

# Nikos C Kyrpides

## List of Publications by Year in Descending Order

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**Version:** 2024-04-09

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

664 papers	49,673 citations	91 h-index	211 g-index
716 ext. papers	73,222 ext. citations	12.6 avg, IF	8.15 L-index

#	Paper	IF	Citations
664	The Genome of the Acid Soil-Adapted Strain OR191 Encodes Determinants for Effective Symbiotic Interaction With Both an Inverted Repeat Lacking Clade and a Phaseoloid Legume Host.. <i>Frontiers in Microbiology</i> , <b>2022</b> , 13, 735911	5.7	0
663	Identifying candidate structured RNAs in CRISPR operons.. <i>RNA Biology</i> , <b>2022</b> , 19, 678-685	4.8	
662	Sodalis ligni Strain 159R Isolated from an Anaerobic Lignin-Degrading Consortium.. <i>Microbiology Spectrum</i> , <b>2022</b> , e0234621	8.9	
661	The Santorini Volcanic Complex as a Valuable Source of Enzymes for Bioenergy. <i>Energies</i> , <b>2021</b> , 14, 14143	3.1	0
660	Genomics, Exometabolomics, and Metabolic Probing Reveal Conserved Proteolytic Metabolism of and Three Candidate Species From China and Japan. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 632731	5.7	2
659	Metagenomic compendium of 189,680 DNA viruses from the human gut microbiome. <i>Nature Microbiology</i> , <b>2021</b> , 6, 960-970	26.6	36
658	Metagenome Sequencing to Explore Phylogenomics of Terrestrial Cyanobacteria. <i>Microbiology Resource Announcements</i> , <b>2021</b> , 10, e0025821	1.3	3
657	DOE JGI Metagenome Workflow. <i>MSystems</i> , <b>2021</b> , 6,	7.6	12
656	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , <b>2021</b> , 184, 3376-3393	36.1	42
655	Genomes OnLine Database (GOLD) v.8: overview and updates. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D723-D733	33.1	47
654	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 499-509	44.5	120
653	A unified catalog of 204,938 reference genomes from the human gut microbiome. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 105-114	44.5	185
652	The IMG/M data management and analysis system v.6.0: new tools and advanced capabilities. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D751-D763	20.1	114
651	IMG/VR v3: an integrated ecological and evolutionary framework for interrogating genomes of uncultivated viruses. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D764-D775	20.1	58
650	CheckV assesses the quality and completeness of metagenome-assembled viral genomes. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 578-585	44.5	104
649	VPF-Class: Taxonomic assignment and host prediction of uncultivated viruses based on viral protein families. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	9
648	Illuminating the Virosphere Through Global Metagenomics. <i>Annual Review of Biomedical Data Science</i> , <b>2021</b> , 4, 369-391	5.6	1

647	The <i>Roseibium album</i> (Labrenzia alba) Genome Possesses Multiple Symbiosis Factors Possibly Underpinning Host-Microbe Relationships in the Marine Benthos. <i>Microbiology Resource Announcements</i> , <b>2021</b> , 10, e0032021	1.3	1
646	<i>Frigoriflavimonas asaccharolytica</i> gen. nov., sp. nov., a novel psychrophilic esterase and protease producing bacterium isolated from Antarctica. <i>Antonie Van Leeuwenhoek</i> , <b>2021</b> , 114, 1991-2002	2.1	0
645	The biogeographic differentiation of algal microbiomes in the upper ocean from pole to pole. <i>Nature Communications</i> , <b>2021</b> , 12, 5483	17.4	3
644	Atypical Divergence of SARS-CoV-2 Orf8 from Orf7a within the Coronavirus Lineage Suggests Potential Stealthy Viral Strategies in Immune Evasion. <i>MBio</i> , <b>2021</b> , 12,	7.8	13
643	Microbial Benthic Communities in the Aegean Sea. <i>Handbook of Environmental Chemistry</i> , <b>2020</b> , 1	0.8	1
642	A synthesis of bacterial and archaeal phenotypic trait data. <i>Scientific Data</i> , <b>2020</b> , 7, 170	8.2	20
641	COVID-19 pandemic reveals the peril of ignoring metadata standards. <i>Scientific Data</i> , <b>2020</b> , 7, 188	8.2	30
640	Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. <i>Nature Medicine</i> , <b>2020</b> , 26, 941-951	50.5	50
639	Novel heavy metal resistance gene clusters are present in the genome of <i>Cupriavidus neocaledonicus</i> STM 6070, a new species of <i>Mimosa pudica</i> microsymbiont isolated from heavy-metal-rich mining site soil. <i>BMC Genomics</i> , <b>2020</b> , 21, 214	4.5	5
638	A scoutRNA Is Required for Some Type V CRISPR-Cas Systems. <i>Molecular Cell</i> , <b>2020</b> , 79, 416-424.e5	17.6	24
637	Structure determination of the HgcAB complex using metagenome sequence data: insights into microbial mercury methylation. <i>Communications Biology</i> , <b>2020</b> , 3, 320	6.7	8
636	Metabolic dependencies govern microbial syntrophies during methanogenesis in an anaerobic digestion ecosystem. <i>Microbiome</i> , <b>2020</b> , 8, 22	16.6	42
635	Giant virus diversity and host interactions through global metagenomics. <i>Nature</i> , <b>2020</b> , 578, 432-436	50.4	94
634	One Complete and Seven Draft Genome Sequences of Subdivision 1 and 3 Isolated from Soil. <i>Microbiology Resource Announcements</i> , <b>2020</b> , 9,	1.3	4
633	Analysis of 1,000+ Type-Strain Genomes Substantially Improves Taxonomic Classification of. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 468	5.7	101
632	IMG-ABC v.5.0: an update to the IMG/Atlas of Biosynthetic Gene Clusters Knowledgebase. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, D422-D430	20.1	33
631	Metagenomes and Metatranscriptomes of a Glucose-Amended Agricultural Soil. <i>Microbiology Resource Announcements</i> , <b>2020</b> , 9,	1.3	1
630	Draft genome of strain 8N4 provides insights into the potential role of this species in its plant host. <i>PeerJ</i> , <b>2020</b> , 8, e8822	3.1	5

629	sp. nov., isolated from air sampling in maritime Antarctica. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2020</b> , 70, 4935-4941	2.2	5
628	Genome-guided analysis allows the identification of novel physiological traits in <i>Trichococcus</i> species. <i>BMC Genomics</i> , <b>2020</b> , 21, 24	4.5	6
627	Genome analysis of the marine bacterium <i>Kiloniella laminariae</i> and first insights into comparative genomics with related <i>Kiloniella</i> species. <i>Archives of Microbiology</i> , <b>2020</b> , 202, 815-824	3	3
626	Insights into the dynamics between viruses and their hosts in a hot spring microbial mat. <i>ISME Journal</i> , <b>2020</b> , 14, 2527-2541	11.9	13
625	Impact of Soil Salinity on the Cowpea Nodule-Microbiome and the Isolation of Halotolerant PGPR Strains to Promote Plant Growth under Salinity Stress. <i>Phytobiomes Journal</i> , <b>2020</b> , 4, 364-374	4.8	4
624	Influence of the polar light cycle on seasonal dynamics of an Antarctic lake microbial community. <i>Microbiome</i> , <b>2020</b> , 8, 116	16.6	15
623	Recombination should not be an afterthought. <i>Nature Reviews Microbiology</i> , <b>2020</b> , 18, 606	22.2	7
622	Molecular Dialogues between Early Divergent Fungi and Bacteria in an Antagonism versus a Mutualism. <i>MBio</i> , <b>2020</b> , 11,	7.8	5
621	A Functional Mini-Integrase in a Two-Protein-type V-C CRISPR System. <i>Molecular Cell</i> , <b>2019</b> , 73, 727-737. <del>43.6</del>	43.6	15
620	Toward unrestricted use of public genomic data. <i>Science</i> , <b>2019</b> , 363, 350-352	33.3	25
619	Improved Draft Genome Sequence of <i>Pseudomonas poae</i> A2-S9, a Strain with Plant Growth-Promoting Activity. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	2
618	Complete Genome Sequence of <i>Serratia quinivorans</i> Strain 124R, a Facultative Anaerobe Isolated on Organosolv Lignin as a Sole Carbon Source. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	1
617	Sulfate-Reducing Bacteria That Produce Exopolymers Thrive in the Calcifying Zone of a Hypersaline Cyanobacterial Mat. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 862	5.7	20
616	Consent insufficient for data release-Response. <i>Science</i> , <b>2019</b> , 364, 446	33.3	4
615	Genome-informed Bradyrhizobium taxonomy: where to from here?. <i>Systematic and Applied Microbiology</i> , <b>2019</b> , 42, 427-439	4.2	41
614	Contrasting Pathways for Anaerobic Methane Oxidation in Gulf of Mexico Cold Seep Sediments. <i>MSystems</i> , <b>2019</b> , 4,	7.6	16
613	Draft Genome of <i>Burkholderia cenocepacia</i> TATl-371, a Strain from the <i>Burkholderia cepacia</i> Complex Retains Antagonism in Different Carbon and Nitrogen Sources. <i>Current Microbiology</i> , <b>2019</b> , 76, 566-574	2.4	3
612	A Comparison of Microbial Genome Web Portals. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 208	5.7	10

611	New insights from uncultivated genomes of the global human gut microbiome. <i>Nature</i> , <b>2019</b> , 568, 505-510.4	10.4	275
610	Large-Scale Analyses of Human Microbiomes Reveal Thousands of Small, Novel Genes. <i>Cell</i> , <b>2019</b> , 178, 1245-1259.e14	56.2	91
609	Microbiomes of Velloziaceae from phosphorus-impooverished soils of the campos rupestres, a biodiversity hotspot. <i>Scientific Data</i> , <b>2019</b> , 6, 140	8.2	3
608	Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes. <i>Nature Microbiology</i> , <b>2019</b> , 4, 1895-1906	26.6	99
607	Microbial metagenomes and metatranscriptomes during a coastal phytoplankton bloom. <i>Scientific Data</i> , <b>2019</b> , 6, 129	8.2	13
606	Analysis of 1,000 Type-Strain Genomes Improves Taxonomic Classification of. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 2083	5.7	66
605	Metagenomes and metatranscriptomes from boreal potential and actual acid sulfate soil materials. <i>Scientific Data</i> , <b>2019</b> , 6, 207	8.2	3
604	High-quality draft genome sequences of DSM 14164, DSM 17497, DSM 15088, DSM 21245 and DSM 16006: taxonomic considerations. <i>Access Microbiology</i> , <b>2019</b> , 1, e000067	1	2
603	Complete Genome Sequence for sp. Strain OR53 and Draft Genome Sequence for sp. Strain OR43, Two Bacteria Tolerant to Uranium. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	3
602	Improved Draft Genome Sequence of sp. Strain LKL04, a Bacterial Endophyte Associated with Switchgrass Plants. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	4
601	Establishment of computational biology in Greece and Cyprus: Past, present, and future. <i>PLoS Computational Biology</i> , <b>2019</b> , 15, e1007532	5	2
600	Diversity, evolution, and classification of virophages uncovered through global metagenomics. <i>Microbiome</i> , <b>2019</b> , 7, 157	16.6	21
599	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , <b>2019</b> , 37, 29-37	44.5	180
598	Genomes OnLine database (GOLD) v.7: updates and new features. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D649-D659	26.59	125
597	IMG/VR v.2.0: an integrated data management and analysis system for cultivated and environmental viral genomes. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D678-D686	20.1	101
596	IMG/M v.5.0: an integrated data management and comparative analysis system for microbial genomes and microbiomes. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D666-D677	20.1	476
595	Genomes of ubiquitous marine and hypersaline <i>Hydrogenovibrio</i> , <i>Thiomicrothabodus</i> and <i>Thiomicrospira</i> spp. encode a diversity of mechanisms to sustain chemolithoautotrophy in heterogeneous environments. <i>Environmental Microbiology</i> , <b>2018</b> , 20, 2686-2708	5.2	14
594	Genome-based evolutionary history of <i>Pseudomonas</i> spp. <i>Environmental Microbiology</i> , <b>2018</b> , 20, 2142-2159	15.9	81

593	Draft Genome Sequence of C7, Isolated from Seawater from the Menai Straits, Wales, United Kingdom. <i>Genome Announcements</i> , <b>2018</b> , 6,		1
592	Arboriscoccus pini gen. nov., sp. nov., an endophyte from a pine tree of the class Alphaproteobacteria, emended description of Geminicoccus roseus, and proposal of Geminicoccaceae fam. nov. <i>Systematic and Applied Microbiology</i> , <b>2018</b> , 41, 94-100	4.2	9
591	Genome-based classification of micromonosporae with a focus on their biotechnological and ecological potential. <i>Scientific Reports</i> , <b>2018</b> , 8, 525	4.9	63
590	Complete Genome Sequence of sp. Strain RBITD, a Butyrate- and Butanol-Producing Thermophile. <i>Genome Announcements</i> , <b>2018</b> , 6,		1
589	HipMCL: a high-performance parallel implementation of the Markov clustering algorithm for large-scale networks. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, e33	20.1	48
588	How Much Do rRNA Gene Surveys Underestimate Extant Bacterial Diversity?. <i>Applied and Environmental Microbiology</i> , <b>2018</b> , 84,	4.8	34
587	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , <b>2018</b> , 36, 359-367	44.5	207
586	Murine colitis reveals a disease-associated bacteriophage community. <i>Nature Microbiology</i> , <b>2018</b> , 3, 1023-1031	103.1	90
585	High-Quality Draft Genome Sequences of Eight Bacteria Isolated from Fungus Gardens Grown by Trachymyrmex septentrionalis Ants. <i>Microbiology Resource Announcements</i> , <b>2018</b> , 7,	1.3	3
584	Draft genome sequence of Chryseobacterium limigenitum SUR2 (LMG 28734) isolated from dehydrated sludge. <i>Brazilian Journal of Microbiology</i> , <b>2018</b> , 49, 5-6	2.2	
583	Genome Sequences of Actinobacteria from Extreme Environments in Colombia. <i>Microbiology Resource Announcements</i> , <b>2018</b> , 7,	1.3	3
582	Draft Genome Sequences of New Isolates and the Known Species of the Family Microbacteriaceae Associated with Plants. <i>Microbiology Resource Announcements</i> , <b>2018</b> , 7,	1.3	1
581	Programmed DNA destruction by miniature CRISPR-Cas14 enzymes. <i>Science</i> , <b>2018</b> , 362, 839-842	33.3	394
580	Genome-Based Taxonomic Classification of the Phylum. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 2007	5.7	297
579	Single-cell genomics of co-sorted Nanoarchaeota suggests novel putative host associations and diversification of proteins involved in symbiosis. <i>Microbiome</i> , <b>2018</b> , 6, 161	16.6	24
578	Genome Sequence of sp. Strain GAS474, a Novel Bacterium Isolated from Soil. <i>Genome Announcements</i> , <b>2018</b> , 6,		3
577	Draft Genome Sequences of Three Strains of a Novel Species Isolated from Forest Soil. <i>Genome Announcements</i> , <b>2018</b> , 6,		2
576	Protein structure determination using metagenome sequence data. <i>Science</i> , <b>2017</b> , 355, 294-298	33.3	346

575	Complete genome sequence of strain YIM 002 (DSM 44835), the type species of the genus and source of new antibiotic compounds. <i>Standards in Genomic Sciences</i> , <b>2017</b> , 12, 21		5
574	IMG-ABC: new features for bacterial secondary metabolism analysis and targeted biosynthetic gene cluster discovery in thousands of microbial genomes. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D560-D565	20.1	61
573	Permanent draft genome of DSM 505, an obligately chemolithoautotrophic member of the. <i>Standards in Genomic Sciences</i> , <b>2017</b> , 12, 10		23
572	High quality draft genome of type strain a rock actinobacterium, and emended description of. <i>Standards in Genomic Sciences</i> , <b>2017</b> , 12, 4		6
571	Succession in the petroleum reservoir microbiome through an oil field production lifecycle. <i>ISME Journal</i> , <b>2017</b> , 11, 2141-2154	11.9	86
570	Paenibacillus aquistagni sp. nov., isolated from an artificial lake accumulating industrial wastewater. <i>Antonie Van Leeuwenhoek</i> , <b>2017</b> , 110, 1189-1197	2.1	6
569	RNA-Dependent Cysteine Biosynthesis in Bacteria and Archaea. <i>MBio</i> , <b>2017</b> , 8,	7.8	16
568	High quality permanent draft genome sequence of DSM 19482, isolated from raw cow milk. <i>Standards in Genomic Sciences</i> , <b>2017</b> , 12, 31		2
567	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 676-683	44.5	161
566	Permanent Draft Genome Sequence of Strain Z-533, a Peptide and Starch Degradar Isolated from Thermal Springs in the Kamchatka Peninsula and Kunashir Island, Russia. <i>Genome Announcements</i> , <b>2017</b> , 5,		2
565	Complete Genome Sequence of ATCC 49181, a Phylogenetically Distinct Ammonia-Oxidizing Bacterium Isolated from Arctic Waters. <i>Genome Announcements</i> , <b>2017</b> , 5,		2
564	Giant viruses with an expanded complement of translation system components. <i>Science</i> , <b>2017</b> , 356, 82-85	33.3	148
563	Evolution of a multi-step phosphorelay signal transduction system in Ensifer: recruitment of the sigma factor RpoN and a novel enhancer-binding protein triggers acid-activated gene expression. <i>Molecular Microbiology</i> , <b>2017</b> , 103, 829-844	4.1	1
562	Critical Assessment of Metagenome Interpretation-a benchmark of metagenomics software. <i>Nature Methods</i> , <b>2017</b> , 14, 1063-1071	21.6	412
561	Draft genome sequence of Actinotignum schaalii DSM 15541T: Genetic insights into the lifestyle, cell fitness and virulence. <i>PLoS ONE</i> , <b>2017</b> , 12, e0188914	3.7	0
560	NAP: The Network Analysis Profiler, a web tool for easier topological analysis and comparison of medium-scale biological networks. <i>BMC Research Notes</i> , <b>2017</b> , 10, 278	2.3	23
559	High-quality genome sequence of the radioresistant bacterium KS 0460. <i>Standards in Genomic Sciences</i> , <b>2017</b> , 12, 46		7
558	Draft genome sequence of strain AHT1, a gram-positive sulfidogenic polyextremophile. <i>Standards in Genomic Sciences</i> , <b>2017</b> , 12, 57		7



557	High-quality draft genome sequence of Mlalz-1, a microsymbiont of (L.) miller collected in Lanzarote, Canary Islands, Spain. <i>Standards in Genomic Sciences</i> , <b>2017</b> , 12, 58		
556	Draft genome sequence of CL-YJ9 (DSM 18822), isolated from the rhizosphere of the coastal tidal-flat plant. <i>Standards in Genomic Sciences</i> , <b>2017</b> , 12, 65		1
555	Draft genome sequences of sp. nov. ERR11 and CCBAU 10071. <i>Standards in Genomic Sciences</i> , <b>2017</b> , 12, 74		19
554	Draft genome sequence of strain USBA-GBX 515 isolated from Superparamo soil samples in Colombian Andes. <i>Standards in Genomic Sciences</i> , <b>2017</b> , 12, 78		3
553	Draft genome of TNe-841, a free-living, nitrogen-fixing, tomato plant-associated bacterium. <i>Standards in Genomic Sciences</i> , <b>2017</b> , 12, 80		7
552	Draft genome sequence of DSM 21565 an anaerobic, slightly halophilic bacterium isolated from a Colombian saline spring. <i>Standards in Genomic Sciences</i> , <b>2017</b> , 12, 86		
551	Genome Sequence of sp. Strain MCTG156(1a), Isolated from a Scottish Coastal Phytoplankton Net Sample. <i>Genome Announcements</i> , <b>2017</b> , 5,		2
550	Genomic Methods and Microbiological Technologies for Profiling Novel and Extreme Environments for the Extreme Microbiome Project (XMP). <i>Journal of Biomolecular Techniques</i> , <b>2017</b> , 28, 31-39	1.1	31
549	Draft Genome Sequence of NE2, an Obligate Methanotroph from Subarctic Soil. <i>Genome Announcements</i> , <b>2017</b> , 5,		10
548	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D457-D465	20.1	115
547	Nontargeted virus sequence discovery pipeline and virus clustering for metagenomic data. <i>Nature Protocols</i> , <b>2017</b> , 12, 1673-1682	18.8	71
546	Feathermoss and epiphytic Nostoc cooperate differently: expanding the spectrum of plant-cyanobacteria symbiosis. <i>ISME Journal</i> , <b>2017</b> , 11, 2821-2833	11.9	35
545	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 725-731	44.5	648
544	Comparative metagenomics of hydrocarbon and methane seeps of the Gulf of Mexico. <i>Scientific Reports</i> , <b>2017</b> , 7, 16015	4.9	32
543	A thermostable Cas9 with increased lifetime in human plasma. <i>Nature Communications</i> , <b>2017</b> , 8, 1424	17.4	88
542	On the Origin of Reverse Transcriptase-Using CRISPR-Cas Systems and Their Hyperdiverse, Enigmatic Spacer Repertoires. <i>MBio</i> , <b>2017</b> , 8,	7.8	34
541	High-quality draft genome sequence of strain STM6155, a microsymbiont from New Caledonia. <i>Standards in Genomic Sciences</i> , <b>2017</b> , 12, 7		1
540	Draft genome sequence of type strain HBR26 and description of sp. nov. <i>Standards in Genomic Sciences</i> , <b>2017</b> , 12, 14		17



539	High-quality-draft genome sequence of the fermenting bacterium type strain GluBS11 (DSM 29698). <i>Standards in Genomic Sciences</i> , <b>2017</b> , 12, 24		4
538	High-quality permanent draft genome sequence of the type strain USDA 76, isolated from (L.) Merr. <i>Standards in Genomic Sciences</i> , <b>2017</b> , 12, 26		4
537	IMG/M: integrated genome and metagenome comparative data analysis system. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D507-D516	20.1	317
536	Genomes OnLine Database (GOLD) v.6: data updates and feature enhancements. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D446-D456	20.1	128
535	Genomic composition and dynamics among Methanomicrobiales predict adaptation to contrasting environments. <i>ISME Journal</i> , <b>2017</b> , 11, 87-99	11.9	19
534	Towards a balanced view of the bacterial tree of life. <i>Microbiome</i> , <b>2017</b> , 5, 140	16.6	44
533	Draft genome sequence of the cellulolytic endophyte A37T2. <i>Standards in Genomic Sciences</i> , <b>2017</b> , 12, 53		5
532	Empirical Comparison of Visualization Tools for Larger-Scale Network Analysis. <i>Advances in Bioinformatics</i> , <b>2017</b> , 2017, 1278932	5.5	32
531	Genomic Analysis of , the Thermophilic Anaerobic Bacterium of the Novel Bacterial Phylum. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 195	5.7	30
530	Genome Data Provides High Support for Generic Boundaries in Ssensu Lato. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 1154	5.7	66
529	Genome-Scale Data Call for a Taxonomic Rearrangement of. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 2501	5.7	33
528	Draft genome and description of Consotaella salsifontis gen. nov. sp. nov., a halophilic, free-living, nitrogen-fixing alphaproteobacterium isolated from an ancient terrestrial saline spring. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2017</b> , 67, 3744-3751	2.2	3
527	Reclassification of a Polynucleobacter cosmopolitanus strain isolated from tropical Lake Victoria as Polynucleobacter victoriensis sp. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2017</b> , 67, 5087-5093	2.2	5
526	Absence of genome reduction in diverse, facultative endohyphal bacteria. <i>Microbial Genomics</i> , <b>2017</b> , 3, e000101	4.4	23
525	Transfer RNAs with novel cloverleaf structures. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, 2776-2785	20.1	16
524	ProDeGe: a computational protocol for fully automated decontamination of genomes. <i>ISME Journal</i> , <b>2016</b> , 10, 269-72	11.9	48
523	Uncovering Earth's virome. <i>Nature</i> , <b>2016</b> , 536, 425-30	50.4	551
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516	High-quality draft genome sequence of strain AK4OH1, a gammaproteobacterium isolated from estuarine sediment. <i>Standards in Genomic Sciences</i> , <b>2016</b> , 11, 66		4
515	An improved high-quality draft genome sequence of <i>Carnobacterium inhibens</i> subsp. <i>inhibens</i> strain K1(T). <i>Standards in Genomic Sciences</i> , <b>2016</b> , 11, 65		2
514	Complete genome sequence of the Antarctic <i>Halorubrum lacusprofundi</i> type strain ACAM 34. <i>Standards in Genomic Sciences</i> , <b>2016</b> , 11, 70		15
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405	Complete Genome sequence of <i>Burkholderia phymatum</i> STM815(T), a broad host range and efficient nitrogen-fixing symbiont of <i>Mimosa</i> species. <i>Standards in Genomic Sciences</i> , <b>2014</b> , 9, 763-74	36
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345	Genome sequence of the lupin-nodulating <i>Bradyrhizobium</i> sp. strain WSM1417. <i>Standards in Genomic Sciences</i> , <b>2013</b> , 9, 273-82	2
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5	Cryptic inoviruses are pervasive in bacteria and archaea across Earth's biomes		2
4	Untapped viral diversity in global soil metagenomes		15
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1	A thermostable Cas9 with increased lifetime in human plasma		2