staphylococcal Genes. <b>2017</b> , 8,	32
1362	Insights into the Geobacillus stearothermophilus species based on phylogenomic principles. <b>2017</b> , 17, 140	30
1361	Phenotypic and genomic survey on organic acid utilization profile of Pseudomonas mendocina strain S5.2, a vineyard soil isolate. <b>2017</b> , 7, 138	5
1360	Draft Genome Sequences of Strains CAPREx SY13 and CAPREx SY21 Isolated from Yams. <b>2017</b> , 5,	
1359	Tripartite species interaction: eukaryotic hosts suffer more from phage susceptible than from phage resistant bacteria. <b>2017</b> , 17, 98	16
1358	Prophages and adaptation of Staphylococcus aureus ST398 to the human clinic. <b>2017</b> , 18, 133	26

1357	Three novel Pseudomonas phages isolated from composting provide insights into the evolution and diversity of tailed phages. <b>2017</b> , 18, 346	14
1356	No evidence for a bovine mastitis Escherichia coli pathotype. <b>2017</b> , 18, 359	26
1355	Comparative genome and transcriptome analysis reveals distinctive surface characteristics and unique physiological potentials of Pseudomonas aeruginosa ATCC 27853. <b>2017</b> , 18, 459	21
1354	Comparative genomics of Enterococcus spp. isolated from bovine feces. <b>2017</b> , 17, 52	39
1353	Emergence and spread of a new community-genotype methicillin-resistant Staphylococcus aureus clone in Colombia. <b>2017</b> , 17, 108	4
1352	Microbial solvent formation revisited by comparative genome analysis. <b>2017</b> , 10, 58	45
1351	Comparative genomic analysis reveals genetic features related to the virulence of FORC_013. <b>2017</b> , 9, 29	4
1350	Potential for hydrogen-oxidizing chemolithoautotrophic and diazotrophic populations to initiate biofilm formation in oligotrophic, deep terrestrial subsurface waters. <b>2017</b> , 5, 37	20
1349	Genome sequencing and analysis of phylotype I strains FJAT-91, FJAT-452 and FJAT-462 isolated from tomato, eggplant, and chili pepper in China. <b>2017</b> , 12, 29	1
1348	Bacteriocins of Non-aureus Staphylococci Isolated from Bovine Milk. <b>2017</b> , 83,	29
1347	Nitrogen fixation in a chemoautotrophic lucinid symbiosis. <b>2016</b> , 2, 16193	36
1346	Mariprofundus micogutta sp. nov., a novel iron-oxidizing zetaproteobacterium isolated from a deep-sea hydrothermal field at the Bayonnaise knoll of the Izu-Ogasawara arc, and a description of Mariprofundales ord. nov. and Zetaproteobacteria classis nov. <b>2017</b> , 199, 335-346	28
1345	Complete genome sequence of sequential Pandoraea apista isolates from the same cystic fibrosis patient supports a model of chronic colonization with in vivo strain evolution over time. <b>2017</b> , 87, 1-6	7
1344	Comparative Genomics Reveals the Diversity of Restriction-Modification Systems and DNA Methylation Sites in Listeria monocytogenes. <b>2017</b> , 83,	16
1343	Genome-Wide Biases in the Rate and Molecular Spectrum of Spontaneous Mutations in Vibrio cholerae and Vibrio fischeri. <b>2017</b> , 34, 93-109	52
1342	Isolation of bacteriophages and their application to control Pseudomonas aeruginosa in planktonic and biofilm models. <b>2017</b> , 168, 194-207	26
1341	Genomic analysis of 495 vancomycin-resistant Enterococcus faecium reveals broad dissemination of a vanA plasmid in more than 19 clones from Copenhagen, Denmark. <b>2017</b> , 72, 40-47	34
1340	Genome sequence of Prevotella intermedia SUNY aB G8-9K-3, a biofilm forming strain with drug-resistance. <b>2017</b> , 48, 5-6	

1339 Hydrocarbon and Lipid Microbiology Protocols. 2017,

1338	The antibiotic resistome of swine manure is significantly altered by association with the Musca domestica larvae gut microbiome. <b>2017</b> , 11, 100-111	72
1337	Identification of IncA/C Plasmid Replication and Maintenance Genes and Development of a Plasmid Multilocus Sequence Typing Scheme. <b>2017</b> , 61,	73
1336	Mining Bacterial Genomes for Secondary Metabolite Gene Clusters. <b>2017</b> , 1520, 23-47	35
1335	Epidemiological Surveillance and Typing Methods to Track Antibiotic Resistant Strains Using High Throughput Sequencing. <b>2017</b> , 1520, 331-356	7
1334	Antibiotics. 2017,	3
1333	Experimental metagenomics and ribosomal profiling of the human skin microbiome. 2017, 26, 211-219	20
1332	The use of Oxford Nanopore native barcoding for complete genome assembly. <b>2017</b> , 6, 1-6	15
1331	Draft Genome Sequence of sp. Strain Sph1(2015), Isolated from a Fouled Membrane Filter Used To Produce Drinking Water. <b>2017</b> , 5,	
1330	Complete Genome Sequence of the Fruiting Myxobacterium Strain DSM 14697, Generated by PacBio Sequencing. <b>2017</b> , 5,	6
1329	Complete Genome Sequence of the New Urolithin-Producing Bacterium DSM 27213. <b>2017</b> , 5,	2
1328	Gut Symbiont Secretes a Eukaryotic-Like Ubiquitin Protein That Mediates Intraspecies Antagonism. <b>2017</b> , 8,	25
1327	Popmarker: Identifying Phylogenetic Markers at the Population Level. <b>2017</b> , 13, 1176934317724404	1
1326	Complete Genome Sequence of Strain B59671, Which Naturally Produces the Broad-Spectrum Bacteriocin Thermophilin 110. <b>2017</b> , 5,	4
1325	Complete Genome Sequence of the Fruiting Myxobacterium DSM 14713. <b>2017</b> , 5,	2
1324	Population Structure and Local Adaptation of MAC Lung Disease Agent Mycobacterium avium subsp. hominissuis. <b>2017</b> , 9, 2403-2417	34
1323	Complete Genome Sequences of Strains CMU, CMS1, CMS2, and CMS3 Isolated from Infant Saliva in South Korea. <b>2017</b> , 5,	7
1322	Reconstructed genomes of novel Dehalococcoides mccartyi strains from 1,2,3,4-tetrachlorodibenzo-p-dioxin-dechlorinating enrichment cultures reveal divergent reductive dehalogenase gene profiles. <b>2017</b> , 93,	9

1321	Genome comparisons indicate recent transfer of Ri-like between sister species and. <b>2017</b> , 7, 9391-9404	37
1320	Searching for Antibiotic Resistance Genes in a Pristine Arctic Wetland. <b>2017</b> , 160, 42-59	14
1319	MICRA: an automatic pipeline for fast characterization of microbial genomes from high-throughput sequencing data. <b>2017</b> , 18, 233	8
1318	Genome Sequence of Strain Ingolstadt Isolated from the Pectoralis Pouch of a Patient with Defibrillator-Related Surgery. <b>2017</b> , 5,	
1317	Computational Methods in Microbial Population Genomics. 2017, 3-29	2
1316	Trajectories and Drivers of Genome Evolution in Surface-Associated Marine Phaeobacter. <b>2017</b> , 9, 3297-3311	8
1315	Population structure of multidrug resistant Klebsiella oxytoca within hospitals across the UK and Ireland identifies sharing of virulence and resistance genes with K. pneumoniae. <b>2017</b> , 9, 574-587	24
1314	First Insights into the Genome Sequence of the Cellulolytic Bacterium DSM 14427. <b>2017</b> , 5,	
1313	Y92-1009 complete genome sequence. <b>2017</b> , 12, 41	5
1312	Draft Genome Sequence of Bacillus sp. FMQ74, a Dairy-Contaminating Isolate from Raw Milk. <b>2017</b> , 5,	
1311	Confronting the catalytic dark matter encoded by sequenced genomes. <b>2017</b> , 45, 11495-11514	38
1310	A molecular portrait of maternal sepsis from Byzantine Troy. <b>2017</b> , 6,	26
1309	Draft Genome Sequence of the Planktic Cyanobacterium , Isolated from Alpine Lentic Freshwater. <b>2017</b> , 5,	5
1308	Genome analysis of E. coli isolated from Crohn's disease patients. <b>2017</b> , 18, 544	15
1307	Genome sequencing of 39 Akkermansia muciniphila isolates reveals its population structure, genomic and functional diverisity, and global distribution in mammalian gut microbiotas. <b>2017</b> , 18, 800	63
1306	Preterm Infant-Associated Clostridium tertium, Clostridium cadaveris, and Clostridium paraputrificum Strains: Genomic and Evolutionary Insights. <b>2017</b> , 9, 2707-2714	27
1305	Genomic Analysis of Third Generation Cephalosporin Resistant Escherichia coli from Dairy Cow Manure. <b>2017</b> , 4,	6
1304	Phenotypic and Genotypic Features of a Heidelberg Strain Isolated in Broilers in Brazil and Their Possible Association to Antibiotics and Short-Chain Organic Acids Resistance and Susceptibility. <b>2017</b> , 4, 184	3

1303	Multiple Locus Variable-Number Tandem-Repeat and Single-Nucleotide Polymorphism-Based Typing Reveals Multiple Lineages in Currently Endemic in China. <b>2017</b> , 4, 215	9
1302	Evolution of mobile genetic element composition in an epidemic methicillin-resistant Staphylococcus aureus: temporal changes correlated with frequent loss and gain events. <b>2017</b> , 18, 684	23
1301	Draft Genome Sequence of Strain Cavy grass 6, Isolated from Domesticated Guinea Pig Fecal Samples. <b>2017</b> , 5,	
1300	Next-Generation Sequencing, Bioinformatics, and Infectious Diseases. <b>2017</b> , 405-420	
1299	Determination of Elizabethkingia Diversity by MALDI-TOF Mass Spectrometry and Whole-Genome Sequencing. <b>2017</b> , 23, 320-323	22
1298	Glimpse into the genome sequence of a multidrug-resistant Acinetobacter pittii ST950 clinical isolate carrying the blaOXA-72 and blaOXA-533 genes in China. <b>2017</b> , 112, 723-727	2
1297	Bioinformatic Analyses of Whole-Genome Sequence Data in a Public Health Laboratory. <b>2017</b> , 23, 1441-1445	24
1296	Characterization of Bacillus Subtilis Viruses vB_BsuM-Goe2 and vB_BsuM-Goe3. <b>2017</b> , 9,	14
1295	Three Draft Genome Sequences of Strains Isolated from Bivalve Hatcheries. 2017, 5,	3
1294	A Review of Bioinformatics Tools for Bio-Prospecting from Metagenomic Sequence Data. <b>2017</b> , 8, 23	97
1293	Complete Genome Sequences of Two Acetic Acid-Producing Strains (Subsp. LMG 1590 and Subsp. LMG 1591). <b>2017</b> , 5, 33	8
1292	Complete Genome Sequences of Two Phages, vB_EcoM_ ESCO5 and vB_EcoM_ESCO13, Which Are Related to phAPEC8. <b>2017</b> , 5,	5
1291	The All-Rounder Sodalis: A New Bacteriome-Associated Endosymbiont of the Lygaeoid Bug Henestaris halophilus (Heteroptera: Henestarinae) and a Critical Examination of Its Evolution. <b>2017</b> , 9, 2893-2910	33
1290	The Serogroup O1 and O2 Lipopolysaccharides Are Encoded by Multiple O-antigen Gene Clusters. <b>2017</b> , 7, 30	15
1289	Genome Dynamics of during Antibiotic Treatment: Transfer, Loss, and Persistence of Genetic Elements of the Infant Gut. <b>2017</b> , 7, 126	30
1288	Nitrile-Degrading Bacteria Isolated from Compost. <b>2017</b> , 5,	21
1287	Genome Analysis of PCR Ribotype 014 Lineage in Australian Pigs and Humans Reveals a Diverse Genetic Repertoire and Signatures of Long-Range Interspecies Transmission. <b>2016</b> , 7, 2138	72
1286	and Inhibit the Growth of Phytopathogenic Species. <b>2016</b> , 7, 2171	36

1285	Key Impact of an Uncommon Plasmid on subsp. S499 Developmental Traits and Lipopeptide Production. <b>2017</b> , 8, 17	9
1284	Uses Specific Domain Rearrangements and Allelic Exchange to Generate Diversity in Surface Virulence Factors. <b>2017</b> , 8, 48	29
1283	Genomic Characterization of Dairy Associated Species and Diversity of Leuconostocs in Undefined Mixed Mesophilic Starter Cultures. <b>2017</b> , 8, 132	31
1282	Enterotoxin C and Enterotoxin-Like L Associated with Post-partum Mastitis. 2017, 8, 173	7
1281	Three Novel Species with Peptidoglycan Cell Walls form the New Genus gen. nov. in the Family Opitutaceae of the Verrucomicrobial Subdivision 4. <b>2017</b> , 8, 202	52
1280	The Histidine Decarboxylase Gene Cluster of Was Gained by Horizontal Gene Transfer and Is Mobile within the Species. <b>2017</b> , 8, 218	19
1279	Characterization of the Prophage Repertoire of African Typhimurium ST313 Reveals High Levels of Spontaneous Induction of Novel Phage BTP1. <b>2017</b> , 8, 235	38
1278	Serpentinization-Influenced Groundwater Harbors Extremely Low Diversity Microbial Communities Adapted to High pH. <b>2017</b> , 8, 308	35
1277	GAMOLA2, a Comprehensive Software Package for the Annotation and Curation of Draft and Complete Microbial Genomes. <b>2017</b> , 8, 346	18
1276	Phosphate Limitation Triggers the Dissolution of Precipitated Iron by the Marine Bacterium sp. FO-BEG1. <b>2017</b> , 8, 364	13
1275	Genotypes Associated with Isolates Displaying Impaired or Enhanced Tolerances to Cold, Salt, Acid, or Desiccation Stress. <b>2017</b> , 8, 369	73
1274	Comparative Genomics of Four Isosphaeraceae Planctomycetes: A Common Pool of Plasmids and Glycoside Hydrolase Genes Shared by PX4, IS1B, DSM 18658, and Strain SH-PL62. <b>2017</b> , 8, 412	33
1273	Comparative Genomics Analysis of a New Strain from Salar de Huasco Reveals a Repertoire of Stress-Related Genes and Arsenic Resistance. <b>2017</b> , 8, 456	24
1272	Untangling Genomes of Novel and Species from Monterey Bay Kelp Forest Metagenomes by Refined Binning. <b>2017</b> , 8, 472	42
1271	Pan-Genomic Analysis Permits Differentiation of Virulent and Non-virulent Strains of That Cohabit spp. and Elucidate Bacterial Virulence Factors. <b>2017</b> , 8, 573	24
1270	A Metagenomic Approach to Cyanobacterial Genomics. <b>2017</b> , 8, 809	54
1269	Insight into Potential Probiotic Markers Predicted in MP-10 Genome Sequence. <b>2017</b> , 8, 891	26
1268	Methane Dynamics in a Tropical Serpentinizing Environment: The Santa Elena Ophiolite, Costa Rica. <b>2017</b> , 8, 916	30

1267	Genome-Wide Analyses Reveal Genes Subject to Positive Selection in. <b>2017</b> , 8, 961	18
1266	Unexpected Dominance of Elusive Acidobacteria in Early Industrial Soft Coal Slags. <b>2017</b> , 8, 1023	21
1265	Structure of O-Antigen and Hybrid Biosynthetic Locus in Clonal Variants Recovered from a Cystic Fibrosis Patient. <b>2017</b> , 8, 1027	9
1264	, an Evolutionary Dead-End Pathogen. <b>2017</b> , 8, 1054	21
1263	A Genome-Wide Association Study to Identify Diagnostic Markers for Human Pathogenic Strains. <b>2017</b> , 8, 1224	27
1262	Evolution of : International Clone II, More Resistance to Ceftazidime, Mutation in. <b>2017</b> , 8, 1256	20
1261	Draft Genome Sequence of the Nitrogen-Fixing Type Strain IS123 Focusing on the Key Genes for Symbiosis with its Host L. <b>2017</b> , 8, 1348	12
1260	Amplicon Sequencing of the Locus Permits Culture-Independent Strain Typing of in Dairy Products. <b>2017</b> , 8, 1380	6
1259	Identification of Secondary Metabolite Gene Clusters in the Genus Reveals Encouraging Biosynthetic Potential toward the Production of Novel Bioactive Compounds. <b>2017</b> , 8, 1494	32
1258	Whole Genome Sequencing of Danish Reveals a Genetically Diverse Collection with Clear Separation from. <b>2017</b> , 8, 1512	28
1257	Evolution of in Cystic Fibrosis Lung over Chronic Infection: A Genomic and Phenotypic Population Study. <b>2017</b> , 8, 1590	43
1256	The Mobilome; A Major Contributor to -Positive O26:H11 Strains Intra-Serotype Diversity. <b>2017</b> , 8, 1625	8
1255	Biology and Genomics of an Historic Therapeutic Bacteriophage Collection. 2017, 8, 1652	10
1254	Environmental Bacteriophages of the Emerging Enterobacterial Phytopathogen, , Show Genomic Conservation and Capacity for Horizontal Gene Transfer between Their Bacterial Hosts. <b>2017</b> , 8, 1654	12
1253	Adaptation of Surface-Associated Bacteria to the Open Ocean: A Genomically Distinct Subpopulation of Colonizes Pacific Mesozooplankton. <b>2017</b> , 8, 1659	13
1252	The Composite 259-kb Plasmid of DSM 17316-A Natural Replicon with Functional RepABC Modules from and. <b>2017</b> , 8, 1787	7
1251	Rapid Gene Turnover as a Significant Source of Genetic Variation in a Recently Seeded Population of a Healthcare-Associated Pathogen. <b>2017</b> , 8, 1817	31
1250	The Bacterial Species Induce Diverse Innate Immune Responses in Human and Avian Intestinal Epithelial Cells. <b>2017</b> , 8, 1840	11

1249	Exploring the Genome and Phenotype of Multi-Drug Resistant of Clinical Origin. 2017, 8, 1913	20
1248	Pathogenicity of Human ST23 to Fish and Genomic Comparison of Pathogenic and Non-pathogenic Isolates. <b>2017</b> , 8, 1933	5
1247	Genome of . Pandoraea novymonadis, an Endosymbiotic Bacterium of the Trypanosomatid. <b>2017</b> , 8, 1940	14
1246	Comparative Genomics of Facultative Bacterial Symbionts Isolated from European Species Reveals an Ancestral Symbiotic Association. <b>2017</b> , 8, 1969	4
1245	Ecogenomics and Taxonomy of Cyanobacteria Phylum. <b>2017</b> , 8, 2132	58
1244	A Novel IncA/C1 Group Conjugative Plasmid, Encoding VIM-1 Metallo-Beta-Lactamase, Mediates the Acquisition of Carbapenem Resistance in ST104 Isolates from Neonates in the Intensive Care Unit of V. Monaldi Hospital in Naples. <b>2017</b> , 8, 2135	18
1243	Bacterial Succession on Sinking Particles in the Ocean's Interior. <b>2017</b> , 8, 2269	24
1242	Toward Understanding Phage:Host Interactions in the Rumen; Complete Genome Sequences of Lytic Phages Infecting Rumen Bacteria. <b>2017</b> , 8, 2340	16
1241	Niche Partitioning of the N Cycling Microbial Community of an Offshore Oxygen Deficient Zone. <b>2017</b> , 8, 2384	32
1240	Clarification of Taxonomic Status within the Species Group Based on a Phylogenomic Analysis. <b>2017</b> , 8, 2422	61
1239	Strong Genomic and Phenotypic Heterogeneity in the Species Complex. <b>2017</b> , 8, 2434	12
1238	Probing Genomic Aspects of the Multi-Host Pathogen Reveals Significant Pangenome Diversity, and a Diverse Array of Virulence Factors. <b>2017</b> , 8, 2485	52
1237	A Potential New Human Pathogen Belonging to Genus, Identified in a Bloodstream Infection. <b>2017</b> , 8, 2533	6
1236	Draft Genome Sequence of a Rare Pigmented subsp. Type C Strain. <b>2017</b> , 5,	
1235	Complete Genome Sequence of Strain G11, a Model Sulfate-Reducing, Hydrogenotrophic, and Syntrophic Partner Organism. <b>2017</b> , 5,	7
1234	Complete Genome and Plasmid Sequences of EDCC 5055 (DSM 28763), Used To Study Implant-Associated Infections. <b>2017</b> , 5,	2
1233	Genome Sequence of Creatinine-Fermenting Strain KRE 4 (DSM 6911). <b>2017</b> , 5,	2
1232	Evolutionary Context of Non-Sorbitol-Fermenting Shiga Toxin-Producing Escherichia coli O55:H7. <b>2017</b> , 23, 1966-1973	6

1231	Bacteriophages are the major drivers of Shigella flexneri serotype 1c genome plasticity: a complete genome analysis. <b>2017</b> , 18, 722	7
1230	Genomic confirmation of vancomycin-resistant Enterococcus transmission from deceased donor to liver transplant recipient. <b>2017</b> , 12, e0170449	15
1229	Within-host whole genome analysis of an antibiotic resistant Pseudomonas aeruginosa strain sub-type in cystic fibrosis. <b>2017</b> , 12, e0172179	23
1228	Assessing biosynthetic potential of agricultural groundwater through metagenomic sequencing: A diverse anammox community dominates nitrate-rich groundwater. <b>2017</b> , 12, e0174930	14
1227	Genomic analyses of the ancestral Manila family of Mycobacterium tuberculosis. 2017, 12, e0175330	5
1226	In silico genomic insights into aspects of food safety and defense mechanisms of a potentially probiotic Lactobacillus pentosus MP-10 isolated from brines of naturally fermented Aloreâ green table olives. <b>2017</b> , 12, e0176801	13
1225	Phylogenetic analysis of emergent Streptococcus pneumoniae serotype 22F causing invasive pneumococcal disease using whole genome sequencing. <b>2017</b> , 12, e0178040	16
1224	Characterization of the emerging zoonotic pathogen Arcobacter thereius by whole genome sequencing and comparative genomics. <b>2017</b> , 12, e0180493	10
1223	Genomic features of "Candidatus Venteria ishoeyi", a new sulfur-oxidizing macrobacterium from the Humboldt Sulfuretum off Chile. <b>2017</b> , 12, e0188371	3
1222	First insights into a type II toxin-antitoxin system from the clinical isolate Mycobacterium sp. MHSD3, similar to epsilon/zeta systems. <b>2017</b> , 12, e0189459	4
1221	Methods for analyzing next-generation sequencing data IX.Genome annotation, visualization, and registration to DDBJ . <b>2017</b> , 28, 3-11	
1220	Draft Genome Sequences of Two Strains of a Newly Described Species,. <b>2017</b> , 5,	O
1219	Genomics-enabled analysis of the emergent disease cotton bacterial blight. <b>2017</b> , 13, e1007003	24
1218	Next generation sequencing reveals the antibiotic resistant variants in the genome of Pseudomonas aeruginosa. <b>2017</b> , 12, e0182524	24
1217	Whole genome sequence of the Treponema pallidum subsp. pallidum strain Amoy: An Asian isolate highly similar to SS14. <b>2017</b> , 12, e0182768	31
1216	Helicobacter pylori gene silencing in vivo demonstrates urease is essential for chronic infection. <b>2017</b> , 13, e1006464	39
1215	Evidence for the evolutionary steps leading to mecA-mediated flactam resistance in staphylococci. <b>2017</b> , 13, e1006674	44
1214	Whole Genome Sequence Analysis of Salmonella Typhi Isolated in Thailand before and after the Introduction of a National Immunization Program. <b>2017</b> , 11, e0005274	14

1213	Nitrogen Fixation Genes and Nitrogenase Activity of the Non-Heterocystous Cyanobacterium Thermoleptolyngbya sp. O-77. <b>2017</b> , 32, 324-329	14
1212	Public health surveillance in the UK revolutionises our understanding of the invasive Salmonella Typhimurium epidemic in Africa. <b>2017</b> , 9, 92	37
1211	Pan-genome and phylogeny of Bacillus cereus sensu lato. <b>2017</b> , 17, 176	59
1210	Association of coral algal symbionts with a diverse viral community responsive to heat shock. <b>2017</b> , 17, 174	15
1209	Longitudinal genomic surveillance of multidrug-resistant Escherichia coli carriage in a long-term care facility in the United Kingdom. <b>2017</b> , 9, 70	27
1208	Within-host evolution of Enterococcus faecium during longitudinal carriage and transition to bloodstream infection in immunocompromised patients. <b>2017</b> , 9, 119	18
1207	Genome analysis of Clostridium perfringens isolates from healthy and necrotic enteritis infected chickens and turkeys. <b>2017</b> , 10, 270	13
1206	Metagenomic analysis reveals potential interactions in an artificial coculture. <b>2017</b> , 7, 193	8
1205	Shifts in coastal sediment oxygenation cause pronounced changes in microbial community composition and associated metabolism. <b>2017</b> , 5, 96	36
1204	Complete genome sequence of sp. CCB-MM1, a halophile isolated from Matang Mangrove Forest, Malaysia. <b>2017</b> , 12, 36	8
1203	Complete genome sequence of the sand-sediment actinobacterium FR1436. <b>2017</b> , 12, 44	2
1202	Complete Genome sequence of the nematicidal MYBT18246. <b>2017</b> , 12, 48	7
1201	Complete genome of strain R3.8, bioremediation potential unraveled with genomic analysis. <b>2017</b> , 12, 52	8
1200	Draft genome sequence and characterization of commensal strain BG1 isolated from bovine gastro-intestinal tract. <b>2017</b> , 12, 61	7
1199	First draft genome sequence of a strain belonging to the genus and its gene expression in situ. <b>2017</b> , 12, 64	5
1198	Draft Genome Sequence of the Fruiting Myxobacterium DSM 71. <b>2017</b> , 5,	1
1197	Genome Sequence of the Homoacetogenic, Gram-Negative, Endospore-Forming Bacterium DSM 3132. <b>2017</b> , 5,	2
1196	Complete Genome Sequence of a Shiga Toxin-Producing Clinical Isolate. <b>2017</b> , 5,	4

	Evolutionary Thrift: Mycobacteria Repurpose Plasmid Diversity during Adaptation of Type VII Secretion Systems. <b>2017</b> , 9, 398-413	24
1194	Draft Genome Sequence of Deep-Sea Alteromonas sp. Strain V450 Isolated from the Marine Sponge Leiodermatium sp. <b>2017</b> , 5,	3
1193	Legionella Becoming a Mutualist: Adaptive Processes Shaping the Genome of Symbiont in the Louse Polyplax serrata. <b>2017</b> , 9, 2946-2957	26
1192	Draft Genome Sequence of PS71, a Multidrug-Resistant Strain Associated with Nosocomial Infections in Greece. <b>2017</b> , 5,	3
1191	Homoacetogenesis in Deep-Sea , as Inferred by Single-Cell Genomics, Provides a Link to Reductive Dehalogenation in Terrestrial. <b>2017</b> , 8,	23
1190	Draft Genome Sequence of the 1,2-Dichloroethane-Utilizing sp. Strain NDB3Y10, Isolated from an Australian Bore Well Producing Coal Seam Gas. <b>2017</b> , 5,	
1189	Draft Genome Sequence of Strain R_RK_3, an Iron-Depositing Isolate of the Genus , Isolated from a Dewatering Well of an Opencast Mine. <b>2017</b> , 5,	0
1188	The genomic sequence of str. N139 reveals a species that thrives in cold waters and extreme environmental conditions. <b>2017</b> , 5, e3162	10
1187	BGDMdocker: a Docker workflow for data mining and visualization of bacterial pan-genomes and biosynthetic gene clusters. <b>2017</b> , 5, e3948	4
1186	Complete Genome Sequences of Two Geographically Distinct Clinical Isolates. <b>2017</b> , 5,	
1185	First Insights into the Genome Sequence of DSM 1045. <b>2017</b> , 5,	3
1185	First Insights into the Genome Sequence of DSM 1045. <b>2017</b> , 5,  Complete Genome Sequences of Legionella pneumophila subsp. fraseri Strains Detroit-1 and Dallas 1E. <b>2017</b> , 5,	3
	Complete Genome Sequences of Legionella pneumophila subsp. fraseri Strains Detroit-1 and Dallas	3 1 5
1184	Complete Genome Sequences of Legionella pneumophila subsp. fraseri Strains Detroit-1 and Dallas 1E. <b>2017</b> , 5,  phyloSkeleton: taxon selection, data retrieval and marker identification for phylogenomics.	1
1184	Complete Genome Sequences of Legionella pneumophila subsp. fraseri Strains Detroit-1 and Dallas 1E. <b>2017</b> , 5,  phyloSkeleton: taxon selection, data retrieval and marker identification for phylogenomics. <i>Bioinformatics</i> , <b>2017</b> , 33, 1230-1232  7-2	5
1184 1183 1182	Complete Genome Sequences of Legionella pneumophila subsp. fraseri Strains Detroit-1 and Dallas 1E. 2017, 5,  phyloSkeleton: taxon selection, data retrieval and marker identification for phylogenomics.  Bioinformatics, 2017, 33, 1230-1232  Phylogenetic Analysis of Klebsiella pneumoniae from Hospitalized Children, Pakistan. 2017, 23, 1872-1875  RNA-seq and Tn-seq reveal fitness determinants of vancomycin-resistant Enterococcus faecium	1 5 26
1184 1183 1182 1181	Complete Genome Sequences of Legionella pneumophila subsp. fraseri Strains Detroit-1 and Dallas 1E. 2017, 5,  phyloSkeleton: taxon selection, data retrieval and marker identification for phylogenomics.  Bioinformatics, 2017, 33, 1230-1232  Phylogenetic Analysis of Klebsiella pneumoniae from Hospitalized Children, Pakistan. 2017, 23, 1872-1875  RNA-seq and Tn-seq reveal fitness determinants of vancomycin-resistant Enterococcus faecium during growth in human serum. 2017, 18, 893  High-Quality Draft Genome Sequence of subsp. Strain 08T0073 Isolated from a Wild European	1 5 26 26

1177	High-Quality Draft Genome Sequence of " Methanoperedens sp." Strain BLZ2, a Nitrate-Reducing Anaerobic Methane-Oxidizing Archaeon Enriched in an Anoxic Bioreactor. <b>2017</b> , 5,	17
1176	Complete plasmid sequence carrying type IV-like and type VII secretion systems from an atypical mycobacteria strain. <b>2017</b> , 112, 514-516	3
1175	Genomic Analysis of Salmonella enterica Serovar Typhimurium DT160 Associated with a 14-Year Outbreak, New Zealand, 1998-2012. <b>2017</b> , 23, 906-913	23
1174	Draft Genome Sequence of sp. Strain SH203, Producing Cellouronate (日,4-Linked Polyglucuronate) Lyase. <b>2017</b> , 5,	1
1173	Draft Genome Sequence of sp. I15G10I2, a Novel Bacterium Isolated from a Coal Seam Gas Water Treatment Pond. <b>2017</b> , 5,	
1172	De novo assembly of genomes from long sequence reads reveals uncharted territories of Propionibacterium freudenreichii. <b>2017</b> , 18, 790	13
1171	Subfunctionalization influences the expansion of bacterial multidrug antibiotic resistance. 2017, 18, 834	2
1170	Draft Genome Sequence of DSM 19640. <b>2017</b> , 5,	1
1169	Sharing of carbapenemase-encoding plasmids between Enterobacteriaceae in UK sewage uncovered by MinION sequencing. <b>2017</b> , 3, e000114	19
1168	Draft Genome Sequences of DSM 17494 and DSM 21029. <b>2017</b> , 5,	1
1168 1167		8
1167		
1167	Draft Genome Sequence of Strain 2873, a Novel Anode-Respiring Bacterium. <b>2017</b> , 5,	8
1167 1166	Draft Genome Sequence of Strain 2873, a Novel Anode-Respiring Bacterium. <b>2017</b> , 5,  Draft Genome Sequences of the Aerobic Strains AL3 and AL5. <b>2017</b> , 5,  Draft Genome Sequence of sp. A-2, an Iodide-Oxidizing Bacterium Isolated from Natural Gas Brine	8
1167 1166 1165	Draft Genome Sequence of Strain 2873, a Novel Anode-Respiring Bacterium. 2017, 5,  Draft Genome Sequences of the Aerobic Strains AL3 and AL5. 2017, 5,  Draft Genome Sequence of sp. A-2, an Iodide-Oxidizing Bacterium Isolated from Natural Gas Brine Water, Chiba, Japan. 2017, 5, 51-53  Evaluating the use of whole-genome sequencing for outbreak investigations in the lack of closely	2
1167 1166 1165	Draft Genome Sequence of Strain 2873, a Novel Anode-Respiring Bacterium. 2017, 5,  Draft Genome Sequences of the Aerobic Strains AL3 and AL5. 2017, 5,  Draft Genome Sequence of sp. A-2, an Iodide-Oxidizing Bacterium Isolated from Natural Gas Brine Water, Chiba, Japan. 2017, 5, 51-53  Evaluating the use of whole-genome sequencing for outbreak investigations in the lack of closely related reference genome. 2018, 59, 1-6  Complete genome sequence of the marine Rhodococcus sp. H-CA8f isolated from Comau fjord in Northern Patagonia, Chile. 2018, 40, 13-17	8 2 2 6
1167 1166 1165 1164 1163	Draft Genome Sequence of Strain 2873, a Novel Anode-Respiring Bacterium. 2017, 5,  Draft Genome Sequences of the Aerobic Strains AL3 and AL5. 2017, 5,  Draft Genome Sequence of sp. A-2, an Iodide-Oxidizing Bacterium Isolated from Natural Gas Brine Water, Chiba, Japan. 2017, 5, 51-53  Evaluating the use of whole-genome sequencing for outbreak investigations in the lack of closely related reference genome. 2018, 59, 1-6  Complete genome sequence of the marine Rhodococcus sp. H-CA8f isolated from Comau fjord in Northern Patagonia, Chile. 2018, 40, 13-17	8 2 2 6

1159	Piggy: a rapid, large-scale pan-genome analysis tool for intergenic regions in bacteria. <b>2018</b> , 7, 1-11	28
1158	Genome-resolved metagenomics identifies genetic mobility, metabolic interactions, and unexpected diversity in perchlorate-reducing communities. <b>2018</b> , 12, 1568-1581	24
1157	Complete Genome Sequencing of Acinetobacter baumannii Strain K50 Discloses the Large Conjugative Plasmid pK50a Encoding Carbapenemase OXA-23 and Extended-Spectrum Lactamase GES-11. <b>2018</b> , 62,	17
1156	Impact of Wastewater Treatment on the Prevalence of Integrons and the Genetic Diversity of Integron Gene Cassettes. <b>2018</b> , 84,	38
1155	Methylophaga muralis Bur 1, a haloalkaliphilic methylotroph isolated from the Khilganta soda lake (Southern Transbaikalia, Buryat Republic). <b>2018</b> , 87, 33-46	7
1154	The MAR databases: development and implementation of databases specific for marine metagenomics. <b>2018</b> , 46, D692-D699	42
1153	Complete Genome Sequence of the Novel Cellulolytic, Anaerobic, Thermophilic Bacterium Type Strain GGR1, Isolated from a Lab Scale Biogas Reactor as Established by Illumina and Nanopore MinION Sequencing. <b>2018</b> , 6,	6
1152	Draft Genome Sequence of Ezakiella peruensis Strain M6.X2, a Human Gut Gram-Positive Anaerobic Coccus. <b>2018</b> , 6,	O
1151	Cladogenesis and Genomic Streamlining in Extracellular Endosymbionts of Tropical Stink Bugs. <b>2018</b> , 10, 680-693	13
1150	Discovery and Biosynthesis of the Antibiotic Bicyclomycin in Distantly Related Bacterial Classes. <b>2018</b> , 84,	23
1149	One More Decade of Agrobacterium Taxonomy. <b>2018</b> , 418, 1-14	6
1148	bla on transferable plasmids in Proteus mirabilis and Providencia rettgeri. <b>2018</b> , 24, 1019.e5-1019.e8	8
1147	Culturing of female bladder bacteria reveals an interconnected urogenital microbiota. 2018, 9, 1557	132
1146	Identification of a novel aminopolycarboxylic acid siderophore gene cluster encoding the biosynthesis of ethylenediaminesuccinic acid hydroxyarginine (EDHA). <b>2018</b> , 10, 722-734	3
1145	Novel plasmid-mediated colistin resistance gene mcr-7.1 in Klebsiella pneumoniae. <b>2018</b> , 73, 1791-1795	206
1144	Draft Genome Sequence of "Nocardia suismassiliense" Strain S-137 (CSUR P4007). <b>2018</b> , 6,	3
1143	Draft Genome Sequence of Burkholderia gladioli Coa14, a Bacterium with Petroleum Bioremediation Potential Isolated from Coari Lake, Amazonas, Brazil. <b>2018</b> , 6,	4
1142	Investigating the Central Metabolism of Clostridium thermosuccinogenes. 2018, 84,	13

1141	Complete Genome Sequence of Loktanella vestfoldensis Strain SMR4r, a Novel Strain Isolated from a Culture of the Chain-Forming Diatom Skeletonema marinoi. <b>2018</b> , 6,	4
1140	Deep mitochondrial origin outside the sampled alphaproteobacteria. <b>2018</b> , 557, 101-105	169
1139	Novel sequencing technologies to support industrial biotechnology. <b>2018</b> , 365,	7
1138	Sporulation capability and amylosome conservation among diverse human colonic and rumen isolates of the keystone starch-degrader Ruminococcus bromii. <b>2018</b> , 20, 324-336	46
1137	Therapy and Outcome of Staphylococcus aureus Infections of Intracorporeal Ventricular Assist Devices. <b>2018</b> , 42, 983-991	7
1136	On the Enigma of Glutathione-Dependent Styrene Degradation in Gordonia rubripertincta CWB2. <b>2018</b> , 84,	27
1135	Complete Genome Sequence of 81009, a Representative of the Sequence Type 131 C1-M27 Clade with a Multidrug-Resistant Phenotype. <b>2018</b> , 6,	7
1134	Extensive Gene Amplification as a Mechanism for Piperacillin-Tazobactam Resistance in Escherichia coli. <b>2018</b> , 9,	27
1133	Clinically Relevant Plasmid-Host Interactions Indicate that Transcriptional and Not Genomic Modifications Ameliorate Fitness Costs of Carbapenemase-Carrying Plasmids. <b>2018</b> , 9,	35
1132	High genetic diversity of extended-spectrum flactamases producing Escherichia coli in feces of horses. <b>2018</b> , 219, 117-122	12
1131	Robinsoniella. <b>2018</b> , 1-8	
1130	A methanotrophic archaeon couples anaerobic oxidation of methane to Fe(III) reduction. <b>2018</b> , 12, 1929-1939	141
1129	Homologous Recombination between Genetically Divergent Campylobacter fetus Lineages Supports Host-Associated Speciation. <b>2018</b> , 10, 716-722	7
1128	The Genome Sequence of "Candidatus Fokinia solitaria": Insights on Reductive Evolution in Rickettsiales. <b>2018</b> , 10, 1120-1126	15
1127	Spread of Clonally Related Escherichia coli Strains Harboring an IncA/C Plasmid Encoding IMP-8 and Its Recruitment into an Unrelated MCR-1-Containing Isolate. <b>2018</b> , 62,	6
1126	Draft Genome Sequence of the Endophyte Strain GM6LP Isolated from. <b>2018</b> , 6,	5
1125	Mechanisms of Persistence of the Ammonia-Oxidizing Bacteria Nitrosomonas to the Biocide Free Nitrous Acid. <b>2018</b> , 52, 5386-5397	32
1124	Bile acid oxidation by Eggerthella lenta strains C592 and DSM 2243. <b>2018</b> , 9, 523-539	31

1123	Two Groups of Cocirculating, Epidemic Clostridiodes difficile Strains Microdiversify through Different Mechanisms. <b>2018</b> , 10, 982-998	7
1122	Structural and functional characterisation of multi-copper oxidase CueO from lignin-degrading bacterium Ochrobactrum sp. reveal its activity towards lignin model compounds and lignosulfonate. <b>2018</b> , 285, 1684-1700	30
1121	Complete Genome Sequence of a New Ruminococcaceae Bacterium Isolated from Anaerobic Biomass Hydrolysis. <b>2018</b> , 6,	4
1120	Phylogenetic signature of lateral exchange of genes for antibiotic production and resistance among bacteria highlights a pattern of global transmission of pathogens between humans and livestock. <b>2018</b> , 125, 255-264	6
1119	Bordetella pseudohinzii targets cilia and impairs tracheal cilia-driven transport in naturally acquired infection in mice. <b>2018</b> , 8, 5681	9
1118	Complete Genome Sequence of subsp. CCM 3239 (Formerly " CCM 3239"), a Producer of the Angucycline-Type Antibiotic Auricin. <b>2018</b> , 6,	7
1117	The reduced genome of Candidatus Kinetoplastibacterium sorsogonicusi, the endosymbiont of Kentomonas sorsogonicus (Trypanosomatidae): loss of the haem-synthesis pathway. <b>2018</b> , 145, 1287-1293	10
1116	Genome Sequence of a Heterotrophic Nitrifier and Aerobic Denitrifier, Paracoccus denitrificans Strain ISTOD1, Isolated from Wastewater. <b>2018</b> , 6,	7
1115	First Insight into the Genome Sequence of Clostridium vincentii DSM 10228, Isolated from Sediment of the McMurdo Ice Shelf, Antarctica. <b>2018</b> , 6,	
1114	Origin, evolution, and distribution of the molecular machinery for biosynthesis of sialylated lipooligosaccharide structures in Campylobacter coli. <b>2018</b> , 8, 3028	8
1113	Genome Sequencing Links Persistent Outbreak of Legionellosis in Sydney (New South Wales, Australia) to an Emerging Clone of Legionella pneumophila Sequence Type 211. <b>2018</b> , 84,	6
1112	Draft Genome Sequence of Strain CIIMS-PH-1, a Serovar 4b Isolate from Infant Septicemia. <b>2018</b> , 6,	1
1111	Analyses Directly in Diarrheal Stool Reveal Large Variations in Bacterial Load and Active Toxin Expression of Enterotoxigenic and. <b>2018</b> , 3,	8
1110	Comparative genomics analysis of Clostridium difficile epidemic strain DH/NAP11/106. <b>2018</b> , 20, 245-253	14
1109	Two Draft Genome Sequences of Isolates from the Rio Negro. <b>2018</b> , 6,	1
1108	Azithromycin Resistance in Shigella spp. in Southeast Asia. <b>2018</b> , 62,	24
1107	Draft Genome Sequence of Strain Acr-14, Isolated from Coral. <b>2018</b> , 6,	3
1106	Updating the genomic taxonomy and epidemiology of Campylobacter hyointestinalis. <b>2018</b> , 8, 2393	18

1105	Use of whole genome sequencing to investigate an increase in Neisseria gonorrhoeae infection among women in urban areas of Australia. <b>2018</b> , 8, 1503	12
1104	Deeply-sourced formate fuels sulfate reducers but not methanogens at Lost City hydrothermal field. <b>2018</b> , 8, 755	45
1103	Pathogenicity Locus Plasmid pCS1-1 Encodes a Novel Clostridial Conjugation Locus. <b>2018</b> , 9,	14
1102	Aether: leveraging linear programming for optimal cloud computing in genomics. <i>Bioinformatics</i> , <b>2018</b> , 34, 1565-1567	5
1101	Draft Genome Sequence of sp. Strain M8, Which Can Degrade a Broad Range of Nitriles. 2018, 6,	2
1100	Comparative genome analysis reveals a complex population structure of Legionella pneumophila subspecies. <b>2018</b> , 59, 172-185	9
1099	Lactobacillus kosoi sp. nov., a fructophilic species isolated from k[so, a Japanese sugar-vegetable fermented beverage. <b>2018</b> , 111, 1149-1156	13
1098	Pan-genome analysis of the genus Finegoldia identifies two distinct clades, strain-specific heterogeneity, and putative virulence factors. <b>2018</b> , 8, 266	12
1097	Comparative Genomics for Prokaryotes. <b>2018</b> , 1704, 55-78	7
1096	A Practical Guide for Comparative Genomics of Mobile Genetic Elements in Prokaryotic Genomes. <b>2018</b> , 1704, 213-242	10
1095	A primer on microbial bioinformatics for nonbioinformaticians. <b>2018</b> , 24, 342-349	33
1094	Prevalence and persistence of Listeria monocytogenes in premises and products of small food business operators in Northern Ireland. <b>2018</b> , 87, 70-78	13
1093	Topical Antibiotic Use Coselects for the Carriage of Mobile Genetic Elements Conferring Resistance to Unrelated Antimicrobials in Staphylococcus aureus. <b>2018</b> , 62,	15
1092	Zoonotic Transfer of Clostridium difficile Harboring Antimicrobial Resistance between Farm Animals and Humans. <b>2018</b> , 56,	75
1091	The incidence of Clostridioides difficile and Clostridium perfringens netF-positive strains in diarrheic dogs. <b>2018</b> , 49, 58-62	22
1090	Successive Emergence of Ceftazidime-Avibactam Resistance through Distinct Genomic Adaptations in -Harboring Klebsiella pneumoniae Sequence Type 307 Isolates. <b>2018</b> , 62,	114
1089	Methylation in Mycobacterium tuberculosis is lineage specific with associated mutations present globally. <b>2018</b> , 8, 160	22
1088	Transcriptomic profiling of interacting nasal staphylococci species reveals global changes in gene and non-coding RNA expression. <b>2018</b> , 365,	7

1087	Analysis of Vibrio seventh pandemic island II and novel genomic islands in relation to attachment sequences among a wide variety of Vibrio cholerae strains. <b>2018</b> , 62, 150-157		4
1086	Genome-enabled metabolic reconstruction of dominant chemosynthetic colonizers in deep-sea massive sulfide deposits. <b>2018</b> , 20, 862-877		18
1085	Draft Genome Sequence of a Red-Pigmented sp. Native to the Hudson Valley Watershed. <b>2018</b> , 6,		6
1084	Identification of a novel botulinum neurotoxin gene cluster in Enterococcus. <b>2018</b> , 592, 310-317		68
1083	Genomic and phenotypic characterization of an atypical Aeromonas salmonicida strain isolated from a lumpfish and producing unusual granular structures. <b>2018</b> , 41, 673-681		7
1082	Transfer of a bla -carrying plasmid between different Escherichia coli strains within the human gut explored by whole genome sequencing analyses. <b>2018</b> , 8, 280		15
1081	DFAST: a flexible prokaryotic genome annotation pipeline for faster genome publication. <i>Bioinformatics</i> , <b>2018</b> , 34, 1037-1039	7.2	371
1080	Whole-Genome Draft Sequences of Nine Asymptomatic Bacteriuria Isolates from Diabetic Patients. <b>2018</b> , 6,		1
1079	Weak Epistasis May Drive Adaptation in Recombining Bacteria. 2018, 208, 1247-1260		30
1078	Comparative Genomics of Bacteriophage of the Genus Seuratvirus. <b>2018</b> , 10, 72-76		19
1077	Evolution of a Dominant Natural Isolate of Escherichia coli in the Human Gut over the Course of a Year Suggests a Neutral Evolution with Reduced Effective Population Size. <b>2018</b> , 84,		31
1076	Methicillin-resistant Staphylococcus pseudintermedius among dogs in the description of novel SCCmec variants. <b>2018</b> , 213, 136-141		8
1075	Genomic analysis reveals different mechanisms of fusidic acid resistance in Staphylococcus aureus from Danish atopic dermatitis patients. <b>2018</b> , 73, 856-861		14
1074	Vibrio coralliirubri sp. nov., a new species isolated from mucus of red coral (Corallium rubrum) collected at Procida island, Italy. <b>2018</b> , 111, 1105-1115		7
1073	Genetic Competence Drives Genome Diversity in Bacillus subtilis. <b>2018</b> , 10, 108-124		29
1072	Genome Sequence of the Bile Salt-Degrading Bacterium sp. Strain Chol11, a Model Organism for Bacterial Steroid Catabolism. <b>2018</b> , 6,		4
1071	Expansion of a urethritis-associated Neisseria meningitidis clade in the United States with concurrent acquisition of N. gonorrhoeae alleles. <b>2018</b> , 19, 176		41
1070	Exploring the arthritogenicity of Streptococcus dysgalactiae subspecies equisimilis. <b>2018</b> , 18, 17		4

1069	A genetically and functionally diverse group of non-diazotrophic Bradyrhizobium spp. colonizes the root endophytic compartment of Arabidopsis thaliana. <b>2018</b> , 18, 61	11
1068	Co-cultivation of the strictly anaerobic methanogen Methanosarcina barkeri with aerobic methanotrophs in an oxygen-limited membrane bioreactor. <b>2018</b> , 102, 5685-5694	12
1067	Discovery and description of a new serogroup 7 Streptococcus pneumoniae serotype, 7D, and structural analysis of 7C and 7D. <b>2018</b> , 463, 24-31	15
1066	Male-killing toxin in a bacterial symbiont of Drosophila. <b>2018</b> , 557, 252-255	69
1065	Draft Genome Sequences of the Obligatory Marine Myxobacterial Strains Enhygromyxa salina SWB005 and SWB007. <b>2018</b> , 6,	7
1064	Draft Genome Sequence of the Fish Pathogen Flavobacterium columnare Genomovar III Strain PH-97028 (=CIP 109753). <b>2018</b> , 6,	2
1063	Clinical and Bacteriologic Analysis of Nontypeable Haemophilus influenzae Strains Isolated from Children with Invasive Diseases in Japan from 2008 to 2015. <b>2018</b> , 56,	13
1062	Invasive Methicillin-Resistant Staphylococcus aureus USA500 Strains from the U.S. Emerging Infections Program Constitute Three Geographically Distinct Lineages. <b>2018</b> , 3,	23
1061	Single-cell metagenomics: challenges and applications. <b>2018</b> , 9, 501-510	41
1060	Genome biology of a novel lineage of planctomycetes widespread in anoxic aquatic environments. <b>2018</b> , 20, 2438-2455	23
1059	Whole-genome comparison of high and low virulent Staphylococcus aureus isolates inducing implant-associated bone infections. <b>2018</b> , 308, 505-513	8
1058	Identification of large cryptic plasmids in Clostridioides (Clostridium) difficile. 2018, 96-97, 25-38	12
1057	Reevaluation of the Complete Genome Sequence of Magnetospirillum gryphiswaldense MSR-1 with Single-Molecule Real-Time Sequencing Data. <b>2018</b> , 6,	12
1056	Emergence of High-Level Colistin Resistance in an Acinetobacter baumannii Clinical Isolate Mediated by Inactivation of the Global Regulator H-NS. <b>2018</b> , 62,	24
1055	Carbapenem-Resistant Hypervirulent Klebsiella pneumoniae of Sequence Type 36. <b>2018</b> , 62,	43
1054	Draft Genome Sequence of Bacillus sp. Strain M21, Isolated from the Arid Area of Matmata, Tunisia. <b>2018</b> , 6,	1
1053	Whole-Genome Sequencing of Aggregatibacter Species Isolated from Human Clinical Specimens and Description of Aggregatibacter kilianii sp. nov. <b>2018</b> , 56,	14
1052	Comparative genomic analysis of the 'pseudofungus'. <b>2018</b> , 8,	20

1051 Draft Genome Sequence of the Endophyte sp. Strain GM2FR Isolated from. <b>2018</b> , 6,	2
1050 Low genomic diversity of Legionella pneumophila within clinical specimens. <b>2018</b> , 24, 1020.e1-10	020.e4 3
Sequence analysis-based characterization and identification of neurovirulence-associated varian of 36 EV71 strains from China. <b>2018</b> , 90, 1310-1317	ts 2
Genome Sequence of Coxiella-Like Endosymbiont Strain CLE-RmD, a Bacterial Agent in the Cattl Tick (Rhipicephalus microplus) Deutsch Strain. <b>2018</b> , 6,	<b>e</b> 6
Community-led comparative genomic and phenotypic analysis of the aquaculture pathogen Pseudomonas baetica a390T sequenced by Ion semiconductor and Nanopore technologies. <b>2018</b> 365,	<b>3,</b> 10
Draft Genome Sequence of sp. Strain ISTPL4, a Psychrotolerant and Halotolerant Bacterium Isolated from Pangong Lake, India. <b>2018</b> , 6,	9
Microbial community and metagenome dynamics during biodegradation of dispersed oil reveals potential key-players in cold Norwegian seawater. <b>2018</b> , 129, 370-378	47
A Single-Nucleotide Insertion in a Drug Transporter Gene Induces a Thermotolerance Phenotype Gluconobacter frateurii by Increasing the NADPH/NADP Ratio via Metabolic Change. <b>2018</b> , 84,	e in 11
Draft Genome Sequence of Methylocella silvestris TVC, a Facultative Methanotroph Isolated fro Permafrost. <b>2018</b> , 6,	m 6
1042 Draft Genome Sequences of Novel , , and [corrected] Strains from a Freshwater Ecosystem. <b>2018</b>	<b>3</b> , 6, 2
The human clone ST22 SCCmec IV methicillin-resistant Staphylococcus aureus isolated from swir herds and wild primates in Nepal: is man the common source?. <b>2018</b> , 94,	ne <sub>16</sub>
GraftM: a tool for scalable, phylogenetically informed classification of genes within metagenom <b>2018</b> , 46, e59	es. 74
Culture of the Insect Endosymbiont Highlights Bacterial Genes Involved in Host-Symbiont Interaction. <b>2018</b> , 9,	35
$_{f 103}8$ Finished Genome Sequence of a Polyurethane-Degrading Pseudomonas Isolate. <b>2018</b> , 6,	o
Metagenomic insight into methanogenic reactors promoting direct interspecies electron transfervia granular activated carbon. <b>2018</b> , 259, 414-422	er 75
1036 Genome variation in nine co-occurring toxic Cylindrospermopsis raciborskii strains. <b>2018</b> , 73, 157	7-166 24
A Novel Glaesserella sp. Isolated from Pigs with Severe Respiratory Infections Has a Mosaic Genome with Virulence Factors Putatively Acquired by Horizontal Transfer. <b>2018</b> , 84,	4
Heterogeneous Antimicrobial Susceptibility Characteristics in Isolates from Cystic Fibrosis Patien 2018, 3,	nts.

1033	Resolving the complete genome of Kuenenia stuttgartiensis from a membrane bioreactor enrichment using Single-Molecule Real-Time sequencing. <b>2018</b> , 8, 4580	27
1032	Comparative analysis of Campylobacter isolates from wild birds and chickens using MALDI-TOF MS, biochemical testing, and DNA sequencing. <b>2018</b> , 30, 354-361	15
1031	Nutritional preferences of human gut bacteria reveal their metabolic idiosyncrasies. 2018, 3, 514-522	119
1030	genome evolution during persistence in the human airways in chronic obstructive pulmonary disease. <b>2018</b> , 115, E3256-E3265	40
1029	Landscape-Scale Factors Affecting the Prevalence of Escherichia coli in Surface Soil Include Land Cover Type, Edge Interactions, and Soil pH. <b>2018</b> , 84,	17
1028	Rapid Global Spread of wRi-like Wolbachia across Multiple Drosophila. <b>2018</b> , 28, 963-971.e8	79
1027	Discovery of new type I toxin-antitoxin systems adjacent to CRISPR arrays in Clostridium difficile. <b>2018</b> , 46, 4733-4751	24
1026	Whole genome sequence and phenotypic characterization of a Cbm serotype e strain of Streptococcus mutans. <b>2018</b> , 33, 257-269	3
1025	Heavy Metal Susceptibility of Escherichia coli Isolated from Urine Samples from Sweden, Germany, and Spain. <b>2018</b> , 62,	14
1024	Microbiome Dynamics in a Large Artificial Seawater Aquarium. <b>2018</b> , 84,	12
1024	Microbiome Dynamics in a Large Artificial Seawater Aquarium. 2018, 84,  Reconstituting the History of Cronobacter Evolution Driven by Differentiated CRISPR Activity. 2018, 84,	12 9
1023	Reconstituting the History of Cronobacter Evolution Driven by Differentiated CRISPR Activity. <b>2018</b>	
1023	Reconstituting the History of Cronobacter Evolution Driven by Differentiated CRISPR Activity. <b>2018</b> , 84,	9
1023	Reconstituting the History of Cronobacter Evolution Driven by Differentiated CRISPR Activity. 2018, 84,  Draft Genome Sequence of sp. Strain ANT_B65, Isolated from Antarctic Marine Sponge. 2018, 6,  Effect of residual doxycycline concentrations on resistance selection and transfer in porcine	9
1023	Reconstituting the History of Cronobacter Evolution Driven by Differentiated CRISPR Activity. 2018, 84,  Draft Genome Sequence of sp. Strain ANT_B65, Isolated from Antarctic Marine Sponge. 2018, 6,  Effect of residual doxycycline concentrations on resistance selection and transfer in porcine commensal Escherichia coli. 2018, 51, 123-127  High Rates of Human Fecal Carriage of mcr-1-Positive Multidrug-Resistant Enterobacteriaceae	9 0 8
1023 1022 1021	Reconstituting the History of Cronobacter Evolution Driven by Differentiated CRISPR Activity. 2018, 84,  Draft Genome Sequence of sp. Strain ANT_B65, Isolated from Antarctic Marine Sponge. 2018, 6,  Effect of residual doxycycline concentrations on resistance selection and transfer in porcine commensal Escherichia coli. 2018, 51, 123-127  High Rates of Human Fecal Carriage of mcr-1-Positive Multidrug-Resistant Enterobacteriaceae Emerge in China in Association With Successful Plasmid Families. 2018, 66, 676-685  Vancomycin-resistant enterococci isolates colonizing and infecting haematology patients: clonality,	9 0 8 41
1023 1022 1021 1020	Reconstituting the History of Cronobacter Evolution Driven by Differentiated CRISPR Activity. 2018, 84,  Draft Genome Sequence of sp. Strain ANT_B65, Isolated from Antarctic Marine Sponge. 2018, 6,  Effect of residual doxycycline concentrations on resistance selection and transfer in porcine commensal Escherichia coli. 2018, 51, 123-127  High Rates of Human Fecal Carriage of mcr-1-Positive Multidrug-Resistant Enterobacteriaceae Emerge in China in Association With Successful Plasmid Families. 2018, 66, 676-685  Vancomycin-resistant enterococci isolates colonizing and infecting haematology patients: clonality, and virulence and resistance profile. 2018, 99, 346-355  Diagnostics for Yaws Eradication: Insights From Direct Next-Generation Sequencing of Cutaneous	9 0 8 41 8

1015	Microbiome and infectivity studies reveal complex polyspecies tree disease in Acute Oak Decline. <b>2018</b> , 12, 386-399	46
1014	Planctomycetes attached to algal surfaces: Insight into their genomes. <b>2018</b> , 110, 231-238	30
1013	panX: pan-genome analysis and exploration. <b>2018</b> , 46, e5	125
1012	Tropical soils are a reservoir for fluorescent Pseudomonas spp. biodiversity. <b>2018</b> , 20, 62-74	15
1011	A fatal outbreak of ST11 carbapenem-resistant hypervirulent Klebsiella pneumoniae in a Chinese hospital: a molecular epidemiological study. <b>2018</b> , 18, 37-46	365
1010	Nutrient and acetate amendment leads to acetoclastic methane production and microbial community change in a non-producing Australian coal well. <b>2018</b> , 11, 626-638	15
1009	Tremblaya phenacola PPER: an evolutionary beta-gammaproteobacterium collage. <b>2018</b> , 12, 124-135	11
1008	Analysis of the prophages carried by human infecting isolates provides new insight into the evolution of Group B Streptococcus species. <b>2018</b> , 24, 514-521	14
1007	selection of a multidrug-resistant during medicinal leech therapy. <b>2018</b> , 21, 23-27	13
1006	Genome and Methylome Variation in Helicobacter pylori With a cag Pathogenicity Island During Early Stages of Human Infection. <b>2018</b> , 154, 612-623.e7	25
1005	Frequency and Mechanisms of Spontaneous Fosfomycin Nonsusceptibility Observed upon Disk Diffusion Testing of Escherichia coli. <b>2018</b> , 56,	23
1004	Complete genome sequence of Granulosicoccus antarcticus type strain IMCC3135, a marine gammaproteobacterium with a putative dimethylsulfoniopropionate demethylase gene. <b>2018</b> , 37, 176-181	15
1003	Integration of Comparative Genomics with Genome-Scale Metabolic Modeling to Investigate Strain-Specific Phenotypical Differences. <b>2018</b> , 1716, 151-175	4
1002	Lactococcus lactis Diversity in Undefined Mixed Dairy Starter Cultures as Revealed by Comparative Genome Analyses and Targeted Amplicon Sequencing of. <b>2018</b> , 84,	16
1001	Metabolic Network Reconstruction and Modeling. 2018,	1
1000	Complete genome of Halomonas aestuarii Hb3, isolated from tidal flat. <b>2018</b> , 37, 43-45	2
999	Biofilm formation, pigment production and motility in Pseudomonas spp. isolated from the dairy industry. <b>2018</b> , 86, 241-248	43
998	Molecular Characterization of an Endozoicomonas-Like Organism Causing Infection in the King Scallop (Pecten maximus L.). <b>2018</b> , 84,	13

997	Multi-omics Reveals the Lifestyle of the Acidophilic, Mineral-Oxidizing Model Species Leptospirillum ferriphilum. <b>2018</b> , 84,	60
996	High Prevalence and Genetic Diversity of Large phiCD211 (phiCDIF1296T)-Like Prophages in Clostridioides difficile. <b>2018</b> , 84,	15
995	Invasive Disease Caused Simultaneously by Dual Serotypes of Streptococcus pneumoniae. 2018, 56,	4
994	Insights from the Genomes of Microbes Thriving in Uranium-Enriched Sediments. <b>2018</b> , 75, 970-984	9
993	Catabolic task division between two near-isogenic subpopulations co-existing in a herbicide-degrading bacterial consortium: consequences for the interspecies consortium metabolic model. <b>2018</b> , 20, 85-96	11
992	Bacteriophages. 2018,	5
991	Mutualism between SGM 81 and in modulating root plasticity and rhizospheric bacterial density. <b>2018</b> , 424, 273-288	16
990	Essential Steps in Characterizing Bacteriophages: Biology, Taxonomy, and Genome Analysis. <b>2018</b> , 1681, 197-215	15
989	Genetic diversity, mobilisation and spread of the yersiniabactin-encoding mobile element ICEKp in Klebsiella pneumoniae populations. <b>2018</b> , 4,	106
988	From plants to nematodes: Serratia grimesii BXF1 genome reveals an adaptation to the modulation of multi-species interactions. <b>2018</b> , 4,	7
987	Draft Genome Sequence of " Moanabacter tarae," Representing a Novel Marine Verrucomicrobial Lineage. <b>2018</b> , 7,	1
986	Draft Genome Sequence of Bacillus anthracis Strain Sterne 09RA8929. <b>2018</b> , 7,	1
985	Complete Genome Sequences of Historic Clostridioides difficile Food-Dwelling Ribotype 078 Strains in Canada Identical to That of the Historic Human Clinical Strain M120 in the United Kingdom. <b>2018</b> , 7,	7
984	Draft Genome Sequence of " Spirobacillus cienkowskii," a Pathogen of Freshwater Species, Reconstructed from Hemolymph Metagenomic Reads. <b>2018</b> , 7,	4
983	The Phylogenomic Diversity of Herbivore-Associated spp. Is Correlated to Lignocellulose-Degrading Potential. <b>2018</b> , 3,	18
982	Complete Genome Sequence of the Multidrug-Resistant Neonatal Meningitis Escherichia coli Serotype O75:H5:K1 Strain mcjchv-1 (NMEC-O75). <b>2018</b> , 7,	5
981	Genomic epidemiology of meticillin-resistant ST22 widespread in communities of the Gaza Strip, 2009. <b>2018</b> , 23,	8
980	Complete Genome Sequences of Bordetella pertussis Clinical Isolate FR5810 and Reference Strain Tohama from Combined Oxford Nanopore and Illumina Sequencing. <b>2018</b> , 7,	5

979	Microbial biodegradation of biuret: defining biuret hydrolases within the isochorismatase superfamily. <b>2018</b> , 20, 2099-2111	6
978	Draft Whole-Genome Sequences of 10 Atypical Enteropathogenic Escherichia coli Strains Isolated in Brazil. <b>2018</b> , 7,	1
977	Genomic Analysis of sp. Br-6, a Bromate Reducing Bacterium Isolated From Soil in Chiba, Japan. <b>2018</b> , 6, 122-126	
976	Final report of ENGAGE - Establishing Next Generation sequencing Ability for Genomic analysis in Europe. <b>2018</b> , 15, 1431E	10
975	Draft Genome Sequence of Mycobacterium parafortuitum Strain P7335. <b>2018</b> , 7,	1
974	Draft Whole-Genome Sequences of Five Klebsiella pneumoniae Isolates from the Subantarctic Islands of New Zealand. <b>2018</b> , 7,	3
973	Complete Genome Sequence of Ferriphaselus amnicola Strain OYT1, a Neutrophilic, Stalk-Forming, Iron-Oxidizing Bacterium. <b>2018</b> , 7,	3
972	Whole-Genome Sequences of Corynebacterium macginleyi CCUG 32361 and Clinical Isolates NML 080212 and NML 120205. <b>2018</b> , 7,	1
971	Draft Genome Sequence of "Bathyarchaeota" Archaeon BE326-BA-RLH, an Uncultured Denitrifier and Putative Anaerobic Methanotroph from South Africa's Deep Continental Biosphere. <b>2018</b> , 7,	8
970	Sputum strains exhibit diversity within and between COPD subjects. <b>2018</b> , 13, 3663-3667	2
969	Draft Genome Sequences of Violacein-Producing Duganella sp. Isolates from a Waterway in Eastern Pennsylvania. <b>2018</b> , 7,	4
968	Draft Genome Sequence of Dyella sp. Strain C9, Isolated from a Malaysian Tropical Peat Swamp Forest. <b>2018</b> , 7,	1
967	Draft Genome Sequence of Mycobacterium shimoidei Strain P7336. <b>2018</b> , 7,	
966	Draft Genome Sequence of Lactobacillus kefiri SGL 13, a Potential Probiotic Strain Isolated from Kefir Grains. <b>2018</b> , 7,	3
965	Draft Genome Sequence of the Shrimp Pathogen Vibrio parahaemolyticus ST17.P5-S1, Isolated in Peninsular Malaysia. <b>2018</b> , 7,	3
964	Complete Genome Sequence of Marinobacter flavimaris LMG 23834, Which Is Potentially Useful in Bioremediation. <b>2018</b> , 6,	3
963	Draft Genome Sequence of Staphylococcus aureus Strain HD1410, Isolated from a Persistent Nasal Carrier. <b>2018</b> , 6,	3
962	Read cloud sequencing elucidates microbiome dynamics in a hematopoietic cell transplant patient. <b>2018</b> , 2018, 234-241	Ο

961	Genome Sequencing and Pan-Genome Analysis of 23 Strains Reveal Unexpected Diversity, With Particular Plasticity of Predatory Gene Sets. <b>2018</b> , 9, 3187	40
960	The Integrative Conjugative Element (ICEclc) of JB2. <b>2018</b> , 9, 1532	7
959	Genotypes and Phenotypes of Enterococci Isolated From Broiler Chickens. 2018, 2,	16
958	Whole genome sequencing for investigations of meningococcal outbreaks in the United States: a retrospective analysis. <b>2018</b> , 8, 15803	12
957	Draft Genome Sequence of Paucibacter aquatile CR182, a Strain with Antimicrobial Activity Isolated from Freshwater of Nakdong River in South Korea. <b>2018</b> , 6,	1
956	Whole-Genome Sequences of Propionibacterium australiense NML (LCDC) 98A072 and NML (LCDC) 98A078, Associated with Granulomatous Bovine Lesions. <b>2018</b> , 7,	1
955	A phylogenetic and evolutionary analysis of antimycin biosynthesis. 2018, 164, 28-39	24
954	Complete Genome Sequence of Bacillus megaterium Strain TG1-E1, a Plant Drought Tolerance-Enhancing Bacterium. <b>2018</b> , 7,	3
953	Genome analysis of clinical multilocus sequence Type 11 Klebsiella pneumoniae from China. <b>2018</b> , 4,	30
952	. 2018,	13
952 951	. 2018,  Genome-wide identification of geographical segregated genetic markers in Salmonella enterica serovar Typhimurium variant 4,[5],12:i:. 2018, 8, 15251	13 16
	Genome-wide identification of geographical segregated genetic markers in Salmonella enterica	
951	Genome-wide identification of geographical segregated genetic markers in Salmonella enterica serovar Typhimurium variant 4,[5],12:i:. <b>2018</b> , 8, 15251  Equine Methicillin-Resistant Sequence Type 398 (MRSA) Harbor Mobile Genetic Elements	16
951	Genome-wide identification of geographical segregated genetic markers in Salmonella enterica serovar Typhimurium variant 4,[5],12:i:. 2018, 8, 15251  Equine Methicillin-Resistant Sequence Type 398 (MRSA) Harbor Mobile Genetic Elements Promoting Host Adaptation. 2018, 9, 2516  Whole genome sequencing analysis of multiple Salmonella serovars provides insights into phylogenetic relatedness, antimicrobial resistance, and virulence markers across humans, food	16 18
951 950 949	Genome-wide identification of geographical segregated genetic markers in Salmonella enterica serovar Typhimurium variant 4,[5],12:i:. 2018, 8, 15251  Equine Methicillin-Resistant Sequence Type 398 (MRSA) Harbor Mobile Genetic Elements Promoting Host Adaptation. 2018, 9, 2516  Whole genome sequencing analysis of multiple Salmonella serovars provides insights into phylogenetic relatedness, antimicrobial resistance, and virulence markers across humans, food animals and agriculture environmental sources. 2018, 19, 801  Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic	16 18 61
951 950 949 948	Genome-wide identification of geographical segregated genetic markers in Salmonella enterica serovar Typhimurium variant 4,[5],12:i:. 2018, 8, 15251  Equine Methicillin-Resistant Sequence Type 398 (MRSA) Harbor Mobile Genetic Elements Promoting Host Adaptation. 2018, 9, 2516  Whole genome sequencing analysis of multiple Salmonella serovars provides insights into phylogenetic relatedness, antimicrobial resistance, and virulence markers across humans, food animals and agriculture environmental sources. 2018, 19, 801  Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic profiles in idiopathic travelers' diarrhea. 2018, 6, 201  Dissemination of Genetic Acquisition/Loss Provides a Variety of Quorum Sensing Regulatory	16 18 61
951 950 949 948 947	Genome-wide identification of geographical segregated genetic markers in Salmonella enterica serovar Typhimurium variant 4,[5],12:i:. 2018, 8, 15251  Equine Methicillin-Resistant Sequence Type 398 (MRSA) Harbor Mobile Genetic Elements Promoting Host Adaptation. 2018, 9, 2516  Whole genome sequencing analysis of multiple Salmonella serovars provides insights into phylogenetic relatedness, antimicrobial resistance, and virulence markers across humans, food animals and agriculture environmental sources. 2018, 19, 801  Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic profiles in idiopathic travelers' diarrhea. 2018, 6, 201  Dissemination of Genetic Acquisition/Loss Provides a Variety of Quorum Sensing Regulatory Properties in Pseudoalteromonas. 2018, 19,  Characterization of Staphylococcal Cassette Chromosome Elements from Methicillin-Resistant	16 18 61 10

943	Global emergence and population dynamics of divergent serotype 3 CC180 pneumococci. 2018, 14, e1007438	37
942	Complete Genome Sequence of an O121:H19 Strain from an Outbreak in Canada Associated with Flour. <b>2018</b> , 6,	5
941	Machine Learning Reveals Missing Edges and Putative Interaction Mechanisms in Microbial Ecosystem Networks. <b>2018</b> , 3,	21
940	Genomic Analysis of the Recent Viral Isolate vB_BthP-Goe4 Reveals Increased Diversity of <b>2</b> 9-Like Phages. <b>2018</b> , 10,	6
939	Examination of Australian Streptococcus suis isolates from clinically affected pigs in a global context and the genomic characterisation of ST1 as a predictor of virulence. <b>2018</b> , 226, 31-40	11
938	Comparative genomic and functional analyses of four sequenced Bacillus cereus genomes reveal conservation of genes relevant to plant-growth-promoting traits. <b>2018</b> , 8, 17009	21
937	The Enterococcus Cassette Chromosome, a Genomic Variation Enabler in Enterococci. 2018, 3,	4
936	Genome-wide analysis of Streptococcus pneumoniae serogroup 19 in the decade after the introduction of pneumococcal conjugate vaccines in Australia. <b>2018</b> , 8, 16969	6
935	Complete Genome Sequence of Avian Pathogenic Escherichia coli Strain APEC O2-211. <b>2018</b> , 7,	3
934	Whole-genome epidemiology, characterisation, and phylogenetic reconstruction of Staphylococcus aureus strains in a paediatric hospital. <b>2018</b> , 10, 82	30
933	Metagenomics-Based, Strain-Level Analysis of From a Time-Series of Microbiome Samples From a Crohn's Disease Patient. <b>2018</b> , 9, 2559	24
932	Genome Sequence Analysis of Two Pseudomonas putida Strains to Identify a 17-Hydroxylase Putatively Involved in Sparteine Degradation. <b>2018</b> , 75, 1649-1654	1
931	Genomes of Escherichia coli bacteraemia isolates originating from urinary tract foci contain more virulence-associated genes than those from non-urinary foci and neutropaenic hosts. <b>2018</b> , 77, 534-543	7
930	Comparative genomic and methylome analysis of non-virulent D74 and virulent Nagasaki Haemophilus parasuis isolates. <b>2018</b> , 13, e0205700	4
929	Pulmonary Isolation of Multidrug resistant "Mycobacterium simulans" and Mycobacterium tuberculosis from a patient in the Horn of Africa. <b>2018</b> , 8, 15341	
928	Whole-Genome Sequence of the First Extended-Spectrum Lactamase-Producing Strain of Salmonella enterica subsp. enterica Serovar Napoli. <b>2018</b> , 7,	10
927	Genome Sequence of the Soybean Cyst Nematode (Heterodera glycines) Endosymbiont "Candidatus Cardinium hertigii" Strain cHgTN10. <b>2018</b> , 6,	5
926	Proteotyping bacteria: Characterization, differentiation and identification of pneumococcus and other species within the Mitis Group of the genus Streptococcus by tandem mass spectrometry proteomics. <b>2018</b> , 13, e0208804	18

925	Single cell genomic and transcriptomic evidence for the use of alternative nitrogen substrates by anammox bacteria. <b>2018</b> , 12, 2706-2722	25
924	Draft Genome Sequences of Three Novel Staphylococcus arlettae Strains Isolated from a Disused Biological Safety Cabinet. <b>2018</b> , 7,	3
923	Complete Genome Sequence of Salmonella enterica subsp. enterica Serotype Derby, Associated with the Pork Sector in France. <b>2018</b> , 7,	4
922	Complete Genome Sequence of Streptococcus agalactiae Serotype III, Multilocus Sequence Type 335 Strain HU-GS5823, Isolated from a Human Patient in Japan with Severe Invasive Infection. <b>2018</b> , 7,	2
921	Complete Genome Sequences of the Potential Zoonotic Pathogens Staphylococcus felis and Staphylococcus kloosii. <b>2018</b> , 6,	4
920	Draft Genome Sequence of NBRC 113063, Isolated from Kľko, a Japanese Sugar-Vegetable Fermented Beverage. <b>2018</b> , 7,	O
919	Whole Genome Characterization of (OPV) Abatino, a Zoonotic Virus Representing a Putative Novel Clade of Old World Orthopoxviruses. <b>2018</b> , 10,	9
918	Antimicrobial Susceptibility and Genomic Structure of Isolates. <b>2018</b> , 9, 3067	8
917	Genome Sequences and Comparative Analysis of Two Extended-Spectrum Extensively-Drug Resistant Strains. <b>2018</b> , 9, 1492	
916	A Novel Inorganic Sulfur Compound Metabolizing -Like Population Is Suggested to Mediate Extracellular Electron Transfer. <b>2018</b> , 9, 2945	5
915	High-Quality Draft Genome Sequence of sp. Strain CPBF 424, a Walnut-Pathogenic Strain with Atypical Features. <b>2018</b> , 7,	6
914	Draft Whole-Genome Sequences of Seven Isolates of Klebsiella pneumoniae from New Zealand Sea Lions. <b>2018</b> , 7,	3
913	Draft Genome Sequence of the Thermophilic Acetogen DSM 23265. <b>2018</b> , 6,	2
912	Draft Genome Sequence of Lactococcus sp. Strain NtB2 (JCM 32569), Isolated from the Gut of the Higher Termite Nasutitermes takasagoensis. <b>2018</b> , 6,	2
911	Draft Genome Sequence of Klebsiella sp. Strain C31 Isolated from a Malaysian Tropical Peat Swamp Forest. <b>2018</b> , 6,	
910	Draft Genome Sequence of Dyella sp. Strain C11, Isolated from a Malaysian Tropical Peat Swamp Forest. <b>2018</b> , 6,	1
909	High-Quality Draft Genome Sequence of Xanthomonas arboricola pv. juglandis CPBF 1521, Isolated from Leaves of a Symptomatic Walnut Tree in Portugal without a Past of Phytosanitary Treatment. <b>2018</b> , 7,	3
908	TIR-Domain Genes Are Part of a Gene Cluster Which Promotes Bacterial Survival in Blood. <b>2018</b> , 2018, 1435820	2

907	Finer-Scale Phylosymbiosis: Insights from Insect Viromes. <b>2018</b> , 3,	15
906	Investigating locally relevant risk factors for infection in Australia: protocol for a case-control study and genomic analysis. <b>2018</b> , 8, e026630	4
905	Draft Genome Sequence of Mariprofundus micogutta Strain ET2. <b>2018</b> , 6,	2
904	Long-Read-Based Genome Sequences of Pandemic and Environmental Vibrio cholerae Strains. <b>2018</b> , 7,	11
903	Species Designations Belie Phenotypic and Genotypic Heterogeneity in Oral Streptococci. 2018, 3,	19
902	Chemical Synergy between Ionophore PBT2 and Zinc Reverses Antibiotic Resistance. <b>2018</b> , 9,	31
901	Evolution of the Population Structure of in France. <b>2018</b> , 9, 3055	16
900	Genome Mining of sp. YIM 130001 Isolated From Lichen Affords New Thiopeptide Antibiotic. <b>2018</b> , 9, 3139	17
899	Update on Tetracycline Susceptibility of Pediococcus acidilactici Based on Strains Isolated from Swiss Cheese and Whey. <b>2018</b> , 81, 1582-1589	7
898	Effect of Vaccination on Pneumococci Isolated from the Nasopharynx of Healthy Children and the Middle Ear of Children with Otitis Media in Iceland. <b>2018</b> , 56,	19
897	Complement Susceptibility in Relation to Genome Sequence of Recent Klebsiella pneumoniae Isolates from Thai Hospitals. <b>2018</b> , 3,	9
896	Gut colonization by a novel Clostridium species is associated with the onset of epizootic rabbit enteropathy. <b>2018</b> , 49, 123	6
895	Transcriptional Landscape of a Plasmid and Response to Imipenem Exposure in TOP10. <b>2018</b> , 9, 2929	6
894	Microevolution of Neisseria lactamica during nasopharyngeal colonisation induced by controlled human infection. <b>2018</b> , 9, 4753	18
893	Draft Genome Sequence of Taylorella equigenitalis Strain 210217RC10635, Isolated from a Pony Stallion in Germany. <b>2018</b> , 7,	1
892	Complete Genome Sequence of Lactobacillus reuteri Byun-re-01, Isolated from Mouse Small Intestine. <b>2018</b> , 7,	1
891	Genomic Analysis of Consecutive Strains From a Single Patient. <b>2018</b> , 9, 2840	5
890	First Insights into the Draft Genome Sequence of the Endophyte Strain GM1FR, Isolated from L. <b>2018</b> , 6,	2

889	Population Structure, Antibiotic Resistance, and Uropathogenicity of Klebsiella variicola. 2018, 9,	34
888	Carbapenemases on the move: it's good to be on ICEs. <b>2018</b> , 9, 37	23
887	Formation of functional, non-amyloidogenic fibres by recombinant Bacillus subtilis TasA. <b>2018</b> , 110, 897-913	20
886	Acquisition and Loss of CTX-M-Producing and Non-Producing Escherichia coli in the Fecal Microbiome of Travelers to South Asia. <b>2018</b> , 9,	13
885	EMBLmyGFF3: a converter facilitating genome annotation submission to European Nucleotide Archive. <b>2018</b> , 11, 584	10
884	Wild bees and their nests host Paenibacillus bacteria with functional potential of avail. <b>2018</b> , 6, 229	14
883	Draft Genome Sequence of Strain NIT02, Isolated from a Laundered Rental Cloth Hot Towel. <b>2018</b> , 6,	0
882	Complete Genome Sequence of WM99c, an Antibiotic-Resistant Acinetobacter baumannii Global Clone 2 (GC2) Strain Representing an Australian GC2 Lineage. <b>2018</b> , 7,	2
881	Prediction of antibiotic resistance in Escherichia coli from large-scale pan-genome data. <b>2018</b> , 14, e1006258	69
880	Antimicrobial resistance prediction and phylogenetic analysis of Neisseria gonorrhoeae isolates using the Oxford Nanopore MinION sequencer. <b>2018</b> , 8, 17596	41
879	The phylogeography and incidence of multi-drug resistant typhoid fever in sub-Saharan Africa. <b>2018</b> , 9, 5094	53
878	USA300 Staphylococcus aureus persists on multiple body sites following an infection. <b>2018</b> , 18, 206	10
877	Draft Genome Sequences of Phenotypically Distinct sp. Isolates Cultured from the Hudson Valley Watershed. <b>2018</b> , 6,	3
876	High frequency of hybrid Escherichia coli strains with combined Intestinal Pathogenic Escherichia coli (IPEC) and Extraintestinal Pathogenic Escherichia coli (ExPEC) virulence factors isolated from human faecal samples. <b>2018</b> , 18, 544	24
875	DNA Sequence Assembly and Annotation of Genes. <b>2018</b> , 9-24	
874	Complete Genome Sequence of Vitreoscilla sp. Strain C1, Source of the First Bacterial Hemoglobin. <b>2018</b> , 7,	1
873	Genome-wide comparison of Corynebacterium diphtheriae isolates from Australia identifies differences in the Pan-genomes between respiratory and cutaneous strains. <b>2018</b> , 19, 869	10
872	Comparative Genomics of Reveals Determinants of Speciation and Diversification of Antimicrobial Defense. <b>2018</b> , 9, 2753	12

## (2018-2018)

871	Co-culture of a Novel Fermentative Bacterium, gen. nov. sp. nov., With the Sulfur Reducer for Enhanced Sulfidogenesis. <b>2018</b> , 9, 3108	10
870	Comparative Genomic Analysis of Members of the Genera and Reveals Distinct Clades with Specific Potential Metabolic Functions. <b>2018</b> , 2018, 7609847	9
869	Functional shifts in microbial mats recapitulate early Earth metabolic transitions. 2018, 2, 1700-1708	21
868	Novel lipooligosaccharide is a determinant of inflammatory potential and virulence. <b>2018</b> , 59, 1893-1905	2
867	Active Crossfire Between Cyanobacteria and Cyanophages in Phototrophic Mat Communities Within Hot Springs. <b>2018</b> , 9, 2039	11
866	Genetic repertoires of anaerobic microbiomes driving generation of biogas. <b>2018</b> , 11, 255	5
865	Unveiling the Multilocus Sequence Typing (MLST) Schemes and Core Genome Phylogenies for Genotyping. <b>2018</b> , 9, 1854	13
864	Revisiting the Taxonomy of the Genus : Getting Order From the Chaos. <b>2018</b> , 9, 2077	66
863	Variant O89 O-Antigen of Is Associated With Group 1 Capsule Loci and Multidrug Resistance. <b>2018</b> , 9, 2026	5
862	Functional Analysis of Methylomonas sp. DH-1 Genome as a Promising Biocatalyst for Bioconversion of Methane to Valuable Chemicals. <b>2018</b> , 8, 117	18
861	Genetic structure of four plasmids found in Acinetobacter baumannii isolate D36 belonging to lineage 2 of global clone 1. <b>2018</b> , 13, e0204357	16
860	Association between possession of ExoU and antibiotic resistance in Pseudomonas aeruginosa. <b>2018</b> , 13, e0204936	24
859	Genomes from uncultivated prokaryotes: a comparison of metagenome-assembled and single-amplified genomes. <b>2018</b> , 6, 173	43
858	Complete Genome Sequence of Geobacter sulfurreducens Strain YM18, Isolated from River Sediment in Japan. <b>2018</b> , 6,	2
857	, a New Species Acquired Carbapenem Resistance. <b>2018</b> , 9, 2170	8
856	Transcriptional and Functional Analysis of Bifidobacterium animalis subsp. lactis Exposure to Tetracycline. <b>2018</b> , 84,	12
855	Complete Genome Sequence of Acidithiobacillus ferridurans JCM 18981. <b>2018</b> , 7,	4
854	Five novel carbapenem-hydrolysing OXA-type Elactamase groups are intrinsic in Acinetobacter spp. <b>2018</b> , 73, 3279-3284	5

853	Draft Genome Sequence of "Candidatus Phycosocius bacilliformis," an Alphaproteobacterial Ectosymbiont of the Hydrocarbon-Producing Green Alga Botryococcus braunii. <b>2018</b> , 6,	О
852	Complete Genome Sequence of a -Positive Klebsiella pneumoniae Strain Isolated from the Effluent of an Urban Sewage Treatment Plant in Japan. <b>2018</b> , 3,	28
851	A metagenomics roadmap to the uncultured genome diversity in hypersaline soda lake sediments. <b>2018</b> , 6, 168	59
850	Comparison of Highly and Weakly Virulent Strains, With a View on the Pangenome and Panregulon of This Species. <b>2018</b> , 9, 1940	22
849	Discovering novel hydrolases from hot environments. <b>2018</b> , 36, 2077-2100	27
848	Complete Genome Sequence and Characterization of Linezolid-Resistant Clinical Isolate KUB3006 Carrying a (B)-Transposon on Its Chromosome and -Plasmid. <b>2018</b> , 9, 2576	19
847	WGS analysis of a penicillin-resistant Neisseria meningitidis strain containing a chromosomal ROB-1 Elactamase gene. <b>2019</b> , 74, 22-28	9
846	An Introduced Crop Plant Is Driving Diversification of the Virulent Bacterial Pathogen Erwinia tracheiphila. <b>2018</b> , 9,	16
845	Genes significantly associated with lineage II food isolates of Listeria monocytogenes. 2018, 19, 708	25
844	Detection of the carbapenemase gene bla in members of the Pseudomonas putida group isolated from polluted Nigerian wetlands. <b>2018</b> , 8, 15116	13
843	Genome hypermobility by lateral transduction. <b>2018</b> , 362, 207-212	103
842	Draft Genome Sequence of Komagataeibacter maltaceti LMG 1529, a Vinegar-Producing Acetic Acid Bacterium Isolated from Malt Vinegar Brewery Acetifiers. <b>2018</b> , 6,	4
841	Genomic heterogeneity differentiates clinical and environmental subgroups of Legionella pneumophila sequence type 1. <b>2018</b> , 13, e0206110	6
840	Comparative Genomics of the First and Complete Genome of "" Supports the Novel Species Hypothesis. <b>2018</b> , 2018, 5261719	6
839	Genome sequence of 4303. <b>2018</b> , 10, 47	1
838	Comparative genomics of clinical strains of Pseudomonas aeruginosa strains isolated from different geographic sites. <b>2018</b> , 8, 15668	28
837	Genetic Signatures of Dairy Group. <b>2018</b> , 9, 2611	11
836	Conversion of Methionine to Cysteine in Depends on the Highly Mobile Gene Cluster. <b>2018</b> , 9, 2415	7

835	pYR4 From a Norwegian Isolate of Is a Putative Virulence Plasmid Encoding Both a Type IV Pilus and a Type IV Secretion System. <b>2018</b> , 8, 373	7
834	A Novel Alkaliphilic Inhibits ESKAPE Pathogens. <b>2018</b> , 9, 2458	23
833	Complete genome of streamlined marine actinobacterium Pontimonas salivibrio strain CL-TW6 adapted to coastal planktonic lifestyle. <b>2018</b> , 19, 625	5
832	Hidden in plain sight-highly abundant and diverse planktonic freshwater Chloroflexi. 2018, 6, 176	47
831	Complete Genome Sequence Reveals Evolutionary Dynamics of an Emerging and Variant Pathovar of Xanthomonas euvesicatoria. <b>2018</b> , 10, 3104-3109	7
830	An investigation into the Omp85 protein BamK in hypervirulent Klebsiella pneumoniae, and its role in outer membrane biogenesis. <b>2018</b> , 109, 584-599	2
829	The transducer-like protein Tlp12 of Campylobacter jejuni is involved in glutamate and pyruvate chemotaxis. <b>2018</b> , 18, 111	8
828	from patients with chronic rhinosinusitis show minimal genetic association between polyp and non-polyp phenotypes. <b>2018</b> , 18, 16	5
827	Comparative Genomics of - Dual Endosymbiosis in a Plant-Parasitic Nematode. <b>2018</b> , 9, 2482	20
826	Comparative Genomics and Infection of Field Clonal Isolates of Biovar 3 Did Not Identify Signature of Host Adaptation. <b>2018</b> , 9, 2505	4
825	Revisiting the Taxonomic Status of the Biomedically and Industrially Important Genus , Using a Phylogenomic Approach. <b>2018</b> , 9, 2281	14
824	The Mycobacterial Cell Envelope: A Relict From the Past or the Result of Recent Evolution?. <b>2018</b> , 9, 2341	30
823	Whole-Genome Sequence of the Novel Strain SMS3, Found in Association with the Marine Diatom. <b>2018</b> , 6, 113-116	2
822	Characterization and Salt Response in Recurrent Halotolerant sp. SH31 Isolated From Sediments of Salar de Huasco, Chilean Altiplano. <b>2018</b> , 9, 2228	18
821	High-quality genome sequences of uncultured microbes by assembly of read clouds. 2018,	60
820	The Occurence of Colistin-Resistant Hypervirulent in China. <b>2018</b> , 9, 2568	24
819	Proteomic analysis of four Clostridium botulinum strains identifies proteins that link biological responses to proteomic signatures. <b>2018</b> , 13, e0205586	8
818	Genomic Characterization of TUA4408L and Evaluation of the Antiviral Activities of its Extracellular Polysaccharides in Porcine Intestinal Epithelial Cells. <b>2018</b> , 9, 2178	20

817	To B or Not to B: Comparative Genomics Suggests as a Source of B Vitamins in Whiteflies. 2018, 9, 2254	30
816	Draft Genome Sequences of Lactobacillus salivarius A3iob and Lactobacillus johnsonii CRL1647, Novel Potential Probiotic Strains for Honeybees (Apis mellifera L.). <b>2018</b> , 7,	4
815	High genomic variability in the plant pathogenic bacterium Pectobacterium parmentieri deciphered from de novo assembled complete genomes. <b>2018</b> , 19, 751	15
814	First whole genome sequencing of Russian isolate of Capnocytophaga canimorsus, opportunistic pathogen causing lethal sepsis. <b>2018</b> , 125, 493-496	
813	Complete genome sequencing of sixteen Francisella noatunensis subsp. orientalis isolates: A genomic approach for molecular characterization and spread dynamics of this clonal population. <b>2018</b> , 110, 442-449	2
812	A genomic infection control study for in two Ghanaian hospitals. <b>2018</b> , 11, 1757-1765	16
811	An Interleukin-23-Interleukin-22 Axis Regulates Intestinal Microbial Homeostasis to Protect from Diet-Induced Atherosclerosis. <b>2018</b> , 49, 943-957.e9	82
810	Draft Genome Sequence of the Butanoic Acid-Producing Bacterium Clostridium luticellarii DSM 29923, Used for Strong Aromatic Chinese Liquor Production. <b>2018</b> , 6,	8
809	Tracking key virulence loci encoding aerobactin and salmochelin siderophore synthesis in Klebsiella pneumoniae. <b>2018</b> , 10, 77	83
808	Bacillus wiedmannii biovar thuringiensis: A Specialized Mosquitocidal Pathogen with Plasmids from Diverse Origins. <b>2018</b> , 10, 2823-2833	12
807	US Immigration Westernizes the Human Gut Microbiome. <b>2018</b> , 175, 962-972.e10	296
806	Draft Genome Sequence of Strain B 225, an Iron-Depositing Isolate of the Genus Novosphingobium. <b>2018</b> , 6,	
805	Gapless, Unambiguous Genome Sequence for Escherichia coli C, a Workhorse of Industrial Biology. <b>2018</b> , 7,	2
804	Antagonistic Pleiotropy in the Bifunctional Surface Protein FadL (OmpP1) during Adaptation of Haemophilus influenzae to Chronic Lung Infection Associated with Chronic Obstructive Pulmonary Disease. <b>2018</b> , 9,	22
803	The complete genomic sequence of a novel cold-adapted bacterium, Y42, isolated from crude oil-contaminated soil. <b>2018</b> , 13, 23	9
802	The chemodiversity of paddy soil dissolved organic matter correlates with microbial community at continental scales. <b>2018</b> , 6, 187	71
801	Draft Genome Sequence of Muricauda sp. Strain K001 Isolated from a Marine Cyanobacterial Culture. <b>2018</b> , 6,	1
800	Genome-scale metabolic reconstructions of multiple Salmonella strains reveal serovar-specific metabolic traits. <b>2018</b> , 9, 3771	52

799	Carriage of blaKPC-2 by a virulence plasmid in hypervirulent Klebsiella pneumoniae. 2018, 73, 3317-3321	46
798	Burkholderia. <b>2018</b> , 1-45	5
797	Draft Genome Sequence of a Strain Isolated from the Urine of an Asymptomatic Dog in Thailand. <b>2018</b> , 6,	4
796	Draft Genome Sequence of the Endophyte Strain GM5LP Isolated from. <b>2018</b> , 6,	1
795	MetaWRAP-a flexible pipeline for genome-resolved metagenomic data analysis. <b>2018</b> , 6, 158	370
794	Draft Genome Sequence of Paraburkholderia sp. Strain C35, Isolated from a Malaysian Tropical Peat Swamp Forest. <b>2018</b> , 6,	
793	Comparative genomics of Czech vaccine strains of Bordetella pertussis. 2018, 76,	5
79 <sup>2</sup>	The changing landscape of vancomycin-resistant Enterococcus faecium in Australia: a population-level genomic study. <b>2018</b> , 73, 3268-3278	19
791	Whole genome sequencing reveals the emergence of a Pseudomonas aeruginosa shared strain sub-lineage among patients treated within a single cystic fibrosis centre. <b>2018</b> , 19, 644	10
790	Creation and Characterization of a Genomically Hybrid Strain in the Nitrogen-Fixing Symbiotic Bacterium Sinorhizobium meliloti. <b>2018</b> , 7, 2365-2378	15
789	Dynamics of microbial populations mediating biogeochemical cycling in a freshwater lake. <b>2018</b> , 6, 165	26
788	A New Freshwater Cyanosiphovirus Harboring Integrase. <b>2018</b> , 9, 2204	11
787	Complete Genome Sequence of Broad-Host-Range Shiga Toxin-Converting Bacteriophage SH2026Stx1, Isolated from Escherichia coli O157:H7. <b>2018</b> , 6,	1
786	Conserved collateral antibiotic susceptibility networks in diverse clinical strains of Escherichia coli. <b>2018</b> , 9, 3673	45
7 <sup>8</sup> 5	Role of plasmid plasticity and mobile genetic elements in the entomopathogen Bacillus thuringiensis serovar israelensis. <b>2018</b> , 42, 829-856	16
7 <sup>8</sup> 4	Novel trimethoprim resistance gene dfrA34 identified in Salmonella Heidelberg in the USA. <b>2019</b> , 74, 38-41	8
783	Genome Analysis, Metabolic Potential, and Predatory Capabilities of Herpetosiphon llansteffanense sp. nov. <b>2018</b> , 84,	16
782	Spfy: an integrated graph database for real-time prediction of bacterial phenotypes and downstream comparative analyses. <b>2018</b> , 2018, 1-10	3

781	Emergence of soil bacterial ecotypes along a climate gradient. <b>2018</b> , 20, 4112-4126	19
78o	Complete Genome Sequence of Lytic Oenococcus oeni Bacteriophage OE33PA. <b>2018</b> , 7,	5
779	Complete Genome Sequence of Escherichia coli Phage vB_EcoS Sa179lw, Isolated from Surface Water in a Produce-Growing Area in Northern California. <b>2018</b> , 6,	2
778	Unraveling the cellulolytic and hemicellulolytic potential of two novel Streptomyces strains. <b>2018</b> , 68, 677-688	3
777	Dynamics of colistin and tobramycin resistance among during prolonged use of selective decontamination of the digestive tract. <b>2018</b> , 7, 67	5
776	Comparative Secretome Analyses of Human and Zoonotic Isolates CC8, CC22, and CC398. <b>2018</b> , 17, 2412-243.	3 16
775	Genome Sequencing Reveals a Large and Diverse Repertoire of Antimicrobial Peptides. 2018, 9, 2012	15
774	Genomic Characterization of Sulphite Reducing Bacteria Isolated From the Dairy Production Chain. <b>2018</b> , 9, 1507	3
773	Comparative Genomics Reveal a Flagellar System, a Type VI Secretion System and Plant Growth-Promoting Gene Clusters Unique to the Endophytic Bacterium. <b>2018</b> , 9, 1997	23
772	Characterizing Mobilized Virulence Factors and Multidrug Resistance Genes in Carbapenemase-Producing in a Sri Lankan Hospital. <b>2018</b> , 9, 2044	9
771	ANNOgesic: a Swiss army knife for the RNA-seq based annotation of bacterial/archaeal genomes. <b>2018</b> , 7,	23
770	Global spread of three multidrug-resistant lineages of Staphylococcus epidermidis. 2018, 3, 1175-1185	120
769	First Report of an OXA-48- and CTX-M-213-Producing Kluyvera Species Clone Recovered from Patients Admitted in a University Hospital in Madrid, Spain. <b>2018</b> , 62,	15
768	A-GAME: improving the assembly of pooled functional metagenomics sequence data. <b>2018</b> , 19, 44	6
767	Genomic repeats, misassembly and reannotation: a case study with long-read resequencing of Porphyromonas gingivalis reference strains. <b>2018</b> , 19, 54	17
766	Distinct Genomic Features Characterize Two Clades of : Proposal of Subsp. Subsp. nov. and Subsp. Subsp. nov. <b>2018</b> , 9, 1743	16
765	Draft Genome Sequence of Mycobacterium porcinum CSURP1564. <b>2018</b> , 6,	2
764	Conserved Genome Organization and Core Transcriptome of the Complex. <b>2018</b> , 9, 1834	1

## (2018-2018)

763	Whole-Genome Sequencing and Bioinformatic Analysis of Isolates from Foodborne Illness Outbreaks of Campylobacter jejuni and Salmonella enterica. <b>2018</b> , 56,	16
762	Comparative genome and phenotypic analysis of three Clostridioides difficile strains isolated from a single patient provide insight into multiple infection of C. difficile. <b>2018</b> , 19, 1	226
761	Hotspot mutations and ColE1 plasmids contribute to the fitness of Salmonella Heidelberg in poultry litter. <b>2018</b> , 13, e0202286	19
760	Whole-genome sequencing enabling the detection of a colistin-resistant hypermutating Citrobacter werkmanii strain harbouring a novel metallo-Elactamase VIM-48. <b>2018</b> , 51, 867-874	8
759	Bloom of a denitrifying methanotroph, 'Candidatus Methylomirabilis limnetica', in a deep stratified lake. <b>2018</b> , 20, 2598-2614	46
758	Genomic analyses reveal two distinct lineages of strains. <b>2018</b> , 25, 7-13	12
757	First Insights into the Genome Sequence of Clostridium thermopalmarium DSM 5974, a Butyrate-Producing Bacterium Isolated from Palm Wine. <b>2018</b> , 6,	
756	Whole-Genome Sequence of Infectious Pancreatic Necrosis Virus Isolated from Farmed Brook Trout (Salvelinus fontinalis) in Pennsylvania. <b>2018</b> , 6,	5
755	American Gut: an Open Platform for Citizen Science Microbiome Research. 2018, 3,	336
754	Draft Genome Sequences of Streptomyces sp. Strains MH60 and 111WW2. <b>2018</b> , 6,	1
753	Canada-Wide Epidemic of Group A Invasive Disease. <b>2018</b> , 5, ofy085	10
75 <sup>2</sup>	Draft Genome Sequence of Riemerella anatipestifer Isolate 17CS0503. <b>2018</b> , 6,	1
751	O-Antigens of Escherichia coli Strains O81 and HS3-104 Are Structurally and Genetically Related, Except O-Antigen Glucosylation in E. coli HS3-104. <b>2018</b> , 83, 534-541	4
750	Pan-genomic approach shows insight of genetic divergence and pathogenic-adaptation of Pasteurella multocida. <b>2018</b> , 670, 193-206	16
749	Complete Closed Genome Sequence of Nontoxigenic Invasive bv. mitis Strain ISS 3319. <b>2018</b> , 6,	2
748	Metagenomic and metatranscriptomic analysis of the microbial community in Swiss-type Maasdam cheese during ripening. <b>2018</b> , 281, 10-22	40
747	Proteomic identification of Axc, a novel beta-lactamase with carbapenemase activity in a meropenem-resistant clinical isolate of Achromobacter xylosoxidans. <b>2018</b> , 8, 8181	4
746	Raphidocelis subcapitata (=Pseudokirchneriella subcapitata) provides an insight into genome evolution and environmental adaptations in the Sphaeropleales. <b>2018</b> , 8, 8058	27

745	Draft Genome Sequences of New Genomospecies "Pectobacterium maceratum" Strains, Which Cause Soft Rot in Plants. <b>2018</b> , 6,	22
744	Genomic and Geographic Context for the Evolution of High-Risk Carbapenem-Resistant Complex Clones ST171 and ST78. <b>2018</b> , 9,	31
743	Marsarchaeota are an aerobic archaeal lineage abundant in geothermal iron oxide microbial mats. <b>2018</b> , 3, 732-740	33
742	Dysbiosis of maternal and neonatal microbiota associated with gestational diabetes mellitus. <b>2018</b> , 67, 1614-1625	168
741	Long-Term, Low-Frequency Cluster of a German-Imipenemase-1-Producing Enterobacter hormaechei ssp. steigerwaltii ST89 in a Tertiary Care Hospital in Germany. <b>2018</b> , 24, 1305-1315	6
740	Phylogenetic uniqueness of Mycobacterium avium subspecies hominissuis isolated from an abnormal pulmonary bovine case. <b>2018</b> , 62, 122-129	1
739	Draft Genome Sequence of Actinobacterial Strain Kineosporia sp. R_H_3, a Neutrophilic Iron-Depositing Bacterium. <b>2018</b> , 6,	
738	Draft Genome Sequence of a Potentially Novel Streptococcus Species Belonging to the Streptococcus mitis Group. <b>2018</b> , 6,	2
737	The impact of serotype-specific vaccination on phylodynamic parameters of Streptococcus pneumoniae and the pneumococcal pan-genome. <b>2018</b> , 14, e1006966	18
736	Comparative genomics of Campylobacter concisus: Analysis of clinical strains reveals genome diversity and pathogenic potential. <b>2018</b> , 7, 116	16
735	Genus-wide comparison of Pseudovibrio bacterial genomes reveal diverse adaptations to different marine invertebrate hosts. <b>2018</b> , 13, e0194368	15
734	Draft Genome Sequence of the Hydrogenogenic Carboxydotroph Moorella stamsii DSM 26271. <b>2018</b> , 6,	3
733	Draft Genome Sequence of Moorella sp. Strain Hama-1, a Novel Acetogenic Bacterium Isolated from a Thermophilic Digestion Reactor. <b>2018</b> , 6,	3
732	Draft Genome Sequence of a Novel Bacterium, sp. Strain MR 02, Capable of Pyomelanin Production, Isolated from the Mahananda River at Siliguri, West Bengal, India. <b>2018</b> , 6,	1
731	An antifungal polyketide associated with horizontally acquired genes supports symbiont-mediated defense in Lagria villosa beetles. <b>2018</b> , 9, 2478	51
730	Sequence, genome organization, annotation and proteomics of the thermophilic, 47.7-kb Geobacillus stearothermophilus bacteriophage TP-84 and its classification in the new Tp84virus genus. <b>2018</b> , 13, e0195449	5
729	Theoretical and Applied Aspects of Systems Biology. 2018,	2
728	Long-read whole genome sequencing and comparative analysis of six strains of the human pathogen Orientia tsutsugamushi. <b>2018</b> , 12, e0006566	18

727	Computational Modeling of Multidrug-Resistant Bacteria. <b>2018</b> , 195-220	1
726	Macroevolution of gastric Helicobacter species unveils interspecies admixture and time of divergence. <b>2018</b> , 12, 2518-2531	13
725	Defining endemic cholera at three levels of spatiotemporal resolution within Bangladesh. 2018, 50, 951-955	22
724	Genomic analysis of a Raoultella ornithinolytica strain causing prosthetic joint infection in an immunocompetent patient. <b>2018</b> , 8, 9462	7
723	A novel adenovirus isolated from the Egyptian fruit bat in South Africa is closely related to recent isolates from China. <b>2018</b> , 8, 9584	8
722	Distribution of Staphylococcus species in dairy cows, workers and shared farm environments. <b>2018</b> , 365,	6
721	Draft Genome Sequence of the Novel Enterobacter cloacae Strain amazonensis, a Highly Heavy Metal-Resistant Bacterium from a Contaminated Stream in Amazonas, Brazil. <b>2018</b> , 6,	1
720	Vertical and horizontal gene transfer tradeoffs direct plasmid fitness.	Ο
719	PneumoKITy: A fast, flexible, specific, and sensitive tool for Streptococcus pneumoniae serotype screening and mixed serotype detection from genome sequence data. <b>2022</b> , 8,	0
718	Collective behavior and virulence arsenal of the fish pathogen Piscirickettsia salmonis in the biofilm realm. 12,	Ο
717	Genomic landscape of prominent XDR Acinetobacter clonal complexes from Dhaka, Bangladesh. <b>2022</b> , 23,	0
716	Comparative Genomics of Lentilactobacillus parabuchneri isolated from dairy, KEM complex, Makgeolli, and Saliva Microbiomes. <b>2022</b> , 23,	O
715	Distribution and Transmission of Colistin Resistance Genes mcr-1 and mcr-3 among Nontyphoidal Salmonella Isolates in China from 2011 to 2020.	0
714	Machine learning and analysis of genomic diversity of Candidatus Liberibacter asiaticus Istrains from 20 citrus production states in Mexico. 13,	O
713	Broad host range may be a key to long-term persistence of bacteriophages infecting intestinal Bacteroidaceae species. <b>2022</b> , 12,	1
712	Global Genomic Epidemiology of Escherichia coli (ExPEC) ST38 Lineage Revealed a Virulome Associated with Human Infections. <b>2022</b> , 10, 2482	O
711	Genome Sequence of a Lytic Staphylococcus aureus Bacteriophage Isolated from Breast Milk. <b>2022</b> , 11,	0
710	Occurrence and Genomic Characterization of mcr-1-Harboring Escherichia coli Isolates from Chicken and Pig Farms in Lima, Peru. <b>2022</b> , 11, 1781	O

709	Characterization and genomic analysis of a novel halovirus infecting Chromohalobacter beijerinckii. 13,	O
708	Reclassification of eight Akkermansia muciniphila strains and description of Akkermansia massiliensis sp. nov. and Candidatus Akkermansia timonensis, isolated from human feces. <b>2022</b> , 12,	O
707	First record of the human infection of Brucella melitensis in Kyrgyzstan: evidence from whole-genome sequencing-based analysis. <b>2022</b> , 11,	O
706	A dynamic epibiont community associated with the bone eating worm Osedax.	O
705	ggMOB: Elucidation of genomic conjugative features and associated cargo genes across bacterial genera using genus-genus mobilization networks. 13,	0
704	Complete Genome Sequence of Variovorax paradoxus JBCE486, Which Alleviates the Salt Stress of the Endemic Plant Ulleung-Sanmaneul.	O
7°3	Cave Thiovulum (Candidatus Thiovulum stygium) differs metabolically and genomically from marine species.	О
702	Effect of Mannan-rich fraction supplementation on commercial broiler intestinum tenue and cecum microbiota. <b>2022</b> , 4,	O
701	New Wolbachia pipientis Genotype Increasing Heat Stress Resistance of Drosophila melanogaster Host Is Characterized by a Large Chromosomal Inversion. <b>2022</b> , 23, 16212	О
700	Characterization of virulence and antimicrobial resistance genes of Aeromonas media strain SD/21🛮 5 from marine sediments in comparison with other Aeromonas spp 13,	1
699	Host-derived protease promotes aggregation of Staphylococcus aureus by cleaving the surface protein SasG.	О
698	Genomic Shift in Population Dynamics of mcr-1-positive Escherichia coli in Human Carriage. <b>2022</b> ,	O
697	Diversity and Prevalence of Clostridium innocuum in the Human Gut Microbiota.	0
696	Comparative Genomic Analysis of the Hydrocarbon-Oxidizing Dibenzothiophene-Desulfurizing Gordonia Strains. <b>2023</b> , 11, 4	1
695	Antibiotic-resistant Escherichia coli from goat farms and the potential treatment by Acalypha indica L. extract. <b>2022</b> , 106889	O
694	Azospirillum Endophyticum sp. nov., an Endophyte of Paris Polyphylla Smith var. Yunnanensis. <b>2023</b> , 80,	O
693	New perspectives on an old grouping: The genomic and phenotypic variability of Oxalobacter formigenes and the implications for calcium oxalate stone prevention. 13,	1
692	An Emerging Lineage of Uropathogenic Extended Spectrum Lactamase Escherichia coli ST127. <b>2022</b> , 10,	O

691	Within-Host Genotypic and Phenotypic Diversity of Contemporaneous Carbapenem-Resistant Klebsiella pneumoniae from Blood Cultures of Patients with Bacteremia. <b>2022</b> , 13,	0
690	Occurrence, Diversity, and Genomes of Candidatus Patescibacterial long the Early Diagenesis of Marine Sediments. <b>2022</b> , 88,	O
689	High-efficiency genome editing of an extreme thermophile Thermus thermophilus using endogenous type I and type III CRISPR-Cas systems. <b>2022</b> , 1, 412-427	0
688	Comparative genomics of trimethoprim-sulfamethoxazole-resistant Achromobacter xylosoxidans clinical isolates from Serbia reveals shortened variant of class 1 integron integrase gene.	O
687	At the threshold of symbiosis: the genome of obligately endosymbiotic Candidatus Nebulobacter yamunensis almost indistinguishable from that of a cultivable strain. <b>2022</b> , 8,	0
686	Characterization of Multiple Alginate Lyases in a Highly Efficient Alginate-Degrading Vibrio Strain and Its Degradation Strategy. <b>2022</b> , 88,	O
685	Microbiome, resistome and mobilome of chlorine-free drinking water treatment systems.	О
684	Bioassay-Guided Fractionation Leads to the Detection of Cholic Acid Generated by the Rare Thalassomonas sp <b>2023</b> , 21, 2	O
683	Microbiome-mediated fructose depletion restricts murine gut colonization by vancomycin-resistant Enterococcus. <b>2022</b> , 13,	0
682	Characterization of a P1-bacteriophage-like plasmid (phage-plasmid) harbouring bla CTX-M-15 in Salmonella enterica serovar Typhi. <b>2022</b> , 8,	O
681	Post-vaccine epidemiology of serotype 3 pneumococci identifies transformation inhibition through prophage-driven alteration of a non-coding RNA. <b>2022</b> , 14,	0
680	Identification of Genetic Markers for the Detection of Bacillus thuringiensis Strains of Interest for Food Safety. <b>2022</b> , 11, 3924	О
679	Transmission of Escherichia coli Causing Pyometra between Two Female Dogs. <b>2022</b> , 10, 2465	О
678	Escherichia coli catheter-associated urinary tract infections are associated with distinctive virulence and biofilm gene determinants.	O
677	Isolation and Characterization of the Lytic Bacteriophages and Its Application in Combination with Amoxicillin againstAeromonas dhakensis.	0
676	Characteristics and adaptability of Flavobacterium panici BSSL-CR3 in tidal flat revealed by comparative genomic and enzymatic analysis. <b>2023</b> , 205,	O
675	Campylobacter majalis sp. nov. and Campylobacter suis sp. nov., novel Campylobacter species isolated from porcine gastrointestinal mucosa. <b>2022</b> , 72,	1
674	Intraglandular mesenchymal stem cell treatment induces changes in the salivary proteome of irradiated patients. <b>2022</b> , 2,	1

673	Streptomyces coriariae sp. nov., a novel streptomycete isolated from actinorhizal nodules of Coriaria intermedia. <b>2022</b> , 72,	O
672	Omic insights into various ceftazidime-avibactam-resistant Klebsiella pneumoniae isolates from two southern Italian regions. 12,	1
671	Consistency across multi-omics layers in a drug-perturbed gut microbial community.	O
670	Molecular Characteristics of an NDM-4 and OXA-181 Co-Producing K51-ST16 Carbapenem-Resistant Klebsiella pneumoniae: Study of Its Potential Dissemination Mediated by Conjugative Plasmids and Insertion Sequences.	O
669	A clinical KPC-producing Klebsiella michiganensis strain carrying IncFII/IncFIA (HI1)/IncFIB (K) multiple replicon plasmid. 13,	O
668	Molecular characterization of a new probiotics Ligilactobacillus salivarius F14 from the gut of Tribes of Odisha.	O
667	All Staphylococcus aureus bacteraemia-inducing strains can cause infective endocarditis: Results of GWAS and experimental animal studies. <b>2023</b> ,	O
666	Phylogenomics of five Pseudanabaena cyanophages and evolutionary traces of horizontal gene transfer. <b>2023</b> , 18,	O
665	Genotypic and phenotypic differences among phase-variable colony variants conserved acrossGardnerellaspp.	O
664	Transmission and microevolution of methicillin-resistant Staphylococcus aureus ST88 strain among patients, healthcare workers, and household contacts at a trauma and orthopedic ward. 10,	O
663	Carbapenemase-Producing Klebsiella pneumoniae in COVID-19 Intensive Care Patients: Identification of IncL-VIM-1 Plasmid in Previously Non-Predominant Sequence Types. <b>2023</b> , 12, 107	1
662	The gut metagenome harbors metabolic and antibiotic resistance signatures of moderate-to-severe asthma.	O
661	Characterization of Cellulomonas sp. HM71 as potential probiotic strain for human health. 12,	O
660	Dissemination of Metallo-Lactamase-Producing Pseudomonas aeruginosa in Serbian Hospital Settings: Expansion of ST235 and ST654 Clones. <b>2023</b> , 24, 1519	O
659	Emerging resistance in Staphylococcus epidermidis during dalbavancin exposure: a case report and in vitro analysis of isolates from prosthetic joint infections.	1
658	Genomic Characteristics and Comparative Genomic Analysis of a Probiotic Bacterial Strain, Lactiplantibacillus plantarum CKDB008. <b>2022</b> , 2,	O
657	Taxonomic Assignment-Based Genome Reconstruction from Apical Periodontal Metagenomes to Identify Antibiotic Resistance and Virulence Factors. <b>2023</b> , 13, 194	O
656	Genome Update for Pseudomonas fluorescens Isolate SBW25.	O

655	Carbon dioxide equivalent emissions from corn silage fermentation. 13,	0
654	Genomics of the flumorigenes lade of the family Rhizobiaceae and description of Rhizobium rhododendrisp. nov	O
653	Antimicrobial Susceptibility and Molecular Features of Colonizing Isolates of Pseudomonas aeruginosa and the Report of a Novel Sequence Type (ST) 3910 from Thailand. <b>2023</b> , 12, 165	O
652	Comparative Genomics and Phenotypic Characterization of Gluconacetobacter entanii, a Highly Acetic Acid-Tolerant Bacterium from Vinegars. <b>2023</b> , 12, 214	Ο
651	Studying the Association between Antibiotic Resistance Genes and Insertion Sequences in Metagenomes: Challenges and Pitfalls. <b>2023</b> , 12, 175	O
650	Genome Characterization of Bacteriophage KPP-1, a Novel Member in the Subfamily Vequintavirinae, and Use of Its Endolysin for the Lysis of Multidrug-Resistant Klebsiella variicola In Vitro. <b>2023</b> , 11, 207	O
649	Novel integrative elements and genomic plasticity in ocean ecosystems. 2023, 186, 47-62.e16	О
648	Features of Mycobacterium bovis Complete Genomes Belonging to 5 Different Lineages. <b>2023</b> , 11, 177	Ο
647	Proteiniphilum and Methanothrix harundinacea became dominant acetate utilizers in a methanogenic reactor operated under strong ammonia stress. 13,	0
646	Genomic analysis of Mycobacterium brumae sustains its nonpathogenic and immunogenic phenotype. 13,	Ο
645	Draft Genome Sequence ofPedococcussp. Strain 5OH_020 Isolated from California Grassland Soil.	0
644	Identification of two distinct phylogenomic lineages and model strains for the understudied cystic fibrosis lung pathogenBurkholderia multivorans.	O
643	Genomic diversity, pathogenicity and antimicrobial resistance of Escherichia coli isolated from poultry in the southern United States. <b>2023</b> , 23,	O
642	Transcriptome Analysis of Arcobacter butzleri Infection in a Mucus-Producing Human Intestinal In Vitro Model.	Ο
641	Combining the In Silico and In Vitro Assays to Identify Strobilanthes cusia Kuntze Bioactives against Penicillin-Resistant Streptococcus pneumoniae. <b>2023</b> , 16, 105	O
640	Relationships between fluid mixing, biodiversity, and chemosynthetic primary productivity in Yellowstone hot springs.	1
639	Unique or not unique? Comparative genetic analysis of bacterial O-antigens from the Oxalobacteraceae family. <b>2023</b> , 26, 810-818	0
638	Genome Sequence of an Ungulate Tetraparvovirus 1 from a Nasal Swab of an Irish Beef-Suckler Calf.	O

637	Infection and Persistence of Coxiella burnetii Clinical Isolate in the Placental Environment. <b>2023</b> , 24, 1209	O
636	Tropodithietic Acid, a Multifunctional Antimicrobial, Facilitates Adaption and Colonization of the Producer, Phaeobacter piscinae.	O
635	Machine learning and metagenomics enhance surveillance of antimicrobial resistance in chicken production in China.	Ο
634	Microcystis pangenome reveals cryptic diversity within and across morphospecies. 2023, 9,	O
633	Carriage of three plasmids in a single human clinical isolate of Clostridioides difficile. 2023, 125, 102669	Ο
632	Conjugation of plasmid harboring blaNDM-1 in a clinical Providencia rettgeri strain through the formation of a fusion plasmid. 13,	O
631	Emergence of plasmid-mediated colistin resistance mcr-3.5 gene in Citrobacter amalonaticus and Citrobacter sedlakii isolated from healthy individual in Thailand. 12,	O
630	Complete Genome Sequence of Sphingopyxis sp. Strain PET50, a Potential Polyethylene Terephthalate (PET)-Degrading Bacterium Isolated from Compost.	O
629	Arcanobacterium pinnipediorum Strain DSM 28752 Isolated from a Harbour Seal: Complete Genome Sequence.	Ο
628	Analyzing the genetic diversity and biotechnological potential of Leuconostoc pseudomesenteroides by comparative genomics. 13,	O
627	Molecular epidemiology of Clostridioides difficile in companion animals: Genetic overlap with human strains and public health concerns. 10,	1
626	Fatty acid overproduction by gut commensal microbiota exacerbates obesity. 2023,	O
625	Insights into the metabolic specificities of pathogenic strains from theRalstonia solanacearum species complex.	O
624	The person-to-person transmission landscape of the gut and oral microbiomes.	4
623	Tricycle surveillance in Antananarivo, Madagascar: circulation of both extended-spectrum beta-lactamase producing Escherichia coli strains and plasmids among humans, chickens and the environment.	O
622	The gut microbiota of people with asthma influences lung inflammation in gnotobiotic mice. <b>2023</b> , 105991	O
621	Whole-genome analysis of gamma-aminobutyric acid producing Psychobiotic Limosilactobacillus reuteri with its Untargeted metabolomics using UHPLC-Q-Tof MS/MS. <b>2023</b> , 147195	0
620	Clostridioides difficile in South American Camelids in Germany: First Insights into Molecular and Genetic Characteristics and Antimicrobial Resistance. <b>2023</b> , 12, 86	O

619	Identification and taxonomy of Streptomyces justiciae strain RA-WS2: a novel setomimycin producing actinobacterium. <b>2023</b> , 13,	O
618	Growth in a biofilm promotes conjugation of ablaNDM-1-bearing plasmid betweenKlebsiella pneumoniaestrains.	O
617	Temperature-specific adaptations and genetic requirements in a biofilm formed by Pseudomonas aeruginosa. 13,	O
616	The DNA Phosphorothioation Restriction-Modification System Influences the Antimicrobial Resistance of Pathogenic Bacteria.	O
615	Clinical and genomic analysis of hypermucoviscous Klebsiella pneumoniae isolates: Identification of new hypermucoviscosity associated genes. 12,	О
614	PPNet: Identifying Functional Association Networks by Phylogenetic Profiling of Prokaryotic Genomes.	O
613	The ESKAPE mobilome contributes to the spread of antimicrobial resistance and CRISPR-mediated conflict between mobile genetic elements. <b>2023</b> , 51, 236-252	1
612	Comparison of R9.4.1/Kit10 and R10/Kit12 Oxford Nanopore flowcells and chemistries in bacterial genome reconstruction. <b>2023</b> , 9,	O
611	Prophage-Derived Regions in Curtobacterium Genomes: Good Things, Small Packages. <b>2023</b> , 24, 1586	1
610	Limosilactobacillus walteri sp. nov., a novel probiotic antimicrobial lipopeptide producing bacterium.	O
609	Anaerobic methanotroph Candidatus Methanoperedens nitroreducens Chas a pleomorphic life cycle.	O
608	Molecular Features and Antimicrobial Susceptibilities of Streptococcus equi ssp. equi Isolates from Strangles Cases in Indonesia. <b>2023</b> , 10, 49	O
607	Spread of the mcr-1 colistin-resistance gene in Escherichia coli through plasmid transmission and chromosomal transposition in French goats. 13,	0
606	Competitiveness and symbiotic efficiency in alfalfa of Rhizobium favelukesii ORY1 strain in which homologous genes of peptidases HrrP and SapA that negatively affect symbiosis were identified. 4,	O
605	An XDR Pseudomonas aeruginosa ST463 Strain with an IncP-2 Plasmid Containing a Novel Transposon Tn 6485f Encoding bla IMP-45 and bla AFM-1 and a Second Plasmid with Two Copies of bla KPC-2.	0
604	Frequent Transmission of Streptococcus pneumoniae Serotype 35B and 35D, Clonal Complex 558 Lineage, across Continents and the Formation of Multiple Clades in Japan.	O
603	Pan-genome association study of Mycobacterium tuberculosis lineage-4 revealed specific genes related to the high and low prevalence of the disease in patients from the North-Eastern area of MedellB, Colombia. 13,	О
602	Diversity and prevalence of type VI secretion system effectors in clinical Pseudomonas aeruginosa isolates. 13,	Ο

601	TransAAP: an automated annotation pipeline for membrane transporter prediction in bacterial genomes. <b>2023</b> , 9,	O
600	Virulence and genomic diversity among clinical isolates of ST1 (BI/NAP1/027)Clostridioides difficile.	O
599	Hiding in Plain Sight: Characterization of Aeromonas Species Isolated from a Recreational Estuary Reveals the Carriage and Putative Dissemination of Resistance Genes. <b>2023</b> , 12, 84	0
598	Multi-Omics Data Analysis for Inflammation Disease Research: Correlation Analysis, Causal Analysis and Network Analysis. <b>2023</b> , 101-118	O
597	The Full Genome Sequences of Pseudomonas sp. Strain MM221 and Pseudoarthrobacter sp. Strain MM222, Isolated from a Meadow in Bielefeld, Germany.	0
596	The bacterial genetic determinants of Escherichia colicapacity to cause bloodstream infections in humans.	O
595	Genomic characterization and assessment of pathogenic potential of Legionella spp. isolates from environmental monitoring. 13,	0
594	Bacterial volatile organic compounds attenuate pathogen virulence via evolutionary trade-offs.	O
593	Allobaculum mucilyticum sp. nov. and Allobaculum fili sp. nov., isolated from the human intestinal tract. <b>2023</b> , 73,	O
592	Multidrug resistance plasmids underlie clonal expansions and international spread ofSalmonella entericaserotype 4,[5],12,i:- ST34 in Southeast Asia.	O
591	CanB is a metabolic mediator of antibiotic resistance in Neisseria gonorrhoeae. <b>2023</b> , 8, 28-39	O
590	Genomic Diversity of the Rarely Observed Genotype of the Mycobacterium tuberculosis Central Asian (CAS) Lineage 3 from North Brazil. <b>2023</b> , 11, 132	O
589	Adaptive Evolution Compensated for the Plasmid Fitness Costs Brought by Specific Genetic Conflicts. <b>2023</b> , 12, 137	0
588	Integrating phylogenetics with intron positions illuminates the origin of the complex spliceosome.	Ο
587	Microbial survival mechanisms within serpentinizing Mariana forearc sediments.	0
586	Molecular features and transmission of NDM-producing Enterobacterales in Israeli hospitals.	Ο
585	Draft genome sequence of Streptomyces sp. KD18, isolated from industrial soil. <b>2023</b> , 13,	0
584	Natural rubber reduces herbivory and alters the microbiome below ground.	O

583	Functional characterization of a novel aminoglycoside phosphotransferase, APH(9)-Ic, and its variant from Stenotrophomonas maltophilia. 12,	О
582	Complete Genome Sequences of 14 Nontuberculous Mycobacteria Type Strains.	О
581	Strategies and tools in illumina and nanopore-integrated metagenomic analysis of microbiome data.	0
580	Complete Genome Sequences of Pseudomonas sp. Strains MM223 and MM227 and Rheinheimera sp. Strain MM224, Isolated from a Pond Edge in Bielefeld, Germany.	O
579	Comparative genomics and molecular epidemiology of colistin-resistant Acinetobacter baumannii. <b>2023</b> , 21, 574-585	3
578	Differential carbon utilization enables co-existence of recently speciated Campylobacteraceae in the cow rumen epithelial microbiome.	O
577	A Genome of Temperate Enterococcus Bacteriophage Placed in a Space of Pooled Viral Dark Matter Sequences. <b>2023</b> , 15, 216	0
576	Selecting for infectivity across metapopulations can increase virulence in the social microbe Bacillus thuringiensis.	О
575	Aging-associated augmentation of gut microbiome virulence capability drives sepsis severity.	О
574	Legionella maioricensis sp. nov., a new species isolated from the hot water distribution systems of a hospital and a shopping center during routine sampling. <b>2023</b> , 73,	O
573	Carriage and Transmission of mcr-1 in Salmonella Typhimurium and Its Monophasic 1,4,[5],12:i:- Variants from Diarrheal Outpatients: a 10-Year Genomic Epidemiology in Guangdong, Southern China.	O
572	A metagenomics and amplicon sequencing combined approach reveals the best primers to study marine aerobic anoxygenic phototrophs.	O
571	Biological Properties of 12 Newly Isolated Acinetobacter baumannii-Specific Bacteriophages. <b>2023</b> , 15, 231	1
570	Natural Recombination among Type I Restriction-Modification Systems Creates Diverse Genomic Methylation Patterns among Xylella fastidiosa Strains.	О
569	Genetic and Phenotypic Characterization of Multidrug-Resistant Klebsiella pneumoniae from Liver Abscess.	О
568	Identification of heat-resistant Bacillus strains in peppers in Sichuan Province, China. <b>2023</b> , 174, 114425	О
567	Pan-genome study underling the extent of genomic variation of invasiveStreptococcus pneumoniaein Malawi.	О
566	Comprehensive characterization of aerobic groundwater biotreatment media. <b>2023</b> , 230, 119587	O

565	Illumina sequencing data of the complete chloroplast genome of rare species Juniperus seravschanica (Cupressaceae) from Kazakhstan. <b>2023</b> , 46, 108866	0
564	Pathogen-associated gene discovery workflows for novel antivirulence therapeutic development. <b>2023</b> , 88, 104429	O
563	Mixed organic and inorganic amendments enhance soil microbial interactions and environmental stress resistance of Tibetan barley on plateau farmland. <b>2023</b> , 330, 117137	0
562	Low-grade intestinal metaplasia in Indonesia: Insights into the expression of proinflammatory cytokines during Helicobacter pylori infection and unique East-Asian CagA characteristics. <b>2023</b> , 163, 156122	o
561	Sulfide intrusion in a habitat forming seagrass can be predicted from relative abundance of sulfur cycling genes in sediments. <b>2023</b> , 864, 161144	0
560	Potential to mitigate nitrogen emissions from paddy runoff: A microbiological perspective. <b>2023</b> , 865, 161306	o
559	Whole-genome sequencing for genetic diversity analysis of Iranian Brucella spp. isolated from humans and livestock. <b>2023</b> , 16, 100483	0
558	Antibiotic Susceptibility, Resistance Gene Determinants and Corresponding Genomic Regions in Lactobacillus amylovorus Isolates Derived from Wild Boars and Domestic Pigs. <b>2023</b> , 11, 103	О
557	Genome sequence analysis and characterization of Bacillus altitudinis B12, a polylactic acid- and keratin-degrading bacterium.	1
556	Association between microbial composition, diversity, and function of the maternal gastrointestinal microbiome with impaired glucose tolerance on the glucose challenge test. <b>2022</b> , 17, e0271261	О
555	A novel SfaNI-like restriction-modification system in Caldicellulosiruptor extents the genetic engineering toolbox for this genus. <b>2022</b> , 17, e0279562	O
554	Genomic Analysis Unveils the Pervasiveness and Diversity of Prophages Infecting Erwinia Species. <b>2023</b> , 12, 44	О
553	Significant Differences in Planktonic Virus Communities Between 【Iellular Fraction【[0.22 ~ 3.0 μ̃m) and 【Viral Fraction【[< 0.22 ਜਿ) in the Ocean.	O
552	A New Kayfunavirus-like Escherichia Phage vB_EcoP-Ro45lw with Antimicrobial Potential of Shiga Toxin-Producing Escherichia coli O45 Strain. <b>2023</b> , 11, 77	О
551	A Salmonella enterica Serovar Oranienburg Clone Caused a Cluster of Bacteremia Cases in Persons With No Recognizable Underlying Diseases in Japan. <b>2023</b> , 10,	O
550	OpenGenomeBrowser: a versatile, dataset-independent and scalable web platform for genome data management and comparative genomics. <b>2022</b> , 23,	О
549	Mechanism of bare patch formation under Haloxylon ammodendron canopies and patch effects on soil microorganisms in the Gurbantunggut Desert, Northern China.	O
548	Design of a multi-epitope vaccine against Haemophilus parasuis based on pan-genome and immunoinformatics approaches. 9,	О

547	Mutational basis of Meropenem resistance in Pseudomonas aeruginosa. 2022, 19-24	0
546	Hybrid Genomic Analysis of Salmonella enterica Serovar Enteritidis SE3 Isolated from Polluted Soil in Brazil. <b>2023</b> , 11, 111	O
545	A one-year genomic investigation of Escherichia coli epidemiology and nosocomial spread at a large US healthcare network. <b>2022</b> , 14,	1
544	Genomic insight into Myroides oncorhynchi sp. nov., a new member of the Myroides genus, isolated from the internal organ of rainbow trout (Oncorhynchus mykiss).	О
543	Variability in Cold Tolerance of Food and Clinical Listeria monocytogenes Isolates. 2023, 11, 65	О
542	Culturable bacteria diversity in stem liquid and resina from Populus euphratica and screening of plant growth-promoting bacteria. <b>2022</b> , 22,	О
541	Alterations of oral microbiota and impact on the gut microbiome in type 1 diabetes mellitus revealed by integrated multi-omic analyses. <b>2022</b> , 10,	1
540	Comparative Genome Analysis of 19 Trueperella pyogenes Strains Originating from Different Animal Species Reveal a Genetically Diverse Open Pan-Genome. <b>2023</b> , 12, 24	O
539	Postglacial adaptations enabled colonization and quasi-clonal dispersal of ammonia-oxidizing archaea in modern European large lakes. <b>2023</b> , 9,	1
538	Accurate and fast graph-based pangenome annotation and clustering with ggCaller.	О
537	Molecular Characterizations of the Coagulase-Negative Staphylococci Species Causing Urinary Tract Infection in Tanzania: A Laboratory-Based Cross-Sectional Study. <b>2023</b> , 12, 180	O
536	Complex organic matter degradation by secondary consumers in chemolithoautotrophy-based subsurface geothermal ecosystems.	О
535	Lutispora saccharofermentans sp. nov., a mesophilic, non-spore-forming bacterium isolated from a lab-scale methanogenic landfill bioreactor digesting anaerobic sludge, and emendation of the genus Lutispora to include species which are non-spore-forming and mesophilic. <b>2023</b> , 73,	О
534	Population genomic analysis of an emerging pathogenLonsdalea quercinaaffecting various species of oaks in western North America.	О
533	Genomic Characterization of Three Novel Bartonella Strains in a Rodent and Two Bat Species from Mexico. <b>2023</b> , 11, 340	О
532	Whole-genome sequencing of the clinical isolate of Legionella pneumophila ALAW1 from the West Bank allows high-resolution typing and determination of pathogenicity mechanisms. <b>2023</b> , 10,	1
531	Anaeromicropila herbilytica gen. nov., sp. nov., a plant polysaccharide-decomposing anaerobic bacterium isolated from anoxic soil subjected to reductive soil disinfestation, and reclassification of Clostridium populeti as Anaeromicropila populeti comb. nov <b>2023</b> , 73,	0
530	Biotin pathway in novel Fodinibius salsisoli sp. nov., isolated from hypersaline soils and	O

529	Using a combination of short- and long-read sequencing to investigate the diversity in plasmid- and chromosomally encoded extended-spectrum beta-lactamases (ESBLs) in clinical Shigella and Salmonella isolates in Belgium. <b>2023</b> , 9,	O
528	Facilitative interaction networks in experimental microbial community dynamics.	0
527	Complete Genome Sequence Analysis of Kribbella sp. CA-293567 and Identification of the Kribbellichelins A & amp; B and Sandramycin Biosynthetic Gene Clusters. <b>2023</b> , 11, 265	0
526	Host Dependent-Transposon for a Plasmid Found in Aeromonas salmonicida subsp. salmonicida That Bears a catB3 Gene for Chloramphenicol Resistance. <b>2023</b> , 12, 257	O
525	ESBL Displace: A Protocol for an Observational Study to Identify Displacing Escherichia coli Strain Candidates from ESBL-Colonized Travel Returners Using Phenotypic, Genomic Sequencing and Metagenome Analysis. <b>2023</b> , 14, 177-189	O
524	Vibrio sinus sp. nov., a marine bacterium isolated from coastal seawater. <b>2023</b> , 73,	Ο
523	Whole-Genome Sequencing of Mycobacterium tuberculosis Isolated from Three Hospitals in South Korea.	О
522	Pathological Features and Genomic Characterization of an Actinobacillus equuli subsp. equuli Bearing Unique Virulence-Associated Genes from an Adult Horse with Pleuropneumonia. <b>2023</b> , 12, 224	Ο
521	Klebsiella pneumoniae carrying multiple alleles of antigen 43-encoding gene of Escherichia coli associated with biofilm formation. <b>2023</b> , 42, 371-377	О
520	Genomic Analysis and In Vitro Investigation of the Hop Resistance Phenotype of Two Novel Loigolactobacillus backii Strains, Isolated from Spoiled Beer. <b>2023</b> , 11, 280	O
519	Split k-mer analysis compared to cgMLST and SNP-based core genome analysis for detecting transmission of vancomycin-resistant enterococci: results from routine outbreak analyses across different hospitals and hospitals networks in Berlin, Germany. <b>2023</b> , 9,	О
518	Strains Colonizing Different Intestinal Sites within an Individual Are Derived from a Single Founder Population.	О
517	Evolutionary diversification of methanotrophic ANME-1 archaea and their expansive virome. <b>2023</b> , 8, 231-245	О
516	Bacteriophage Infection of the Marine Bacterium Shewanella glacialimarina Induces Dynamic Changes in tRNA Modifications. <b>2023</b> , 11, 355	O
515	In vitro gut microbiome response to carbohydrate supplementation is acutely affected by a sudden change in diet. <b>2023</b> , 23,	О
514	Identification of levoglucosan degradation pathways in bacteria and sequence similarity network analysis.	O
513	Plant growth promotion of the forage plant Lupinus albus Var. Orden Dorado using Pseudomonas agronomica sp. nov. and Bacillus pretiosus sp. nov. added over a valorized agricultural biowaste. 13,	О
512	Targeting Enterococci with Antimicrobial Activity against Clostridium perfringens from Poultry. <b>2023</b> , 12, 231	O

511	Extensively drug-resistant Acinetobacter baumannii: role of conjugative plasmids in transferring resistance. 11, e14709	O
510	Cryptic Diversity of Black Band Disease Cyanobacteria in Siderastrea siderea Corals Revealed by Chemical Ecology and Comparative Genome-Resolved Metagenomics. <b>2023</b> , 21, 76	1
509	Genomic and physiological characterization of Novosphingobium terrae sp. nov., an alphaproteobacterium isolated from Cerrado soil containing a mega-sized chromid.	0
508	Genome-centered metagenomics illuminates adaptations of core members to a partial Nitritation Anammox bioreactor under periodic microaeration. 14,	O
507	Retrospective Study of the Epidemiology of Clostridioides difficile Infection in the Neurosurgery Department of a Tertiary Hospital in China. Volume 16, 545-554	O
506	Geography shapes the genomics and antimicrobial resistance of Salmonella enterica Serovar Enteritidis isolated from humans. <b>2023</b> , 13,	O
505	Metagenomic analysis of ecological niche overlap and community collapse in microbiome dynamics.	O
504	Prevalence and genetic characteristics of fosB-positive Staphylococcus aureus in duck farms in Guangdong, China in 2020.	O
503	The Impact of Species Tree Estimation Error on Cophylogenetic Reconstruction.	O
502	Does kimchi deserve the status of a probiotic food?. 1-14	O
502 501	Does kimchi deserve the status of a probiotic food?. 1-14  Draft genome of Raoultella planticola, a high lead resistance bacterium from industrial wastewater. 2023, 13,	0
	Draft genome of Raoultella planticola, a high lead resistance bacterium from industrial wastewater.	
501	Draft genome of Raoultella planticola, a high lead resistance bacterium from industrial wastewater. <b>2023</b> , 13,  Assessing Antimicrobial and Metal Resistance Genes in Escherichia Coli from Domestic	0
501	Draft genome of Raoultella planticola, a high lead resistance bacterium from industrial wastewater.  2023, 13,  Assessing Antimicrobial and Metal Resistance Genes in Escherichia Coli from Domestic Groundwater Supplies in Rural Ireland.  Genome sequencing of Pseudomonas fluorescens phage UFJF_PfSW6: a novel lytic Pijolavirus	0
501 500 499	Draft genome of Raoultella planticola, a high lead resistance bacterium from industrial wastewater.  2023, 13,  Assessing Antimicrobial and Metal Resistance Genes in Escherichia Coli from Domestic Groundwater Supplies in Rural Ireland.  Genome sequencing of Pseudomonas fluorescens phage UFJF_PfSW6: a novel lytic Pijolavirus specie with potential for biocontrol in the dairy industry. 2023, 13,  Whole-Genome Sequencing of Clinical Isolates of Mycobacterium tuberculosis Isolated before and	0 0
501 500 499 498	Draft genome of Raoultella planticola, a high lead resistance bacterium from industrial wastewater. 2023, 13,  Assessing Antimicrobial and Metal Resistance Genes in Escherichia Coli from Domestic Groundwater Supplies in Rural Ireland.  Genome sequencing of Pseudomonas fluorescens phage UFJF_PfSW6: a novel lytic Pijolavirus specie with potential for biocontrol in the dairy industry. 2023, 13,  Whole-Genome Sequencing of Clinical Isolates of Mycobacterium tuberculosis Isolated before and after Treatment.	0 0
501 500 499 498 497	Draft genome of Raoultella planticola, a high lead resistance bacterium from industrial wastewater. 2023, 13,  Assessing Antimicrobial and Metal Resistance Genes in Escherichia Coli from Domestic Groundwater Supplies in Rural Ireland.  Genome sequencing of Pseudomonas fluorescens phage UFJF_PfSW6: a novel lytic Pijolavirus specie with potential for biocontrol in the dairy industry. 2023, 13,  Whole-Genome Sequencing of Clinical Isolates of Mycobacterium tuberculosis Isolated before and after Treatment.  Lociq: A Loci-Seeking Approach for Enhanced Plasmid Subtyping and Structural Characterization.  Avian strains of emerging pathogen Escherichia fergusonii are phylogenetically diverse and harbor the greatest AMR dissemination potential among different sources: Comparative genomic	<ul><li>0</li><li>0</li><li>0</li><li>0</li><li>0</li></ul>

493	Exploring the Potential Molecular Mechanisms of Interactions between a Probiotic Consortium and Its Coral Host.	0
492	Phylogenomic analysis of Wolbachia genomes from the Darwin Tree of Life biodiversity genomics project. <b>2023</b> , 21, e3001972	o
491	Galaxy ASIST: A web-based platform for mapping and assessment of global standards of antimicrobial susceptibility: A case study in Acinetobacter baumannii genomes. 13,	O
490	Virulence and antibiotic-resistance genes in Enterococcus faecalis associated with streptococcosis disease in fish. <b>2023</b> , 13,	o
489	First complete genome sequence of lumpy skin disease virus directly from a clinical sample in South India.	0
488	Description and Genomic Analysis of the First Facultatively Lithoautotrophic, Thermophilic Bacteria of the Genus Thermaerobacter Isolated from Low-temperature Sediments of Lake Baikal.	o
487	Chryseobacterium paludis sp. nov. and Chryseobacterium foetidum sp. nov. Isolated from the Aquatic Environment, South Korea. <b>2023</b> , 61, 37-47	O
486	Rapid metagenomic sequencing for diagnosis and antimicrobial sensitivity prediction of canine bacterial infections.	o
485	GardnerellaDiversity and Ecology in Pregnancy and Preterm Birth.	O
484	Genome sequence and genomic analysis of liver abscess caused by hypervirulent Klebsiella pneumoniae. <b>2023</b> , 13,	О
483	Genomic relatedness and dissemination of blaNDM-5 among Acinetobacter baumannii isolated from hospital environments and clinical specimens in Thailand. 11, e14831	0
482	Uncovering the determinants of model Escherichia coli strain C600 susceptibility and resistance to lytic T4-like and T7-like phage. <b>2023</b> , 325, 199048	О
481	Comparative genomic and functional annotation of Pseudomonas spp. genomes responsible for blue discoloration of Brazilian fresh soft cheese. <b>2023</b> , 140, 105605	0
480	STRESS AND IMMUNITY OF NODULE BACTERIA SINORHIZOBIUM MELILOTI: LOCALIZATION, POLYMORPHISM AND PHYLOGENY OF GENETIC DETERMINANTS. <b>2022</b> ,	o
479	Genomic view of the diversity and functional role of archaea and bacteria in the skeleton of the reef-building corals Porites lutea and Isopora palifera. <b>2022</b> , 12,	1
478	Description of Defluviimonas salinarumsp. nov. with the potential of benzene-degradation isolated from saltern in the Yellow Seacoast. <b>2023</b> , 370,	O
477	Unitig level assembly graph based metagenome-assembled genome refiner (UGMAGrefiner): A tool to increase completeness and resolution of metagenome-assembled genomes. <b>2023</b> , 21, 2394-2404	0
476	Genome-centric view of the microbiome in a new deep-sea glass sponge species Bathydorus sp 14,	О

475	Cross-protection and cross-feeding between Klebsiella pneumoniae and Acinetobacter baumannii promotes their co-existence. <b>2023</b> , 14,	О
474	Metaphor - A workflow for streamlined assembly and binning of metagenomes.	O
473	The genome of Bacillus tequilensis EA-CB0015 sheds light into its epiphytic lifestyle and potential as a biocontrol agent. 14,	0
472	A male-killing Wolbachia endosymbiont is concealed by another endosymbiont and a nuclear suppressor. <b>2023</b> , 21, e3001879	O
471	Increased clonal dissemination of OXA-232-producing ST15 Klebsiella pneumoniae in Zhejiang, China from 2018 to 2021. <b>2023</b> , 12,	О
470	Emergence and clonal expansion of Vibrio aestuarianus lineages pathogenic for oysters in Europe.	O
469	Discovery of the Streamlined Haloarchaeon Halorutilus salinus , Comprising a New Order Widespread in Hypersaline Environments across the World.	0
468	Competition between lysogenic and sensitive bacteria is determined by the fitness costs of the different emerging phage-resistance strategies. 12,	O
467	Structure and gene cluster annotation of the O-antigen of Aeromonas sobria strain K928 isolated from common carp and classified into the new Aeromonas PGO1 serogroup. <b>2023</b> , 108809	О
466	Whole-Genome Sequencing and Comparative Genomics Analysis of a Newly Emerged Multidrug-Resistant Klebsiella pneumoniae Isolate of ST967.	O
465	Deep Divergence and Genomic Diversification of Gut Symbionts of Neotropical Stingless Bees.	0
464	Convergence of resistance and evolutionary responses in Escherichia coliand Salmonella entericaco-inhabiting chicken farms in China.	O
463	First detection of tet(X4)-positive Enterobacterales in retail vegetables and clonal spread of Escherichia coli ST195 producing Tet(X4) in animals, foods, and humans across China and Thailand. <b>2023</b> , 391-393, 110145	0
462	Adaptive Radioresistance of Enterohemorrhagic Escherichia coli O157:H7 Results in Genomic Loss of Shiga Toxin-Encoding Prophages.	O
461	Genome analyses of Weissella strains isolated from Campos das Vertentes, Minas Gerais, Brazil revealed new bacteriocins with a large spectrum of activity. <b>2023</b> , 52, 102421	0
460	A multiplex PCR assay for the differentiation of Mycobacterium tuberculosis complex reveals high rates of mixed-lineage tuberculosis infections among patients in Ghana. 13,	О
459	Characterization of Phietavirus Henu 2 in the virome of individuals with acute gastroenteritis.	0
458	Metagenomic Insight into Microbiome and Antibiotic Resistance Genes of High Clinical Concern in Urban and Rural Hospital Wastewater of Northern India Origin: a Major Reservoir of Antimicrobial Resistance. <b>2023</b> , 11,	O

457	Epidemiology and Genetic Characteristics of Carbapenem-Resistant Escherichia coli in Chinese Intensive Care Unit Analyzed by Whole-Genome Sequencing: a Prospective Observational Study. <b>2023</b> , 11,	О
456	Gallocin A, an Atypical Two-Peptide Bacteriocin with Intramolecular Disulfide Bonds Required for Activity. <b>2023</b> , 11,	O
455	Genome-resolved metagenomics revealed metal-resistance, geochemical cycles in a Himalayan hot spring.	О
454	IS1-related large-scale deletion of chromosomal regions harbouring oxygen-insensitive nitroreductase genenfsBcauses nitrofurantoin heteroresistance inEscherichia coli.	О
453	Diversity of the type VI secretion systems in the Neisseria spp. <b>2023</b> , 9,	О
452	Dissemination of Pseudomonas aeruginosa bla NDM-1 -Positive ST308 Clone in Singapore.	O
451	A Transducing Bacteriophage Infecting Staphylococcus epidermidis Contributes to the Expansion of a Novel Siphovirus Genus and Implies the Genus Is Inappropriate for Phage Therapy.	О
450	GenoVi, an open-source automated circular genome visualizer for bacteria and archaea. <b>2023</b> , 19, e1010998	O
449	A novel ssDNA Bidnavirus in the giant freshwater prawn Macrobrachium rosenbergii. 2023, 568, 739340	О
448	Burkholderia semiarida sp. nov. and Burkholderia sola sp. nov., two novel B. cepacia complex species causing onion sour skin. <b>2023</b> , 46, 126415	О
447	Dominance of mixed ether/ester, intact polar membrane lipids in five species of the order Rubrobacterales: Another group of bacteria not obeying the <b>I</b> lpid divide <b>12023</b> , 46, 126404	О
446	Phage-based therapy against biofilm producers in gram-negative ESKAPE pathogens. <b>2023</b> , 178, 106064	O
445	Characterizing prophages in the genus Fusobacterium. <b>2023</b> , 80, 102718	О
444	Genome-guided approaches and evaluation of the strategies to influence bioprocessing assisted morphological engineering of Streptomyces cell factories. <b>2023</b> , 376, 128836	О
443	Whole genome characterization of a multidrug-resistant hypervirulent Pasteurella multocida with a new drug-resistant plasmid. <b>2023</b> , 102, 102583	О
442	Foremost report of the whole genome of Spirabiliibacterium mucosae from India and comparative genomics of the novel genus Spirabiliibacterium. <b>2023</b> , 867, 147359	О
441	A novel lytic bacteriophage against colistin-resistant Escherichia coli isolated from different animals. <b>2023</b> , 329, 199090	О
440	Genomic analysis of Paenibacillus larvae isolates from the Czech Republic and the neighbouring regions of Slovakia. <b>2023</b> , 158, 34-40	О

439	First reported detection of the mobile colistin resistance genes, mcr-8 and mcr-9, in the Irish environment. <b>2023</b> , 876, 162649	0
438	QSP: An open sequence database for quorum sensing related gene analysis with an automatic annotation pipeline. <b>2023</b> , 235, 119814	Ο
437	DIET-like mutualism of Geobacter and methanogens at specific electrode potential boosts production of both methane and hydrogen from propionate. <b>2023</b> , 235, 119911	0
436	Study on characteristic and mechanism involved in the formation of N-nitrosodimethylamine precursors during microbial metabolism of amino acids. <b>2023</b> , 874, 162469	O
435	First report of enterotoxigenic Staphylococcus argenteus as a foodborne pathogen. 2023, 394, 110182	O
434	Exploration of urease-mediated biomineralization for defluoridation by Proteus columbae MLN9 with an emphasis on its genomic characterization. <b>2023</b> , 11, 109791	Ο
433	One global disseminated 193 kb high-risk hybrid plasmid harboring tet(X4), mcr or blaNDM threatening public health. <b>2023</b> , 876, 162807	О
432	New insights into the role of key microorganisms and wooden barrels during lambic beer fermentation and maturation. <b>2023</b> , 394, 110163	Ο
431	Pan-genome analysis of the Burkholderia gladioli PV. Cocovenenans reveal the extent of variation in the toxigenic gene cluster. <b>2023</b> , 113, 104249	1
430	Comprehensive genome analysis of Burkholderia contaminans SK875, a quorum-sensing strain isolated from the swine. <b>2023</b> , 13,	Ο
429	Myeloid TLR4 signaling promotes post-injury withdrawal resolution of murine liver fibrosis. <b>2023</b> , 26, 106220	O
428	Genomic characterization of endemic diarrheagenic Escherichia coli and Escherichia albertii from infants with diarrhea in Vietnam. <b>2023</b> , 17, e0011259	O
427	Microbial community composition and metabolic potential during a succession of algal blooms from Skeletonema sp. to Phaeocystis sp 14,	0
426	Characterization of phytopathogen-preying Hyalangium versicolor sp. nov., and proposal for the reclassification of Cystobacter gracilis as Hyalangium gracile comb. Nov. <b>2023</b> , 205,	O
425	Potential reservoirs of antimicrobial resistance in livestock waste and treated wastewater that can be disseminated to agricultural land. <b>2023</b> , 872, 162194	0
424	Dissolved storage glycans shaped the community composition of abundant bacterioplankton clades during a North Sea spring phytoplankton bloom. <b>2023</b> , 11,	O
423	Activity and diversity of prophages harbored by wheat phyllosphere bacteria.	О
422	A Multiplexed, Tiled PCR Method for Rapid Whole-Genome Sequencing of Infectious Spleen and Kidney Necrosis Virus (ISKNV) in Tilapia. <b>2023</b> , 15, 965	O

421	Bacterial benz(a)anthracene catabolic networks in contaminated soils and their modulation by other co-occurring HMW-PAHs. <b>2023</b> , 328, 121624	О
420	River sediment microbial community composition and function impacted by thallium spill. <b>2023</b> , 880, 163101	О
419	Complete genome sequence data of Leuconostoc mesenteroides KNU-2 and Weissella hellenica MBEL1842 isolated from kimchi. <b>2023</b> , 47, 108919	0
418	Description of Dryocola gen. nov. and two novel species, Dryocola boscaweniae sp. nov. and Dryocola clanedunensis sp. nov. isolated from the rhizosphere of native British oaks. <b>2023</b> , 46, 126399	O
417	Surveillance of 16 UK native bat species through conservationist networks uncovers coronaviruses with zoonotic potential.	0
416	Characterization of isogenic mutants with single or double deletions of four phenolic acid esterases in Lactiplantibacillus plantarum TMW1.460. <b>2023</b> , 388, 110100	О
415	Rapid fluorescence visualization of Yersinia enterocolitica by CRISPR/Cas12a using novel specific target obtained by pan-genome analysis. <b>2023</b> , 175, 114500	0
414	A novel higher polyhydroxybutyrate producer Halomonas halmophila 18H with unique cell factory attributes. <b>2023</b> , 372, 128669	О
413	Agrobacterium cucumeris sp. nov. isolated from crazy roots on cucumber (Cucumis sativus). <b>2023</b> , 46, 126402	О
412	Molecular characterization of Arcobacter butzleri isolates from poultry in rural Ghana. 13,	О
411	Genome Analysis Identifies a Novel Type III Secretion System (T3SS) Category in Vibrio Species. <b>2023</b> , 11, 290	0
410	Genome sequencing and comparative genomic analysis of bovine mastitis-associated Staphylococcus aureus strains from India. <b>2023</b> , 24,	O
409	Closed genomes uncover a saltwater species of Candidatus Electronema and shed new light on the boundary between marine and freshwater cable bacteria. <b>2023</b> , 17, 561-569	0
408	Rapid emergence of extensively drug-resistant Shigella sonnei in France. 2023, 14,	O
407	The persistence of time: the lifespan of Bacillus anthracis spores in environmental reservoirs. 2023, 104029	0
406	Airborne antibiotic resistome and human health risk in railway stations during COVID-19 pandemic. <b>2023</b> , 172, 107784	O
405	High abundance of hydrocarbon-degrading Alcanivorax in plumes of hydrothermally active volcanoes in the South Pacific Ocean. <b>2023</b> , 17, 600-610	0
404	Evaluation of novel isolates of Lacticaseibacillus rhamnosus Probio-M9 derived through space mutagenesis. <b>2023</b> , 52, 102456	О

403	The Impact of Colistin Resistance on the Activation of Innate Immunity by Lipopolysaccharide Modification. <b>2023</b> , 91,	O
402	The diversity and metabolism of culturable nitrate-reducing bacteria from the photic zone of the Western North Pacific Ocean.	Ο
401	Tracking the Emergence and Dissemination of a bla NDM-23 Gene in a Multidrug Resistance Plasmid of Klebsiella pneumoniae. <b>2023</b> , 11,	0
400	Comparative metagenomics at Solfatara and Pisciarelli hydrothermal systems in Italy reveal that ecological differences across substrates are not ubiquitous. 14,	O
399	Comparative Genomic Analysis Reveals the Functional Traits and Safety Status of Lactic Acid Bacteria Retrieved from Artisanal Cheeses and Raw Sheep Milk. <b>2023</b> , 12, 599	O
398	Contrasting Genetic Diversity of Listeria Pathogenicity Islands 3 and 4 Harbored by Nonpathogenic Listeria spp <b>2023</b> , 89,	O
397	Genome-based reclassification of Anoxybacillus salavatliensis Cihan et al. 2011 as a later heterotypic synonym of Anoxybacillus gonensis Belduz et al. 2003.	0
396	Genomic epidemiology of the primary methicillin-resistantStaphylococcus aureusclones causing invasive infections in Paraguayan children.	O
395	Genomic epidemiology of Mycobacterium avium subsp. paratuberculosis isolates from Canadian dairy herds provides evidence for multiple infection events. 14,	0
394	Whole-genome analysis of a Vibrio cholerae O1 biotype classical strain isolated in 1946 in Sasebo city, Nagasaki prefecture, from a returnee from the northeast part of China. <b>2023</b> , 51,	O
393	Functional analysis of metalloenzymes from human gut microbiota and their role in ulcerative colitis. <b>2023</b> , 134,	0
392	Genome-wide association and dissociation studies in Pantoea ananatis reveal potential virulence factors affecting Allium porrum and Allium fistulosum []Allium cepa hybrid. 13,	O
391	Genome-wide transcriptional response of Escherichia coli O157:H7 to light-emitting diodes with various wavelengths. <b>2023</b> , 13,	0
390	Identifying and tracking mobile elements in evolving compost communities yields insights into the nanobiome.	O
389	Evidence for a core set of microbial lichen symbionts from a global survey of metagenomes.	0
388	Proteus mirabilis isolated from untreated hospital wastewater, Ibadan, Southwestern Nigeria showed low-level resistance to fluoroquinolone and carried qnrD3 on Col3M plasmids. <b>2023</b> , 30, 47158-47167	0
387	Genetic determinants of host tropism in Klebsiella phages. <b>2023</b> , 42, 112048	2
386	Diverse secondary metabolites are expressed in particle-associated and free-living microorganisms of the permanently anoxic Cariaco Basin. <b>2023</b> , 14,	О

385	Microbiota-derived acetate enhances host antiviral response via NLRP3. 2023, 14,	1
384	Laboratory strains of Escherichia coli K-12: things are seldom what they seem. <b>2023</b> , 9,	О
383	A molecular epidemiological study on Escherichia coli in young chicks with colibacillosis identified two possible outbreaks across farms. <b>2023</b> , 54,	0
382	Phenotypic and genetic alterations of Burkholderia pseudomallei in patients during relapse and persistent infections. 14,	O
381	Guild-Level Microbiome Signature Associated with COVID-19 Severity and Prognosis. 2023, 14,	0
380	Supergroup F Wolbachia with extremely reduced genome: transition to obligate insect symbionts. <b>2023</b> , 11,	О
379	Interspecies Horizontal Transfer and Specific Integration of the Mosquitocidal Toxin-Encoding Plasmid pTAND672-2 from Bacillus thuringiensis subsp. israelensis to Lysinibacillus sphaericus. <b>2023</b> , 89,	O
378	Aristophania vespae gen. nov., sp. nov., isolated from wasps, is related to Bombella and Oecophyllibacter, isolated from bees and ants. <b>2023</b> , 73,	О
377	Insights into the genome of Methylobacterium sp. NMS14P, a novel bacterium for growth promotion of maize, chili, and sugarcane. <b>2023</b> , 18, e0281505	O
376	Copper removal capability and genomic insight into the lifestyle of copper mine inhabiting Micrococcus yunnanensis GKSM13. <b>2023</b> , 223, 115431	O
375	Dynamics of the MRSA Population in A Chilean Hospital: A Phylogenomic Analysis (2000-2016).	O
374	Marine Picoplankton Metagenomes from Eleven Vertical Profiles Obtained by the Malaspina Expedition in the Tropical and Subtropical Oceans.	O
373	A nontuberculous mycobacterium could solve the mystery of the lady from the Franciscan church in Basel, Switzerland. <b>2023</b> , 21,	0
372	Corynebacterium megadyptis sp. nov. with two subspecies, Corynebacterium megadyptis subsp. megadyptis subsp. nov. and Corynebacterium megadyptis subsp. dunedinense subsp. nov. isolated from yellow-eyed penguins. <b>2023</b> , 73,	O
371	Phocaeicola oris sp. nov., an anaerobic bacterium isolated from the saliva of a patient with oral squamous cell carcinoma. <b>2023</b> , 73,	0
370	PanViTa: Pan Virulence and resisTance analysis. 3,	1
369	CeftazidimeBvibactam resistance in Klebsiella pneumoniae sequence type 37: a decade of persistence and concealed evolution. <b>2023</b> , 9,	О
368	Adding context to the pneumococcal core genes using bioinformatic analysis of the intergenic pangenome of Streptococcus pneumoniae. 3,	O

367	How Can Omics Inform Diabetic Foot Ulcer Clinical Management? A Whole Genome Comparison of Four Clinical Strains of Staphylococcus aureus. <b>2023</b> , 27, 51-61	0
366	Within-host resistance evolution of a fatal ST11 hypervirulent carbapenem-resistant Klebsiella pneumoniae. <b>2023</b> , 61, 106747	O
365	Can non-typeable Haemophilus influenzae carriage surveillance data infer antimicrobial resistance associated with otitis media?. <b>2023</b> , 7, 13-22	0
364	Hypervirulent Klebsiella pneumoniae Causing Neonatal Bloodstream Infections: Emergence of NDM-1-Producing Hypervirulent ST11-K2 and ST15-K54 Strains Possessing pLVPK-Associated Markers. <b>2023</b> , 11,	O
363	Metagenomic Analysis of Anaerobic Microbial Communities Degrading Short-Chain Fatty Acids as Sole Carbon Sources. <b>2023</b> , 11, 420	0
362	Discovery of the gut microbial enzyme responsible for bilirubin reduction to urobilinogen.	O
361	Temporal Dynamics of Genetically Heterogeneous Extended-Spectrum Cephalosporin ResistantEscherichia coliBloodstream Infections.	О
360	One to host them all: genomics of the diverse bacterial endosymbionts of the spider Oedothorax gibbosus. <b>2023</b> , 9,	O
359	Identification of phenotypic and genotypic properties and cold adaptive mechanisms of novel freezethaw stress-resistant strain Pseudomonas mandelii from Antarctica. <b>2023</b> , 46, 169-183	О
358	A global virome of methanogenic archaea highlights novel diversity and adaptations to the gut environment.	O
357	Genomic Epidemiology of Streptococcus pneumoniae Isolated in a Tertiary Hospital in Beijing, China, from 2018 to 2022. <b>2023</b> , 12, 284	О
356	Extracellular proteases are an essential public good supportingBacillus subtilisgrowth through exogenous protein degradation.	O
355	Nanofibers with genotyped Bacillus strains exhibiting antibacterial and immunomodulatory activity. <b>2023</b> , 355, 371-384	Ο
354	Enrichment of tetracycline-degrading bacterial consortia: Microbial community succession and degradation characteristics and mechanism. <b>2023</b> , 448, 130984	O
353	Next-generation sequencing approach to investigate genome variability of Parapoxvirus in Canadian muskoxen (Ovibos moschatus). <b>2023</b> , 109, 105414	0
352	Comparative Genomics of Legionella pneumophila Isolates from the West Bank and Germany Support Molecular Epidemiology of LegionnairesDisease. <b>2023</b> , 11, 449	O
351	Phylogenetic distance and structural diversity directing a reclassification of glycopeptide antibiotics.	0
350	Genomic analysis of the international high-risk clonal lineage Klebsiella pneumoniae sequence type 395. <b>2023</b> , 15,	O

349	Comparative genomics reveals the acquisition of mobile genetic elements by the plant growth-promoting Pantoea eucrina OB49 in polluted environments. <b>2023</b> , 115, 110579	Ο
348	Characterization of Bacillus Strains from Natural Honeybee Products with High Keratinolytic Activity and Antimicrobial Potential. <b>2023</b> , 11, 456	O
347	Periodontal disease is associated with increased gut colonization of pathogenic Haemophilus parainfluenzae in patients with Crohn disease. <b>2023</b> , 42, 112120	O
346	Aeromonas salmonicida isolates from Canada demonstrate wide distribution and clustering among mesophilic strains.	О
345	Genomic insights into antibiotic resistance and mobilome of lactic acid bacteria and bifidobacteria. <b>2023</b> , 6, e202201637	O
344	Comparative Genomics Identifies Novel Genetic Changes Associated with Oxacillin, Vancomycin and Daptomycin Susceptibility in ST100 Methicillin-Resistant Staphylococcus aureus. <b>2023</b> , 12, 372	O
343	Phenotypic Characterization and Comparative Genomic Analysis of Novel Salmonella Bacteriophages Isolated from a Tropical Rainforest. <b>2023</b> , 24, 3678	O
342	Expansion of Kuravirus-like Phage Sequences within the Past Decade, including Escherichia Phage YF01 from Japan, Prompt the Creation of Three New Genera. <b>2023</b> , 15, 506	O
341	Genome Sequences of Comamonadaceae Bacteria OS-1 and OS-4, Two Highly H 2 O 2 -Sensitive Strains Isolated from Pond Water. <b>2023</b> , 12,	0
340	Biotechnologically potential genes in a polysaccharide-degrading epibiont of the Indonesian brown algae Hydroclathrus sp <b>2023</b> , 21,	O
339	Comparison of the relative impacts of acute consumption of an inulin-enriched diet, milk kefir or a commercial probiotic product on the human gut microbiome and metabolome.	O
338	Plasmids manipulate bacterial behaviour through translational regulatory crosstalk. <b>2023</b> , 21, e3001988	O
337	Transcriptome and Proteome of Methicillin-Resistant Staphylococcus aureus Small-Colony Variants Reveal Changed Metabolism and Increased Immune Evasion. <b>2023</b> , 11,	O
336	Ecology, more than antibiotics consumption, is the major predictor for the global distribution of aminoglycoside-modifying enzymes. 12,	1
335	Diverse Populations of Staphylococcus pseudintermedius Colonize the Skin of Healthy Dogs. <b>2023</b> , 11,	O
334	Streptococcus suis outbreak caused by an emerging zoonotic strain with acquired multi-drug resistance in Thailand. <b>2023</b> , 9,	O
333	Increased Amino Acid Absorption Mediated by Lacticaseibacillus rhamnosus IDCC 3201 in High-Protein Diet-Fed Mice. <b>2023</b> ,	0
332	Horizontal Gene Transfer, Fitness Costs and Mobility Shape the Spread of Antibiotic Resistance Genes into Experimental Populations of Acinetobacter Baylyi. <b>2023</b> , 40,	O

331	Maribacter halichondrissp. nov., isolated from the marine spongeHalichondria panicea.	O
330	Fructilactobacillus cliffordii sp. nov., Fructilactobacillus hinvesii sp. nov., Fructilactobacillus myrtifloralis sp. nov., Fructilactobacillus carniphilus sp. nov. and Fructobacillus americanaquae sp. nov., five novel lactic acid bacteria isolated from insects or flowers of Kangaroo Island, South	O
329	A diverse repertoire of anti-defense systems is encoded in the leading region of plasmids.	O
328	Comparative genome identification of accessory genes associated with strong biofilm formation in Vibrio parahaemolyticus. <b>2023</b> , 166, 112605	O
327	Co-cultivation is a powerful approach to produce a robust functionally designed synthetic consortium as a live biotherapeutic product (LBP). <b>2023</b> , 15,	0
326	Genomic diversity in Fructobacillus spp. isolated from fructose-rich niches. <b>2023</b> , 18, e0281839	O
325	MGnify Genomes: A Resource for Biome-specific Microbial Genome Catalogues. 2023, 168016	0
324	First insights into the gut microbiome of Diatraea saccharalis: From a sugarcane pest to a reservoir of new bacteria with biotechnological potential. 11,	O
323	Emergence and Evolution of OXA-23-Producing ST46Pas-ST462Oxf-KL28-OCL1 Carbapenem-Resistant Acinetobacter baumannii Mediated by a Novel ISAba1-Based Tn7534 Transposon. <b>2023</b> , 12, 396	O
322	The NagY regulator: A member of the BglG/SacY antiterminator family conserved in Enterococcus faecalis and involved in virulence. 13,	O
321	ABUNDANCE OF PHAGE-RELATED SEQUENCES ON NON-SYMBIOTIC PLASMIDS OF SINORHIZOBIUM MELILOTI FROM CENTERS OF LEGUME PLANTS DIVERSITY. <b>2022</b> ,	O
320	A novel variant of theListeria monocytogenestype VII secretion system EssC component is associated with an Rhs toxin.	O
319	Genome-resolved metagenomics inferred novel insights into the microbial community, metabolic pathways, and biomining potential of Malanjkhand acidic copper mine tailings. <b>2023</b> , 30, 50864-50882	O
318	Population genomics-guided engineering of phenazine biosynthesis inPseudomonas chlororaphis.	O
317	Evidence of structural rearrangements in ESBL-positive pESI(like) megaplasmids of S.Infantis. <b>2023</b> , 370,	O
316	Computational Insight into Intraspecies Distinctions in Pseudoalteromonas distincta: Carotenoid-like Synthesis Traits and Genomic Heterogeneity. <b>2023</b> , 24, 4158	O
315	High-throughput microbial culturomics using automation and machine learning.	1
314	Genome-centric metagenomic insights into the role of Chloroflexi in anammox, activated sludge and methanogenic reactors. <b>2023</b> , 23,	O

313	Genomic Epidemiological Analysis of Antimicrobial-Resistant Bacteria with Nanopore Sequencing. <b>2023</b> , 227-246	0
312	Genomic and clinical characteristics of carbapenem-resistant Enterobacter cloacae complex isolates collected in a Chinese tertiary hospital during 2013\( \begin{align*} 2013\(	O
311	Whole-genome-based characterization of Campylobacter jejuni from human patients with gastroenteritis collected over an 18 year period reveals increasing prevalence of antimicrobial resistance. <b>2023</b> , 9,	0
310	Community composition and the environment modulate the population dynamics of type VI secretion in human gut bacteria.	О
309	Collection of Annotated Acinetobacter Genome Sequences. 2023, 12,	O
308	Development of Synbiotic Preparations That Restore the Properties of Cattle Feed Affected by Toxin-Forming Micromycetes. <b>2023</b> , 13, 523	O
307	Genome-Based Analysis of the Potential Bioactivity of the Terrestrial Streptomyces vinaceusdrappus Strain AC-40. <b>2023</b> , 12, 345	O
306	Characteristics of Extended-Spectrum Lactamase Producing Enterobacterales Isolated from Dogs and Cats, 2011 2021. <b>2023</b> , 10, 178	О
305	Draft Genome Sequences of Spacecraft-Associated Microbes Isolated from Six NASA Missions. <b>2023</b> , 12,	О
304	Genetic and enzymatic characterization of two novel blaNDM-36, -37 variants in Escherichia coli strains. <b>2023</b> , 42, 471-480	О
303	Comparative Genomic Analysis and Physiological Properties of Limosilactobacillus fermentum SMFM2017-NK2 with Ability to Inflammatory Bowel Disease. <b>2023</b> , 11, 547	o
302	Draft Genome Sequences of Three Bacterial Species from Aquatic Habitats near Washington, DC. <b>2023</b> , 12,	О
301	Improved Genomic Prediction of Staphylococcus epidermidis Isolation Sources with a Novel Polygenic Score. <b>2023</b> , 61,	0
300	Complete Genome Sequences of Bioluminescent Staphylococcus aureus Strains Xen31 and Xen36, Derived from Two Clinical Isolates. <b>2023</b> , 12,	О
299	High-Throughput Mutagenesis Reveals a Role for Antimicrobial Resistance- and Virulence-Associated Mobile Genetic Elements in Staphylococcus aureus Host Adaptation. <b>2023</b> , 11,	0
298	Oxygen intrusions sustain aerobic nitrite oxidation in anoxic marine zones.	О
297	Strain-level bacterial typing directly from patient samples using optical DNA mapping. 2023, 3,	0
296	Highly conserved composite transposon harbouring aerobactin iuc3 in Klebsiella pneumoniae from pigs. <b>2023</b> , 9,	О

295	Genomic, metabolomic, and functional characterisation of beneficial properties of Pediococcus pentosaceus ST58, isolated from human oral cavity. <b>2023</b> , 14, 57-72	0
294	In Silico Evidence of the Multifunctional Features of Lactiplantibacillus pentosus LPG1, a Natural Fermenting Agent Isolated from Table Olive Biofilms. <b>2023</b> , 12, 938	1
293	Extending and improving metagenomic taxonomic profiling with uncharacterized species using MetaPhlAn 4.	0
292	PCR Assay for Rapid Taxonomic Differentiation of Virulent Staphylococcus aureus and Klebsiella pneumoniae Bacteriophages. <b>2023</b> , 24, 4483	O
291	The gastrointestinal antibiotic resistome in pediatric leukemia and lymphoma patients. 13,	0
<b>2</b> 90	Multiomic spatial analysis reveals a distinct mucosa-associated virome. 2023, 15,	O
289	Detection of Streptococcus pyogenes M1UK in Australia and characterization of the mutation driving enhanced expression of superantigen SpeA. <b>2023</b> , 14,	0
288	Saccharomyces cerevisiae fermentation product improves robustness of equine gut microbiome upon stress. 10,	O
287	Revealing within-species diversity in uncultured human gut bacteria with single-cell long-read sequencing. 14,	0
286	Genomic characterization and molecular dating of the novel bacterium Permianibacter aggregans HW001T, which originated from Permian ground water. <b>2023</b> , 5, 12-27	O
285	Genomic Comparative Analysis of Two Multi-Drug Resistance (MDR) Acinetobacter baumannii Clinical Strains Assigned to International Clonal Lineage II Recovered Pre- and Post-COVID-19 Pandemic. <b>2023</b> , 12, 358	0
284	Draft genomes of three closely related low light-adapted Prochlorococcus. 2023, 24,	O
283	Thermomonas paludicola sp. nov., isolated from a lotus wetland. 2023, 73,	О
282	Identification of further variation at the lipooligosaccharide outer core locus inAcinetobacter baumanniigenomes and extension of the OCL reference sequence database forKaptive.	O
281	Actinobacillus pleuropneumoniaeencodes multiple phase-variable DNA methyltransferases that control distinct phasevarions.	0
280	Comparative Genomics of Halobacterium salinarum Strains Isolated from Salted Foods Reveals Protechnological Genes for Food Applications. <b>2023</b> , 11, 587	O
279	Whole-genome sequence analysis of clinically isolated carbapenem resistant Escherichia coli from Iran. <b>2023</b> , 23,	O
278	Circulating androgen regulation by androgen-catabolizing gut bacteria in male mouse gut. <b>2023</b> , 15,	O

277	Genomic Characterization of a Vancomycin-Resistant Strain of Enterococcus faecium Harboring a rep2 Plasmid. Volume 16, 1153-1158	Ο
276	Whole genome sequencing ofBorrelia burgdorferiisolates reveals linked clusters of plasmid-borne accessory genome elements associated with virulence.	O
275	Protein embeddings improve phage-host interaction prediction.	О
274	Can Probiotics, Particularly Limosilactobacillus fermentum UCO-979C and Lacticaseibacillus rhamnosus UCO-25A, Be Preventive Alternatives against SARS-CoV-2?. <b>2023</b> , 12, 384	O
273	Associations between picocyanobacterial ecotypes and cyanophage host genes across ocean basins and depth. 11, e14924	0
272	Insights into the Evolution of P. aeruginosa Antimicrobial Resistance in a Patient Undergoing Intensive Therapy. <b>2023</b> , 12, 483	0
271	Molecular Characterization and Clinical Relevance of Taxonomic Reassignment of Staphylococcus schleiferi Subspecies into Two Separate Species, Staphylococcus schleiferi and Staphylococcus coagulans. <b>2023</b> , 11,	O
270	Emergence of Carbapenemase-Producing Hypervirulent Klebsiella pneumoniae in Switzerland.	O
269	Complete Genome Sequences of Oryctes rhinoceros nudivirus Strains Detected in Haplotype-G Oryctes rhinoceros from Johor, Malaysia. <b>2023</b> , 12,	0
268	The Prevalence of Plasmid-Mediated Colistin Resistance Gene mcr-1 and Different Transferability and Fitness of mcr-1 -Bearing IncX4 Plasmids in Escherichia coli from Pigeons. <b>2023</b> , 11,	O
267	Clonal Expansion of Multidrug-Resistant Streptococcus dysgalactiae Subspecies equisimilis Causing Bacteremia, Japan, 2005[021. <b>2023</b> , 29, 528-539	0
266	Complete Genome Sequence of an Escherichia coli Strain Isolated from Laboratory Mouse Stool for Use as a Chassis for Transgene Delivery to the Murine Microbiome. <b>2023</b> , 12,	O
265	Genomic attributes of Vibrio cholerae O1 responsible for 2022 massive cholera outbreak in Bangladesh. <b>2023</b> , 14,	0
264	Identification and pathogenic (toxicogenic) potential of Staphylococcus haemolyticus and Bacillus paranthracis consortia isolated from bovine mastitis in Russia.	O
263	Challenges of Whole Genome Sequencing based Molecular Identification of Zoonotic Tuberculosis caused by Mycobacterium orygis.	0
262	The Space Environment Activates Capsular Polysaccharide Production in Lacticaseibacillus rhamnosus Probio-M9 by Mutating the wze ( ywqD ) Gene. <b>2023</b> , 11,	O
261	Antimicrobial resistance in Campylobacter fetus: emergence and genomic evolution. 2023, 9,	0
<b>2</b> 60	Comparative genomic analysis provides insights into taxonomy and temperature adaption of Aeromonas salmonicida. <b>2023</b> , 46, 545-561	O

259	Shifts from cooperative to individual-based predation defense determine microbial predator-prey dynamics. <b>2023</b> , 17, 775-785	O
258	A bacterial genome assembly and annotation laboratory using a virtual machine.	O
257	Genomic Characterization and Wetland Occurrence of a Novel Campylobacter Isolate from Canada Geese. <b>2023</b> , 11, 648	0
256	Exploring microbial functional biodiversity at the protein family level!From metagenomic sequence reads to annotated protein clusters. 3,	O
255	Identification and characterization of opportunistic pathogen Pectobacterium polonicum causing potato blackleg in China. 14,	O
254	Whole-genome sequencing-based characterization of Streptomyces sp. 6(4): focus on natural product. <b>2023</b> , 5,	O
253	Conservation of Genomic Information in Multiple Displacement Amplified Low-Quantity Metagenomic Material from Marine Invertebrates. <b>2023</b> , 21, 165	0
252	Bioinformatic survey of CRISPR loci across 15 Serratia species. <b>2023</b> , 12,	O
251	Whole Genome Sequence of a Novel Bacteriophage APT65 Infecting Aeromonas hydrophila. <b>2023</b> , 4, 46-50	0
250	PhaGAA: an integrated web server platform for phage genome annotation and analysis. 2023, 39,	O
249	Screening for Clostridioides difficile colonization at admission to the hospital: a multi-centre study. <b>2023</b> ,	O
248	Class 1 integrons and multiple mobile genetic elements in clinical isolates of the Klebsiella pneumoniae complex from a tertiary hospital in eastern China. 14,	O
247	Genomic Features Predict Bacterial Life History Strategies in Soil, as Identified by Metagenomic Stable Isotope Probing.	O
246	Genome-resolved metagenomics reveals abundant nitrate reducers and partitioning of nitrite usage within global oxygen deficient zones.	O
245	The abundance of the potential pathogen Staphylococcus hominis in the air microbiome in a dental clinic and its susceptibility to far-UVC light. <b>2023</b> , 12,	0
244	Spontaneous Genomic Variation as a Survival Strategy of Nosocomial Staphylococcus haemolyticus. <b>2023</b> , 11,	O
243	Virus diversity and activity is driven by snowmelt and host dynamics in a high-altitude watershed soil ecosystem.	0
242	Experimental evolution forcing Oenococcus oeni acid tolerance highlights critical role of the citrate locus. <b>2023</b> , 104048	О

241	Genetic Characterization of Listeria from Food of Non-Animal Origin Products and from Producing and Processing Companies in Bavaria, Germany. <b>2023</b> , 12, 1120	0
240	Impacts of Domestication and Veterinary Treatment on Mobile Genetic Elements and Resistance Genes in Equine Fecal Bacteria. <b>2023</b> , 89,	O
239	The terrestrial isopod symbiont Candidatus Hepatincola porcellionumlis a potential nutrient scavenger related to Holosporales symbionts of protists. <b>2023</b> , 3,	0
238	Closely relatedBacteroidesof the murine intestinal microbiota affect each other growth positively or negatively.	O
237	Hologenome analysis reveals independent evolution to chemosymbiosis by deep-sea bivalves. <b>2023</b> , 21,	0
236	Core genome multilocus sequence typing scheme for Bacillus cereus group bacteria. <b>2023</b> , 104050	O
235	Genome Analysis of Pseudomonas aeruginosa Strains from Chronically Infected Patients with High Levels of Persister Formation. <b>2023</b> , 12, 426	0
234	Draft Genomes of Two Fusobacterium simiae Strains. <b>2023</b> , 12,	O
233	Development of the oral resistome during the first decade of life. 2023, 14,	О
232	A hydrogenotrophic Sulfurimonas is globally abundant in deep-sea oxygen-saturated hydrothermal plumes. <b>2023</b> , 8, 651-665	O
231	Genus-Wide Genomic Characterization of Macrococcus: Insights into Evolution, Population Structure, and Functional Potential.	0
230	Genomic determinants of soil depth niche partitioning in Gagatemarchaeaceae, a novel family of deeply-rooted Thaumarchaeota.	O
229	Phenotypic and genotypic survey of antibiotic resistance in Salmonella enterica isolates from dairy farms in Uruguay. 10,	O
228	Circulation of enterotoxigenic Escherichia coli (ETEC) isolates expressing CS23 from the environment to clinical settings.	O
227	Bacterial aerobic methane cycling by the marine sponge-associated microbiome. 2023, 11,	0
226	Inference and reconstruction of the heimdallarchaeial ancestry of eukaryotes.	O
225	Mechanisms of low susceptibility to the disinfectant benzalkonium chloride in a multidrug-resistant environmental isolate of Aeromonas hydrophila.	0
224	Comammox Nitrospira and Ammonia-Oxidizing Archaea Are Dominant Ammonia Oxidizers in Sediments of an Acid Mine Lake Containing High Ammonium Concentrations. <b>2023</b> , 89,	O

223	Comparative Genomic Analysis of Enterococci across Sectors of the One Health Continuum. <b>2023</b> , 11, 727	O
222	A phylogenomic analysis of Limosilactobacillus reuteri reveals ancient and stable evolutionary relationships with rodents and birds and zoonotic transmission to humans. <b>2023</b> , 21,	O
221	Genome Analysis of Two Pseudomonas syringae pv. aptata Strains with Different Virulence Capacity Isolated from Sugar Beet: Features of Successful Pathogenicity in the Phyllosphere Microbiome. <b>2023</b> , 11,	О
220	Distinct Wolbachia localization patterns in oocytes of diverse host species reveal multiple strategies of maternal transmission.	O
219	The tropical cookbook: Termite diet and phylogenetics Dver geographical origin Drive the microbiome and functional genetic structure of nests. 14,	О
218	Extended-Spectrum Lactamase Genes Traverse the Escherichia coli Populations of Intensive Care Unit Patients, Staff, and Environment. <b>2023</b> , 11,	O
217	Brevicillin, a novel lanthipeptide from the genusBrevibacilluswith antimicrobial, antifungal, and antiviral activity. <b>2023</b> , 134,	О
216	Beta-Lactam Susceptibility Profiles of Bacteria Isolated from the Ozama River in Santo Domingo, Dominican Republic. <b>2023</b> , 15, 5109	O
215	New insights into the impact of microbiome on horizontal and vertical transmission of a tick-borne pathogen. <b>2023</b> , 11,	О
214	Metabolic Versatility of the Family Halieaceae Revealed by the Genomics of Novel Cultured Isolates. <b>2023</b> , 11,	O
213	Genotypic and Phenotypic Characterization of Some psms Hypervirulent Clinical Isolates of Staphylococcus aureus in a Tertiary Hospital in Hefei, Anhui. Volume 16, 1471-1484	O
212	Activating a dormant metabolic pathway for high-temperature l-alanine production in Bacillus licheniformis. <b>2023</b> , 26, 106397	O
211	Whole genome sequencing revealed a high level of antimicrobial resistance genes and virulence factors in a multidrug-resistant Citrobacter freundii BAU_TM8 strain isolated from a domesticated duck in Bangladesh.	0
210	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,	O
209	TheHaemophilus influenzaein vivo gene expression reveals major clues about bacterial central metabolism, acquisition of trace elements, and other essential pathways during infection of the human lung.	О
208	A swapped genetic code prevents viral infections and gene transfer. <b>2023</b> , 615, 720-727	O
207	Unlocking the microbial studies through computational approaches: how far have we reached?. <b>2023</b> , 30, 48929-48947	О
206	Genomic Characterization of Staphylococcus aureus in Wildlife. 2023, 13, 1064	O

205	Phylogenomic analysis of the genus Rosenbergiella and description of Rosenbergiella gaditana sp. nov., Rosenbergiella metrosideri sp. nov., Rosenbergiella epipactidis subsp. nov., Rosenbergiella epipactidis subsp. californiensis subsp. nov., Rosenbergiella epipactidis subsp.	Ο
204	japonicus subsp. nov., Rosenbergiella nectarea subsp. nectarea subsp. nov. and Rosenbergiella Ligilactobacillus ubinensis sp. nov., a novel species isolated from the wild ferment of a durian fruit (Durio zibethinus). <b>2023</b> , 73,	Ο
203	A pangenome approach-based loop-mediated isothermal amplification assay for the specific and early detection of Bordetella pertussis. <b>2023</b> , 13,	0
202	Mobile genetic elements drive the multidrug resistance and spread of Salmonella serotypes along a poultry meat production line. 14,	O
201	Taxonomic distribution of metabolic functions underpins nutrient cycling inTrichodesmiumconsortia.	0
200	Monitoring Longitudinal Trends and Assessment of the Health Risk of Shigella flexneri Antimicrobial Resistance. <b>2023</b> , 57, 4971-4983	O
199	A food poisoning caused by ST7 Staphylococcal aureus harboring sea gene in Hainan province, China. 14,	0
198	Spatial profiling of microbial communities by sequential FISH with error-robust encoding. <b>2023</b> , 14,	O
197	Tamlana laminarinivorans sp. nov. and Tamlana sargassicola sp. nov., two novel species isolated from Sargassum, show genomic and physiological adaptations for a Sargassum-associated lifestyle. <b>2023</b> , 73,	О
196	Systematic analysis of prophage elements in actinobacterial genomes reveals a remarkable phylogenetic diversity. <b>2023</b> , 13,	O
195	Plasmid-Mediated Colistin Resistance Genes mcr-1 and mcr-4 in Multidrug-Resistant Escherichia coli Strains Isolated from a Healthy Pig in Portugal. <b>2023</b> , 29, 78-84	0
194	Adaptation Strategies to High Hydrostatic Pressures in Pseudothermotoga species Revealed by Transcriptional Analyses. <b>2023</b> , 11, 773	O
193	Emergence of Mobile Colistin Resistance Genes within Los Angeles County Wastewater. <b>2023</b> , 10, 316-321	0
192	Characterization of a Plant Growth-Promoting Endohyphal Bacillus subtilis in Fusarium acuminatum from Spiranthes sinensis. <b>2023</b> , 72, 29-37	O
191	Metagenomic sequencing reveals swine lung microbial communities and metagenome-assembled genomes associated with lung lesions pilot study.	0
190	Diverse and Abundant Viruses Exploit Conjugative Plasmids.	O
189	Endogenous Plasmids and Chromosomal Genome Reduction in the Cardinium Endosymbiont of Dermatophagoides farinae. <b>2023</b> , 8,	0
188	Luteimonas galliterrae sp. nov., isolated from poultry farm soil. <b>2023</b> , 73,	O

187	Elucidating the genomic history of commercially used Bacillus thuringiensis subsp. tenebrionis strain NB176. 13,	O
186	A Representative Collection of Commensal Extended-Spectrum- and AmpC-FLactamase-Producing Escherichia coli of Animal Origin for Phage Sensitivity Studies. <b>2023</b> , 4, 35-45	O
185	Diversity of the genus Cryobacterium and proposal of 19 novel species isolated from glaciers. 14,	0
184	Vancomycin Resistance in Enterococcus faecium from the Dallas, Texas, Area Is Conferred Predominantly on pRUM-Like Plasmids. <b>2023</b> , 8,	O
183	Sifting through the core-genome to identify putative cross-protective antigens against Riemerella anatipestifer. <b>2023</b> , 107, 3085-3098	О
182	Potential selection and maintenance of manure-originated multi-drug resistant plasmids at sub-clinical antibiotic concentrations.	O
181	Citrobacter meridianamericanus sp. nov., isolated from a soil sample. <b>2023</b> , 73,	O
180	Development and Clinical Application of a Multilocus Sequence Typing Scheme for Bacteroides fragilis Based on Whole-Genome Sequencing Data. <b>2023</b> , 11,	O
179	Evidence for a Putative Isoprene Reductase in Acetobacterium wieringae.	0
178	Contingency, Repeatability and Predictability in the Evolution of a Prokaryotic Pangenome.	O
177	Toward novel treatment against filariasis: Insight into genome-wide co-evolutionary analysis of filarial nematodes and Wolbachia. 14,	0
176	Isolation and characterisation of novel Methanocorpusculum species indicates the genus is ancestrally host-associated. <b>2023</b> , 21,	0
175	Rapid adaptations of Legionella pneumophila to the human host. <b>2023</b> , 9,	O
174	Comparative genomics of Mycoplasma feriruminatoris, a fast-growing pathogen of wild Caprinae.	O
173	Multi-faceted metagenomic analysis of spacecraft associated surfaces reveal planetary protection relevant microbial composition. <b>2023</b> , 18, e0282428	О
172	Phylogroup-specific variation shapes the clustering of antimicrobial resistance genes and defence systems across regions of genome plasticity in Pseudomonas aeruginosa. <b>2023</b> , 90, 104532	O
171	Complete Genome Sequence and Analysis of a ST573 Multidrug-Resistant Methicillin-Resistant Staphylococcus aureus SauR3 Clinical Isolate from Terengganu, Malaysia. <b>2023</b> , 12, 502	1
170	Uncovering plant microbiomes using long-read metagenomic sequencing.	O

169	Comparison of the colonization ability of Burkholderia strain B23 in the citrus rhizoplane and rhizosphere and assessment of the underlying mechanisms using full-length 16S rDNA amplicon and metatranscriptomic analyses.	O
168	Novosphingobium kaempferiae sp. nov., a phosphate-solubilizing bacterium isolated from stem of Kaempferia marginata Carey. <b>2023</b> , 73,	O
167	The COVID-19 Pandemic Sparked Off a Large-Scale Outbreak of Carbapenem-Resistant Acinetobacter baumannii from the Endemic Strains at an Italian Hospital. <b>2023</b> , 11,	О
166	Bartonella Prevalence and Genome Sequences in Rodents in Some Regions of Xinjiang, China.	O
165	Gram-positive anaerobic cocci guard skin homeostasis by regulating host-defense mechanisms. <b>2023</b> , 26, 106483	O
164	Inoviridaeprophage dynamics during diversification, succession and Atlantic invasion of Pacific-nativeVibrio parahaemolyticus.	O
163	Analysis of bacterial pangenomes reduces CRISPR dark matter and reveals strong association between membranome and CRISPR-Cas systems. <b>2023</b> , 9,	О
162	Global scenario of the RmtE pan-aminoglycoside-resistance mechanism: emergence of the rmtE4 gene in South America associated with a hospital-related IncL plasmid. <b>2023</b> , 9,	O
161	Group AStreptococcusstrains causing meningitis without distinct invasive phenotype.	О
160	New insights into the neuroprotective and beta-secretase1 inhibitor profiles of tirandamycin B isolated from a newly found Streptomyces composti sp. nov <b>2023</b> , 13,	O
159	Horizontal transfer of probable chicken-pathogenicity chromosomal islands betweenStaphylococcus aureusandStaphylococcus agnetis.	О
158	Nuclease genes occupy boundaries of genetic exchange between bacteriophages.	O
157	Isolation and whole genome characterization of antagonisticPaenibacillus polymyxa188 and its biocontrol potential against several fungi.	О
156	Metabiotics Signature through Genome Sequencing and In Vitro Inhibitory Assessment of a Novel Lactococcus lactis Strain UTNCys6-1 Isolated from Amazonian Camu-Camu Fruits. <b>2023</b> , 24, 6127	O
155	The genomic landscape of reference genomes of cultivated human gut bacteria. 2023, 14,	О
154	Genomic analysis of Vibrio harveyi strain PH1009, a potential multi-drug resistant pathogen due to acquisition of toxin genes. <b>2023</b> , 9, e14926	O
153	UropathogenicEscherichia colipopulation structure and antimicrobial susceptibility in Norfolk, UK.	О
152	Altered infective competence of the human gut microbiome in COVID-19. <b>2023</b> , 11,	O

151	Potato root-associated microbiomes adapt to combined water and nutrient limitation and have a plant genotype-specific role for plant stress mitigation. <b>2023</b> , 18,	0
150	Core genome sequencing and genotyping of Leptospira interrogans in clinical samples by target capture sequencing. <b>2023</b> , 23,	O
149	The genomic epidemiology of Escherichia albertii infecting humans and birds in Great Britain. <b>2023</b> , 14,	0
148	Genomic dissection of endemic carbapenem resistance: metallo-beta-lactamase gene dissemination through clonal, plasmid and integron transfer pathways.	O
147	Analysis of the Genomics and Mouse Virulence of an Emergent Clone of Streptococcus dysgalactiae Subspecies equisimilis. <b>2023</b> , 11,	O
146	Cultivation of SAR202 Bacteria from the Ocean.	O
145	Epidemiological and genomic analyses of human isolates of Streptococcus suis between 2005 and 2021 in Shenzhen, China. 14,	0
144	Emergence of hypervirulent Pseudomonas aeruginosa pathotypically armed with co-expressed T3SS effectors ExoS and ExoU. <b>2023</b> ,	Ο
143	Complete Genome Sequences of Two Clonal Complex 398 Methicillin-resistant Staphylococcus aureus Strains Isolated from Patients in Korea. <b>2023</b> , 51, 132-133	0
142	Evolution of an alternative genetic code in theProvidenciasymbiont of the haematophagous leechHaementeria acuecueyetzin.	Ο
141	Enterococcal Linear Plasmids Adapt to Enterococcus faecium and Spread within Multidrug-Resistant Clades. <b>2023</b> , 67,	О
140	Genomics of Invasive Cutibacterium acnes Isolates from Deep-Seated Infections. 2023, 11,	Ο
139	Epidemiological Description and Detection of Antimicrobial Resistance in Various Aquatic Sites in Marseille, France. <b>2023</b> , 11,	Ο
138	Comparative genomic analysis of Colistin resistant Escherichia coli isolated from pigs, a human and wastewater on colistin withdrawn pig farm. <b>2023</b> , 13,	O
137	Characterization of resistance genes and plasmids from sick children caused by Salmonella enterica resistance to azithromycin in Shenzhen, China. 13,	0
136	Pathobionts from chemically disrupted gut microbiota induce insulin-dependent diabetes in mice. <b>2023</b> , 11,	0
135	Genome Characterization and Infectivity Potential of Vibriophage-?LV6 with Lytic Activity against Luminescent Vibrios of Penaeus vannamei Shrimp Aquaculture. <b>2023</b> , 15, 868	O
134	Genomic characterization and identification of virulence-related genes in Vibrio nigripulchritudo isolated from white leg shrimp Penaeus vannamei.	Ο

133	Genome-resolved analyses of oligotrophic groundwater microbial communities along phenol pollution in a continuous-flow biodegradation model system. 14,	О
132	Genome-Wide Pathway Exploration of the Epidermidibacterium keratini EPI-7T. <b>2023</b> , 11, 870	O
131	The evolution of morphological development is congruent with the species phylogeny in the genus Streptomyces. 14,	0
130	Nitrite accumulation and anammox bacterial niche partitioning in Arctic Mid-Ocean Ridge sediments. <b>2023</b> , 3,	O
129	RND pumps across the genus Acinetobacter: AdeIJK is the universal efflux pump. 2023, 9,	0
128	Spanish Outbreak Isolates Bridge Phylogenies of European and American Bacillus anthracis. <b>2023</b> , 11, 889	O
127	Parallel host shifts in a bacterial plant pathogen suggest independent genetic solutions.	0
126	Responses to organic pollutants in the tropical Pacific and subtropical Atlantic Oceans by pelagic marine bacteria. 11,	O
125	Temperate bacteriophages infecting the mucin-degrading bacterium Ruminococcus gnavus from the human gut. <b>2023</b> , 15,	0
124	Enrichment Culture but Not Metagenomic Sequencing Identified a Highly Prevalent Phage Infecting Lactiplantibacillus plantarum in Human Feces.	O
123	Bacterial defences interact synergistically by disrupting phage cooperation.	0
122	Comparative genomics of 40 Weissella paramesenteroides strains. 14,	O
121	Flavobacterium frigoritolerans sp. nov. and Flavobacterium shii sp. nov., isolated from glaciers on the Tibetan Plateau. <b>2023</b> , 73,	0
120	Streptococcus canis genomic epidemiology reveals the potential for zoonotic transfer. <b>2023</b> , 9,	O
119	Genomics of the Eumorigenes Lade of the family Rhizobiaceae and description of Rhizobium rhododendri sp. nov <b>2023</b> , 12,	0
118	A First Insight into the Microbial and Viral Communities of Comau FjordA Unique Human-Impacted Ecosystem in Patagonia (42? S). <b>2023</b> , 11, 904	O
117	Bursts in biosynthetic gene cluster transcription are accompanied by surges of natural compound production in the myxobacterium Sorangium sp	0
116	A novel proteinaceous molecule produced by Lysinibacillus sp. OF-1 depends on the Ami oligopeptide transporter to kill Streptococcus pneumoniae. <b>2023</b> , 169,	O

115	Vagococcus luciliae sp. nov., isolated from the common green bottle fly Lucilia sericata. 2023, 73,	О
114	Temporal colonization of the gut microbiome in neonatalBos taurusat single nucleotide resolution.	Ο
113	Metagenomic analysis of plant viruses in tropical fresh and wastewater.	0
112	CRISPR-Cas9 enrichment, a new strategy in microbial metagenomics to investigate complex genomic regions: The case of an environmental integron.	O
111	Flavobacterium pygoscelis sp. nov., isolated from a chinstrap penguin chick (Pygoscelis antarcticus). <b>2023</b> , 73,	O
110	Rothia from the Human Nose Inhibit Moraxella catarrhalis Colonization with a Secreted Peptidoglycan Endopeptidase.	O
109	Roseomonas fluvialis sp. nov., an aerobic bacteriochlorophyll a-containing freshwater bacterium isolated from river epilithic biofilm. <b>2023</b> , 73,	0
108	Differences in vertical and horizontal transmission dynamics shape plasmid distribution in clinical enterobacteria.	O
107	A Novel Bacterial Speciation Process Observed in a Symbiotic Marine Population.	0
106	Metagenome-Assembled Genomes from Appalachian Acid Mine Drainage Sites.	O
105	Comprehensive genomic analysis of hypocholesterolemic probiotic Enterococcus faecium LR13	
	reveals unique proteins involved in cholesterol-assimilation. 10,	O
104		0
	reveals unique proteins involved in cholesterol-assimilation. 10,  Assessment of plasmids for relating the 2020 Salmonella enterica serovar Newport onion outbreak	
104	reveals unique proteins involved in cholesterol-assimilation. 10,  Assessment of plasmids for relating the 2020 Salmonella enterica serovar Newport onion outbreak to farms implicated by the outbreak investigation. 2023, 24,  Identification of levoglucosan degradation pathways in bacteria and sequence similarity network	Ο
104	reveals unique proteins involved in cholesterol-assimilation. 10,  Assessment of plasmids for relating the 2020 Salmonella enterica serovar Newport onion outbreak to farms implicated by the outbreak investigation. 2023, 24,  Identification of levoglucosan degradation pathways in bacteria and sequence similarity network analysis. 2023, 205,  Enhancement of micropollutant biotransformation by adding manganese sand in constructed	0
104	reveals unique proteins involved in cholesterol-assimilation. 10,  Assessment of plasmids for relating the 2020 Salmonella enterica serovar Newport onion outbreak to farms implicated by the outbreak investigation. 2023, 24,  Identification of levoglucosan degradation pathways in bacteria and sequence similarity network analysis. 2023, 205,  Enhancement of micropollutant biotransformation by adding manganese sand in constructed wetlands. 2023, 9, e15092  Application of a novel lytic Jerseyvirus phage LPSent1 for the biological control of the	0 0
104 103 102	reveals unique proteins involved in cholesterol-assimilation. 10,  Assessment of plasmids for relating the 2020 Salmonella enterica serovar Newport onion outbreak to farms implicated by the outbreak investigation. 2023, 24,  Identification of levoglucosan degradation pathways in bacteria and sequence similarity network analysis. 2023, 205,  Enhancement of micropollutant biotransformation by adding manganese sand in constructed wetlands. 2023, 9, e15092  Application of a novel lytic Jerseyvirus phage LPSent1 for the biological control of the multidrug-resistant Salmonella Enteritidis in foods. 14,  First insights into antimicrobial resistance, toxigenic profiles, and genetic diversity in Bacillus	0 0

97	Whole genome sequencing to study antimicrobial resistance and RTX virulence genes in equine Actinobacillus isolates. <b>2023</b> , 54,	0
96	Spontaneously Produced Lysogenic Phages Are an Important Component of the Soybean Bradyrhizobium Mobilome.	O
95	Isolation and pan-genome analysis of Enterobacter hormaechei Z129, a ureolytic bacterium, from the rumen of dairy cow. 14,	0
94	Viruses interact with hosts that span distantly related microbial domains in dense hydrothermal mats.	O
93	Nocardia pulmonis sp. nov., an actinomycete isolated from a patient with pulmonary infection. <b>2023</b> , 73,	O
92	Intrinsic Resistance to Colistin in the Genus Hafnia.	Ο
91	Characterization and Association of Rips Repertoire to Host Range of Novel Ralstonia solanacearum Strains by In Silico Approaches. <b>2023</b> , 11, 954	О
90	Vibrio aestuarianusClade A and Clade B isolates are associated with Pacific oyster (Crassostrea gigas) disease outbreaks across Ireland.	Ο
89	First Report of OXA-181-Producing Enterobacterales Isolates in Latin America.	0
88	Quantifying Shared and Unique Gene Content across 17 Microbial Ecosystems.	O
87	Genomic Modification of TonB and Emergence of Small-Colony Phenotype in VIM- and NDM-Producing Escherichia coli following Cefiderocol Exposure In Vitro.	0
86	Metagenomic insights into the composition and function of the gut microbiota of mice infected with Toxoplasma gondii. 14,	O
85	Genetic characterization of ESBL-producing and ciprofloxacin-resistant Escherichia coli from Belgian broilers and pigs. 14,	0
84	The evolution and international spread of extensively drug resistant Shigella sonnei. 2023, 14,	Ο
83	Description of Agathobaculum massiliense sp. nov., a new bacterial species prevalent in the human gut and predicted to produce indole and tryptophan based on genomic analysis.	О
82	Global Marine Cold Seep Metagenomes Reveal Diversity of Taxonomy, Metabolic Function, and Natural Products.	O
81	Isolation and Genomic Characteristics of Cat-Borne Campylobacter felis sp. nov. and Sheep-Borne Campylobacter ovis sp. nov. <b>2023</b> , 11, 971	О
80	A Culturomics-Based Bacterial Synthetic Community for Improving Resilience towards Arsenic and Heavy Metals in the Nutraceutical Plant Mesembryanthemum crystallinum. <b>2023</b> , 24, 7003	Ο

79	Genome-wide association reveals host-specific genomic traits in Escherichia coli. 2023, 21,	O
78	Paenibacillus dendrobii sp. nov., an indole-3-acetic acid-producing endophytic bacterium isolated from Dendrobium nobile. <b>2023</b> , 73,	Ο
77	Comparative Genomics Analysis of Habitat Adaptation by Lactobacillus kefiranofaciens. <b>2023</b> , 12, 1606	Ο
76	Vibrio paucivorans sp. nov. and Vibrio qingdaonensis sp. nov., two marine bacteria. <b>2023</b> , 73,	O
75	Facilitative interaction networks in experimental microbial community dynamics. 14,	O
74	Highly sensitive quantitative phase microscopy and deep learning aided with whole genome sequencing for rapid detection of infection and antimicrobial resistance. 14,	1
73	Monkeypox virus: phylogenomics, hostpathogen interactome and mutational cascade. <b>2023</b> , 9,	0
72	On-person adaptive evolution of Staphylococcus aureus during treatment for atopic dermatitis. <b>2023</b> , 31, 593-603.e7	O
71	Large-scale phage cultivation for commensal human gut bacteria. 2023, 31, 665-677.e7	O
70	Genomic Epidemiology of Corynebacterium diphtheriae in New Caledonia.	O
70 69	Genomic Epidemiology of Corynebacterium diphtheriae in New Caledonia.  Pangenomic Study of Fusobacterium nucleatum Reveals the Distribution of Pathogenic Genes and Functional Clusters at the Subspecies and Strain Levels.	0
	Pangenomic Study of Fusobacterium nucleatum Reveals the Distribution of Pathogenic Genes and	
69	Pangenomic Study of Fusobacterium nucleatum Reveals the Distribution of Pathogenic Genes and Functional Clusters at the Subspecies and Strain Levels.	0
69 68	Pangenomic Study of Fusobacterium nucleatum Reveals the Distribution of Pathogenic Genes and Functional Clusters at the Subspecies and Strain Levels.  Staphylococcal diversity in atopic dermatitis from an individual to a global scale. 2023, 31, 578-592.e6  Genomic investigation of antimicrobial resistance in Brucella abortus strains isolated from cattle in	0
69 68 67	Pangenomic Study of Fusobacterium nucleatum Reveals the Distribution of Pathogenic Genes and Functional Clusters at the Subspecies and Strain Levels.  Staphylococcal diversity in atopic dermatitis from an individual to a global scale. 2023, 31, 578-592.e6  Genomic investigation of antimicrobial resistance in Brucella abortus strains isolated from cattle in Brazil. 2023, 31, 101777  Prevalence and Genomic Characteristics of mcr -Positive Escherichia coli Strains Isolated from	0 0
69 68 67 66	Pangenomic Study of Fusobacterium nucleatum Reveals the Distribution of Pathogenic Genes and Functional Clusters at the Subspecies and Strain Levels.  Staphylococcal diversity in atopic dermatitis from an individual to a global scale. 2023, 31, 578-592.e6  Genomic investigation of antimicrobial resistance in Brucella abortus strains isolated from cattle in Brazil. 2023, 31, 101777  Prevalence and Genomic Characteristics of mcr -Positive Escherichia coli Strains Isolated from Humans, Pigs, and Foods in China.  Whole-Genome Sequencing of Lactobacillus johnsonii MT4, a Novel Strain Isolated from the Oral	0 0
69 68 67 66 65	Pangenomic Study of Fusobacterium nucleatum Reveals the Distribution of Pathogenic Genes and Functional Clusters at the Subspecies and Strain Levels.  Staphylococcal diversity in atopic dermatitis from an individual to a global scale. 2023, 31, 578-592.e6  Genomic investigation of antimicrobial resistance in Brucella abortus strains isolated from cattle in Brazil. 2023, 31, 101777  Prevalence and Genomic Characteristics of mcr-Positive Escherichia coli Strains Isolated from Humans, Pigs, and Foods in China.  Whole-Genome Sequencing of Lactobacillus johnsonii MT4, a Novel Strain Isolated from the Oral Cavity of C57BL/6 Mice.	0 0 0

61	Antimicrobial Activity of Cefiderocol against the Carbapenemase-Producing Enterobacter cloacae Complex and Characterization of Reduced Susceptibility Associated with Metallo-Lactamase VIM-1.	O
60	Genome Organization of Four Brazilian Xanthomonas albilineans Strains Does Not Correlate with Aggressiveness.	O
59	Stutzerimonas frequens strain TF18 with superior heterotrophic nitrification-aerobic denitrification ability for the treatment of aquaculture effluent. <b>2023</b> , 130, 156-165	О
58	Children with autism show differences in the gut DNA virome compared to non-autistic children: a case control study. <b>2023</b> , 23,	O
57	Design and validation of Dolosigranulum pigrum specific PCR primers using the bacterial core genome. <b>2023</b> , 13,	0
56	Core-Genome Multilocus Sequence Typing for Epidemiological and Evolutionary Analyses of Phytopathogenic Xanthomonas citri.	O
55	Brevundimonas brasiliensis sp. nov.: a New Multidrug-Resistant Species Isolated from a Patient in Brazil.	0
54	Benzo[a]pyrene stress impacts adaptive strategies and ecological functions of earthworm intestinal viromes.	Ο
53	Variation in Sphingomonas traits across habitats and phylogenetic clades. 14,	Ο
52	Antimicrobial-Resistant Enterobacterales Recovered from the Environment of Two Zoological Institutions Include Enterobacter cloacae Complex ST171 Producing KPC-4 Carbapenemase.	Ο
51	Genomic analysis and characterization of phages infecting the marine Roseobacter CHAB-I-5 lineage reveal a globally distributed and abundant phage genus. 14,	Ο
50	De novogenome assembly resolving repetitive structures enables genomic analysis of 35 EuropeanMycoplasma bovisstrains.	O
49	Outbreak report of polymyxin-carbapenem-resistant Klebsiella pneumoniae causing untreatable infections evidenced by synergy tests and bacterial genomes. <b>2023</b> , 13,	0
48	Three marine species of the genus Fulvivirga, rich sources of carbohydrate-active enzymes degrading alginate, chitin, laminarin, starch, and xylan. <b>2023</b> , 13,	O
47	Complete Genome Sequence of Citrobacter braakii GW-Imi-1b1, Isolated from Hospital Wastewater in Greifswald, Germany.	0
46	Probable Airborne Transmission of Burkholderia pseudomallei Causing an Urban Outbreak of Melioidosis during Typhoon Season in Hong Kong, China	O
45	A 1.5 Mb continuous endogenous viral element region in the arbuscular mycorrhizal fungusRhizophagus irregularis.	0
44	Genomic Insights into Bacterial Resistance to Proline-Rich Antimicrobial Peptide Bac7. <b>2023</b> , 13, 438	O

43	Genome profiling of uropathogenic E. coli from strictly defined community-acquired UTI in paediatric patients: a multicentric study. <b>2023</b> , 12,	0
42	Virotyping and genetic antimicrobial susceptibility testing of porcine ETEC/STEC strains and associated plasmid types. 14,	О
41	Ecophysiological analysis reveals distinct environmental preferences in closely related Baltic Sea picocyanobacteria.	0
40	Genomic features, antimicrobial susceptibility, and epidemiological insights into Burkholderia cenocepacia clonal complex 31 isolates from bloodstream infections in India. 13,	О
39	Colonization and transmission of Staphylococcus aureus in schools: a citizen science project. <b>2023</b> , 9,	0
38	The Identification of Streptococcus pasteurianus Obtained from Six Regions in China by Multiplex PCR Assay and the Characteristics of Pathogenicity and Antimicrobial Resistance of This Zoonotic Pathogen. <b>2023</b> , 12, 615	O
37	E. coli ST11 (O157:H7) does not encode a functional AcrF efflux pump. <b>2023</b> , 169,	O
36	Complete genome sequence of Aeromonas phage GomatiRiver_11, a novel T4-like bacteriophage that infects Aeromonas hydrophila.	O
35	Comparative genomic insights into habitat adaptation of coral-associated Prosthecochloris. 14,	0
34	Genomic analysis of the population structure of Paenibacillus larvae in New Zealand. 14,	0
33	Defense systems are pervasive across chromosomally integrated mobile genetic elements and are inversely correlated to virulence and antimicrobial resistance.	O
32	Protein language model-based end-to-end type II polyketide prediction without sequence alignment.	О
31	Dissecting the genotypic features of a fluoroquinolone-resistant Pseudomonas aeruginosa ST316 sublineage causing ear infections in Shanghai, China. <b>2023</b> , 9,	O
30	Epidemiological and Genetic Characteristics of Clinical Carbapenem-Resistant Pseudomonas aeruginosa Strains in Guangdong Province, China.	О
29	Integrated computational approaches to aid precision medicine for cancer therapy: Present scenario and future prospects. <b>2023</b> , 403-424	0
28	A novel Nitrospira lineage isolated from activated sludge using elevated temperatures.	О
27	A Pseudomonas Lysogenic Bacteriophage Crossing the Antarctic and Arctic, Representing a New Genus of Autographiviridae. <b>2023</b> , 24, 7662	0
26	Characterization and Genomic Analysis of the Naphthalene-Degrading Delftia tsuruhatensis ULwDis3 Isolated from Seawater. <b>2023</b> , 11, 1092	o

25	Cuticle supplementation and nitrogen recycling by a dual bacterial symbiosis in a family of xylophagous beetles.	O
24	Metapangenomics of wild and cultivated banana microbiome reveals a plethora of host-associated protective functions. <b>2023</b> , 18,	O
23	Comparative genomic analyses of the clinically-derived Winkia strain NY0527: the reassignment of W. neuii subsp. neuii and W. neuii subsp. antitratus into two separate species and insights into their virulence characteristics. 14,	0
22	New Representative of the Species <b>P</b> rosthecodimorpha hirschiil <b>F</b> rom a Methanotrophic Enrichment Culture: Phenotypic Traits and Genome Analysis. <b>2023</b> , 92, 129-136	O
21	Identification of core therapeutic targets for Monkeypox virus and repurposing potential of drugs against them: An in silico approach. <b>2023</b> , 106971	O
20	Genomic characterization of a pandrug-resistantKlebsiella pneumoniaebelonging to the high-risk ST11 in the Brazilian Amazon region.	O
19	Characterization of two multidrug-resistant Klebsiella pneumoniae harboring tigecycline-resistant gene tet(X4) in China. 14,	0
18	Genomic Correlates of Tailocin Sensitivity inPseudomonas syringae.	Ο
17	Phylogenomics of Globally Spread Clonal Groups 14 and 15 of Klebsiella pneumoniae.	0
16	A multiomic approach to defining the essential genome of the globally important pathogen Corynebacterium diphtheriae. <b>2023</b> , 19, e1010737	O
15	Sellimonas catena sp. nov., isolated from human faeces. <b>2023</b> , 73,	O
14	Pathogen genomics and phage-based solutions for accurately identifying and controlling Salmonella pathogens. 14,	O
13	Roles of adenine methylation in the physiology of Lacticaseibacillus paracasei. 2023, 14,	0
12	A Metagenomic and Amplicon Sequencing Combined Approach Reveals the Best Primers to Study Marine Aerobic Anoxygenic Phototrophs.	O
11	Genomic analysis reveals the presence of emerging pathogenicKlebsiellalineages aboard the International Space Station.	0
10	Dissemination of carbapenemase-producing Enterobacterales through wastewater and gulls at a wastewater treatment plant in Sweden. <b>2023</b> , 886, 163997	O
9	Near-Complete Genome Sequence of White Spot Syndrome Virus Infecting Cultivated Shrimp (Penaeus vannamei) in Peru.	0
8	Whole Genome Analysis and Assessment of the Metabolic Potential of Gordonia rubripertincta Strain 112, a Degrader of Aromatic and Aliphatic Compounds. <b>2023</b> , 12, 721	O

## CITATION REPORT

7	Staphylococcus aureus biofilm properties and chronic rhinosinusitis severity scores correlate positively with total CD4 + T- cell frequencies and inversely with its Th1, Th17 and regulatory cell frequencies.	O
6	Characterization of two novel colistin resistance gene mcr-1 variants originated from Moraxella spp 14,	O
5	Complete genome analysis of Tequatrovirus ufvareg1, a Tequatrovirus species inhibiting Escherichia coli O157:H7. 13,	O
4	Whole-genome sequencing of multidrug resistance Salmonella Typhi clinical strains isolated from Balochistan, Pakistan. 11,	O
3	Geography, not lifestyle, explains the population structure of free-living and host-associated deep-sea hydrothermal vent snail symbionts. <b>2023</b> , 11,	O
2	N/S element transformation modulating lithospheric microbial communities by single-species manipulation. <b>2023</b> , 11,	O
1	Repression of Staphylococcus aureus and Escherichia coli by Lactiplantibacillus plantarum Strain AG10 in Drosophila melanogaster In Vivo Model. <b>2023</b> , 11, 1297	О