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FastTree 2--approximately maximum-likelihood trees for large alignments

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2280	The threshold bootstrap clustering: a new approach to find families or transmission clusters within molecular quasispecies. <i>PLoS ONE</i> , <b>2010</b> , 5, e13619	3.7	14
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2276	Evolutionary relationships of wild hominids recapitulated by gut microbial communities. <b>2010</b> , 8, e1000546		364
2275	Phylogenetic and phyletic studies of informational genes in genomes highlight existence of a 4 domain of life including giant viruses. <i>PLoS ONE</i> , <b>2010</b> , 5, e15530	3.7	108
2274	An insect nidovirus emerging from a primary tropical rainforest. <b>2011</b> , 2, e00077-11		89
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2265	PATRIC: the comprehensive bacterial bioinformatics resource with a focus on human pathogenic species. <b>2011</b> , 79, 4286-98		198
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2256	Toward an efficient method of identifying core genes for evolutionary and functional microbial phylogenies. <i>PLoS ONE</i> , <b>2011</b> , 6, e24704	3-7	67
2255	RAXML and FastTree: comparing two methods for large-scale maximum likelihood phylogeny estimation. <i>PLoS ONE</i> , <b>2011</b> , 6, e27731	3-7	124
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2242	Algorithms, data structures, and numerics for likelihood-based phylogenetic inference of huge trees. <b>2011</b> , 12, 470	40
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2236	The phylogeny of advanced snakes (Colubroidea), with discovery of a new subfamily and comparison of support methods for likelihood trees. <b>2011</b> , 58, 329-42	221
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2234	FastSP: linear time calculation of alignment accuracy. <b>2011</b> , 27, 3250-8	36
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2231	Ortholog identification in the presence of domain architecture rearrangement. <b>2011</b> , 12, 413-22	23
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2226	Phylogenetic and functional characterization of the hAT transposon superfamily. <b>2011</b> , 188, 45-57	56
2225	Bacterial community structures are unique and resilient in full-scale bioenergy systems. <b>2011</b> , 108, 4158-63	325
2224	Antennal transcriptome of <i>Manduca sexta</i> . <b>2011</b> , 108, 7449-54	210
2223	Comparative genomics of 28 <i>Salmonella enterica</i> isolates: evidence for CRISPR-mediated adaptive sublineage evolution. <b>2011</b> , 193, 3556-68	127
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2202	Evolution of a large, conserved, and syntenic gene family in insects. <b>2012</b> , 2, 313-9		40
2201	Estimating optimal species trees from incomplete gene trees under deep coalescence. <b>2012</b> , 19, 591-605		25
2200	Abiotic factors shape microbial diversity in Sonoran Desert soils. <b>2012</b> , 78, 7527-37		137
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2192	SuperFine: fast and accurate supertree estimation. <b>2012</b> , 61, 214-27	42
2191	Comparative genomics and stx phage characterization of LEE-negative Shiga toxin-producing Escherichia coli. <b>2012</b> , 2, 133	66
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2189	Insights from the architecture of the bacterial transcription apparatus. <b>2012</b> , 179, 299-319	36
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2187	Draft Genome sequence of Escherichia coli AI27, a porcine isolate belonging to phylogenetic group B1. <b>2012</b> , 194, 6640-1	1
2186	Dysfunction of the intestinal microbiome in inflammatory bowel disease and treatment. <b>2012</b> , 13, R79	1668
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2184	Characterisation of retroviruses in the horse genome and their transcriptional activity via transcriptome sequencing. <b>2012</b> , 433, 55-63	14
2183	Population genomics of early events in the ecological differentiation of bacteria. <b>2012</b> , 336, 48-51	366
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2177	The shared antibiotic resistome of soil bacteria and human pathogens. <b>2012</b> , 337, 1107-11	980
2176	SATe-II: very fast and accurate simultaneous estimation of multiple sequence alignments and phylogenetic trees. <b>2012</b> , 61, 90-106	257

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2172	Ter-dependent stress response systems: novel pathways related to metal sensing, production of a nucleoside-like metabolite, and DNA-processing. <b>2012</b> , 8, 3142-65	61
2171	Structural and functional characterization of microcin C resistance peptidase MccF from <i>Bacillus anthracis</i> . <b>2012</b> , 420, 366-83	19
2170	In silico cloning of genes encoding neuropeptides, neurohormones and their putative G-protein coupled receptors in a spider mite. <b>2012</b> , 42, 277-95	81
2169	MergeAlign: improving multiple sequence alignment performance by dynamic reconstruction of consensus multiple sequence alignments. <b>2012</b> , 13, 117	51
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2167	FluShuffle and FluResort: new algorithms to identify reassorted strains of the influenza virus by mass spectrometry. <b>2012</b> , 13, 208	17
2166	A scalable method for identifying frequent subtrees in sets of large phylogenetic trees. <b>2012</b> , 13, 256	3
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2163	The evolution of cardiolipin biosynthesis and maturation pathways and its implications for the evolution of eukaryotes. <b>2012</b> , 12, 32	29
2162	Distribution of nitrogen fixation and nitrogenase-like sequences amongst microbial genomes. <b>2012</b> , 13, 162	257
2161	Lateral gene transfer of an ABC transporter complex between major constituents of the human gut microbiome. <b>2012</b> , 12, 248	15
2160	The tomato RLK superfamily: phylogeny and functional predictions about the role of the LRRIL-RLK subfamily in antiviral defense. <b>2012</b> , 12, 229	87
2159	Archaeal origin of tubulin. <b>2012</b> , 7, 10	64
2158	Polymorphic toxin systems: Comprehensive characterization of trafficking modes, processing, mechanisms of action, immunity and ecology using comparative genomics. <b>2012</b> , 7, 18	309

2157	Proteorhodopsin genes in giant viruses. <b>2012</b> , 7, 34		72
2156	ALOG domains: provenance of plant homeotic and developmental regulators from the DNA-binding domain of a novel class of DIRS1-type retroposons. <b>2012</b> , 7, 39		29
2155	Updated clusters of orthologous genes for Archaea: a complex ancestor of the Archaea and the byways of horizontal gene transfer. <b>2012</b> , 7, 46		120
2154	Proteins from the FLOWERING LOCUS T-like subclade of the PEBP family act antagonistically to regulate floral initiation in tobacco. <b>2012</b> , 72, 908-21		78
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2151	Millimeter-scale patterns of phylogenetic and trait diversity in a salt marsh microbial mat. <b>2012</b> , 3, 293		34
2150	Microbial 16S rRNA Ion Tag and community metagenome sequencing using the Ion Torrent (PGM) Platform. <b>2012</b> , 91, 80-8		143
2149	Phylogenomics of prokaryotic ribosomal proteins. <i>PLoS ONE</i> , <b>2012</b> , 7, e36972	3-7	180
2148	Identification of soil bacteria susceptible to TiO <sub>2</sub> and ZnO nanoparticles. <b>2012</b> , 78, 6749-58		195
2147	An improved Greengenes taxonomy with explicit ranks for ecological and evolutionary analyses of bacteria and archaea. <b>2012</b> , 6, 610-8		3287
2146	Adenylylation control by intra- or intermolecular active-site obstruction in Fic proteins. <b>2012</b> , 482, 107-10		114
2145	Identification of novel components of NAD-utilizing metabolic pathways and prediction of their biochemical functions. <b>2012</b> , 8, 1661-77		46
2144	Estimating variation within the genes and inferring the phylogeny of 186 sequenced diverse <i>Escherichia coli</i> genomes. <b>2012</b> , 13, 577		137
2143	Reconciling taxonomy and phylogenetic inference: formalism and algorithms for describing discord and inferring taxonomic roots. <b>2012</b> , 7, 8		8
2142	Treelength optimization for phylogeny estimation. <i>PLoS ONE</i> , <b>2012</b> , 7, e33104	3-7	5
2141	Adaptive evolution of HIV at HLA epitopes is associated with ethnicity in Canada. <i>PLoS ONE</i> , <b>2012</b> , 7, e36933	3-7	4
2140	Evolution and diversity of the Microviridae viral family through a collection of 81 new complete genomes assembled from virome reads. <i>PLoS ONE</i> , <b>2012</b> , 7, e40418	3-7	123

2139	The relation between oral <i>Candida</i> load and bacterial microbiome profiles in Dutch older adults. <i>PLoS ONE</i> , <b>2012</b> , 7, e42770	3.7	86
2138	Designing and testing broadly-protective filoviral vaccines optimized for cytotoxic T-lymphocyte epitope coverage. <i>PLoS ONE</i> , <b>2012</b> , 7, e44769	3.7	19
2137	Combining epidemiological and genetic networks signifies the importance of early treatment in HIV-1 transmission. <i>PLoS ONE</i> , <b>2012</b> , 7, e46156	3.7	12
2136	Glutamine versus ammonia utilization in the NAD synthetase family. <i>PLoS ONE</i> , <b>2012</b> , 7, e39115	3.7	30
2135	HIV-1 subtypes and recombinants in Northern Tanzania: distribution of viral quasispecies. <i>PLoS ONE</i> , <b>2012</b> , 7, e47605	3.7	12
2134	Phylogenomic investigation of phospholipid synthesis in archaea. <b>2012</b> , 2012, 630910		35
2133	Discovery of Novel DENN Proteins: Implications for the Evolution of Eukaryotic Intracellular Membrane Structures and Human Disease. <b>2012</b> , 3, 283		187
2132	Gene flow and biological conflict systems in the origin and evolution of eukaryotes. <b>2012</b> , 2, 89		53
2131	FastJoin, an improved neighbor-joining algorithm. <b>2012</b> , 11, 1909-22		14
2130	Rapid identification of high-confidence taxonomic assignments for metagenomic data. <b>2012</b> , 40, e111		50
2129	Gut microbiota composition correlates with diet and health in the elderly. <b>2012</b> , 488, 178-84		1987
2128	Diversity and structure of soil bacterial communities associated with vultures in an African savanna. <b>2012</b> , 3, art47		17
2127	Phylomark, a tool to identify conserved phylogenetic markers from whole-genome alignments. <b>2012</b> , 78, 4884-92		31
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2125	Comparative microbial diversity analyses of modern marine thrombolitic mats by barcoded pyrosequencing. <b>2012</b> , 14, 82-100		52
2124	Experimental and analytical tools for studying the human microbiome. <b>2011</b> , 13, 47-58		491
2123	The orange carotenoid protein in photoprotection of photosystem II in cyanobacteria. <b>2012</b> , 1817, 158-66		140
2122	Environmental actinorhodopsin expression revealed by a new in situ filtration and fixation sampler. <b>2012</b> , 4, 491-7		14

2121	Diversity of methyl halide-degrading microorganisms in oceanic and coastal waters. <b>2012</b> , 334, 111-8	8
2120	Identification of olfactory receptor genes in Atlantic salmon <i>Salmo salar</i> . <b>2012</b> , 81, 559-75	28
2119	Environment or kin: whence do bees obtain acidophilic bacteria?. <b>2012</b> , 21, 1754-68	99
2118	On the culture-independent assessment of the diversity and distribution of <i>Prochlorococcus</i> . <b>2012</b> , 14, 567-79	8
2117	TPV1, the first virus isolated from the hyperthermophilic genus <i>Thermococcus</i> . <b>2012</b> , 14, 503-16	61
2116	Anaerobic methane oxidation in metalliferous hydrothermal sediments: influence on carbon flux and decoupling from sulfate reduction. <b>2012</b> , 14, 2726-40	82
2115	Female <i>Anopheles gambiae</i> antennae: increased transcript accumulation of the mosquito-specific odorant-binding-protein OBP2. <b>2012</b> , 5, 27	6
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2113	Mimiviridae: clusters of orthologous genes, reconstruction of gene repertoire evolution and proposed expansion of the giant virus family. <b>2013</b> , 10, 106	86
2112	Draft genome of the mountain pine beetle, <i>Dendroctonus ponderosae</i> Hopkins, a major forest pest. <b>2013</b> , 14, R27	212
2111	Insights into archaeal evolution and symbiosis from the genomes of a nanoarchaeon and its inferred crenarchaeal host from Obsidian Pool, Yellowstone National Park. <b>2013</b> , 8, 9	80
2110	In silico analysis of the fucosylation-associated genome of the human blood fluke <i>Schistosoma mansoni</i> : cloning and characterization of the enzymes involved in GDP-L-fucose synthesis and Golgi import. <b>2013</b> , 6, 201	5
2109	Phylogenetic models of molecular evolution: next-generation data, fit, and performance. <b>2013</b> , 76, 351-2	13
2108	Anaerobic oxidation of methane coupled to nitrate reduction in a novel archaeal lineage. <b>2013</b> , 500, 567-70	750
2107	Impacts of inundation and drought on eukaryote biodiversity in semi-arid floodplain soils. <b>2013</b> , 22, 1746-58	46
2106	Structural and evolutionary adaptation of rhoptyry kinases and pseudokinases, a family of coccidian virulence factors. <b>2013</b> , 13, 117	57
2105	Beyond classification: gene-family phylogenies from shotgun metagenomic reads enable accurate community analysis. <b>2013</b> , 14, 419	6
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2103	Baseline survey of the anatomical microbial ecology of an important food plant: <i>Solanum lycopersicum</i> (tomato). <b>2013</b> , 13, 114	152
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2097	Genome-wide transcript analysis of early maize leaf development reveals gene cohorts associated with the differentiation of C4 Kranz anatomy. <b>2013</b> , 75, 656-70	76
2096	Characterization of bacterial and archaeal communities in air-cathode microbial fuel cells, open circuit and sealed-off reactors. <b>2013</b> , 97, 9885-95	79
2095	Enrichment of lung microbiome with supraglottic taxa is associated with increased pulmonary inflammation. <b>2013</b> , 1, 19	262
2094	Kinesin-5: cross-bridging mechanism to targeted clinical therapy. <b>2013</b> , 531, 133-49	48
2093	Optimizing SNP microarray probe design for high accuracy microbial genotyping. <b>2013</b> , 94, 303-10	13
2092	Selective occurrence of Rhizobiales in frost flowers on the surface of young sea ice near Barrow, Alaska and distribution in the polar marine rare biosphere. <b>2013</b> , 5, 575-82	12
2091	Naive binning improves phylogenomic analyses. <b>2013</b> , 29, 2277-84	111
2090	SIV-induced instability of the chimpanzee gut microbiome. <b>2013</b> , 14, 340-5	62
2089	Rare variants in hypermutable genes underlie common morphology and growth traits in wild <i>Saccharomyces paradoxus</i> . <b>2013</b> , 195, 513-25	12
2088	Laccase is necessary and nonredundant with peroxidase for lignin polymerization during vascular development in <i>Arabidopsis</i> . <b>2013</b> , 25, 3976-87	280
2087	Adaptation of a membrane bioreactor to 1,2-dichloroethane revealed by 16S rDNA pyrosequencing and <i>dhlA</i> qPCR. <b>2013</b> , 47, 13668-76	11
2086	Chimeric viruses blur the borders between the major groups of eukaryotic single-stranded DNA viruses. <b>2013</b> , 4, 2700	74

2085	Bacterial, archaeal and viral-like rhodopsins from the Red Sea. <b>2013</b> , 5, 475-82	39
2084	Broad-scale phylogenomics provides insights into retrovirus-host evolution. <b>2013</b> , 110, 20146-51	65
2083	Identifying reaction modules in metabolic pathways: bioinformatic deduction and experimental validation of a new putative route in purine catabolism. <b>2013</b> , 7, 99	9
2082	Pandoraviruses are highly derived phycodnaviruses. <b>2013</b> , 8, 25	52
2081	Comparative genomics of actinomycetes with a focus on natural product biosynthetic genes. <b>2013</b> , 14, 611	124
2080	Analysis of the gut microbiota of walking sticks (Phasmatodea). <b>2013</b> , 6, 368	31
2079	Conserved microstructure of the Brassica B Genome of Brassica nigra in relation to homologous regions of Arabidopsis thaliana, B. rapa and B. oleracea. <b>2013</b> , 14, 250	34
2078	Comparative genomics in acid mine drainage biofilm communities reveals metabolic and structural differentiation of co-occurring archaea. <b>2013</b> , 14, 485	75
2077	Genome resolved analysis of a premature infant gut microbial community reveals a Varibaculum cambriense genome and a shift towards fermentation-based metabolism during the third week of life. <b>2013</b> , 1, 30	39
2076	TRAPID: an efficient online tool for the functional and comparative analysis of de novo RNA-Seq transcriptomes. <b>2013</b> , 14, R134	89
2075	Community differentiation of the cutaneous microbiota in psoriasis. <b>2013</b> , 1, 31	245
2074	Comparison of the Legionella pneumophila population structure as determined by sequence-based typing and whole genome sequencing. <b>2013</b> , 13, 302	34
2073	snp-search: simple processing, manipulation and searching of SNPs from high-throughput sequencing. <b>2013</b> , 14, 326	5
2072	Utilizing novel diversity estimators to quantify multiple dimensions of microbial biodiversity across domains. <b>2013</b> , 13, 259	9
2071	Genomes of "Spiribacter", a streamlined, successful halophilic bacterium. <b>2013</b> , 14, 787	37
2070	Characterization of the trunk neural crest in the bamboo shark, Chiloscylidium punctatum. <b>2013</b> , 521, 3303-20	6
2069	A Generic Vectorization Scheme and a GPU Kernel for the Phylogenetic Likelihood Library. <b>2013</b> ,	8
2068	The extent of mycorrhizal colonization of roots and its influence on plant growth and phosphorus content. <b>2013</b> , 371, 1-13	163

2067	Minimizing the average distance to a closest leaf in a phylogenetic tree. <b>2013</b> , 62, 824-36	8
2066	Reactor performance in terms of COD and nitrogen removal and bacterial community structure of a three-stage rotating bioelectrochemical contactor. <b>2013</b> , 47, 881-94	69
2065	Surveying the microbiome of ants: comparing 454 pyrosequencing with traditional methods to uncover bacterial diversity. <b>2013</b> , 79, 525-34	89
2064	Widespread horizontal transfer of retrotransposons. <b>2013</b> , 110, 1012-6	92
2063	16S rRNA survey revealed complex bacterial communities and evidence of bacterial interference on human adenoids. <b>2013</b> , 15, 535-47	27
2062	Stability analysis of phylogenetic trees. <b>2013</b> , 29, 166-74	4
2061	Mechanism of tetracycline resistance by ribosomal protection protein Tet(O). <b>2013</b> , 4, 1477	74
2060	Small core communities and high variability in bacteria associated with the introduced ascidian <i>Styela plicata</i> . <b>2013</b> , 59, 35-46	18
2059	Bioinformatics for microbial genotyping of equine encephalitis viruses, orthopoxviruses, and hantaviruses. <b>2013</b> , 193, 112-20	2
2058	Evolution of cyclic amidohydrolases: a highly diversified superfamily. <b>2013</b> , 77, 70-80	8
2057	pA506, a conjugative plasmid of the plant epiphyte <i>Pseudomonas fluorescens</i> A506. <b>2013</b> , 79, 5272-82	10
2056	Phylogenetic detection of novel Cryptomycota in an Iowa (United States) aquifer and from previously collected marine and freshwater targeted high-throughput sequencing sets. <b>2013</b> , 15, 2333-41	33
2055	Phylogenetic and demographic characterization of HIV-1 transmission in Madrid, Spain. <b>2013</b> , 14, 232-9	21
2054	A cornucopia of human polyomaviruses. <b>2013</b> , 11, 264-76	236
2053	Immune status, antibiotic medication and pH are associated with changes in the stomach fluid microbiota. <b>2013</b> , 7, 1354-66	99
2052	An arbuscular mycorrhizal fungus significantly modifies the soil bacterial community and nitrogen cycling during litter decomposition. <b>2013</b> , 15, 1870-81	196
2051	Next-generation phylogenomics. <b>2013</b> , 8, 3	91
2050	The tracrRNA and Cas9 families of type II CRISPR-Cas immunity systems. <b>2013</b> , 10, 726-37	233

2049	Phylogenetic analyses of phylum Actinobacteria based on whole genome sequences. <b>2013</b> , 164, 718-28	29
2048	Treertrimmer: a method for phylogenetic dataset size reduction. <b>2013</b> , 6, 145	15
2047	Successful establishment and global dispersal of genotype VI avian paramyxovirus serotype 1 after cross species transmission. <b>2013</b> , 17, 260-8	20
2046	Vanadate and acetate biostimulation of contaminated sediments decreases diversity, selects for specific taxa, and decreases aqueous V5+ concentration. <b>2013</b> , 47, 6500-9	58
2045	RubisCO-based CO2 fixation and C1 metabolism in the actinobacterium <i>Pseudonocardia dioxanivorans</i> CB1190. <b>2013</b> , 15, 3040-53	28
2044	Gene invasion in distant eukaryotic lineages: discovery of mutually exclusive genetic elements reveals marine biodiversity. <b>2013</b> , 7, 1764-74	21
2043	Pelagic Oxygen Minimum Zone Microbial Communities. <b>2013</b> , 113-122	12
2042	Genome sequences of rare, uncultured bacteria obtained by differential coverage binning of multiple metagenomes. <b>2013</b> , 31, 533-8	869
2041	pH dominates variation in tropical soil archaeal diversity and community structure. <b>2013</b> , 86, 303-11	65
2040	In situ chemistry and microbial community compositions in five deep-sea hydrothermal fluid samples from Irina II in the Logatchev field. <b>2013</b> , 15, 1551-60	36
2039	Impact of Mangrove Roots on Bacterial Composition. <b>2013</b> , 1081-1088	
2038	Genome sequences of 65 <i>Helicobacter pylori</i> strains isolated from asymptomatic individuals and patients with gastric cancer, peptic ulcer disease, or gastritis. <b>2013</b> , 68, 39-43	13
2037	Phylogenetic stratigraphy in the Guerrero Negro hypersaline microbial mat. <b>2013</b> , 7, 50-60	147
2036	A molecular phylogeny of nephilid spiders: evolutionary history of a model lineage. <b>2013</b> , 69, 961-79	70
2035	Influence of oxic/anoxic fluctuations on ammonia oxidizers and nitrification potential in a wet tropical soil. <b>2013</b> , 85, 179-94	45
2034	The effects of model choice and mitigating bias on the ribosomal tree of life. <b>2013</b> , 69, 17-38	51
2033	Automated analysis of phylogenetic clusters. <b>2013</b> , 14, 317	218
2032	Superiority of a mechanistic codon substitution model even for protein sequences in phylogenetic analysis. <b>2013</b> , 13, 257	7

2031	The basic building blocks and evolution of CRISPR-CAS systems. <b>2013</b> , 41, 1392-400	120
2030	Phylogenomic Databases and Orthology Prediction. <b>2013</b> , 99-124	
2029	Symbiotic prokaryotic communities from different populations of the giant barrel sponge, <i>Xestospongia muta</i> . <b>2013</b> , 2, 938-52	31
2028	Probiotic dosing of <i>Ruminococcus flavefaciens</i> affects rumen microbiome structure and function in reindeer. <b>2013</b> , 66, 840-9	13
2027	Elucidating the microbial resuscitation cascade in biological soil crusts following a simulated rain event. <b>2013</b> , 15, 2799-815	73
2026	Archaeology of eukaryotic DNA replication. <b>2013</b> , 5, a012963	56
2025	The evolutionary pattern and the regulation of stearyl-CoA desaturase genes. <b>2013</b> , 2013, 856521	17
2024	Global analysis of fission yeast mating genes reveals new autophagy factors. <b>2013</b> , 9, e1003715	59
2023	The Subtelomeric khipu Satellite Repeat from <i>Phaseolus vulgaris</i> : Lessons Learned from the Genome Analysis of the Andean Genotype G19833. <b>2013</b> , 4, 109	17
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2021	Upper Arctic Ocean water masses harbor distinct communities of heterotrophic flagellates. <b>2013</b> , 10, 4273-4286	21
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2019	Effects of diet on resource utilization by a model human gut microbiota containing <i>Bacteroides cellulosilyticus</i> WH2, a symbiont with an extensive glycobiome. <b>2013</b> , 11, e1001637	184
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2012	The individual-specific and diverse nature of the preterm infant microbiota. <b>2013</b> , 98, F334-40	83	
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2010	Surface microbes in the neonatal intensive care unit: changes with routine cleaning and over time. <b>2013</b> , 51, 2617-24	55	
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2008	Whole-genome sequencing of gentamicin-resistant <i>Campylobacter coli</i> isolated from U.S. retail meats reveals novel plasmid-mediated aminoglycoside resistance genes. <b>2013</b> , 57, 5398-405	64	
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2002	The PhyloFacts FAT-CAT web server: ortholog identification and function prediction using fast approximate tree classification. <b>2013</b> , 41, W242-8	23	
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1996	Expanding the marine virosphere using metagenomics. <b>2013</b> , 9, e1003987		183

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1984	The expanding superfamily of gelsolin homology domain proteins. <b>2013</b> , 70, 775-95		32
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1969	Novel group of podovirus infecting the marine bacterium. <b>2013</b> , 3, e24766	16
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1961	A microbial clock provides an accurate estimate of the postmortem interval in a mouse model system. <b>2013</b> , 2, e01104	183
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1953	Assembly-driven community genomics of a hypersaline microbial ecosystem. <i>PLoS ONE</i> , <b>2013</b> , 8, e61692	3.7	71
1952	Monitoring Seasonal Changes in Winery-Resident Microbiota. <i>PLoS ONE</i> , <b>2013</b> , 8, e66437	3.7	131
1951	The Ecology of Microbial Communities Associated with <i>Macrocystis pyrifera</i> . <i>PLoS ONE</i> , <b>2013</b> , 8, e67480	3.7	47
1950	Comparison of DNA extraction methods in analysis of salivary bacterial communities. <i>PLoS ONE</i> , <b>2013</b> , 8, e67699	3.7	62
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1939	Molecular characterization of the fecal microbiota in patients with nonalcoholic steatohepatitis--a longitudinal study. <i>PLoS ONE</i> , <b>2013</b> , 8, e62885	3.7	205
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1932	The personal human oral microbiome obscures the effects of treatment on periodontal disease. <i>PLoS ONE</i> , <b>2014</b> , 9, e86708	3.7	66
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1930	The impact of modelling rate heterogeneity among sites on phylogenetic estimates of intraspecific evolutionary rates and timescales. <i>PLoS ONE</i> , <b>2014</b> , 9, e95722	3.7	36
1929	Host control of symbiont natural product chemistry in cryptic populations of the tunicate <i>Lissoclinum patella</i> . <i>PLoS ONE</i> , <b>2014</b> , 9, e95850	3.7	18
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1927	HIV-1 tropism dynamics and phylogenetic analysis from longitudinal ultra-deep sequencing data of CCR5- and CXCR4-using variants. <i>PLoS ONE</i> , <b>2014</b> , 9, e102857	3.7	15
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1925	Identification of transcription factor genes and their correlation with the high diversity of stramenopiles. <i>PLoS ONE</i> , <b>2014</b> , 9, e111841	3.7	6
1924	Evolution of acyl-substrate recognition by a family of acyl-homoserine lactone synthases. <i>PLoS ONE</i> , <b>2014</b> , 9, e112464	3.7	14

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1922	HIV-1 diversity, transmission dynamics and primary drug resistance in Angola. <i>PLoS ONE</i> , <b>2014</b> , 9, e113626	3-7	12
1921	Early canine plaque biofilms: characterization of key bacterial interactions involved in initial colonization of enamel. <i>PLoS ONE</i> , <b>2014</b> , 9, e113744	3-7	43
1920	IM-TORNADO: a tool for comparison of 16S reads from paired-end libraries. <i>PLoS ONE</i> , <b>2014</b> , 9, e114804	3-7	76
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1918	Temporal dynamics in the ruminal microbiome of dairy cows during the transition period. <b>2014</b> , 92, 4014-22		64
1917	High frequency of phylogenetically diverse reductive dehalogenase-homologous genes in deep seafloor sedimentary metagenomes. <b>2014</b> , 5, 80		47
1916	Two distinct microbial communities revealed in the sponge <i>Cinachyrella</i> . <b>2014</b> , 5, 581		27
1915	The hermit crab's nose-antennal transcriptomics. <b>2013</b> , 7, 266		23
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1913	Evaluating topological conflict in centipede phylogeny using transcriptomic data sets. <b>2014</b> , 31, 1500-13		54
1912	Characterization of the fecal microbiome in different swine groups by high-throughput sequencing. <b>2014</b> , 28, 157-62		34
1911	Evidence for the retention of two evolutionary distinct plastids in dinoflagellates with diatom endosymbionts. <b>2014</b> , 6, 2321-34		36
1910	A phylogenomic view of ecological specialization in the Lachnospiraceae, a family of digestive tract-associated bacteria. <b>2014</b> , 6, 703-13		402
1909	Probiotics and virulent human rotavirus modulate the transplanted human gut microbiota in gnotobiotic pigs. <b>2014</b> , 6, 39		44
1908	Metagenomic analyses of bacteria on human hairs: a qualitative assessment for applications in forensic science. <b>2014</b> , 5, 16		52
1907	FastMG: a simple, fast, and accurate maximum likelihood procedure to estimate amino acid replacement rate matrices from large data sets. <b>2014</b> , 15, 341		5
1906	Lineage-specific expansions of TET/JBP genes and a new class of DNA transposons shape fungal genomic and epigenetic landscapes. <b>2014</b> , 111, 1676-83		41

1905	An expanded genomic representation of the phylum cyanobacteria. <b>2014</b> , 6, 1031-45	186
1904	Functional phylogenomics analysis of bacteria and archaea using consistent genome annotation with UniFam. <b>2014</b> , 14, 207	14
1903	Cyclic nucleotide-gated ion channel gene family in rice, identification, characterization and experimental analysis of expression response to plant hormones, biotic and abiotic stresses. <b>2014</b> , 15, 853	79
1902	Genome sequence of <i>Vibrio diabolicus</i> and identification of the exopolysaccharide HE800 biosynthesis locus. <b>2014</b> , 98, 10165-76	14
1901	Transposable element-assisted evolution and adaptation to host plant within the <i>Leptosphaeria maculans</i> - <i>Leptosphaeria biglobosa</i> species complex of fungal pathogens. <b>2014</b> , 15, 891	111
1900	FOAM (Functional Ontology Assignments for Metagenomes): a Hidden Markov Model (HMM) database with environmental focus. <b>2014</b> , 42, e145	66
1899	LotuS: an efficient and user-friendly OTU processing pipeline. <b>2014</b> , 2, 30	186
1898	Dietary supplementation with lactose or artificial sweetener enhances swine gut <i>Lactobacillus</i> population abundance. <b>2014</b> , 111 Suppl 1, S30-5	64
1897	MyTaxa: an advanced taxonomic classifier for genomic and metagenomic sequences. <b>2014</b> , 42, e73	240
1896	Life in an unusual intracellular niche: a bacterial symbiont infecting the nucleus of amoebae. <b>2014</b> , 8, 1634-44	32
1895	In silico detection of phylogenetic informative Y-chromosomal single nucleotide polymorphisms from whole genome sequencing data. <b>2014</b> , 35, 3102-10	5
1894	Human germline and pan-cancer variomes and their distinct functional profiles. <b>2014</b> , 42, 11570-88	20
1893	Bloodstream infections due to <i>Peptoniphilus</i> spp.: report of 15 cases. <b>2014</b> , 20, O857-60	27
1892	tRNA signatures reveal a polyphyletic origin of SAR11 strains among alphaproteobacteria. <b>2014</b> , 10, e1003454	6
1891	A taxonomy of bacterial microcompartment loci constructed by a novel scoring method. <b>2014</b> , 10, e1003898	170
1890	Whole-genome sequencing and epidemiological analysis do not provide evidence for cross-transmission of <i>Mycobacterium abscessus</i> in a cohort of pediatric cystic fibrosis patients. <b>2015</b> , 60, 1007-16	58
1889	The contribution of viral genotype to plasma viral set-point in HIV infection. <b>2014</b> , 10, e1004112	33
1888	Applications of Next-Generation Sequencing Technologies to the Study of the Human Microbiome. <b>2014</b> , 75-106	

1887	Convergent bacterial microbiotas in the fungal agricultural systems of insects. <b>2014</b> , 5, e02077	68
1886	A novel Bayesian method for detection of APOBEC3-mediated hypermutation and its application to zoonotic transmission of simian foamy viruses. <b>2014</b> , 10, e1003493	15
1885	Recoding of the stop codon UGA to glycine by a BD1-5/SN-2 bacterium and niche partitioning between Alpha- and Gammaproteobacteria in a tidal sediment microbial community naturally selected in a laboratory chemostat. <b>2014</b> , 5, 231	26
1884	16S rDNA-based analysis reveals cosmopolitan occurrence but limited diversity of two cyanobacterial lineages with contrasted patterns of intracellular carbonate mineralization. <b>2014</b> , 5, 331	25
1883	The evolution of fungal metabolic pathways. <b>2014</b> , 10, e1004816	121
1882	Evolution of replicative DNA polymerases in archaea and their contributions to the eukaryotic replication machinery. <b>2014</b> , 5, 354	51
1881	Large-scale genomic analysis of codon usage in dengue virus and evaluation of its phylogenetic dependence. <b>2014</b> , 2014, 851425	20
1880	The contribution of the genomes of a termite and a locust to our understanding of insect neuropeptides and neurohormones. <b>2014</b> , 5, 454	83
1879	A compositional look at the human gastrointestinal microbiome and immune activation parameters in HIV infected subjects. <b>2014</b> , 10, e1003829	259
1878	High temporal and spatial diversity in marine RNA viruses implies that they have an important role in mortality and structuring plankton communities. <b>2014</b> , 5, 703	29
1877	Late winter under ice pelagic microbial communities in the high Arctic Ocean and the impact of short-term exposure to elevated CO2 levels. <b>2014</b> , 5, 490	18
1876	Comparative dynamics and distribution of influenza drug resistance acquisition to protein m2 and neuraminidase inhibitors. <b>2014</b> , 31, 355-63	19
1875	Seeking the source of <i>Pseudomonas aeruginosa</i> infections in a recently opened hospital: an observational study using whole-genome sequencing. <b>2014</b> , 4, e006278	69
1874	Exposure to a social stressor disrupts the community structure of the colonic mucosa-associated microbiota. <b>2014</b> , 14, 189	203
1873	RapidTree: A solution to rapid reconstruction phylogenetic tree. <b>2014</b> ,	
1872	Bioinformatic genome comparisons for taxonomic and phylogenetic assignments using <i>Aeromonas</i> as a test case. <b>2014</b> , 5, e02136	155
1871	Recovery of a medieval <i>Brucella melitensis</i> genome using shotgun metagenomics. <b>2014</b> , 5, e01337-14	54
1870	Absence of patient-to-patient intrahospital transmission of <i>Staphylococcus aureus</i> as determined by whole-genome sequencing. <b>2014</b> , 5, e01692-14	58

1869	Evolution of bacterial protein-tyrosine kinases and their relaxed specificity toward substrates. <b>2014</b> , 6, 800-17	32
1868	Detection of evolutionarily distinct avian influenza A viruses in Antarctica. <b>2014</b> , 5, e01098-14	70
1867	A conserved proline triplet in Val-tRNA synthetase and the origin of elongation factor P. <b>2014</b> , 9, 476-83	25
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1865	A phylogenetic perspective on species diversity, diversity and biogeography for the microbial world. <b>2014</b> , 23, 5868-76	18
1864	Microscale sulfur cycling in the phototrophic pink berry consortia of the Sippewissett Salt Marsh. <b>2014</b> , 16, 3398-415	59
1863	AliView: a fast and lightweight alignment viewer and editor for large datasets. <b>2014</b> , 30, 3276-8	1320
1862	Relationships between phyllosphere bacterial communities and plant functional traits in a neotropical forest. <b>2014</b> , 111, 13715-20	302
1861	Bacterial communities of traditional salted and fermented seafoods from Jeju Island of Korea using 16S rRNA gene clone library analysis. <b>2014</b> , 79, M927-34	30
1860	Evolutionary dynamics of leucine-rich repeat receptor-like kinases and related genes in plants: A phylogenomic approach. <b>2014</b> , 56, 648-662	10
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1858	Bacterial community structure and soil properties of a subarctic tundra soil in Council, Alaska. <b>2014</b> , 89, 465-75	74
1857	First ancient mitochondrial human genome from a prepastoralist southern African. <b>2014</b> , 6, 2647-53	34
1856	Inferring influenza global transmission networks without complete phylogenetic information. <b>2014</b> , 7, 403-12	2
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1853	Revised and updated nomenclature for highly pathogenic avian influenza A (H5N1) viruses. <b>2014</b> , 8, 384-8	128
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1851	Culture-dependent and culture-independent analyses reveal no prokaryotic community shifts or recovery of <i>Serratia marcescens</i> in <i>Acropora palmata</i> with white pox disease. <b>2014</b> , 88, 457-67	26
1850	Phylogenetic signal in the community structure of host-specific microbiomes of tropical marine sponges. <b>2014</b> , 5, 532	107
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1846	Alkane hydroxylase genes in psychrophile genomes and the potential for cold active catalysis. <b>2014</b> , 15, 1120	18
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1844	Bacterial community composition of chronic periodontitis and novel oral sampling sites for detecting disease indicators. <b>2014</b> , 2, 32	54
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1835	Phylogenetic analyses reveal HIV-1 infections between men misclassified as heterosexual transmissions. <b>2014</b> , 28, 1967-75	58
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1831	Protein quality and the protein to carbohydrate ratio within a high fat diet influences energy balance and the gut microbiota in C57BL/6J mice. <i>PLoS ONE</i> , <b>2014</b> , 9, e88904	3-7 57
1830	DBatVir: the database of bat-associated viruses. <b>2014</b> , 2014, bau021	84
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1828	Orthology inference in nonmodel organisms using transcriptomes and low-coverage genomes: improving accuracy and matrix occupancy for phylogenomics. <b>2014</b> , 31, 3081-92	161
1827	Prevalence and pathogenic potential of campylobacter isolates from free-living, human-commensal american crows. <b>2014</b> , 80, 1639-44	33
1826	Spaced words and kmacs: fast alignment-free sequence comparison based on inexact word matches. <b>2014</b> , 42, W7-11	54
1825	A systematic computational analysis of biosynthetic gene cluster evolution: lessons for engineering biosynthesis. <b>2014</b> , 10, e1004016	118
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1821	Importance of saprotrophic freshwater fungi for pollen degradation. <i>PLoS ONE</i> , <b>2014</b> , 9, e94643	3-7 74
1820	PASTA: Ultra-Large Multiple Sequence Alignment. <b>2014</b> , 177-191	37
1819	A pluralistic account of homology: adapting the models to the data. <b>2014</b> , 31, 501-16	32
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1816	PlantTFDB 3.0: a portal for the functional and evolutionary study of plant transcription factors. <b>2014</b> , 42, D1182-7	611

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1814	The functions of DNA methylation by CcrM in <i>Caulobacter crescentus</i> : a global approach. <b>2014</b> , 42, 3720-35	94
1813	The amphibian skin-associated microbiome across species, space and life history stages. <b>2014</b> , 23, 1238-50	220
1812	Unearthing carrion beetles' microbiome: characterization of bacterial and fungal hindgut communities across the Silphidae. <b>2014</b> , 23, 1251-67	65
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1810	Host-specific adaptation governs the interaction of the marine diatom, <i>Pseudo-nitzschia</i> and their microbiota. <b>2014</b> , 8, 63-76	85
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1804	Arsenic(V) reduction in relation to Iron(III) transformation and molecular characterization of the structural and functional microbial community in sediments of a basin-fill aquifer in Northern Utah. <b>2014</b> , 80, 3198-208	43
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1801	Comparative genomics of unintegrated <i>Campylobacter coli</i> clades 2 and 3. <b>2014</b> , 15, 129	31
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1799	Developmental pathway for potent V1V2-directed HIV-neutralizing antibodies. <b>2014</b> , 509, 55-62	537
1798	Gene-targeted metagenomic analysis of glucan-branching enzyme gene profiles among human and animal fecal microbiota. <b>2014</b> , 8, 493-503	23

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1795	Why are some microbes more ubiquitous than others? Predicting the habitat breadth of soil bacteria. <b>2014</b> , 17, 794-802	147
1794	Molecular and ultrastructural analysis of forisome subunits reveals the principles of forisome assembly. <b>2014</b> , 113, 1121-37	14
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1792	Enzymatic synthesis of bioinformatically predicted microcin C-like compounds encoded by diverse bacteria. <b>2014</b> , 5, e01059-14	21
1791	Microbial community dynamics and stability during an ammonia-induced shift to syntrophic acetate oxidation. <b>2014</b> , 80, 3375-83	100
1790	Stop codon reassignments in the wild. <b>2014</b> , 344, 909-13	83
1789	The genetic potential for key biogeochemical processes in Arctic frost flowers and young sea ice revealed by metagenomic analysis. <b>2014</b> , 89, 376-87	21
1788	Rapid single-colony whole-genome sequencing of bacterial pathogens. <b>2014</b> , 69, 1275-81	42
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1786	Spatial and temporal variations of microbial community in a mixed plug-flow loop reactor fed with dairy manure. <b>2014</b> , 7, 332-46	41
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1783	Signature protein of the PVC superphylum. <b>2014</b> , 80, 440-5	18
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1779	Endosymbiotic gene transfer in tertiary plastid-containing dinoflagellates. <b>2014</b> , 13, 246-55	39
1778	The impact of automated filtering of BLAST-determined homologs in the phylogenetic detection of horizontal gene transfer from a transcriptome assembly. <b>2014</b> , 71, 184-92	8
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1774	Key roles for freshwater Actinobacteria revealed by deep metagenomic sequencing. <b>2014</b> , 23, 6073-90	104
1773	Exopolysaccharide-producing probiotic Lactobacilli reduce serum cholesterol and modify enteric microbiota in ApoE-deficient mice. <b>2014</b> , 144, 1956-62	60
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1771	Phylogeny of Cas9 determines functional exchangeability of dual-RNA and Cas9 among orthologous type II CRISPR-Cas systems. <b>2014</b> , 42, 2577-90	251
1770	Microbial biogeography of wine grapes is conditioned by cultivar, vintage, and climate. <b>2014</b> , 111, E139-48	557
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1768	Formation and release behavior of iron corrosion products under the influence of bacterial communities in a simulated water distribution system. <b>2014</b> , 16, 576-85	37
1767	Molecular phylogenetic analysis of Hawaiian Rutaceae ( <i>Melicope</i> , <i>Platydesma</i> and <i>Zanthoxylum</i> ) and their different colonization patterns. <b>2014</b> , 174, 425-448	25
1766	Responsiveness of cardiometabolic-related microbiota to diet is influenced by host genetics. <b>2014</b> , 25, 583-99	48
1765	Discovery of a novel methanogen prevalent in thawing permafrost. <b>2014</b> , 5, 3212	131
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1762	Effect of domestication on the spread of the [PIN+] prion in <i>Saccharomyces cerevisiae</i> . <b>2014</b> , 197, 1007-24	9

1761	Molecular analysis for screening human bacterial pathogens in municipal wastewater treatment and reuse. <b>2014</b> , 48, 11610-9	56
1760	A molecular phylogeny of <i>Acronychia</i> , <i>Euodia</i> , <i>Melicope</i> and relatives (Rutaceae) reveals polyphyletic genera and key innovations for species richness. <b>2014</b> , 79, 54-68	28
1759	Symbiont shift towards <i>Rhizobium</i> nodulation in a group of phylogenetically related <i>Phaseolus</i> species. <b>2014</b> , 79, 1-11	13
1758	Coinfection. Virus-helminth coinfection reveals a microbiota-independent mechanism of immunomodulation. <b>2014</b> , 345, 578-82	195
1757	The natural history of ADP-ribosyltransferases and the ADP-ribosylation system. <b>2015</b> , 384, 3-32	72
1756	The evolutionary journey of Argonaute proteins. <b>2014</b> , 21, 743-53	240
1755	Correlation between viral production and carbon mineralization under nitrate-reducing conditions in aquifer sediment. <b>2014</b> , 8, 1691-703	25
1754	Phylogenomic analysis of spiders reveals nonmonophyly of orb weavers. <b>2014</b> , 24, 1772-7	102
1753	TCS: a new multiple sequence alignment reliability measure to estimate alignment accuracy and improve phylogenetic tree reconstruction. <b>2014</b> , 31, 1625-37	132
1752	Contrasting diversity of epibiotic bacteria and surrounding bacterioplankton of a common submerged macrophyte, <i>Potamogeton crispus</i> , in freshwater lakes. <b>2014</b> , 90, 551-62	40
1751	Dense genomic sampling identifies highways of pneumococcal recombination. <b>2014</b> , 46, 305-309	269
1750	Genomes of <i>Alteromonas australica</i> , a world apart. <b>2014</b> , 15, 483	23
1749	Comparative assessment of the bacterial communities associated with <i>Aedes aegypti</i> larvae and water from domestic water storage containers. <b>2014</b> , 7, 391	43
1748	Characterization of the nasopharyngeal microbiota in health and during rhinovirus challenge. <b>2014</b> , 2, 22	87
1747	Cultivation reveals physiological diversity among defensive ' <i>Streptomyces philanthi</i> ' symbionts of beewolf digger wasps (Hymenoptera, Crabronidae). <b>2014</b> , 14, 202	13
1746	Silicified Biota in High-Altitude, Geothermally Influenced Ignimbrites at El Tatio Geysir Field, Andean Cordillera (Chile). <b>2014</b> , 31, 493-508	15
1745	Six subgroups and extensive recent duplications characterize the evolution of the eukaryotic tubulin protein family. <b>2014</b> , 6, 2274-88	70
1744	A roadmap for natural product discovery based on large-scale genomics and metabolomics. <b>2014</b> , 10, 963-8	343

1743	Origin of giant viruses from smaller DNA viruses not from a fourth domain of cellular life. <b>2014</b> , 466-467, 38-52	109
1742	Shallow water marine sediment bacterial community shifts along a natural CO <sub>2</sub> gradient in the Mediterranean Sea off Vulcano, Italy. <b>2014</b> , 67, 819-28	48
1741	Analyses of dryland biological soil crusts highlight lichens as an important regulator of microbial communities. <b>2014</b> , 23, 1735-1755	53
1740	Early lignin pathway enzymes and routes to chlorogenic acid in switchgrass ( <i>Panicum virgatum</i> L.). <b>2014</b> , 84, 565-76	50
1739	Soil bacterial communities of different natural forest types in Northeast China. <b>2014</b> , 383, 203-216	57
1738	Genomic analysis of <i>Chthonomonas calidirosea</i> , the first sequenced isolate of the phylum Armatimonadetes. <b>2014</b> , 8, 1522-33	30
1737	Bacterial diversity associated with feeding dry forage at different dietary concentrations in the rumen contents of Mehshana buffalo ( <i>Bubalus bubalis</i> ) using 16S pyrotags. <b>2014</b> , 25, 31-41	49
1736	Effects of season and host physiological state on the diversity, density, and activity of the arctic ground squirrel cecal microbiota. <b>2014</b> , 80, 5611-22	52
1735	Rapid Evolution of Cellulosome Modules by Comparative Analyses of Five Clostridiales Genomes. <b>2014</b> , 7, 1369-1381	
1734	Improvement of domain-level ortholog clustering by optimizing domain-specific sum-of-pairs score. <b>2014</b> , 15, 148	7
1733	Metavir 2: new tools for viral metagenome comparison and assembled virome analysis. <b>2014</b> , 15, 76	165
1732	A survey of plant and algal genomes and transcriptomes reveals new insights into the evolution and function of the cellulose synthase superfamily. <b>2014</b> , 15, 260	41
1731	Predicting the fungal CUG codon translation with Bagheera. <b>2014</b> , 15, 411	14
1730	Processing faecal samples: a step forward for standards in microbial community analysis. <b>2014</b> , 14, 112	99
1729	Polymicrobial airway bacterial communities in adult bronchiectasis patients. <b>2014</b> , 14, 130	38
1728	Zearalenone lactonohydrolase activity in <i>Hypocreales</i> and its evolutionary relationships within the epoxide hydrolase subset of a/b-hydrolases. <b>2014</b> , 14, 82	28
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1726	A near-full length genotypic assay for HCV1b. <b>2014</b> , 209, 126-35	11

1725	Promiscuous nickel import in human pathogens: structure, thermodynamics, and evolution of extracytoplasmic nickel-binding proteins. <b>2014</b> , 22, 1421-32	26
1724	Variation in the hindgut microbial communities of the Florida manatee, <i>Trichechus manatus latirostris</i> over winter in Crystal River, Florida. <b>2014</b> , 87, 601-15	24
1723	The source of inoculum plays a defining role in the development of MEC microbial consortia fed with acetic and propionic acid mixtures. <b>2014</b> , 182-183, 11-8	42
1722	Anaerobic oxidation of long-chain n-alkanes by the hyperthermophilic sulfate-reducing archaeon, <i>Archaeoglobus fulgidus</i> . <b>2014</b> , 8, 2153-66	68
1721	Seasonal fluctuations in ionic concentrations drive microbial succession in a hypersaline lake community. <b>2014</b> , 8, 979-90	58
1720	Genomic V exons from whole genome shotgun data in reptiles. <b>2014</b> , 66, 479-92	15
1719	New sequencing technologies, the development of genomics tools, and their applications in evolutionary arachnology. <b>2014</b> , 42, 1-15	13
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1541	Intranuclear bacteria: inside the cellular control center of eukaryotes. <b>2015</b> , 25, 339-46	39
1540	Arginine-rhamnosylation as new strategy to activate translation elongation factor P. <b>2015</b> , 11, 266-70	82
1539	Application of whole-genome sequencing for bacterial strain typing in molecular epidemiology. <b>2015</b> , 53, 1072-9	185
1538	Pan-vertebrate comparative genomics unmasks retrovirus macroevolution. <b>2015</b> , 112, 464-9	92
1537	Extending the conserved phylogenetic core of archaea disentangles the evolution of the third domain of life. <b>2015</b> , 32, 1242-54	44
1536	Deflating trees: improving Bayesian branch-length estimates using informed priors. <b>2015</b> , 64, 441-7	5
1535	Molecular characterization of HIV-1 infection in Northwest Spain (2009-2013): Investigation of the subtype F outbreak. <b>2015</b> , 30, 96-101	18
1534	Bioinformatic analysis of a PLP-dependent enzyme superfamily suitable for biocatalytic applications. <b>2015</b> , 33, 566-604	152
1533	Lateral gene transfer and gene duplication played a key role in the evolution of <i>Mastigamoeba</i> <i>balamuthi</i> hydrogenosomes. <b>2015</b> , 32, 1039-55	50
1532	Defining the phylogenomics of <i>Shigella</i> species: a pathway to diagnostics. <b>2015</b> , 53, 951-60	57
1531	Spatial variation of the colonic microbiota in patients with ulcerative colitis and control volunteers. <b>2015</b> , 64, 1553-61	154
1530	Hydrogen export from intertidal cyanobacterial mats: sources, fluxes and the influence of community composition. <b>2015</b> , 17, 3738-53	13
1529	Discovery of novel genes derived from transposable elements using integrative genomic analysis. <b>2015</b> , 32, 1487-506	38
1528	V genes in primates from whole genome sequencing data. <b>2015</b> , 67, 211-28	7

1527	Species-specific duplications driving the recent expansion of NBS-LRR genes in five Rosaceae species. <b>2015</b> , 16, 77	30
1526	The genome and transcriptome of the zoonotic hookworm <i>Ancylostoma ceylanicum</i> identify infection-specific gene families. <b>2015</b> , 47, 416-22	68
1525	NIK1-mediated translation suppression functions as a plant antiviral immunity mechanism. <b>2015</b> , 520, 679-82	132
1524	Bacterial and archaeal community structures in the Arctic deep-sea sediment. <b>2015</b> , 34, 93-113	9
1523	Comparative Metagenomics of Eight Geographically Remote Terrestrial Hot Springs. <b>2015</b> , 70, 411-24	79
1522	The utility and public health implications of PCR and whole genome sequencing for the detection and investigation of an outbreak of Shiga toxin-producing <i>Escherichia coli</i> serogroup O26:H11. <b>2015</b> , 143, 1672-80	32
1521	Geometric Constraints Dominate the Antigenic Evolution of Influenza H3N2 Hemagglutinin. <b>2015</b> , 11, e1004940	34
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1519	16S rDNA analysis of archaea indicates dominance of <i>Methanobacterium</i> and high abundance of <i>Methanomassiliicoccaceae</i> in rumen of Nili-Ravi buffalo. <b>2015</b> , 35, 3-10	14
1518	Expansion of the CRF19_cpx Variant in Spain. <b>2015</b> , 69, 146-9	13
1517	Gut microbiota mediate caffeine detoxification in the primary insect pest of coffee. <b>2015</b> , 6, 7618	194
1516	Distinct <i>SagA</i> from Hospital-Associated Clade A1 <i>Enterococcus faecium</i> Strains Contributes to Biofilm Formation. <b>2015</b> , 81, 6873-82	17
1515	Genomes of planktonic Acidimicrobiales: widening horizons for marine Actinobacteria by metagenomics. <b>2015</b> , 6,	64
1514	A primase subunit essential for efficient primer synthesis by an archaeal eukaryotic-type primase. <b>2015</b> , 6, 7300	13
1513	Detection of the NS3 Q80K polymorphism by Sanger and deep sequencing in hepatitis C virus genotype 1a strains in the UK. <b>2015</b> , 21, 1033-9	19
1512	Most of the Dominant Members of Amphibian Skin Bacterial Communities Can Be Readily Cultured. <b>2015</b> , 81, 6589-600	29
1511	Effect of headspace carbon dioxide sequestration on microbial biohydrogen communities. <b>2015</b> , 40, 9966-9976	11
1510	Diverse small circular DNA viruses circulating amongst estuarine molluscs. <b>2015</b> , 31, 284-95	44

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1508	Is Planktonic Diversity Well Recorded in Sedimentary DNA? Toward the Reconstruction of Past Protistan Diversity. <b>2015</b> , 70, 865-75	43
1507	The power of next-generation sequencing as illustrated by the neuropeptidome of the crayfish <i>Procambarus clarkii</i> . <b>2015</b> , 224, 84-95	73
1506	The secreted proteins of <i>Achlya hypogyna</i> and <i>Thraustotheca clavata</i> identify the ancestral oomycete secretome and reveal gene acquisitions by horizontal gene transfer. <b>2014</b> , 7, 120-35	18
1505	Rapid draft sequencing and real-time nanopore sequencing in a hospital outbreak of <i>Salmonella</i> . <b>2015</b> , 16, 114	211
1504	Structural and biochemical characterization of the N-acetylglucosaminidase from <i>Thermotoga maritima</i> : toward rationalization of mechanistic knowledge in the GH73 family. <b>2015</b> , 25, 319-30	19
1503	A phylogenomic and molecular markers based analysis of the phylum Chlamydiae: proposal to divide the class Chlamydia into two orders, Chlamydiales and Parachlamydiales ord. nov., and emended description of the class Chlamydia. <b>2015</b> , 108, 765-81	16
1502	Hologenome theory supported by cooccurrence networks of species-specific bacterial communities in siphonous algae ( <i>Caulerpa</i> ). <b>2015</b> , 91,	28
1501	A Cyclic GMP-Dependent K <sup>+</sup> Channel in the Blastocladiomycete Fungus <i>Blastocladiella emersonii</i> . <b>2015</b> , 14, 958-63	16
1500	The impact of clinical, demographic and risk factors on rates of HIV transmission: a population-based phylogenetic analysis in British Columbia, Canada. <b>2015</b> , 211, 926-35	73
1499	Proton Pump Inhibitors Alter Specific Taxa in the Human Gastrointestinal Microbiome: A Crossover Trial. <b>2015</b> , 149, 883-5.e9	192
1498	Genomic characteristics and environmental distributions of the uncultivated Far-T4 phages. <b>2015</b> , 6, 199	15
1497	Ultra-Large Alignments Using Ensembles of Hidden Markov Models. <b>2015</b> , 259-260	1
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1495	Evolutionary Analysis of the B56 Gene Family of PP2A Regulatory Subunits. <b>2015</b> , 16, 10134-57	11
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1491	Analysis of the history and spread of HIV-1 in Uganda using phylodynamics. <b>2015</b> , 96, 1890-8	24
1490	Whole-Genome Sequencing Allows for Improved Identification of Persistent <i>Listeria monocytogenes</i> in Food-Associated Environments. <b>2015</b> , 81, 6024-37	98
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1488	Structure, mineralogy, and microbial diversity of geothermal spring microbialites associated with a deep oil drilling in Romania. <b>2015</b> , 6, 253	18
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1483	Comparative genomics of Australian isolates of the wheat stem rust pathogen <i>Puccinia graminis</i> f. sp. <i>tritici</i> reveals extensive polymorphism in candidate effector genes. <b>2014</b> , 5, 759	64
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1481	A molecular phylogenetics-based approach for identifying recent hepatitis C virus transmission events. <b>2015</b> , 33, 101-9	18
1480	Contrasting taxonomic stratification of microbial communities in two hypersaline meromictic lakes. <b>2015</b> , 9, 2642-56	55
1479	Isolation of a significant fraction of non-phototroph diversity from a desert Biological Soil Crust. <b>2015</b> , 6, 277	37
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1477	Comparison of Bacterial Community Composition of Primary and Persistent Endodontic Infections Using Pyrosequencing. <b>2015</b> , 41, 1226-33	54
1476	The Microbiome of Field-Caught and Laboratory-Adapted Australian Tephritid Fruit Fly Species with Different Host Plant Use and Specialisation. <b>2015</b> , 70, 498-508	70
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1469	Perturbation of the intestinal microbiota of mice infected with <i>Cryptosporidium parvum</i> . <b>2015</b> , 45, 567-73	43
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1463	Effects of diurnal variation of gut microbes and high-fat feeding on host circadian clock function and metabolism. <b>2015</b> , 17, 681-9	440
1462	Whole-genome sequencing for national surveillance of Shiga toxin-producing <i>Escherichia coli</i> O157. <b>2015</b> , 61, 305-12	123
1461	Gut microbiome compositional and functional differences between tumor and non-tumor adjacent tissues from cohorts from the US and Spain. <b>2015</b> , 6, 161-72	63
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1456	Emergence and subsequent functional specialization of kindlins during evolution of cell adhesiveness. <b>2015</b> , 26, 786-96	14

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1409	The Genome of Winter Moth ( <i>Operophtera brumata</i> ) Provides a Genomic Perspective on Sexual Dimorphism and Phenology. <b>2015</b> , 7, 2321-32	53
1408	PlantOrDB: a genome-wide ortholog database for land plants and green algae. <b>2015</b> , 15, 161	10
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1373	Large-scale genomic sequencing of extraintestinal pathogenic <i>Escherichia coli</i> strains. <b>2015</b> , 25, 119-28	116
1372	Global origin and transmission of hepatitis C virus nonstructural protein 3 Q80K polymorphism. <b>2015</b> , 211, 1288-95	42
1371	Response of bacterioplankton communities to cadmium exposure in coastal water microcosms with high temporal variability. <b>2015</b> , 81, 231-40	23
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1326	Proteomic Stable Isotope Probing Reveals Biosynthesis Dynamics of Slow Growing Methane Based Microbial Communities. <b>2016, 7, 563</b>	20
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1312	Fungal Assemblages in Different Habitats in an Erman's Birch Forest. <b>2016, 7, 1368</b>	14

1311	Phytoplankton-Associated Bacterial Community Composition and Succession during Toxic Diatom Bloom and Non-Bloom Events. <b>2016</b> , 7, 1433	29
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1300	A scalability study of phylogenetic network inference methods using empirical datasets and simulations involving a single reticulation. <b>2016</b> , 17, 422	25
1299	The complete genome of the tospovirus Zucchini lethal chlorosis virus. <b>2016</b> , 13, 123	6
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1297	Novel <i>Borrelia</i> species detected in echidna ticks, <i>Bothriocroton concolor</i> , in Australia. <b>2016</b> , 9, 339	47
1296	PhyloBot: A Web Portal for Automated Phylogenetics, Ancestral Sequence Reconstruction, and Exploration of Mutational Trajectories. <b>2016</b> , 12, e1004976	34
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1272	Functional interactions of archaea, bacteria and viruses in a hypersaline endolithic community. <b>2016</b> , 18, 2064-77	66
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1258	Characterization of pollen and bacterial community composition in brood provisions of a small carpenter bee. <b>2016</b> , 25, 2302-11	62

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1208	A beak size locus in Darwin's finches facilitated character displacement during a drought. <b>2016</b> , 352, 470-4	151
1207	Genomic and functional analyses of <i>Mycobacterium tuberculosis</i> strains implicate <i>ald</i> in D-cycloserine resistance. <b>2016</b> , 48, 544-51	108
1206	Divergent evolution for diverse substrate recognition by family 31 glycoside hydrolases. <b>2016</b> , 94, 323-30	1
1205	Culturing of 'unculturable' human microbiota reveals novel taxa and extensive sporulation. <b>2016</b> , 533, 543-546	672
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1202	Burkholderia: an update on taxonomy and biotechnological potential as antibiotic producers. <b>2016</b> , 100, 5215-29	145
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1200	A novel nuclear genetic code alteration in yeasts and the evolution of codon reassignment in eukaryotes. <b>2016</b> , 26, 945-55	49
1199	Fast Coalescent-Based Computation of Local Branch Support from Quartet Frequencies. <b>2016</b> , 33, 1654-68	355
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1195	Effects of Proton Pump Inhibitors on the Gastric Mucosa-Associated Microbiota in Dyspeptic Patients. <b>2016</b> , 82, 6633-6644	53
1194	Distinctive gut microbial community structure in both the wild and farmed Swan goose ( <i>Anser cygnoides</i> ). <b>2016</b> , 56, 1299-1307	25
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1186	Pyrosequencing of the broiler chicken gastrointestinal tract reveals the regional similarity and dissimilarity of microbial community. <b>2016</b> , 302-313	7

1185	Concomitant emergence of the antisense protein gene of HIV-1 and of the pandemic. <b>2016</b> , 113, 11537-11542	42
1184	Treatment of groundwater containing Mn(II), Fe(II), As(III) and Sb(III) by bioaugmented quartz-sand filters. <b>2016</b> , 106, 126-134	54
1183	Possible healthcare-associated transmission as a cause of secondary infection and population structure of <i>Staphylococcus aureus</i> isolates from two wound treatment centres in Ghana. <b>2016</b> , 13, 92-101	16
1182	Transmission of MDR MRSA between primates, their environment and personnel at a United States primate centre. <b>2016</b> , 71, 2798-803	22
1181	Highlighting the microbial diversity of 12 French cheese varieties. <b>2016</b> , 238, 265-273	60
1180	Sequence amplification via cell passaging creates spurious signals of positive adaptation in influenza virus H3N2 hemagglutinin. <b>2016</b> , 2,	28
1179	Fine-Tuning Motile Cilia and Flagella: Evolution of the Dynein Motor Proteins from Plants to Humans at High Resolution. <b>2016</b> , 33, 3249-3267	36
1178	LINEs between Species: Evolutionary Dynamics of LINE-1 Retrotransposons across the Eukaryotic Tree of Life. <b>2016</b> , 8, 3301-3322	42
1177	Identification of combinatorial host-specific signatures with a potential to affect host adaptation in influenza A H1N1 and H3N2 subtypes. <b>2016</b> , 17, 529	3
1176	Divergent evolutionary and epidemiological dynamics of cassava mosaic geminiviruses in Madagascar. <b>2016</b> , 16, 182	15
1175	Phylogenomics of Lophotrochozoa with Consideration of Systematic Error. <b>2017</b> , 66, 256-282	111
1174	The outer membrane phospholipase A is essential for membrane integrity and type III secretion in <i>Shigella flexneri</i> . <b>2016</b> , 6,	7
1173	Identification of distinctive molecular traits that are characteristic of the phylum "Deinococcus-Thermus" and distinguish its main constituent groups. <b>2016</b> , 39, 453-463	12
1172	A large outbreak of <i>Campylobacter jejuni</i> infection in a university college caused by chicken liver pE, Australia, 2013. <b>2016</b> , 144, 2971-2978	27
1171	Long-term antibiotic exposure in soil is associated with changes in microbial community structure and prevalence of class 1 integrons. <b>2016</b> , 92,	34
1170	Moleculo Long-Read Sequencing Facilitates Assembly and Genomic Binning from Complex Soil Metagenomes. <b>2016</b> , 1,	51
1169	Analysis of the chronic wound microbiota of 2,963 patients by 16S rDNA pyrosequencing. <b>2016</b> , 24, 163-74	176
1168	Rapid annotation of <i>nifH</i> gene sequences using classification and regression trees facilitates environmental functional gene analysis. <b>2016</b> , 8, 905-916	17

1167	<i>Coccomyxa actinabiotis</i> sp. nov. (Trebouxiophyceae, Chlorophyta), a new green microalga living in the spent fuel cooling pool of a nuclear reactor. <b>2016</b> , 52, 689-703	26
1166	Molecular Microbiological Profile of Chronic Suppurative Otitis Media. <b>2016</b> , 54, 2538-46	35
1165	Fate and impact of zero-valent copper nanoparticles on geographically-distinct soils. <b>2016</b> , 573, 661-670	23
1164	Cutaneous microbiome effects of fluticasone propionate cream and adjunctive bleach baths in childhood atopic dermatitis. <b>2016</b> , 75, 481-493.e8	84
1163	UAP56 is a conserved crucial component of a divergent mRNA export pathway in <i>Toxoplasma gondii</i> . <b>2016</b> , 102, 672-689	13
1162	Assessment of the bacterial community in directly brined Aloreã de Mãga table olive fermentations by metagenetic analysis. <b>2016</b> , 236, 47-55	23
1161	Genetic features of livestock-associated <i>Staphylococcus aureus</i> ST9 isolates from Chinese pigs that carry the <i>lsa(E)</i> gene for quinupristin/dalfopristin resistance. <b>2016</b> , 306, 722-729	16
1160	The Trichoptera barcode initiative: a strategy for generating a species-level Tree of Life. <b>2016</b> , 371,	49
1159	Experimental sulfate amendment alters peatland bacterial community structure. <b>2016</b> , 566-567, 1289-1296	12
1158	Bacterial Communities Associated with Different <i>Anthurium andraeanum</i> L. Plant Tissues. <b>2016</b> , 31, 321-8	17
1157	Characterising the interspecific variations and convergence of gut microbiota in Anseriformes herbivores at wintering areas. <b>2016</b> , 6, 32655	29
1156	Temperature mediates continental-scale diversity of microbes in forest soils. <b>2016</b> , 7, 12083	271
1155	MyTH4-FERM myosins have an ancient and conserved role in filopod formation. <b>2016</b> , 113, E8059-E8068	15
1154	Draft genome of the living fossil <i>Ginkgo biloba</i> . <b>2016</b> , 5, 49	161
1153	Nutrient enrichment induces dormancy and decreases diversity of active bacteria in salt marsh sediments. <b>2016</b> , 7, 12881	74
1152	Draft Genome Sequence of <i>Streptomyces</i> sp. Strain PTY08712, Isolated from <i>Styela canopus</i> , a Panamanian Tunicate. <b>2016</b> , 4,	1
1151	Gut microbiota are linked to increased susceptibility to hepatic steatosis in low-aerobic-capacity rats fed an acute high-fat diet. <b>2016</b> , 311, G166-79	22
1150	Multiplexed next-generation sequencing and de novo assembly to obtain near full-length HIV-1 genome from plasma virus. <b>2016</b> , 236, 98-104	18

1149	Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. <b>2016</b> , 537, 689-693	400
1148	Bark Beetle Research in the Postgenomic Era. <b>2016</b> , 50, 265-293	5
1147	Microbial electrochemical systems outperform fixed-bed biofilters in cleaning up urban wastewater. <b>2016</b> , 2, 984-993	44
1146	Neonatal gut microbiota associates with childhood multisensitized atopy and T cell differentiation. <b>2016</b> , 22, 1187-1191	548
1145	Origin, imports and exports of HIV-1 subtype C in South Africa: A historical perspective. <b>2016</b> , 46, 200-208	22
1144	Antibiotics, birth mode, and diet shape microbiome maturation during early life. <b>2016</b> , 8, 343ra82	680
1143	Silencing of natural transformation by an RNA chaperone and a multitarget small RNA. <b>2016</b> , 113, 8813-8	76
1142	HIV Infection Linked to Injection Use of Oxymorphone in Indiana, 2014-2015. <b>2016</b> , 375, 229-39	395
1141	Nomadic lifestyle of <i>Lactobacillus plantarum</i> revealed by comparative genomics of 54 strains isolated from different habitats. <b>2016</b> , 18, 4974-4989	106
1140	Comparative metagenomics unveils functions and genome features of microbialite-associated communities along a depth gradient. <b>2016</b> , 18, 4990-5004	20
1139	Antibiotics Suppress Activation of Intestinal Mucosal Mast Cells and Reduce Dietary Lipid Absorption in Sprague-Dawley Rats. <b>2016</b> , 151, 923-932	36
1138	Bacterial and fungal symbionts of parasitic <i>Dendroctonus</i> bark beetles. <b>2016</b> , 92,	22
1137	Mobile genes in the human microbiome are structured from global to individual scales. <b>2016</b> , 535, 435-439	148
1136	Here We Are, But Where Do We Go? A Systematic Review of Crustacean Transcriptomic Studies from 2014-2015. <b>2016</b> , 56, 1055-1066	16
1135	Modeling central metabolism and energy biosynthesis across microbial life. <b>2016</b> , 17, 568	22
1134	The dissemination of multidrug-resistant <i>Enterobacter cloacae</i> throughout the UK and Ireland. <b>2016</b> , 1, 16173	16
1133	A high-resolution map of the gut microbiota in Atlantic salmon ( <i>Salmo salar</i> ): A basis for comparative gut microbial research. <b>2016</b> , 6, 30893	151
1132	Genome-based microbial ecology of anammox granules in a full-scale wastewater treatment system. <b>2016</b> , 7, 11172	248

1131	A perspective on 16S rRNA operational taxonomic unit clustering using sequence similarity. <b>2016</b> , 2, 16004	126
1130	Cytolethal distending toxin producing <i>Escherichia coli</i> O157:H43 strain T22 represents a novel evolutionary lineage within the O157 serogroup. <b>2016</b> , 46, 110-117	1
1129	Ecological dynamics of influenza A viruses: cross-species transmission and global migration. <b>2016</b> , 6, 36839	19
1128	Genomics of high molecular weight plasmids isolated from an on-farm biopurification system. <b>2016</b> , 6, 28284	12
1127	Neuropeptide Evolution: Chelicerate Neurohormone and Neuropeptide Genes may reflect one or more whole genome duplications. <b>2016</b> ,	2
1126	Evidence for an Alternative Mechanism of Toxin Production in the Box Jellyfish <i>Alatina alata</i> . <b>2016</b> , 56, 973-988	11
1125	Membrane Proteins Are Dramatically Less Conserved than Water-Soluble Proteins across the Tree of Life. <b>2016</b> , 33, 2874-2884	35
1124	Draft Genome Sequence of <i>Gordonia</i> sp. Strain UCD-TK1 (Phylum Actinobacteria). <b>2016</b> , 4,	2
1123	Endemic hydrothermal vent species identified in the open ocean seed bank. <b>2016</b> , 1, 16086	32
1122	Compartmentalized HIV rebound in the central nervous system after interruption of antiretroviral therapy. <b>2016</b> , 2, vew020	28
1121	The effect of DNA extraction methodology on gut microbiota research applications. <b>2016</b> , 9, 365	45
1120	Gut microbiota of dung beetles correspond to dietary specializations of adults and larvae. <b>2016</b> , 25, 6092-6106	40
1119	The <i>Cardamine hirsuta</i> genome offers insight into the evolution of morphological diversity. <b>2016</b> , 2, 16167	56
1118	Birth mode-dependent association between pre-pregnancy maternal weight status and the neonatal intestinal microbiome. <b>2016</b> , 6, 23133	87
1117	Reconstructing contact network parameters from viral phylogenies. <b>2016</b> , 2, vew029	7
1116	Impact of dengue virus (DENV) co-infection on clinical manifestations, disease severity and laboratory parameters. <b>2016</b> , 16, 406	34
1115	Genes conserved for arbuscular mycorrhizal symbiosis identified through phylogenomics. <b>2016</b> , 2, 15208	129
1114	Tracing ancestor rice of Suriname Maroons back to its African origin. <b>2016</b> , 2, 16149	18

1113	A Direct Comparison of Two Densely Sampled HIV Epidemics: The UK and Switzerland. <b>2016</b> , 6, 32251	11
1112	Evolution of 2009 H1N1 influenza viruses during the pandemic correlates with increased viral pathogenicity and transmissibility in the ferret model. <b>2016</b> , 6, 28583	15
1111	Developing a genetic manipulation system for the Antarctic archaeon, <i>Halorubrum lacusprofundi</i> : investigating acetamidase gene function. <b>2016</b> , 6, 34639	14
1110	Genomic and enzymatic evidence for acetogenesis among multiple lineages of the archaeal phylum Bathyarchaeota widespread in marine sediments. <b>2016</b> , 1, 16035	178
1109	Antibiotic-induced perturbations in gut microbial diversity influences neuro-inflammation and amyloidosis in a murine model of Alzheimer's disease. <b>2016</b> , 6, 30028	314
1108	Genomes of Abundant and Widespread Viruses From the Deep Ocean. <b>2016</b> , 7,	52
1107	Improving Re-annotation of Annotated Eukaryotic Genomes. <b>2016</b> , 171-195	2
1106	Next generation sequencing data of a defined microbial mock community. <b>2016</b> , 3, 160081	55
1105	The Last Common Ancestor of Most Bilaterian Animals Possessed at Least Nine Opsins. <b>2016</b> , 8, 3640-3652	60
1104	Vertical distribution of bacterial community is associated with the degree of soil organic matter decomposition in the active layer of moist acidic tundra. <b>2016</b> , 54, 713-723	25
1103	A De-Novo Genome Analysis Pipeline (DeNoGAP) for large-scale comparative prokaryotic genomics studies. <b>2016</b> , 17, 260	14
1102	MycocAP - Mycobacterium Comparative Analysis Platform. <b>2015</b> , 5, 18227	2
1101	Evolutionary Dynamics and Complicated Genetic Transmission Network Patterns of HIV-1 CRF01_AE among MSM in Shanghai, China. <b>2016</b> , 6, 34729	26
1100	Evolutionary plasticity of restorer-of-fertility-like proteins in rice. <b>2016</b> , 6, 35152	32
1099	Streptococcal group B integrative and mobilizable element IMESag-rpsI encodes a functional relaxase involved in its transfer. <b>2016</b> , 6,	6
1098	Resurrecting ancestral structural dynamics of an antiviral immune receptor: adaptive binding pocket reorganization repeatedly shifts RNA preference. <b>2016</b> , 16, 241	5
1097	The multiple evolutionary origins of the eukaryotic N-glycosylation pathway. <b>2016</b> , 11, 36	30
1096	Altered gut microbiota in Rett syndrome. <b>2016</b> , 4, 41	69

1095	Comparison of placenta samples with contamination controls does not provide evidence for a distinct placenta microbiota. <b>2016</b> , 4, 29	326
1094	New observations of the enigmatic West African Cellana limpet (Mollusca: Gastropoda: Nacellidae). <b>2016</b> , 9,	1
1093	Anchoring quartet-based phylogenetic distances and applications to species tree reconstruction. <b>2016</b> , 17, 783	12
1092	Scaling statistical multiple sequence alignment to large datasets. <b>2016</b> , 17, 764	9
1091	A performance study of the impact of recombination on species tree analysis. <b>2016</b> , 17, 785	7
1090	Coreceptor usage of Chinese HIV-1 and impact of X4/DM transmission clusters among recently infected men who have sex with men. <b>2016</b> , 95, e5017	8
1089	Climate and edaphic controllers influence rhizosphere community assembly for a wild annual grass. <b>2016</b> , 97, 1307-18	72
1088	Analysis of metagenomic data reveals common features of halophilic viral communities across continents. <b>2016</b> , 18, 889-903	31
1087	Metabarcoding reveals strong spatial structure and temporal turnover of zooplankton communities among marine and freshwater ports. <b>2016</b> , 22, 493-504	60
1086	Geography and Location Are the Primary Drivers of Office Microbiome Composition. <b>2016</b> , 1,	84
1085	Genomic and transcriptomic analysis of the streptomycin-dependent Mycobacterium tuberculosis strain 18b. <b>2016</b> , 17, 190	16
1084	Comparative study on the in vitro replication and genomic variability of Argentinean field isolates of bovine herpesvirus type 4 (BoHV-4). <b>2016</b> , 52, 372-8	6
1083	Applications of Bio-molecular Databases in Bioinformatics. <b>2016</b> , 329-351	2
1082	Evolution of hepatitis C virus in HIV coinfecting patients under antiretroviral therapy. <b>2016</b> , 43, 186-96	1
1081	Comparative genomic analyses reveal broad diversity in botulinum-toxin-producing Clostridia. <b>2016</b> , 17, 180	56
1080	Evaluation of 16S rRNA amplicon sequencing using two next-generation sequencing technologies for phylogenetic analysis of the rumen bacterial community in steers. <b>2016</b> , 127, 132-140	48
1079	Effects of Gene Duplication, Positive Selection, and Shifts in Gene Expression on the Evolution of the Venom Gland Transcriptome in Widow Spiders. <b>2016</b> , 8, 228-42	26
1078	Genus-Wide Comparative Genome Analyses of Colletotrichum Species Reveal Specific Gene Family Losses and Gains during Adaptation to Specific Infection Lifestyles. <b>2016</b> , 8, 1467-81	50

1077	Associations among Wine Grape Microbiome, Metabolome, and Fermentation Behavior Suggest Microbial Contribution to Regional Wine Characteristics. <b>2016</b> , 7,	205
1076	A Silenced vanA Gene Cluster on a Transferable Plasmid Caused an Outbreak of Vancomycin-Variable Enterococci. <b>2016</b> , 60, 4119-27	24
1075	Prebiotics and Bioactive Milk Fractions Affect Gut Development, Microbiota, and Neurotransmitter Expression in Piglets. <b>2016</b> , 63, 688-697	43
1074	nana plant2 Encodes a Maize Ortholog of the Arabidopsis Brassinosteroid Biosynthesis Gene DWARF1, Identifying Developmental Interactions between Brassinosteroids and Gibberellins. <b>2016</b> , 171, 2633-47	55
1073	The origin of the supernumerary subunits and assembly factors of complex I: A treasure trove of pathway evolution. <b>2016</b> , 1857, 971-9	37
1072	Prevalence of Cryptosporidium and Giardia in the water resources of the Kuang River catchment, Northern Thailand. <b>2016</b> , 562, 701-713	20
1071	Highly diverse nirK genes comprise two major clades that harbour ammonium-producing denitrifiers. <b>2016</b> , 17, 155	40
1070	SuperPhy: predictive genomics for the bacterial pathogen Escherichia coli. <b>2016</b> , 16, 65	9
1069	Bacterial community composition and fhs profiles of low- and high-ammonia biogas digesters reveal novel syntrophic acetate-oxidising bacteria. <b>2016</b> , 9, 48	119
1068	Large genomic differences between Moraxella bovoculi isolates acquired from the eyes of cattle with infectious bovine keratoconjunctivitis versus the deep nasopharynx of asymptomatic cattle. <b>2016</b> , 47, 31	24
1067	Composition of the Cutaneous Bacterial Community in Japanese Amphibians: Effects of Captivity, Host Species, and Body Region. <b>2016</b> , 72, 460-9	38
1066	Large differences in potential denitrification and sediment microbial communities across the Laurentian great lakes. <b>2016</b> , 128, 353-368	27
1065	Genetic diversity of hepatitis B virus (HBV) in Madagascar. <b>2016</b> , 88, 2138-2144	4
1064	An extended single-index multiplexed 16S rRNA sequencing for microbial community analysis on MiSeq illumina platforms. <b>2016</b> , 56, 321-6	76
1063	Intermediate divergence levels maximize the strength of structure-sequence correlations in enzymes and viral proteins. <b>2016</b> , 25, 1341-53	4
1062	ncRNA orthologies in the vertebrate lineage. <b>2016</b> , 2016,	14
1061	Origin and mechanism of crassulacean acid metabolism in orchids as implied by comparative transcriptomics and genomics of the carbon fixation pathway. <b>2016</b> , 86, 175-85	21
1060	Deterministic processes dominate nematode community structure in the Fynbos Mediterranean heathland of South Africa. <b>2016</b> , 30, 685-701	15

1059	Indoor air bacterial communities in Hong Kong households assemble independently of occupant skin microbiomes. <b>2016</b> , 18, 1754-63	38
1058	Ice cover extent drives phytoplankton and bacterial community structure in a large north-temperate lake: implications for a warming climate. <b>2016</b> , 18, 1704-19	45
1057	A phylotranscriptomic analysis of gene family expansion and evolution in the largest order of pleurocarpous mosses (Hypnales, Bryophyta). <b>2016</b> , 98, 29-40	24
1056	Comprehensive curation and analysis of fungal biosynthetic gene clusters of published natural products. <b>2016</b> , 89, 18-28	76
1055	Genome-Based Infection Tracking Reveals Dynamics of Clostridium difficile Transmission and Disease Recurrence. <b>2016</b> , 62, 746-752	52
1054	Dissecting Japan's Dengue Outbreak in 2014. <b>2016</b> , 94, 409-412	46
1053	Recent Mobility of Casposons, Self-Synthesizing Transposons at the Origin of the CRISPR-Cas Immunity. <b>2016</b> , 8, 375-86	26
1052	Dengue in China: Comprehensive Phylogenetic Evaluation Reveals Evidence of Endemicity and Complex Genetic Diversity. <b>2016</b> , 94, 198-202	16
1051	Myelin in cartilaginous fish. <b>2016</b> , 1641, 34-42	8
1050	Genomic Epidemiology: Whole-Genome-Sequencing-Powered Surveillance and Outbreak Investigation of Foodborne Bacterial Pathogens. <b>2016</b> , 7, 353-74	111
1049	Perfluoroalkyl Acids Inhibit Reductive Dechlorination of Trichloroethene by Repressing Dehalococcoides. <b>2016</b> , 50, 240-8	32
1048	HGTree: database of horizontally transferred genes determined by tree reconciliation. <b>2016</b> , 44, D610-9	24
1047	Analysis of cbbL, nifH, and pufLM in Soils from the Sør Rondane Mountains, Antarctica, Reveals a Large Diversity of Autotrophic and Phototrophic Bacteria. <b>2016</b> , 71, 131-49	23
1046	Effects of organic&horganic compound fertilizer with reduced chemical fertilizer application on crop yields, soil biological activity and bacterial community structure in a rice&wheat cropping system. <b>2016</b> , 99, 1-12	173
1045	Spatial variability of microbial richness and diversity and relationships with soil organic carbon, texture and structure across an agricultural field. <b>2016</b> , 103, 44-55	51
1044	A polyphenol-rich fraction obtained from table grapes decreases adiposity, insulin resistance and markers of inflammation and impacts gut microbiota in high-fat-fed mice. <b>2016</b> , 31, 150-65	72
1043	Transmission dynamics of HIV-1 subtype B in the Basque Country, Spain. <b>2016</b> , 40, 91-97	9
1042	The human milk oligosaccharide 2'-fucosyllactose augments the adaptive response to extensive intestinal. <b>2016</b> , 310, G427-38	26

1041	Analysis of factors contributing to variation in the C57BL/6J fecal microbiota across German animal facilities. <b>2016</b> , 306, 343-355	97
1040	Mesophyll Chloroplast Investment in C3, C4 and C2 Species of the Genus <i>Flaveria</i> . <b>2016</b> , 57, 904-18	20
1039	Contrasting Patterns of Evolutionary Diversification in the Olfactory Repertoires of Reptile and Bird Genomes. <b>2016</b> , 8, 470-80	13
1038	Bacterioplankton community resilience to ocean acidification: evidence from microbial network analysis. <b>2016</b> , 73, 865-875	48
1037	High-throughput sequencing reveals the core gut microbiome of Bar-headed goose ( <i>Anser indicus</i> ) in different wintering areas in Tibet. <b>2016</b> , 5, 287-95	29
1036	Effects of sequence diversity and recombination on the accuracy of phylogenetic trees estimated by kSNP. <b>2016</b> , 32, 90-99	5
1035	Microbial diversity drives multifunctionality in terrestrial ecosystems. <b>2016</b> , 7, 10541	699
1034	Diverse circular replication-associated protein encoding viruses circulating in invertebrates within a lake ecosystem. <b>2016</b> , 39, 304-316	51
1033	Probing fatty acid metabolism in bacteria, cyanobacteria, green microalgae and diatoms with natural and unnatural fatty acids. <b>2016</b> , 12, 1299-312	16
1032	16S metagenomics reveals changes in the soil bacterial community driven by soil organic C, N-fertilizer and tillage-crop residue management. <b>2016</b> , 159, 1-8	56
1031	Characterization of a Drinking Water Distribution Pipeline Terminally Colonized by <i>Naegleria fowleri</i> . <b>2016</b> , 50, 2890-8	26
1030	Direct and Indirect Horizontal Transmission of the Antifungal Probiotic Bacterium <i>Janthinobacterium lividum</i> on Green Frog ( <i>Lithobates clamitans</i> ) Tadpoles. <b>2016</b> , 82, 2457-2466	30
1029	Full Mitochondrial Genome Sequence of the Sugar Beet Wireworm <i>Limonius californicus</i> (Coleoptera: Elateridae), a Common Agricultural Pest. <b>2016</b> , 4,	5
1028	Changes of soil prokaryotic communities after clear-cutting in a karst forest: evidences for cutting-based disturbance promoting deterministic processes. <b>2016</b> , 92,	22
1027	A phylogenomic reappraisal of family-level divisions within the class Halobacteria: proposal to divide the order Halobacteriales into the families Halobacteriaceae, Haloarculaceae fam. nov., and Halococcaceae fam. nov., and the order Haloferacales into the families, Haloferacaceae and Halorubraceae fam nov. <b>2016</b> , 109, 565-87	85
1026	Nutrient limitation of microbial phototrophs on a debris-covered glacier. <b>2016</b> , 95, 156-163	37
1025	Xenacoelomorpha is the sister group to Nephrozoa. <b>2016</b> , 530, 89-93	210
1024	Late acquisition of mitochondria by a host with chimaeric prokaryotic ancestry. <b>2016</b> , 531, 101-4	161

1023	Real-time, portable genome sequencing for Ebola surveillance. <b>2016</b> , 530, 228-232	845
1022	Responses of Soil Bacterial Communities to Nitrogen Deposition and Precipitation Increment Are Closely Linked with Aboveground Community Variation. <b>2016</b> , 71, 974-89	55
1021	Increased water contamination and grow-out Pekin duck mortality when raised with water troughs compared to pin-metered water lines using a United States management system. <b>2016</b> , 95, 736-48	7
1020	Fast and accurate branch lengths estimation for phylogenomic trees. <b>2016</b> , 17, 23	10
1019	Detection and Diversity of Fungal Nitric Oxide Reductase Genes (p450nor) in Agricultural Soils. <b>2016</b> , 82, 2919-2928	35
1018	Virological failure in patients with HIV-1 subtype C receiving antiretroviral therapy: an analysis of a prospective national cohort in Sweden. <b>2016</b> , 3, e166-74	35
1017	Aflatoxin B1 Induced Compositional Changes in Gut Microbial Communities of Male F344 Rats. <b>2016</b> , 150, 54-63	54
1016	Gut bacterial communities across tadpole ecomorphs in two diverse tropical anuran faunas. <b>2016</b> , 103, 25	46
1015	Cervical Microbiota Associated with Higher Grade Cervical Intraepithelial Neoplasia in Women Infected with High-Risk Human Papillomaviruses. <b>2016</b> , 9, 357-66	66
1014	Fungal root endophytes of tomato from Kenya and their nematode biocontrol potential. <b>2016</b> , 15, 1	26
1013	Neuropeptide evolution: Chelicerate neurohormone and neuropeptide genes may reflect one or more whole genome duplications. <b>2016</b> , 229, 41-55	29
1012	Perchlorate Reductase Is Distinguished by Active Site Aromatic Gate Residues. <b>2016</b> , 291, 9190-202	46
1011	Genomic Analysis of Salmonella enterica Serovar Typhimurium Characterizes Strain Diversity for Recent U.S. Salmonellosis Cases and Identifies Mutations Linked to Loss of Fitness under Nitrosative and Oxidative Stress. <b>2016</b> , 7, e00154	15
1010	Comparative Genomics of Candidate Phylum TM6 Suggests That Parasitism Is Widespread and Ancestral in This Lineage. <b>2016</b> , 33, 915-27	50
1009	ISC, a Novel Group of Bacterial and Archaeal DNA Transposons That Encode Cas9 Homologs. <b>2015</b> , 198, 797-807	26
1008	Impact of gene family evolutionary histories on phylogenetic species tree inference by gene tree parsimony. <b>2016</b> , 96, 9-16	1
1007	Community shift of biofilms developed in a full-scale drinking water distribution system switching from different water sources. <b>2016</b> , 544, 499-506	28
1006	Evolution of geographical place and niche space: Patterns of diversification in the North American sedge (Cyperaceae) flora. <b>2016</b> , 95, 183-95	26

1005	Skin bacterial diversity of Panamanian frogs is associated with host susceptibility and presence of <i>Batrachochytrium dendrobatidis</i> . <b>2016</b> , 10, 1682-95	98
1004	Genome Reconstruction from Metagenomic Data Sets Reveals Novel Microbes in the Brackish Waters of the Caspian Sea. <b>2016</b> , 82, 1599-1612	29
1003	Microbial composition of biofilms associated with lithifying rubble of <i>Acropora palmata</i> branches. <b>2016</b> , 92,	7
1002	Evolutionary Divergence of <i>Aggregatibacter actinomycetemcomitans</i> . <b>2016</b> , 95, 94-101	35
1001	Effects of salinity build-up on the performance and bacterial community structure of a membrane bioreactor. <b>2016</b> , 200, 305-10	65
1000	Utility of Whole-Genome Sequencing in Characterizing <i>Acinetobacter</i> Epidemiology and Analyzing Hospital Outbreaks. <b>2016</b> , 54, 593-612	60
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964	Widespread Historical Contingency in Influenza Viruses. <b>2017</b> , 205, 409-420	7
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932	Microbiomic differences in tumor and paired-normal tissue in head and neck squamous cell carcinomas. <b>2017</b> , 9, 14	64
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916	An introduction to metagenomic data generation, analysis, visualization, and interpretation. <b>2017</b> , 94-126	2

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913	WGS-based surveillance of third-generation cephalosporin-resistant <i>Escherichia coli</i> from bloodstream infections in Denmark. <b>2017</b> , 72, 1922-1929	47
912	How Long Does <i>Wolbachia</i> Remain on Board?. <b>2017</b> , 34, 1183-1193	61
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569	Metabarcoding airborne pollen from subtropical and temperate eastern Australia over multiple years reveals pollen aerobiome diversity and complexity. <b>2023</b> , 862, 160585	0
568	Description of <i>Pseudogemmobacter faecipullorum</i> sp. nov., isolated from poultry manure. <b>2022</b> , 369,	0
567	DRUG RESISTANCE MUTATIONS AND TRANSMISSION CLUSTERS OF THE HIV-1 CRF01_AE SUB-EPIDEMIC IN BULGARIA. <b>2022</b> , 49, 12-19	0
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562	Characteristic alterations of gut microbiota in uncontrolled gout. <b>2022</b> , 60, 1178-1190	2
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558	Intake of slow-digesting carbohydrates is related to changes in the microbiome and its functional pathways in growing rats with obesity induced by diet. 9,	1
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407	Integrating phylogenetics with intron positions illuminates the origin of the complex spliceosome.	0
406	Altered gastrointestinal tract structure and microbiome following cerebral malaria infection.	0
405	Epiphytic Microbiome of Alvarinho Wine Grapes from Different Geographic Regions in Portugal. <b>2023</b> , 12, 146	0
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403	SARS-CoV-2 escape from cytotoxic T cells during long-term COVID-19. <b>2023</b> , 14,	0
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399	<i>Moraxella nasicaprae</i> sp. nov., Isolated from a Goat with Respiratory Disease. <b>2023</b> , 80,	0
398	A bittersweet fate: detection of serotype switching in <i>Pseudomonas aeruginosa</i> . <b>2023</b> , 9,	0
397	Inflammatory Responses Induced by the Monophasic Variant of <i>Salmonella</i> Typhimurium in Pigs Play a Role in the High Shedder Phenotype and Fecal Microbiota Composition.	2
396	Comparative genome analysis reveals high-level drug resistance markers in a clinical isolate of <i>Mycobacterium fortuitum</i> subsp. <i>fortuitum</i> MF GZ001. 12,	0
395	Geography and elevation as drivers of cloacal microbiome assemblages of a passerine bird distributed across Sulawesi, Indonesia. <b>2023</b> , 5,	0
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