

CITATION REPORT

List of articles citing

The RAST Server: rapid annotations using subsystems technoc

DOI: 10.1186/1471-2164-9-75
BMC Genomics, 2008, 9, 75.

Source: <https://exaly.com/paper-pdf/43752676/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
2283	The metagenomics RAST server - a public resource for the automatic phylogenetic and functional analysis of metagenomes. 2008 , 9, 386		2527
2282	MetaMine--a tool to detect and analyse gene patterns in their environmental context. 2008 , 9, 459		6
2281	Streptococcus iniae M-like protein contributes to virulence in fish and is a target for live attenuated vaccine development. 2008 , 3, e2824		67
2280	An outlook into ultra-scale visualization of large-scale biological data. 2008 ,		2
2279	The smallest cells pose the biggest problems: high-performance computing and the analysis of metagenome sequence data. 2008 , 125, 012050		
2278	Origin of saxitoxin biosynthetic genes in cyanobacteria. 2009 , 4, e5758		95
2277	Gene order phylogeny and the evolution of methanogens. 2009 , 4, e6069		27
2276	Comparative genomics reveals mechanism for short-term and long-term clonal transitions in pandemic Vibrio cholerae. 2009 , 106, 15442-7		297
2275	Molecular diversity of a North Carolina wastewater treatment plant as revealed by pyrosequencing. 2009 , 75, 1688-96		124
2274	Role of flagella in virulence of the coral pathogen Vibrio coralliilyticus. 2009 , 75, 5704-7		43
2273	Analysis of the genome of the Escherichia coli O157:H7 2006 spinach-associated outbreak isolate indicates candidate genes that may enhance virulence. 2009 , 77, 3713-21		122
2272	DIYA: a bacterial annotation pipeline for any genomics lab. 2009 , 25, 962-3		61
2271	Adaptations to submarine hydrothermal environments exemplified by the genome of Nautilia profundicola. 2009 , 5, e1000362		105
2270	A parsimony approach to biological pathway reconstruction/inference for genomes and metagenomes. 2009 , 5, e1000465		266
2269	Novel electrochemically active bacterium phylogenetically related to Arcobacter butzleri, isolated from a microbial fuel cell. 2009 , 75, 7326-34		138
2268	FIGfams: yet another set of protein families. 2009 , 37, 6643-54		101
2267	Text-mining of PubMed abstracts by natural language processing to create a public knowledge base on molecular mechanisms of bacterial enteropathogens. 2009 , 10, 177		14

2266	The Genome Reverse Compiler: an explorative annotation tool. 2009 , 10, 35	11
2265	Analysis and comparison of very large metagenomes with fast clustering and functional annotation. 2009 , 10, 359	88
2264	JANE: efficient mapping of prokaryotic ESTs and variable length sequence reads on related template genomes. 2009 , 10, 391	5
2263	Reconstructing the virulome of the human pathogen <i>Streptococcus pyogenes</i> using NMPDR subsystems-based annotation. 2009 , 10,	78
2262	UFO: a web server for ultra-fast functional profiling of whole genome protein sequences. <i>BMC Genomics</i> , 2009 , 10, 409	4-5 14
2261	Genome-wide dissection of globally emergent multi-drug resistant serotype 19A <i>Streptococcus pneumoniae</i> . <i>BMC Genomics</i> , 2009 , 10, 642	4-5 81
2260	Recombination and insertion events involving the botulinum neurotoxin complex genes in <i>Clostridium botulinum</i> types A, B, E and F and <i>Clostridium butyricum</i> type E strains. 2009 , 7, 66	117
2259	The case for biocentric microbiology. 2009 , 1, 16	7
2258	Reconstruction of biochemical networks in microorganisms. 2009 , 7, 129-43	699
2257	Metagenomic analysis of stressed coral holobionts. 2009 , 11, 2148-63	410
2256	The effect of diet on the human gut microbiome: a metagenomic analysis in humanized gnotobiotic mice. 2009 , 1, 6ra14	1977
2255	Harnessing genomics for evolutionary insights. 2009 , 24, 192-200	119
2254	Metagenomic analysis of respiratory tract DNA viral communities in cystic fibrosis and non-cystic fibrosis individuals. 2009 , 4, e7370	297
2253	iBsu1103: a new genome-scale metabolic model of <i>Bacillus subtilis</i> based on SEED annotations. 2009 , 10, R69	122
2252	Application of high-performance computing to the reconstruction, analysis, and optimization of genome-scale metabolic models. 2009 , 180, 012025	8
2251	Two genome sequences of the same bacterial strain, <i>Gluconacetobacter diazotrophicus</i> PAI 5, suggest a new standard in genome sequence submission. 2010 , 2, 309-17	24
2250	Nutriproteomics and Proteogenomics: Cultivating Two Novel Hybrid Fields of Personalized Medicine with Added Societal Value. 2010 , 8, 240-244	9
2249	Genomics and Enzymology of NAD Biosynthesis. 2010 , 213-257	15

2248	Graph methods for the investigation of metabolic networks in parasitology. 2010 , 137, 1393-407		17
2247	DraGnET: software for storing, managing and analyzing annotated draft genome sequence data. 2010 , 11, 100		6
2246	BiGG: a Biochemical Genetic and Genomic knowledgebase of large scale metabolic reconstructions. 2010 , 11, 213		399
2245	Accessing the SEED genome databases via Web services API: tools for programmers. 2010 , 11, 319		99
2244	IPRStats: visualization of the functional potential of an InterProScan run. 2010 , 11 Suppl 12, S13		11
2243	Genomic encyclopedia of sugar utilization pathways in the <i>Shewanella</i> genus. <i>BMC Genomics</i> , 2010 , 11, 494	4-5	71
2242	A three-way comparative genomic analysis of <i>Mannheimia haemolytica</i> isolates. <i>BMC Genomics</i> , 2010 , 11, 535	4-5	19
2241	Genomic survey of the ectoparasitic mite <i>Varroa destructor</i> , a major pest of the honey bee <i>Apis mellifera</i> . <i>BMC Genomics</i> , 2010 , 11, 602	4-5	99
2240	A genomic perspective on the potential of <i>Actinobacillus succinogenes</i> for industrial succinate production. <i>BMC Genomics</i> , 2010 , 11, 680	4-5	85
2239	Unprecedented loss of ammonia assimilation capability in a urease-encoding bacterial mutualist. <i>BMC Genomics</i> , 2010 , 11, 687	4-5	30
2238	Comparative genomics of the bacterial genus <i>Listeria</i> : Genome evolution is characterized by limited gene acquisition and limited gene loss. <i>BMC Genomics</i> , 2010 , 11, 688	4-5	151
2237	Comparative genomic analysis reveals evidence of two novel <i>Vibrio</i> species closely related to <i>V. cholerae</i> . 2010 , 10, 154		44
2236	Characterization and genomic analysis of chromate resistant and reducing <i>Bacillus cereus</i> strain SJ1. 2010 , 10, 221		66
2235	Production of haemolysins by strains of the <i>Actinobacillus minor</i> /"porcitonsillarum" complex. 2010 , 141, 332-41		6
2234	Marine microbial genomics in Europe: current status and perspectives. 2010 , 3, 523-30		24
2233	Genome (re-)annotation and open-source annotation pipelines. 2010 , 3, 362-9		22
2232	Biosynthesis of rhizocticins, antifungal phosphonate oligopeptides produced by <i>Bacillus subtilis</i> ATCC6633. 2010 , 17, 28-37		71
2231	Subsystems-based servers for rapid annotation of genomes and metagenomes. 2010 , 11,		3

2230	A mixed community of actinomycetes produce multiple antibiotics for the fungus farming ant <i>Acromyrmex octospinosus</i> . 2010 , 8, 109	170
2229	Comparative systems biology: from bacteria to man. 2010 , 2, 518-532	14
2228	Viral and microbial community dynamics in four aquatic environments. 2010 , 4, 739-51	305
2227	Fine-scale evolution: genomic, phenotypic and ecological differentiation in two coexisting <i>Salinibacter ruber</i> strains. 2010 , 4, 882-95	58
2226	A new chlorophyll d-containing cyanobacterium: evidence for niche adaptation in the genus <i>Acaryochloris</i> . 2010 , 4, 1456-69	47
2225	High-throughput generation, optimization and analysis of genome-scale metabolic models. 2010 , 28, 977-82	745
2224	GenePRIMP: a gene prediction improvement pipeline for prokaryotic genomes. 2010 , 7, 455-7	441
2223	A protocol for generating a high-quality genome-scale metabolic reconstruction. 2010 , 5, 93-121	1156
2222	The metavirome of a hypersaline environment. 2010 , 12, 2965-76	56
2221	De Novo assembly of the complete genome of an enhanced electricity-producing variant of <i>Geobacter sulfurreducens</i> using only short reads. 2010 , 5, e10922	29
2220	Sequencing and genetic variation of multidrug resistance plasmids in <i>Klebsiella pneumoniae</i> . 2010 , 5, e10141	33
2219	Genome sequencing reveals widespread virulence gene exchange among human <i>Neisseria</i> species. 2010 , 5, e11835	141
2218	The Use of Subsystems to Encode Biosynthesis of Vitamins and Cofactors. 2010 , 141-159	9
2217	The novel polysaccharide deacetylase homologue Pdi contributes to virulence of the aquatic pathogen <i>Streptococcus iniae</i> . 2010 , 156, 543-554	42
2216	Complete genome sequence of <i>Halalkalicoccus jeotgali</i> B3(T), an extremely halophilic archaeon. 2010 , 192, 4528-9	21
2215	Transposases are the most abundant, most ubiquitous genes in nature. 2010 , 38, 4207-17	196
2214	Differential gene retention in plastids of common recent origin. 2010 , 27, 1530-7	85
2213	Genome sequence of <i>Leuconostoc argentinum</i> KCTC 3773. 2010 , 192, 6490-1	6

2212	Population Genomics of Bacteria. 2010 , 121-151	3
2211	Emergence of resistance among USA300 methicillin-resistant <i>Staphylococcus aureus</i> isolates causing invasive disease in the United States. 2010 , 54, 3804-11	127
2210	Complete genome sequence of the diesel-degrading <i>Acinetobacter</i> sp. strain DR1. 2010 , 192, 4794-5	51
2209	Genome of <i>Helicobacter pylori</i> strain 908. 2010 , 192, 6488-9	23
2208	FragGeneScan: predicting genes in short and error-prone reads. 2010 , 38, e191	535
2207	Enterotoxigenic <i>Escherichia coli</i> elicits immune responses to multiple surface proteins. 2010 , 78, 3027-35	58
2206	Virulence factors encoded by <i>Legionella longbeachae</i> identified on the basis of the genome sequence analysis of clinical isolate D-4968. 2010 , 192, 1030-44	53
2205	Complete genome sequence of <i>Staphylococcus lugdunensis</i> strain HKU09-01. 2010 , 192, 1471-2	52
2204	Comparative genomics of clinical and environmental <i>Vibrio mimicus</i> . 2010 , 107, 21134-9	40
2203	A computational genomics pipeline for prokaryotic sequencing projects. 2010 , 26, 1819-26	62
2202	Advanced computational algorithms for microbial community analysis using massive 16S rRNA sequence data. 2010 , 38, e205	37
2201	Genome sequence of hybrid <i>Vibrio cholerae</i> O1 MJ-1236, B-33, and CIRS101 and comparative genomics with <i>V. cholerae</i> . 2010 , 192, 3524-33	87
2200	Draft genome sequence of <i>Streptomyces clavuligerus</i> NRRL 3585, a producer of diverse secondary metabolites. 2010 , 192, 6317-8	48
2199	Comparative analyses of two thermophilic enzymes exhibiting both beta-1,4 mannosidic and beta-1,4 glucosidic cleavage activities from <i>Caldanaerobius polysaccharolyticus</i> . 2010 , 192, 4111-21	36
2198	A functional metagenomic approach for expanding the synthetic biology toolbox for biomass conversion. 2010 , 6, 360	54
2197	Transcriptomic analyses of xylan degradation by <i>Prevotella bryantii</i> and insights into energy acquisition by xylanolytic bacteroidetes. 2010 , 285, 30261-73	79
2196	Functional characterization of pGKT2, a 182-kilobase plasmid containing the xplAB genes, which are involved in the degradation of hexahydro-1,3,5-trinitro-1,3,5-triazine by <i>Gordonia</i> sp. strain KTR9. 2010 , 76, 6329-37	39
2195	Metagenomic analysis of apple orchard soil reveals antibiotic resistance genes encoding predicted bifunctional proteins. 2010 , 76, 4396-401	129

2194	Functional diversity of four glycoside hydrolase family 3 enzymes from the rumen bacterium <i>Prevotella bryantii</i> B14. 2010 , 192, 2335-45	37
2193	A timescale for evolution, population expansion, and spatial spread of an emerging clone of methicillin-resistant <i>Staphylococcus aureus</i> . 2010 , 6, e1000855	132
2192	An Ergatis-based prokaryotic genome annotation web server. 2010 , 26, 1122-4	81
2191	Human hypervirulent <i>Clostridium difficile</i> strains exhibit increased sporulation as well as robust toxin production. 2010 , 192, 4904-11	215
2190	Using comparative genome analysis to identify problems in annotated microbial genomes. 2010 , 156, 1909-1917	78
2189	Evolutionary genomics of <i>Staphylococcus aureus</i> reveals insights into the origin and molecular basis of ruminant host adaptation. 2010 , 2, 454-66	147
2188	Community and gene composition of a human dental plaque microbiota obtained by metagenomic sequencing. 2010 , 25, 391-405	64
2187	The pre-seventh pandemic <i>Vibrio cholerae</i> BX 330286 El Tor genome: evidence for the environment as a genome reservoir. 2010 , 2, 208-16	3
2186	Unraveling the First <i>Xylella fastidiosa</i> Subsp. <i>Fastidiosa</i> Genome from Texas. 2010 , 35, 479-483	21
2185	RATT: Rapid Annotation Transfer Tool. 2011 , 39, e57	224
2184	Complete genome sequence of the haloaromatic acid-degrading bacterium <i>Achromobacter xylosoxidans</i> A8. 2011 , 193, 791-2	30
2183	Draft genome sequence of the polycyclic aromatic hydrocarbon-degrading, genetically engineered bioluminescent bioreporter <i>Pseudomonas fluorescens</i> HK44. 2011 , 193, 5009-10	11
2182	Complete genome sequence of highly multidrug-resistant <i>Pseudomonas aeruginosa</i> NCGM2.S1, a representative strain of a cluster endemic to Japan. 2011 , 193, 7010	36
2181	Genome sequence of the abyssomicin- and proximicin-producing marine actinomycete <i>Verrucospora maris</i> AB-18-032. 2011 , 193, 3391-2	20
2180	Draft genome of <i>Streptomyces zinciresistens</i> K42, a novel metal-resistant species isolated from copper-zinc mine tailings. 2011 , 193, 6408-9	9
2179	Genome sequence of <i>Lactococcus garvieae</i> 21881, isolated in a case of human septicemia. 2011 , 193, 4033-4	32
2178	A Parsimony Approach to Biological Pathway Reconstruction/Inference for Metagenomes. 2011 , 453-460	1
2177	Metagenomic Approaches in Systems Biology. 2011 , 473-489	4

2176	Detection of Large Numbers of Novel Sequences in the Metatranscriptomes of Complex Marine Microbial Communities. 2011 , 277-286	3
2175	Pathogen comparative genomics in the next-generation sequencing era: genome alignments, pangenomics and metagenomics. 2011 , 10, 322-33	30
2174	Synergistic use of plant-prokaryote comparative genomics for functional annotations. <i>BMC Genomics</i> , 2011 , 12 Suppl 1, S2	4-5 33
2173	Complete genome sequence of a carbon monoxide-utilizing acetogen, <i>Eubacterium limosum</i> KIST612. 2011 , 193, 307-8	53
2172	Genome sequence of <i>Sphingomonas</i> sp. S17, isolated from an alkaline, hyperarsenic, and hypersaline volcano-associated lake at high altitude in the Argentinean Puna. 2011 , 193, 3686-7	31
2171	Complete genome sequence of <i>Rickettsia heilongjiangensis</i> , an emerging tick-transmitted human pathogen. 2011 , 193, 5564-5	13
2170	Integrative genome-scale metabolic analysis of <i>Vibrio vulnificus</i> for drug targeting and discovery. 2011 , 7, 460	128
2169	Peptidoglycan remodeling and conversion of an inner membrane into an outer membrane during sporulation. 2011 , 146, 799-812	75
2168	The genome of th17 cell-inducing segmented filamentous bacteria reveals extensive auxotrophy and adaptations to the intestinal environment. 2011 , 10, 260-72	142
2167	Connecting genotype to phenotype in the era of high-throughput sequencing. 2011 , 1810, 967-77	24
2166	Isolation of <i>Succinivibrionaceae</i> implicated in low methane emissions from Tammar wallabies. 2011 , 333, 646-8	119
2165	PATRIC: the comprehensive bacterial bioinformatics resource with a focus on human pathogenic species. 2011 , 79, 4286-98	198
2164	The pathogenic potential of <i>Yersinia enterocolitica</i> 1A. 2011 , 301, 556-61	36
2163	Whole genome sequencing of environmental <i>Vibrio cholerae</i> O1 from 10 nanograms of DNA using short reads. 2011 , 87, 208-12	14
2162	<i>Pseudomonas fluorescens</i> BBc6R8 type III secretion mutants no longer promote ectomycorrhizal symbiosis. 2011 , 3, 203-10	43
2161	Searching in microbial genomes for encoded small proteins. 2011 , 4, 308-13	9
2160	Short communication: the complete genome sequence of <i>Bifidobacterium animalis</i> subspecies <i>animalis</i> ATCC 25527(T) and comparative analysis of growth in milk with <i>B. animalis</i> subspecies <i>lactis</i> DSM 10140(T). 2011 , 94, 5864-70	10
2159	Draft Genome Sequences of <i>Xanthomonas sacchari</i> and Two Banana-Associated <i>Xanthomonads</i> Reveal Insights into the <i>Xanthomonas</i> Group 1 Clade. 2011 , 2, 1050-65	38

2158	Genomic signatures of strain selection and enhancement in <i>Bacillus atrophaeus</i> var. <i>globigii</i> , a historical biowarfare simulant. 2011 , 6, e17836		31
2157	AGeS: a software system for microbial genome sequence annotation. 2011 , 6, e17469		15
2156	Global distribution of <i>Polaromonas</i> phylotypes--evidence for a highly successful dispersal capacity. 2011 , 6, e23742		90
2155	Phylogenomic analysis of <i>Odysella thessalonicensis</i> fortifies the common origin of Rickettsiales, <i>Pelagibacter ubique</i> and <i>Reclimonas americana</i> mitochondrion. 2011 , 6, e24857		46
2154	Sequence and role in virulence of the three plasmid complement of the model tumor-inducing bacterium <i>Pseudomonas savastanoi</i> pv. <i>savastanoi</i> NCPPB 3335. 2011 , 6, e25705		28
2153	Solving the Problem: Genome Annotation Standards before the Data Deluge. 2011 , 5, 168-93		46
2152	Draft genome sequence of <i>Caminibacter mediatlanticus</i> strain TB-2, an epsilonproteobacterium isolated from a deep-sea hydrothermal vent. 2011 , 5, 135-43		15
2151	Genome of alkaliphilic <i>Bacillus pseudofirmus</i> OF4 reveals adaptations that support the ability to grow in an external pH range from 7.5 to 11.4. 2011 , 13, 3289-309		63
2150	Coral-mucus-associated <i>Vibrio</i> integrons in the Great Barrier Reef: genomic hotspots for environmental adaptation. 2011 , 5, 962-72		32
2149	Genomic and proteomic analyses of the coral pathogen <i>Vibrio coralliilyticus</i> reveal a diverse virulence repertoire. 2011 , 5, 1471-83		75
2148	Horizontal gene transfer in <i>Histophilus somni</i> and its role in the evolution of pathogenic strain 2336, as determined by comparative genomic analyses. <i>BMC Genomics</i> , 2011 , 12, 570	4-5	20
2147	Hydrogen is an energy source for hydrothermal vent symbioses. 2011 , 476, 176-80		175
2146	Comparative genomic analysis of bacteriophage EP23 infecting <i>Shigella sonnei</i> and <i>Escherichia coli</i> . 2011 , 49, 927-34		19
2145	Simultaneous genome sequencing of symbionts and their hosts. 2011 , 55, 119-126		26
2144	A novel antifungal <i>Pseudomonas fluorescens</i> isolated from potato soils in Greenland. 2011 , 62, 1185-92		24
2143	Metabolic network reconstruction and genome-scale model of butanol-producing strain <i>Clostridium beijerinckii</i> NCIMB 8052. 2011 , 5, 130		82
2142	CloVR: a virtual machine for automated and portable sequence analysis from the desktop using cloud computing. 2011 , 12, 356		220
2141	Comparative supragenomic analyses among the pathogens <i>Staphylococcus aureus</i> , <i>Streptococcus pneumoniae</i> , and <i>Haemophilus influenzae</i> using a modification of the finite supragenome model. <i>BMC Genomics</i> , 2011 , 12, 187	4-5	44

2140	Yersinia enterocolitica palearctica serobiotype O:3/4--a successful group of emerging zoonotic pathogens. <i>BMC Genomics</i> , 2011 , 12, 348	4-5	19
2139	Genome sequencing reveals diversification of virulence factor content and possible host adaptation in distinct subpopulations of Salmonella enterica. <i>BMC Genomics</i> , 2011 , 12, 425	4-5	99
2138	WebMGA: a customizable web server for fast metagenomic sequence analysis. <i>BMC Genomics</i> , 2011 , 12, 444	4-5	440
2137	Genomic and proteomic analyses of Mycobacterium bovis BCG Mexico 1931 reveal a diverse immunogenic repertoire against tuberculosis infection. <i>BMC Genomics</i> , 2011 , 12, 493	4-5	20
2136	Comparative genomics of Helicobacter pylori and the human-derived Helicobacter bizzozeronii CIII-1 strain reveal the molecular basis of the zoonotic nature of non-pylori gastric Helicobacter infections in humans. <i>BMC Genomics</i> , 2011 , 12, 534	4-5	30
2135	Status quo in physiological proteomics of the uncultured Riftia pachyptila endosymbiont. 2011 , 11, 3106-17		28
2134	Ongoing purifying selection on intergenic spacers in group A streptococcus. 2011 , 11, 343-8		7
2133	Genomics for key players in the N cycle from guinea pigs to the next frontier. 2011 , 496, 289-318		3
2132	Genome reduction by deletion of paralogs in the marine cyanobacterium Prochlorococcus. 2011 , 28, 2751-60		38
2131	Evidence-based annotation of transcripts and proteins in the sulfate-reducing bacterium Desulfovibrio vulgaris Hildenborough. 2011 , 193, 5716-27		24
2130	Genome sequence of Lactobacillus cypricasei KCTC 13900. 2011 , 193, 5053-4		7
2129	Role of Sphingomonas sp. strain Fr1 PhyR-NepR-EcfG cascade in general stress response and identification of a negative regulator of PhyR. 2011 , 193, 6629-38		51
2128	Genome of multidrug-resistant uropathogenic Escherichia coli strain NA114 from India. 2011 , 193, 4272-3		53
2127	Whole-genome sequencing of Staphylococcus aureus strain RN4220, a key laboratory strain used in virulence research, identifies mutations that affect not only virulence factors but also the fitness of the strain. 2011 , 193, 2332-5		132
2126	Genome sequence of Sphingomonas elodea ATCC 31461, a highly productive industrial strain of gellan gum. 2011 , 193, 7015-6		13
2125	Draft genome sequence of Kocuria rhizophila P7-4. 2011 , 193, 4286-7		8
2124	Genome sequence of Bifidobacterium breve DPC 6330, a strain isolated from the human intestine. 2011 , 193, 6799-800		5
2123	Complete genome sequence of Bacillus amyloliquefaciens LL3, which exhibits glutamic acid-independent production of poly-β-glutamic acid. 2011 , 193, 3393-4		33

2122	Complete genome sequence of the proteolytic <i>Clostridium botulinum</i> type A5 (B3') strain H04402 065. 2011 , 193, 2351-2	24
2121	Genome analysis of a <i>Mycoplasma hyorhinis</i> strain derived from a primary human melanoma cell line. 2011 , 193, 4543-4	15
2120	Draft genome sequence of <i>Nesterenkonia</i> sp. strain F, isolated from Aran-Bidgol Salt Lake in Iran. 2011 , 193, 5580	10
2119	Complete genome sequencing of <i>Lactobacillus acidophilus</i> 30SC, isolated from swine intestine. 2011 , 193, 2882-3	16
2118	Genome sequence of <i>Acinetobacter baumannii</i> MDR-TJ. 2011 , 193, 2365-6	25
2117	Genome sequence of strain IMCC2047, a novel marine member of the Gammaproteobacteria. 2011 , 193, 3688-9	6
2116	Genome sequence of <i>Bacillus pumilus</i> S-1, an efficient isoeugenol-utilizing producer for natural vanillin. 2011 , 193, 6400-1	10
2115	Genome sequence of <i>Pasteurella multocida</i> subsp. <i>gallicida</i> Anand1_poultry. 2011 , 193, 5604	12
2114	Genome sequences of two <i>Staphylococcus aureus</i> ovine strains that induce severe (strain O11) and mild (strain O46) mastitis. 2011 , 193, 2353-4	23
2113	Genome sequence of clinical isolate <i>Mycobacterium tuberculosis</i> NCGM2209. 2011 , 193, 6792	5
2112	Draft genome of <i>Phaeobacter gallaeciensis</i> ANG1, a dominant member of the accessory nidamental gland of <i>Euprymna scolopes</i> . 2011 , 193, 3397-8	12
2111	Complete genome sequence of the obligate piezophilic hyperthermophilic archaeon <i>Pyrococcus yanosii</i> CH1. 2011 , 193, 4297-8	43
2110	Characterization and quantitation of a novel β -lactamase gene found in a wastewater treatment facility and the surrounding coastal ecosystem. 2011 , 77, 8226-33	34
2109	Genome sequence of <i>Vibrio rotiferianus</i> strain DAT722. 2011 , 193, 3381-2	13
2108	Genome sequence of <i>Rhodococcus erythropolis</i> XP, a biodesulfurizing bacterium with industrial potential. 2011 , 193, 6422-3	23
2107	Genome sequence of the 17 β -estradiol-utilizing bacterium <i>Sphingomonas</i> strain KC8. 2011 , 193, 4266-7	14
2106	Genome sequence of <i>Lactobacillus suebicus</i> KCTC 3549. 2011 , 193, 5532-3	4
2105	Genome sequence of <i>Lactobacillus farciminis</i> KCTC 3681. 2011 , 193, 1790-1	10

2104	The <i>Photobacterium damsela</i> subsp. <i>damsela</i> hemolysins <i>damselysin</i> and <i>HlyA</i> are encoded within a new virulence plasmid. 2011 , 79, 4617-27	51
2103	Genome sequence of the bacteriocin-producing oral probiotic <i>Streptococcus salivarius</i> strain M18. 2011 , 193, 6402-3	32
2102	Complete genome sequence of <i>Melissococcus plutonius</i> ATCC 35311. 2011 , 193, 4029-30	19
2101	Genome sequence of strain IMCC1989, a novel member of the marine gammaproteobacteria. 2011 , 193, 3672-3	5
2100	Genome sequence of strain IMCC3088, a proteorhodopsin-containing marine bacterium belonging to the OM60/NOR5 clade. 2011 , 193, 3415-6	11
2099	Complete genome sequence of the marine fish pathogen <i>Vibrio anguillarum</i> harboring the pJM1 virulence plasmid and genomic comparison with other virulent strains of <i>V. anguillarum</i> and <i>V. ordalii</i> . 2011 , 79, 2889-900	87
2098	Genome sequence of <i>Lactococcus garvieae</i> 8831, isolated from rainbow trout lactococcosis outbreaks in Spain. 2011 , 193, 4263-4	32
2097	Genome sequence of <i>Pseudomonas putida</i> strain B6-2, a superdegrader of polycyclic aromatic hydrocarbons and dioxin-like compounds. 2011 , 193, 6789-90	25
2096	Genome sequence of strain IMCC9480, a xanthorhodopsin-bearing betaproteobacterium isolated from the Arctic Ocean. 2011 , 193, 3421	7
2095	Draft genome sequence of the biocontrol bacterium <i>Chromobacterium</i> sp. strain C-61. 2011 , 193, 6803-4	8
2094	Genome sequence of <i>Sphingobium yanoikuyae</i> XLDN2-5, an efficient carbazole-degrading strain. 2011 , 193, 6404-5	11
2093	Genome Sequence of <i>Leuconostoc gelidum</i> KCTC 3527, Isolated from Kimchi. 2011 , 193, 799-800	5
2092	Genome sequence of <i>Lactobacillus coryniformis</i> subsp. <i>coryniformis</i> KCTC 3167. 2011 , 193, 1014-5	3
2091	Major families of multiresistant plasmids from geographically and epidemiologically diverse staphylococci. 2011 , 1, 581-91	68
2090	Genome sequence of <i>Leuconostoc carnosum</i> KCTC 3525. 2011 , 193, 6100-1	4
2089	Genome Sequence of <i>Weissella cibaria</i> KACC 11862. 2011 , 193, 797-8	16
2088	Genome sequence of <i>Salinisphaera shabanensis</i> , a gammaproteobacterium from the harsh, variable environment of the brine-seawater interface of the Shaban Deep in the Red Sea. 2011 , 193, 4555-6	15
2087	Genome sequence of <i>Escherichia coli</i> AA86, isolated from cow feces. 2011 , 193, 3681	7

2086	Common ancestry and novel genetic traits of <i>Francisella novicida</i> -like isolates from North America and Australia as revealed by comparative genomic analyses. 2011 , 77, 5110-22	26
2085	Whole-genome sequence of <i>Streptococcus pseudopneumoniae</i> isolate IS7493. 2011 , 193, 6102-3	20
2084	Genome of a novel isolate of <i>Paracoccus denitrificans</i> capable of degrading N,N-dimethylformamide. 2011 , 193, 5598-9	36
2083	Draft genome sequences of two <i>Pseudomonas aeruginosa</i> clinical isolates with different antibiotic susceptibilities. 2011 , 193, 5573	5
2082	Draft genome sequence of the <i>Paenibacillus polymyxa</i> type strain (ATCC 842T), a plant growth-promoting bacterium. 2011 , 193, 5026-7	28
2081	Complete genome sequence of <i>Yersinia enterocolitica</i> subsp. <i>paleartica</i> serogroup O:3. 2011 , 193, 2067	23
2080	Complete genome sequence of <i>Campylobacter jejuni</i> strain S3. 2011 , 193, 1491-2	12
2079	Genome sequence of <i>Lactobacillus johnsonii</i> PF01, isolated from piglet feces. 2011 , 193, 5030-1	13
2078	Genome sequence of <i>Pseudomonas putida</i> Idaho, a unique organic-solvent-tolerant bacterium. 2011 , 193, 7011-2	17
2077	Complete genome sequence of <i>Vibrio vulnificus</i> MO6-24/O. 2011 , 193, 2062-3	55
2076	Genome sequence of strain TW25, a novel member of the genus <i>Ornithinibacillus</i> in the family Bacillaceae. 2011 , 193, 2884-5	3
2075	Genome sequence of <i>Leuconostoc fallax</i> KCTC 3537. 2011 , 193, 588-9	5
2074	Complete genome sequence of the hyperthermophilic, piezophilic, heterotrophic, and carboxydrotrophic archaeon <i>Thermococcus barophilus</i> MP. 2011 , 193, 1481-2	47
2073	Genome sequence of <i>Taylorella equigenitalis</i> MCE9, the causative agent of contagious equine metritis. 2011 , 193, 1785	20
2072	Genome sequence of strain TW15, a novel member of the genus <i>Ruegeria</i> , belonging to the marine Roseobacter clade. 2011 , 193, 3401-2	5
2071	Complete genome of <i>Pseudomonas mendocina</i> NK-01, which synthesizes medium-chain-length polyhydroxyalkanoates and alginate oligosaccharides. 2011 , 193, 3413-4	19
2070	<i>Streptococcus pneumoniae</i> serotype 6C: an intra- and interclonal complex comparison. 2011 , 193, 3409-10	3
2069	Genome sequence of <i>Lactococcus garvieae</i> UNIUD074, isolated in Italy from a lactococcosis outbreak. 2011 , 193, 3684-5	28

2068	Genome sequence of <i>Acinetobacter</i> sp. strain P8-3-8, isolated from <i>Fistularia commersonii</i> in Vietnam. 2011 , 193, 4288-9	5
2067	Draft genome sequence of <i>Methylophaga aminisulfidivorans</i> MP T. 2011 , 193, 4265	9
2066	Genome sequence of the halotolerant marine bacterium <i>Myxococcus fulvus</i> HW-1. 2011 , 193, 5015-6	43
2065	Genome sequence of <i>Rheinheimera</i> sp. strain A13L, isolated from Pangong Lake, India. 2011 , 193, 5873-4	18
2064	Genome sequence of <i>Idiomarina</i> sp. strain A28L, isolated from Pangong Lake, India. 2011 , 193, 5875-6	9
2063	First draft genome sequence of a strain from the genus <i>Citricoccus</i> . 2011 , 193, 6092-3	5
2062	<i>Chlamydia psittaci</i> genetic variants differ in virulence by modulation of host immunity. 2011 , 204, 654-63	24
2061	Two Strains of <i>Crocospaera watsonii</i> with Highly Conserved Genomes are Distinguished by Strain-Specific Features. 2011 , 2, 261	26
2060	Complete genome sequence of strain HTCC2503T of <i>Parvularcula bermudensis</i> , the type species of the order "Parvularculales" in the class Alphaproteobacteria. 2011 , 193, 305-6	6
2059	Genome sequence of <i>Lactobacillus salivarius</i> GJ-24, a probiotic strain isolated from healthy adult intestine. 2011 , 193, 5021-2	12
2058	Genome sequence of <i>Helicobacter bizzozeronii</i> strain CIII-1, an isolate from human gastric mucosa. 2011 , 193, 4565-6	19
2057	Complete genome sequence of strain IMCC9063, belonging to SAR11 subgroup 3, isolated from the Arctic Ocean. 2011 , 193, 3379-80	24
2056	Genome sequence of <i>Oceanicaulis</i> sp. strain HTCC2633, isolated from the Western Sargasso Sea. 2011 , 193, 317-8	8
2055	Genomes of two chronological isolates (<i>Helicobacter pylori</i> 2017 and 2018) of the West African <i>Helicobacter pylori</i> strain 908 obtained from a single patient. 2011 , 193, 3385-6	27
2054	Biochemical analyses of multiple endoxylanases from the rumen bacterium <i>Ruminococcus albus</i> 8 and their synergistic activities with accessory hemicellulose-degrading enzymes. 2011 , 77, 5157-69	34
2053	Draft genome sequence of <i>Lactobacillus malefermentans</i> KCTC 3548. 2011 , 193, 5537	4
2052	Draft genome sequence of <i>Lactobacillus zeae</i> KCTC 3804. 2011 , 193, 5023	4
2051	Genome sequence of <i>Halorhabdus tiamatea</i> , the first archaeon isolated from a deep-sea anoxic brine lake. 2011 , 193, 4553-4	22

2050	Genome sequence of <i>Lactobacillus animalis</i> KCTC 3501. 2011 , 193, 1280-1	8
2049	Genome sequence of <i>Lactobacillus versmoldensis</i> KCTC 3814. 2011 , 193, 5589-90	2
2048	Whole-genome shotgun sequencing of the sulfur-oxidizing chemoautotroph <i>Tetrathlobacter kashmirensis</i> . 2011 , 193, 5553-4	27
2047	Complete genome sequence of the hyperthermophilic archaeon <i>Thermococcus</i> sp. strain AM4, capable of organotrophic growth and growth at the expense of hydrogenogenic or sulfidogenic oxidation of carbon monoxide. 2011 , 193, 7019-20	22
2046	Genome sequence of <i>Leuconostoc pseudomesenteroides</i> KCTC 3652. 2011 , 193, 4299	9
2045	Genome sequence of multidrug-resistant <i>Pseudomonas aeruginosa</i> NCGM1179. 2011 , 193, 6397	9
2044	Complete genome sequence of the veterinary pathogen <i>Staphylococcus pseudintermedius</i> strain HKU10-03, isolated in a case of canine pyoderma. 2011 , 193, 1783-4	29
2043	Genome sequence of the newly isolated chemolithoautotrophic <i>Bradyrhizobiaceae</i> strain SG-6C. 2011 , 193, 5057	7
2042	Genome sequence of <i>Leuconostoc inhae</i> KCTC 3774, isolated from Kimchi. 2011 , 193, 1278-9	5
2041	Metagenomic analysis of kimchi, a traditional Korean fermented food. 2011 , 77, 2264-74	342
2040	Misannotations of rRNA can now generate 90% false positive protein matches in metatranscriptomic studies. 2011 , 39, 8792-802	37
2039	Genome sequence of <i>Brachybacterium squillarum</i> M-6-3(T), isolated from salt-fermented seafood. 2011 , 193, 6416-7	6
2038	Draft genome sequence of the biocontrol bacterium <i>Pseudomonas putida</i> B001, an oligotrophic bacterium that induces systemic resistance to plant diseases. 2011 , 193, 6795-6	19
2037	Draft genome sequence of <i>Lactobacillus mali</i> KCTC 3596. 2011 , 193, 5037	1
2036	Genome sequence of strain HTCC2083, a novel member of the marine clade <i>Roseobacter</i> . 2011 , 193, 319-20	8
2035	Genome sequence of the plant-pathogenic bacterium <i>Dickeya dadantii</i> 3937. 2011 , 193, 2076-7	78
2034	Draft genome sequence of <i>Caloramator australicus</i> strain RC3T, a thermoanaerobe from the Great Artesian Basin of Australia. 2011 , 193, 2664-5	7
2033	Genome sequence of the thermophilic strain <i>Bacillus coagulans</i> XZL4, an efficient pentose-utilizing producer of chemicals. 2011 , 193, 6398-9	12

2032	The FGGY carbohydrate kinase family: insights into the evolution of functional specificities. 2011 , 7, e1002318	40
2031	Directed evaluation of enterotoxigenic <i>Escherichia coli</i> autotransporter proteins as putative vaccine candidates. 2011 , 5, e1428	28
2030	Genome majority vote improves gene predictions. 2011 , 7, e1002284	11
2029	Draft genome sequence of <i>Streptomyces</i> strain S4, a symbiont of the leaf-cutting ant <i>Acromyrmex octospinosus</i> . 2011 , 193, 4270-1	23
2028	Integrative genomic analysis identifies isoleucine and CodY as regulators of <i>Listeria monocytogenes</i> virulence. 2012 , 8, e1002887	86
2027	Identification and removal of ribosomal RNA sequences from metatranscriptomes. 2012 , 28, 433-5	148
2026	Genomic and transcriptomic studies of an RDX (hexahydro-1,3,5-trinitro-1,3,5-triazine)-degrading actinobacterium. 2012 , 78, 7798-800	20
2025	Genome sequence of multidrug-resistant <i>Escherichia coli</i> EC302/04, isolated from a human tracheal aspirate. 2012 , 194, 6691-2	5
2024	The genome of the heartworm, <i>Dirofilaria immitis</i> , reveals drug and vaccine targets. 2012 , 26, 4650-61	105
2023	Genome sequence of cold-adapted <i>Pseudomonas mandelii</i> strain JR-1. 2012 , 194, 3263	24
2022	Draft genome sequence of <i>Enterobacter cloacae</i> subsp. <i>cloacae</i> strain 08XA1, a fecal bacterium of giant pandas. 2012 , 194, 6928-9	2
2021	Temperature regulation of virulence factors in the pathogen <i>Vibrio coralliilyticus</i> . 2012 , 6, 835-46	149
2020	Whole-genome shotgun sequence of the sulfur-oxidizing chemoautotroph <i>Pseudaminobacter salicylatoxidans</i> KCT001. 2012 , 194, 4743-4	10
2019	Whole genome analysis of <i>Leptospira licerasiae</i> provides insight into leptospiral evolution and pathogenicity. 2012 , 6, e1853	52
2018	Genome sequence of the methanotrophic poly- β -hydroxybutyrate producer <i>Methylocystis parvus</i> OBBP. 2012 , 194, 5709-10	23
2017	Genome sequence of the alkaliphilic bacterium <i>Nitritalea halalkaliphila</i> type strain LW7, isolated from Lonar Lake, India. 2012 , 194, 5688-9	10
2016	Patterns of gene flow define species of thermophilic Archaea. 2012 , 10, e1001265	152
2015	CRISPR/cas loci of type II <i>Propionibacterium acnes</i> confer immunity against acquisition of mobile elements present in type I <i>P. acnes</i> . 2012 , 7, e34171	48

2014	Bacteriophages MR299-2 and NH-4 can eliminate <i>Pseudomonas aeruginosa</i> in the murine lung and on cystic fibrosis lung airway cells. 2012 , 3, e00029-12	162
2013	Genome sequence of <i>Pseudomonas chlororaphis</i> GP72, a root-colonizing biocontrol strain. 2012 , 194, 1269-70	28
2012	Complete genome sequence of <i>Lactococcus lactis</i> subsp. <i>cremoris</i> A76. 2012 , 194, 1241-2	22
2011	Genome sequence of the bacteriocin-producing strain <i>Lactococcus garvieae</i> DCC43. 2012 , 194, 6976-7	15
2010	Draft genome sequence of Arctic marine Bacterium <i>Pseudoalteromonas issachenkonii</i> PAMC 22718. 2012 , 194, 4140	5
2009	Genome sequence of the Antarctic psychrophile bacterium <i>Planococcus antarcticus</i> DSM 14505. 2012 , 194, 4465	11
2008	Complete genome sequence of <i>Methanomassiliicoccus luminyensis</i> , the largest genome of a human-associated Archaea species. 2012 , 194, 4745	64
2007	Whole-genome sequence of <i>Nocardiosis alba</i> strain ATCC BAA-2165, associated with honeybees. 2012 , 194, 6358-9	15
2006	Genome sequence of the unclassified marine Gammaproteobacterium BDW918. 2012 , 194, 3753-4	4
2005	Genome sequence of <i>Pseudomonas stutzeri</i> SDM-LAC, a typical strain for studying the molecular mechanism of lactate utilization. 2012 , 194, 894-5	20
2004	Genome sequence of <i>Peptoniphilus rhinitidis</i> 1-13T, an anaerobic coccus strain isolated from clinical specimens. 2012 , 194, 2405-6	6
2003	First genome sequence of a <i>Burkholderia pseudomallei</i> isolate in China, strain BPC006, obtained from a melioidosis patient in Hainan. 2012 , 194, 6604-5	15
2002	Complete genome sequence of the bacteriophages ECBP1 and ECBP2 isolated from two different <i>Escherichia coli</i> strains. 2012 , 86, 12439-40	11
2001	Complete resequencing and reannotation of the <i>Lactobacillus plantarum</i> WCFS1 genome. 2012 , 194, 195-6	92
2000	Genome sequence of an OXA23-producing, carbapenem-resistant <i>Acinetobacter baumannii</i> strain of sequence type ST75. 2012 , 194, 6000-1	9
1999	Genome sequence of <i>Stenotrophomonas maltophilia</i> S028, an isolate harboring the AmpR-L2 resistance module. 2012 , 194, 6696	4
1998	Genome sequence of <i>Staphylococcus arlettae</i> strain CVD059, isolated from the blood of a cardiovascular disease patient. 2012 , 194, 6615-6	9
1997	Genome sequence of extracellular-protease-producing <i>Alishewanella jeotgali</i> isolated from traditional Korean fermented seafood. 2012 , 194, 2097	13

1996	Draft genome sequence of <i>Pedobacter agri</i> PB92T, which belongs to the family Sphingobacteriaceae. 2012 , 194, 3738	3
1995	Draft genome sequence of <i>Staphylococcus vitulinus</i> F1028, a strain isolated from a block of fermented soybean. 2012 , 194, 5961-2	5
1994	Genome sequence of <i>Kocuria atrinae</i> C3-8, isolated from Jeotgal, a traditional Korean fermented seafood. 2012 , 194, 5996	5
1993	Draft genome sequence of <i>Pontibacter</i> sp. nov. BAB1700, a halotolerant, industrially important bacterium. 2012 , 194, 6329-30	9
1992	Genome sequence of <i>Escherichia coli</i> J53, a reference strain for genetic studies. 2012 , 194, 3742-3	36
1991	Genome sequence of <i>Reyranella massiliensis</i> , a bacterium associated with amoebae. 2012 , 194, 5698	6
1990	Draft genome sequence of the quality control strain <i>Enterococcus faecalis</i> ATCC 29212. 2012 , 194, 6006-7	21
1989	Draft genome sequence of <i>Bacillus endophyticus</i> 2102. 2012 , 194, 5705-6	8
1988	Genome sequence of a cold-adaptable sulfamethoxazole-degrading bacterium, <i>Pseudomonas psychrophila</i> HA-4. 2012 , 194, 5721	9
1987	Genome sequence of <i>Brucella melitensis</i> strain 128, an isolate of biovar 3 of sequence type 8. 2012 , 194, 6960	1
1986	Genome sequence of <i>Staphylococcus epidermidis</i> strain AU12-03, isolated from an intravascular catheter. 2012 , 194, 6639	2
1985	Draft genome sequence of <i>Bacillus anthracis</i> UR-1, isolated from a German heroin user. 2012 , 194, 5997-8	12
1984	Draft genome sequence of <i>Pseudomonas fuscovaginae</i> , a broad-host-range pathogen of plants. 2012 , 194, 2765-6	10
1983	Complete Genome Sequence of IME13, a <i>Stenotrophomonas maltophilia</i> bacteriophage with large burst size and unique plaque polymorphism. 2012 , 86, 11392-3	14
1982	Genome sequence of <i>Pseudomonas putida</i> S12, a potential platform strain for industrial production of valuable chemicals. 2012 , 194, 5985-6	11
1981	Genome sequence of a highly efficient aerobic denitrifying bacterium, <i>Pseudomonas stutzeri</i> T13. 2012 , 194, 5720	29
1980	Genome sequence of the plant growth-promoting rhizobacterium <i>Bacillus</i> sp. strain JS. 2012 , 194, 3760-1	27
1979	Genome sequence of the halophilic archaeon <i>Halococcus hamelinensis</i> . 2012 , 194, 2100-1	12

1978	Genome sequence of the halotolerant bacterium <i>Imtechella halotolerans</i> K1T. 2012 , 194, 3731	3
1977	Complete genome sequence of <i>Brucella abortus</i> strain BCB034, a strain of biovar 2 isolated from human. 2012 , 194, 6943	
1976	Draft genome sequence of <i>Lactobacillus rossiae</i> DSM 15814(T). 2012 , 194, 5460-1	5
1975	Complete genome sequence of the dairy isolate <i>Streptococcus macedonicus</i> ACA-DC 198. 2012 , 194, 1838-9	25
1974	Complete genome sequence of <i>Salmonella enterica</i> serovar pullorum RKS5078. 2012 , 194, 744	19
1973	pEI1573 Carrying blaIMP-4, from Sydney, Australia, is closely related to other IncL/M plasmids. 2012 , 56, 6029-32	55
1972	Genome sequence and comparative pathogenomics analysis of a <i>Salmonella enterica</i> Serovar Typhi strain associated with a typhoid carrier in Malaysia. 2012 , 194, 5970-1	18
1971	Insights from the genome sequence of a <i>Salmonella enterica</i> serovar Typhi strain associated with a sporadic case of typhoid fever in Malaysia. 2012 , 194, 5124-5	7
1970	Genome sequence of <i>Lactobacillus fructivorans</i> KCTC 3543. 2012 , 194, 2111-2	4
1969	Genome sequence of <i>Lysinibacillus boronitolerans</i> F1182, isolated from a traditional Korean fermented soybean product. 2012 , 194, 5988	6
1968	Draft genome sequence of <i>Mycobacterium abscessus</i> subsp. <i>bolletii</i> BD(T). 2012 , 194, 2756-7	27
1967	Genome sequence of the marine bacterium <i>Marinilabilia salmonicolor</i> JCM 21150T. 2012 , 194, 3746	5
1966	Genome sequences of two plant growth-promoting fluorescent <i>Pseudomonas</i> strains, R62 and R81. 2012 , 194, 3272-3	21
1965	Genome sequences of <i>Burkholderia</i> sp. strains CCGE1002 and H160, isolated from legume nodules in Mexico and Brazil. 2012 , 194, 6927	33
1964	Genome sequence of <i>Mycobacterium abscessus</i> strain M152. 2012 , 194, 6662	3
1963	Draft genome sequence of the human pathogen <i>Streptomyces somaliensis</i> , a significant cause of actinomycetoma. 2012 , 194, 3544-5	21
1962	Genomic comparison of <i>Kingella kingae</i> strains. 2012 , 194, 5972	10
1961	Whole-genome sequence of <i>Stenotrophomonas maltophilia</i> D457, a clinical isolate and a model strain. 2012 , 194, 3563-4	34

1960	Draft genome sequence of the cyanide-utilizing bacterium <i>Pseudomonas fluorescens</i> strain NCIMB 11764. 2012 , 194, 6618-9	8
1959	Genome sequence of <i>Parascardovia denticolens</i> IPLA 20019, isolated from human breast milk. 2012 , 194, 4776-7	9
1958	Genome sequence of the lactate-utilizing <i>Pseudomonas aeruginosa</i> strain XMG. 2012 , 194, 4751-2	13
1957	Genome sequence of strain IMCC14465, isolated from the East Sea, belonging to the PS1 clade of Alphaproteobacteria. 2012 , 194, 6952-3	6
1956	Draft genome sequence of <i>Agrobacterium albertimagni</i> strain AOL15. 2012 , 194, 6986-7	4
1955	Complete genome sequence of <i>Actinobacillus suis</i> H91-0380, a virulent serotype O2 strain. 2012 , 194, 6686-7	12
1954	Genome sequences of two thermophilic <i>Bacillus licheniformis</i> strains, efficient producers of platform chemical 2,3-butanediol. 2012 , 194, 4133-4	14
1953	Genome sequence of <i>Staphylococcus lentus</i> F1142, a strain isolated from Korean soybean paste. 2012 , 194, 5987	7
1952	Genetic fine structure of a <i>Salmonella enterica</i> serovar Typhi strain associated with the 2005 outbreak of typhoid fever in Kelantan, Malaysia. 2012 , 194, 3565-6	16
1951	Draft genome sequence of <i>Paenisporosarcina</i> sp. strain TG-14, a psychrophilic bacterium isolated from sediment-laden stratified basal ice from Taylor Glacier, McMurdo Dry Valleys, Antarctica. 2012 , 194, 6656-7	7
1950	Draft genome sequence of the nitrogen-fixing symbiotic bacterium <i>Bradyrhizobium elkanii</i> 587. 2012 , 194, 3547-8	15
1949	Key enzymes enabling the growth of <i>Arthrobacter</i> sp. strain JBH1 with nitroglycerin as the sole source of carbon and nitrogen. 2012 , 78, 3649-55	11
1948	Genome sequence of the welan gum-producing strain <i>Sphingomonas</i> sp. ATCC 31555. 2012 , 194, 5989-90	20
1947	Draft genome sequence of <i>Thermus</i> sp. strain RL, isolated from a hot water spring located atop the Himalayan ranges at Manikaran, India. 2012 , 194, 3534	26
1946	Complete genome sequence of the porcine isolate <i>Enterococcus faecalis</i> D32. 2012 , 194, 5490-1	14
1945	Genome sequence of <i>Sphingomonas</i> sp. strain PAMC 26605, isolated from Arctic lichen (<i>Ochrolechia</i> sp.). 2012 , 194, 1607	7
1944	Complete genome sequences of two <i>Persicivirga</i> bacteriophages, P12024S and P12024L. 2012 , 86, 8907-8	15
1943	Genome sequence of the plant growth-promoting bacterium <i>Enterobacter cloacae</i> GS1. 2012 , 194, 4479	5

1942	Genome sequence of the broad-host-range <i>Pseudomonas</i> phage Φ 51. 2012 , 86, 10239	10
1941	Draft genome sequence of <i>Flavobacterium</i> sp. strain F52, isolated from the rhizosphere of bell pepper (<i>Capsicum annuum</i> L. cv. Maccabi). 2012 , 194, 5462-3	28
1940	Draft genome sequence of <i>Paenibacillus peoriae</i> strain KCTC 3763T. 2012 , 194, 1237-8	9
1939	Genomic comparison of <i>Escherichia coli</i> O104:H4 isolates from 2009 and 2011 reveals plasmid, and prophage heterogeneity, including shiga toxin encoding phage stx2. 2012 , 7, e48228	94
1938	Genotypic and phenotypic evaluation of the evolution of high-level daptomycin nonsusceptibility in vancomycin-resistant <i>Enterococcus faecium</i> . 2012 , 56, 6051-3	49
1937	Draft genome sequence of <i>Methanobacterium formicicum</i> DSM 3637, an Archaeobacterium isolated from the methane producer amoeba <i>Pelomyxa palustris</i> . 2012 , 194, 6967-8	12
1936	Frontiers in metabolic reconstruction and modeling of plant genomes. 2012 , 63, 2247-58	62
1935	Complete genome sequence of <i>Brucella suis</i> VBI22, isolated from bovine milk. 2012 , 194, 910	9
1934	Complete annotated genome sequence of <i>Mycobacterium tuberculosis</i> Erdman. 2012 , 194, 2770	14
1933	Genome sequence of the bacteriocin-producing <i>Lactobacillus curvatus</i> strain CRL705. 2012 , 194, 538-9	29
1932	Genome sequence of enterohemorrhagic <i>Escherichia coli</i> NCCP15658. 2012 , 194, 3749-50	7
1931	Genome sequence of " <i>Candidatus Methanomethylophilus alvus</i> " Mx1201, a methanogenic archaeon from the human gut belonging to a seventh order of methanogens. 2012 , 194, 6944-5	112
1930	Genome sequence of <i>Oscillibacter ruminantium</i> strain GH1, isolated from rumen of Korean native cattle. 2012 , 194, 6362	19
1929	Draft genome sequence of <i>Halomonas</i> sp. strain HAL1, a moderately halophilic arsenite-oxidizing bacterium isolated from gold-mine soil. 2012 , 194, 199-200	31
1928	Draft genome sequence of <i>Moritella dasanensis</i> strain ArB 0140, a psychrophilic bacterium isolated from the Arctic Ocean. 2012 , 194, 5452-3	4
1927	Genome sequence of <i>Lactococcus raffinolactis</i> strain 4877, isolated from natural dairy starter culture. 2012 , 194, 6364	14
1926	Bacterial responses to a simulated colon tumor microenvironment. 2012 , 11, 851-62	31
1925	Genome sequence of <i>Pseudomonas putida</i> strain SJTE-1, a bacterium capable of degrading estrogens and persistent organic pollutants. 2012 , 194, 4781-2	25

1924	Genome sequence of the rice pathogen <i>Pseudomonas fuscovaginae</i> CB98818. 2012 , 194, 5479-80	9
1923	Genome sequences for six <i>Rhodanobacter</i> strains, isolated from soils and the terrestrial subsurface, with variable denitrification capabilities. 2012 , 194, 4461-2	47
1922	Characterization of the ELPhiS prophage from <i>Salmonella enterica</i> serovar Enteritidis strain LK5. 2012 , 78, 1785-93	20
1921	Draft genome sequence of <i>Enterococcus mundtii</i> CRL1656. 2012 , 194, 550	10
1920	Draft genome sequence of <i>Herbaspirillum lusitanum</i> P6-12, an endophyte isolated from root nodules of <i>Phaseolus vulgaris</i> . 2012 , 194, 4136-7	18
1919	Complete genome sequence of the giant <i>Pseudomonas</i> phage Lu11. 2012 , 86, 6369-70	24
1918	Complete genome sequence of <i>Mycobacterium xenopi</i> type strain RIVM700367. 2012 , 194, 3282-3	3
1917	Draft genome sequence of <i>Mycobacterium bolletii</i> strain M24, a rapidly growing mycobacterium of contentious taxonomic status. 2012 , 194, 4475	10
1916	Annotated genome sequence of <i>Mycobacterium massiliense</i> strain M154, belonging to the recently created taxon <i>Mycobacterium abscessus</i> subsp. <i>bolletii</i> comb. nov. 2012 , 194, 4778	11
1915	Genome sequence of <i>Klebsiella pneumoniae</i> LZ, a potential platform strain for 1,3-propanediol production. 2012 , 194, 4457-8	6
1914	Draft genome sequence of the human pathogen <i>Halomonas stevensii</i> S18214T. 2012 , 194, 5143	7
1913	A <i>Rickettsia</i> genome overrun by mobile genetic elements provides insight into the acquisition of genes characteristic of an obligate intracellular lifestyle. 2012 , 194, 376-94	115
1912	Insight into the transmission biology and species-specific functional capabilities of tsetse (Diptera: glossinidae) obligate symbiont <i>Wigglesworthia</i> . 2012 , 3,	76
1911	Complete genome sequence of <i>Celeribacter</i> bacteriophage P12053L. 2012 , 86, 8339-40	26
1910	Draft genome sequence of the antifungal-producing plant-benefiting bacterium <i>Burkholderia pyrrocinia</i> CH-67. 2012 , 194, 6649-50	8
1909	Draft genome sequence of <i>Paenibacillus polymyxa</i> OSY-DF, which coproduces a lantibiotic, paenibacillin, and polymyxin E1. 2012 , 194, 4739-40	26
1908	Genome sequence of n-alkane-degrading <i>Hydrocarboniphaga effusa</i> strain AP103T (ATCC BAA-332T). 2012 , 194, 5120	3
1907	Genome sequences of two freshwater betaproteobacterial isolates, <i>Limnohabitans</i> species strains Rim28 and Rim47, indicate their capabilities as both photoautotrophs and ammonia oxidizers. 2012 , 194, 6302-3	33

1906	Genome sequence of the plant growth-promoting rhizobacterium <i>Pseudomonas putida</i> S11. 2012 , 194, 6015	2
1905	Draft genome sequence of <i>Rhodovulum</i> sp. strain PH10, a phototrophic alphaproteobacterium isolated from a soil sample of mangrove of Namkhana, India. 2012 , 194, 6363	3
1904	Draft genome sequence of the thermophilic bacterium <i>Anoxybacillus kamchatkensis</i> G10. 2012 , 194, 6684-5	10
1903	Genome sequence of the highly efficient arsenite-oxidizing bacterium <i>Achromobacter arsenitoxydans</i> SY8. 2012 , 194, 1243-4	27
1902	Draft genome sequence of <i>Serratia</i> sp. strain M24T3, isolated from pinewood disease nematode <i>Bursaphelenchus xylophilus</i> . 2012 , 194, 3764	20
1901	Bacteriophage cocktail significantly reduces <i>Escherichia coli</i> O157: H7 contamination of lettuce and beef, but does not protect against recontamination. 2012 , 2, 178-185	83
1900	The mitochondrial genome of <i>Paraminabea aldersladei</i> (Cnidaria: Anthozoa: Octocorallia) supports intramolecular recombination as the primary mechanism of gene rearrangement in octocoral mitochondrial genomes. 2012 , 4, 994-1006	51
1899	Draft genome sequence of <i>Pantoea ananatis</i> B1-9, a nonpathogenic plant growth-promoting bacterium. 2012 , 194, 729	24
1898	Global transcriptome response to ionic liquid by a tropical rain forest soil bacterium, <i>Enterobacter lignolyticus</i> . 2012 , 109, E2173-82	81
1897	Draft genome sequence of the methane-oxidizing bacterium <i>Methylococcus capsulatus</i> (Texas). 2012 , 194, 6626	15
1896	Genome sequence of <i>Pseudomonas aeruginosa</i> strain SJTD-1, a bacterium capable of degrading long-chain alkanes and crude oil. 2012 , 194, 4783-4	19
1895	Biochemical and structural insights into xylan utilization by the thermophilic bacterium <i>Caldanaerobius polysaccharolyticus</i> . 2012 , 287, 34946-34960	38
1894	Draft genome sequence of <i>Pseudomonas</i> sp. strain M47T1, carried by <i>Bursaphelenchus xylophilus</i> isolated from <i>Pinus pinaster</i> . 2012 , 194, 4789-90	8
1893	Identification and characterization of a novel incompatibility group X3 plasmid carrying <i>bla</i> NDM-1 in <i>Enterobacteriaceae</i> isolates with epidemiological links to multiple geographical areas in China. 2012 , 1, e39	97
1892	Genome sequence of the plant growth-promoting rhizobacterium <i>Bacillus</i> sp. strain 916. 2012 , 194, 5467-8	13
1891	Genome and physiology of a model Epsilonproteobacterium responsible for sulfide detoxification in marine oxygen depletion zones. 2012 , 109, 506-10	113
1890	Draft genome sequence of <i>Pseudomonas</i> sp. strain Ag1, isolated from the midgut of the malaria mosquito <i>Anopheles gambiae</i> . 2012 , 194, 5449	15
1889	Genome sequence of <i>Myroides injenensis</i> M09-0166(T), isolated from clinical specimens. 2012 , 194, 2748-9	9

1888	Draft genome sequence of <i>Bacillus anthracis</i> BF-1, isolated from Bavarian cattle. 2012 , 194, 6360-1	10
1887	Draft genome sequence of the soil bacterium <i>Burkholderia terrae</i> strain BS001, which interacts with fungal surface structures. 2012 , 194, 4480-1	13
1886	Complete genome sequence of <i>Klebsiella oxytoca</i> E718, a New Delhi metallo- β -lactamase-1-producing nosocomial strain. 2012 , 194, 5454	23
1885	Draft genome sequence of the novel enteric bacterium <i>Galloisinimonas intestini</i> B14T KCTC 32180, isolated from the gut of a Galloisiana species (Notoptera: Grylloblattidae) fossil insect. 2012 , 194, 6648	
1884	Genome sequence of <i>Pseudomonas</i> sp. strain PAMC 25886, isolated from alpine glacial cryoconite. 2012 , 194, 1844	4
1883	Genome sequence of " <i>Candidatus Aquiluna</i> " sp. strain IMCC13023, a marine member of the Actinobacteria isolated from an arctic fjord. 2012 , 194, 3550-1	40
1882	Draft genome sequence of the fish pathogen <i>Vibrio harveyi</i> strain ZJ0603. 2012 , 194, 6644-5	11
1881	Complete genome sequence of <i>Brucella canis</i> strain 118, a strain isolated from canine. 2012 , 194, 6680	3
1880	Draft genome sequence of <i>Achromobacter piechaudii</i> strain HLE. 2012 , 194, 6355	8
1879	Genome sequence of the hemolytic-uremic syndrome-causing strain <i>Escherichia coli</i> NCCP15647. 2012 , 194, 3747-8	9
1878	Complete genome sequence of <i>Marinomonas bacteriophage</i> P12026. 2012 , 86, 8909-10	9
1877	Genome sequence of <i>Mycobacterium massiliense</i> M18, isolated from a lymph node biopsy specimen. 2012 , 194, 4125	11
1876	Genome sequence of the polychlorinated-biphenyl degrader <i>Pseudomonas pseudoalcaligenes</i> KF707. 2012 , 194, 4426-7	21
1875	Draft genome sequences of <i>Enterobacter</i> sp. isolate Ag1 from the midgut of the malaria mosquito <i>Anopheles gambiae</i> . 2012 , 194, 5481	16
1874	Vitamin B(12) synthesis and salvage pathways were acquired by horizontal gene transfer to the Thermotogales. 2012 , 4, 730-9	15
1873	Complete genome sequence of the African dairy isolate <i>Streptococcus infantarius</i> subsp. <i>infantarius</i> strain CJ18. 2012 , 194, 2105-6	10
1872	Genome sequence of the rice pathogen <i>Dickeya zeae</i> strain ZJU1202. 2012 , 194, 4452-3	17
1871	Complete genome sequence of <i>Klebsiella pneumoniae</i> 1084, a hypermucoviscosity-negative K1 clinical strain. 2012 , 194, 6316	30

1870	Complete genome sequence of <i>Brucella melitensis</i> 133, an isolate of biovar 1 of sequence type 32. 2012 , 194, 6932	
1869	Molecular and biochemical analyses of the GH44 module of CbMan5B/Cel44A, a bifunctional enzyme from the hyperthermophilic bacterium <i>Caldicellulosiruptor bescii</i> . 2012 , 78, 7048-59	31
1868	Draft genome sequence of the bean-nodulating <i>Sinorhizobium fredii</i> strain GR64. 2012 , 194, 6978	2
1867	Genome sequences of <i>Brucella melitensis</i> 16M and its two derivatives 16M1w and 16M13w, which evolved in vivo. 2012 , 194, 5489	10
1866	Draft genome sequence of <i>Sinorhizobium meliloti</i> CCNWSX0020, a nitrogen-fixing symbiont with copper tolerance capability isolated from lead-zinc mine tailings. 2012 , 194, 1267-8	18
1865	Draft genome sequence of the biocontrol bacterium <i>Bacillus amyloliquefaciens</i> strain M27. 2012 , 194, 6934-5	18
1864	FSL J1-208, a virulent uncommon phylogenetic lineage IV <i>Listeria monocytogenes</i> strain with a small chromosome size and a putative virulence plasmid carrying internalin-like genes. 2012 , 78, 1876-89	31
1863	Draft genome sequence of the nitrophenol-degrading actinomycete <i>Rhodococcus imtechensis</i> RKJ300. 2012 , 194, 3543	11
1862	Draft genome sequence of plant growth-promoting rhizobium <i>Mesorhizobium amorphae</i> , isolated from zinc-lead mine tailings. 2012 , 194, 736-7	31
1861	Genome sequence of <i>Afipia birgiae</i> , a rare bacterium associated with <i>Amoebae</i> . 2012 , 194, 7018	3
1860	Genome sequence of the thermophile <i>Bacillus coagulans</i> Hammer, the type strain of the species. 2012 , 194, 6294-5	9
1859	Genome sequence of <i>Nitratireductor aquibiodomus</i> strain RA22. 2012 , 194, 6307	5
1858	Genome sequence of <i>Diplorickettsia massiliensis</i> , an emerging <i>Ixodes ricinus</i> -associated human pathogen. 2012 , 194, 3287	7
1857	Genome sequence and comparative genomics analysis of a <i>Vibrio cholerae</i> O1 strain isolated from a cholera patient in Malaysia. 2012 , 194, 6933	5
1856	Draft genome sequence of <i>Bacillus pumilus</i> BA06, a producer of alkaline serine protease with leather-dehairing function. 2012 , 194, 6668-9	15
1855	Whole-genome sequences and comparative genomics of <i>Salmonella enterica</i> serovar Typhi isolates from patients with fatal and nonfatal typhoid fever in Papua New Guinea. 2012 , 194, 5122-3	10
1854	Genome sequence of <i>Janthinobacterium</i> sp. strain PAMC 25724, isolated from alpine glacier cryoconite. 2012 , 194, 2096	27
1853	Genome sequence of a novel member of the genus <i>Psychrobacter</i> isolated from Antarctic soil. 2012 , 194, 2403	22

1852	MicrobeDB: a locally maintainable database of microbial genomic sequences. 2012 , 28, 1947-8	13
1851	Draft genome sequence of <i>Gillisia</i> sp. strain CBA3202, a novel member of the genus <i>Gillisia</i> , which belongs to the family Flavobacteriaceae. 2012 , 194, 3739	6
1850	Use of recombinase-based in vivo expression technology to characterize <i>Enterococcus faecalis</i> gene expression during infection identifies in vivo-expressed antisense RNAs and implicates the protease Eep in pathogenesis. 2012 , 80, 539-49	40
1849	Draft genome sequence of <i>Sphingomonas echinoides</i> ATCC 14820. 2012 , 194, 1843	9
1848	Draft genome sequence of <i>Halomonas smyrnensis</i> AAD6T. 2012 , 194, 5690-1	13
1847	Genomic analysis of <i>Mycobacterium abscessus</i> strain M139, which has an ambiguous subspecies taxonomic position. 2012 , 194, 6002-3	10
1846	Complete genome sequence of the endophytic bacterium <i>Burkholderia</i> sp. strain KJ006. 2012 , 194, 4432-3	32
1845	Complete genome sequence of <i>Mycobacterium vaccae</i> type strain ATCC 25954. 2012 , 194, 6339-40	7
1844	Virioplankton community structure in Tunisian solar salterns. 2012 , 78, 7429-37	32
1843	Draft genome sequence of <i>Virgibacillus halodenitrificans</i> 1806. 2012 , 194, 6332-3	7
1842	Complete genome sequence of <i>Mycobacterium fortuitum</i> subsp. <i>fortuitum</i> type strain DSM46621. 2012 , 194, 6337-8	5
1841	Draft genome sequence of the plant growth-promoting bacterium <i>Bacillus siamensis</i> KCTC 13613T. 2012 , 194, 4148-9	29
1840	Genome sequence of <i>Moraxella catarrhalis</i> RH4, an isolate of seroresistant lineage. 2012 , 194, 6969	11
1839	Genome sequence of <i>Vibrio</i> sp. strain EJY3, an agarolytic marine bacterium metabolizing 3,6-anhydro-L-galactose as a sole carbon source. 2012 , 194, 2773-4	20
1838	Genome sequence of the polyhydroxybutyrate producer <i>Pseudomonas extremaustralis</i> , a highly stress-resistant Antarctic bacterium. 2012 , 194, 2381-2	27
1837	Genome sequence of the biocontrol strain <i>Pseudomonas fluorescens</i> F113. 2012 , 194, 1273-4	57
1836	Whole-genome shotgun sequencing of the extremophile <i>Alkalibacillus haloalkaliphilus</i> C-5, of Indian origin. 2012 , 194, 4775	3
1835	Draft genome sequence of <i>Paenibacillus</i> sp. strain OSY-SE, a bacterium producing the novel broad-spectrum lipopeptide antibiotic paenibacterin. 2012 , 194, 6306	7

1834	Draft genome sequence of <i>Leucobacter chromiirestiens</i> , an extremely chromium-tolerant strain. 2012 , 194, 540-1	12
1833	Analysis of the genome of <i>Mycobacterium abscessus</i> strain M94 reveals an uncommon cluster of tRNAs. 2012 , 194, 5724	6
1832	Genome sequence of <i>Sphingomonas</i> sp. strain PAMC 26621, an Arctic-lichen-associated bacterium isolated from a <i>Cetraria</i> sp. 2012 , 194, 3030	16
1831	Genome sequence of <i>Enterobacter cloacae</i> subsp. <i>dissolvens</i> SDM, an efficient biomass-utilizing producer of platform chemical 2,3-butanediol. 2012 , 194, 897-8	21
1830	Draft genome sequence of the hydrocarbon-degrading and emulsan-producing strain <i>Acinetobacter venetianus</i> RAG-1T. 2012 , 194, 4771-2	13
1829	Genome sequence of <i>Leuconostoc pseudomesenteroides</i> strain 4882, isolated from a dairy starter culture. 2012 , 194, 6637	17
1828	Draft genome sequence of <i>Pseudomonas psychrotolerans</i> L19, isolated from copper alloy coins. 2012 , 194, 1623-4	7
1827	Genome sequence of <i>Brucella melitensis</i> S66, an isolate of sequence type 8, prevalent in China. 2012 , 194, 5451	4
1826	pJIE137 carrying blaCTX-M-62 is closely related to p271A carrying blaNDM-1. 2012 , 56, 2166-8	25
1825	Comparative analysis of genome sequences covering the seven <i>Cronobacter</i> species. 2012 , 7, e49455	96
1824	Genome sequence of a novel nicotine-degrading strain, <i>Pseudomonas geniculata</i> N1. 2012 , 194, 3553-4	9
1823	Identification and characterization of a lipopolysaccharide α ,3-sialyltransferase from the human pathogen <i>Helicobacter bizzozeronii</i> . 2012 , 194, 2540-50	13
1822	Complete genome sequence of the fruiting myxobacterium <i>Coralloccoccus coralloides</i> DSM 2259. 2012 , 194, 3012-3	43
1821	Draft genome sequence of <i>Commensalibacter intestini</i> A911T, a symbiotic bacterium isolated from <i>Drosophila melanogaster</i> intestine. 2012 , 194, 1246	9
1820	Genome sequence of "Candidatus <i>Microthrix parvicella</i> " Bio17-1, a long-chain-fatty-acid-accumulating filamentous actinobacterium from a biological wastewater treatment plant. 2012 , 194, 6670-1	25
1819	Antimicrobial treatment and containment measures for an extremely drug-resistant <i>Klebsiella pneumoniae</i> ST101 isolate carrying pKPN101-IT, a novel fully sequenced bla(KPC-2) plasmid. 2012 , 50, 3768-72	36
1818	Complete genome sequence of <i>Melissococcus plutonius</i> DAT561, a strain that shows an unusual growth profile and is representative of an endemic cluster in Japan. 2012 , 194, 3014	10
1817	Draft genome sequence of <i>Ureibacillus thermosphaericus</i> strain thermo-BF, isolated from Ramsar hot springs in Iran. 2012 , 194, 4431	5

1816	Draft genome sequences of the <i>Pseudomonas fluorescens</i> biocontrol strains Wayne1R and Wood1R. 2012 , 194, 724-5	9
1815	Molecular characterization of the 2011 Hong Kong scarlet fever outbreak. 2012 , 206, 341-51	72
1814	Complete genome sequence of <i>Liberibacter crescens</i> BT-1. 2012 , 7, 271-83	74
1813	Genome sequence of the bacterioplanktonic, mixotrophic <i>Vibrio campbellii</i> strain PEL22A, isolated in the Abrolhos Bank. 2012 , 194, 2759-60	10
1812	Genomic Analysis of <i>Mycobacterium massiliense</i> strain M115, an isolate from human sputum. 2012 , 194, 4786	11
1811	Genome sequence of <i>Helicobacter pylori</i> hpEurope strain N6. 2012 , 194, 3725-6	19
1810	Genome sequence of the plant pathogen <i>Pseudomonas syringae</i> pv. <i>panici</i> LMG 2367. 2012 , 194, 5693-4	7
1809	Genome sequence of <i>Acinetobacter</i> sp. strain HA, isolated from the gut of the polyphagous insect pest <i>Helicoverpa armigera</i> . 2012 , 194, 5156	16
1808	Quantifying homologous replacement of loci between haloarchaeal species. 2012 , 4, 1223-44	49
1807	Identification and characterization of a bile salt hydrolase from <i>Lactobacillus salivarius</i> for development of novel alternatives to antibiotic growth promoters. 2012 , 78, 8795-802	56
1806	Identification of the herboxidiene biosynthetic gene cluster in <i>Streptomyces chromofuscus</i> ATCC 49982. 2012 , 78, 2034-8	20
1805	Complete genome sequence of <i>Oceanimonas</i> sp. GK1, a halotolerant bacterium from Gavkhouni Wetland in Iran. 2012 , 194, 2123-4	12
1804	Draft genome sequence of the shrimp pathogen <i>Vibrio harveyi</i> CAIM 1792. 2012 , 194, 2104	8
1803	Genome sequence of <i>Sphingomonas wittichii</i> DP58, the first reported phenazine-1-carboxylic acid-degrading strain. 2012 , 194, 3535-6	12
1802	Genome sequence of the probiotic bacterium <i>Sporolactobacillus vineae</i> SL153T. 2012 , 194, 3015-6	3
1801	Genome sequence of the nitroaromatic compound-degrading Bacterium <i>Burkholderia</i> sp. strain SJ98. 2012 , 194, 3286	14
1800	Genome sequence of the Shiga toxin-producing <i>Escherichia coli</i> strain NCCP15657. 2012 , 194, 3751-2	5
1799	Complete genome sequences of probiotic strains <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> B420 and Bi-07. 2012 , 194, 4131-2	20

1798	Draft genome sequence and comparative analysis of the superb aromatic-hydrocarbon degrader <i>Rhodococcus</i> sp. strain DK17. 2012 , 194, 4440	11
1797	Genome sequence of a novel indigo-producing strain, <i>Pseudomonas monteilii</i> QM. 2012 , 194, 4459-60	9
1796	Genome sequence of <i>Sphingobium indicum</i> B90A, a hexachlorocyclohexane-degrading bacterium. 2012 , 194, 4471-2	29
1795	Draft genome sequence of <i>Alcaligenes faecalis</i> subsp. <i>faecalis</i> NCIB 8687 (CCUG 2071). 2012 , 194, 5153	19
1794	Genome sequence of a nicotine-degrading strain of <i>Arthrobacter</i> . 2012 , 194, 5714-5	9
1793	Complete genome sequence of the endophytic <i>Enterobacter cloacae</i> subsp. <i>cloacae</i> strain ENHKU01. 2012 , 194, 5965	31
1792	Draft genome sequence of <i>Paenisporosarcina</i> sp. strain TG-20, a psychrophilic bacterium isolated from the basal ice of Taylor Glacier. 2012 , 194, 6636	
1791	Draft genome sequence of <i>Bacillus oceanisediminis</i> 2691. 2012 , 194, 6351-2	6
1790	Genome sequence of <i>Janibacter hoylei</i> MTCC8307, isolated from the stratospheric air. 2012 , 194, 6629-30	5
1789	Genome sequence of <i>Rhizobium grahamii</i> CCGE502, a broad-host-range symbiont with low nodulation competitiveness in <i>Phaseolus vulgaris</i> . 2012 , 194, 6651-2	5
1788	Complete genome sequence of <i>Brucella canis</i> BCB018, a strain isolated from a human patient. 2012 , 194, 6697-8	6
1787	Complete genome sequence of <i>Brucella suis</i> field strain BCB025 of sequence type ST22. 2012 , 194, 6959	
1786	Genome sequence of OXA-48 carbapenemase-producing <i>Klebsiella pneumoniae</i> KpO3210. 2012 , 194, 6981	8
1785	Shotgun genome sequence of a <i>Yersinia enterocolitica</i> isolate from the Philippines. 2012 , 194, 542-3	2
1784	Genome sequence of benzo(a)pyrene-degrading bacterium <i>Novosphingobium pentaromativorans</i> US6-1. 2012 , 194, 907	34
1783	Draft genome sequences of the biocontrol bacterium <i>Mitsuaria</i> sp. strain H24L5A. 2012 , 194, 734-5	8
1782	Genome sequence of deep-sea manganese-oxidizing bacterium <i>Marinobacter manganoxydans</i> Mni7-9. 2012 , 194, 899-900	26
1781	Genome sequence of the arsenite-oxidizing strain <i>Agrobacterium tumefaciens</i> 5A. 2012 , 194, 903	13

1780	Draft genome of <i>Pseudomonas stutzeri</i> strain ZoBell (CCUG 16156), a marine isolate and model organism for denitrification studies. 2012 , 194, 1277-8	26
1779	Draft genome sequence of <i>Gluconobacter morbifer</i> G707T, a pathogenic gut bacterium isolated from <i>Drosophila melanogaster</i> intestine. 2012 , 194, 1245	9
1778	Complete genome sequence of the highly hemolytic strain <i>Bacillus cereus</i> F837/76. 2012 , 194, 1630	5
1777	Complete genome sequence of the beer spoilage organism <i>Pediococcus clausenii</i> ATCC BAA-344T. 2012 , 194, 1271-2	31
1776	Complete genome sequence of <i>Brucella abortus</i> 134, a biovar 1 strain isolated from human. 2012 , 194, 6658	1
1775	Complete genome sequence of <i>Croceibacter bacteriophage</i> P2559S. 2012 , 86, 8912-3	8
1774	Genome sequence of the anaerobic bacterium <i>Clostridium arbusti</i> SL206(T). 2012 , 194, 2758	2
1773	Genome sequence of <i>Herbaspirillum</i> sp. strain GW103, a plant growth-promoting bacterium. 2012 , 194, 4150	15
1772	The chimeric genome of <i>Sphaerochaeta</i> : nonspiral spirochetes that break with the prevalent dogma in spirochete biology. 2012 , 3,	44
1771	Comparative genomics of early-diverging <i>Brucella</i> strains reveals a novel lipopolysaccharide biosynthesis pathway. 2012 , 3, e00246-12	23
1770	Conceptualizing a Genomics Software Institute (GSI). 2012 , 6, 136-44	1
1769	Genome sequence of strain HIMB624, a cultured representative from the OM43 clade of marine Betaproteobacteria. 2012 , 6, 11-20	27
1768	Complete Genome Sequence of <i>Paenibacillus</i> strain Y4.12MC10, a Novel <i>Paenibacillus lautus</i> strain Isolated from Obsidian Hot Spring in Yellowstone National Park. 2012 , 6, 381-400	27
1767	Complete genome sequence of bacteriophage VvAW1, which infects <i>Vibrio vulnificus</i> . 2012 , 6, 415-26	11
1766	Metagenomic evidence for h(2) oxidation and h(2) production by serpentinite-hosted subsurface microbial communities. 2012 , 2, 268	130
1765	XagR, a LuxR homolog, contributes to the virulence of <i>Xanthomonas axonopodis</i> pv. <i>glycines</i> to soybean. 2012 , 25, 1104-17	42
1764	Genome sequence of <i>Staphylococcus aureus</i> Newbould 305, a strain associated with mild bovine mastitis. 2012 , 194, 6292-3	20
1763	Metagenome analysis reveals yet unexplored reductive dechlorinating potential of <i>Dehalobacter</i> sp. E1 growing in co-culture with <i>Sedimentibacter</i> sp. 2012 , 4, 604-16	46

1762	Genetic barcodes for improved environmental tracking of an anthrax simulant. 2012 , 78, 8272-80	18
1761	Draft genome sequence of high-melanin-yielding <i>Aeromonas media</i> strain WS. 2012 , 194, 6693-4	23
1760	Molybdoenzyme that catalyzes the anaerobic hydroxylation of a tertiary carbon atom in the side chain of cholesterol. 2012 , 287, 36905-16	49
1759	Mathematical optimization applications in metabolic networks. 2012 , 14, 672-86	100
1758	Genome sequence of the immunomodulatory strain <i>Bifidobacterium bifidum</i> LMG 13195. 2012 , 194, 6997	2
1757	Identification and characterization of <i>Cronobacter</i> iron acquisition systems. 2012 , 78, 6035-50	39
1756	Characterization of the <i>Salmonella</i> bacteriophage vB_SenS-Ent1. 2012 , 93, 2046-2056	22
1755	Genome sequences of <i>Lactococcus garvieae</i> TB25, isolated from Italian cheese, and <i>Lactococcus garvieae</i> LG9, isolated from Italian rainbow trout. 2012 , 194, 1249-50	23
1754	Public good dynamics drive evolution of iron acquisition strategies in natural bacterioplankton populations. 2012 , 109, 20059-64	213
1753	Genome analysis of <i>Mycobacterium massiliense</i> strain M172, which contains a putative mycobacteriophage. 2012 , 194, 5128	7
1752	Genome analysis of bovine-mastitis-associated <i>Escherichia coli</i> O32:H37 strain P4. 2012 , 194, 3732	16
1751	Genome sequences of three live attenuated vaccine strains of <i>Brucella</i> species and implications for pathogenesis and differential diagnosis. 2012 , 194, 6012-3	10
1750	<i>Shigella sonnei</i> genome sequencing and phylogenetic analysis indicate recent global dissemination from Europe. 2012 , 44, 1056-9	203
1749	Forward genetic in planta screen for identification of plant-protective traits of <i>Sphingomonas</i> sp. strain Fr1 against <i>Pseudomonas syringae</i> DC3000. 2012 , 78, 5529-35	41
1748	A metagenomic study of diet-dependent interaction between gut microbiota and host in infants reveals differences in immune response. 2012 , 13, r32	173
1747	Reconstruction of the <i>Saccharopolyspora erythraea</i> genome-scale model and its use for enhancing erythromycin production. 2012 , 102, 493-502	32
1746	Reconstruction and analysis of a genome-scale metabolic model of the vitamin C producing industrial strain <i>Ketogulonicigenium vulgare</i> WSH-001. 2012 , 161, 42-8	30
1745	Microbial virus genome annotation-mustering the troops to fight the sequence onslaught. 2012 , 434, 175-80	12

1744	Next-generation sequencing and de novo assembly, genome organization, and comparative genomic analyses of the genomes of two <i>Helicobacter pylori</i> isolates from duodenal ulcer patients in India. 2012 , 194, 5963-4	12
1743	Genome sequence of <i>Xanthomonas campestris</i> JX, an industrially productive strain for Xanthan gum. 2012 , 194, 4755-6	24
1742	Genome sequence and mutational analysis of plant-growth-promoting bacterium <i>Agrobacterium tumefaciens</i> CCNWGS0286 Isolated from a zinc-lead mine tailing. 2012 , 78, 5384-94	54
1741	Genome sequence of a <i>Salinibacterium</i> sp. isolated from Antarctic soil. 2012 , 194, 2404	7
1740	Genome sequence of the psychrophilic deep-sea bacterium <i>Moritella marina</i> MP-1 (ATCC 15381). 2012 , 194, 6296-7	9
1739	Draft genome sequence of a <i>Sphingomonas</i> sp., an endosymbiotic bacterium isolated from an arctic lichen <i>Umbilicaria</i> sp. 2012 , 194, 3010-1	7
1738	Complete genome sequence of IME11, a new N4-like bacteriophage. 2012 , 86, 13861	12
1737	Complete genome sequence of IME15, the first T7-like bacteriophage lytic to pan-antibiotic-resistant <i>Stenotrophomonas maltophilia</i> . 2012 , 86, 13839-40	14
1736	Genetic and functional characterization of cyclic lipopeptide white-line-inducing principle (WLIP) production by rice rhizosphere isolate <i>Pseudomonas putida</i> RW10S2. 2012 , 78, 4826-34	49
1735	Genome sequence of thermotolerant <i>Bacillus methanolicus</i> : features and regulation related to methylophony and production of L-lysine and L-glutamate from methanol. 2012 , 78, 5170-81	55
1734	Analysis of a <i>Streptococcus pyogenes</i> puerperal sepsis cluster by use of whole-genome sequencing. 2012 , 50, 2224-8	47
1733	A metabolic network approach for the identification and prioritization of antimicrobial drug targets. 2012 , 20, 113-23	76
1732	Computational systems biology and in silico modeling of the human microbiome. 2012 , 13, 769-80	75
1731	Genome sequence of the marine bacterium <i>Vibrio campbellii</i> DS40M4, isolated from open ocean water. 2012 , 194, 904	15
1730	Complete genome sequence of <i>Acinetobacter baumannii</i> MDR-TJ and insights into its mechanism of antibiotic resistance. 2012 , 67, 2825-32	57
1729	Metabolic specialization and the assembly of microbial communities. 2012 , 6, 1985-91	87
1728	Genome sequences of the ethanol-tolerant <i>Lactobacillus vini</i> strains LMG 23202T and JP7.8.9. 2012 , 194, 3018	9
1727	Genome sequence of <i>Lactobacillus salivarius</i> SMXD51, a potential probiotic strain isolated from chicken cecum, showing anti-campylobacter activity. 2012 , 194, 3008-9	15

1726	BLANNOTATOR: enhanced homology-based function prediction of bacterial proteins. 2012 , 13, 33		12
1725	A comparative genomics perspective on the genetic content of the alkaliphilic haloarchaeon <i>Natrialba magadii</i> ATCC 43099T. <i>BMC Genomics</i> , 2012 , 13, 165	4-5	33
1724	Genome-wide characterization of <i>Vibrio</i> phage β p2 with unique arrangements of the mob-like genes. <i>BMC Genomics</i> , 2012 , 13, 224	4-5	15
1723	Comparative metagenomics of three Dehalococcoides-containing enrichment cultures: the role of the non-dechlorinating community. <i>BMC Genomics</i> , 2012 , 13, 327	4-5	80
1722	Genetic diversity within the genus <i>Francisella</i> as revealed by comparative analyses of the genomes of two North American isolates from environmental sources. <i>BMC Genomics</i> , 2012 , 13, 422	4-5	11
1721	Tracing genomic variations in two highly virulent <i>Yersinia enterocolitica</i> strains with unequal ability to compete for host colonization. <i>BMC Genomics</i> , 2012 , 13, 467	4-5	14
1720	The <i>Caulobacter crescentus</i> phage phiCbK: genomics of a canonical phage. <i>BMC Genomics</i> , 2012 , 13, 542	4-5	59
1719	Comparative genomics of the classical <i>Bordetella</i> subspecies: the evolution and exchange of virulence-associated diversity amongst closely related pathogens. <i>BMC Genomics</i> , 2012 , 13, 545	4-5	82
1718	Comparative genomics of bacteria in the genus <i>Providencia</i> isolated from wild <i>Drosophila melanogaster</i> . <i>BMC Genomics</i> , 2012 , 13, 612	4-5	22
1717	Genomic basis of broad host range and environmental adaptability of <i>Rhizobium tropici</i> CIAT 899 and <i>Rhizobium</i> sp. PRF 81 which are used in inoculants for common bean (<i>Phaseolus vulgaris</i> L.). <i>BMC Genomics</i> , 2012 , 13, 735	4-5	96
1716	Extensive remodeling of the <i>Pseudomonas syringae</i> pv. <i>avellanae</i> type III secretome associated with two independent host shifts onto hazelnut. 2012 , 12, 141		41
1715	Changes in human gut flora with age: an Indian familial study. 2012 , 12, 222		29
1714	Analysis of a unique <i>Clostridium botulinum</i> strain from the Southern hemisphere producing a novel type E botulinum neurotoxin subtype. 2012 , 12, 245		32
1713	MESSA: MEta-Server for protein Sequence Analysis. 2012 , 10, 82		33
1712	Phylogenetic and functional diversity of metagenomic libraries of phenol degrading sludge from petroleum refinery wastewater treatment system. 2012 , 2, 18		36
1711	Dissemination and characterization of NDM-1-producing <i>Acinetobacter pittii</i> in an intensive care unit in China. 2012 , 18, E506-13		66
1710	Oxygen minimum zones harbour novel viral communities with low diversity. 2012 , 14, 3043-65		54
1709	Fighting outbreaks with bacterial genomics: case review and workflow proposal. 2012 , 15, 341-51		10

1708	High-throughput bacterial genome sequencing: an embarrassment of choice, a world of opportunity. 2012 , 10, 599-606	326
1707	CINPER: an interactive web system for pathway prediction for prokaryotes. 2012 , 7, e51252	4
1706	Development of constraint-based system-level models of microbial metabolism. 2012 , 881, 531-49	
1705	Bacterial genome annotation. 2012 , 881, 471-503	7
1704	Physiological homogeneity among the endosymbionts of <i>Riftia pachyptila</i> and <i>Tevnia jerichonana</i> revealed by proteogenomics. 2012 , 6, 766-76	61
1703	Genome sequence of <i>Pseudomonas aeruginosa</i> DQ8, an efficient degrader of n-alkanes and polycyclic aromatic hydrocarbons. 2012 , 194, 6304-5	10
1702	In silico method for modelling metabolism and gene product expression at genome scale. 2012 , 3, 929	194
1701	Isolating antifungals from fungus-growing ant symbionts using a genome-guided chemistry approach. 2012 , 517, 47-70	15
1700	Functional divergence in the genus <i>Oenococcus</i> as predicted by genome sequencing of the newly-described species, <i>Oenococcus kitaharae</i> . 2012 , 7, e29626	21
1699	Genomic characterization of the <i>Taylorella</i> genus. 2012 , 7, e29953	21
1698	Sigma E regulators control hemolytic activity and virulence in a shrimp pathogenic <i>Vibrio harveyi</i> . 2012 , 7, e32523	22
1697	<i>Pseudomonas syringae</i> pv. <i>actinidiae</i> (PSA) isolates from recent bacterial canker of kiwifruit outbreaks belong to the same genetic lineage. 2012 , 7, e36518	102
1696	Genome-wide study of the defective sucrose fermenter strain of <i>Vibrio cholerae</i> from the Latin American cholera epidemic. 2012 , 7, e37283	12
1695	Metagenomic and metabolic profiling of nonlithifying and lithifying stromatolitic mats of Highborne Cay, The Bahamas. 2012 , 7, e38229	41
1694	Predictive sequence analysis of the <i>Candidatus Liberibacter asiaticus</i> proteome. 2012 , 7, e41071	19
1693	Identification and characterization of novel <i>Salmonella</i> mobile elements involved in the dissemination of genes linked to virulence and transmission. 2012 , 7, e41247	46
1692	Phylogenetic and functional metagenomic profiling for assessing microbial biodiversity in environmental monitoring. 2012 , 7, e43630	38
1691	Intestinal tissues induce an SNP mutation in <i>Pseudomonas aeruginosa</i> that enhances its virulence: possible role in anastomotic leak. 2012 , 7, e44326	116

1690	Diversity of <i>Melissococcus plutonius</i> from honeybee larvae in Japan and experimental reproduction of European foulbrood with cultured atypical isolates. 2012 , 7, e33708	58
1689	Diversification of the <i>Salmonella</i> fimbriae: a model of macro- and microevolution. 2012 , 7, e38596	68
1688	SEED servers: high-performance access to the SEED genomes, annotations, and metabolic models. 2012 , 7, e48053	121
1687	Molecular evidence for the thriving of <i>Campylobacter jejuni</i> ST-4526 in Japan. 2012 , 7, e48394	27
1686	BG7: a new approach for bacterial genome annotation designed for next generation sequencing data. 2012 , 7, e49239	38
1685	Survey of endosymbionts in the <i>Diaphorina citri</i> metagenome and assembly of a <i>Wolbachia</i> wDi draft genome. 2012 , 7, e50067	59
1684	Cyanobacteria of the genus <i>prochlorothrix</i> . 2012 , 3, 173	13
1683	Redundancy and modularity in membrane-associated dissimilatory nitrate reduction in <i>Bacillus</i> . 2012 , 3, 371	36
1682	Comparative genomics of the <i>Staphylococcus intermedius</i> group of animal pathogens. 2012 , 2, 44	33
1681	A framework for assessing the concordance of molecular typing methods and the true strain phylogeny of <i>Campylobacter jejuni</i> and <i>C. coli</i> using draft genome sequence data. 2012 , 2, 57	22
1680	Untangling genomes from metagenomes: revealing an uncultured class of marine Euryarchaeota. 2012 , 335, 587-90	355
1679	In vitro and in vivo characterization and strain safety of <i>Lactobacillus reuteri</i> NCIMB 30253 for probiotic applications. 2012 , 58, 776-87	11
1678	Comparative genomic analyses of 17 clinical isolates of <i>Gardnerella vaginalis</i> provide evidence of multiple genetically isolated clades consistent with subspeciation into genovars. 2012 , 194, 3922-37	115
1677	Complete genome sequence of a sucrose-nonfermenting epidemic strain of <i>Vibrio cholerae</i> O1 from Brazil. 2012 , 194, 2772	6
1676	Evolutionary perspective on the origin of Haitian cholera outbreak strain. 2012 , 30, 338-46	7
1675	Complete genome sequence of <i>Mycobacterium phlei</i> type strain RIVM601174. 2012 , 194, 3284-5	10
1674	Analysis of the antimicrobial susceptibility of the ionizing radiation-resistant bacterium <i>Deinococcus radiodurans</i> : implications for bioremediation of radioactive waste. 2012 , 62, 493-500	4
1673	Phage-bacteria relationships and CRISPR elements revealed by a metagenomic survey of the rumen microbiome. 2012 , 14, 207-27	82

1672	Comparative genomics of <i>Neisseria weaveri</i> clarifies the taxonomy of this species and identifies genetic determinants that may be associated with virulence. 2012 , 328, 100-5	11
1671	Novel <i>Streptococcus infantarius</i> subsp. <i>infantarius</i> variants harboring lactose metabolism genes homologous to <i>Streptococcus thermophilus</i> . 2012 , 31, 33-42	26
1670	The genome sequence of the lactic acid bacterium, <i>Carnobacterium maltaromaticum</i> ATCC 35586 encodes potential virulence factors. 2012 , 152, 107-15	33
1669	Next generation sequencing and bioinformatic bottlenecks: the current state of metagenomic data analysis. 2012 , 23, 9-15	243
1668	Comparative genomics of bacteria from the genus <i>Collimonas</i> : linking (dis)similarities in gene content to phenotypic variation and conservation. 2012 , 4, 424-32	12
1667	Isolation of new <i>Pseudomonas tolaasii</i> bacteriophages and genomic investigation of the lytic phage BF7. 2012 , 332, 162-9	16
1666	Inheritance of the <i>Salmonella</i> virulence plasmids: mostly vertical and rarely horizontal. 2012 , 12, 1058-63	34
1665	Comparative genomics of multiple plasmids from APEC associated with clonal outbreaks demonstrates major similarities and identifies several potential vaccine-targets. 2012 , 158, 384-93	20
1664	ArxA, a new clade of arsenite oxidase within the DMSO reductase family of molybdenum oxidoreductases. 2012 , 14, 1635-45	103
1663	The eroded genome of a <i>Psychotria</i> leaf symbiont: hypotheses about lifestyle and interactions with its plant host. 2012 , 14, 2757-69	46
1662	Metagenomics - a guide from sampling to data analysis. 2012 , 2, 3	507
1661	Genomic analysis reveals multiple [FeFe] hydrogenases and hydrogen sensors encoded by treponemes from the H(2)-rich termite gut. 2012 , 63, 282-94	19
1660	The metagenome of the marine anammox bacterium ' <i>Candidatus Scalindua profunda</i> ' illustrates the versatility of this globally important nitrogen cycle bacterium. 2013 , 15, 1275-89	199
1659	Insights into archaeal evolution and symbiosis from the genomes of a nanoarchaeon and its inferred crenarchaeal host from Obsidian Pool, Yellowstone National Park. 2013 , 8, 9	80
1658	Evidence of a new metabolic capacity in an emerging diarrheal pathogen: lessons from the draft genomes of <i>Vibrio fluvialis</i> strains PG41 and I21563. 2013 , 5, 20	4
1657	Beginner's guide to comparative bacterial genome analysis using next-generation sequence data. 2013 , 3, 2	87
1656	<i>Stomatobaculum longum</i> gen. nov., sp. nov., an obligately anaerobic bacterium from the human oral cavity. 2013 , 63, 1450-1456	21
1655	Comparative genome characterization of <i>Achromobacter</i> members reveals potential genetic determinants facilitating the adaptation to a pathogenic lifestyle. 2013 , 97, 6413-25	31

1654	Genomic analysis of the biocontrol strain <i>Pseudomonas fluorescens</i> Pf29Arp with evidence of T3SS and T6SS gene expression on plant roots. 2013 , 5, 393-403		36
1653	Condensing the omics fog of microbial communities. 2013 , 21, 325-33		62
1652	Multifactorial diversity sustains microbial community stability. 2013 , 7, 2126-36		113
1651	MetaPathways: a modular pipeline for constructing pathway/genome databases from environmental sequence information. 2013 , 14, 202		75
1650	A semi-automated genome annotation comparison and integration scheme. 2013 , 14, 172		10
1649	Design and validation of a supragenome array for determination of the genomic content of <i>Haemophilus influenzae</i> isolates. <i>BMC Genomics</i> , 2013 , 14, 484	4-5	13
1648	Genomic characterization provides new insight into <i>Salmonella</i> phage diversity. <i>BMC Genomics</i> , 2013 , 14, 481	4-5	54
1647	Pan-genome analysis of the emerging foodborne pathogen <i>Cronobacter</i> spp. suggests a species-level bidirectional divergence driven by niche adaptation. <i>BMC Genomics</i> , 2013 , 14, 366	4-5	62
1646	Comparative genomics of <i>Salmonella enterica</i> serovars Derby and Mbandaka, two prevalent serovars associated with different livestock species in the UK. <i>BMC Genomics</i> , 2013 , 14, 365	4-5	31
1645	Comparative genomic analysis of four representative plant growth-promoting rhizobacteria in <i>Pseudomonas</i> . <i>BMC Genomics</i> , 2013 , 14, 271	4-5	98
1644	Genome sequencing of bacteria: sequencing, de novo assembly and rapid analysis using open source tools. <i>BMC Genomics</i> , 2013 , 14, 211	4-5	36
1643	Comparisons of infant <i>Escherichia coli</i> isolates link genomic profiles with adaptation to the ecological niche. <i>BMC Genomics</i> , 2013 , 14, 81	4-5	10
1642	Phenotypic and genotypic properties of <i>Microbacterium yannicii</i> , a recently described multidrug resistant bacterium isolated from a lung transplanted patient with cystic fibrosis in France. 2013 , 13, 97		16
1641	Genome-level homology and phylogeny of <i>Vibrionaceae</i> (Gammaproteobacteria: Vibrionales) with three new complete genome sequences. 2013 , 13, 80		9
1640	Mealybugs nested endosymbiosis: going into the 'matryoshka' system in <i>Planococcus citri</i> in depth. 2013 , 13, 74		32
1639	Characterization of a group of pyrroloquinoline quinone-dependent dehydrogenases that are involved in the conversion of L-sorbose to 2-Keto-L-gulonic acid in <i>Ketogulonicigenium vulgare</i> WSH-001. 2013 , 29, 1398-404		20
1638	Identification and characterization of the actinomycin G gene cluster in <i>Streptomyces iakyrus</i> . 2013 , 9, 1286-9		13
1637	Quantitative proteomic analysis of ibuprofen-degrading <i>Patulibacter</i> sp. strain I11. 2013 , 24, 615-30		53

1636	A combinatorial approach to the structure elucidation of a pyoverdine siderophore produced by a <i>Pseudomonas putida</i> isolate and the use of pyoverdine as a taxonomic marker for typing <i>P. putida</i> subspecies. 2013 , 26, 561-75	14
1635	Expanding the diversity of oenococcal bacteriophages: insights into a novel group based on the integrase sequence. 2013 , 166, 331-40	24
1634	Molecular Characterization of an Atypical IncX3 Plasmid pKPC-NY79 Carrying bla KPC-2 in a <i>Klebsiella pneumoniae</i> . 2013 , 67, 493-8	36
1633	High-resolution transcriptional analysis of the regulatory influence of cell-to-cell signalling reveals novel genes that contribute to <i>Xanthomonas</i> phytopathogenesis. 2013 , 88, 1058-69	43
1632	Assembly and features of secondary metabolite biosynthetic gene clusters in <i>Streptomyces</i> ansochromogenes. 2013 , 56, 609-18	10
1631	Genome sequencing identifies <i>Listeria fleischmannii</i> subsp. <i>coloradonensis</i> subsp. nov., isolated from a ranch. 2013 , 63, 3257-3268	31
1630	Complete genome sequence of Φ P51, a temperate bacteriophage of <i>Clostridium perfringens</i> . 2013 , 158, 2015-7	16
1629	Plasmid-mediated fosfomycin resistance in <i>Escherichia coli</i> isolated from pig. 2013 , 162, 964-967	26
1628	Functional assignment of <i>Mycobacterium tuberculosis</i> proteome revealed by genome-scale fold-recognition. 2013 , 93, 40-6	13
1627	Draft genome sequences of five recent human uropathogenic <i>Escherichia coli</i> isolates. 2013 , 69, 66-70	13
1626	Genome sequence analysis indicates that the model eukaryote <i>Nematostella vectensis</i> harbors bacterial consorts. 2013 , 79, 6868-73	21
1625	Reannotation of translational start sites in the genome of <i>Mycobacterium tuberculosis</i> . 2013 , 93, 18-25	19
1624	The genome sequence of the hydrocarbon-degrading <i>Acinetobacter venetianus</i> VE-C3. 2013 , 164, 439-49	26
1623	Insights from the draft genome of <i>Paenibacillus lentimorbus</i> NRRL B-30488, a promising plant growth promoting bacterium. 2013 , 168, 737-8	6
1622	Organic cofactors in the metabolism of <i>Dehalococcoides mccartyi</i> strains. 2013 , 368, 20120321	45
1621	Comparative genomics of two 'Candidatus <i>Accumulibacter</i> ' clades performing biological phosphorus removal. 2013 , 7, 2301-14	75
1620	Complete nucleotide sequence of a blaKPC-harboring IncI2 plasmid and its dissemination in New Jersey and New York hospitals. 2013 , 57, 5019-25	68
1619	Identification and characterization of five new molecular serogroups of <i>Cronobacter</i> spp. 2013 , 10, 343-52	28

1618	Methylophaga nitratireducentiscrescens sp. nov. and Methylophaga frappieri sp. nov., isolated from the biofilm of the methanol-fed denitrification system treating the seawater at the Montreal Biodome. 2013 , 63, 2216-2222		31
1617	Mono-dimensional blue native-PAGE and bi-dimensional blue native/urea-PAGE or/SDS-PAGE combined with nLC-ESI-LIT-MS/MS unveil membrane protein heteromeric and homomeric complexes in Streptococcus thermophilus. 2013 , 94, 240-61		18
1616	The comprehensive antibiotic resistance database. 2013 , 57, 3348-57		1045
1615	Sulfide oxidation, nitrate respiration, carbon acquisition, and electron transport pathways suggested by the draft genome of a single orange Guaymas Basin Beggiatoa (Cand. Maribeggiatoa) sp. filament. 2013 , 11, 53-65		30
1614	The genome of the alga-associated marine flavobacterium Formosa agariphila KMM 3901T reveals a broad potential for degradation of algal polysaccharides. 2013 , 79, 6813-22		137
1613	Genome sequences of two dehalogenation specialists Dehalococcoides mccartyi strains BTF08 and DCMB5 enriched from the highly polluted Bitterfeld region. 2013 , 343, 101-4		64
1612	Genome Sequence of Salt-Tolerant Bacillus safensis Strain VK, Isolated from Saline Desert Area of Gujarat, India. 2013 , 1,		21
1611	Massively parallel polymerase cloning and genome sequencing of single cells using nanoliter microwells. 2013 , 31, 1126-32		188
1610	Improvement of plant growth and seed yield in Jatropha curcas by a novel nitrogen-fixing root associated Enterobacter species. 2013 , 6, 140		27
1609	Microbes, metagenomes and marine mammals: enabling the next generation of scientist to enter the genomic era. <i>BMC Genomics</i> , 2013 , 14, 600	4.5	18
1608	Comparative genomics of Campylobacter concisus isolates reveals genetic diversity and provides insights into disease association. <i>BMC Genomics</i> , 2013 , 14, 585	4.5	32
1607	Comparing the genomes of Helicobacter pylori clinical strain UM032 and Mice-adapted derivatives. 2013 , 5, 25		12
1606	Rapid construction of metabolic models for a family of Cyanobacteria using a multiple source annotation workflow. 2013 , 7, 142		26
1605	A phylogenomic approach to bacterial subspecies classification: proof of concept in Mycobacterium abscessus. <i>BMC Genomics</i> , 2013 , 14, 879	4.5	17
1604	Biochemical and molecular characterization of Treponema phagedenis-like spirochetes isolated from a bovine digital dermatitis lesion. 2013 , 13, 280		23
1603	Draft genome sequences of two Bifidobacterium sp. from the honey bee (Apis mellifera). 2013 , 5, 42		14
1602	Genome anatomy of the gastrointestinal pathogen, Vibrio parahaemolyticus of crustacean origin. 2013 , 5, 37		7
1601	Draft genome sequence of Xanthomonas fragariae reveals reductive evolution and distinct virulence-related gene content. <i>BMC Genomics</i> , 2013 , 14, 829	4.5	25

1600	SHARP: genome-scale identification of gene-protein-reaction associations in cyanobacteria. 2013 , 118, 181-90	5
1599	Insights of biosurfactant producing <i>Serratia marcescens</i> strain W2.3 isolated from diseased tilapia fish: a draft genome analysis. 2013 , 5, 29	20
1598	Streptococcal collagen-like protein A and general stress protein 24 are immunomodulating virulence factors of group A <i>Streptococcus</i> . 2013 , 27, 2633-43	10
1597	Comparative genomics of IncP-1 β plasmids from water environments reveals diverse and unique accessory genetic elements. 2013 , 70, 412-9	8
1596	Prevalence and molecular epidemiology of plasmid-mediated fosfomycin resistance genes among blood and urinary <i>Escherichia coli</i> isolates. 2013 , 62, 1707-1713	66
1595	Coupling FACS and genomic methods for the characterization of uncultivated symbionts. 2013 , 531, 45-60	4
1594	The genome sequence of <i>Streptomyces lividans</i> 66 reveals a novel tRNA-dependent peptide biosynthetic system within a metal-related genomic island. 2013 , 5, 1165-75	83
1593	Whole genome comparison of six <i>Crocospaera watsonii</i> strains with differing phenotypes. 2013 , 49, 786-801	38
1592	Next-generation annotation of prokaryotic genomes with EuGene-P: application to <i>Sinorhizobium meliloti</i> 2011. 2013 , 20, 339-54	61
1591	Applying systems and synthetic biology approaches to the production of food ingredients, enzymes and nutraceuticals by bacteria. 2013 , 81-96	
1590	In silico modeling and evaluation of <i>Gordonia alkanivorans</i> for biodesulfurization. 2013 , 9, 2530-40	36
1589	Draft Genome Sequence of <i>Brucella abortus</i> BCB027, a Strain Isolated from a Domestic Deer. 2013 , 1,	1
1588	The rhizome of the multidrug-resistant <i>Enterobacter aerogenes</i> genome reveals how new "killer bugs" are created because of a sympatric lifestyle. 2013 , 30, 369-83	83
1587	Bacteriophage genes that inactivate the CRISPR/Cas bacterial immune system. 2013 , 493, 429-32	495
1586	Identification of accessory genome regions in poultry <i>Clostridium perfringens</i> isolates carrying the netB plasmid. 2013 , 195, 1152-66	50
1585	The mercury resistance (<i>mer</i>) operon in a marine gliding flavobacterium, <i>Tenacibaculum discolor</i> 9A5. 2013 , 83, 135-48	9
1584	Real-time sequencing to decipher the molecular mechanism of resistance of a clinical pan-drug-resistant <i>Acinetobacter baumannii</i> isolate from Marseille, France. 2013 , 57, 592-6	57
1583	Geoarchaeota: a new candidate phylum in the Archaea from high-temperature acidic iron mats in Yellowstone National Park. 2013 , 7, 622-34	68

1582	An indigoidine biosynthetic gene cluster from <i>Streptomyces chromofuscus</i> ATCC 49982 contains an unusual IndB homologue. 2013 , 40, 159-68	47
1581	Genomic analysis of HAdV-B14 isolate from the outbreak of febrile respiratory infection in China. 2013 , 102, 448-55	11
1580	Evaluation of whole-genome sequencing as a genotyping tool for <i>Campylobacter jejuni</i> in comparison with pulsed-field gel electrophoresis and flaA typing. 2013 , 92, 573-80	21
1579	Identification and characterization of a periplasmic trilactone esterase, Cee, revealed unique features of ferric enterobactin acquisition in <i>Campylobacter</i> . 2013 , 87, 594-608	32
1578	Systems-level characterization of a host-microbe metabolic symbiosis in the mammalian gut. 2013 , 4, 28-40	155
1577	Research resources for tuberculosis at the National Institute of Allergy and Infectious Diseases. 2013 , 93, 6-11	
1576	Database resources for the tuberculosis community. 2013 , 93, 12-7	23
1575	Marine microbial symbiosis heats up: the phylogenetic and functional response of a sponge holobiont to thermal stress. 2013 , 7, 991-1002	148
1574	Automated genome annotation and metabolic model reconstruction in the SEED and Model SEED. 2013 , 985, 17-45	97
1573	Merging multiple omics datasets in silico: statistical analyses and data interpretation. 2013 , 985, 459-70	15
1572	A Microbial Metagenome (<i>Leucobacter</i> sp.) in <i>Caenorhabditis</i> Whole Genome Sequences. 2013 , 7, 55-72	19
1571	Exploiting New Systems-Based Strategies to Elucidate PlantBacterial Interactions in the Rhizosphere. 2013 , 57-68	8
1570	Type 1 and type 2 strains of <i>Mycoplasma pneumoniae</i> form different biofilms. 2013 , 159, 737-747	49
1569	Comparative genome analysis of <i>Streptococcus infantarius</i> subsp. <i>infantarius</i> CJ18, an African fermented camel milk isolate with adaptations to dairy environment. <i>BMC Genomics</i> , 2013 , 14, 200	4-5 37
1568	Bioinformatic progress and applications in metaproteogenomics for bridging the gap between genomic sequences and metabolic functions in microbial communities. 2013 , 13, 2786-804	39
1567	New linear lipopeptides produced by <i>Pseudomonas cichorii</i> SF1-54 are involved in virulence, swarming motility, and biofilm formation. 2013 , 26, 585-98	37
1566	Genomic deletions disrupt nitrogen metabolism pathways of a cyanobacterial diatom symbiont. 2013 , 4, 1767	80
1565	Metatranscriptomic analysis of lactic acid bacterial gene expression during kimchi fermentation. 2013 , 163, 171-9	107

1564	RubisCO-based CO ₂ fixation and C ₁ metabolism in the actinobacterium <i>Pseudonocardia dioxanivorans</i> CB1190. 2013 , 15, 3040-53	28
1563	Isolation and characterization of <i>Staphylococcus aureus</i> strains from a Paso del Norte dairy. 2013 , 96, 3535-42	13
1562	Genome sequences of rare, uncultured bacteria obtained by differential coverage binning of multiple metagenomes. 2013 , 31, 533-8	869
1561	Identification of micromonolactam, a new polyene macrocyclic lactam from two marine <i>Micromonospora</i> strains using chemical and molecular methods: clarification of the biosynthetic pathway from a glutamate starter unit. 2013 , 66, 431-41	40
1560	Identification of new protein coding sequences and signal peptidase cleavage sites of <i>Helicobacter pylori</i> strain 26695 by proteogenomics. 2013 , 86, 27-42	32
1559	<i>Bordetella holmesii</i> : initial genomic analysis of an emerging opportunist. 2013 , 67, 132-5	10
1558	Genome characterization of a novel <i>Burkholderia cepacia</i> complex genomovar isolated from dieback affected mango orchards. 2013 , 29, 2033-44	6
1557	Fast induction of biosynthetic polysaccharide genes <i>lpxA</i> , <i>lpxE</i> , and <i>rklI</i> of <i>Rhizobium</i> sp. strain PRF 81 by common bean seed exudates is indicative of a key role in symbiosis. 2013 , 13, 275-83	6
1556	Single-cell and metagenomic analyses indicate a fermentative and saccharolytic lifestyle for members of the OP9 lineage. 2013 , 4, 1854	143
1555	Draft genome of <i>Ochrobactrum intermedium</i> strain M86 isolated from non-ulcer dyspeptic individual from India. 2013 , 5, 7	11
1554	Metagenomic approaches for exploiting uncultivated bacteria as a resource for novel biosynthetic enzymology. 2013 , 20, 636-47	110
1553	Genome Sequence of <i>Lactobacillus fermentum</i> Strain MTCC 8711, a Probiotic Bacterium Isolated from Yogurt. 2013 , 1,	13
1552	In vivo emergence of colistin resistance in <i>Klebsiella pneumoniae</i> producing KPC-type carbapenemases mediated by insertional inactivation of the PhoQ/PhoP mgrB regulator. 2013 , 57, 5521-6	239
1551	Mobile elements in a single-filament orange Guaymas Basin <i>Beggiatoa</i> ("Candidatus <i>Maribeggiatoa</i> ") sp. draft genome: evidence for genetic exchange with cyanobacteria. 2013 , 79, 3974-85	23
1550	Processing of cellulose synthase (<i>AcsAB</i>) from <i>Gluconacetobacter hansenii</i> 23769. 2013 , 529, 92-8	9
1549	The automatic annotation of bacterial genomes. 2013 , 14, 1-12	86
1548	Why orange Guaymas Basin <i>Beggiatoa</i> spp. are orange: single-filament-genome-enabled identification of an abundant octaheme cytochrome with hydroxylamine oxidase, hydrazine oxidase, and nitrite reductase activities. 2013 , 79, 1183-90	32
1547	Candidate phylum TM6 genome recovered from a hospital sink biofilm provides genomic insights into this uncultivated phylum. 2013 , 110, E2390-9	144

1546	Litorilinea aerophila gen. nov., sp. nov., an aerobic member of the class Caldilineae, phylum Chloroflexi, isolated from an intertidal hot spring. 2013 , 63, 1149-1154	20
1545	Complete Genome Sequence of Serratia liquefaciens Strain ATCC 27592. 2013 , 1,	16
1544	Genome Sequence of the Butanol Hyperproducer Clostridium saccharoperbutylacetonicum N1-4. 2013 , 1, e0007013	17
1543	Genome Sequences of Multidrug-Resistant Acinetobacter baumannii Strains from Nosocomial Outbreaks in Japan. 2013 , 1,	3
1542	Draft Genome Sequence of the Human-Pathogenic Bacterium Vibrio alginolyticus E0666. 2013 , 1,	2
1541	Genome Sequences of Two Lactococcus garvieae Strains Isolated from Meat. 2013 , 1,	11
1540	Draft Genome Sequence of Fructophilic Lactobacillus florum. 2013 , 1,	8
1539	Draft Genome Sequence of the Paenibacillus sp. Strain ICGEB2008 (MTCC 5639) Isolated from the Gut of Helicoverpa armigera. 2013 , 1,	6
1538	Genome Sequence of Helicobacter heilmannii Sensu Stricto ASB1 Isolated from the Gastric Mucosa of a Kitten with Severe Gastritis. 2013 , 1,	17
1537	Draft Genome of Klebsiella pneumoniae Sequence Type 512, a Multidrug-Resistant Strain Isolated during a Recent KPC Outbreak in Italy. 2013 , 1,	4
1536	Draft Genome Sequence of the Phyllosphere Model Bacterium Pantoea agglomerans 299R. 2013 , 1,	27
1535	Complete Genome Sequence of Escherichia Phage ADB-2 Isolated from a Fecal Sample of Poultry. 2013 , 1, e0004313	4
1534	Draft Genome Sequence of Escherichia coli Strain ATCC 23502 (Serovar O5:K4:H4). 2013 , 1, e0004613	8
1533	Draft Genome Sequence of the Opportunistic Human Pathogen Morganella morganii SC01. 2013 , 1,	5
1532	Draft genome sequences of five strains in the genus thauera. 2013 , 1,	13
1531	Draft Genome Sequences of Pseudomonas fluorescens BS2 and Pusillimonas noertemannii BS8, Soil Bacteria That Cooperate To Degrade the Poly- β -Glutamic Acid Anthrax Capsule. 2013 , 1,	6
1530	Draft Genome Sequences of Two Virulent Serotypes of Avian Pasteurella multocida. 2013 , 1,	2
1529	Whole-Genome Sequences of an Aerobic Anoxygenic Phototroph, Blastomonas sp. Strain AAP53, Isolated from a Freshwater Desert Lake in Inner Mongolia, China. 2013 , 1, e0007113	7

1528	Draft Genome Sequences of Two Clinical Isolates of <i>Lactobacillus rhamnosus</i> from Initial Stages of Dental Pulp Infection. 2013 , 1,	7
1527	Draft Genome Sequence of <i>Vibrio mimicus</i> Strain CAIM 602T. 2013 , 1, e0008413	3
1526	Draft genome sequence of an Actinobacterium, <i>Brachybacterium muris</i> strain UCD-AY4. 2013 , 1, e0008613	9
1525	Complete genome sequence of <i>Myxococcus stipitatus</i> strain DSM 14675, a fruiting myxobacterium. 2013 , 1, e0010013	21
1524	Draft Genome Sequence of VIM-2-Producing Multidrug-Resistant <i>Pseudomonas aeruginosa</i> ST175, an Epidemic High-Risk Clone. 2013 , 1, e0011213	8
1523	Whole-Genome Shotgun Sequence of <i>Pseudomonas viridiflava</i> , a Bacterium Species Pathogenic to <i>Arabisidopsis thaliana</i> . 2013 , 1,	5
1522	Draft Genome Sequence of the Type Species of the Genus <i>Citrobacter</i> , <i>Citrobacter freundii</i> MTCC 1658. 2013 , 1,	10
1521	Draft Genome Sequence of <i>Microbacterium</i> sp. Strain UCD-TDU (Phylum Actinobacteria). 2013 , 1, e0012013	5
1520	Genome Sequence of the Pathogenic Bacterium <i>Vibrio vulnificus</i> Biotype 3. 2013 , 1, e0013613	12
1519	Draft Genome Sequence of a Clinical Strain of <i>Yersinia enterocolitica</i> (IP10393) of Bioserotype 4/O:3 from France. 2013 , 1,	1
1518	Complete Genome Sequence of the Probiotic <i>Enterococcus faecalis</i> Symbioflor 1 Clone DSM 16431. 2013 , 1,	28
1517	Draft Genome Sequence of <i>Kocuria</i> sp. Strain UCD-OTCP (Phylum Actinobacteria). 2013 , 1,	5
1516	Genome Sequence of <i>Klebsiella pneumoniae</i> HSL4, a New Strain Isolated from Mangrove Sediment for Biosynthesis of 1,3-Propanediol. 2013 , 1,	1
1515	Draft Genome Sequence of <i>Stenotrophomonas maltophilia</i> Strain EPM1, Found in Association with a Culture of the Human Parasite <i>Giardia duodenalis</i> . 2013 , 1, e0018213	6
1514	Genome Sequence of <i>Halanaerobium saccharolyticum</i> subsp. <i>saccharolyticum</i> Strain DSM 6643T, a Halophilic Hydrogen-Producing Bacterium. 2013 , 1,	11
1513	Draft Genome Sequence of the Nitrate- and Phosphate-Accumulating <i>Bacillus</i> sp. Strain MCC0008. 2013 , 1,	1
1512	Complete Genome Sequence of the Probiotic <i>Bifidobacterium thermophilum</i> Strain RBL67. 2013 , 1,	12
1511	Genome Sequence of <i>Campylobacter showae</i> UNSWCD, Isolated from a Patient with Crohn's Disease. 2013 , 1,	2

1510	Genome Sequence of <i>Stenotrophomonas maltophilia</i> Strain AU12-09, Isolated from an Intravascular Catheter. 2013 , 1,	9
1509	Draft Genome Sequence of <i>Erwinia toletana</i> , a Bacterium Associated with Olive Knots Caused by <i>Pseudomonas savastanoi</i> pv. <i>Savastanoi</i> . 2013 , 1,	8
1508	Whole-Genome Sequences of <i>Streptococcus tigurinus</i> Type Strain AZ_3a and <i>S. tigurinus</i> 1366, a Strain Causing Prosthetic Joint Infection. 2013 , 1,	11
1507	Draft Genome Sequence of the Steroid Degradator <i>Rhodococcus ruber</i> Strain Chol-4. 2013 , 1,	7
1506	Genome Sequence of Non-O1 <i>Vibrio cholerae</i> PS15. 2013 , 1,	9
1505	Draft Genome Sequence of <i>Curtobacterium flaccumfaciens</i> Strain UCD-AKU (Phylum Actinobacteria). 2013 , 1,	6
1504	Genome Sequence of <i>Xanthomonas arboricola</i> pv. <i>Corylina</i> , Isolated from Turkish Filbert in Colorado. 2013 , 1,	18
1503	Whole-Genome Sequencing and Comparative Analysis of <i>Yersinia pestis</i> , the Causative Agent of a Plague Outbreak in Northern Peru. 2013 , 1,	6
1502	Draft Genome Sequence of <i>Herbaspirillum huttiense</i> subsp. <i>putei</i> IAM 15032, a Strain Isolated from Well Water. 2013 , 1,	4
1501	Draft Genome Sequence of <i>Salinibacillus aidingensis</i> Strain MSP4, an Obligate Halophilic Bacterium Isolated from a Salt Crystallizer of the Rann of Kutch, India. 2013 , 1,	5
1500	Draft Genome Sequence of a Nitrate- and Phosphate-Removing <i>Bacillus</i> sp., WBUNB009. 2013 , 1,	1
1499	Complete Genome of a <i>Methanosarcina mazei</i> Strain Isolated from Sediment Samples from an Amazonian Flooded Area. 2013 , 1,	8
1498	Draft Genome Sequences of Two Multidrug-Resistant <i>Acinetobacter baumannii</i> Strains of Sequence Type ST92 and ST96. 2013 , 1,	1
1497	Draft Genome Sequence of <i>Vibrio parahaemolyticus</i> V110, Isolated from Shrimp in Hong Kong. 2013 , 1,	10
1496	Genome Sequence of <i>Proteus mirabilis</i> Strain PR03, Isolated from a Local Hospital in Malaysia. 2013 , 1,	5
1495	Draft Genome Sequence of <i>Streptococcus agalactiae</i> PR06. 2013 , 1,	1
1494	Genome Sequence of the <i>Pectobacterium atrosepticum</i> Strain CFBP6276, Causing Blackleg and Soft Rot Diseases on Potato Plants and Tubers. 2013 , 1,	8
1493	Draft Genome Sequence of the Antarctic Psychrophilic Bacterium <i>Pseudomonas syringae</i> Strain Lz4W. 2013 , 1,	7

1492	Draft Genome Sequence of <i>Pseudomonas fluorescens</i> LMG 5329, a White Line-Inducing Principle-Producing Bioindicator for the Mushroom Pathogen <i>Pseudomonas tolaasii</i> . 2013 , 1,	2
1491	First draft genome sequence from a member of the genus <i>Agrococcus</i> , isolated from modern microbialites. 2013 , 1,	5
1490	Genome Sequence of <i>Plesiomonas shigelloides</i> Strain 302-73 (Serotype O1). 2013 , 1,	10
1489	Genome Sequence of the Vancomycin-Producing <i>Amycolatopsis orientalis</i> subsp. <i>orientalis</i> Strain KCTC 9412T. 2013 , 1,	12
1488	Draft Genome Sequence of Ammonia-Producing <i>Acinetobacter</i> sp. Strain MCC2139 from Dairy Effluent. 2013 , 1,	0
1487	Draft Genome Sequence of <i>Klebsiella pneumoniae</i> Isolate PR04. 2013 , 1,	
1486	Draft Genome Sequence of Multidrug-Resistant <i>Pseudomonas aeruginosa</i> Strain VRFP02, Isolated from a Septicemic Patient in India. 2013 , 1,	8
1485	Complete Genome Sequence of <i>Mycobacterium massiliense</i> Clinical Strain Asan 50594, Belonging to the Type II Genotype. 2013 , 1,	18
1484	Draft Genome Sequences of <i>Elizabethkingia meningoseptica</i> . 2013 , 1,	14
1483	Draft Genome Sequence of <i>Arthrobacter crystallopoietes</i> Strain BAB-32, Revealing Genes for Bioremediation. 2013 , 1,	6
1482	Genome Sequence of "Candidatus <i>Methanomassiliicoccus intestinalis</i> " Isoire-Mx1, a Third Thermoplasmatales-Related Methanogenic Archaeon from Human Feces. 2013 , 1,	67
1481	Draft Genome Sequence of the Hydrogen- and Ethanol-Producing Anaerobic Alkalithermophilic Bacterium <i>Caloramator celer</i> . 2013 , 1,	6
1480	Draft Genome Sequences of <i>Porphyromonas crevioricanis</i> JCM 15906T and <i>Porphyromonas cansulci</i> JCM 13913T Isolated from a Canine Oral Cavity. 2013 , 1,	2
1479	Draft Genome Sequence of <i>Arcticibacter svalbardensis</i> Strain MN12-7T, a Member of the Family Sphingobacteriaceae Isolated from an Arctic Soil Sample. 2013 , 1,	3
1478	Draft Genome Sequence of <i>Helicobacter fennelliae</i> Strain MRY12-0050, Isolated from a Bacteremia Patient. 2013 , 1,	5
1477	Draft Genome Sequence of <i>Indibacter alkaliphilus</i> Strain LW1T, Isolated from Lonar Lake, a Haloalkaline Lake in the Buldana District of Maharashtra, India. 2013 , 1,	1
1476	Draft Genome Sequence of an Oscillatorian Cyanobacterium, Strain ESFC-1. 2013 , 1,	5
1475	Genome Sequence of <i>Clostridium diolis</i> Strain DSM 15410, a Promising Natural Producer of 1,3-Propanediol. 2013 , 1,	6

1474	Genome Sequence of <i>Staphylococcus massiliensis</i> Strain S46, Isolated from the Surface of Healthy Human Skin. 2013 , 1,	3
1473	Genome Sequence of <i>Salmonella bongori</i> Strain N268-08 [corrected]. 2013 , 1,	2
1472	Genome Sequence of <i>Klebsiella pneumoniae</i> Strain ATCC 25955, an Oxygen-Insensitive Producer of 1,3-Propanediol. 2013 , 1,	2
1471	Draft Genome Sequence of Strain SA_ST125_MupR of Methicillin-Resistant <i>Staphylococcus aureus</i> ST125, a Major Clone in Spain. 2013 , 1,	1
1470	Draft Genome Sequence of the Fast-Growing Marine Bacterium <i>Vibrio natriegens</i> Strain ATCC 14048. 2013 , 1,	21
1469	Draft Genome Sequence of <i>Exiguobacterium pavilionensis</i> Strain RW-2, with Wide Thermal, Salinity, and pH Tolerance, Isolated from Modern Freshwater Microbialites. 2013 , 1,	14
1468	Genome Sequence of the 2,4,5-Trichlorophenoxyacetate-Degrading Bacterium <i>Burkholderia phenoliruptrix</i> Strain AC1100. 2013 , 1,	3
1467	High-Quality Draft Genome Sequence of <i>Pseudomonas syringae</i> pv. <i>Syringae</i> Strain SM, Isolated from Wheat. 2013 , 1,	12
1466	Draft Genome Sequence of <i>Clostridium tyrobutyricum</i> Strain UC7086, Isolated from Grana Padano Cheese with Late-Blowing Defect. 2013 , 1,	14
1465	Genome Sequence of a Novel Polymer-Grade L-Lactate-Producing Alkaliphile, <i>Exiguobacterium</i> sp. Strain 8-11-1. 2013 , 1,	12
1464	Draft Genome Sequence of <i>Lactobacillus rhamnosus</i> CRL1505, an Immunobiotic Strain Used in Social Food Programs in Argentina. 2013 , 1,	
1463	Draft Genome Sequence of <i>Winogradskyella psychrotolerans</i> RS-3T, Isolated from the Marine Transect of Kongsfjorden, Ny-Alesund, Svalbard, Arctic Ocean. 2013 , 1,	2
1462	Draft Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Manhattan Strain 111113, from an Outbreak of Human Infections in Northern Italy. 2013 , 1,	2
1461	Draft Genome Sequence of <i>Alicyclobacillus acidoterrestris</i> Strain ATCC 49025. 2013 , 1,	5
1460	Genome Sequence of the Probiotic Strain <i>Lactobacillus rhamnosus</i> (Formerly <i>Lactobacillus casei</i>) LOCK900. 2013 , 1,	26
1459	Draft Genome Sequence of <i>Cyclobacterium qasimii</i> Strain M12-11BT, Isolated from Arctic Marine Sediment. 2013 , 1,	1
1458	Draft Genome Sequence of the Fast-Growing Bacterium <i>Vibrio natriegens</i> Strain DSMZ 759. 2013 , 1,	27
1457	Draft Genome Sequence of <i>Mycobacterium massiliense</i> Strain M159, Showing Phenotypic Resistance to β -Lactam and Tetracycline Antibiotics. 2013 , 1,	

1456	Draft Genome Sequence of <i>Sphingobium chinhatense</i> Strain IP26T, Isolated from a Hexachlorocyclohexane Dumpsite. 2013 , 1,	17
1455	Whole-Genome Sequences of <i>Staphylococcus aureus</i> ST398 Strains of Animal Origin. 2013 , 1,	4
1454	Whole-Genome Sequence of the Ancestral Animal-Borne ST398 <i>Staphylococcus aureus</i> Strain S123. 2013 , 1,	4
1453	Draft Genome Sequence of <i>Pseudomonas pelagia</i> CL-AP6, a Psychrotolerant Bacterium Isolated from Culture of Antarctic Green Alga <i>Pyramimonas gelidicola</i> . 2013 , 1,	4
1452	Draft Genome Sequence of Ammonia-Producing <i>Aeromonas</i> sp. MDS8 Strain MCC2167 from Sludge of a Dairy Effluent Treatment Plant. 2013 , 1,	3
1451	Genome Sequence of <i>Novosphingobium lindaniclasticum</i> LE124T, Isolated from a Hexachlorocyclohexane Dumpsite. 2013 , 1,	8
1450	First Whole-Genome Sequence of <i>Mycobacterium iranicum</i> , a Newly Reported Mycobacterial Species. 2013 , 1,	2
1449	Draft Genome Sequence of <i>Sphingobium</i> sp. Strain HDIPO4, an Avid Degradator of Hexachlorocyclohexane. 2013 , 1,	12
1448	Draft Genome Sequence of Multidrug-Resistant <i>Mycobacterium tuberculosis</i> Clinical Isolate OSDD515, Belonging to the Uganda I Genotype. 2013 , 1,	1
1447	Whole-Genome Shotgun Sequencing of <i>Rhodococcus erythropolis</i> Strain P27, a Highly Radiation-Resistant Actinomycete from Antarctica. 2013 , 1,	4
1446	Draft Genome Sequence of <i>Bacillus subtilis</i> Strain S1-4, Which Degrades Feathers Efficiently. 2013 , 1,	5
1445	Complete Genome Sequence of <i>Vibrio anguillarum</i> M3, a Serotype O1 Strain Isolated from Japanese Flounder in China. 2013 , 1,	11
1444	Genome Sequences of <i>Listeria monocytogenes</i> Serotype 4b Variant Strains Isolated from Clinical and Environmental Sources. 2013 , 1,	9
1443	Genome Sequence of the Fructan-Degrading Organism <i>Marinimicrobium</i> sp. Strain LS-A18, Isolated from a Marine Solar Saltern. 2013 , 1,	1
1442	Draft Genome Sequence of the Earliest <i>Cronobacter sakazakii</i> Sequence Type 4 Strain, NCIMB 8272. 2013 , 1,	8
1441	Draft Genome Sequences of Three Newly Identified Species in the Genus <i>Cronobacter</i> , <i>C. helveticus</i> LMG23732T, <i>C. pulveris</i> LMG24059, and <i>C. zurichensis</i> LMG23730T. 2013 , 1,	11
1440	Draft Genome Sequence of <i>Vibrio coralliilyticus</i> Strain OCN008, Isolated from Kane'ohe Bay, Hawai'i. 2013 , 1,	9
1439	Draft Genome Sequence of <i>Brucella melitensis</i> Strain ADMAS-G1, Isolated from Placental Fluids of an Aborted Goat. 2013 , 1,	2

1438	Genome Sequences of <i>Salmonella enterica</i> Serotype Typhimurium Blood Clinical Isolate ST4848/06 and Stool Isolate ST1489/06. 2013 , 1,	
1437	Draft Genome Sequence of a Meningitic Isolate of <i>Cronobacter sakazakii</i> Clonal Complex 4, Strain 8399. 2013 , 1,	4
1436	Draft Genome Sequences of <i>Bordetella hinzii</i> and <i>Bordetella trematum</i> . 2013 , 1,	5
1435	Draft Genome Sequences of Multidrug-Resistant <i>Acinetobacter</i> sp. Strains from Colombian Hospitals. 2013 , 1,	2
1434	Complete Genome Sequence of the <i>Mesoplasma florum</i> W37 Strain. 2013 , 1,	6
1433	Draft Genome Sequence of Beta-Hemolytic <i>Streptococcus iniae</i> KCTC 11634. 2013 , 1,	2
1432	Draft Genome Sequence of <i>Bacillus</i> sp. Strain NSP2.1, a Nonhalophilic Bacterium Isolated from the Salt Marsh of the Great Rann of Kutch, India. 2013 , 1,	2
1431	Draft Genome Sequence of <i>Psychrobacter aquaticus</i> Strain CMS 56T, Isolated from a Cyanobacterial Mat Sample Collected from Water Bodies in the McMurdo Dry Valley Region of Antarctica. 2013 , 1,	2
1430	Genome Sequence of a Strain of the Human Pathogenic Bacterium <i>Pseudomonas alcaligenes</i> That Caused Bloodstream Infection. 2013 , 1,	14
1429	Draft Genome Sequence of <i>Loktanella cinnabarina</i> LL-001T, Isolated from Deep-Sea Floor Sediment. 2013 , 1,	
1428	Draft Genome Sequence of an Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> Clinical Isolate of the Ural Strain OSDD493. 2013 , 1,	1
1427	Complete Genome Sequence of Channel Catfish Gastrointestinal Septicemia Isolate <i>Edwardsiella tarda</i> C07-087. 2013 , 1,	18
1426	Genome Sequence of <i>Dyella ginsengisoli</i> Strain LA-4, an Efficient Degradator of Aromatic Compounds. 2013 , 1,	9
1425	Draft Genome Sequence of a Multidrug-Resistant Clinical Isolate of <i>Mycobacterium tuberculosis</i> Belonging to a Novel Spoligotype. 2013 , 1,	
1424	Genome Sequences of Clinical <i>Vibrio cholerae</i> Isolates from an Oyster-Borne Cholera Outbreak in Florida. 2013 , 1,	5
1423	Draft Genome Sequence of <i>Serratia fonticola</i> UTAD54, a Carbapenem-Resistant Strain Isolated from Drinking Water. 2013 , 1,	3
1422	Draft Genome Sequence of <i>Serratia fonticola</i> LMG 7882T Isolated from Freshwater. 2013 , 1,	2
1421	Genome Sequence of <i>Rickettsia gravesii</i> , Isolated from Western Australian Ticks. 2013 , 1,	5

1420	Draft Genome Sequence of <i>Veillonella parvula</i> HSIVP1, Isolated from the Human Small Intestine. 2013 , 1,	7
1419	Complete Genome Sequence of <i>Carnobacterium gilichinskyi</i> Strain WN1359T (DSM 27470T). 2013 , 1,	7
1418	Draft Genome Sequence of <i>Pseudomonas</i> sp. Strain CMAA 1215, a Plant Growth-Promoting Bacterium Isolated from a Brazilian Mangrove. 2013 , 1,	5
1417	Genome Sequence of <i>Enterobacter turicensis</i> Strain 610/05 (LMG 23731), Isolated from Fruit Powder. 2013 , 1,	4
1416	Draft Genome Sequence of <i>Lactobacillus jensenii</i> Strain MD IIE-70(2). 2013 , 1,	2
1415	Draft Genome Sequence of <i>Lactobacillus fermentum</i> Strain 3872. 2013 , 1,	12
1414	Complete Genome Sequence of <i>Staphylococcus aureus</i> Z172, a Vancomycin-Intermediate and Daptomycin-Nonsusceptible Methicillin-Resistant Strain Isolated in Taiwan. 2013 , 1,	12
1413	Draft Genome Sequence of <i>Enterococcus</i> sp. Strain HSIEG1, Isolated from the Human Small Intestine. 2013 , 1,	3
1412	Draft Genome Sequence of the Psychrophilic and Alkaliphilic <i>Rhodonellum psychrophilum</i> Strain GCM71T. 2013 , 1,	1
1411	Draft Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serotype Oranienburg Strain S-76, Isolated from an Aquatic Environment. 2013 , 1,	5
1410	Complete Genome Sequence of <i>Exiguobacterium</i> sp. Strain MH3, Isolated from Rhizosphere of <i>Lemna minor</i> . 2013 , 1,	15
1409	Complete Genome Sequence of Bacteroidales Strain CF from a Chloroform-Dechlorinating Enrichment Culture. 2013 , 1,	7
1408	Complete Genome Sequence of <i>Pediococcus pentosaceus</i> Strain SL4. 2013 , 1,	11
1407	Genome Sequence of the Pigment-Producing Bacterium <i>Pseudogulbenkiania ferrooxidans</i> , Isolated from Loktak Lake. 2013 , 1,	6
1406	Evolutionary Genomics of <i>Salmonella enterica</i> Subspecies. 2013 , 4,	90
1405	Small, smaller, smallest: the origins and evolution of ancient dual symbioses in a Phloem-feeding insect. 2013 , 5, 1675-88	189
1404	Draft Genome Sequence of the Plant Pathogen <i>Dickeya zeae</i> DZ2Q, Isolated from Rice in Italy. 2013 , 1,	11
1403	Genome Sequences of Four <i>Yersinia enterocolitica</i> Bioserotype 4/O:3 Isolates from Mammals. 2013 , 1,	

1402	Draft Genome Sequence of the Arsenite-Oxidizing Strain Aliihoeflea sp. 2WW, Isolated from Arsenic-Contaminated Groundwater. 2013 , 1,	6
1401	Draft Genome Sequence of the Obligate Halophilic Bacillus sp. Strain NSP22.2, Isolated from a Seasonal Salt Marsh of the Great Rann of Kutch, India. 2013 , 1,	
1400	Genome Sequencing of <i>Ralstonia solanacearum</i> FQY_4, Isolated from a Bacterial Wilt Nursery Used for Breeding Crop Resistance. 2013 , 1,	17
1399	Comparative genomic analysis of rapid evolution of an extreme-drug-resistant <i>Acinetobacter baumannii</i> clone. 2013 , 5, 807-18	32
1398	Complete sequence of pOZ176, a 500-kilobase IncP-2 plasmid encoding IMP-9-mediated carbapenem resistance, from outbreak isolate <i>Pseudomonas aeruginosa</i> 96. 2013 , 57, 3775-82	53
1397	Genome sequence of <i>Methanobrevibacter</i> sp. strain jh1, isolated from rumen of Korean native cattle. 2013 , 1,	19
1396	Genome Sequences and Photosynthesis Gene Cluster Composition of a Freshwater Aerobic Anoxygenic Phototroph, <i>Sandarakinorhabdus</i> sp. Strain AAP62, Isolated from the Shahu Lake in Ningxia, China. 2013 , 1,	2
1395	Draft Genome Sequence of <i>Escherichia coli</i> Strain ATCC 23506 (Serovar O10:K5:H4). 2013 , 1, e0004913	8
1394	Draft Genome Sequence of the 2-Chloro-4-Nitrophenol-Degrading Bacterium <i>Arthrobacter</i> sp. Strain SJCon. 2013 , 1, e0005813	10
1393	Draft genome sequence of a subarctic humic substance-degrading pseudomonad. 2013 , 1,	1
1392	Whole-Genome Sequencing of <i>Micrococcus luteus</i> Strain Modasa, of Indian Origin. 2013 , 1, e0007613	3
1391	Draft Genome Sequence of <i>Rhodococcus qingshengii</i> Strain BKS 20-40. 2013 , 1, e0012813	2
1390	Draft Genome Sequence of <i>Rhodococcus triatomae</i> Strain BKS 15-14. 2013 , 1, e0012913	3
1389	Draft Genome Sequence of <i>Acinetobacter baumannii</i> Strain MSP4-16. 2013 , 1, e0013713	1
1388	Draft Genome Sequence of <i>Amycolatopsis decaplanina</i> Strain DSM 44594T. 2013 , 1, e0013813	3
1387	Draft Genome Sequence of <i>Rhodococcus ruber</i> Strain BKS 20-38. 2013 , 1, e0013913	0
1386	Draft Genome Sequence of <i>Rhodococcus opacus</i> Strain M213 Shows a Diverse Catabolic Potential. 2013 , 1,	9
1385	Draft Genome Sequence of <i>Streptomyces gancidicus</i> Strain BKS 13-15. 2013 , 1, e0015013	3

1384	Draft Genome Sequence of a Humic Substance-Degrading <i>Paenibacillus</i> sp. Isolated from the Subarctic Grasslands at Low Temperature. 2013 , 1,	
1383	Draft Genome Sequence of <i>Ochrobactrum pseudogrignonense</i> Strain CDB2, a Highly Efficient Arsenate-Resistant Soil Bacterium from Arsenic-Contaminated Cattle Dip Sites. 2013 , 1, e0017313	9
1382	Draft Genome Sequence of <i>Myxococcus xanthus</i> Wild-Type Strain DZ2, a Model Organism for Predation and Development. 2013 , 1,	29
1381	Draft Genome Sequence of <i>Bacillus atrophaeus</i> UCMB-5137, a Plant Growth-Promoting Rhizobacterium. 2013 , 1,	3
1380	Genome Sequence of Naphthalene-Degrading Soil Bacterium <i>Pseudomonas putida</i> CSV86. 2013 , 1,	15
1379	Genome Sequence of <i>Alcaligenes</i> sp. Strain HPC1271. 2013 , 1,	5
1378	Genome of the Psychrophilic Bacterium <i>Bacillus psychrosaccharolyticus</i> , a Potential Source of 2'-Deoxyribosyltransferase for Industrial Nucleoside Synthesis. 2013 , 1,	5
1377	Draft Genome Sequence of <i>Agarivorans albus</i> Strain MKT 106T, an Agarolytic Marine Bacterium. 2013 , 1,	1
1376	Draft Genome of a Type 4 Pilus Defective <i>Myxococcus xanthus</i> Strain, DZF1. 2013 , 1,	16
1375	Draft Genome Sequence of <i>Euryhalocalulis caribicus</i> Strain JL2009T, a New Member of the Family Hyphomonadaceae Isolated from the Caribbean Sea. 2013 , 1,	
1374	Genome Sequence of <i>Streptococcus agalactiae</i> Strain 09mas018883, Isolated from a Swedish Cow. 2013 , 1,	8
1373	Draft Genome Sequence of a Highly Flagellated, Fast-Swimming Archaeon, <i>Methanocaldococcus villosus</i> Strain KIN24-T80 (DSM 22612). 2013 , 1,	3
1372	Complete Genome Sequence of the Carbazole Degrader <i>Pseudomonas resinovorans</i> Strain CA10 (NBRC 106553). 2013 , 1,	9
1371	Genome Sequence of <i>Thermus thermophilus</i> ATCC 33923, a Thermostable Trehalose-Producing Strain. 2013 , 1,	6
1370	Draft Genome Sequence of <i>Enterococcus faecium</i> Strain CRL 1879, Isolated from a Northwestern Argentinian Artisanal Cheese. 2013 , 1,	
1369	Genome Sequences of <i>Amycolatopsis orientalis</i> subsp. <i>orientalis</i> Strains DSM 43388 and DSM 46075. 2013 , 1,	5
1368	Draft Genome Sequence of the Brazilian Toxic Bloom-Forming Cyanobacterium <i>Microcystis aeruginosa</i> Strain SPC777. 2013 , 1,	11
1367	Draft Genome Sequence of <i>Pseudomonas putida</i> Strain MTCC5279. 2013 , 1,	5

1366	Genome Sequence of the Cheese-Starter Strain <i>Lactobacillus delbrueckii</i> subsp. <i>lactis</i> CRL 581. 2013, 1,	5
1365	Genome Sequence of the Quorum-Quenching <i>Agrobacterium tumefaciens</i> Strain WRT31. 2013, 1,	1
1364	Genome Sequence of the Melanin-Producing Extremophile <i>Aeromonas salmonicida</i> subsp. <i>pectinolytica</i> Strain 34melT. 2013, 1,	8
1363	Draft Whole-Genome Sequence of VIM-1-Producing Multidrug-Resistant <i>Enterobacter cloacae</i> EC_38VIM1. 2013, 1,	
1362	Draft Genome Sequences of <i>Helicobacter pylori</i> Strains HPARG63 and HPARG8G, Cultured from Patients with Chronic Gastritis and Gastric Ulcer Disease. 2013, 1,	1
1361	Draft Genome Sequence of <i>Sphingobium quisquiliarum</i> Strain P25T, a Novel Hexachlorocyclohexane (HCH)-Degrading Bacterium Isolated from an HCH Dumpsite. 2013, 1,	14
1360	Draft Genome Sequence of a Hexachlorocyclohexane-Degrading Bacterium, <i>Sphingobium baderi</i> Strain LL03T. 2013, 1,	9
1359	Draft Genome Sequence of <i>Xylella fastidiosa</i> subsp. <i>multiplex</i> Strain Griffin-1 from <i>Quercus rubra</i> in Georgia. 2013, 1,	14
1358	Genome Sequence of <i>Streptococcus parauberis</i> Strain KCTC11980, Isolated from Diseased <i>Paralichthys olivaceus</i> . 2013, 1,	6
1357	Draft Genome Sequence of the <i>Mycobacterium tuberculosis</i> Strain 43-16836, Belonging to the Indo-Oceanic Lineage, Isolated From Tuberculous Meningitis in Thailand. 2013, 1,	4
1356	Draft Genome Sequence of <i>Bacillus</i> sp. Strain SB47, an Obligate Extreme Halophile Isolated from a Salt Pan of the Little Rann of Kutch, India. 2013, 1,	5
1355	Draft Genome Sequence of <i>Bacillus</i> sp. Strain NSP9.1, a Moderately Halophilic Bacterium Isolated from the Salt Marsh of the Great Rann of Kutch, India. 2013, 1,	4
1354	Draft Genome Sequence of the Extremely Halophilic <i>Bacillus</i> sp. Strain SB49, Isolated from a Salt Crystallizer Pond of the Little Rann of Kutch, India. 2013, 1,	6
1353	Draft Genome Sequence of <i>Sphingobium</i> sp. Strain KK22, a High-Molecular-Weight Polycyclic Aromatic Hydrocarbon-Degrading Bacterium Isolated from Cattle Pasture Soil. 2013, 1,	11
1352	Draft Genome Sequence of <i>Corynebacterium pseudodiphtheriticum</i> Strain 090104 "Sokolov". 2013, 1,	7
1351	Draft Genome Sequence of a Plant Growth-Promoting Rhizobacterium, <i>Serratia fonticola</i> Strain AU-P3(3). 2013, 1,	6
1350	Draft Genome Sequence of Plant Growth-Promoting Rhizobacterium <i>Pantoea</i> sp. Strain AS-PWVM4. 2013, 1,	3
1349	Complete Genome Sequence of <i>Lactococcus lactis</i> subsp. <i>lactis</i> KLDS4.0325. 2013, 1,	14

1348	Draft Genome Sequence of Plant-Growth-Promoting Rhizobacterium <i>Serratia fonticola</i> Strain AU-AP2C, Isolated from the Pea Rhizosphere. 2013 , 1,	2
1347	Characterization of <i>Aeromonas hydrophila</i> wound pathotypes by comparative genomic and functional analyses of virulence genes. 2013 , 4, e00064-13	54
1346	Complete Genome Sequence of the Broad-Host-Range Paenibacillus larvae Phage phiIBB_PL23. 2013 , 1,	20
1345	Draft Genome Sequence of <i>Pseudomonas veronii</i> Strain 1YdBTEX2. 2013 , 1,	10
1344	Draft Genome Sequences of Two Multidrug Resistant <i>Klebsiella pneumoniae</i> ST258 Isolates Resistant to Colistin. 2013 , 1,	6
1343	Genome Sequence of <i>Rhodococcus</i> sp. Strain BCP1, a Biodegrader of Alkanes and Chlorinated Compounds. 2013 , 1,	7
1342	Draft Genome Sequence of a Clinical Isolate of Multidrug-Resistant <i>Mycobacterium tuberculosis</i> East African Indian Strain OSDD271. 2013 , 1,	2
1341	Complete Genome Sequence of <i>Staphylococcus aureus</i> Tager 104, a Sequence Type 49 Ancestor. 2013 , 1,	6
1340	Draft Genome Sequence of Vancomycin-Heteroresistant <i>Staphylococcus epidermidis</i> Strain UC7032, Isolated from Food. 2013 , 1,	3
1339	Complete Genome Sequence of the Probiotic Strain <i>Lactobacillus casei</i> (Formerly <i>Lactobacillus paracasei</i>) LOCK919. 2013 , 1,	20
1338	Draft Genome Sequence of <i>Brevibacillus</i> sp. Strain BAB-2500, a Strain That Might Play an Important Role in Agriculture. 2013 , 1,	5
1337	Draft Genome Sequence of <i>Sphingobium lactosutens</i> Strain DS20T, Isolated from a Hexachlorocyclohexane Dumpsite. 2013 , 1,	5
1336	Draft Genome Sequence of <i>Pseudomonas plecoglossicida</i> Strain NB2011, the Causative Agent of White Nodules in Large Yellow Croaker (<i>Larimichthys crocea</i>). 2013 , 1,	23
1335	Genome Sequence of <i>Lactobacillus saerimneri</i> 30a (Formerly <i>Lactobacillus</i> sp. Strain 30a), a Reference Lactic Acid Bacterium Strain Producing Biogenic Amines. 2013 , 1,	9
1334	Complete Genome Sequence of the Epidemic and Highly Virulent CTX-M-15-Producing H30-Rx Subclone of <i>Escherichia coli</i> ST131. 2013 , 1,	38
1333	Genome Sequence of <i>Lysinibacillus sphaericus</i> Strain KCTC 3346T. 2013 , 1,	4
1332	Complete genome sequence of <i>Bacillus thuringiensis</i> subsp. <i>thuringiensis</i> strain IS5056, an isolate highly toxic to <i>Trichoplusia ni</i> . 2013 , 1, e0010813	35
1331	Draft Genome Sequence of Chromate-Resistant and Biofilm-Producing Strain <i>Pseudomonas alcaliphila</i> 34. 2013 , 1,	3

1330	Bacterial growth at -15 °C; molecular insights from the permafrost bacterium <i>Planococcus halocryophilus</i> Or1. 2013 , 7, 1211-26	211
1329	Draft Genome Sequence of <i>Escherichia coli</i> Strain Nissle 1917 (Serovar O6:K5:H1). 2013 , 1, e0004713	25
1328	RubisCO gene clusters found in a metagenome microarray from acid mine drainage. 2013 , 79, 2019-26	21
1327	Draft Genome Sequence of <i>Mycobacterium abscessus</i> subsp. <i>bolletii</i> INCQS 00594. 2013 , 1,	
1326	The genome organization of <i>Thermotoga maritima</i> reflects its lifestyle. 2013 , 9, e1003485	31
1325	Whole-genome sequences of five oyster-associated bacteria show potential for crude oil hydrocarbon degradation. 2013 , 1,	18
1324	Semi-automated curation of metabolic models via flux balance analysis: a case study with <i>Mycoplasma gallisepticum</i> . 2013 , 9, e1003208	12
1323	Nearly finished genomes produced using gel microdroplet culturing reveal substantial intraspecies genomic diversity within the human microbiome. 2013 , 23, 878-88	46
1322	Reconstitution of a thermostable xylan-degrading enzyme mixture from the bacterium <i>Caldicellulosiruptor bescii</i> . 2013 , 79, 1481-90	37
1321	Explaining microbial phenotypes on a genomic scale: GWAS for microbes. 2013 , 12, 366-80	38
1320	Proteogenomic analysis of <i>Bradyrhizobium japonicum</i> USDA110 using GenoSuite, an automated multi-algorithmic pipeline. 2013 , 12, 3388-97	35
1319	Bacterial DNA sifted from the <i>Trichoplax adhaerens</i> (Animalia: Placozoa) genome project reveals a putative rickettsial endosymbiont. 2013 , 5, 621-45	60
1318	<i>Lactobacillus paracasei</i> comparative genomics: towards species pan-genome definition and exploitation of diversity. 2013 , 8, e68731	111
1317	Draft Genome Sequence of <i>Aeromonas veronii</i> Hm21, a Symbiotic Isolate from the Medicinal Leech Digestive Tract. 2013 , 1,	19
1316	Genome Sequence of the Autotrophic Acetogen <i>Clostridium autoethanogenum</i> JA1-1 Strain DSM 10061, a Producer of Ethanol from Carbon Monoxide. 2013 , 1,	19
1315	Draft Genome Sequence of <i>Sphingobium ummariense</i> Strain RL-3, a Hexachlorocyclohexane-Degrading Bacterium. 2013 , 1,	7
1314	A Rex family transcriptional repressor influences H ₂ O ₂ accumulation by <i>Enterococcus faecalis</i> . 2013 , 195, 1815-24	46
1313	H-NS is a negative regulator of the two hemolysin/cytotoxin gene clusters in <i>Vibrio anguillarum</i> . 2013 , 81, 3566-76	21

1312	Complete sequence of pSAM7, an IncX4 plasmid carrying a novel blaCTX-M-14b transposition unit isolated from <i>Escherichia coli</i> and <i>Enterobacter cloacae</i> from cattle. 2013 , 57, 4590-4	14
1311	Presence of entomobirnaviruses in Chinese mosquitoes in the absence of Dengue virus co-infection. 2013 , 94, 663-667	17
1310	Complete sequence of a bla(KPC-2)-harboring IncFII(K1) plasmid from a <i>Klebsiella pneumoniae</i> sequence type 258 strain. 2013 , 57, 1542-5	46
1309	Complete Genome Sequence of a <i>Francisella tularensis</i> subsp. <i>holarctica</i> Strain from Germany Causing Lethal Infection in Common Marmosets. 2013 , 1,	10
1308	Draft Genome Sequence of the Bisphenol A-Degrading Bacterium <i>Sphingobium</i> sp. Strain YL23. 2013 , 1,	10
1307	The use of metagenomic approaches to analyze changes in microbial communities. 2013 , 6, 37-48	49
1306	Draft Genome Sequence of <i>Agrobacterium</i> sp. Strain UHFBA-218, Isolated from Rhizosphere Soil of Crown Gall-Infected Cherry Rootstock Colt. 2013 , 1,	6
1305	Draft Genome Sequence of <i>Lactobacillus plantarum</i> Strain WJL, a <i>Drosophila</i> Gut Symbiont. 2013 , 1,	12
1304	Draft genome sequences for oil-degrading bacterial strains from beach sands impacted by the deepwater horizon oil spill. 2013 , 1,	19
1303	Two multidrug-resistant clinical isolates of <i>Bacteroides fragilis</i> carry a novel metronidazole resistance <i>nim</i> gene (<i>nimJ</i>). 2013 , 57, 3767-74	43
1302	Distinct lipopeptide production systems for WLIP (white line-inducing principle) in <i>Pseudomonas fluorescens</i> and <i>Pseudomonas putida</i> . 2013 , 5, 160-9	22
1301	Whole-Genome Sequence of Fish-Pathogenic <i>Mycobacterium</i> sp. Strain 012931, Isolated from Yellowtail (<i>Seriola quinqueradiata</i>). 2013 , 1,	2
1300	Comparative genome analysis of <i>Lactobacillus casei</i> strains isolated from Actimel and Yakult products reveals marked similarities and points to a common origin. 2013 , 6, 576-87	26
1299	Structure and evolution of chlorate reduction composite transposons. 2013 , 4,	49
1298	<i>Xanthomonas arboricola</i> pv. <i>fragariae</i> : what's in a name?. 2013 , 62, 1123-1131	23
1297	Comparative genomics of Japanese <i>Erwinia pyrifoliae</i> strain Ejp617 with closely related erwinias. 2013 , 56, 83-90	3
1296	Complete Genome Sequence of Probiotic Strain <i>Lactobacillus acidophilus</i> La-14. 2013 , 1,	23
1295	Investigation of <i>Mannheimia haemolytica</i> bacteriophages relative to host diversity. 2013 , 114, 1592-603	6

1294	Adaptation and modification of three CRISPR loci in two closely related cyanobacteria. 2013 , 10, 852-64	62
1293	Precipitation of alacranite (As8S9) by a novel As(V)-respiring anaerobe strain MPA-C3. 2013 , 15, 2748-60	8
1292	Complete nucleotide sequences of blaKPC-4- and blaKPC-5-harboring IncN and IncX plasmids from <i>Klebsiella pneumoniae</i> strains isolated in New Jersey. 2013 , 57, 269-76	68
1291	Draft Genome Sequence of <i>Pseudoalteromonas luteoviolacea</i> Strain B (ATCC 29581). 2013 , 1, e0004813	9
1290	Draft Genome Sequence of the Polyextremophilic <i>Exiguobacterium</i> sp. Strain S17, Isolated from Hyperarsenic Lakes in the Argentinian Puna. 2013 , 1,	34
1289	Genome signature-based dissection of human gut metagenomes to extract subliminal viral sequences. 2013 , 4, 2420	60
1288	Genome Sequence of the Extreme Obligate Alkaliphile <i>Bacillus marmarensis</i> Strain DSM 21297. 2013 , 1,	7
1287	Role of energy sensor TlpD of <i>Helicobacter pylori</i> in gerbil colonization and genome analyses after adaptation in the gerbil. 2013 , 81, 3534-51	26
1286	Genetic analysis of capsular polysaccharide synthesis gene clusters from all serotypes of <i>Streptococcus suis</i> : potential mechanisms for generation of capsular variation. 2013 , 79, 2796-806	69
1285	Tracking the establishment of local endemic populations of an emergent enteric pathogen. 2013 , 110, 17522-7	89
1284	Draft Genome Sequence of an Obligate and Moderately Halophilic Bacterium, <i>Thalassobacillus devorans</i> Strain MSP14, the First Draft Genome of the Genus <i>Thalassobacillus</i> . 2013 , 1,	2
1283	Genome Sequence of <i>Clostridium butyricum</i> Strain DSM 10702, a Promising Producer of Biofuels and Biochemicals. 2013 , 1,	6
1282	Genome sequence of the moderately halophilic bacterium <i>Salinicoccus carniancri</i> type strain Crm(T) (= DSM 23852(T)). 2013 , 8, 255-63	6
1281	Applying Shannon's information theory to bacterial and phage genomes and metagenomes. 2013 , 3, 1033	22
1280	Re-annotation of the <i>Saccharopolyspora erythraea</i> genome using a systems biology approach. <i>BMC Genomics</i> , 2013 , 14, 699	4-5 18
1279	Draft genome sequence of <i>Rhodococcus rhodochrous</i> strain ATCC 17895. 2013 , 9, 175-84	13
1278	Draft genome sequence of the chronic, nonclonal cystic fibrosis isolate <i>Pseudomonas aeruginosa</i> strain 18A. 2013 , 1, e0000113	3
1277	Genome Sequence of <i>Sphingomonas xenophaga</i> QYY, an Anthraquinone-Degrading Strain. 2013 , 1,	4

1276	Draft Genome Sequences of Two Bulgarian <i>Bacillus anthracis</i> Strains. 2013 , 1, e0015213	2
1275	Draft Genome Sequence of <i>Methylophaga lonarensis</i> MPLT, a Haloalkaliphilic (Non-Methane-Utilizing) Methylophag. 2013 , 1,	2
1274	Draft Genome Sequence of the Halophilic Bacterium <i>Halobacillus</i> sp. Strain BAB-2008. 2013 , 1,	2
1273	Draft Genome Sequence of a Clinical Isolate of <i>Mycobacterium tuberculosis</i> Strain PR05. 2013 , 1,	2
1272	The Draft Genome Sequence of <i>Sphingomonas paucimobilis</i> Strain HER1398 (Proteobacteria), Host to the Giant PAU Phage, Indicates That It Is a Member of the Genus <i>Sphingobacterium</i> (Bacteroidetes). 2013 , 1,	8
1271	Draft Genome Sequence of Exopolysaccharide-Producing Thermophilic Bacterium <i>Brevibacillus thermoruber</i> Strain 423. 2013 , 1,	4
1270	Draft Genome Sequence of <i>Lactobacillus brevis</i> Strain EW, a <i>Drosophila</i> Gut Pathobiont. 2013 , 1,	4
1269	High-Quality Draft Genome Sequence of <i>Bifidobacterium longum</i> E18, Isolated from a Healthy Adult. 2013 , 1,	5
1268	Draft Genome Sequence of an Alphaproteobacterium, <i>Caenispirillum salinarum</i> AK4(T), Isolated from a Solar Saltern. 2013 , 1,	1
1267	Draft Genome Sequence of the Rice Endophyte <i>Burkholderia kururiensis</i> M130. 2013 , 1, e0022512	9
1266	Draft Genome Sequence of Strain JLT2015T, Belonging to the Family Sphingomonadaceae of the Alphaproteobacteria. 2013 , 1,	1
1265	Genome Sequences of Two Morphologically Distinct and Thermophilic <i>Bacillus coagulans</i> Strains, H-1 and XZL9. 2013 , 1,	7
1264	Genome Sequence of <i>Lactobacillus sakei</i> subsp. <i>sakei</i> LS25, a Commercial Starter Culture Strain for Fermented Sausage. 2013 , 1,	10
1263	Whole-Genome Sequences of Two <i>Staphylococcus aureus</i> ST398 Strains of Human Origin, S94 and S100. 2013 , 1,	6
1262	Genome Sequence of Marine Bacterium <i>Idiomarina</i> sp. Strain 28-8, Isolated from Korean Ark Shells. 2013 , 1,	0
1261	Draft Genome Sequence of the Arsenate-Respiring Bacterium <i>Chrysiogenes arsenatis</i> Strain DSM 11915. 2013 , 1,	2
1260	Genome Sequences of Two <i>Enterobacter pulveris</i> Strains, 601/05T (=LMG 24057T =DSM 19144T) and 1160/04 (=LMG 24058 =DSM 19146), Isolated from Fruit Powder. 2013 , 1,	3
1259	Non-contiguous finished genome sequence and description of <i>Salmonella enterica</i> subsp. <i>houtenae</i> str. RKS3027. 2013 , 8, 198-205	1

1258	Non contiguous-finished genome sequence of <i>Pseudomonas syringae</i> pathovar <i>syringae</i> strain B64 isolated from wheat. 2013 , 8, 420-9	10
1257	Draft Genome Sequence of <i>Amphibacillus jilensis</i> Y1(T), a Facultatively Anaerobic, Alkaliphilic and Halotolerant Bacterium. 2013 , 8, 491-9	0
1256	Genome sequence and description of the heavy metal tolerant bacterium <i>Lysinibacillus sphaericus</i> strain OT4b.31. 2013 , 9, 42-56	31
1255	Non-contiguous finished genome sequence and description of <i>Oceanobacillus massiliensis</i> sp. nov. 2013 , 9, 370-84	17
1254	Non-contiguous finished genome sequence of <i>Phocaecicola abscessus</i> type strain 7401987(T). 2013 , 9, 351-8	0
1253	Genome sequence of the chromate-resistant bacterium <i>Leucobacter salsicius</i> type strain M1-8(T). 2014 , 9, 495-504	7
1252	Bacterial genomes: what they teach us about cellulose degradation. 2013 , 4, 669-681	25
1251	Genome Sequence of <i>Parvimonas micra</i> Strain A293, Isolated from an Abdominal Abscess from a Patient in the United Kingdom. 2013 , 1,	7
1250	Whole Genome Sequencing and Comparative Analysis of <i>Bartonella bacilliformis</i> Strain INS, the Causative Agent of Carrion's Disease. 2013 , 1,	4
1249	Complete Genome Sequence of <i>Bacillus subtilis</i> Strain PY79. 2013 , 1,	35
1248	Whole-genome sequence of a freshwater aerobic anoxygenic phototroph, <i>Porphyrobacter</i> sp. strain AAP82, isolated from the Huguangyan Maar Lake in Southern China. 2013 , 1, e0007213	3
1247	Draft Genome Sequence of <i>Leucobacter</i> sp. Strain UCD-THU (Phylum Actinobacteria). 2013 , 1,	5
1246	Draft Genome Sequence of the Dimorphic Prosthecate Bacterium <i>Brevundimonas abyssalis</i> TAR-001T. 2013 , 1,	1
1245	Draft Genome Sequence of <i>Rhodococcus erythropolis</i> DN1, a Crude Oil Biodegrader. 2013 , 1,	8
1244	Whole-Genome Sequencing of <i>Lactobacillus shenzhenensis</i> Strain LY-73T. 2013 , 1,	
1243	Complete Genome Sequence of the <i>Campylobacter coli</i> Clinical Isolate 15-537360. 2013 , 1,	15
1242	Whole-Genome Shotgun Sequencing of <i>Mycobacterium abscessus</i> M156, an Emerging Clinical Pathogen in Malaysia. 2013 , 1,	2
1241	Genome Sequence of an <i>Enterobacter helveticus</i> Strain, 1159/04 (LMG 23733), Isolated from Fruit Powder. 2013 , 1,	4

1240	Genome Sequence of <i>Staphylococcus pseudintermedius</i> Strain E140, an ST71 European-Associated Methicillin-Resistant Isolate. 2013 , 1, e0020712	13
1239	Draft Genome Sequence of a Phosphate-Accumulating <i>Bacillus</i> sp., WBUNB004. 2013 , 1,	4
1238	Draft Genome Sequence of <i>Catellibacillus marimammalium</i> , a Novel Species Commonly Found in Gull Feces. 2013 , 1,	8
1237	Draft Genome Sequence of <i>Lactobacillus pobuzihii</i> E100301T. 2013 , 1,	1
1236	Draft Genome Sequence of <i>Dietzia</i> sp. Strain UCD-THP (Phylum Actinobacteria). 2013 , 1,	5
1235	Genome Sequence of Methicillin-Resistant <i>Staphylococcus pseudintermedius</i> Sequence Type 233 (ST233) Strain K7, of Human Origin. 2013 , 1,	5
1234	Draft Genome Sequence of <i>Leifsonia rubra</i> Strain CMS 76RT, Isolated from a Cyanobacterial Mat Sample from a Pond in Wright Valley, McMurdo, Antarctica. 2013 , 1,	2
1233	Genome Sequence of the Quorum-Sensing-Signal-Producing Nonpathogen <i>Agrobacterium tumefaciens</i> Strain P4. 2013 , 1,	4
1232	Draft Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serotype Saintpaul Strain S-70, Isolated from an Aquatic Environment. 2013 , 1,	5
1231	Genome Sequence of <i>Vibrio cholerae</i> G4222, a South African Clinical Isolate. 2013 , 1, e0004013	1
1230	Genome Sequence of <i>Clostridium tyrobutyricum</i> ATCC 25755, a Butyric Acid-Overproducing Strain. 2013 , 1,	24
1229	Genome Sequences of Two Pathogenic <i>Streptococcus agalactiae</i> Isolates from the One-Humped Camel <i>Camelus dromedarius</i> . 2013 , 1,	6
1228	Multivariate analysis of functional metagenomes. 2013 , 4, 41	38
1227	The genome sequences of <i>Cellulomonas fimi</i> and " <i>Cellvibrio gilvus</i> " reveal the cellulolytic strategies of two facultative anaerobes, transfer of " <i>Cellvibrio gilvus</i> " to the genus <i>Cellulomonas</i> , and proposal of <i>Cellulomonas gilvus</i> sp. nov. 2013 , 8, e53954	44
1226	Exploring the diversity of <i>Arcobacter butzleri</i> from cattle in the UK using MLST and whole genome sequencing. 2013 , 8, e55240	35
1225	Genome sequence of <i>Lactobacillus pentosus</i> KCA1: vaginal isolate from a healthy premenopausal woman. 2013 , 8, e59239	36
1224	Genomic comparison between <i>Salmonella Gallinarum</i> and <i>Pullorum</i> : differential pseudogene formation under common host restriction. 2013 , 8, e59427	25
1223	Insights into the physiology and ecology of the brackish-water-adapted Cyanobacterium <i>Nodularia spumigena</i> CCY9414 based on a genome-transcriptome analysis. 2013 , 8, e60224	66

1222	The detection and sequencing of a broad-host-range conjugative IncP-1 β plasmid in an epidemic strain of <i>Mycobacterium abscessus</i> subsp. <i>bolletii</i> . 2013 , 8, e60746	27
1221	Genomic and enzymatic results show <i>Bacillus cellulosilyticus</i> uses a novel set of LPXTA carbohydrases to hydrolyze polysaccharides. 2013 , 8, e61131	9
1220	Identification of genes and pathways related to phenol degradation in metagenomic libraries from petroleum refinery wastewater. 2013 , 8, e61811	37
1219	Reduce manual curation by combining gene predictions from multiple annotation engines, a case study of start codon prediction. 2013 , 8, e63523	11
1218	Adaptability and persistence of the emerging pathogen <i>Bordetella petrii</i> . 2013 , 8, e65102	12
1217	Context-dependent competition in a model gut bacterial community. 2013 , 8, e67210	19
1216	Complete genome sequence of the cystic fibrosis pathogen <i>Achromobacter xylosoxidans</i> NH44784-1996 complies with important pathogenic phenotypes. 2013 , 8, e68484	59
1215	Identification and characterization of three novel lipases belonging to families II and V from <i>Anaerovibrio lipolyticus</i> 5ST. 2013 , 8, e69076	27
1214	Genomic investigation into strain heterogeneity and pathogenic potential of the emerging gastrointestinal pathogen <i>Campylobacter ureolyticus</i> . 2013 , 8, e71515	16
1213	Genome analysis coupled with physiological studies reveals a diverse nitrogen metabolism in <i>Methylocystis</i> sp. strain SC2. 2013 , 8, e74767	38
1212	Genetic variation in the <i>Staphylococcus aureus</i> 8325 strain lineage revealed by whole-genome sequencing. 2013 , 8, e77122	39
1211	Comparative genome analysis of <i>Megasphaera</i> sp. reveals niche specialization and its potential role in the human gut. 2013 , 8, e79353	73
1210	Soil bacterial community shifts after chitin enrichment: an integrative metagenomic approach. 2013 , 8, e79699	64
1209	<i>Streptococcus pneumoniae</i> serine protease HtrA, but not SFP or PrtA, is a major virulence factor in pneumonia. 2013 , 8, e80062	29
1208	Implication of lateral genetic transfer in the emergence of <i>Aeromonas hydrophila</i> isolates of epidemic outbreaks in channel catfish. 2013 , 8, e80943	68
1207	The genome sequence of 'Mycobacterium massiliense' strain CIP 108297 suggests the independent taxonomic status of the <i>Mycobacterium abscessus</i> complex at the subspecies level. 2013 , 8, e81560	44
1206	Novel insight into the genetic context of the <i>cadAB</i> genes from a 4-chloro-2-methylphenoxyacetic acid-degrading <i>Sphingomonas</i> . 2013 , 8, e83346	21
1205	Comparative genomics analysis of <i>Streptococcus</i> isolates from the human small intestine reveals their adaptation to a highly dynamic ecosystem. 2013 , 8, e83418	42

1204	Genome implosion elicits host-confinement in <i>Alcaligenaceae</i> : evidence from the comparative genomics of <i>Tetrathiodacter kashmirensis</i> , a pathogen in the making. 2013 , 8, e64856	8
1203	Mechanistic model of <i>Rothia mucilaginosa</i> adaptation toward persistence in the CF lung, based on a genome reconstructed from metagenomic data. 2013 , 8, e64285	38
1202	Comparative Genomic Analyses of <i>Streptococcus pseudopneumoniae</i> Provide Insight into Virulence and Commensalism Dynamics. 2013 , 8, e65670	18
1201	Metagenomic insights into the dominant Fe(II) oxidizing Zetaproteobacteria from an iron mat at Līhi, Hawaiī. 2013 , 4, 52	25
1200	Complete genome sequence and phenotype microarray analysis of <i>Cronobacter sakazakii</i> SP291: a persistent isolate cultured from a powdered infant formula production facility. 2013 , 4, 256	30
1199	Evidence supporting dissimilatory and assimilatory lignin degradation in <i>Enterobacter lignolyticus</i> SCF1. 2013 , 4, 280	70
1198	Insight into the evolution of <i>Vibrio vulnificus</i> biotype 3's genome. 2013 , 4, 393	17
1197	A comparative pan-genome perspective of niche-adaptable cell-surface protein phenotypes in <i>Lactobacillus rhamnosus</i> . 2014 , 9, e102762	36
1196	<i>Pseudomonas putida</i> CSV86: a candidate genome for genetic bioaugmentation. 2014 , 9, e84000	31
1195	Scrutinizing virus genome termini by high-throughput sequencing. 2014 , 9, e85806	44
1194	Application of microarray and functional-based screening methods for the detection of antimicrobial resistance genes in the microbiomes of healthy humans. 2014 , 9, e86428	45
1193	Genome sequencing of <i>Listeria monocytogenes</i> "Quargel" listeriosis outbreak strains reveals two different strains with distinct in vitro virulence potential. 2014 , 9, e89964	45
1192	New hydrocarbon degradation pathways in the microbial metagenome from Brazilian petroleum reservoirs. 2014 , 9, e90087	69
1191	Analysis of <i>Anoxybacillus</i> genomes from the aspects of lifestyle adaptations, prophage diversity, and carbohydrate metabolism. 2014 , 9, e90549	42
1190	Comparative genome analysis of <i>Lactobacillus rhamnosus</i> clinical isolates from initial stages of dental pulp infection: identification of a new exopolysaccharide cluster. 2014 , 9, e90643	21
1189	Genomic evidence reveals the extreme diversity and wide distribution of the arsenic-related genes in Burkholderiales. 2014 , 9, e92236	31
1188	Characterization of nontypable <i>Haemophilus influenzae</i> isolates recovered from adult patients with underlying chronic lung disease reveals genotypic and phenotypic traits associated with persistent infection. 2014 , 9, e97020	24
1187	Insights from the genome annotation of <i>Elizabethkingia anophelis</i> from the malaria vector <i>Anopheles gambiae</i> . 2014 , 9, e97715	33

1186	Comparative genomic characterization of a Thailand-Myanmar isolate, MS6, of <i>Vibrio cholerae</i> O1 El Tor, which is phylogenetically related to a "US Gulf Coast" clone. 2014 , 9, e98120	13
1185	Exopolysaccharide (EPS) synthesis by <i>Oenococcus oeni</i> : from genes to phenotypes. 2014 , 9, e98898	46
1184	Resistance determinants and mobile genetic elements of an NDM-1-encoding <i>Klebsiella pneumoniae</i> strain. 2014 , 9, e99209	85
1183	Variable characteristics of bacteriocin-producing <i>Streptococcus salivarius</i> strains isolated from Malaysian subjects. 2014 , 9, e100541	22
1182	The first complete genome sequence of the class Fimbriimonadia in the phylum Armatimonadetes. 2014 , 9, e100794	8
1181	6-hydroxy-3-succinoylpyridine hydroxylase catalyzes a central step of nicotine degradation in <i>Agrobacterium tumefaciens</i> S33. 2014 , 9, e103324	15
1180	Closely related NDM-1-encoding plasmids from <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> in Taiwan. 2014 , 9, e104899	28
1179	Genome-scale reconstruction of metabolic networks of <i>Lactobacillus casei</i> ATCC 334 and 12A. 2014 , 9, e110785	24
1178	Genome annotation provides insight into carbon monoxide and hydrogen metabolism in <i>Rubrivivax gelatinosus</i> . 2014 , 9, e114551	14
1177	Complete genome sequence and comparative genomic analysis of <i>Mycobacterium massiliense</i> JCM 15300 in the <i>Mycobacterium abscessus</i> group reveal a conserved genomic island MmGI-1 related to putative lipid metabolism. 2014 , 9, e114848	15
1176	Global genome comparative analysis reveals insights of resistome and life-style adaptation of <i>Pseudomonas putida</i> strain T2-2 in oral cavity. 2014 , 2014, 930727	7
1175	Unique characteristics of the pyrrolysine system in the 7th order of methanogens: implications for the evolution of a genetic code expansion cassette. 2014 , 2014, 374146	44
1174	VibrioBase: a model for next-generation genome and annotation database development. 2014 , 2014, 569324	4
1173	Emerging strategies and integrated systems microbiology technologies for biodiscovery of marine bioactive compounds. 2014 , 12, 3516-59	54
1172	Phages of non-dairy lactococci: isolation and characterization of Φ 47, a phage infecting the grass isolate <i>Lactococcus lactis</i> ssp. <i>cremoris</i> DPC6860. 2014 , 4, 417	8
1171	Development of pVCR94 \times from <i>Vibrio cholerae</i> , a prototype for studying multidrug resistant IncA/C conjugative plasmids. 2014 , 5, 44	37
1170	Population and genomic analysis of the genus <i>Halorubrum</i> . 2014 , 5, 140	37
1169	Bacteriophages of <i>leuconostoc</i> , <i>oenococcus</i> , and <i>weissella</i> . 2014 , 5, 186	42

1168	High-Throughput Sequencing, a Versatile Weapon to Support Genome-Based Diagnosis in Infectious Diseases: Applications to Clinical Bacteriology. 2014 , 3, 258-79	19
1167	Genomics-Based Exploration of Virulence Determinants and Host-Specific Adaptations of <i>Pseudomonas syringae</i> Strains Isolated from Grasses. 2014 , 3, 121-48	11
1166	The Family Succinivibrionaceae. 2014 , 639-648	9
1165	Proteogenomics in microbiology: taking the right turn at the junction of genomics and proteomics. 2014 , 14, 2360-675	24
1164	Draft Genome Sequences of Four Strains of <i>Vibrio parahaemolyticus</i> , Three of Which Cause Early Mortality Syndrome/Acute Hepatopancreatic Necrosis Disease in Shrimp in China and Thailand. 2014 , 2,	102
1163	Draft Genome Sequence of <i>Vibrio parahaemolyticus</i> Strain M0605, Which Causes Severe Mortalities of Shrimps in Mexico. 2014 , 2,	69
1162	PATRIC, the bacterial bioinformatics database and analysis resource. 2014 , 42, D581-91	823
1161	Draft genome sequence of the extremely halophilic archaeon <i>Halococcus sediminicola</i> CBA1101 isolated from a marine sediment sample. 2014 , 18PB, 145-146	2
1160	Draft genome sequence of <i>Methanoculleus</i> sp. MH98A, a novel methanogen isolated from sub-seafloor methane hydrate deposits in Krishna Godavari basin. 2014 , 18PB, 139-140	5
1159	Draft genomic DNA sequence of strain <i>Halomonas</i> sp. FS-N4 exhibiting high catalase activity. 2014 , 18 Pt B, 119-21	1
1158	Draft Genome Sequence of <i>Methylobacterium</i> sp. Strain L2-4, a Leaf-Associated Endophytic N-Fixing Bacterium Isolated from <i>Jatropha curcas</i> L. 2014 , 2,	10
1157	Draft genome sequence of <i>Halolamina rubra</i> CBA1107(T), an agarolytic haloarchaeon isolated from solar salt. 2014 , 18 Pt B, 127-8	1
1156	Draft genome sequence of <i>Halapricum salinum</i> CBA1105(T), an extremely halophilic archaeon isolated from solar salt. 2014 , 18 Pt B, 133-4	3
1155	Permanent draft genome of the malachite-green-tolerant bacterium <i>Rhizobium</i> sp. MGL06. 2014 , 18 Pt B, 87-8	2
1154	Characterization and genome sequence of Dev2, a new T7-like bacteriophage infecting <i>Cronobacter turicensis</i> . 2014 , 159, 3013-9	6
1153	Complete Genome Sequence of <i>Pseudomonas aeruginosa</i> Strain YL84, a Quorum-Sensing Strain Isolated from Compost. 2014 , 2,	11
1152	<i>Oenococcus alcoholitolerans</i> sp. nov., a lactic acid bacteria isolated from cachaça and ethanol fermentation processes. 2014 , 106, 1259-67	18
1151	Molecular analysis of OXA-48-carrying conjugative IncL/M-like plasmids in clinical isolates of <i>Klebsiella pneumoniae</i> in Ireland. 2014 , 20, 270-4	18

1150	Whole genome sequence and comparative genomic analysis of multidrug-resistant <i>Staphylococcus capitis</i> subsp. <i>urealyticus</i> strain LNZR-1. 2014 , 6, 45		7
1149	The genomic landscape of the verrucomicrobial methanotroph <i>Methylacidiphilum fumariolicum</i> SolV. <i>BMC Genomics</i> , 2014 , 15, 914	4.5	28
1148	Comparative genomic analysis of nine <i>Sphingobium</i> strains: insights into their evolution and hexachlorocyclohexane (HCH) degradation pathways. <i>BMC Genomics</i> , 2014 , 15, 1014	4.5	55
1147	Functional phylogenomics analysis of bacteria and archaea using consistent genome annotation with UniFam. 2014 , 14, 207		14
1146	Comparative genomics of planktonic Flavobacteriaceae from the Gulf of Maine using metagenomic data. 2014 , 2, 34		14
1145	Draft Genome Sequence of <i>Clostridium perfringens</i> Strain JJC, a Highly Efficient Hydrogen Producer Isolated from Landfill Leachate Sludge. 2014 , 2,		7
1144	Comparative analysis of surface-exposed virulence factors of <i>Acinetobacter baumannii</i> . <i>BMC Genomics</i> , 2014 , 15, 1020	4.5	76
1143	Complete genome sequence of bacteriophage vB_YenP_AP5 which infects <i>Yersinia enterocolitica</i> of serotype O:3. 2014 , 11, 188		13
1142	Impact of analytic provenance in genome analysis. <i>BMC Genomics</i> , 2014 , 15 Suppl 8, S1	4.5	8
1141	Genome analysis of <i>Campylobacter jejuni</i> strains isolated from a waterborne outbreak. <i>BMC Genomics</i> , 2014 , 15, 768	4.5	27
1140	Genomic evidence for the emergence and evolution of pathogenicity and niche preferences in the genus <i>Campylobacter</i> . 2014 , 6, 2392-405		25
1139	Genome Sequence of the Quorum-Quenching <i>Rhodococcus erythropolis</i> Strain R138. 2014 , 2,		8
1138	Complete Genome Sequences of <i>Pseudomonas monteilii</i> SB3078 and SB3101, Two Benzene-, Toluene-, and Ethylbenzene-Degrading Bacteria Used for Bioaugmentation. 2014 , 2,		10
1137	Single cell genomic study of <i>Dehalococcoidetes</i> species from deep-sea sediments of the Peruvian Margin. 2014 , 8, 1831-42		59
1136	Workload characterization for MG-RAST metagenomic data analytics service in the cloud. 2014 ,		4
1135	Genomic versatility and functional variation between two dominant heterotrophic symbionts of deep-sea <i>Osedax</i> worms. 2014 , 8, 908-24		21
1134	Comparative genome-scale reconstruction of gapless metabolic networks for present and ancestral species. 2014 , 10, e1003465		59
1133	Draft Genome Sequences of Cyclodextrin-Producing Alkaliphilic <i>Bacillus</i> Strains JCM 19045, JCM 19046, and JCM 19047. 2014 , 2,		1

1132	Mutations in global regulators lead to metabolic selection during adaptation to complex environments. 2014 , 10, e1004872	39
1131	Genome and metabolic network of "Candidatus Phaeomarinobacter ectocarpi" Ec32, a new candidate genus of Alphaproteobacteria frequently associated with brown algae. 2014 , 5, 241	23
1130	Phylogenetically driven sequencing of extremely halophilic archaea reveals strategies for static and dynamic osmo-response. 2014 , 10, e1004784	95
1129	Dissemination of cephalosporin resistance genes between <i>Escherichia coli</i> strains from farm animals and humans by specific plasmid lineages. 2014 , 10, e1004776	213
1128	Draft Genome Sequence of Textile Azo Dye-Decolorizing and -Degrading <i>Pseudomonas aeruginosa</i> Strain PFK10, Isolated from the Common Effluent Treatment Plant of the Ankleshwar Industrial Area of Gujarat, India. 2014 , 2,	4
1127	Genome Sequence of <i>Bacillus cereus</i> Strain A1, an Efficient Starch-Utilizing Producer of Hydrogen. 2014 , 2,	12
1126	Whole-genome single-nucleotide-polymorphism analysis for discrimination of <i>Clostridium botulinum</i> group I strains. 2014 , 80, 2125-32	28
1125	Draft Genome Sequence of "Candidatus <i>Cronobacter colletis</i> " NCTC 14934T, a New Species in the Genus <i>Cronobacter</i> . 2014 , 2,	6
1124	Draft Genome Sequences of the Onion Center Rot Pathogen <i>Pantoea ananatis</i> PA4 and Maize Brown Stalk Rot Pathogen <i>P. ananatis</i> BD442. 2014 , 2,	6
1123	Draft Genome Sequences of Nine <i>Salmonella enterica</i> Serovar <i>Bovismorbificans</i> Isolates from Various Sources. 2014 , 2,	1
1122	Next-Generation Sequencing. 2014 , 125-145	2
1121	Evolution and comparative genomics of <i>Campylobacter jejuni</i> ST-677 clonal complex. 2014 , 6, 2424-38	14
1120	Safety of the surrogate microorganism <i>Enterococcus faecium</i> NRRL B-2354 for use in thermal process validation. 2014 , 80, 1899-909	75
1119	A scalable and accurate targeted gene assembly tool (SAT-Assembler) for next-generation sequencing data. 2014 , 10, e1003737	21
1118	Three classes of plasmid (47-63 kb) carry the type B neurotoxin gene cluster of group II <i>Clostridium botulinum</i> . 2014 , 6, 2076-87	20
1117	Palaeosymbiosis revealed by genomic fossils of <i>Wolbachia</i> in a strongyloidean nematode. 2014 , 10, e1004397	40
1116	Presence of extensive <i>Wolbachia</i> symbiont insertions discovered in the genome of its host <i>Glossina morsitans morsitans</i> . 2014 , 8, e2728	55
1115	Effect of the strain <i>Bacillus amyloliquefaciens</i> FZB42 on the microbial community in the rhizosphere of lettuce under field conditions analyzed by whole metagenome sequencing. 2014 , 5, 252	70

1114	Vertical transmission of highly similar bla CTX-M-1-harboring IncI1 plasmids in Escherichia coli with different MLST types in the poultry production pyramid. 2014 , 5, 519	58
1113	Enterobacter asburiae strain L1: complete genome and whole genome optical mapping analysis of a quorum sensing bacterium. 2014 , 14, 13913-24	14
1112	Draft Genome Sequence of Actibacterium mucosum KCTC 23349, a Marine Alphaproteobacterium with Complex Ionic Requirements Isolated from Mediterranean Seawater at Malvarrosa Beach, Valencia, Spain. 2014 , 2,	
1111	Draft Genome Sequence of the Anti-Algal Marine Actinomycete Streptomyces sp. JS01. 2014 , 2,	2
1110	First draft genome sequence of a member of the genus planomicrobium, isolated from the chandra river, India. 2014 , 2,	6
1109	The characteristics of ubiquitous and unique Leptospira strains from the collection of Russian centre for leptospirosis. 2014 , 2014, 649034	9
1108	Draft Genome Sequence of the Mannitol-Producing Strain Lactobacillus mucosae CRL573. 2014 , 2,	7
1107	Characterization and comparative analysis of antibiotic resistance plasmids isolated from a wastewater treatment plant. 2014 , 5, 558	28
1106	Hypervariable pili and flagella genes provide suitable new targets for DNA high-resolution melt-based genotyping of dairy Geobacillus spp. 2014 , 77, 1715-22	
1105	Draft Genome Sequence of Pseudoalteromonas sp. Strain NW 4327 (MTCC 11073, DSM 25418), a Pathogen of the Great Barrier Reef Sponge Rhopaloeides odorabile. 2014 , 2,	6
1104	First Complete Genome Sequence of Escherichia albertii Strain KF1, a New Potential Human Enteric Pathogen. 2014 , 2,	20
1103	Whole-Genome Shotgun Sequence of Bacillus amyloliquefaciens Strain UASWS BA1, a Bacterium Antagonistic to Plant Pathogenic Fungi. 2014 , 2,	5
1102	Draft Genome Sequence of the Toxic Bloom-Forming Cyanobacterium Aphanizomenon flos-aquae NIES-81. 2014 , 2,	7
1101	Draft Genome Sequence of Multidrug-Resistant Acinetobacter baumannii Strain MMC4, Isolated from a Patient in Tennessee. 2014 , 2,	
1100	Genome Sequence of Lactobacillus fabifermentans Strain T30PCM01, Isolated from Fermenting Grape Marc. 2014 , 2,	4
1099	Draft Genome Sequences of Two Cellulolytic Paenibacillus sp. Strains, MAEPY1 and MAEPY2, from Malaysian Landfill Leachate. 2014 , 2,	4
1098	Genome Sequences of Streptococcus thermophilus Strains MTH17CL396 and M17PTZA496 from Fontina, an Italian PDO Cheese. 2014 , 2,	17
1097	Draft Genome Sequence of Bacteroides reticulotermitis Strain JCM 10512T, Isolated from the Gut of a Termite. 2014 , 2,	2

1096	Draft Genome Sequencing of <i>Methanobrevibacter oralis</i> Strain JMR01, Isolated from the Human Intestinal Microbiota. 2014 , 2,	11
1095	Draft Genome Sequence of <i>Clostridium bifermentans</i> Strain WYM, a Promising Biohydrogen Producer Isolated from Landfill Leachate Sludge. 2014 , 2,	6
1094	Draft Genome Sequence of <i>Campylobacter coli</i> Strain IPSID-1 Isolated from a Patient with Immunoproliferative Small Intestinal Disease. 2014 , 2,	4
1093	Draft Genome Sequence of mc251, a Highly Hydrogen Peroxide-Resistant <i>Mycobacterium smegmatis</i> Mutant Strain. 2014 , 2,	6
1092	Draft genome sequences of two <i>arcobacter</i> strains isolated from human feces. 2014 , 2,	6
1091	Genome Sequence of a <i>Bacillus anthracis</i> Outbreak Strain from Zambia, 2011. 2014 , 2,	12
1090	Genome Sequences of Four Italian <i>Streptococcus thermophilus</i> Strains of Dairy Origin. 2014 , 2,	13
1089	Complete Nucleotide Sequence of pVv01, a P1-Like Plasmid Prophage of <i>Vibrio vulnificus</i> . 2014 , 2,	6
1088	Complete Genome Sequence of <i>Vibrio parahaemolyticus</i> Environmental Strain UCM-V493. 2014 , 2,	18
1087	Draft Genome Sequence of the Naphthalene Degradier <i>Herbaspirillum</i> sp. Strain RV1423. 2014 , 2,	6
1086	Draft Genome Sequence of the Antarctic Polyextremophile <i>Nesterenkonia</i> sp. Strain AN1. 2014 , 2,	2
1085	Draft Genome Sequence of <i>Paenibacillus pini</i> JCM 16418T, Isolated from the Rhizosphere of Pine Tree. 2014 , 2,	4
1084	Draft Genome Sequence of <i>Pectobacterium wasabiae</i> Strain CFIA1002. 2014 , 2,	2
1083	Draft Genome Sequence of <i>Escherichia coli</i> MS499, Isolated from the Infected Uterus of a Postpartum Cow with Metritis. 2014 , 2,	13
1082	Complete Genome Sequence for the Fusarium Head Blight Antagonist <i>Bacillus amyloliquefaciens</i> Strain TrigoCor 1448. 2014 , 2,	7
1081	Draft Genome Sequence of <i>Magnetospirillum</i> sp. Strain SO-1, a Freshwater Magnetotactic Bacterium Isolated from the Ol'khovka River, Russia. 2014 , 2,	11
1080	Improved Hybrid Genome Assemblies of Two Strains of <i>Bacteroides xylanisolvens</i> , SD_CC_1b and SD_CC_2a, Obtained Using Illumina and 454 Sequencing Technologies. 2014 , 2,	
1079	Complete Genome Sequences of Nitrofurantoin-Sensitive and -Resistant <i>Escherichia coli</i> ST540 and ST2747 Strains. 2014 , 2,	7

1078	Draft Genome Sequence of the Novel Thermoacidophilic Archaeon <i>Acidianus copahuensis</i> Strain ALE1, Isolated from the Copahue Volcanic Area in Neuquen, Argentina. 2014, 2,	12
1077	Complete Genome Sequences of Four Novel <i>Lactococcus lactis</i> Phages Distantly Related to the Rare 1706 Phage Species. 2014, 2,	5
1076	Draft Genome Sequence of Methicillin-Resistant <i>Staphylococcus aureus</i> KT/Y21, a Sequence Type 772 (ST772) Strain Isolated from a Pediatric Blood Sample in Terengganu, Malaysia. 2014, 2,	4
1075	Draft Genome Sequence of the Multidrug-Resistant <i>Escherichia coli</i> Strain LR09, Isolated from a Wastewater Treatment Plant. 2014, 2,	
1074	Draft Genome Sequences of <i>Psychrobacter</i> Strains JCM 18900, JCM 18901, JCM 18902, and JCM 18903, Isolated Preferentially from Frozen Aquatic Organisms. 2014, 2,	5
1073	Draft Genome Sequences of Six <i>Listeria monocytogenes</i> Strains Isolated from Dairy Products from a Processing Plant in Southern Italy. 2014, 2,	9
1072	Genome Sequence of <i>Burkholderia cenocepacia</i> H111, a Cystic Fibrosis Airway Isolate. 2014, 2,	25
1071	Draft Genome Sequence of <i>Lysobacter capsici</i> AZ78, a Bacterium Antagonistic to Plant-Pathogenic Oomycetes. 2014, 2,	9
1070	Draft Genome Sequence of <i>Geobacillus</i> sp. Strain FW23, Isolated from a Formation Water Sample. 2014, 2,	4
1069	Draft Genome Sequence of <i>Erwinia mallotivora</i> BT-MARDI, Causative Agent of Papaya Dieback Disease. 2014, 2,	11
1068	Draft genome sequences of three <i>arcobacter</i> strains of pig and dairy cattle manure origin. 2014, 2,	8
1067	Draft Genome Sequence of Acid-Tolerant <i>Clostridium drakei</i> SL1T, a Potential Chemical Producer through Syngas Fermentation. 2014, 2,	10
1066	Complete Genome Sequences of <i>Lactobacillus johnsonii</i> Strain N6.2 and <i>Lactobacillus reuteri</i> Strain TD1. 2014, 2,	12
1065	Draft Whole-Genome Sequence of a New Variant of <i>Vibrio cholerae</i> O1 El Tor Strain Isolated from a Cholera Patient in Russia. 2014, 2,	
1064	Draft Genome Sequence of <i>Xanthomonas arboricola</i> pv. <i>pruni</i> Strain Xap33, Causal Agent of Bacterial Spot Disease on Almond. 2014, 2,	12
1063	Draft Genome Sequence of the Nonstarter Bacteriocin-Producing Strain <i>Enterococcus mundtii</i> CRL35. 2014, 2,	5
1062	Complete Genome Sequence of <i>Staphylococcus aureus</i> XN108, an ST239-MRSA-SCCmec III Strain with Intermediate Vancomycin Resistance Isolated in Mainland China. 2014, 2,	10
1061	Draft Genome Sequence of <i>Streptococcus parauberis</i> Strain SK-417, Isolated from Diseased <i>Sebastes ventricosus</i> in Kagoshima, Japan. 2014, 2,	5

1060	Draft Genome Sequence of blaNDM-1-Positive <i>Escherichia coli</i> O25b-ST131 Clone Isolated from an Environmental Sample. 2014 , 2,	8
1059	Draft Genome Sequence of <i>Cupriavidus</i> sp. Strain SK-4, a di-ortho-Substituted Biphenyl-Utilizing Bacterium Isolated from Polychlorinated Biphenyl-Contaminated Sludge. 2014 , 2,	3
1058	Genome Sequences of Two <i>Leuconostoc pseudomesenteroides</i> Strains Isolated from Danish Dairy Starter Cultures. 2014 , 2,	5
1057	Complete Genome Sequence of <i>Winogradskyella</i> sp. Strain PG-2, a Proteorhodopsin-Containing Marine Flavobacterium. 2014 , 2,	1
1056	Draft Genome Sequence of <i>Pseudomonas</i> sp. Strain Ant30-3, a Psychrotolerant Bacterium with Biodegradative Attribute Isolated from Antarctica. 2014 , 2,	
1055	Draft Genome Sequence of the <i>Mycobacterium tuberculosis</i> Clinical Isolate C2, Belonging to the Latin American-Mediterranean Family. 2014 , 2,	2
1054	Genome Sequence of a Promising Hydrogen-Producing Facultative Anaerobic Bacterium, <i>Brevundimonas naejangsanensis</i> Strain B1. 2014 , 2,	7
1053	Draft Genome Sequence of <i>Geobacillus thermopakistaniensis</i> Strain MAS1. 2014 , 2,	13
1052	Draft Genome Sequences of <i>Geobacillus</i> sp. Strains CAMR5420 and CAMR12739. 2014 , 2,	5
1051	Genome Sequences of Strain ATCC 29281 and Pin and Northern Red Oak Isolates of <i>Lonsdalea quercina</i> subsp. <i>quercina</i> . 2014 , 2,	2
1050	Genome Sequence of meso-2,3-Butanediol-Producing Strain <i>Serratia marcescens</i> ATCC 14041. 2014 , 2,	5
1049	Complete Genome Sequences of Three Iberian <i>Brucella suis</i> Biovar 2 Strains Isolated from Wild Boars. 2014 , 2,	3
1048	Draft Genome Sequence of <i>Bacillus subtilis</i> strain KATMIRA1933. 2014 , 2,	8
1047	Draft Genome Sequences of <i>Geomicrobium</i> sp. Strains JCM 19037, JCM 19038, JCM 19039, and JCM 19055, Isolated from Aquatic Samples. 2014 , 2,	
1046	Draft Genome Sequence of <i>Enterococcus faecalis</i> MB5259. 2014 , 2,	
1045	Draft Genome Sequence of <i>Cupriavidus</i> sp. Strain SK-3, a 4-Chlorobiphenyl- and 4-Chlorobenzoic Acid-Degrading Bacterium. 2014 , 2,	2
1044	Complete Genome Sequences of Two Central European <i>Brucella suis</i> bv. 2 Haplotype 2c Strains Isolated from Wild Boars. 2014 , 2,	1
1043	Genome Sequence of " <i>Candidatus Arthromitus</i> " sp. Strain SFB-Mouse-NL, a Commensal Bacterium with a Key Role in Postnatal Maturation of Gut Immune Functions. 2014 , 2,	27

1042	Draft Genome Sequence of the Endosymbiont "Candidatus Ruthia magnifica" UCD-CM (Phylum Proteobacteria). 2014 , 2,	
1041	Draft Genome Sequence of Lutibaculum baratangense Strain AMV1T, Isolated from a Mud Volcano in Andamans, India. 2014 , 2,	2
1040	Whole-Genome Sequence of Streptococcus macedonicus Strain 33MO, Isolated from the Curd of Morlacco Cheese in the Veneto Region (Italy). 2014 , 2,	8
1039	Whole-Genome Shotgun Sequence of Arthrospira platensis Strain Paraca, a Cultivated and Edible Cyanobacterium. 2014 , 2,	11
1038	Draft Genome Sequence of Pasteurella multocida subsp. multocida B:2 Strain VTCCBAA264 Isolated from Bubalus bubalis in North India. 2014 , 2,	5
1037	Complete Genome Sequence of Bacillus anthracis HYU01, Isolated from Soil Samples in the Korean Peninsula. 2014 , 2,	3
1036	Draft Genome Sequence of a Hypersensitive Reaction-Inducing Pantoea agglomerans Strain Isolated from Olive Knots Caused by Pseudomonas savastanoi pv. savastanoi. 2014 , 2,	4
1035	Draft Genome Sequence of Microbacterium sp. Strain CH12i, Isolated from Shallow Groundwater in Cape Hallett, Antarctica. 2014 , 2,	5
1034	Closed Genome Sequence of Noninvasive Streptococcus pyogenes M/emm3 Strain STAB902. 2014 , 2,	6
1033	Draft Genome Sequence of Nonlabens ulvanivorans, an Ulvan-Degrading Bacterium. 2014 , 2,	12
1032	Draft Genome Sequence of Haloferax sp. Strain ATB1, Isolated from a Semi-Arid Region in the Brazilian Caatinga. 2014 , 2,	4
1031	Draft Genome Sequence of Falsirhodobacter sp. Strain alg1, an Alginate-Degrading Bacterium Isolated from Fermented Brown Algae. 2014 , 2,	5
1030	Draft Genome Sequence of the Pyridinediol-Fermenting Bacterium Synergistes jonesii 78-1. 2014 , 2,	1
1029	Draft Genome Sequence of Rifamycin Derivatives Producing Amycolatopsis mediterranei Strain DSM 46096/S955. 2014 , 2,	4
1028	Draft Genome Sequence of Pseudomonas sp. Strain JMM, a Sediment-Hosted Environmental Isolate. 2014 , 2,	1
1027	Complete Genome Sequence of Actinobaculum schaalii Strain CCUG 27420. 2014 , 2,	8
1026	Draft Genome Sequence of the Shellfish Bacterial Pathogen Vibrio sp. Strain B183. 2014 , 2,	
1025	First Genome Sequence of Potential Mycotoxin-Degrading Bacterium Devosia nanyangense DDB001. 2014 , 2,	3

1024	Genome Sequence of the Boron-Tolerant and -Requiring Bacterium <i>Bacillus boroniphilus</i> . 2014 , 2,	1
1023	Genome Sequence of <i>Porphyromonas gingivalis</i> Strain HG66 (DSM 28984). 2014 , 2,	11
1022	Draft Genome Sequence of the Oyster Larval Probiotic Bacterium <i>Vibrio</i> sp. Strain OY15. 2014 , 2,	1
1021	Draft Genome Sequence of <i>Thermoanaerobacterium saccharolyticum</i> Strain NTOU1, a Thermophilic Bacterium Isolated from Marine Shallow Hydrothermal Vents. 2014 , 2,	
1020	Draft Genome Sequence of <i>Cellulosimicrobium</i> sp. Strain MM, Isolated from Arsenic-Rich Microbial Mats of a Himalayan Hot Spring. 2014 , 2,	19
1019	Draft Genome Sequences of Vancomycin-Susceptible <i>Staphylococcus aureus</i> Related to Heterogeneous Vancomycin-Intermediate <i>S. aureus</i> . 2014 , 2,	2
1018	Complete Genome Sequence of a Dimethyl Sulfide-Utilizing Bacterium, <i>Acinetobacter guillouiae</i> Strain 20B (NBRC 110550). 2014 , 2,	4
1017	Draft Genome Sequence of <i>Buttiauxella agrestis</i> , Isolated from Surface Water. 2014 , 2,	3
1016	Draft Genome Sequence of <i>Raoultella planticola</i> , Isolated from River Water. 2014 , 2,	7
1015	Genome Sequences of <i>Brucella abortus</i> and <i>Brucella suis</i> Strains Isolated from Bovine in Zimbabwe. 2014 , 2,	5
1014	Draft Genome Sequence of the Polyextremophilic <i>Halorubrum</i> sp. Strain AJ67, Isolated from Hyperarsenic Lakes in the Argentinian Puna. 2014 , 2,	11
1013	Draft Genome Sequence of <i>Pseudomonas aeruginosa</i> ATCC 33988, a Bacterium Highly Adapted to Fuel-Polluted Environments. 2014 , 2,	8
1012	Draft Genome Sequence of <i>Saccharopolyspora rectivirgula</i> . 2014 , 2,	7
1011	Whole-Genome Sequences of <i>Streptococcus thermophilus</i> Strains TH1435 and TH1436, Isolated from Raw Goat Milk. 2014 , 2,	20
1010	Insight into the First Draft Genome Sequence of the Genus <i>Sediminibacillus</i> , <i>Sediminibacillus halophilus</i> Strain NSP9.3. 2014 , 2,	1
1009	Complete Genome Sequence of <i>Cellulophaga lytica</i> HI1 Using PacBio Single-Molecule Real-Time Sequencing. 2014 , 2,	4
1008	Draft genome sequence of atrazine-utilizing bacteria isolated from Indian agricultural soil. 2014 , 2,	6
1007	Genome Sequence of <i>Borrelia crocidurae</i> Strain 03-02, a Clinical Isolate from Senegal. 2014 , 2,	4

1006	Draft Genome Sequence of the Iron-Oxidizing Acidophile <i>Leptospirillum ferriphilum</i> Type Strain DSM 14647. 2014 , 2,	16
1005	Draft Genome Sequence of the Halophilic and Highly Halotolerant Gammaproteobacteria Strain MFB021. 2014 , 2,	3
1004	Draft Genome Sequences of Marine Flavobacterium <i>Nonlabens</i> Strains NR17, NR24, NR27, NR32, NR33, and Ara13. 2014 , 2,	2
1003	Draft Genome Sequence of Psychrotrophic <i>Acinetobacter</i> sp. Strain MN12 (MTCC 10786), Which Produces a Low-Temperature-Active and Alkaline-Stable Peptidase. 2014 , 2,	2
1002	Draft Genome Sequences of Marine Flavobacterium <i>Algibacter lectus</i> Strains SS8 and NR4. 2014 , 2,	3
1001	Complete Genome Sequence of <i>Streptococcus pyogenes</i> M/emm44 Strain STAB901, Isolated in a Clonal Outbreak in French Brittany. 2014 , 2,	2
1000	Draft genome sequences of two novel <i>Aeromonas</i> species recovered in association with cyanobacterial blooms. 2014 , 2,	1
999	Whole-Genome Sequencing of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar <i>Cubana</i> Strains Isolated from Agricultural Sources. 2014 , 2,	1
998	Draft Genome Sequence of <i>Cryobacterium roopkundensis</i> Strain RuGl7, Isolated from a Soil Sample in the Vicinity of Roopkund Lake, Himalayas, India. 2014 , 2,	2
997	Complete Genome Sequence of <i>Mycobacterium tuberculosis</i> Strain MtURU-001, Isolated from a Rapidly Progressing Outbreak in Uruguay. 2014 , 2,	
996	Draft Genome Sequence of <i>Lactobacillus crispatus</i> 2029. 2014 , 2,	3
995	Draft Genome Sequence of Fish Pathogenic <i>Vibrio vulnificus</i> Biotype 2. 2014 , 2,	2
994	Draft Genome Sequence of <i>Pseudomonas chlororaphis</i> YL-1, a Biocontrol Strain Suppressing Plant Microbial Pathogens. 2014 , 2,	4
993	<i>Kingella kingae</i> KK247, an Atypical Pulsed-Field Gel Electrophoresis Clone A Strain. 2014 , 2,	2
992	Draft Genome Sequence of Marine Flavobacterium <i>Jejuia pallidilutea</i> Strain 11shimoA1 and Pigmentation Mutants. 2014 , 2,	
991	Draft Genome Sequence of <i>Chryseobacterium</i> sp. Strain P1-3, a Keratinolytic Bacterium Isolated from Poultry Waste. 2014 , 2,	6
990	Whole-Genome Sequences of Six <i>Salmonella enterica</i> Serovar <i>Bovismorbificans</i> Isolates Associated with a 2011 Multistate Hummus-Borne Outbreak. 2014 , 2,	3
989	Draft Genome Sequences of Three Strains of <i>Bacteroides pyogenes</i> Isolated from a Cat and Swine. 2014 , 2,	3

988	Whole-Genome Sequencing Identifies an Atypical <i>Listeria monocytogenes</i> Strain Isolated from Pet Foods. 2014 , 2,	10
987	Draft Genome Sequence of an Aniline-Degrading Bacterium, <i>Burkholderia</i> sp. K24. 2014 , 2,	3
986	Draft Genome Sequence of the Nicotinate-Metabolizing Soil Bacterium <i>Bacillus niacini</i> DSM 2923. 2014 , 2,	5
985	Complete Genome Sequence of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> , Isolated from Human Breast Milk. 2014 , 2,	13
984	Draft Genome Sequence of <i>Pseudoalteromonas</i> sp. Strain PLSV, an Ulvan-Degrading Bacterium. 2014 , 2,	6
983	Draft Genome Sequence of <i>Bacillus subtilis</i> GXA-28, a Thermophilic Strain with High Productivity of Poly- γ -Glutamic Acid. 2014 , 2,	1
982	Draft Genome Sequence of <i>Kocuria palustris</i> PEL. 2014 , 2,	2
981	Draft Genome Sequence of <i>Pseudomonas nitroreducens</i> Strain TX1, Which Degrades Nonionic Surfactants and Estrogen-Like Alkylphenols. 2014 , 2,	10
980	Draft Genome Sequence and Annotation of the Entomopathogenic Bacterium <i>Photorhabdus luminescens</i> LN2, Which Shows Nematicidal Activity against <i>Heterorhabditis bacteriophora</i> H06 Nematodes. 2014 , 2,	1
979	Genome Sequence of the Emerging Plant Pathogen <i>Dickeya solani</i> Strain RNS 08.23.3.1A. 2014 , 2,	13
978	Draft Genome Sequence of the Versatile Alkane-Degrading Bacterium <i>Aquabacterium</i> sp. Strain NJ1. 2014 , 2,	14
977	Draft Genome Sequence of <i>Erwinia oleae</i> , a Bacterium Associated with Olive Knots Caused by <i>Pseudomonas savastanoi</i> pv. <i>savastanoi</i> . 2014 , 2,	4
976	Complete Genome Sequence of <i>Vibrio coralliilyticus</i> Strain OCN014, Isolated from a Diseased Coral at Palmyra Atoll. 2014 , 2,	12
975	Genome Sequences of Three Highly Copper-Resistant <i>Salmonella enterica</i> subsp. I Serovar Typhimurium Strains Isolated from Pigs in Denmark. 2014 , 2,	10
974	Do rumen Bacteroidetes utilize an alternative mechanism for cellulose degradation?. 2014 , 5, e01401-14	94
973	Draft Genome Sequence of <i>Tatumella</i> sp. Strain UCD-D_suzukii (Phylum Proteobacteria) Isolated from <i>Drosophila suzukii</i> Larvae. 2014 , 2,	3
972	Structural and functional diversity of free-living microorganisms in reef surface, Kra island, Thailand. <i>BMC Genomics</i> , 2014 , 15, 607	4-5 11
971	Draft Genome Sequence of <i>Pseudomonas aeruginosa</i> Strain RB, a Bacterium Capable of Synthesizing Cadmium Selenide Nanoparticles. 2014 , 2,	2

970	Streptococcus mitis strains causing severe clinical disease in cancer patients. 2014 , 20, 762-71	77
969	Genome Sequence of the Sulfite-reducing Bacterium <i>Sulfiteobacter</i> sp. Strain 2047-Infecting Lytic Phage {Phi}CB2047-B. 2014 , 2,	12
968	Draft Genome Sequence of <i>Sphingopyxis</i> sp. Strain MWB1, a Crude-Oil-Degrading Marine Bacterium. 2014 , 2,	9
967	Draft Genome Sequences of <i>Escherichia coli</i> Strains Isolated from Septic Patients. 2014 , 2,	2
966	The oxygen-independent metabolism of cyclic monoterpenes in <i>Castellaniella defragrans</i> 65Phen. 2014 , 14, 164	16
965	Characterization, sequencing and comparative genomic analysis of vB_AbaM-IME-AB2, a novel lytic bacteriophage that infects multidrug-resistant <i>Acinetobacter baumannii</i> clinical isolates. 2014 , 14, 181	43
964	Complete Genome Sequence of the Model Rhizosphere Strain <i>Azospirillum brasilense</i> Az39, Successfully Applied in Agriculture. 2014 , 2,	32
963	Genome Sequence of <i>Pseudomonas azelaica</i> HBP1, Which Catabolizes 2-Hydroxybiphenyl Fungicide. 2014 , 2,	9
962	Draft Genome Sequence of <i>Arcobacter cibarius</i> Strain LMG21996T, Isolated from Broiler Carcasses. 2014 , 2,	6
961	<i>Curtobacterium</i> sp. Genome Sequencing Underlines Plant Growth Promotion-Related Traits. 2014 , 2,	10
960	Draft Genome Sequence of <i>Deinococcus</i> sp. Strain RL Isolated from Sediments of a Hot Water Spring. 2014 , 2,	12
959	Draft Genome Sequence of <i>Clostridium manganotii</i> TR, Isolated from the Fecal Material of a Timber Rattlesnake. 2014 , 2,	
958	Draft Genome Sequence of a Psychrophilic Bacterium, <i>Sphingomonas antarcticum</i> , Isolated from the Soils of Schirmacher Oasis, Antarctica. 2014 , 2,	3
957	Whole-Genome Sequence of CMY-2 β -Lactamase-Producing <i>Salmonella enterica</i> Serovar Typhimurium Strain L-3553. 2014 , 2,	1
956	Draft Genome Sequence of <i>Hymenobacter</i> sp. Strain IS2118, Isolated from a Freshwater Lake in Schirmacher Oasis, Antarctica, Reveals Diverse Genes for Adaptation to Cold Ecosystems. 2014 , 2,	7
955	Complete Genome Sequence of <i>Bacillus subtilis</i> BAB-1, a Biocontrol Agent for Suppression of Tomato Gray Mold. 2014 , 2,	10
954	Draft Genome Sequence of <i>Amycolatopsis mediterranei</i> DSM 40773, a Tangible Antibiotic Producer. 2014 , 2,	3
953	Draft Genome Sequence of Hexachlorohexane (HCH)-Degrading <i>Sphingobium lucknowense</i> Strain F2T, Isolated from an HCH Dumpsite. 2014 , 2,	5

952	Draft Genome Sequence of <i>Brucella abortus</i> S99: Designated Antigenic Smooth Reference Strain Used in Diagnostic Tests in India. 2014 , 2,	1
951	Genome Sequence of <i>Rhodococcus opacus</i> Strain R7, a Biodegrader of Mono- and Polycyclic Aromatic Hydrocarbons. 2014 , 2,	8
950	Draft Genome Sequence of the Moderately Thermophilic Bacterium <i>Schleiferia thermophila</i> Strain Yellowstone (<i>Bacteroidetes</i>). 2014 , 2,	4
949	Draft Genome Sequence of a Sulfide-Oxidizing, Autotrophic Filamentous Anoxygenic Phototrophic Bacterium, <i>Chloroflexus</i> sp. Strain MS-G (<i>Chloroflexi</i>). 2014 , 2,	12
948	Draft Genome Sequence of Strain BF-4, a Lysinibacillus-Like <i>Bacillus</i> Isolated during an Anthrax Outbreak in Bavaria. 2014 , 2,	1
947	Draft Genome Sequence of <i>Serratia grimesii</i> Strain A2. 2014 , 2,	4
946	Draft Genome Sequence of <i>Bacillus subtilis</i> Strain D7XPN1, Isolated from Commercial Bioreactor-Degrading Food Waste. 2014 , 2,	1
945	Draft Genome Sequences of <i>Devosia</i> sp. Strain 17-2-E-8 and <i>Devosia riboflavina</i> Strain IFO13584. 2014 , 2,	14
944	Draft Genome Sequence of "Candidatus <i>Liberibacter asiaticus</i> " from California. 2014 , 2,	12
943	Draft Genome Sequences of Two Antimicrobial-Producing <i>Burkholderia</i> sp. Strains, MSh1 and MSh2, Isolated from Malaysian Tropical Peat Swamp Forest Soil. 2014 , 2,	3
942	Metagenomic assessment of the eastern oyster-associated microbiota. 2014 , 2,	27
941	Draft Genome Sequence of Gephyronic Acid Producer <i>Cystobacter violaceus</i> Strain Cb vi76. 2014 , 2,	12
940	Whole-Genome Sequence of "Candidatus <i>Liberibacter solanacearum</i> " Strain R1 from California. 2014 , 2,	7
939	Metagenome-wide association of microbial determinants of host phenotype in <i>Drosophila melanogaster</i> . 2014 , 5, e01631-14	86
938	Draft Genome Sequence of Petroleum Hydrocarbon-Degrading <i>Pseudomonas aeruginosa</i> Strain PK6, Isolated from the Saurashtra Region of Gujarat, India. 2014 , 2,	4
937	Genome Sequence of <i>Fusobacterium nucleatum</i> Strain W1481, a Possible New Subspecies Isolated from a Periodontal Pocket. 2014 , 2,	3
936	Draft Genome Sequence of <i>Clostridium</i> sp. Strain Ade.TY, a New Biohydrogen- and Biochemical-Producing Bacterium Isolated from Landfill Leachate Sludge. 2014 , 2,	1
935	Draft Genome Sequence of the Boron-Tolerant and Moderately Halotolerant Bacterium <i>Gracilibacillus boracitolerans</i> JCM 21714T. 2014 , 2,	2

934	Genome Sequence of the Probiotic Strain <i>Lactobacillus rhamnosus</i> (Formerly <i>Lactobacillus casei</i>) LOCK908. 2014, 2,	13
933	Comparative Genomic Analysis of Multidrug-Resistant <i>Pseudomonas aeruginosa</i> Clinical Isolates VRFPA06 and VRFPA08 with VRFPA07. 2014, 2,	14
932	Draft Genome Sequence of the Antitrypanosomally Active Sponge-Associated Bacterium <i>Actinokineospora</i> sp. Strain EG49. 2014, 2,	13
931	Draft Genome Sequence of <i>Xylella fastidiosa</i> Pear Leaf Scorch Strain in Taiwan. 2014, 2,	18
930	Draft Genome Sequence of <i>Bacillus thuringiensis</i> Serovar Tolworthi Strain Na205-3, an Isolate Toxic for <i>Helicoverpa armigera</i> . 2014, 2,	5
929	Whole-Genome Sequence of " <i>Candidatus Liberibacter asiaticus</i> " from Guangdong, China. 2014, 2,	35
928	Complete Genome Sequence of a Virulent <i>Streptococcus agalactiae</i> Strain, 138P, Isolated from Diseased Nile Tilapia. 2014, 2,	5
927	Draft Genome Sequence of <i>Fervidicella metallireducens</i> Strain AeBT, an Iron-Reducing Thermoanaerobe from the Great Artesian Basin. 2014, 2,	1
926	Complete Genome of the Attenuated Sparfloxacin-Resistant <i>Streptococcus agalactiae</i> Strain 138spar. 2014, 2,	3
925	Draft Genome Sequence of Insecticidal <i>Streptomyces</i> sp. Strain PCS3-D2, Isolated from Mangrove Soil in Philippines. 2014, 2,	1
924	Complete Genome Sequence of the Highly Virulent <i>Aeromonas hydrophila</i> AL09-71 Isolated from Diseased Channel Catfish in West Alabama. 2014, 2,	7
923	Complete Genome Sequence of a Moderately Virulent <i>Aeromonas hydrophila</i> Strain, pc104A, Isolated from Soil of a Catfish Pond in West Alabama. 2014, 2,	7
922	Draft Genome Sequence of a <i>Legionella pneumophila</i> Serogroup 4 Strain Causing Legionellosis. 2014, 2,	
921	Genome Sequence of Thermophilic <i>Bacillus licheniformis</i> Strain 3F-3, an Efficient Pentose-Utilizing Producer of 2,3-Butanediol. 2014, 2,	3
920	Genome Sequence of <i>Streptomyces wadayamensis</i> Strain A23, an Endophytic Actinobacterium from <i>Citrus reticulata</i> . 2014, 2,	9
919	Draft Genome Sequence of <i>Bacillus amyloliquefaciens</i> B-1895. 2014, 2,	13
918	Draft Genome Sequence of the Rifamycin Producer <i>Amycolatopsis rifamycinica</i> DSM 46095. 2014, 2,	7
917	Draft Genome Sequence of the Alga-Aggregating Bacterium <i>Bacillus</i> sp. Strain RP1137. 2014, 2,	

916	Complete Genome Sequence of the <i>Pseudomonas aeruginosa</i> Bacteriophage phiBB-PAA2. 2014 , 2,	4
915	Draft Genome Sequence of the Alkaliphilic and Xylanolytic <i>Paenibacillus</i> sp. Strain JCM 10914, Isolated from the Gut of a Soil-Feeding Termite. 2014 , 2,	3
914	Draft Genome Sequence of a Human-Associated Isolate of <i>Methanobrevibacter arboriphilicus</i> , the Lowest-G+C-Content Archaeon. 2014 , 2,	11
913	Draft Genome Sequence of <i>Lactobacillus rhamnosus</i> 2166. 2014 , 2,	
912	Draft Genome Sequence of <i>Bacillus thuringiensis</i> Strain BrMgv02-JM63, a Chitinolytic Bacterium Isolated from Oil-Contaminated Mangrove Soil in Brazil. 2014 , 2,	4
911	Genome Sequence of <i>Streptomyces exfoliatus</i> DSMZ 41693, a Source of Poly(3-Hydroxyalkanoate)-Degrading Enzymes. 2014 , 2,	4
910	Comparison of widely used <i>Listeria monocytogenes</i> strains EGD, 10403S, and EGD-e highlights genomic variations underlying differences in pathogenicity. 2014 , 5, e00969-14	140
909	Genome Sequence of <i>Sporolactobacillus terrae</i> DSM 11697, the Type Strain of the Species. 2014 , 2,	3
908	Genome Sequence of <i>Mycobacterium tuberculosis</i> C2, a Cerebrospinal Fluid Clinical Isolate from Central India. 2014 , 2,	1
907	Genome Sequence of <i>Bacillus anthracis</i> STI, a Sterne-Like Georgian/Soviet Vaccine Strain. 2014 , 2,	5
906	Draft Genome Sequence of <i>Clostridium scatologenes</i> ATCC 25775, a Chemolithoautotrophic Acetogenic Bacterium Producing 3-Methylindole and 4-Methylphenol. 2014 , 2,	5
905	Genome Sequence of <i>Bacillus amyloliquefaciens</i> GB03, an Active Ingredient of the First Commercial Biological Control Product. 2014 , 2,	36
904	Draft Genome Sequence of <i>Pseudomonas</i> sp. Strain 2-92, a Biological Control Strain Isolated from a Field Plot Under Long-Term Mineral Fertilization. 2014 , 2,	1
903	Draft Genome Sequence of <i>Bacillus subtilis</i> Strain NKYL29, an Antimicrobial-Peptide-Producing Strain from Soil. 2014 , 2,	
902	Draft Genome Sequence of <i>Escherichia coli</i> Strain VKPM B-10182, Producing the Enzyme for Synthesis of Cephalosporin Acids. 2014 , 2,	
901	Draft Genome Sequences of Two Ulvan-Degrading Isolates, Strains LTR and LOR, That Belong to the <i>Alteromonas</i> Genus. 2014 , 2,	8
900	Complete Genome Sequence of Highly Adherent <i>Pseudomonas aeruginosa</i> Small-Colony Variant SCV20265. 2014 , 2,	13
899	Draft Genome Sequence of a Moderately Halophilic <i>Bacillus megaterium</i> Strain, MSP20.1, Isolated from a Saltern of the Little Rann of Kutch, India. 2014 , 2,	6

898	Draft Genome Sequence of the <i>Gluconobacter oxydans</i> Strain DSM 2003, an Important Biocatalyst for Industrial Use. 2014 , 2,	2
897	Draft Genome Sequence of <i>Rhizobium rhizogenes</i> Strain ATCC 15834. 2014 , 2,	10
896	Draft Genome Sequence of <i>Pantoea ananatis</i> Strain LMG 2665T, a Bacterial Pathogen of Pineapple Fruitlets. 2014 , 2,	9
895	Draft Genome Sequence of Methicillin-Resistant <i>Staphylococcus epidermidis</i> Strain ET-024, Isolated from an Endotracheal Tube Biofilm of a Mechanically Ventilated Patient. 2014 , 2,	4
894	Draft Genome Sequence of Petroleum Oil-Degrading Marine Bacterium <i>Pseudomonas taeanensis</i> Strain MS-3, Isolated from a Crude Oil-Contaminated Seashore. 2014 , 2,	4
893	Draft Genome Sequence of <i>Corynebacterium ulcerans</i> FRC58, Isolated from the Bronchitic Aspiration of a Patient in France. 2014 , 2,	5
892	Complete Genome Sequence of <i>Hyphomicrobium nitratorans</i> Strain NL23, a Denitrifying Bacterium Isolated from Biofilm of a Methanol-Fed Denitrification System Treating Seawater at the Montreal Biodome. 2014 , 2,	11
891	Genome Sequence of <i>Marteella</i> sp. Strain AD-3, a Moderately Halophilic Polycyclic Aromatic Hydrocarbon-Degrading Bacterium. 2014 , 2,	7
890	Genome Sequence of SCB34, a Sequence Type 131 Multidrug-Resistant <i>Escherichia coli</i> Isolate Causing Neonatal Early-Onset Sepsis. 2014 , 2,	5
889	Genome Sequence of <i>Streptomyces olindensis</i> DAUFPE 5622, Producer of the Antitumoral Anthracycline Cosmomylin D. 2014 , 2,	5
888	Draft Genome Sequence of <i>Stenotrophomonas maltophilia</i> SeITE02, a Gammaproteobacterium Isolated from Selenite-Contaminated Mining Soil. 2014 , 2,	4
887	Cryptic ecology among host generalist <i>Campylobacter jejuni</i> in domestic animals. 2014 , 23, 2442-51	80
886	<i>Youngiibacter fragilis</i> gen. nov., sp. nov., isolated from natural gas production-water and reclassification of <i>Acetivibrio multivorans</i> as <i>Youngiibacter multivorans</i> comb. nov. 2014 , 64, 198-205	12
885	Whole-genome sequence analysis of the naturally competent <i>Acinetobacter baumannii</i> clinical isolate A118. 2014 , 6, 2235-9	32
884	Draft Genome Sequence of an Extreme Haloarchaeon 3A1-DGR Isolated from a Saltern Crystallizer of the Little Rann of Kutch, India. 2014 , 54, 471-3	2
883	Characterization of pFOX-7a, a conjugative IncL/M plasmid encoding the FOX-7 AmpC-type β -lactamase, involved in a large outbreak in a neonatal intensive care unit. 2014 , 69, 2620-4	11
882	Fluoroacetate biosynthesis from the marine-derived bacterium <i>Streptomyces xinghaiensis</i> NRRL B-24674. 2014 , 12, 4828-31	39
881	Revolutionizing Prokaryotic Systematics Through Next-Generation Sequencing. 2014 , 75-101	6

880	Genome Sequence of the Plant Endophyte <i>Bacillus pumilus</i> INR7, Triggering Induced Systemic Resistance in Field Crops. 2014 , 2,	18
879	A unique megaplasmid contributes to stress tolerance and pathogenicity of an emergent <i>Salmonella enterica</i> serovar Infantis strain. 2014 , 16, 977-94	87
878	<i>Halomonas sulfidaeris</i> -dominated microbial community inhabits a 1.8 km-deep subsurface Cambrian Sandstone reservoir. 2014 , 16, 1695-708	46
877	Strategy for genome sequencing analysis and assembly for comparative genomics of <i>Pseudomonas</i> genomes. 2014 , 1149, 565-77	3
876	Draft Genome Sequence of <i>Nitrocola</i> sp. Strain A-D6, an Arsenic-Resistant Gammaproteobacterium Isolated from a Salt Flat. 2014 , 2,	5
875	The gill chamber epibiosis of deep-sea shrimp <i>Rimicaris exoculata</i> : an in-depth metagenomic investigation and discovery of Zetaproteobacteria. 2014 , 16, 2723-38	41
874	Pathways and substrate-specific regulation of amino acid degradation in <i>Phaeobacter inhibens</i> DSM 17395 (archetype of the marine <i>Roseobacter</i> clade). 2014 , 16, 218-38	24
873	Tolerance of a phage element by <i>Streptococcus pneumoniae</i> leads to a fitness defect during colonization. 2014 , 196, 2670-80	19
872	Complete nucleotide sequence of a conjugative IncF plasmid from an <i>Escherichia coli</i> isolate of equine origin containing blaCMY-2 within a novel genetic context. 2014 , 352, 123-7	8
871	Draft genome sequence of <i>Sphingobium</i> sp. strain ba1, resistant to kanamycin and nickel ions. 2014 , 361, 8-9	11
870	Genome Sequence of <i>Bacillus thuringiensis</i> subsp. <i>kurstaki</i> Strain HD-1. 2014 , 2,	7
869	Draft Genome Sequence of <i>Aeromonas hydrophila</i> Strain Ae34, Isolated from a Septicemic and Moribund Koi Carp (<i>Cyprinus carpio koi</i>), a Freshwater Aquarium Fish. 2014 , 2,	8
868	Disruption of a methyltransferase gene in actinomycin G gene cluster in <i>Streptomyces iakyrus</i> increases the production of phenazinomycin. 2014 , 352, 62-8	6
867	ARG-ANNOT, a new bioinformatic tool to discover antibiotic resistance genes in bacterial genomes. 2014 , 58, 212-20	752
866	Draft Genome Sequence of a Deep-Sea Bacterium, <i>Bacillus niacini</i> Strain JAM F8, Involved in the Degradation of Glycosaminoglycans. 2014 , 2,	7
865	Complete Genome Sequences of Beijing and Manila Family Strains of <i>Mycobacterium tuberculosis</i> . 2014 , 2,	4
864	Complete Genome Sequence of the Attenuated Novobiocin-Resistant <i>Streptococcus iniae</i> Vaccine Strain ISNO. 2014 , 2,	1
863	Complete Genome Sequence of a Virulent Strain, <i>Streptococcus iniae</i> ISET0901, Isolated from Diseased Tilapia. 2014 , 2,	3

862	Acetic acid bacteria genomes reveal functional traits for adaptation to life in insect guts. 2014 , 6, 912-20	53
861	Genome Sequence of the Octopine-Type <i>Agrobacterium tumefaciens</i> Strain Ach5. 2014 , 2,	18
860	Comparative genomics of closely related <i>Salmonella enterica</i> serovar Typhi strains reveals genome dynamics and the acquisition of novel pathogenic elements. <i>BMC Genomics</i> , 2014 , 15, 1007	4-5 15
859	Construction of a dairy microbial genome catalog opens new perspectives for the metagenomic analysis of dairy fermented products. <i>BMC Genomics</i> , 2014 , 15, 1101	4-5 51
858	High resolution assembly and characterization of genomes of Canadian isolates of <i>Salmonella</i> Enteritidis. <i>BMC Genomics</i> , 2014 , 15, 713	4-5 8
857	Complete genome determination and analysis of <i>Acholeplasma oculi</i> strain 19L, highlighting the loss of basic genetic features in the <i>Acholeplasmataceae</i> . <i>BMC Genomics</i> , 2014 , 15, 931	4-5 5
856	From microbial gene essentiality to novel antimicrobial drug targets. <i>BMC Genomics</i> , 2014 , 15, 958	4-5 39
855	Genome sequence and phenotypic analysis of a first German <i>Francisella</i> sp. isolate (W12-1067) not belonging to the species <i>Francisella tularensis</i> . 2014 , 14, 169	22
854	Comparative analysis of <i>Klebsiella pneumoniae</i> genomes identifies a phospholipase D family protein as a novel virulence factor. 2014 , 12, 41	87
853	Differences in carbon source utilisation distinguish <i>Campylobacter jejuni</i> from <i>Campylobacter coli</i> . 2014 , 14, 262	19
852	Investigation of a new acetogen isolated from an enrichment of the tammar wallaby forestomach. 2014 , 14, 314	22
851	Genome sequencing and genomic characterization of a tigecycline-resistant <i>Klebsiella pneumoniae</i> strain isolated from the bile samples of a cholangiocarcinoma patient. 2014 , 6, 40	10
850	Nonclinical and clinical <i>Enterococcus faecium</i> strains, but not <i>Enterococcus faecalis</i> strains, have distinct structural and functional genomic features. 2014 , 80, 154-65	40
849	Draft Genome Sequences of Two Genetic Variant Strains of <i>Edwardsiella piscicida</i> , JF1305 and RSB1309, Isolated from Olive Flounder (<i>Paralichthys olivaceus</i>) and Red Sea Bream (<i>Pagrus major</i>) Cultured in Japan, Respectively. 2014 , 2,	8
848	Insight into the Draft Genome Sequence of Human Isolate <i>Lactobacillus rhamnosus</i> LR231, a Bacterium with Probiotic Potential. 2014 , 2,	2
847	Effect of <i>sypQ</i> gene on poly-N-acetylglucosamine biosynthesis in <i>Vibrio parahaemolyticus</i> and its role in infection process. 2014 , 24, 351-8	13
846	Contribution of the highly conserved EaeH surface protein to enterotoxigenic <i>Escherichia coli</i> pathogenesis. 2014 , 82, 3657-66	25
845	Reconstruction of Metabolic Network from Genome Information and its Structural and Functional Analysis. 2014 , 113-131	

- 844 Single-cell genomics reveals metabolic strategies for microbial growth and survival in an oligotrophic aquifer. **2014**, 160, 362-72 10
- 843 The complete nucleotide sequence of the carbapenem resistance-conferring conjugative plasmid pLD209 from a *Pseudomonas putida* clinical strain reveals a chimeric design formed by modules derived from both environmental and clinical bacteria. **2014**, 58, 1816-21 9
- 842 Phylogenomic and MALDI-TOF MS analysis of *Streptococcus sinensis* HKU4T reveals a distinct phylogenetic clade in the genus *Streptococcus*. **2014**, 6, 2930-43 14
- 841 Complete Genome Sequence of *Vibrio anguillarum* Phage CHOED Successfully Used for Phage Therapy in Aquaculture. **2014**, 2, 6
- 840 Insights into organohalide respiration and the versatile catabolism of *Sulfurospirillum multivorans* gained from comparative genomics and physiological studies. **2014**, 16, 3562-80 66
- 839 Genome sequence of *Candidatus Riesia pediculischaeffi*, endosymbiont of chimpanzee lice, and genomic comparison of recently acquired endosymbionts from human and chimpanzee lice. **2014**, 4, 2189-95 19
- 838 SIMAP--the database of all-against-all protein sequence similarities and annotations with new interfaces and increased coverage. **2014**, 42, D279-84 15
- 837 PGP: parallel prokaryotic proteogenomics pipeline for MPI clusters, high-throughput batch clusters and multicore workstations. **2014**, 30, 1469-70 19
- 836 Draft Genome Sequence of *trh+* *Vibrio parahaemolyticus* VP-49, Isolated from Seafood Harvested along the Mangalore Coast, India. **2014**, 2, 6
- 835 Genome sequence of *Mycobacterium aromaticivorans* JS19b1(T), a novel isolate from Hawaiian soil. **2014**, 186, 137-8 10
- 834 Community-integrated omics links dominance of a microbial generalist to fine-tuned resource usage. **2014**, 5, 5603 56
- 833 In vivo function and comparative genomic analyses of the *Drosophila* gut microbiota identify candidate symbiosis factors. **2014**, 5, 576 51
- 832 Draft Genome Sequence of *Lactobacillus plantarum* CMPG5300, a Human Vaginal Isolate. **2014**, 2, 12
- 831 Draft Genome Sequence of *Lactobacillus plantarum* wikim18, Isolated from Korean Kimchi. **2014**, 2, 3
- 830 Draft Genome Sequence of *Lactobacillus plantarum* 2165. **2014**, 2, 3
- 829 Whole genome sequencing and analysis of plant growth promoting bacteria isolated from the rhizosphere of plantation crops coconut, cocoa and arecanut. **2014**, 9, e104259 58
- 828 Draft Genome Sequence of Urease-Producing *Sporosarcina pasteurii* with Potential Application in Biocement Production. **2014**, 2, 6
- 827 Fusobase: an online *Fusobacterium* comparative genomic analysis platform. **2014**, 2014, 5

826	Identification of a Highly Efficient Aerobic Denitrifying Bacterium in SBR and Denitrification Optimization. 2014 , 955-959, 376-382	3
825	Genomic analysis of three African strains of <i>Bacillus anthracis</i> demonstrates that they are part of the clonal expansion of an exclusively pathogenic bacterium. 2014 , 2, 161-9	12
824	Draft Genome Sequence of Root-Colonizing Bacterium <i>Bacillus</i> sp. Strain PTS-394. 2014 , 2,	4
823	Genome Sequencing of a Mung Bean Plant Growth Promoting Strain of <i>P. aeruginosa</i> with Biocontrol Ability. 2014 , 2014, 123058	11
822	Draft genome sequences of two <i>Bacillus thuringiensis</i> strains and characterization of a putative 41.9-kDa insecticidal toxin. 2014 , 6, 1490-504	21
821	The Ellis Island Effect: A novel mobile element in a multi-drug resistant clinical isolate includes a mosaic of resistance genes from Gram-positive bacteria. 2014 , 4, e29801	10
820	Small but powerful, the primary endosymbiont of moss bugs, <i>Candidatus Evansia muelleri</i> , holds a reduced genome with large biosynthetic capabilities. 2014 , 6, 1875-93	24
819	Draft Genome Sequence of Enterotoxigenic <i>Escherichia coli</i> Strain W25K. 2014 , 2,	18
818	Draft Genome Sequence of the Aromatic Hydrocarbon-Degrading Bacterium <i>Sphingobium</i> sp. Strain Ant17, Isolated from Antarctic Soil. 2014 , 2,	5
817	Genome Sequence of <i>Lactobacillus plantarum</i> EGD-AQ4, Isolated from Fermented Product of Northeast India. 2014 , 2,	3
816	Comparative genomics of <i>Lactobacillus crispatus</i> suggests novel mechanisms for the competitive exclusion of <i>Gardnerella vaginalis</i> . <i>BMC Genomics</i> , 2014 , 15, 1070	4-5 74
815	Gene clusters of <i>Hafnia alvei</i> strain FB1 important in survival and pathogenesis: a draft genome perspective. 2014 , 6, 29	10
814	A draft genome of <i>Escherichia coli</i> sequence type 127 strain 2009-46. 2014 , 6, 32	7
813	The genome of <i>Clostridium difficile</i> 5.3. 2014 , 6, 4	13
812	StaphyloBase: a specialized genomic resource for the staphylococcal research community. 2014 , 2014, bau010	3
811	Draft genome sequence of <i>Rhodospirillum rubrum</i> strain JA643T with special reference to hopanoid biosynthesis. 2014 , 21, 639-47	14
810	Comparative genomic analysis and virulence differences in closely related <i>Salmonella enterica</i> serotype Heidelberg isolates from humans, retail meats, and animals. 2014 , 6, 1046-68	91
809	<i>Synechococcus</i> : 3 billion years of global dominance. 2014 , 23, 5538-51	68

808	Purification and characterization of phosphonoglycans from <i>Glycomyces</i> sp. strain NRRL B-16210 and <i>Stackebrandtia nassauensis</i> NRRL B-16338. 2014 , 196, 1768-79		14
807	Interspecies systems biology uncovers metabolites affecting <i>C. elegans</i> gene expression and life history traits. 2014 , 156, 759-70		111
806	Draft genome of formaldehyde-degrading strain, <i>Pseudomonas monteilii</i> IOFA19. 2014 , 15, 1-2		4
805	Draft genome sequence of <i>Bacillus firmus</i> DS1. 2014 , 177, 20-1		8
804	Genomic insights into the taxonomic status of the three subspecies of <i>Bacillus subtilis</i> . 2014 , 37, 95-9		19
803	Genome sequencing and annotation of <i>Amycolatopsis vancoresmycina</i> strain DSM 44592(T). 2014 , 2, 16-7		4
802	Genome sequencing, annotation of <i>Citrobacter freundii</i> strain GTC 09479. 2014 , 2, 40-1		3
801	Complete genome of a new Firmicutes species belonging to the dominant human colonic microbiota (' <i>Ruminococcus bicirculans</i> ') reveals two chromosomes and a selective capacity to utilize plant glucans. 2014 , 16, 2879-90		40
800	Genome sequencing of a single cell of the widely distributed marine subsurface Dehalococcoidia, phylum Chloroflexi. 2014 , 8, 383-97		106
799	pIMP-PH114 carrying bla IMP-4 in a <i>Klebsiella pneumoniae</i> strain is closely related to other multidrug-resistant IncA/C2 plasmids. 2014 , 68, 227-32		25
798	Comparative genomics of enterohemorrhagic <i>Escherichia coli</i> O145:H28 demonstrates a common evolutionary lineage with <i>Escherichia coli</i> O157:H7. <i>BMC Genomics</i> , 2014 , 15, 17	4-5	58
797	I7EP: an integrated toolkit for exploration of microbial pan-genomes. <i>BMC Genomics</i> , 2014 , 15, 8	4-5	77
796	Draft Genome Sequence of the Methyl Parathion (Pesticide) Degrading Bacterium <i>Pseudomonas</i> spp. MR3. 2014 , 54, 120-1		6
795	Draft Genome Sequence of the Endophytic Bacterium <i>Enterobacter</i> spp. MR1, Isolated from Drought Tolerant Plant (<i>Butea monosperma</i>). 2014 , 54, 118-9		4
794	Phenotypic and genomic characterization of the Antarctic bacterium <i>Gillisia</i> sp. CAL575, a producer of antimicrobial compounds. 2014 , 18, 35-49		19
793	Genome Sequence of the Thermophilic Cyanobacterium <i>Thermosynechococcus</i> sp. Strain NK55a. 2014 , 2,		12
792	Prokka: rapid prokaryotic genome annotation. 2014 , 30, 2068-9		6439
791	Genome Sequence of the AcrySTALLIFEROUS <i>Bacillus thuringiensis</i> Serovar Israelensis Strain 4Q7, Widely Used as a Recombination Host. 2014 , 2,		7

790	Purification and biochemical characterization of halophilic, alkalithermophilic protease AbCP from <i>Alkalibacillus</i> sp. NM-Fa4. 2014 , 105, 74-81	26
789	Identification of bacteriophages for biocontrol of the kiwifruit canker phytopathogen <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> . 2014 , 80, 2216-28	58
788	Comparative analysis of the full genome of <i>Helicobacter pylori</i> isolate Sahul64 identifies genes of high divergence. 2014 , 196, 1073-83	22
787	Mining locus tags in PubMed Central to improve microbial gene annotation. 2014 , 15, 43	
786	Comparative genomics of unintegrated <i>Campylobacter coli</i> clades 2 and 3. <i>BMC Genomics</i> , 2014 , 15, 129	4-5 31
785	Genome sequence and comparative analysis of a <i>Vibrio cholerae</i> O139 strain E306 isolated from a cholera case in China. 2014 , 6, 3	8
784	Close relationship of a novel Flavobacteriaceae α -amylase with archaeal α -amylases and good potentials for industrial applications. 2014 , 7, 18	26
783	Leveraging big data bioinformatics approaches to extract knowledge from public omics data.. 2022 , 1-23	
782	Expression and functional analysis of the type III secretion system effector repertoire of the xylem pathogen on cucurbits.. 2022 ,	0
781	sp. nov., an actinomycete isolated from compost of (Lam.).. 2022 , 72,	0
780	gen. nov., sp. nov., isolated from larvae of mealworm L., and a proposal to transfer Liu . 2016 to a new genus as comb. nov.. 2022 , 72,	0
779	Construction and Analysis of the Complete Genome Sequence of Leprosy Agent <i>Mycobacterium lepromatosis</i> .. 2022 , e0169221	0
778	Genomic and Experimental Analysis of the Biostimulant and Antagonistic Properties of Phytopathogens of and .. 2022 , 10,	1
777	Optimizing the Parametrization of Homologue Classification in the Pan-Genome Computation for a Bacterial Species: Case Study <i>Streptococcus pyogenes</i> .. 2022 , 2449, 299-324	0
776	Evolutionary Genome Mining for the Discovery and Engineering of Natural Product Biosynthesis.. 2022 , 2489, 129-155	
775	Cyanobacterial Genome Sequencing, Annotation, and Bioinformatics.. 2022 , 2489, 269-287	
774	Whole Genome Sequence Analysis of a Novel <i>Apilactobacillus</i> Species from Giant Honeybee (<i>Apis dorsata</i>) Gut Reveals Occurrence of Genetic Elements Coding Prebiotic and Probiotic Traits. 2022 , 10, 904	0
773	Zoonotic Transmission of to Caretakers From Sick Pen Calves Carrying a Mixed Population of Strains With and Without Guillain Barré Syndrome-Associated Lipooligosaccharide Loci.. 2022 , 13, 800269	0

772	Exploration of genomic and functional features of chitinolytic bacterium RC1830, isolated from Chilika Lake, India.. 2022 , 12, 120	
771	Characterization of the Upper Respiratory Bacterial Microbiome in Critically Ill COVID-19 Patients. 2022 , 10, 982	0
770	sp. nov., a novel hexadecane-degrading species isolated from plastic waste.. 2022 , 72,	0
769	A Highly Unstable and Elusive Plasmid That Encodes the Type III Secretion System Is Necessary for Full Virulence in the Marine Fish Pathogen subsp. ... 2022 , 23,	1
768	gen. nov. sp. nov., a neutrophilic, microaerobic iron- and thiosulfate-oxidizing bacterium isolated from iron-rich wetland sediment.. 2022 , 72,	0
767	Genetic Evidences of Biosurfactant Production in Two Strains MB415 and MB418 Isolated From Oil Contaminated Soil.. 2022 , 10, 855762	
766	Whole genome sequencing and phylogenomic analyses of a novel glufosinate-tolerant species.. 2022 , 12, 123	0
765	Transferability of ESBL-encoding IncN and IncI1 plasmids among field strains of different Salmonella serovars and Escherichia coli.. 2022 ,	0
764	Soil-derived sp. GMR22 producing antibiofilm activity against : bioassay, untargeted LC-HRMS, and gene cluster analysis.. 2022 , 8, e09333	0
763	Genomic and Physiological Characterization of Metabacillus flavus sp. nov., a Novel Carotenoid-Producing Bacilli Isolated from Korean Marine Mud. 2022 , 10, 979	1
762	Microbiome "Inception": an Intestinal Cestode Shapes a Hierarchy of Microbial Communities Nested within the Host.. 2022 , e0067922	1
761	Flavobacterium hungaricum sp. nov. a novel soil inhabitant, cellulolytic bacterium isolated from plough field.. 2022 , 204, 301	
760	Opportunities and challenges of using metagenomic data to bring uncultured microbes into cultivation.. 2022 , 10, 76	5
759	Polyphasic Analysis Reveals Potential Petroleum Hydrocarbon Degradation and Biosurfactant Production by Rare Biosphere Thermophilic Bacteria From Deception Island, an Active Antarctic Volcano. 2022 , 13,	0
758	sp. nov., isolated from the stem of in north-west China.. 2022 , 72,	0
757	New Beta-lactamases in Candidate Phyla Radiation: Owing Pleiotropic Enzymes Is a Smart Paradigm for Microorganisms with a Reduced Genome. 2022 , 23, 5446	0
756	The Broad Host Range Plant Pathogen Dickeya dianthicola Shows a High Genetic Diversity. 2022 , 10, 1024	
755	Identification of a phage-derived depolymerase specific for KL47 capsule of Klebsiella pneumoniae and its therapeutic potential in mice.. 2022 ,	2

754	sp. AC04842: Genomic Insights and Functional Expression of Its Latex Clearing Protein Genes (and) When Cultivated With Natural and Vulcanized Rubber as the Sole Carbon Source.. 2022 , 13, 854427	0
753	Emerging resistance to ceftriaxone treatment owing to different ampD mutations in <i>Enterobacter roggenkampii</i> .. 2022 , 105301	
752	KPC-3-, GES-5-, and VIM-1-Producing Enterobacterales Isolated from Urban Ponds. 2022 , 19, 5848	0
751	Comparative Genomic Analysis Revealed Distinct Molecular Components and Organization of CO ₂ -Concentrating Mechanism in Thermophilic Cyanobacteria. 2022 , 13,	2
750	Cryptic Genes for Interbacterial Antagonism Distinguish Species Infecting Blacklegged Ticks From Other Pathogens.. 2022 , 12, 880813	0
749	Physiological and genomic characterisation of <i>Luteimonas fraxinea</i> sp. nov., a bacterial species associated with trees tolerant to ash dieback. 2022 , 126333	1
748	Complete Genome Sequence of <i>Enterobacter</i> Phage vB_EcRAM-01, a New against the <i>Enterobacter cloacae</i> Complex.. 2022 , e0004522	
747	Development of Phage Cocktails to Treat <i>E. coli</i> Catheter-Associated Urinary Tract Infection and Associated Biofilms. 2022 , 13,	2
746	Cold-adaptive traits identified by comparative genomic analysis of a lipase-producing <i>Pseudomonas</i> sp. HS6 isolated from snow-covered soil of Sikkim Himalaya and molecular simulation of lipase for wide substrate specificity.. 2022 ,	
745	sp. nov., isolated from Yongle Blue Hole in the South China Sea.. 2022 , 72,	1
744	<i>Panacibacter microcystis</i> sp. nov., isolated from a eutrophic reservoir during the <i>Microcystis</i> bloom period.. 2022 , 204, 291	1
743	gen. nov., sp. nov., a member of the family isolated from seawater of the Indian Ocean and intertidal zone.. 2022 , 72,	0
742	subsp. subsp. nov., a lactic acid bacterium isolated from naturally fermented dairy product.. 2022 , 72,	0
741	Antimicrobial Resistance and Comparative Genomic Analysis of <i>Elizabethkingia anophelis</i> subsp. <i>endophytica</i> Isolated from Raw Milk. 2022 , 11, 648	
740	A putatively new family of alphaproteobacterial chloromethane degraders from a deciduous forest soil revealed by stable isotope probing and metagenomics.. 2022 , 17, 24	
739	Genomic analysis of <i>Thalassospira</i> sp. SW-3-3 reveals its genetic potential for phthalate pollution remediation.. 2022 , 63, 100953	
738	Nitrogen fixation and other biogeochemically important features of Atacama Desert giant horsetail plant microbiomes inferred from metagenomic contig analysis.. 2022 ,	
737	Description of the two novel species of the genus <i>Helicobacter</i> : <i>Helicobacter anatolicus</i> sp. nov., and <i>Helicobacter kayseriensis</i> sp. nov., isolated from feces of urban wild birds.. 2022 , 45, 126326	1

- 736 Emergence of bla, bla, bla and bla carrying plasmids in Raoultella spp. in the environment.. **2022**, 306, 119437 2
- 735 Draft genome sequence of Bacillus sp. strain FSQ1, a biological control agent against white mold in common bean (*Phaseolus vulgaris* L.). **2022**, 100138
- 734 Description and characterization of three endophytic from the halophyte gen. nov., sp. nov. sp. nov. and sp. nov.. **2022**, 72, 0
- 733 Genomic Features of High-Level Gentamicin-Resistant Enterococcus faecalis Strain LREF-1 from India.. **2022**, e0118721
- 732 Genome mining of Burkholderia ambifaria strain T16, a rhizobacterium able to produce antimicrobial compounds and degrade the mycotoxin fusaric acid.. **2022**, 38, 114 0
- 731 The Notable Achievements and the Prospects of Bacterial Pathogen Genomics. **2022**, 10, 1040 1
- 730 PrrT/A, a Pseudomonas aeruginosa Bacterial Encoded Toxin-Antitoxin System Involved in Prophage Regulation and Biofilm Formation.. **2022**, e0118222 1
- 729 Impacts of restriction-modification systems on pan-epigenome dynamics and genome plasticity.. **2022**, 8,
- 728 Oceanisphaera pacifica sp. nov., isolated from the intestine of Trichiurus japonicus.. **2022**, 204, 338
- 727 A genomic overview including polyphasic taxonomy of Thalassoroseus pseudoceratinae gen. nov., sp. nov. isolated from a marine sponge, Pseudoceratina sp.. **2022**,
- 726 Comprehensive genome analysis of Lentzea reveals repertoire of polymer-degrading enzymes and bioactive compounds with clinical relevance.. **2022**, 12, 8409 1
- 725 Genomic, morphological, and biochemical analyses of a multi-metal resistant but multi-drug susceptible strain of Bordetella petrii from hospital soil.. **2022**, 12, 8439 1
- 724 Full Issue PDF.. **2022**, 35, 439-508
- 723 sp. nov., isolated from rhizosphere of plant with antioxidative potential.. **2022**, 72, 0
- 722 sp. nov., a methylotrophic methanogen isolated from sediment of the East China Sea.. **2022**, 72, 0
- 721 Genome mining reveals polysaccharide-degrading potential and new antimicrobial gene clusters of novel intestinal bacterium Paenibacillus jilinensis sp. nov.. *BMC Genomics*, **2022**, 23, 380 4.5 1
- 720 Mircubactin B rescues the lethal effect of cell wall biosynthesis mutations in Bacillus subtilis.
- 719 Genetic Resistance Determinants in Clinical Acinetobacter pittii Genomes. **2022**, 11, 676 0

718	Health-Promoting Nature of <i>Lactococcus lactis</i> IBB109 and <i>Lactococcus lactis</i> IBB417 Strains Exhibiting Proliferation Inhibition and Stimulation of Interleukin-18 Expression in Colorectal Cancer Cells. 2022 , 13,	1
717	Genomic characterization of <i>Lelliottia amnigena</i> PTJIT1005, a nitrate tolerant strain isolated from water sample of Yamuna River, Delhi, India.	
716	Extremophilic Bacterium <i>Halomonas desertis</i> G11 as a Cell Factory for Poly-3-Hydroxybutyrate-co-3-Hydroxyvalerate Copolymer β Production. 2022 , 10,	0
715	Comparative Genomics of Acetic Acid Bacteria within the Genus <i>Bombella</i> in Light of Beehive Habitat Adaptation. 2022 , 10, 1058	
714	Phage resistance profiling identifies new genes required for biogenesis and modification of the corynebacterial cell envelope.	
713	Emergence of a Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Isolate Co-harbours Dual blaNDM β 6-Carrying Plasmids in China. 2022 , 13,	0
712	Spontaneous genomic variation as a survival strategy of nosocomial <i>S. haemolyticus</i> .	
711	Identification of <i>Pseudomonas asiatica</i> subsp. <i>bavariensis</i> str. JM1 as the first N β -carboxy(m)ethyllysine degrading soil bacterium.	0
710	Isolation and Genome Analysis of an Amoeba-Associated Bacterium <i>Dyella terrae</i> Strain Ely Copper Mine From Acid Rock Drainage in Vermont, United States. 2022 , 13,	0
709	Characterization and application of bacteriophages for the biocontrol of Shiga-toxin producing <i>Escherichia coli</i> in Romaine lettuce. 2022 , 140, 109109	0
708	Selection and Development of Nontoxic Nonproteolytic <i>Clostridium botulinum</i> Surrogate Strains for Food Challenge Testing. 2022 , 11, 1577	1
707	<i>Apilactobacillus zhangquensis</i> sp. nov. and <i>Apilactobacillus xinyiensis</i> sp. nov., isolated from the gut of honeybee (<i>Apis mellifera</i>). 2022 , 72,	0
706	An expanding arsenal of immune systems that protect bacteria from phages.	0
705	<i>Bifidobacterium mizhiense</i> sp. nov., isolated from the gut of honeybee (<i>Apis mellifera</i>). 2022 , 72,	0
704	Isolation and characterization of the novel bacteriophage vB_SmaS_BUCT626 against <i>Stenotrophomonas maltophilia</i> .	0
703	<i>Thalassolituus alkanivorans</i> sp. nov., a hydrocarbon-utilizing bacterium isolated from the Mariana Trench. 2022 , 72,	0
702	Pangenome analyses of <i>Bacillus pumilus</i> , <i>Bacillus safensis</i> , and <i>Priestia megaterium</i> exploring the plant-associated features of bacilli strains isolated from canola.	1
701	Deciphering the Virus Signal Within the Marine Dissolved Organic Matter Pool. 2022 , 13,	0

- 700 Genome sequence and Carbohydrate Active Enzymes (CAZymes) repertoire of the thermophilic *Caldicoprobacter algeriensis* TH7C1T. **2022**, 21, 0
- 699 A prevalence and molecular characterization of novel pathogenic strains of *Macrocooccus caseolyticus* isolated from external wounds of donkeys in Khartoum State Sudan. **2022**, 18, 0
- 698 Emergent marine toxins risk assessment using molecular and chemical approaches. **2022**, 20, 0
- 697 Metagenomes of Red Sea Subpopulations Challenge the Use of Marker Genes and Morphology to Assess *Trichodesmium* Diversity. **2022**, 13, 0
- 696 Spontaneously produced lysogenic phages are an important component of the soybean *Bradyrhizobium mobilome*. 0
- 695 The Complete Genome Sequence of *Bacillus safensis* BRM1 Isolated from Brazilian Mangrove Sediment: A Potential Source of Biomass Converting Enzymes. **2022**, 16, 0
- 694 Complete Genome Sequence of the N4-like *Pseudomonas aeruginosa* Bacteriophage vB_PaeP_CMS1. 0
- 693 Draft Genome Sequence of *Tenacibaculum ovolyticum* To-7Br, Recovered from a Farmed Atlantic Salmon (*Salmo salar*). 0
- 692 Bioprospecting the microbiome of Red Sea Atlantis II brine pool for peptidases and biosynthetic genes with promising antibacterial activity. **2022**, 21, 0
- 691 Genomic characteristics, virulence and antimicrobial resistance in avian pathogenic *Escherichia coli* MTR_BAU02 strain isolated from layer farms in Bangladesh. **2022**, 2
- 690 Impact of Modified Atmospheres on Growth and Metabolism of Meat-Spoilage Relevant *Photobacterium* spp. as Predicted by Comparative Proteomics. **2022**, 13, 0
- 689 Unusual Hypermucoviscous Clinical Isolate of *Klebsiella pneumoniae* with No Known Determinants of Hypermucoviscosity. 1
- 688 *Evansella halocellulosilytica* sp. nov., an alkali-halotolerant and cellulose-dissolving bacterium isolated from bauxite residue. **2022**, 26, 0
- 687 Coexistence of *tmexCD-toprJ*, *bla* NDM-1, and *bla* IMP-4 in One Plasmid Carried by Clinical *Klebsiella* spp.. 1
- 686 Physiological and biochemical characterization and genome analysis of *Rhodococcus qingshengii* strain 7B capable of crude oil degradation and plant stimulation. **2022**, 35, e00741 0
- 685 Chromosomal integration of *bla*CTX-M genes in diverse *Escherichia coli* isolates recovered from river water in Japan. **2022**, 3, 100144 1
- 684 Genomic characterization and phytostimulative effect of a novel *Serratia* species. **2022**, 54, 341-367 0
- 683 NDM-5-Producing *Escherichia coli* Co-Harboring *mcr-1* Gene in Companion Animals in China. **2022**, 12, 1310 0

- 682 *Thauera sedimentorum* sp. nov., Isolated from Coastal Sediment. **2022**, 79,
- 681 Phylogenomic Analysis of *Salmonella enterica* subsp. *enterica* Serovar *Bovismorbificans* from Clinical and Food Samples Using Whole Genome Wide Core Genes and kmer Binning Methods to Identify Two Distinct Polyphyletic Genome Pathotypes. **2022**, 10, 1199
- 680 Suggestion for a new bacteriophage genus for the *Klebsiella pneumoniae* phage ν B_KpnS-Carvaje. 0
- 679 Genomic characterization of denitrifying methylotrophic *Pseudomonas aeruginosa* strain AAK/M5 isolated from municipal solid waste landfill soil. **2022**, 38,
- 678 *Photobacterium arenosum* WH24, Isolated from the Gill of Pacific Oyster *Crassostrea gigas* from the North Sea of Germany: Co-cultivation and Prediction of Virulence. **2022**, 79, 1
- 677 Mutual Exclusion of *Methanobrevibacter* Species in the Human Gut Microbiota Facilitates Directed Cultivation of a Candidatus *Methanobrevibacter Intestini* Representative.
- 676 *Saccharopolyspora soli* sp. nov., isolated from Northern Cyprus soil. **2022**, 204, 1
- 675 Genome Sequence and Characterization of a Xanthorhodopsin-Containing, Aerobic Anoxygenic Phototrophic *Rhodobacter* Species, Isolated from Mesophilic Conditions at Yellowstone National Park. **2022**, 10, 1169 0
- 674 Isolation, Molecular Characterization, and Antimicrobial Resistance of Selected Culturable Bacteria From Crayfish (*Procambarus clarkii*). 13,
- 673 *Sedimentimonas flavescens* gen. nov., sp. nov., isolated from sediment of Clam Island, Liaoning Province.
- 672 Complete Genome Sequence of *Salmonella* Phage ν B_SenA_SM5, Active against Multidrug-Resistant *Salmonella enterica* Serovar Typhi Isolates. 1
- 671 *Microvirga terricola* sp. nov. and *Microvirga solisilvae* sp. nov, isolated from forest soil. **2022**, 204,
- 670 Resistance of *Dickeya solani* strain IPO 2222 to lytic bacteriophage $\mathbb{D}5$ results in fitness tradeoffs for the bacterium during infection. **2022**, 12, 0
- 669 Sustainable bioethanol production from enzymatically hydrolyzed second-generation *Posidonia oceanica* waste using stable *Microbacterium metallidurans* carbohydrate-active enzymes as biocatalysts.
- 668 Characterization of *Kordiimonas marina* sp. nov. and *Kordiimonas laminariae* sp. nov. and Comparative Genomic Analysis of the Genus *Kordiimonas*, A Marine-Adapted Taxon. 9, 1
- 667 *Pseudonocardia terrae* sp. nov., an actinobacterium isolated from rice rhizosphere soil in Thailand. **2022**, 72, 0
- 666 Identification of *Mucilaginibacter conchicola* sp. nov., *Mucilaginibacter achroorhodeus* sp. nov. and *Mucilaginibacter pallidroseus* sp. nov. and emended description of the genus *Mucilaginibacter*. **2022**, 72, 1
- 665 Genomic Analysis Reveals That Isolation Temperature on Selective Media Introduces Genetic Variation in *Campylobacter jejuni* from Bovine Feces. **2022**, 11, 678 0

- 664 Discovery of the First Lytic *Staphylococcus pseudintermedius*/*Staphylococcus aureus* Polyvalent Bacteriophages. **2022**, 3, 116-124
- 663 Growth Fitness, Heme Uptake and Genomic Variants in Mutants of Oxygen-tolerant *Lactacaseibacillus casei* and *Lactiplantibacillus plantarum* Strains. **2022**, 127096
- 662 Opportunistic pathogen virulence is maintained by the presence of predators.
- 661 Genomic analysis of a novel active prophage of *Hafnia paralvei*.
- 660 A new bacterial tRNA enhances antibiotic production in *Streptomyces* by circumventing inefficient wobble base-pairing. 1
- 659 Characterization and genome analysis of *Pseudomonas aeruginosa* phage vB_PaeP_Lx18 and the antibacterial activity of its lysozyme. 0
- 658 The CRISPR/Cas Machinery Evolution and Gene Flow in the Hot Spring Cyanobacterium *Thermotichus*. **2022**, 14, 502
- 657 Heterotrophic Sulfur Oxidation of *Halomonas titanicae* SOB56 and Its Habitat Adaptation to the Hydrothermal Environment. 13, 0
- 656 Evaluating the Contribution of the Predicted Toxin/Antitoxin System HigBA to Persistence, Biofilm Formation, and Virulence in *Burkholderia pseudomallei*.
- 655 Duck sewage source coliphage P762 can lyse STEC and APEC. 0
- 654 Microbiome Restructuring: Dominant Coral Bacterium *Endozoicomonas* Species Respond Differentially to Environmental Changes. 1
- 653 Genome-scale metabolic modelling enables deciphering ethanol metabolism via the acrylate pathway in the propionate-producer *Anaerotignum neopropionicum*. **2022**, 21, 1
- 652 Turnover in Life-Strategies Recapitulates Marine Microbial Succession Colonizing Model Particles. 13, 0
- 651 Genomic Characterization of *Escherichia coli* O8 Strains Producing Shiga Toxin 2l Subtype. **2022**, 10, 1245 0
- 650 High diversity of pathogenic *Escherichia coli* clones carrying *mcr-1* among gulls underlines the need for strategies at the environment-livestock-human interface. 0
- 649 Draft Genome Sequences of *Flavobacterium covae* Strains LSU-066-04 and LV-359-01.
- 648 Bacterial Associates of a Desert Specialist Fungus-Growing Ant Antagonize Competitors with a Nocamycin Analog. 0
- 647 Ribosomal RNA operons define a central functional compartment in the *Streptomyces* chromosome.

- 646 Novel Insights Into the Phylogeny and Biotechnological Potential of *Weissella* Species. 13, 1
- 645 Isolation of Three Coliphages and the Evaluation of Their Phage Cocktail for Biocontrol of Shiga Toxin-Producing *Escherichia coli* O157 in Milk. **2022**, 79, 0
- 644 Genome analysis uncovers the prolific antagonistic and plant growth-promoting potential of endophyte *Bacillus velezensis* K1. **2022**, 836, 146671 2
- 643 Comparative genomics analysis of *Bacillus velezensis* LOH112 isolated from a nonagenarian provides insights into its biocontrol and probiotic traits. **2022**, 835, 146644 0
- 642 Molecular approaches to uncover phage-lactic acid bacteria interactions in a model community simulating fermented beverages. **2022**, 107, 104069 1
- 641 An essential role for tungsten in the ecology and evolution of a previously uncultivated lineage of anaerobic, thermophilic Archaea. **2022**, 13, 2
- 640 Coexistence of Heavy Metal Tolerance and Antibiotic Resistance in Thermophilic Bacteria Belonging to Genus *Geobacillus*. 13,
- 639 *Variovorax terrae* sp. nov. Isolated from Soil with Potential Antioxidant Activity. **2022**, 1
- 638 Rational selection and Characterisation of bile acid (BA) metabolising species of infant origin.
- 637 Genome-based reclassification of *Anoxybacillus karvacharensis* Panosyan et al. as a later heterotypic synonym of *Anoxybacillus kestanbolensis* Dulger et al. 2004; *A. flavithermus* subsp. *yunnanensis* CCTCC AB2010187T Dai et al. 2011 as a later heterotypic synonym of *A. lengchongensis* DSM 23211T Zhang et al. 2011. **2022**, 204,
- 636 Novel *Pseudomonas* sp. SCA7 Promotes Plant Growth in Two Plant Families and Induces Systemic Resistance in *Arabidopsis thaliana*. 13,
- 635 Virioplankton assemblages from Challenger Deep, the deepest place in the oceans. **2022**, 104680 0
- 634 Bacteriophage-Resistant Mutant of *Enterococcus faecalis* Is Impaired in Biofilm Formation. 13, 1
- 633 Comparative genomic insights into bacterial induction of larval settlement and metamorphosis in the upside-down jellyfish *Cassiopea*.
- 632 Whole genome sequencing and comparative genomic analyses of *Pseudomonas aeruginosa* strain isolated from arable soil reveal novel insights into heavy metal resistance and codon biology. **2022**, 68, 481-503 0
- 631 Co-transfer of functionally interdependent genes contributes to genome mosaicism in lambdoid phages.
- 630 Prevalence and risk factors of tet(X4)-positive Enterobacteriaceae in human gut microbiota. **2022**, 0
- 629 Incomplete denitrification phenotypes in diverse *Thermus* species from diverse geothermal spring sediments and adjacent soils in southwest China. **2022**, 26, 0

- 628 Characterization of Pathway-Specific Regulator NigR for High Yield Production of Nigericin in *Streptomyces malaysiensis* F913. **2022**, 11, 938 1
- 627 Draft Genome Sequence of *Xanthobacter aminoxidans* ATCC BAA-299 T.
- 626 Comparative Genome Analysis of Two Heterotrophic Nitrifying *Pseudomonas putida* Strains Isolated from Freshwater Shrimp Ponds in Soc Trang Province. **2022**, 8, 336
- 625 Genomic analysis of heavy metal-resistant *Halobacterium salinarum* isolated from Sfax solar saltern sediments. **2022**, 26, 0
- 624 Characterization and Genomic Analysis of a New Phage Infecting *Helicobacter pylori*. **2022**, 23, 7885 0
- 623 Carbohydrate-Active Enzymes of a Novel Halotolerant Alkalihalobacillus Species for Hydrolysis of Starch and Other Algal Polysaccharides. 0
- 622 *Lelliottia steviae* sp. nov. isolated from *Stevia rebaudiana* Bertoni. **2022**, 204,
- 621 *Paludisphaera rhizosphaerae* sp. nov., a new member of the family Isosphaeraceae, isolated from the rhizosphere soil of *Erianthus ravennae*.
- 620 Genome Analysis of ESBL-Producing *Escherichia coli* Isolated from Pigs. **2022**, 11, 776 0
- 619 Isolation and Characterization of Novel Lytic Bacteriophage vB_RsoP_BMB50 infecting *Ralstonia solanacearum*. **2022**, 79,
- 618 *Fictibacillus marinisediminis* sp. nov., a nitrate-reducing bacterium isolated from marine sediment in Hupo Basin, Republic of Korea. **2022**, 204, 1
- 617 Comparative genomics of the plant-growth promoting bacterium *Sphingobium* sp. strain AEW4 isolated from the rhizosphere of the beachgrass *Ammophila breviligulata*. *BMC Genomics*, **2022**, 23, 4-5 1
- 616 *Subtercola endophyticus* sp. nov., a cold-adapted bacterium isolated from *Abies koreana*. **2022**, 12,
- 615 Arsenic and chromium resistance mechanisms in the *Micrococcus luteus* group. **2022**,
- 614 Proteomining-Based Elucidation of Natural Product Biosynthetic Pathways in *Streptomyces*. 13,
- 613 Evolutionary Instability of Collateral Susceptibility Networks in Ciprofloxacin-Resistant Clinical *Escherichia coli* Strains.
- 612 Characterization of *Cronobacter sakazakii* Strains Originating from Plant-Origin Foods Using Comparative Genomic Analyses and Zebrafish Infectivity Studies. **2022**, 10, 1396
- 611 Studies on the interaction of three lytic bacteriophages with a wide collection of *Escherichia coli* strains implicated in swine enteric colibacillosis.

610	Comparative genomics of <i>Nocardia seriolae</i> reveals recent importation and subsequent widespread dissemination in mariculture farms in the South Central Coast region, Vietnam. 2022 , 8,	
609	Microbial liberation of N-methylserotonin from orange fiber in gnotobiotic mice and humans. 2022 , 185, 2495-2509.e11	1
608	Detection of OXA-181-producing <i>Pseudomonas aeruginosa</i> in Germany. 2022 , 312, 151557	
607	Within-host evolution of a gut pathobiont facilitates liver translocation.	2
606	<i>Serinicoccus kebangsaanensis</i> sp. nov, a new bacterium isolated from the toxic diatom, <i>Nitzschia navis-varingica</i> . 2022 , 101005	
605	Phylogenetic analysis and accessory genome diversity reveal insight into the evolutionary history of <i>Streptococcus dysgalactiae</i> . 13,	
604	Identification of a broad-spectrum lytic Myoviridae bacteriophage using multidrug resistant <i>Salmonella</i> isolates from pig slaughterhouses as the indicator and its application in combating <i>Salmonella</i> infections. 2022 , 18,	
603	Alterations in the Microbiota of Caged Honeybees in the Presence of <i>Nosema ceranae</i> Infection and Related Changes in Functionality.	0
602	Prosthecate aerobic anoxygenic phototrophs <i>Photocaulis sulfatitolerans</i> gen. nov. sp. nov. and <i>Photocaulis rubescens</i> sp. nov. isolated from alpine meromictic lakes in British Columbia, Canada. 2022 , 204,	1
601	Genome sequencing and comparative analysis of <i>Wolbachia</i> strain wAlbA reveals <i>Wolbachia</i> -associated plasmids are common.	0
600	<i>Humibacter ginsenosidimutans</i> sp. nov., with ginsenoside-converting activity isolated from activated sludge. 2022 , 72,	0
599	Molecular cloning, characterization, and in-silico analysis of l-asparaginase from Himalayan <i>Pseudomonas</i> sp. PCH44. 2022 , 12,	0
598	Genomic Analysis of the <i>Serratia marcescens</i> Bacteriophage BUCT660.	1
597	Genome Analysis of <i>Enterobacter asburiae</i> and <i>Lelliottia</i> spp. Proliferating in Oligotrophic Drinking Water Reservoirs and Lakes.	1
596	<i>Shewanella azerbaijanica</i> sp. nov. a novel aquatic species with high bioremediation abilities. 2022 , 204,	2
595	Characterization of a Lytic Bacteriophage vB_SurP-PSU3 Infecting <i>Staphylococcus ureilyticus</i> and Its Efficacy Against Biofilm. 13,	
594	Genomic and physiological evaluation of two root associated <i>Pseudomonas</i> from <i>Coffea arabica</i> . 2022 , 127129	0
593	<i>Winogradskyella luteola</i> sp. nov., <i>Erythrobacter ani</i> sp. nov., and <i>Erythrobacter crassostrea</i> sp. nov., isolated from the hemolymph of the Pacific Oyster <i>Crassostrea gigas</i> . 2022 , 204,	1

- 592 *Rhodohalobacter sulfatireducens* sp. nov., isolated from a marine solar saltern. **2022**, 204, 0
- 591 Whole genome sequencing and in vitro activity data of Escherichia phage NTEC3 against multidrug-resistant Uropathogenic and extensively drug-resistant Uropathogenic *E. coli* isolates. **2022**, 108479 0
- 590 Genetic Characteristics and Enzymatic Activities of *Bacillus velezensis* KS04AU as a Stable Biocontrol Agent against Phytopathogens. **2022**, 13, 201-223 0
- 589 *Roseomonas rosulenta* sp. nov., isolated from rice paddy soil. **2022**, 204, 0
- 588 Genomic characterization of lytic bacteriophages AϕL and AϕM infecting ESBL *K. pneumoniae* and its therapeutic potential on biofilm dispersal and in-vivo bacterial clearance. **2022**, 262, 127104 0
- 587 *Actinospica acidithermotolerans* sp. nov., a novel actinomycete isolated from sediment from an Indonesian hot spring. **2022**, 204, 0
- 586 Genomic evaluation of BC4, a consortium of four *Alkalihalobacillus clausii* isolates, confirms its probiotic potential and safety in usage. 0
- 585 Effect of a bacteriocin-producing *Streptococcus salivarius* on the pathogen *Fusobacterium nucleatum* in a model of the human distal colon. **2022**, 14, 0
- 584 High-resolution spatial and genomic characterization of coral-associated microbial aggregates in the coral *Stylophora pistillata*. **2022**, 8, 0
- 583 Novel Insights into bla_{GES} Mobilome Reveal Extensive Genetic Variation in Hospital Effluents. 0
- 582 Insights from cyanobacterial genomic and transcriptomic analyses into adaptation strategies in terrestrial environments. **2022**, 110438 0
- 581 Draft-genome analysis provides insights into the virulence properties and genome plasticity of *Vibrio fluvialis* organisms isolated from shrimp farms and Turag river in Bangladesh. **2022**, 204, 0
- 580 Virulent Phages Isolated from a Smear-Ripened Cheese Are Also Detected in Reservoirs of the Cheese Factory. **2022**, 14, 1620 0
- 579 Molecular Characterization of pBOq-*IncQ* and pBOq-95LK Plasmids of *Escherichia coli* BOq 01, a New Isolated Strain from Poultry Farming, Involved in Antibiotic Resistance. **2022**, 10, 1509 1
- 578 Whole genome sequencing of the multidrug-resistant *Chryseobacterium indologenes* isolated from a patient in Brazil. 9, 2
- 577 Coastal Transient Niches Shape the Microdiversity Pattern of a Bacterioplankton Population with Reduced Genomes. 1
- 576 Multiple Adaptive Strategies of Himalayan *Iodobacter* sp. PCH194 to High-Altitude Stresses. 13, 0
- 575 Isolation and genomic characterization of a novel Autographiviridae bacteriophage IME184 with lytic activity against *Klebsiella pneumoniae*. **2022**, 319, 198873 1

- 574 Characterization of *Lactiplantibacillus plantarum* Tw226 strain and its use for the production of a new membrane-bound biosurfactant. **2022**, 363, 119889
- 573 Complete Genome Sequence of *Chryseobacterium mulctrae* KACC 21234T: A Potential Proteolytic and Lipolytic Bacteria Isolated from Bovine Raw Milk. **2022**, 40, 86-91
- 572 Metabolic network models of *Gardnerella* pangenome identify interactions in the vaginal environment.
- 571 Exploring the Antibiotic Production Potential of Heterotrophic Bacterial Communities Isolated from the Marine Sponges *Crateromorpha meyeri*, *Pseudaxinella reticulata*, *Farrea similaris*, and *Caulophacus arcticus* through Synergistic Metabolomic and Genomic Analyses. **2022**, 20, 463 ○
- 570 Phylogenomic analysis and metabolic role reconstruction of mutualistic Rhizobiales hindgut symbionts of *Acromyrmex* leaf-cutting ants. **2022**, 98,
- 569 Genetic editing of multi-resistance plasmids in *Escherichia coli* isolated from meat during transfer. **2022**, 122, 102640
- 568 Within-farm dynamics of ESBL-producing *Escherichia coli* in dairy cattle: Resistance profiles and molecular characterization by long-read whole-genome sequencing. 13, 1
- 567 Impact of a phage cocktail targeting *Escherichia coli* and *Enterococcus faecalis* as members of a gut bacterial consortium in vitro and in vivo. 13,
- 566 Methanol utilizers of the rhizosphere and phyllosphere of a common grass and forb host species. **2022**, 17,
- 565 A Cocktail of Three Virulent Phages Controls Multidrug-Resistant *Salmonella* Enteritidis Infection in Poultry. 13, ○
- 564 Prophage Diversity Across *Salmonella* and Verotoxin-Producing *Escherichia coli* in Agricultural Niches of British Columbia, Canada. 13, 1
- 563 Insights into the Antimicrobial Resistance Profile of a Next Generation Probiotic *Akkermansia muciniphila* DSM 22959. **2022**, 19, 9152 1
- 562 Metagenome-Assembled Genome of *Cyanocohniella* sp. LLY from the Cyanosphere of Llayta, an Edible Andean Cyanobacterial Macrocolony. **2022**, 10, 1517 ○
- 561 Comprehensive Phylogenomics of *Methylobacterium* Reveals Four Evolutionary Distinct Groups and Underappreciated Phyllosphere Diversity. **2022**, 14, ○
- 560 *Limnobacter parvuscolonica* sp. nov., thiosulfate-oxidizing bacterium isolated from lake water.
- 559 Intrinsic tet(L) sub-class in *Bacillus velezensis* and *Bacillus amyloliquefaciens* is associated with a reduced susceptibility toward tetracycline. 13,
- 558 High impact of bacterial predation on cyanobacteria in soil biocrusts. **2022**, 13, ○
- 557 *Shewanella shenzhenensis* sp. nov., a novel Fe(III)-reducing bacterium with abundant possible cytochrome genes, isolated from mangrove sediment. ○

- 556 Comprehensive deciphering prophages in genus *Acetobacter* on the ecology, genomic features, toxin-antitoxin system, and linkage with CRISPR-Cas system. 13, 0
- 555 *Pelagibacterium xiamenense* sp. nov., isolated from intertidal sediment. **2022**, 72, 0
- 554 Comparative genomics provides insights into the potential biocontrol mechanism of two *Lysobacter* enzymogenes strains with distinct antagonistic activities. 13, 0
- 553 Bioinformatics and its role in the study of the evolution and probiotic potential of lactic acid bacteria. 2
- 552 Characterization of Metagenome Assembled Genomes from the International Space Station. 0
- 551 *Sphingomonas folii* sp. nov., *Sphingomonas citri* sp. nov. and *Sphingomonas citricola* sp. nov., isolated from citrus phyllosphere. **2022**, 72, 0
- 550 Co-occurrence of *mcr-2* and *mcr-3* genes on chromosome of multidrug-resistant *Escherichia coli* isolated from healthy individuals in Thailand. **2022**, 106662 0
- 549 Plant growth-promoting properties of *Streptomyces* spp. isolates and their impact on mung bean plantlets' rhizosphere microbiome. 13, 0
- 548 Draft genome sequencing data of the moderately halophilic bacterium, *Allobacillus halotolerans* SKP2-8 from shrimp paste (ka-pi). **2022**, 108549 0
- 547 *Nitrosomonas supralitoralis* sp. nov., an ammonia-oxidizing bacterium from beach sand in a supralittoral zone. **2022**, 204, 0
- 546 *Maridesulfovibrio caeruleilacunae* sp. nov. and *Maridesulfovibrio oucae* sp. nov., two sulfate-reducing bacteria isolated from Yongle Blue Hole of the South China Sea. 0
- 545 First Report of *Bartonella* spp. in Marsupials from Brazil, with a Description of *Bartonella harrusi* sp. nov. and a New Proposal for the Taxonomic Reclassification of Species of the Genus *Bartonella*. **2022**, 10, 1609 1
- 544 *Pseudovibrio flavus* sp. nov. isolated from the sea sponge *Verongula gigantea*. **2022**, 72, 0
- 543 *Sediminibacillus dalangtanensis* sp. nov., a moderate halophile isolated from hypersaline sediments of the Qaidam Basin in Northwest China. **2022**, 71, 0
- 542 Description of *Aestuariivivens marinum* sp. nov., *Aestuariivivens sediminis* sp. nov. and *Aestuariivivens sediminicola* sp. nov., three new species isolated from the upper layer of tidal flat sediment. **2022**, 126355 0
- 541 Phenotypic and genomic characteristics of *Brevibacterium zhoupengii* sp. nov., a novel halotolerant actinomycete isolated from bat feces. 0
- 540 Transcriptomic Analysis of *Staphylococcus equorum* KM1031, Isolated from the High-Salt Fermented Seafood Jeotgal, under Salt Stress. **2022**, 8, 403 0
- 539 Infant Gut Microbial Metagenome Mining of α -Fucosidases with Activity on Fucosylated Human Milk Oligosaccharides and Glycoconjugates. 1

- 538 Emergence of uncommon KL38-OCL6-ST220 carbapenem-resistant *Acinetobacter pittii* strain, co-producing chromosomal NDM-1 and OXA-820 carbapenemases. 12,
- 537 A Framework for the Systematic Selection of Biosensor Chassis for Environmental Synthetic Biology. ○
- 536 The diversity in antimicrobial resistance of MDR Enterobacteriaceae among Chinese broiler and laying farms and two mcr-1 positive plasmids revealed their resistance-transmission risk. 13, ○
- 535 Mexican Strains of *Anaplasma marginale*: A First Comparative Genomics and Phylogeographic Analysis. 2022, 11, 873
- 534 Complete Genome Sequencing of a Community-Associated Methicillin-Resistant *Staphylococcus aureus* USA300 Strain JICS127, a Uniquely Evolved USA300 Lineage in Japan.
- 533 *Lightella neohaematopini*: A new lineage of highly reduced endosymbionts coevolving with chipmunk lice of the genus *Neohaematopinus*. 13,
- 532 Detection of interphylum transfers of the magnetosome gene cluster in magnetotactic bacteria. 13, ○
- 531 Integrating metagenomic binning with flux balance analysis to unravel syntrophies in anaerobic CO₂ methanation. 2022, 10, ○
- 530 In silico Analysis of ACE2 Receptor to Find Potential Herbal Drugs in COVID-19 Associated Neurological Dysfunctions. 2022, 17, 1934578X2211185 2
- 529 Probiogenomic Analysis of *Lactiplantibacillus* sp. LM14-2 from Fermented Mussel (Hoi-dong), and Evaluation of its Cholesterol-lowering and Immunomodulation Effects.
- 528 Ecophysiological and genomic analyses of a representative isolate of highly abundant *Bacillus cereus* strains in contaminated subsurface sediments. ○
- 527 *Metabacillus rhizolycopersici* sp. nov., Isolated from the Rhizosphere Soil of Tomato Plants. 2022, 79, ○
- 526 The microbiome of a bacterivorous marine choanoflagellate contains a resource-demanding obligate bacterial associate. 2022, 7, 1466-1479 ○
- 525 A tale of two plasmids: contributions of plasmid associated phenotypes to epidemiological success among *Shigella*. 2022, 289, ○
- 524 Complete Genome Sequence of *Micrococcus yunnanensis* TT9, Isolated from a Healthy Volunteer. ○
- 523 Unraveling the Genomic Potential of the Thermophilic Bacterium *Anoxybacillus flavithermus* from an Antarctic Geothermal Environment. 2022, 10, 1673 ○
- 522 An Inu (A)-Carrying Multi-Resistance Plasmid Derived from Sequence Type 3 Methicillin-Resistant *Staphylococcus lugdunensis* May Contribute to Antimicrobial Resistance in Staphylococci. 2022, 66,
- 521 An in silico reverse vaccinology study of *Brachyspira pilosicoli*, the causative organism of intestinal spirochaetosis, to identify putative vaccine candidates. 2022,

- 520 Complete genome sequencing of a Tequintavirus bacteriophage with a broad host range against *Salmonella Abortus equi* isolates from donkeys. 13, 1
- 519 Fecal Carriage of *Escherichia coli* Harboring the tet(X4)-IncX1 Plasmid from a Tertiary Class-A Hospital in Beijing, China. **2022**, 11, 1068 0
- 518 The landscape in the gut microbiome of long-lived families reveals new insights on longevity and aging [r]elevant neural and immune function. **2022**, 14, 1
- 517 Classification and molecular characteristics of tet(X)-carrying plasmids in *Acinetobacter* species. 13,
- 516 *Aquibacillus saliphilus* sp. nov., a moderately halophilic bacterium isolated from a grey saltern. **2022**, 72,
- 515 Microbiota Communities of Healthy and Bacterial Pustule Diseased Soybean. **2022**, 38, 372-382 0
- 514 Development and evaluation of temperature-sensitive *Mycoplasma anserisalpingitidis* clones as vaccine candidates. 1-15
- 513 Machine learning algorithm to characterize antimicrobial resistance associated with the International Space Station surface microbiome. **2022**, 10, 0
- 512 Accumulation of defense systems drives panphage resistance in *Pseudomonas aeruginosa*. 0
- 511 ReNoteWeb - Web platform for the improvement of assembly result and annotation of prokaryotic genomes. **2022**, 146819
- 510 Co-Occurrence of β -Lactam and Aminoglycoside Resistance Determinants among Clinical and Environmental Isolates of *Klebsiella pneumoniae* and *Escherichia coli*: A Genomic Approach. **2022**, 15, 1011 1
- 509 Complete Genome Sequencing of Polar *Arthrobacter* sp. PAMC25284, Copper Tolerance Potential Unraveled with Genomic Analysis. **2022**, 2022, 1-12 0
- 508 Draft Genome Sequence of a Multiple Antibiotic Resistant *Staphylococcus aureus* NCTC 6571-UB Laboratory Strain.
- 507 Genomic Analysis Reveals Adaptation of *Vibrio campbellii* to the Hadal Ocean. **2022**, 88,
- 506 *Parasphingorhabdus cellanae* sp. nov., isolated from the gut of a Korean limpet, *Cellana toreuma*. **2022**, 72,
- 505 Genomic characteristics of two most widely used BCG vaccine strains: Danish 1331 and Pasteur 1173P2. **2022**, 23,
- 504 *Bacillus megaterium* HgT21: a Promising Metal Multiresistant Plant Growth-Promoting Bacteria for Soil Bioremediation. 1
- 503 Draft genome sequences of hydrocarbon degrading *Haloferax* sp. AB510, *Haladaptatus* sp. AB618 and *Haladaptatus* sp. AB643 isolated from the estuarine sediments of Sundarban mangrove forests, India. **2022**, 12,

- 502 Genome Sequence of SN1, a Bacteriophage That Infects *Sphaerotilus natans* and *Pseudomonas aeruginosa*.
- 501 Genomic characteristics of clinical multidrug-resistant *Proteus* isolates from a tertiary care hospital in southwest China. 13, ○
- 500 Draft Genome Sequences of Three Nitrogen-Fixing Strains Isolated from Soil Cooled for Growing Temperate Root Crops in a Tropical Climate.
- 499 UV and chemically induced *Halomonas smyrnensis* mutants for enhanced levan productivity. **2022**, 356, 19-29 ○
- 498 Genomic insights into a free-living, nitrogen-fixing but non nodulating novel species of *Bradyrhizobium sediminis* from freshwater sediment: Three isolates with the smallest genome within the genus *Bradyrhizobium*. **2022**, 45, 126353 1
- 497 Gut microbiome and metabolome of sea cucumber (*Stichopus ocellatus*) as putative markers for monitoring the marine sediment pollution in Pahang, Malaysia. **2022**, 182, 114022 1
- 496 A genome-led study on the pathogenesis of *Fusobacterium necrophorum* infections. **2022**, 840, 146770
- 495 Seasonal variation in the phytoremediation by *Pontederia crassipes* (Mart) Solms (water hyacinth) and its associated microbiota. **2022**, 183, 106744
- 494 Phages against non-capsulated *Klebsiella pneumoniae*: broader host range, slower resistance. ○
- 493 Comparative genomic analysis of the genus *Marinomonas* and taxonomic study of *Marinomonas algarum* sp. nov., isolated from red algae *Gelidium amansii*. **2022**, 204, ○
- 492 A Novel Freshwater Cyanophage Mae-Yong1326-1 Infecting Bloom-Forming Cyanobacterium *Microcystis aeruginosa*. **2022**, 14, 2051 ○
- 491 Genome mining to unravel potential metabolic pathways linked to gallium bioleaching ability of bacterial mine isolates. 13, ○
- 490 Rhizosphere microbiome analysis of healthy and infected Cumin (*Cuminum cyminum* L.) varieties from Gujarat, India. **2022**, 100163 ○
- 489 Characterization of a *Vibrio*-infecting bacteriophage, VPMCC5, and proposal of its incorporation as a new genus in the *Zobellviridae* family. **2022**, 321, 198904 ○
- 488 Characterization and complete genome analysis of a bacteriophage vB_EcoM_DE7 infecting donkey-derived *Escherichia coli*. **2022**, 321, 198913 ○
- 487 Molecular, biochemical, and comparative genome analysis of a rhizobacterial strain *Klebsiella* Sp. KBG6.2 imparting salt stress tolerance to *Oryza sativa* L.. **2022**, 203, 105066 ○
- 486 *Clostridium perfringens* associated with dairy farm systems show diverse genotypes. **2022**, 382, 109933 ○
- 485 Genome sequence data of *Bacillus* sp. CCB-MMP212 isolated from Malaysian mangrove: A potential strain in arsenic resistance with Arsl, CAs lyase. **2022**, 45, 108597 ○

- 484 Region-specific genomic signatures of multidrug-resistant *Helicobacter pylori* isolated from East and South India. **2022**, 847, 146857 ○
- 483 Mangrove microbial community recovery and their role in early stages of forest recolonization within shrimp ponds. **2023**, 855, 158863 ○
- 482 A multi-layer genome mining and phylogenomic analysis to construct efficient and autonomous efflux system for medium chain fatty acids. **2022**, 2, 1-14 ○
- 481 Computational design and characterization of a multiepitope vaccine against carbapenemase-producing *Klebsiella pneumoniae* strains, derived from antigens identified through reverse vaccinology. **2022**, 20, 4446-4463 1
- 480 New-Age Genomic Measures for Uncovering Plant-Microbiome Interactions: Tools, Pipelines and Guidance Map for Genomic Data Mining. **2022**, 207-232 ○
- 479 An Integrative and Conjugative Element (ICE) Found in *Shewanella halifaxensis*; Isolated from Marine Fish Intestine May Connect Genetic Materials between Human and Marine Environments. **2022**, 37, n/a ○
- 478 Genome-Resolved Metagenomics Informs the Functional Ecology of Uncultured Acidobacteria in Redox Oscillated Sphagnum Peat. ○
- 477 In silico analysis and a comparative genomics approach to predict pathogenic trehalase genes in the complete genome of Antarctica *Shigella* sp. PAMC28760. **2022**, 13, 1502-1514 ○
- 476 *Nanobdella aerobiophila* gen. nov., sp. nov., a thermoacidophilic, obligate ectosymbiotic archaeon, and proposal of Nanobdellaceae fam. nov., Nanobdellales ord. nov. and Nanobdellia class. nov.. **2022**, 72, 1
- 475 From Farm to Fork: *Streptococcus suis* as a Model for the Development of Novel Phage-Based Biocontrol Agents. **2022**, 14, 1996 ○
- 474 Metagenomics-resolved genomics provides novel insights into chitin turnover, metabolic specialization, and niche partitioning in the octocoral microbiome. **2022**, 10, ○
- 473 Draft Genome Sequence of *Pseudomonas mandelii* Strain 29, Isolated from the Desert Truffle *Terfezia claveryi*. ○
- 472 *Polymorphobacter megasporae* sp. nov., isolated from an Antarctic lichen. **2022**, 72, ○
- 471 Persistence of Rare *Salmonella Typhi* Genotypes Susceptible to First-Line Antibiotics in the Remote Islands of Samoa. 1
- 470 Novel bacterial taxa in a minimal lignocellulolytic consortium and their potential for lignin and plastics transformation. **2022**, 2, ○
- 469 Genome Sequences of the Human-Skin-Originated *Brevundimonas albigilva* TT17 and the Soil-Originated *B. albigilva* KEME 9005-016 T. ○
- 468 Withdrawal of antibiotic growth promoters in China and its impact on the foodborne pathogen *Campylobacter coli* of swine origin. 13, ○
- 467 Functional genomics analysis of a phyllospheric *Pseudomonas* spp with potential for biological control against coffee rust. **2022**, 22, ○

466	Rhizobium quercicola sp. nov., isolated from the leaf of Quercus variabilis in China. 2022 , 204,	0
465	Genome sequencing and comparative analysis of Wolbachia strain wAlbA reveals Wolbachia-associated plasmids are common. 2022 , 18, e1010406	0
464	Paracandidimonas lactea sp. nov., a urea-utilizing bacterium isolated from landfill. 2022 , 204,	1
463	Genomic characteristics of listeria that caused invasive listeriosis during the COVID-19 pandemic.	0
462	Genomic characterization of a novel bacteriophage STP55 revealed its prominent capacity in disrupting the dual-species biofilm formed by Salmonella Typhimurium and Escherichia coli O157: H7 strains. 2022 , 204,	1
461	Genome-Guided Investigation Provides New Insights into Secondary Metabolites of Streptomyces parvulus SX6 from Aegiceras corniculatum. 2022 , 71, 381-394	0
460	Bioinformatics study of expression from genomes of epidemiologically related MRSA CC398 isolates from human and wild animal samples. 2022 , 268, 104714	0
459	Curtobacterium allii sp. nov., the actinobacterial pathogen causing onion bulb rot.	0
458	Genome analysis and phenotypic characterization of Halomonas hibernica isolated from a traditional food process with novel quorum quenching and catalase activities. 2022 , 168,	0
457	Genome Sequences of 16 Escherichia coli Bacteriophages Isolated from Wastewater, Pond Water, Cow Manure, and Bird Feces.	2
456	Structural insight into a glucomannan-type extracellular polysaccharide produced by a marine Bacillus altitudinis SORB11 from Southern Ocean. 2022 , 12,	0
455	A Plasmid Carrying blaIMP-56 in Pseudomonas aeruginosa Belonging to a Novel Resistance Plasmid Family. 2022 , 10, 1863	1
454	In silico prediction of the enzymes involved in the degradation of the herbicide molinate by Gulosibacter molinivorax ON4T. 2022 , 12,	0
453	A stable home for an equine pathogen: valid publication of the binomial Prescottella equi gen. nov., comb. nov., and reclassification of four rhodococcal species into the genus Prescottella.. 2022 , 72,	0
452	Breaking the ICE: an easy workflow for identifying and analyzing integrative and conjugative elements in bacterial genomes.	2
451	Apilactobacillus apisilvae sp. nov., Nicolia spurrieriana gen. nov. sp. nov., Bombilactobacillus folatiphilus sp. nov. and Bombilactobacillus thymidiniphilus sp. nov., four new lactic acid bacterial isolates from stingless bees Tetragonula carbonaria and Austroplebeia australis. 2022 , 72,	2
450	Empirical genomic methods for tracking plasmid spread among healthcare-associated bacteria.	0
449	Characterization of Phage Resistance and Their Impacts on Bacterial Fitness in Pseudomonas aeruginosa.	1

- 448 Complete Genome Sequence of *Bacillus amyloliquefaciens* KNU-28 Isolated from Peach Leaves (*Prunus Persica* [L.] Batsch). ○
- 447 Isolation and genomic characterization of metal-resistant *Stenotrophomonas maltophilia* SRM01 from the marine environment. ○
- 446 *Robiginitalea marina* sp. nov., isolated from coastal sediment. **2022**, 204, 1
- 445 Development of a Bacteriophage Cocktail against *Pectobacterium carotovorum* Subsp. *carotovorum* and Its Effects on *Pectobacterium* Virulence. ○
- 444 Comparative Genome Analysis of a Novel Alkaliphilic Actinobacterial Species *Nesterenkonia haasae*. **2022**, 71, 453-461 ○
- 443 *Streptomyces*: Derived Active Extract Inhibits *Candida albicans* Biofilm Formation. **2022**, 79, ○
- 442 Liposomal Delivery of Newly Identified Prophage Lysins in a *Pseudomonas aeruginosa* Model. **2022**, 23, 10143 1
- 441 Draft Genome Sequence of *Lentilactobacillus kosonis* NBRC 111893, Isolated from a Japanese Sugar-Vegetable Fermented Beverage called *Kijiso*. ○
- 440 Characterization of *TeLE*, an LXG effector of *Streptococcus gallolyticus*, antagonized by a non-canonical immunity protein. ○
- 439 Comparative genomics reveals the evolution of antimicrobial resistance in *Bacteroides nordii*. **2022**, 105811 ○
- 438 Recent O-antigen diversification masks highly pathogenic STEC O104:H4. ○
- 437 New Multidrug Efflux Systems in a Microcystin-Degrading Bacterium *Blastomonas fulva* and Its Genomic Feature. **2022**, 23, 10856 ○
- 436 Description of *Deefgea piscis* sp. nov., and *Deefgea tanakiae* sp. nov., isolated from the gut of Korean indigenous fish. ○
- 435 Complete Genome Sequence of a Multidrug-Resistant *Klebsiella pneumoniae* Strain Carrying *blaOXA181* and *blaKPC-125* Carbapenemase. **2022**, 28, 916-920 ○
- 434 Genomic analysis of two *Bacillus safensis* isolated from Merzouga desert reveals desert adaptive and potential plant growth-promoting traits. ○
- 433 Genome Insight and Description of Previously Uncultured N₂-Fixing Bacterium *Rhizobium terricola* sp. nov., Isolated from Forest Rhizospheric Soil by Using Modified Culture Method. **2022**, 14, 733 1
- 432 Enterococcal linear plasmids adapt to *Enterococcus faecium* and spread within multidrug-resistant clades. ○
- 431 *Geoalkalibacter halelectricus* SAP -1 sp. nov. possessing extracellular electron transfer and mineral-reducing capabilities from a haloalkaline environment. ○

- 430 Genomic description and prevalence of two new Candidatus Saccharibacteria species from the human gut in different samples and countries. ○
- 429 Monitoring phage-induced lysis of Gram-negatives in real time using a fluorescent DNA dye. ○
- 428 *Vibrio tarriae* sp. nov., a novel member of the Cholerae clade. **2022**, 72, 2
- 427 Whole genome sequencing and global metabolome profiling of clinical *Mycobacterium tuberculosis* isolates provide insights to their drug resistance status. ○
- 426 Converting the genomic knowledge base to build protein specific machine learning prediction models; a classification study on thermophilic serine protease. ○
- 425 An Update of Bovine Hemoplasmas Based on Phylogenetic and Genomics Analysis. **2022**, 10, 1916 ○
- 424 Sequestration of gut pathobionts in intraluminal casts, a mechanism to avoid dysregulated T cell activation by pathobionts. **2022**, 119, 1
- 423 Draft Genome Sequence of Two *Salmonella enterica* Subspecies *enterica* Serovar Minnesota Strains Harboring *Mcr-1.1* Gene Isolated from Chicken Meat in Saudi Arabia. ○
- 422 Genome Sequence of *Halomonas* sp. Strain MS1, a Metallophore-Producing, Algal Growth-Promoting Marine Bacterium Isolated from the Green Seaweed *Ulva mutabilis* (Chlorophyta). ○
- 421 First report of the whole genome of *Moraxella bovoculi* genotype 1 from India and comparative genomics of *Moraxella bovoculi* to identify genotype-specific markers. **2022**, 204, ○
- 420 Frequent dissemination and carriage of an SCCmec-mecC hybrid in methicillin-resistant *Mammaliococcus sciuri* in farm animals from Tunisia. **2022**, 1
- 419 Metagenomic and genomic characterization of heavy metal tolerance and resistance genes in the rhizosphere microbiome of *Avicennia germinans* in a semi-arid mangrove forest in the tropics. **2022**, 184, 114204 ○
- 418 Antifungal cultures and metabolites of lactic acid bacteria for use in dairy fermentations. **2022**, 383, 109938 ○
- 417 pST15-IncHI2 plasmids co-harboring *mcr-9* and several other antibiotic resistance genes in heavy metal tolerant *Enterobacter cloacae* complex isolates from hospital infections. **2022**, 31, 187-188 ○
- 416 Insights on Microbial Communities Inhabiting Non-Volcanic Hot Springs. **2022**, 23, 12241 1
- 415 Description of *Halosolutus amylolyticus* gen. nov., sp. nov., *Halosolutus halophilus* sp. nov. and *Halosolutus gelatinilyticus* sp. nov., and genome-based taxonomy of genera *Natribaculum* and *Halovarius*. **2022**, 72, ○
- 414 Genome-Scale Modeling and Systems Metabolic Engineering of *Vibrio natriegens* for the Production of 1,3-Propanediol. **2023**, 209-220 ○
- 413 Complete nucleotide sequence of *cfr*-harbouring multidrug-resistant plasmid, pFJ6683, from avian *Pasteurella multocida*. ○

412	Comparative genomic and functional analysis of <i>Arthrobacter</i> sp. UMCV2 reveals the presence of luxR-related genes inducible by the biocompound N, N-dimethylhexadecylamine. 13,	2
411	A Clinical Outcome of the Anti-PD-1 Therapy of Melanoma in Polish Patients Is Mediated by Population-Specific Gut Microbiome Composition. 2022 , 14, 5369	0
410	Draft Genome Sequences of Seven <i>Limosilactobacillus fermentum</i> Indigenously Isolated Probiotic Strains from the Artisanal Fermented Milk Product Dahi.	0
409	Identification, characterization, and genome sequencing of <i>Brevibacterium sediminis</i> MG-1 isolate with growth-promoting properties. 2022 , 12,	0
408	Detection of IMP-4 and SFO-1 co-producing ST51 <i>Enterobacter hormaechei</i> clinical isolates. 12,	0
407	Genomic and Phylogenetic Characterization of <i>Rhodopseudomonas infernalis</i> sp. nov., Isolated from the Hell Creek Watershed (Nebraska). 2022 , 10, 2024	0
406	Complete whole genome sequencing of <i>Vibrio parahaemolyticus</i> strain UMP001VA, isolated from sea cucumber <i>Holothuria leucospilota</i> from Malaysia harbouring bla gene. 2022 ,	0
405	Draft Genome Sequences for 6 Isolates of Endospore-Forming Class Bacilli Species Isolated from Soil from a Suburban, Wooded, Developed Space.	0
404	Genomic Variability Correlates with Biofilm Phenotypes in Multidrug Resistant Clinical Isolates of <i>Pseudomonas aeruginosa</i> .	0
403	Emergence of a Novel Lineage and Wide Spread of a blaCTX-M-15/IncHI2/ST1 Plasmid among Nosocomial <i>Enterobacter</i> in Guadeloupe. 2022 , 11, 1443	0
402	Adaptations to high pressure of <i>Nautilia</i> sp. strain PV -1, a piezophilic <i>Campylobacterium</i> (aka <i>Epsilonproteobacterium</i>) isolated from a deep-sea hydrothermal vent.	1
401	Plasticity of the adult human small intestinal stoma microbiota. 2022 ,	1
400	Metabolic Characteristics of Porcine LA-MRSA CC398 and CC9 Isolates from Germany and China via Biolog Phenotype MicroArrayTM. 2022 , 10, 2116	0
399	Mirubactin C rescues the lethal effect of cell wall biosynthesis mutations in <i>Bacillus subtilis</i> . 13,	0
398	Comparative Genomic Analysis of Phytopathogenic <i>Xanthomonas</i> Species Suggests High Level of Genome Plasticity Related to Virulence and Host Adaptation. 2022 , 1, 218-241	0
397	Comparative genome analysis of mycobacteria focusing on tRNA and non-coding RNA. 2022 , 23,	0
396	Friend or Foe: Draft Genome Sequence of <i>Bradyrhizobium</i> sp. Strain SRS-191.	0
395	Predominance of Methanomicrobiales and diverse hydrocarbon-degrading taxa in the Appalachian coalbed biosphere revealed through metagenomics and genome-resolved metabolisms..	0

- 394 *Hephaestia mangrovi* sp. nov., a novel endophytic bacterium isolated from *Aegiceras corniculatum*. **2022**, 72, ○
- 393 *Metallosphaera javensis* sp. nov., a novel species of thermoacidophilic archaea, isolated from a volcanic area. **2022**, 72, ○
- 392 *Salinimicrobium sediminilitoris* sp. nov., Isolated from a Tidal Flat. **2022**, 79, ○
- 391 *Gordonia zhenghanii* sp. nov. and *Gordonia liuliyuniae* sp. nov., isolated from bat faeces. **2022**, 72, ○
- 390 *Fructobacillus cardui* sp. nov., isolated from a thistle (*Carduus nutans*) flower. **2022**, 72, ○
- 389 Complete Genome Sequence of *Brucella abortus* 2308, Isolated from an Abortion Storm on a Dairy Farm in India. ○
- 388 Potential autotrophic carbon-fixer and Fe(II)-oxidizer *Alcanivorax* sp. MM125-6 isolated from Wocan hydrothermal field. 13, ○
- 387 *Zavarzinia marina* sp. nov., a novel hydrocarbon-degrading bacterium isolated from deep chlorophyll maximum layer seawater of the West Pacific Ocean and emended description of the genus *Zavarzinia*. **2022**, 72, ○
- 386 *Streptococcus salivarius* 24SMBc Genome Analysis Reveals New Biosynthetic Gene Clusters Involved in Antimicrobial Effects on *Streptococcus pneumoniae* and *Streptococcus pyogenes*. **2022**, 10, 2042 ○
- 385 Genome sequence of the entomopathogenic *Serratia entomophila* isolate 626 and characterisation of the species specific itaconate degradation pathway. **2022**, 23, ○
- 384 High Titer of (S)-Equol Synthesis from Daidzein in *Escherichia coli*. ○
- 383 *Bacillus velezensis* TSA32-1 as a Promising Agent for Biocontrol of Plant Pathogenic Fungi. **2022**, 8, 1053 ○
- 382 Insights from the genome sequence of *Bacillus tropicus* EMB20, an efficient β -lactamase-producing bacterium. **2022**, 12, ○
- 381 *Rasiella rasia* gen. nov. sp. nov. within the family Flavobacteriaceae isolated from seawater recirculating aquaculture system. **2022**, 60, 1070-1076 ○
- 380 Comprehensive multi-omics characterization of gut microbiome extracellular vesicles reveals a connection to gut-brain axis signaling. ○
- 379 Glycogen degrading activities of catalytic domains of α -amylase and α -amylase-pullulanase enzymes conserved in *Gardnerella* spp. from the vaginal microbiome. 1
- 378 Genome Mining Reveals High Biosynthetic Potential of Biocontrol Agent *Bacillus velezensis* B.BV10. **2022**, 13, 1984 ○
- 377 Isolation of Genes Encoding Carbon Metabolism Pathways from Complex Microbial Communities. **2023**, 115-123 ○

- 376 The deep-sea coral, *Callogorgia delta*, associates with bacteria belonging to a novel marine branch of the Mollicutes. 0
- 375 An expanded arsenal of immune systems that protect bacteria from phages. **2022**, 2
- 374 Genomic Diversity of NDM-Producing *Klebsiella* Species from Brazil, 2013-2022. **2022**, 11, 1395 0
- 373 Dissemination of bla_{NDM-5} and mcr-8.1 in carbapenem-resistant *Klebsiella pneumoniae* and *Klebsiella quasipneumoniae* in an animal breeding area in Eastern China. 13, 0
- 372 Monochloramine Induces Release of DNA and RNA from Bacterial Cells: Quantification, Sequencing Analyses, and Implications. 0
- 371 Phylogenomic analysis of a metagenome-assembled genome indicates a new taxon of an anoxygenic phototroph bacterium in the family Chromatiaceae and the proposal of *Candidatus Thioaporphodococcus* gen. nov. **2022**, 204, 0
- 370 Endophytic *Bosea spartocytisi* sp. nov. Coexists with rhizobia in root nodules of *Spartocytisus supranubius* growing in soils of Teide National Park (Canary Islands). **2022**, 45, 126374 1
- 369 Draft Genome Sequence of *Stutzerimonas stutzeri* NT-I, Which Reduces Selenium Oxyanions into Elemental Selenium and Volatile Selenium Species. 0
- 368 Silicon and plant nutrition: Dynamics, mechanisms of transport, and role of silicon solubilizer microbiomes in sustainable agriculture. **2022**, 2
- 367 *Lysobacter sedimenti* sp. nov., Isolated from the Sediment, and Reclassification of *Luteimonas lumbrici* as *Lysobacter lumbrici* comb. nov. **2022**, 79, 0
- 366 *Portibacter marinus* sp. nov., isolated from the sediment on the surface of plastics and proposal of a novel genus *Neolewinella* gen. nov. based on the genome-based phylogeny of the family Lewinellaceae. **2022**, 72, 0
- 365 Isolation and characterization of novel *Fusobacterium nucleatum* bacteriophages. 13, 0
- 364 Genomic insights into phage-host interaction in the deep-sea chemolithoautotrophic *Campylobacterota*, *Nitratiruptor*. **2022**, 2, 0
- 363 Transport and utilization of glycogen breakdown products by *Gardnerella* spp. from the human vaginal microbiome. 0
- 362 Novel species of *Frankia*, *Frankia gtarii* sp. nov. and *Frankia tisai* sp. nov., isolated from a root nodule of *Alnus glutinosa*. **2022**, 126377 0
- 361 First report of a multidrug-resistant *Salmonella enterica* Serovar *Infantis* carrying pESI megaplasmid isolated from marine shrimp in India. **2022**, 31, 248-251 0
- 360 A new enantioselective dioxygenase for the (S)-enantiomer of the chiral herbicide dichlorprop in *Sphingopyxis* sp. DBS4. **2023**, 176, 105511 0
- 359 *Citrobacter portucalensis* Sb-2 contains a metalloid resistance determinant transmitted by *Citrobacter* phage *Chris1*. **2023**, 443, 130184 0

- 358 Explainable Deep Learning Approach for Multilabel Classification of Antimicrobial Resistance With Missing Labels. **2022**, 10, 113073-113085 ○
- 357 Characterization of the lytic phage MSP1 for the inhibition of multidrug-resistant *Salmonella enterica* serovars Thompson and its biofilm. **2023**, 385, 110010 1
- 356 Genomic characterization and application of a novel bacteriophage STG2 capable of reducing planktonic and biofilm cells of *Salmonella*. **2023**, 385, 109999 ○
- 355 A Review of Extremophile Protein Classification Using Machine Learning. **2022**, ○
- 354 Genomic Analysis of Halotolerant Bacterial Strains *Marteella soudanensis* NC18T and NC20. **2022**, ○
- 353 Genotype-phenotype correlations within the Geodermatophilaceae. 13, 1
- 352 Draft Genome Sequence of a Ketoprofen Degradator, *Rhodococcus erythropolis* IEGM 746. ○
- 351 Novel *Aeromonas* Phage Ahy-Yong1 and Its Protective Effects against *Aeromonas hydrophila* in Brocade Carp (*Cyprinus* aka Koi). **2022**, 14, 2498 ○
- 350 Genome Report of Emergent Fish Pathogen *Edwardsiella piscicida* Recovered from *Pseudoplatystoma corruscans* in Brazil. ○
- 349 Biocontrol of methicillin-resistant *Staphylococcus aureus* using a virulent bacteriophage derived from a temperate one. **2022**, 127258 ○
- 348 Extraintestinal survival and host immune response to *Vibrio cholerae*. ○
- 347 Comparative genomics study of *Staphylococcus aureus* isolated from cattle and humans reveals virulence patterns exclusively associated with bovine clinical mastitis strains. 13, 1
- 346 Bioremediation of Multiple Heavy Metals Mediated by Antarctic Marine Isolated *Dietzia psychrhalcaliphila* J11D. **2022**, 10, 1669 ○
- 345 First Record of the Rare Species *Aeromonas lusitana* from Rainbow Trout (*Oncorhynchus mykiss*, Walbaum): Comparative Analysis with the Existing Strains. **2022**, 11, 1299 ○
- 344 Quorum sensing activities and genomic insights of plant growth-promoting rhizobacteria isolated from Assam tea. ○
- 343 Characterization and whole-genome sequencing of an extreme arsenic tolerant *Citrobacter freundii* SRS1 strain isolated from Savar area in Bangladesh. ○
- 342 Characterization of antibiotic-resistance traits in *Akkermansia muciniphila* strains of human origin. **2022**, 12, ○
- 341 Modeling multiphage-bacteria kinetics to predict phage therapy potency and longevity. ○

- 340 Globally Disseminated Multidrug Resistance Plasmids Revealed by Complete Assembly of Multidrug Resistant *Escherichia coli* and *Klebsiella pneumoniae* Genomes from Diarrheal Disease in Botswana. **2022**, 2, 934-949 ○
- 339 *Lacrimispora defluvii* PI-S10-B5AT sp. nov., an Obligate Anaerobe, Isolated from an Industrial Waste and Reclassification of *Hungatella xylanolytica* as *Lacrimispora xylanolytica* and *Clostridium indicum* as *Lacrimispora indica* Comb. nov.. **2022**, 79, ○
- 338 Isolation, characterization, and genomic analysis of vB_PaeS_TUMS_P81, a lytic bacteriophage against *Pseudomonas aeruginosa*. ○
- 337 *Paracrocinitomix mangrovi* gen. nov., sp. nov., isolated from a mangrove sediment: proposal of two new families, *Phaeocystidibacteraceae* fam. nov. and *Owenweeksiaceae* fam. nov., and emended description of the family *Schleiferiaceae*. ○
- 336 *Jiella avicenniae* sp. nov., a novel endophytic bacterium isolated from bark of *Avicennia marina*. **2022**, 204, ○
- 335 *Gramella sediminis* sp. nov., isolated from a tidal flat of the Yellow Sea. **2022**, 72, 1
- 334 *Marinobacterium sedimentorum* sp. nov., Isolated from the Bottom Sediments of the Okhotsk Sea. **2022**, 14, 944 ○
- 333 Complete Genome Sequence and Comparative Genome Analysis of *Variovorax* sp. Strains PAMC28711, PAMC26660, and PAMC28562 and Trehalose Metabolic Pathways in Antarctica Isolates. **2022**, 2022, 1-13 ○
- 332 Draft genome of *Sporosarcina* sp. NCCP-2222T isolated from rhizosphere of mangrove plant *Ceriops tagal* reveals its potential as a plant biostimulant and constitutes a novel species. **2022**, 102543 ○
- 331 Phage resistance profiling identifies new genes required for biogenesis and modification of the corynebacterial cell envelope. 11, ○
- 330 Genomic analysis of *Paenibacillus* sp. MDMC362 from the Merzouga desert leads to the identification of a potentially thermostable catalase. ○
- 329 Metagenomic insights into microorganisms and antibiotic resistance genes of waste antibiotic fermentation residues along production, storage and treatment processes. **2022**, 1, 1
- 328 Physiological niche informs evolution of metabolic function and corresponding drug targets of pathobionts. ○
- 327 Prevalence and Genetic Analysis of Resistance Mechanisms of Linezolid-Nonsusceptible Enterococci in a Tertiary Care Hospital Examined via Whole-Genome Sequencing. **2022**, 11, 1624 ○
- 326 Genomic Analysis of a Novel Heavy Metal Resistant Isolate from a Black Sea Contaminated Sediment with the Potential to Degrade Alkanes: *Plantactinospora alkalitolerans* sp. nov.. **2022**, 14, 947 1
- 325 Insights into Genomic Evolution and the Potential Genetic Basis of *Klebsiella variicola* subsp. *variicola* ZH07 Reveal Its Potential for Plant Growth Promotion and Autotoxin Degradation. ○
- 324 Whole Genome Analyses Accurately Identify *Neisseria* spp. and Limit Taxonomic Ambiguity. **2022**, 23, 13456 ○
- 323 Genomic Diversity of *Campylobacter lari* Group Isolates from Europe and Australia in a One Health Context. ○

- 322 Identification of a 17 β -estradiol-degrading *Microbacterium hominis* SJTG1 With High Adaptability and Characterization of the Genes for Estrogen Degradation. **2022**, 130371 ○
- 321 Introducing the Bacterial and Viral Bioinformatics Resource Center (BV-BRC): a resource combining PATRIC, IRD and ViPR. 10
- 320 Genomic potential for exopolysaccharide production and differential polysaccharide degradation in closely related *Alteromonas* sp. PRIM-21 and *Alteromonas fortis* 1T. ○
- 319 Taxonomic and genomic characterization of *Sporosarcina cyprini* sp. nov., moderately tolerant of Cr+6 and Cd+2 isolated from the gut of invasive fish *Cyprinus carpio* var. *communis* (Linn., 1758). ○
- 318 Divergent gene expression responses in two Baltic Sea heterotrophic model bacteria to dinoflagellate dissolved organic matter. **2022**, 17, e0243406 ○
- 317 Role of stress-induced proteins RpoS and YicC in the persistence of *Salmonella enterica* subsp. *enterica* serotype Typhimurium in tomato plants. ○
- 316 Analysis of pCl107 a large plasmid carried by an ST25 *Acinetobacter baumannii* strain reveals a complex evolutionary history and links to multiple antibiotic resistance and metabolic pathways. ○
- 315 Genomes of *Vibrio metoecus* co-isolated with *Vibrio cholerae* extend our understanding of differences between these closely related species. **2022**, 14, ○
- 314 Characterization and the host specificity of Pet-CM3 Φ , a new phage infecting *Cronobacter* and *Enterobacter* strains. **2023**, 324, 199025 ○
- 313 Comparative analysis unravels genetic recombination events of *Vibrio parahaemolyticus* recA gene. **2023**, 107, 105396 ○
- 312 Whole genome sequence data of a marine bacterium, *Marinobacter adhaerens* PBVC038, associated with toxic harmful algal bloom. **2023**, 46, 108768 ○
- 311 CAM-21, a novel lytic phage with high specificity towards *Escherichia coli* O157:H7 in food products. **2023**, 386, 110026 ○
- 310 Genomic analysis of *Marinimicrobium* sp. C6131 reveals its genetic potential involved in chitin metabolism. **2023**, 67, 101007 ○
- 309 Use of kefir-derived lactic acid bacteria for the preparation of a fermented soy drink with increased estrogenic activity. **2023**, 164, 112322 1
- 308 Whole genome and 16S rRNA dataset of *Pectobacterium carotovorum* strain 21TX0081 isolated from a symptomatic onion foliage in Texas. **2023**, 46, 108823 ○
- 307 Differential impacts of salinity on antibiotic resistance genes during cattle manure stockpiling are linked to mobility potentials revealed by metagenomic sequencing. **2023**, 445, 130590 ○
- 306 Comparison of functional classification systems. **2022**, 4, ○
- 305 Effects of *Klebsiella pneumoniae* Bacteriophages on IRAK3 Knockdown/Knockout THP-1 Monocyte Cell Lines. **2022**, 14, 2582 ○

304	Consumption of N ₂ O by <i>Flavobacterium azooxidireducens</i> sp. nov. Isolated from Decomposing Leaf Litter of <i>Phragmites australis</i> (Cav.). 2022 , 10, 2304	1
303	<i>Zunongwangia pacifica</i> sp. nov., isolated from surface seawater of the Western Pacific Ocean. 2022 , 72,	0
302	Plasmids of the urinary microbiota. 2022 , 4,	0
301	Genomic and probiotic attributes of <i>Lactobacillus</i> strains from rice-based fermented foods of North Eastern India.	0
300	ARCHE: A HIERARCHICAL, EASY TO DOWNLOAD, FUNCTIONAL-OPTIMIZED ANNOTATOR FOR MICROBIAL META(GENOMES).	0
299	Genomic analysis and in vivo efficacy of <i>Pediococcus acidilactici</i> as a potential probiotic to prevent hyperglycemia, hypercholesterolemia and gastrointestinal infections. 2022 , 12,	1
298	NDM-1 and OXA-48-Like Carbapenemases (OXA-48, OXA-181 and OXA-252) Co-Producing <i>Shewanella xiamenensis</i> from Hospital Wastewater, China. Volume 15, 6927-6938	0
297	<i>Endozoicomonas-chlamydiae</i> interactions in cell-associated microbial aggregates of the coral <i>Pocillopora acuta</i> .	0
296	<i>Mangrovimonas futianensis</i> sp. nov., a novel species isolated from mangrove sediment. 2022 , 72,	0
295	Co-transfer of functionally interdependent genes contributes to genome mosaicism in lambdoid phages. 2022 , 8,	0
294	<i>Anianabacter salinae</i> gen. nov., sp. nov. ASV31T, a Facultative Alkaliphilic and Extremely Halotolerant Bacterium Isolated from Brine of a Millennial Continental Saltern. 2022 , 14, 1009	0
293	Ribosomal RNA operons define a central functional compartment in the <i>Streptomyces</i> chromosome. 2022 , 50, 11654-11669	0
292	The Long and Short of Genome Sequencing: Using a Hybrid Sequencing Strategy to Sequence Oral Microbial Genomes. 2023 , 75-89	0
291	Probiogenomic In-Silico Analysis and Safety Assessment of <i>Lactiplantibacillus plantarum</i> DJF10 Strain Isolated from Korean Raw Milk. 2022 , 23, 14494	1
290	Potential application of a newly isolated phage BUCT609 infecting <i>Stenotrophomonas maltophilia</i> . 13,	0
289	Identification of a growth factor required for culturing specific fastidious oral bacteria. 2023 , 15,	0
288	The first host-associated anaerobic isolate of <i>Psychrilyobacter</i> provides insights into its potential roles in the abalone gut.	0
287	Prophages regulate <i>Shewanella fidelis</i> 3313 motility and biofilm formation: implications for gut colonization dynamics in <i>Ciona robusta</i> .	0

- 286 Genomic profiling of *Nitrospira* species reveals ecological success of comammox *Nitrospira*. **2022**, 10, ○
- 285 *Limnobacter parvus* sp. nov., a Thiosulfate-Oxidizing Bacterium Isolated from Lake Water. **2023**, 80, ○
- 284 Phylogenomic analysis of *Citrobacter* sp. strain AAK_AS5 and its metabolic capabilities to support nitrogen removal behavior. ○
- 283 Various mobile genetic elements carrying *optrA* in *Enterococcus faecium* and *Enterococcus faecalis* isolates from swine within the same farm. ○
- 282 In Vitro and Pre-Clinical Evaluation of Locally Isolated Phages, vB_Pae_SMP1 and vB_Pae_SMP5, Formulated as Hydrogels against Carbapenem-Resistant *Pseudomonas aeruginosa*. **2022**, 14, 2760 ○
- 281 Draft Genome Sequence of *Mycobacterium tuberculosis* Strain SNMICRO 2047-20, Isolated from Intraocular Infection. ○
- 280 Genomic Insights into Two Endophytic Strains: *Stenotrophomonas geniculata* NWUBe21 and *Pseudomonas carnis* NWUBe30 from Cowpea with Plant Growth-Stimulating Attributes. **2022**, 12, 12953 1
- 279 The use of filamentous hemagglutinin adhesin to detect immune responses to *Campylobacter hepaticus* infections in layer hens. 9, ○
- 278 Comparative genomics of drug-resistant strains of *Mycobacterium tuberculosis* in Ecuador. **2022**, 23, ○
- 277 Complete genome sequence analysis of a plant growth-promoting phylloplane *Bacillus altitudinis* FD48 offers mechanistic insights into priming drought stress tolerance in rice. **2022**, 110550 1
- 276 A computational model of *Pseudomonas syringae* metabolism unveils the role of branched-chain amino acids in virulence expression at the early stages of *Arabidopsis* colonization. ○
- 275 *Staphylococcus aureus* populations from the gut and the blood are not distinguished by virulence traits—critical role of host barrier integrity. **2022**, 10, ○
- 274 *Nocardioides palaemonis* sp. nov. and *Tessaracoccus palaemonis* sp. nov., isolated from the gastrointestinal tract of lake prawn. **2022**, 72, ○
- 273 *Emiliana huxleyi* Bacteria Interactions under Increasing CO₂ Concentrations. **2022**, 10, 2461 ○
- 272 Adaptive lifestyle of bacteria determines phage-bacteria interaction. 13, ○
- 271 Phylogenomic diversity of *Vibrio* species and other Gammaproteobacteria isolated from Pacific oysters (*Crassostrea gigas*) during a summer mortality outbreak. **2022**, 8, ○
- 270 The draft genome of Andean *Rhodopseudomonas* sp. strain AZUL predicts genome plasticity and adaptation to chemical homeostasis. **2022**, 22, ○
- 269 Exploring the Interspecific Interactions and the Metabolome of the Soil Isolate *Hylemonella gracilis*. ○

- 268 *Levilactobacillus humaensis* sp. nov. and *Lapidilactobacillus luobeiensis* sp. nov., isolated from traditional Chinese pickle. **2022**, 72, 0
- 267 Specialized metabolic convergence in the gut microbiomes of cycad-feeding insects tolerant to Ethylamino-L-alanine (BMAA). 0
- 266 *Gordonia tangerina* sp. nov., isolated from seawater. **2022**, 72, 0
- 265 Safety Evaluation of *Bacillus subtilis* IDCC1101, Newly Isolated from Cheonggukjang, for Industrial Applications. **2022**, 10, 2494 2
- 264 *Paenibacillus xylinteritus* sp. nov., a novel bacterial species isolated from grapevine wood. 0
- 263 Genomic analysis of *Mycobacterium brumaes* sustains its nonpathogenic and immunogenic phenotype. 0
- 262 IS26-mediated in vivo acquisition of blaKPC-2 in an ST11-K64 *Klebsiella pneumoniae* isolate from a senile inpatient. 0
- 261 *Halocatena salina* sp. nov., a filamentous halophilic archaeon isolated from Aiding Salt Lake. **2022**, 72, 0
- 260 Heterologous production and characterization of a pyomelanin of Antarctic *Pseudomonas* sp. ANT_H4: a metabolite protecting against UV and free radicals, interacting with iron from minerals and exhibiting priming properties toward plant hairy roots. **2022**, 21, 0
- 259 Disproportionation of Inorganic Sulfur Compounds by Mesophilic Chemolithoautotrophic *Campylobacterota*. 0
- 258 *Streptomyces Spinosirectus* sp. nov., Isolated From the Medicinal Plant *Xanthium Sibiricum*. **2023**, 80, 0
- 257 Outbreak of carbapenem-resistant enterobacteria in a thoracic-oncology unit through clonal and plasmid-mediated transmission of the blaOXA-48 gene in Southern France. 12, 0
- 256 Draft Genome Sequences of Four Methicillin-Resistant *Staphylococcus aureus* Strains (M080_2017, M106_2017, M181_2017, and M191_2017), Isolated from a Malaysian Teaching Hospital. **2022**, 11, 0
- 255 Metagenomic-based surveillance systems for antibiotic resistance in non-clinical settings. 13, 0
- 254 Pharokka: a fast scalable bacteriophage annotation tool. 0
- 253 Description of *Microbacterium neungamense* sp. nov. isolated from a hot spring. **2023**, 205, 0
- 252 *Nitratireductor luteus* sp. nov. isolated from saline-alkali land. 0
- 251 Genome-based taxonomic rearrangement of *Oceanobacter*-related bacteria including the description of *Thalassolituus hydrocarbonoclasticus* sp. nov. and *Thalassolituus pacificus* sp. nov. and emended description of the genus *Thalassolituus*. 13, 0

- 250 *Janthinobacterium kumbetense* sp. nov., a violacein producing bacterium isolated from spring water in Turkey, and investigation of antimicrobial activity of violacein. ○
- 249 Genomic Characterization of Livestock-Associated Methicillin-Resistant *Staphylococcus aureus* ST7 Isolates from a Case of Human Bacteremia in China. Volume 15, 7449-7457 ○
- 248 Phenotypic and Genotypic Characterization of Carbapenem-Resistant Enterobacteriaceae Recovered from a Single Hospital in China, 2013 to 2017. Volume 15, 7679-7690 ○
- 247 Vertical and horizontal gene transfer tradeoffs direct plasmid fitness. ○
- 246 Comparative Genomics of *Lentilactobacillus parabuchneri* isolated from dairy, KEM complex, Makgeolli, and Saliva Microbiomes. **2022**, 23, ○
- 245 Characterization of three *Stenotrophomonas* strains isolated from different ecosystems and proposal of *Stenotrophomonas mori* sp. nov. and *Stenotrophomonas lacuserhaii* sp. nov.. 13, ○
- 244 *Devosia oryisoli* sp. nov., a novel moderately halotolerant bacterium isolated from the roots of rice plants and genome mining revealed the biosynthesis potential as plant growth promoter. ○
- 243 Unexpected finding of *Fusobacterium varium* abundance in cattle rumen: implications for liver abscess interventions. ○
- 242 Complete Genome Sequence of *Variovorax paradoxus* JBCE486, Which Alleviates the Salt Stress of the Endemic Plant *Ulleung-Sanmaneu*. ○
- 241 Intracellular Transposition of Mobile Genetic Elements Associated with the Colistin Resistance Gene *mcr-1*. ○
- 240 Cave *Thiovulum* (*Candidatus Thiovulum stygium*) differs metabolically and genomically from marine species. ○
- 239 Comparative genomic analyses of four novel *Ramlibacter* species and the cellulose-degrading properties of *Ramlibacter cellulolyticus* sp. nov.. **2022**, 12, ○
- 238 Evidence of p-nitrophenol Biodegradation and Study of Genomic Attributes from a Newly Isolated Aquatic Bacterium *Pseudomonas Asiatica* Strain PNPG3. 1-18 ○
- 237 Carbapenem resistance in *Acinetobacter pittii* isolates mediated by metallo-β-lactamases. ○
- 236 Comparative Genomic Analysis of the Hydrocarbon-Oxidizing Dibenzothiophene-Desulfurizing *Gordonia* Strains. **2023**, 11, 4 1
- 235 Revisiting the taxonomy of the genus *Rhodopirellula* with the proposal for reclassification of the genus to *Rhodopirellula sensu stricto*, *Aporhodopirellula* gen. nov., *Allorhodopirellula* gen. nov. and *Neorhodopirellula* gen. nov. ○
- 234 Metabolic Network Models of the *Gardnerella* Pangenome Identify Key Interactions with the Vaginal Environment. ○
- 233 Potential Biocontrol Activities of *Populus* Endophytes against Several Plant Pathogens Using Different Inhibitory Mechanisms. **2023**, 12, 13 1

- 232 Isolation, characterization, and genomic analysis of vB_PaeP_TUMS_P121, a new lytic bacteriophage infecting *Pseudomonas aeruginosa*. **2023**, 168, 0
- 231 Characterization and genomic Analysis of a novel *Pseudomonas* phage vB_PsaP_M1, representing a new viral family, Psaeviridae. 9, 0
- 230 Molecular Characterization of Five Novel Plasmids from *Enterococcus italicus* SD1 Isolated from Fermented Milk: An Insight into Understanding Plasmid Incompatibility. **2022**, 147154 0
- 229 *Paraconexibacter antarcticus* sp. nov., a novel actinobacterium isolated from Antarctic tundra soil. **2022**, 72, 0
- 228 Physiological and comparative proteomic characterization of *Desulfolithobacter dissulfuricans* gen. nov., sp. nov., a novel mesophilic, sulfur-disproportionating chemolithoautotroph from a deep-sea hydrothermal vent. 13, 1
- 227 Recombination Drives Evolution of Carbapenem-Resistant *Klebsiella pneumoniae* Sequence Type 11 KL47 to KL64 in China. 1
- 226 Genomic Characteristics and Comparative Genomic Analysis of a Probiotic Bacterial Strain, *Lactiplantibacillus plantarum* CKDB008. **2022**, 2, 0
- 225 Draft Genome Sequence of *Lactiplantibacillus plantarum* Strain ISO1, a Potential Probiotic Bacterium Isolated from the Milk of South African Saanen Goats. 0
- 224 Comparative Genomics and Phenotypic Characterization of *Gluconacetobacter entanii*, a Highly Acetic Acid-Tolerant Bacterium from Vinegars. **2023**, 12, 214 0
- 223 Commensal *Lactobacilli* Metabolically Contribute to Cervical Epithelial Homeostasis in a Species-Specific Manner. 0
- 222 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. **2023**, 11, 207 0
- 221 Genomic analysis of *Mycobacterium brumae* sustains its nonpathogenic and immunogenic phenotype. 13, 0
- 220 *Weizmannia acidilactici* sp. nov., a lactic acid producing bacterium isolated from soils. **2023**, 46, 126389 0
- 219 *Halorarius litoreus* gen. nov., sp. nov., *Halorarius halobius* sp. nov., *Haloglomus halophilum* sp. nov., *Haloglomus salinum* sp. nov., and *Natronomonas marina* sp. nov., extremely halophilic archaea isolated from tidal flat and marine solar salt. 10, 0
- 218 Draft Genome Sequence and Annotation of *Pseudomonas carnis* Strain 20TX0167, Isolated from an Onion (*Allium cepa*). 0
- 217 *Pseudarthrobacter humi* sp. nov., an actinobacterium isolated from soil. **2023**, 73, 0
- 216 Genomic and Transcriptomic Insights into Salinity Tolerance-Based Niche Differentiation of *Synechococcus* Clades in Estuarine and Coastal Waters. 0
- 215 Monitoring phage-induced lysis of gram-negatives in real time using a fluorescent DNA dye. **2023**, 13, 2

- 214 Alicyclobacillus chiapanensis PA2T, a novel species with specific adaptation in a bacterial cell wall isolated from an active volcano. ○
- 213 Genomic insights of Leclercia adecarboxylata strains linked to an outbreak in public hospitals in Mexico. ○
- 212 Emergence of plasmid-mediated colistin resistance mcr-3.5 gene in Citrobacter amalonaticus and Citrobacter sedlakii isolated from healthy individual in Thailand. 12, ○
- 211 Bacillus subtilis phage phi18: genomic analysis and receptor identification. **2023**, 168, ○
- 210 Genomic Characterization of Salmonella enterica serovar Weltevreden Associated with Human Diarrhea. ○
- 209 Complete Genome Sequences of Two Lytic Phages of Salmonella enterica. ○
- 208 Meningitis-associated pneumococcal serotype 8, ST 53, strain is hypervirulent in a rat model and has non-haemolytic pneumolysin which can be attenuated by liposomes. 12, ○
- 207 Nisin E, a New Nisin Variant Produced by Streptococcus equinus MDC1. **2023**, 13, 1186 ○
- 206 Tracing of persistent Listeria monocytogenes contamination in ewe's milk farm. ○
- 205 Characterization and genome analysis of Vibrio phage vB_VhaP_PG11, representing a new viral genus. 9, ○
- 204 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. ○
- 203 Pseudomonas citri sp. nov., a potential novel plant growth promoting bacterium isolated from rhizosphere soil of citrus. ○
- 202 Draft Genome Sequences of Two Enterobacter hormaechei subsp. xiangfangensis Strains Isolated from the Moroccan Sahara. ○
- 201 Electrochemically mediated bioconversion and integrated purification greatly enhanced co-production of 1,3-propanediol and organic acids from glycerol in an industrial bioprocess. ○
- 200 Susceptible bacteria survive antibiotic treatment in the mammalian gastrointestinal tract without evolving resistance. ○
- 199 Comparative Genomics Revealed a Potential Threat of Aeromonas rivipollensis G87 Strain and Its Antibiotic Resistance. **2023**, 12, 131 ○
- 198 Enterococcus faecium Bacteriophage vB_EfaH_163, a New Member of the Herelleviridae Family, Reduces the Mortality Associated with an E. faecium vanR Clinical Isolate in a Galleria mellonella Animal Model. **2023**, 15, 179 1
- 197 Real-time polymerase chain reaction methods for strain specific identification and enumeration of strain Lactocaseibacillus paracasei 8700:2. 13, ○

- 196 Draft genome sequence of *Streptomyces* sp. KD18, isolated from industrial soil. **2023**, 13, ○
- 195 Draft Genome Sequences of Three *Pseudomonas chengduensis* Strains Isolated from Desert Soil in Morocco. ○
- 194 A Genome of Temperate Enterococcus Bacteriophage Placed in a Space of Pooled Viral Dark Matter Sequences. **2023**, 15, 216 ○
- 193 *Flaviumibacter fluminis* sp. nov., a novel thermotolerant bacterium isolated from river silt. **2023**, 73, ○
- 192 Phylogenomic analysis of the genus *Alcanivorax*: proposal for division of this genus into the emended genus *Alcanivorax* and two novel genera *Alloalcanivorax* gen. nov. and *Isoalcanivorax* gen. nov.. **2023**, 73, ○
- 191 Whole-genome sequencing, annotation, and biological characterization of a novel Siphoviridae phage against multi-drug resistant *Propionibacterium acne*. 13, ○
- 190 Whole genome sequencing and annotation of a lysogenic phage vB_EcoP_DE5 isolated from donkey-derived *Escherichia coli*. ○
- 189 Dataset of the complete genome of *Streptomyces cavourensis* strain 2BA6PGT isolated from sediment from the bottom of the salt lake Verkhnee Beloe (Buryatia, Russia). **2023**, 46, 108877 ○
- 188 Multi-omics approach reveals elevated potential of bacteria for biodegradation of imidacloprid. **2023**, 221, 115271 ○
- 187 Description and genomic characterization of *Nocardioides bruguierae* sp. nov., isolated from *Bruguiera gymnorhiza*. **2023**, 46, 126391 ○
- 186 De Novo Genome Sequencing, Annotation, and Taxonomy of Unknown Bacteria. **2023**, 2023, pdb.top107847 ○
- 185 Systems biology approach for analysis of mobile genetic elements in chicken gut microbiome. **2022**, ○
- 184 The inside scoop: Comparative genomics of two intranuclear bacteria, *Candidatus Berkiella cookevillensis* and *Candidatus Berkiella aquae* **2022**, 17, e0278206 ○
- 183 Diversity of Mixotrophic Neutrophilic Thiosulfate- and Iron-Oxidizing Bacteria from Deep-Sea Hydrothermal Vents. **2023**, 11, 100 ○
- 182 Characterization of a lytic phage KFS-EC3 infecting multiple foodborne pathogens. **2022**, 29, 1022-1034 ○
- 181 Genome-scale metabolic reconstruction of 7,302 human microorganisms for personalized medicine. 1
- 180 A Maverick-like cluster in the genome of a pathogenic, moderately virulent strain of *Gallibacterium anatis*, ESV200, a transient biofilm producer. 14, ○
- 179 Seeds of *Stevia rebaudiana* Bertoni as a Source of Plant Growth-Promoting Endophytic Bacteria with the Potential to Synthesize Rebaudioside A. **2023**, 24, 2174 ○

- 178 *Streptomyces macrolidinus* sp. nov., a novel soil actinobacterium with potential anticancer and antimalarial activity. **2023**, 73, ○
- 177 Multidrug-resistant toxigenic *Corynebacterium diphtheriae* sublineage 453 with two novel resistance genomic islands. **2023**, 9, ○
- 176 *Amycolatopsis* from Desert Specialist Fungus-Growing Ants Suppresses Contaminant Fungi Using the Antibiotic ECO-0501. ○
- 175 Characterization and genome analysis of *Escherichia* phage fBC-Eco01, isolated from wastewater in Tunisia. **2023**, 168, ○
- 174 *Vibrio sinus* sp. nov., a marine bacterium isolated from coastal seawater. **2023**, 73, ○
- 173 Draft Genome Sequence of *Vibrio parahaemolyticus* PSU5579, Isolated during an Outbreak of Acute Hepatopancreatic Necrosis Disease in Thailand. ○
- 172 Comparative Genomics of a Polyvalent *Escherichia*-*Salmonella* Phage fp01 and In Silico Analysis of Its Receptor Binding Protein and Conserved Enterobacteriaceae Phage Receptor. **2023**, 15, 379 ○
- 171 Complete genome sequence of the temperate bacteriophage phiSTEC1575-Stx2k induced from Shiga toxin-producing *Escherichia coli*. ○
- 170 Whole genome sequencing of bovine *Pasteurella multocida* type B isolated from haemorrhagic septicaemia during 2020 major outbreak in East Coast, Malaysia. **2023**, ○
- 169 Genomic insight into the environmental adaptations and toxigenic features of endophytic *Bacillus cereus* CaB1 isolated from *Capsicum annum* L.. **2023**, 13, ○
- 168 Characterization and comprehensive genome analysis of novel bacteriophage, vB_Kpn_ZCKp20p, with lytic and anti-biofilm potential against clinical multidrug-resistant *Klebsiella pneumoniae*. 13, 1
- 167 Pathometagenomics reveals susceptibility to intestinal infection by *Morganella* to be mediated by the blood group-related B4galnt2 gene in wild mice. **2023**, 15, ○
- 166 Biosynthetic novelty index reveals the metabolic potential of rare actinobacteria isolated from highly oligotrophic sediments. **2023**, 9, ○
- 165 Genome Assembly of a Putative Plant Growth-Stimulating Bacterial Sweet Pepper Fruit Isolate, *Enterobacter hormaechei* SRU4.4. ○
- 164 Characteristics of Environmental *Klebsiella pneumoniae* and *Klebsiella oxytoca* Bacteriophages and Their Therapeutic Applications. **2023**, 15, 434 ○
- 163 Evaluation of the Antimicrobial Potential and Characterization of Novel T7-Like *Erwinia* Bacteriophages. **2023**, 12, 180 ○
- 162 Efficacy in *Galleria mellonella* Larvae and Application Potential Assessment of a New Bacteriophage BUCT700 Extensively Lyse *Stenotrophomonas maltophilia*. ○
- 161 Extensively drug-resistant *Acinetobacter baumannii*: role of conjugative plasmids in transferring resistance. 11, e14709 ○

- 160 Retrospective Study of the Epidemiology of *Clostridioides difficile* Infection in the Neurosurgery Department of a Tertiary Hospital in China. Volume 16, 545-554 ○
- 159 Draft genome of *Raoultella planticola*, a high lead resistance bacterium from industrial wastewater. **2023**, 13, ○
- 158 Isolation of vB_AsaM_LPM4 reveals the dynamics of Prophage 3 in *Aeromonas salmonicida* subsp. *salmonicida*. **2023**, 168, ○
- 157 Phenotypic characterization and genome analysis reveal the probiotic potential of a banyan endophyte *Bacillus velezensis* K1. **2023**, 134, ○
- 156 Whole-genome sequencing of *Histophilus somni* strains isolated in Russia. 272-280 ○
- 155 Characterization of Pseudorabies Virus Associated with Severe Respiratory and Neuronal Signs in Old Pigs. **2023**, 2023, 1-12 ○
- 154 *Abyssibius alkaniclasticus* gen. nov., sp. nov., a novel member of the family Rhodobacteraceae, isolated from the Mariana Trench. **2023**, 73, ○
- 153 Phenotypic and Genotypic Characterization of Newly Isolated *Xanthomonas euvesicatoria*-Specific Bacteriophages and Evaluation of Their Biocontrol Potential. **2023**, 12, 947 ○
- 152 Molecular characterization of *Paenibacillus antarcticus* IPAC21, a bioemulsifier producer isolated from Antarctic soil. 14, ○
- 151 Management factors influence *Salmonella* persistence in reused poultry litter over three successive flocks. ○
- 150 Genome Sequence of a Bangladeshi Strain of *Raoultella ornithinolytica*, a Pathogen with Metal and Antimicrobial Resistance Genes Isolated from a Pet Cat. ○
- 149 *Collinsella urealyticum* sp. nov., a urease-positive bacterial strain isolated from swine faeces. **2023**, 205, ○
- 148 Genome analyses of *Weissella* strains isolated from Campos das Vertentes, Minas Gerais, Brazil revealed new bacteriocins with a large spectrum of activity. **2023**, 52, 102421 ○
- 147 *Spiribacter salilacus* sp. nov., a novel moderately halophilic bacterium isolated from a saline lake in China. **2023**, 205, ○
- 146 Isolation, characterization and genomic analysis of a novel phage IME178 with lytic activity against *Escherichia coli*. **2023**, 106099 ○
- 145 Diversity of the type VI secretion systems in the *Neisseria* spp. **2023**, 9, ○
- 144 Microcosm-omics centric investigation reveals elevated bacterial degradation of imidacloprid. **2023**, 324, 121402 ○
- 143 Function of the algicidal bacterium *Pseudomonas* sp. Go58 isolated from the biofilm on a water plant, and its active compounds, pyoluteorins. **2023**, 872, 162088 ○

- 142 A K-17 serotype specific Klebsiella phage JKP2 with biofilm reduction potential. **2023**, 329, 199107 ○
- 141 Genome-guided approaches and evaluation of the strategies to influence bioprocessing assisted morphological engineering of Streptomyces cell factories. **2023**, 376, 128836 ○
- 140 Whole genome sequence analysis enabled affirmation of the probiotic potential of marine sporulater Bacillus amyloliquefaciens BTSS3 isolated from Centroscyllium fabricii. **2023**, 864, 147305 ○
- 139 Foremost report of the whole genome of Spirabilibacterium mucosae from India and comparative genomics of the novel genus Spirabilibacterium. **2023**, 867, 147359 ○
- 138 A novel lytic bacteriophage against colistin-resistant Escherichia coli isolated from different animals. **2023**, 329, 199090 ○
- 137 Ancylobacter mangrovi sp. nov., a novel endophytic bacterium isolated form mangrove plant. **2023**, 46, 126419 ○
- 136 Bioprospecting of the Antarctic Bacillus subtilis strain for potential application in leaching hydrocarbons and trace elements from contaminated environments based on functional and genomic analysis. **2023**, 227, 115785 ○
- 135 Exploration of urease-mediated biomineralization for defluoridation by Proteus columbae MLN9 with an emphasis on its genomic characterization. **2023**, 11, 109791 ○
- 134 Whole genome sequence data of an Antarctic bacterium, Arthrobacter sp. ES1 from the Schirmacher Oasis, East Antarctica. **2023**, 48, 109052 ○
- 133 Characterization and genomic analysis of novel bacteriophage NK20 to revert colistin resistance and combat pandrug-resistant Klebsiella pneumoniae in a rat respiratory infection model. **2023**, 322, 121639 ○
- 132 Genomic evidence for two pathways of formaldehyde oxidation and denitrification capabilities of the species Paracoccus methylovorus sp. nov.. **2022**, 72, ○
- 131 Quorum sensing activities and genomic insights of plant growth-promoting rhizobacteria isolated from Assam tea. **2023**, 39, ○
- 130 From farm to fork: persistence of clinically-relevant multidrug-resistant and copper-tolerant Klebsiella pneumoniae along after colistin withdrawal in poultry production. ○
- 129 Characterization of phytopathogen-preying Hyalangium versicolor sp. nov., and proposal for the reclassification of Cystobacter gracilis as Hyalangium gracile comb. Nov. **2023**, 205, ○
- 128 (Meta)genomics -assisted screening of novel antibacterial lactic acid bacteria strains from traditional fermented milk from Western China and their bioprotective effects on cheese. **2023**, 175, 114507 ○
- 127 Molecular characterization of Arcobacter butzleri isolates from poultry in rural Ghana. 13, ○
- 126 Genome sequencing and comparative genomic analysis of bovine mastitis-associated Staphylococcus aureus strains from India. **2023**, 24, ○
- 125 Resistance to critically important antibiotics in hospital wastewater from the largest Croatian city. **2023**, 870, 161805 ○

- 124 Characterization of small plasmids carrying florfenicol resistance gene floR in *Actinobacillus pleuropneumoniae* and *Pasteurella multocida* isolates from swine in China. 10, ○
- 123 Characterization of metagenome-assembled genomes of two endo-archaea of *Candida tropicalis*. 1, ○
- 122 Genome-based reclassification of *Anoxybacillus salavatliensis* Cihan et al. 2011 as a later heterotypic synonym of *Anoxybacillus gonensis* Belduz et al. 2003. ○
- 121 Competitiveness and Phylogenetic Relationship of Rhizobial Strains with Different Symbiotic Efficiency in *Trifolium repens*: Conversion of Parasitic into Non-Parasitic Rhizobia by Natural Symbiotic Gene Transfer. **2023**, 12, 243 ○
- 120 Supergroup F Wolbachia with extremely reduced genome: transition to obligate insect symbionts. **2023**, 11, ○
- 119 Insights into the genome of *Methylobacterium* sp. NMS14P, a novel bacterium for growth promotion of maize, chili, and sugarcane. **2023**, 18, e0281505 ○
- 118 Copper removal capability and genomic insight into the lifestyle of copper mine inhabiting *Micrococcus yunnanensis* GKSM13. **2023**, 223, 115431 ○
- 117 *Muricauda spongiicola* sp. nov., isolated from the sponge *Callyspongia elongata*. **2023**, 73, ○
- 116 Ceftazidime–avibactam resistance in *Klebsiella pneumoniae* sequence type 37: a decade of persistence and concealed evolution. **2023**, 9, ○
- 115 How Can Omics Inform Diabetic Foot Ulcer Clinical Management? A Whole Genome Comparison of Four Clinical Strains of *Staphylococcus aureus*. **2023**, 27, 51-61 ○
- 114 Identification of AHL Synthase in *Desulfovibrio vulgaris* Hildenborough Using an In-Silico Methodology. **2023**, 13, 364 ○
- 113 Nisin E Is a Novel Nisin Variant Produced by Multiple *Streptococcus equinus* Strains. **2023**, 11, 427 ○
- 112 Comparative genomics of *Bacillus cereus* sensu lato spp. biocontrol strains in correlation to in-vitro phenotypes and plant pathogen antagonistic capacity. 14, ○
- 111 Dynamic state of plasmid genomic architectures resulting from XerC/D-mediated site-specific recombination in *Acinetobacter baumannii* Rep_3 superfamily resistance plasmids carrying blaOXA-58- and TnaphA6-resistance modules. 14, ○
- 110 Metabolic handoffs between multiple symbionts may benefit the deep-sea bathymodioline mussels. ○
- 109 A bacterial cold-active dye-decolorizing peroxidase from an Antarctic *Pseudomonas* strain. **2023**, 107, 1707-1724 ○
- 108 Draft Genome Sequence of an Epibiotic Bacterium, *Bacillus cereus*, Isolated from Cyanobacterial Blooms in Lake Taihu, China. **2023**, 12, ○
- 107 A Highly Effective Bacteriophage-1252 to Control Multiple Serovars of *Salmonella enterica*. **2023**, 12, 797 ○

- 106 Comparative whole-genome analysis of novel marine *Vibrio campbellii* from pure and non-axenic cultures reveals a unique plasmid. ○
- 105 Morphological and genomic characteristics of two novel actinomycetes, *Ornithinimicrobium* *sufpigmenti* sp. nov. and *Ornithinimicrobium* *faecis* sp. nov. isolated from bat faeces (*Rousettus* *leschenaultia* and *Taphozous perforates*). 13, ○
- 104 *Mucilaginibacter straminoryzae* sp. nov., isolated from rice straw used for growing periphyton. 2023, 73, ○
- 103 Salmonella Phage CKT1 Effectively Controls the Vertical Transmission of Salmonella Pullorum in Adult Broiler Breeders. 2023, 12, 312 ○
- 102 *Maribacter halichondri* sp. nov., isolated from the marine sponge *Halichondria panicea*. ○
- 101 Characterization of a lytic *Escherichia coli* phage CE1 and its potential use in therapy against avian pathogenic *Escherichia coli* infections. 14, ○
- 100 Staying below the Radar: Unraveling a New Family of Ubiquitous λ -Cryptic Non-Tailed Temperate Vibriophages and Implications for Their Bacterial Hosts. 2023, 24, 3937 ○
- 99 Physiological and genomic insights into abiotic stress of halophilic archaeon *Natrinema altunense* 4.1R isolated from a saline ecosystem of Tunisian desert. 2023, 151, 133-152 ○
- 98 First insights into the gut microbiome of *Diatraea saccharalis*: From a sugarcane pest to a reservoir of new bacteria with biotechnological potential. 11, ○
- 97 Optimization and elucidation of organophosphorus and pyrethroid degradation pathways by a novel bacterial consortium C3 using RSM and GC-MS-based metabolomics. 2023, 144, 104744 ○
- 96 Description of *Fervidibacillus* gen. nov. with Two Species, *Fervidibacillus albus* sp. nov., and *Fervidibacillus halotolerans* sp. nov., Isolated from Tidal Flat Sediments and Emendation of Misclassified Taxa in the Genus *Caldibacillus*. 2023, 61, 175-187 ○
- 95 Resistance to the Bacteriocin Lcn972 Deciphered by Genome Sequencing. 2023, 11, 501 ○
- 94 Evidence of structural rearrangements in ESBL-positive pESI(like) megaplasmids of *S. Infantis*. 2023, 370, ○
- 93 Genomic Islands Identified in Highly Resistant *Serratia* sp. HRI: A Pathway to Discover New Disinfectant Resistance Elements. 2023, 11, 515 ○
- 92 Characterization and Genomic Analysis of a Novel Lytic Phage DCp1 against *Clostridium perfringens* Biofilms. 2023, 24, 4191 1
- 91 Characterization of a Potential Probiotic *Lactiplantibacillus plantarum* LRCC5310 by Comparative Genomic Analysis and its Vitamin B6 Production Ability. 2023, ○
- 90 Synergy between Genome Mining, Metabolomics, and Bioinformatics Uncovers Antibacterial Chlorinated Carbazole Alkaloids and Their Biosynthetic Gene Cluster from *Streptomyces tubbatahanensis* sp. nov., a Novel Actinomycete Isolated from Sulu Sea, Philippines. 2023, 11, ○
- 89 Comparison of four multilocus sequence typing schemes and amino acid biosynthesis based on genomic analysis of *Bacillus subtilis*. 2023, 18, e0282092 ○

- 88 Bacterial origins of thymidylate metabolism in Asgard archaea and Eukarya. **2023**, 14, ○
- 87 Genome-Based Analysis of the Potential Bioactivity of the Terrestrial *Streptomyces vinaceusdrappus* Strain AC-40. **2023**, 12, 345 ○
- 86 Genomic insights of an alkaliphilic bacterium *Halalkalibacter alkaliphilus* sp. nov. isolated from an Indian Soda Lake. ○
- 85 Complete Genome Sequence of *Campylobacter hepaticus* RBCL71delta, Associated with Spotty Liver Disease in Organic Pasture-Raised Laying Hens in Georgia, USA. **2023**, 12, ○
- 84 Bipartite Genomes in Enterobacterales: Independent Origins of Chromids, Elevated Openness and Donors of Horizontally Transferred Genes. **2023**, 24, 4292 ○
- 83 Characterization of a novel cold-adapted intracellular serine protease from the extremophile *Planococcus halocryophilus* Or1. 14, ○
- 82 Functional annotation and comparative analysis of four *Botrytis cinerea* mitogenomes reported from Punjab, Pakistan. **2023**, 30, 103605 ○
- 81 *Arthrobacter mangrovi* sp. nov., an actinobacterium isolated from the rhizosphere of a mangrove. **2023**, 73, ○
- 80 *Serratia silvae* sp. nov., Isolated from Forest Soil. **2023**, 80, ○
- 79 Temperature-induced modulation of stress-tolerant PGP genes bioprospected from *Bacillus* sp. IHBT-705 associated with saffron (*Crocus sativus*) rhizosphere: A natural -treasure trove of microbial biostimulants. 14, ○
- 78 Stingray epidermal microbiomes are species-specific with local adaptations. 14, ○
- 77 Genomic Comparisons Reveal Selection Pressure and Functional Variation Between Nutritional Endosymbionts of Cave-Adapted and Epigeal Hawaiian Planthoppers. **2023**, 15, ○
- 76 *Blastopirellula sediminis* sp. nov. a new member of Pirellulaceae isolated from the Andaman and Nicobar Islands. ○
- 75 A new class A beta-lactamase gene blaCAE-1 coexists with blaAFM-1 in a novel untypable plasmid in *Comamonas aquatica*. **2023**, 13, ○
- 74 *Corynebacterium guaraldiae* sp. nov.: a new species of *Corynebacterium* from human infections. ○
- 73 Metagenomics-Based Analysis of Candidate Lactate Utilizers from the Rumen of Beef Cattle. **2023**, 11, 658 ○
- 72 *Rhodococcus* Strains from the Specialized Collection of Alkanotrophs for Biodegradation of Aromatic Compounds. **2023**, 28, 2393 ○
- 71 Spontaneous Genomic Variation as a Survival Strategy of Nosocomial *Staphylococcus haemolyticus*. **2023**, 11, ○

- 70 Near-Complete Whole-Genome Sequence of *Paenibacillus* sp. nov. Strain J5C2022, a Sucrotolerant and Endospore-Forming Bacterium Isolated from Highly Concentrated Sugar Brine. **2023**, 12, ○
- 69 Abundance and composition of particles and their attached microbiomes along an Atlantic Meridional Transect. 10, ○
- 68 A unique symbiosome in an anaerobic single-celled eukaryote. ○
- 67 Investigation of a *Listeria monocytogenes* Chromosomal Immigration Control Region Reveals Diverse Restriction Modification Systems with Complete Sequence Type Conservation. **2023**, 11, 699 ○
- 66 *Halocatena marina* sp. nov., a novel filamentous halophilic archaeon isolated from marine tidal flat and emended description of the genus *Halocatena*. **2023**, 27, ○
- 65 Characterization of a lytic *Pseudomonas aeruginosa* phage vB_PaeP_ASP23 and functional analysis of its lysin LysASP and holin HolASP. 14, ○
- 64 Beta-Lactam Susceptibility Profiles of Bacteria Isolated from the Ozama River in Santo Domingo, Dominican Republic. **2023**, 15, 5109 ○
- 63 Transport and Utilization of Glycogen Breakdown Products by *Gardnerella* spp. from the Human Vaginal Microbiome. **2023**, 11, ○
- 62 Unlocking the microbial studies through computational approaches: how far have we reached?. **2023**, 30, 48929-48947 ○
- 61 Characterization of Molecular Diversity and Organization of Phycobilisomes in Thermophilic Cyanobacteria. **2023**, 24, 5632 ○
- 60 A Novel Strategy to Identify Endolysins with Lytic Activity against Methicillin-Resistant *Staphylococcus aureus*. **2023**, 24, 5772 ○
- 59 Snow Microorganisms Colonise Arctic Soils Following Snow Melt. ○
- 58 *Brevundimonas* and *Serratia* as host systems for assessing associated environmental viromes and phage diversity by complementary approaches. 14, ○
- 57 Potential selection and maintenance of manure-originated multi-drug resistant plasmids at sub-clinical antibiotic concentrations. ○
- 56 Predicting human risk with multidrug resistant *Enterobacter hormaechei* MS2 with MCR 9 gene isolated from the feces of healthy broiler through whole genome sequence based analysis.. ○
- 55 Whole genome characterization of thermophilic *Campylobacter* species isolated from dairy manure in small specialty crop farms of Northeast Ohio. 14, ○
- 54 Prospecting the functional potential of *Bacillus altitudinis* 1.4 isolated from sediment in association with *Bradyrhizobium japonicum*. ○
- 53 Design of Phage-Cocktail Containing Hydrogel for the Treatment of *Pseudomonas aeruginosa* Infected Wounds. **2023**, 15, 803 ○

- 52 Effect of phage vB_EcoM_FJ1 on the reduction of ETEC O9:H9 infection in a neonatal pig cell line. **2023**, 54, ○
- 51 Isolation and characterization of bioactive metabolites of *Bacillus enclensis* CARE-V7 strain from southeast coast of India. ○
- 50 *Novosphingobium kaempferiae* sp. nov., a phosphate-solubilizing bacterium isolated from stem of *Kaempferia marginata* Carey. **2023**, 73, ○
- 49 Genomes of four *Streptomyces* strains reveal insights into putative new species and pathogenicity of scab-causing organisms. **2023**, 24, ○
- 48 *Gordonia aquimaris* sp. nov., a novel marine actinobacterium isolated from seawater in the upper gulf of Thailand. **2023**, 73, ○
- 47 Genetic diversity of listeria found in the meat processing environment. **2023**, 41, 24 ○
- 46 Genomic analysis of *Vibrio harveyi* strain PH1009, a potential multi-drug resistant pathogen due to acquisition of toxin genes. **2023**, 9, e14926 ○
- 45 Description of *Ornithinimicrobium cryptoxanthini* sp. nov., a Novel Actinomycete Producing Cryptoxanthin Isolated from the Tongtian River Sediments. ○
- 44 Analysis of the speciation process suggests a dual lifestyle in the plant pathogen *Ralstonia solanacearum* species complex. ○
- 43 Genomics assisted characterization of plant growth-promoting and metabolite producing psychrotolerant Himalayan *Chryseobacterium cucumeris* PCH239. **2023**, 205, ○
- 42 Enterococcal Linear Plasmids Adapt to *Enterococcus faecium* and Spread within Multidrug-Resistant Clades. **2023**, 67, ○
- 41 Pioneer colonizers: Bacteria that alter the chicken intestinal morphology and development of the microbiota. 14, ○
- 40 Description of a Novel Fish Pathogen, *Plesiomonas shigelloides* subsp. *oncorhynchi*, Isolated from Rainbow Trout (*Oncorhynchus mykiss*): First Genome Analysis and Comparative Genomics. **2023**, 8, 179 ○
- 39 Comparative Genomics and Directed Evolution Reveal Genetic Determinants of Extreme UVC Radiation Tolerance in Bacteria Recovered from the Stratosphere. ○
- 38 Can beta-lactamase resistance genes in anaerobic Gram-negative gut bacteria transfer to gut aerobes?. ○
- 37 Diverse Repertoire and Relationship of Exopolysaccharide Genes in Cold-Adapted *Acinetobacter* sp. CUI-P1 Revealed by Comparative Genome Analysis. **2023**, 11, 885 ○
- 36 *Natrinema caseinilyticum* sp. nov., *Natrinema gelatinilyticum* sp. nov., *Natrinema marinum* sp. nov., *Natrinema zhouii* sp. nov., extremely halophilic archaea isolated from marine environments and a salt mine. **2023**, 27, ○
- 35 *Membranihabitans maritimus* sp. nov., a marine bacterium isolated from deep seawater. **2023**, 73, ○

- 34 Genomic profiling and characteristics of a C1 degrading heterotrophic fresh-water bacterium *Paracoccus* sp. strain DMF. ○
- 33 Whole genome sequencing of a novel *Bacillus thuringiensis* isolated from Assam soil. **2023**, 23, ○
- 32 Draft Genome Sequences of 18 Bacteroidetes Strains Isolated from a Human Stool Sample. ○
- 31 Spontaneously Produced Lysogenic Phages Are an Important Component of the Soybean *Bradyrhizobium Mobilome*. ○
- 30 *Shewanella subflava* sp. nov., a novel multi-resistant bacterium, isolated from the estuary of the Fenhe River into the Yellow River. ○
- 29 *Parvularcula maris* sp. nov., an algicidal bacterium isolated from seawater. **2023**, 73, ○
- 28 *Limimanicola litoreus* sp. nov., isolated from intertidal sand of the Yellow Sea. **2023**, 73, ○
- 27 Isolation, screening and characterization of phage. **2023**, ○
- 26 *Aestuariibaculum lutulentum* sp. nov., a marine bacterium isolated from coastal sediment in Beihai. **2023**, 205, ○
- 25 New Insights on Metabolic Features of *Bacillus subtilis* Based on Multistrain Genome-Scale Metabolic Modeling. **2023**, 24, 7091 ○
- 24 Draft Genome Sequence Resource of *Erwinia* sp. Strain INIA01, a Phytopathogen Isolated from a Diseased Stalk of Peruvian Maize. ○
- 23 Coliphages of the human urinary microbiota. **2023**, 18, e0283930 ○
- 22 Characterization of the heteropolysaccharides produced by *Liquorilactobacillus sicerae* CUPV261 and *Secundilactobacillus collinoides* CUPV237 isolated from cider. **2023**, 397, 110199 ○
- 21 *Brevundimonas brasiliensis* sp. nov.: a New Multidrug-Resistant Species Isolated from a Patient in Brazil. ○
- 20 Genomic analysis and characterization of phages infecting the marine *Roseobacter* CHAB-I-5 lineage reveal a globally distributed and abundant phage genus. 14, ○
- 19 Complete Genome Sequence of *Klebsiella pneumoniae* Bacteriophage KpS110, Encoding Five Tail-Associated Proteins with Putative Polysaccharide Depolymerase Domains. ○
- 18 *Microbulbifer zhoushanensis* sp. nov., *Microbulbifer sediminum* sp. nov. and *Microbulbifer guangxiensis* sp. nov., three marine bacteria isolated from a tidal flat. **2023**, 73, ○
- 17 In planta interactions of a novel bacteriophage against *Pseudomonas syringae* pv. tomato. ○

- 16 *Solitalea agri* sp. nov., a new member of the genus *Solitalea* isolated from rhizospheric soil of a jujube tree. **2023**, 73, ○
- 15 Characterization of the newly isolated phage Y3Z against multi-drug resistant *Cutibacterium acnes*. **2023**, 106111 ○
- 14 *Tahibacter harae* sp. nov., isolated from pig farm soil in Guangdong, PR China. **2023**, 73, ○
- 13 *Streptomyces beihaiensis* sp. nov., a chitin-degrading actinobacterium, isolated from shrimp pond soil. **2023**, 73, ○
- 12 Diversity of Plant Growth-Promoting Endophytic Bacteria, Genome Analysis of Strain Sx8-8 and Its Rice Germination Promoting Activity. **2023**, 92, 269-283 ○
- 11 Description of *Sporanaerobium hydrogeniformans* gen. nov., sp. nov., an obligately anaerobic, hydrogen producing bacterium of Lachnospiraceae family isolated from Aravali hot spring in India. ○
- 10 Temperate phage influence virulence and biofilm-forming of *Salmonella* Typhimurium and enhance the ability to contaminate food product. **2023**, 110223 ○
- 9 Complete Genome of *Candidatus Phytoplasma rubi* RS, a Phytopathogenic Bacterium Associated with Rubus Stunt Disease. **2023**, 12, ○
- 8 *Alteromonas salexigens* sp. nov., isolated from coastal seawater. ○
- 7 Roles of adenine methylation in the physiology of *Lactocaseibacillus paracasei*. **2023**, 14, ○
- 6 Home-based microbial solution to boost crop growth in low-fertility soil. ○
- 5 Dissemination of carbapenemase-producing Enterobacterales through wastewater and gulls at a wastewater treatment plant in Sweden. **2023**, 886, 163997 ○
- 4 Genome sequence data of *Burkholderia* sp. IMCC1007 isolated from maize rhizosphere: A potential strain in fusaric acid mycotoxin biodegradation. **2023**, 48, 109204 ○
- 3 Whole Genome Analysis and Assessment of the Metabolic Potential of *Gordonia rubripertincta* Strain 112, a Degradar of Aromatic and Aliphatic Compounds. **2023**, 12, 721 ○
- 2 Microbes with higher metabolic independence are enriched in human gut microbiomes under stress. ○
- 1 Repression of *Staphylococcus aureus* and *Escherichia coli* by *Lactiplantibacillus plantarum* Strain AG10 in *Drosophila melanogaster* In Vivo Model. **2023**, 11, 1297 ○