

Nikos C Kyrpides

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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	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , 2012 , 486, 207-14	50.4	6938
663	A framework for human microbiome research. <i>Nature</i> , 2012 , 486, 215-21	50.4	1722
662	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013 , 499, 431-7	50.4	1484
661	The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon <i>Archaeoglobus fulgidus</i> . <i>Nature</i> , 1997 , 390, 364-70	50.4	1257
660	Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. <i>Nature</i> , 2007 , 450, 560-5	50.4	990
659	The minimum information about a genome sequence (MIGS) specification. <i>Nature Biotechnology</i> , 2008 , 26, 541-7	44.5	964
658	IMG: the Integrated Microbial Genomes database and comparative analysis system. <i>Nucleic Acids Research</i> , 2012 , 40, D115-22	20.1	953
657	Protein interaction maps for complete genomes based on gene fusion events. <i>Nature</i> , 1999 , 402, 86-90	50.4	896
656	A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea. <i>Nature</i> , 2009 , 462, 1056-60	50.4	803
655	IMG ER: a system for microbial genome annotation expert review and curation. <i>Bioinformatics</i> , 2009 , 25, 2271-8	7.2	742
654	Genome sequence of <i>Bacillus cereus</i> and comparative analysis with <i>Bacillus anthracis</i> . <i>Nature</i> , 2003 , 423, 87-91	50.4	670
653	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017 , 35, 725-731	44.5	648
652	Experimental determination and system level analysis of essential genes in <i>Escherichia coli</i> MG1655. <i>Journal of Bacteriology</i> , 2003 , 185, 5673-84	3.5	598
651	Uncovering Earth's virome. <i>Nature</i> , 2016 , 536, 425-30	50.4	551
650	Metagenomic analysis of two enhanced biological phosphorus removal (EBPR) sludge communities. <i>Nature Biotechnology</i> , 2006 , 24, 1263-9	44.5	541
649	A catalog of reference genomes from the human microbiome. <i>Science</i> , 2010 , 328, 994-9	33.3	508
648	Minimum Information about a Biosynthetic Gene cluster. <i>Nature Chemical Biology</i> , 2015 , 11, 625-31	11.7	498

647	Toward an online repository of Standard Operating Procedures (SOPs) for (meta)genomic annotation. <i>OMICS A Journal of Integrative Biology</i> , 2008 , 12, 137-41	3.8	491
646	CRISPR recognition tool (CRT): a tool for automatic detection of clustered regularly interspaced palindromic repeats. <i>BMC Bioinformatics</i> , 2007 , 8, 209	3.6	482
645	IMG/M v.5.0: an integrated data management and comparative analysis system for microbial genomes and microbiomes. <i>Nucleic Acids Research</i> , 2019 , 47, D666-D677	20.1	476
644	The genomic basis of trophic strategy in marine bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 15527-33	11.5	472
643	The Wolbachia genome of <i>Brugia malayi</i> : endosymbiont evolution within a human pathogenic nematode. <i>PLoS Biology</i> , 2005 , 3, e121	9.7	452
642	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. <i>Nature Biotechnology</i> , 2011 , 29, 415-20	44.5	445
641	IMG 4 version of the integrated microbial genomes comparative analysis system. <i>Nucleic Acids Research</i> , 2014 , 42, D560-7	20.1	444
640	GenePRIMP: a gene prediction improvement pipeline for prokaryotic genomes. <i>Nature Methods</i> , 2010 , 7, 455-7	21.6	441
639	The genome sequence of the facultative intracellular pathogen <i>Brucella melitensis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 443-8	11.5	439
638	Microbial species delineation using whole genome sequences. <i>Nucleic Acids Research</i> , 2015 , 43, 6761-71	20.1	433
637	Critical Assessment of Metagenome Interpretation-a benchmark of metagenomics software. <i>Nature Methods</i> , 2017 , 14, 1063-1071	21.6	412
636	Complete sequence and comparative genome analysis of the dairy bacterium <i>Streptococcus thermophilus</i> . <i>Nature Biotechnology</i> , 2004 , 22, 1554-8	44.5	397
635	Programmed DNA destruction by miniature CRISPR-Cas14 enzymes. <i>Science</i> , 2018 , 362, 839-842	33.3	394
634	The Genomes OnLine Database (GOLD) v.4: status of genomic and metagenomic projects and their associated metadata. <i>Nucleic Acids Research</i> , 2012 , 40, D571-9	20.1	375
633	Comparison of the complete genome sequences of <i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a and pv. <i>tomato</i> DC3000. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 11064-9	11.5	354
632	Protein structure determination using metagenome sequence data. <i>Science</i> , 2017 , 355, 294-298	33.3	346
631	Symbiosis insights through metagenomic analysis of a microbial consortium. <i>Nature</i> , 2006 , 443, 950-5	50.4	339
630	The Genomes On Line Database (GOLD) in 2009: status of genomic and metagenomic projects and their associated metadata. <i>Nucleic Acids Research</i> , 2010 , 38, D346-54	20.1	331

629	Genomics. Genome project standards in a new era of sequencing. <i>Science</i> , 2009 , 326, 236-7	33.3	326
628	IMG/M: integrated genome and metagenome comparative data analysis system. <i>Nucleic Acids Research</i> , 2017 , 45, D507-D516	20.1	317
627	The integrated microbial genomes (IMG) system. <i>Nucleic Acids Research</i> , 2006 , 34, D344-8	20.1	306
626	Direct comparisons of Illumina vs. Roche 454 sequencing technologies on the same microbial community DNA sample. <i>PLoS ONE</i> , 2012 , 7, e30087	3.7	305
625	Genome-Based Taxonomic Classification of the Phylum. <i>Frontiers in Microbiology</i> , 2018 , 9, 2007	5.7	297
624	The Genomes On Line Database (GOLD) in 2007: status of genomic and metagenomic projects and their associated metadata. <i>Nucleic Acids Research</i> , 2008 , 36, D475-9	20.1	276
623	New insights from uncultivated genomes of the global human gut microbiome. <i>Nature</i> , 2019 , 568, 505-514	10.4	275
622	IMG/M: a data management and analysis system for metagenomes. <i>Nucleic Acids Research</i> , 2008 , 36, D534-8	20.1	268
621	Genome sequence and analysis of the oral bacterium <i>Fusobacterium nucleatum</i> strain ATCC 25586. <i>Journal of Bacteriology</i> , 2002 , 184, 2005-18	3.5	268
620	Complete genome sequence of DSM 30083(T), the type strain (U5/41(T)) of <i>Escherichia coli</i> , and a proposal for delineating subspecies in microbial taxonomy. <i>Standards in Genomic Sciences</i> , 2014 , 9, 2		267
619	The Genomes OnLine Database (GOLD) v.5: a metadata management system based on a four level (meta)genome project classification. <i>Nucleic Acids Research</i> , 2015 , 43, D1099-106	20.1	258
618	Use of simulated data sets to evaluate the fidelity of metagenomic processing methods. <i>Nature Methods</i> , 2007 , 4, 495-500	21.6	257
617	The M5nr: a novel non-redundant database containing protein sequences and annotations from multiple sources and associated tools. <i>BMC Bioinformatics</i> , 2012 , 13, 141	3.6	215
616	A korarchaeal genome reveals insights into the evolution of the Archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 8102-7	11.5	214
615	IMG/M 4 version of the integrated metagenome comparative analysis system. <i>Nucleic Acids Research</i> , 2014 , 42, D568-73	20.1	212
614	The integrated microbial genomes system: an expanding comparative analysis resource. <i>Nucleic Acids Research</i> , 2010 , 38, D382-90	20.1	210
613	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , 2018 , 36, 359-367	44.5	207
612	IMG/M: the integrated metagenome data management and comparative analysis system. <i>Nucleic Acids Research</i> , 2012 , 40, D123-9	20.1	207

611	The evolution of host specialization in the vertebrate gut symbiont <i>Lactobacillus reuteri</i> . <i>PLoS Genetics</i> , 2011 , 7, e1001314	6	203
610	The SPFH domain: implicated in regulating targeted protein turnover in stomatins and other membrane-associated proteins. <i>Trends in Biochemical Sciences</i> , 1999 , 24, 425-7	10.3	201
609	Prepublication data sharing. <i>Nature</i> , 2009 , 461, 168-70	50.4	197
608	The complete genome sequence of the algal symbiont <i>Dinoroseobacter shibae</i> : a hitchhiker's guide to life in the sea. <i>ISME Journal</i> , 2010 , 4, 61-77	11.9	187
607	Meeting report: the terabase metagenomics workshop and the vision of an Earth microbiome project. <i>Standards in Genomic Sciences</i> , 2010 , 3, 243-8		187
606	The Genomes On Line Database (GOLD) v.2: a monitor of genome projects worldwide. <i>Nucleic Acids Research</i> , 2006 , 34, D332-4	20.1	187
605	A unified catalog of 204,938 reference genomes from the human gut microbiome. <i>Nature Biotechnology</i> , 2021 , 39, 105-114	44.5	185
604	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019 , 37, 29-37	44.5	180
603	The DOE-JGI Standard Operating Procedure for the Annotations of Microbial Genomes. <i>Standards in Genomic Sciences</i> , 2009 , 1, 63-7		177
602	The standard operating procedure of the DOE-JGI Microbial Genome Annotation Pipeline (MGAP v.4). <i>Standards in Genomic Sciences</i> , 2015 , 10, 86		174
601	The ERGO genome analysis and discovery system. <i>Nucleic Acids Research</i> , 2003 , 31, 164-71	20.1	173
600	Genome sequence and analysis of the soil cellulolytic actinomycete <i>Thermobifida fusca</i> YX. <i>Journal of Bacteriology</i> , 2007 , 189, 2477-86	3.5	167
599	The integrated microbial genomes (IMG) system in 2007: data content and analysis tool extensions. <i>Nucleic Acids Research</i> , 2008 , 36, D528-33	20.1	167
598	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. <i>Nature Biotechnology</i> , 2017 , 35, 676-683	44.5	161
597	Giant viruses with an expanded complement of translation system components. <i>Science</i> , 2017 , 356, 82-85	33.3	148
596	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , 2014 , 12, e1001920	9.7	146
595	The Earth Microbiome Project: Meeting report of the "1 EMP meeting on sample selection and acquisition" at Argonne National Laboratory October 6 2010. <i>Standards in Genomic Sciences</i> , 2010 , 3, 249-53		146
594	The Genomic Standards Consortium. <i>PLoS Biology</i> , 2011 , 9, e1001088	9.7	143

593	Metagenomics uncovers gaps in amplicon-based detection of microbial diversity. <i>Nature Microbiology</i> , 2016 , 1, 15032	26.6	132
592	Genomes OnLine Database (GOLD) v.6: data updates and feature enhancements. <i>Nucleic Acids Research</i> , 2017 , 45, D446-D456	20.1	128
591	Genomes OnLine database (GOLD) v.7: updates and new features. <i>Nucleic Acids Research</i> , 2019 , 47, D649-D659	20.1	125
590	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021 , 39, 499-509	44.5	120
589	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2017 , 45, D457-D465	20.1	115
588	Genome-Based Taxonomic Classification of. <i>Frontiers in Microbiology</i> , 2016 , 7, 2003	5.7	114
587	The IMG/M data management and analysis system v.6.0: new tools and advanced capabilities. <i>Nucleic Acids Research</i> , 2021 , 49, D751-D763	20.1	114
586	Comparative metagenomic and metatranscriptomic analysis of hindgut paunch microbiota in wood- and dung-feeding higher termites. <i>PLoS ONE</i> , 2013 , 8, e61126	3.7	113
585	KOW: a novel motif linking a bacterial transcription factor with ribosomal proteins. <i>Trends in Biochemical Sciences</i> , 1996 , 21, 425-6	10.3	113
584	The fast changing landscape of sequencing technologies and their impact on microbial genome assemblies and annotation. <i>PLoS ONE</i> , 2012 , 7, e48837	3.7	112
583	CheckV assesses the quality and completeness of metagenome-assembled viral genomes. <i>Nature Biotechnology</i> , 2021 , 39, 578-585	44.5	104
582	Analysis of 1,000+ Type-Strain Genomes Substantially Improves Taxonomic Classification of. <i>Frontiers in Microbiology</i> , 2020 , 11, 468	5.7	101
581	IMG/VR v.2.0: an integrated data management and analysis system for cultivated and environmental viral genomes. <i>Nucleic Acids Research</i> , 2019 , 47, D678-D686	20.1	101
580	Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes. <i>Nature Microbiology</i> , 2019 , 4, 1895-1906	26.6	99
579	Multiple syntrophic interactions in a terephthalate-degrading methanogenic consortium. <i>ISME Journal</i> , 2011 , 5, 122-30	11.9	99
578	Giant virus diversity and host interactions through global metagenomics. <i>Nature</i> , 2020 , 578, 432-436	50.4	94
577	Complete genome sequence of Kytococcus sedentarius type strain (541). <i>Standards in Genomic Sciences</i> , 2009 , 1, 12-20		94
576	Identification of a haloalkaliphilic and thermostable cellulase with improved ionic liquid tolerance. <i>Green Chemistry</i> , 2011 , 13, 2083	10	93

575	A genomic analysis of the archaeal system <i>Ignicoccus hospitalis</i> - <i>Nanoarchaeum equitans</i> . <i>Genome Biology</i> , 2008 , 9, R158	18.3	92
574	Large-Scale Analyses of Human Microbiomes Reveal Thousands of Small, Novel Genes. <i>Cell</i> , 2019 , 178, 1245-1259.e14	56.2	91
573	Individual genome assembly from complex community short-read metagenomic datasets. <i>ISME Journal</i> , 2012 , 6, 898-901	11.9	91
572	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. <i>Nature Communications</i> , 2016 , 7, 10476	17.4	90
571	Murine colitis reveals a disease-associated bacteriophage community. <i>Nature Microbiology</i> , 2018 , 3, 1023-1031	16.3	90
570	A thermostable Cas9 with increased lifetime in human plasma. <i>Nature Communications</i> , 2017 , 8, 1424	17.4	88
569	Succession in the petroleum reservoir microbiome through an oil field production lifecycle. <i>ISME Journal</i> , 2017 , 11, 2141-2154	11.9	86
568	High level of intergenera gene exchange shapes the evolution of haloarchaea in an isolated Antarctic lake. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 16939-44	11.5	85
567	Large-scale contamination of microbial isolate genomes by Illumina PhiX control. <i>Standards in Genomic Sciences</i> , 2015 , 10, 18		85
566	Genomic characterization of methanomicrobiales reveals three classes of methanogens. <i>PLoS ONE</i> , 2009 , 4, e5797	3.7	85
565	The complete multipartite genome sequence of <i>Cupriavidus necator</i> JMP134, a versatile pollutant degrader. <i>PLoS ONE</i> , 2010 , 5, e9729	3.7	84
564	Stop codon reassignments in the wild. <i>Science</i> , 2014 , 344, 909-13	33.3	83
563	Genome-based evolutionary history of <i>Pseudomonas</i> spp. <i>Environmental Microbiology</i> , 2018 , 20, 2142-2159	15.2	81
562	The standard operating procedure of the DOE-JGI Metagenome Annotation Pipeline (MAP v.4). <i>Standards in Genomic Sciences</i> , 2016 , 11, 17		81
561	Engineering <i>Escherichia coli</i> for biodiesel production utilizing a bacterial fatty acid methyltransferase. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 8052-61	4.8	81
560	Whole-genome comparative analysis of three phytopathogenic <i>Xylella fastidiosa</i> strains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 12403-8	11.5	81
559	IMG-ABC: A Knowledge Base To Fuel Discovery of Biosynthetic Gene Clusters and Novel Secondary Metabolites. <i>MBio</i> , 2015 , 6, e00932	7.8	80
558	Complete genome sequence of the <i>Medicago</i> microsymbiont <i>Ensifer</i> (<i>Sinorhizobium</i>) <i>medicae</i> strain WSM419. <i>Standards in Genomic Sciences</i> , 2010 , 2, 77-86		80

557	Universal protein families and the functional content of the last universal common ancestor. <i>Journal of Molecular Evolution</i> , 1999 , 49, 413-23	3.1	80
556	Fifteen years of microbial genomics: meeting the challenges and fulfilling the dream. <i>Nature Biotechnology</i> , 2009 , 27, 627-32	44.5	73
555	Genomics of aerobic cellulose utilization systems in actinobacteria. <i>PLoS ONE</i> , 2012 , 7, e39331	3.7	73
554	Genomic Encyclopedia of Type Strains, Phase I: The one thousand microbial genomes (KMG-I) project. <i>Standards in Genomic Sciences</i> , 2014 , 9, 1278-84		72
553	Non-contiguous finished genome sequence and contextual data of the filamentous soil bacterium <i>Ktedonobacter racemifer</i> type strain (SOSP1-21). <i>Standards in Genomic Sciences</i> , 2011 , 5, 97-111		72
552	An experimental metagenome data management and analysis system. <i>Bioinformatics</i> , 2006 , 22, e359-67	7.2	72
551	The genome of the obligately intracellular bacterium <i>Ehrlichia canis</i> reveals themes of complex membrane structure and immune evasion strategies. <i>Journal of Bacteriology</i> , 2006 , 188, 4015-23	3.5	72
550	Nontargeted virus sequence discovery pipeline and virus clustering for metagenomic data. <i>Nature Protocols</i> , 2017 , 12, 1673-1682	18.8	71
549	Sequencing of multiple clostridial genomes related to biomass conversion and biofuel production. <i>Journal of Bacteriology</i> , 2010 , 192, 6494-6	3.5	71
548	Complete genome sequences of six strains of the genus <i>Methylobacterium</i> . <i>Journal of Bacteriology</i> , 2012 , 194, 4746-8	3.5	70
547	Genome analysis of <i>F. nucleatum</i> sub spp <i>vincentii</i> and its comparison with the genome of <i>F. nucleatum</i> ATCC 25586. <i>Genome Research</i> , 2003 , 13, 1180-9	9.7	67
546	Genomes OnLine Database (GOLD 1.0): a monitor of complete and ongoing genome projects world-wide. <i>Bioinformatics</i> , 1999 , 15, 773-4	7.2	67
545	Analysis of 1,000 Type-Strain Genomes Improves Taxonomic Classification of. <i>Frontiers in Microbiology</i> , 2019 , 10, 2083	5.7	66
544	Genome Data Provides High Support for Generic Boundaries in <i>Sensu Lato</i> . <i>Frontiers in Microbiology</i> , 2017 , 8, 1154	5.7	66
543	Comparative genome analysis of <i>Bacillus cereus</i> group genomes with <i>Bacillus subtilis</i> . <i>FEMS Microbiology Letters</i> , 2005 , 250, 175-84	2.9	64
542	Genome-based classification of micromonosporae with a focus on their biotechnological and ecological potential. <i>Scientific Reports</i> , 2018 , 8, 525	4.9	63
541	Complete genome sequence of <i>Odoribacter splanchnicus</i> type strain (1651/6). <i>Standards in Genomic Sciences</i> , 2011 , 4, 200-9		62
540	The emergence of major cellular processes in evolution. <i>FEBS Letters</i> , 1996 , 390, 119-23	3.8	62

539	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> , 2017 , 45, D560-D565	20.1	61
538	Complete genome of the cellulolytic ruminal bacterium <i>Ruminococcus albus</i> 7. <i>Journal of Bacteriology</i> , 2011 , 193, 5574-5	3.5	61
537	Novel insights into the diversity of catabolic metabolism from ten haloarchaeal genomes. <i>PLoS ONE</i> , 2011 , 6, e20237	3.7	60
536	Complete genome sequence of "Enterobacter lignolyticus" SCF1. <i>Standards in Genomic Sciences</i> , 2011 , 5, 69-85		60
535	Draft sequencing and comparative genomics of <i>Xylella fastidiosa</i> strains reveal novel biological insights. <i>Genome Research</i> , 2002 , 12, 1556-63	9.7	59
534	IMG/VR v3: an integrated ecological and evolutionary framework for interrogating genomes of uncultivated viruses. <i>Nucleic Acids Research</i> , 2021 , 49, D764-D775	20.1	58
533	Complete genome sequence of the aerobic marine methanotroph <i>Methylomonas methanica</i> MC09. <i>Journal of Bacteriology</i> , 2011 , 193, 7001-2	3.5	57
532	Complete genome sequence of <i>Chitinophaga pinensis</i> type strain (UQM 2034). <i>Standards in Genomic Sciences</i> , 2010 , 2, 87-95		57
531	Functional and genomic diversity of methylotrophic Rhodocyclaceae: description of <i>Methyloversatilis discipulorum</i> sp. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015 , 65, 2227-2233	2.2	56
530	Genome sequence of the Fleming strain of <i>Micrococcus luteus</i> , a simple free-living actinobacterium. <i>Journal of Bacteriology</i> , 2010 , 192, 841-60	3.5	55
529	Focus: Synergistetes. <i>Environmental Microbiology</i> , 2009 , 11, 1327-9	5.2	55
528	Genome analysis of the anaerobic thermohalophilic bacterium <i>Halothermothrix orenii</i> . <i>PLoS ONE</i> , 2009 , 4, e4192	3.7	54
527	Whole-genome sequence annotation: 'Going wrong with confidence'. <i>Molecular Microbiology</i> , 1999 , 32, 886-7	4.1	54
526	Complete genome sequence of <i>Haliangium ochraceum</i> type strain (SMP-2). <i>Standards in Genomic Sciences</i> , 2010 , 2, 96-106		53
525	On the evolution of arginases and related enzymes. <i>Journal of Molecular Evolution</i> , 1994 , 39, 101-4	3.1	53
524	Archaeal and bacterial hyperthermophiles: horizontal gene exchange or common ancestry?. <i>Trends in Genetics</i> , 1999 , 15, 298-9	8.5	52
523	Complete genome sequence of "Thioalkalivibrio sulfidophilus" HL-EbGr7. <i>Standards in Genomic Sciences</i> , 2011 , 4, 23-35		51
522	Gene context analysis in the Integrated Microbial Genomes (IMG) data management system. <i>PLoS ONE</i> , 2009 , 4, e7979	3.7	51

521	Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. <i>Nature Medicine</i> , 2020 , 26, 941-951	50.5	50
520	Improving microbial genome annotations in an integrated database context. <i>PLoS ONE</i> , 2013 , 8, e54859	3.7	49
519	Complete genome sequences for the anaerobic, extremely thermophilic plant biomass-degrading bacteria <i>Caldicellulosiruptor hydrothermalis</i> , <i>Caldicellulosiruptor kristjanssonii</i> , <i>Caldicellulosiruptor kronotskyensis</i> , <i>Caldicellulosiruptor owensensis</i> , and <i>Caldicellulosiruptor lactoaceticus</i> . <i>Journal of Bacteriology</i> , 2011 , 193, 1483-4	3.5	49
518	Complete genome sequence of <i>Geodermatophilus obscurus</i> type strain (G-20). <i>Standards in Genomic Sciences</i> , 2010 , 2, 158-67		49
517	Genome sequence of <i>Thermofilum pendens</i> reveals an exceptional loss of biosynthetic pathways without genome reduction. <i>Journal of Bacteriology</i> , 2008 , 190, 2957-65	3.5	49
516	ProDeGe: a computational protocol for fully automated decontamination of genomes. <i>ISME Journal</i> , 2016 , 10, 269-72	11.9	48
515	Genomic Encyclopedia of Bacterial and Archaeal Type Strains, Phase III: the genomes of soil and plant-associated and newly described type strains. <i>Standards in Genomic Sciences</i> , 2015 , 10, 26		48
514	HipMCL: a high-performance parallel implementation of the Markov clustering algorithm for large-scale networks. <i>Nucleic Acids Research</i> , 2018 , 46, e33	20.1	48
513	Complete genome sequence of <i>Thauera aminoaromatica</i> strain MZ1T. <i>Standards in Genomic Sciences</i> , 2012 , 6, 325-35		47
512	Genomes OnLine Database (GOLD) v.8: overview and updates. <i>Nucleic Acids Research</i> , 2021 , 49, D723-D733	1	47
511	A Genomic Encyclopedia of the Root Nodule Bacteria: assessing genetic diversity through a systematic biogeographic survey. <i>Standards in Genomic Sciences</i> , 2015 , 10, 14		46
510	Draft genome sequence of <i>Frankia</i> sp. strain CN3, an atypical, noninfective (Nod-) ineffective (Fix-) isolate from <i>Coriaria nepalensis</i> . <i>Genome Announcements</i> , 2013 , 1, e0008513		46
509	Comparative genomic analysis of the microbiome [corrected] of herbivorous insects reveals eco-environmental adaptations: biotechnology applications. <i>PLoS Genetics</i> , 2013 , 9, e1003131	6	46
508	Complete genome sequences of <i>Desulfosporosinus orientis</i> DSM765T, <i>Desulfosporosinus youngiae</i> DSM17734T, <i>Desulfosporosinus meridiei</i> DSM13257T, and <i>Desulfosporosinus acidiphilus</i> DSM22704T. <i>Journal of Bacteriology</i> , 2012 , 194, 6300-1	3.5	46
507	Complete genome sequence of the termite hindgut bacterium <i>Spirochaeta coccoides</i> type strain (SPN1(T)), reclassification in the genus <i>Sphaerochaeta</i> as <i>Sphaerochaeta coccoides</i> comb. nov. and emendations of the family Spirochaetaceae and the genus <i>Sphaerochaeta</i> . <i>Standards in Genomic Sciences</i> , 2012 , 6, 194-209		46
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