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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.

460 papers	25,035 citations	70 h-index	147 g-index
482 ext. papers	32,287 ext. citations	12.8 avg, IF	6.32 L-index

#	Paper	IF	Citations
460	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013 , 499, 431-7	50.4	1484
459	Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. <i>Nature</i> , 2007 , 450, 560-5	50.4	990
458	IMG: the Integrated Microbial Genomes database and comparative analysis system. <i>Nucleic Acids Research</i> , 2012 , 40, D115-22	20.1	953
457	A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea. <i>Nature</i> , 2009 , 462, 1056-60	50.4	803
456	IMG ER: a system for microbial genome annotation expert review and curation. <i>Bioinformatics</i> , 2009 , 25, 2271-8	7.2	742
455	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
454	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
453	Uncovering Earth's virome. <i>Nature</i> , 2016 , 536, 425-30	50.4	551
452	Metagenomic analysis of two enhanced biological phosphorus removal (EBPR) sludge communities. <i>Nature Biotechnology</i> , 2006 , 24, 1263-9	44.5	541
451	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
450	Dissecting biological "dark matter" with single-cell genetic analysis of rare and uncultivated TM7 microbes from the human mouth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 11889-94	11.5	464
449	The <i>Wolbachia</i> genome of <i>Brugia malayi</i> : endosymbiont evolution within a human pathogenic nematode. <i>PLoS Biology</i> , 2005 , 3, e121	9.7	452
448	IMG 4 version of the integrated microbial genomes comparative analysis system. <i>Nucleic Acids Research</i> , 2014 , 42, D560-7	20.1	444
447	GenePRIMP: a gene prediction improvement pipeline for prokaryotic genomes. <i>Nature Methods</i> , 2010 , 7, 455-7	21.6	441
446	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
445	Microbial species delineation using whole genome sequences. <i>Nucleic Acids Research</i> , 2015 , 43, 6761-71	20.1	433
444	Symbiosis insights through metagenomic analysis of a microbial consortium. <i>Nature</i> , 2006 , 443, 950-5	50.4	339

443	IMG/M: integrated genome and metagenome comparative data analysis system. <i>Nucleic Acids Research</i> , 2017 , 45, D507-D516	20.1	317
442	The integrated microbial genomes (IMG) system. <i>Nucleic Acids Research</i> , 2006 , 34, D344-8	20.1	306
441	IMG/M: a data management and analysis system for metagenomes. <i>Nucleic Acids Research</i> , 2008 , 36, D534-8	20.1	268
440	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
439	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
438	Use of simulated data sets to evaluate the fidelity of metagenomic processing methods. <i>Nature Methods</i> , 2007 , 4, 495-500	21.6	257
437	High-resolution metagenomics targets specific functional types in complex microbial communities. <i>Nature Biotechnology</i> , 2008 , 26, 1029-34	44.5	226
436	IMG/M 4 version of the integrated metagenome comparative analysis system. <i>Nucleic Acids Research</i> , 2014 , 42, D568-73	20.1	212
435	The integrated microbial genomes system: an expanding comparative analysis resource. <i>Nucleic Acids Research</i> , 2010 , 38, D382-90	20.1	210
434	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , 2018 , 36, 359-367	44.5	207
433	IMG/M: the integrated metagenome data management and comparative analysis system. <i>Nucleic Acids Research</i> , 2012 , 40, D123-9	20.1	207
432	The evolution of host specialization in the vertebrate gut symbiont <i>Lactobacillus reuteri</i> . <i>PLoS Genetics</i> , 2011 , 7, e1001314	6	203
431	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019 , 37, 29-37	44.5	180
430	The DOE-JGI Standard Operating Procedure for the Annotations of Microbial Genomes. <i>Standards in Genomic Sciences</i> , 2009 , 1, 63-7		177
429	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
428	The ERGO genome analysis and discovery system. <i>Nucleic Acids Research</i> , 2003 , 31, 164-71	20.1	173
427	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
426	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

425	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
424	Targeted discovery of glycoside hydrolases from a switchgrass-adapted compost community. <i>PLoS ONE</i> , 2010 , 5, e8812	3.7	154
423	The complete genome sequence of <i>Fibrobacter succinogenes</i> S85 reveals a cellulolytic and metabolic specialist. <i>PLoS ONE</i> , 2011 , 6, e18814	3.7	152
422	Giant viruses with an expanded complement of translation system components. <i>Science</i> , 2017 , 356, 82-85	33.3	148
421	The genome sequence of <i>Psychrobacter arcticus</i> 273-4, a psychroactive Siberian permafrost bacterium, reveals mechanisms for adaptation to low-temperature growth. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 2304-12	4.8	134
420	Metagenomics uncovers gaps in amplicon-based detection of microbial diversity. <i>Nature Microbiology</i> , 2016 , 1, 15032	26.6	132
419	The genome sequence of the psychrophilic archaeon, <i>Methanococcoides burtonii</i> : the role of genome evolution in cold adaptation. <i>ISME Journal</i> , 2009 , 3, 1012-35	11.9	128
418	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021 , 39, 499-509	44.5	120
417	A bacterial metapopulation adapts locally to phage predation despite global dispersal. <i>Genome Research</i> , 2008 , 18, 293-7	9.7	119
416	Millimeter-scale genetic gradients and community-level molecular convergence in a hypersaline microbial mat. <i>Molecular Systems Biology</i> , 2008 , 4, 198	12.2	118
415	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2017 , 45, D457-D465	20.1	115
414	Genome-Based Taxonomic Classification of. <i>Frontiers in Microbiology</i> , 2016 , 7, 2003	5.7	114
413	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
412	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
411	A metagenomic insight into freshwater methane-utilizing communities and evidence for cooperation between the Methylococcaceae and the Methylophilaceae. <i>PeerJ</i> , 2013 , 1, e23	3.1	104
410	Architecture of thermal adaptation in an <i>Exiguobacterium sibiricum</i> strain isolated from 3 million year old permafrost: a genome and transcriptome approach. <i>BMC Genomics</i> , 2008 , 9, 547	4.5	103
409	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
408	Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes. <i>Nature Microbiology</i> , 2019 , 4, 1895-1906	26.6	99

407	Complete genome sequence of <i>Kytococcus sedentarius</i> type strain (541). <i>Standards in Genomic Sciences</i> , 2009 , 1, 12-20		94
406	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
405	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. <i>Nature Communications</i> , 2016 , 7, 10476	17.4	90
404	Genome sequence of "Candidatus <i>Frankia datisciae</i> " Dg1, the uncultured microsymbiont from nitrogen-fixing root nodules of the dicot <i>Datisca glomerata</i> . <i>Journal of Bacteriology</i> , 2011 , 193, 7017-8	3.5	87
403	Large-scale contamination of microbial isolate genomes by Illumina PhiX control. <i>Standards in Genomic Sciences</i> , 2015 , 10, 18		85
402	Genomic potential of <i>Marinobacter aquaeolei</i> , a biogeochemical "opportunitroph". <i>Applied and Environmental Microbiology</i> , 2011 , 77, 2763-71	4.8	85
401	Stop codon reassignments in the wild. <i>Science</i> , 2014 , 344, 909-13	33.3	83
400	Single-cell genomics reveals complex carbohydrate degradation patterns in poribacterial symbionts of marine sponges. <i>ISME Journal</i> , 2013 , 7, 2287-300	11.9	83
399	Exploring the symbiotic pangenome of the nitrogen-fixing bacterium <i>Sinorhizobium meliloti</i> . <i>BMC Genomics</i> , 2011 , 12, 235	4.5	83
398	The standard operating procedure of the DOE-JGI Metagenome Annotation Pipeline (MAP v.4). <i>Standards in Genomic Sciences</i> , 2016 , 11, 17		81
397	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
396	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
395	Complete genome sequence of the Medicago microsymbiont <i>Ensifer</i> (<i>Sinorhizobium</i>) <i>medicae</i> strain WSM419. <i>Standards in Genomic Sciences</i> , 2010 , 2, 77-86		80
394	Genomics of aerobic cellulose utilization systems in actinobacteria. <i>PLoS ONE</i> , 2012 , 7, e39331	3.7	73
393	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
392	An experimental metagenome data management and analysis system. <i>Bioinformatics</i> , 2006 , 22, e359-67	7.2	72
391	Nontargeted virus sequence discovery pipeline and virus clustering for metagenomic data. <i>Nature Protocols</i> , 2017 , 12, 1673-1682	18.8	71
390	Complete genome sequences of six strains of the genus <i>Methylobacterium</i> . <i>Journal of Bacteriology</i> , 2012 , 194, 4746-8	3.5	70

389	Metatranscriptomic array analysis of 'Candidatus Accumulibacter phosphatis'-enriched enhanced biological phosphorus removal sludge. <i>Environmental Microbiology</i> , 2010 , 12, 1205-17	5.2	67
388	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
387	Genome Data Provides High Support for Generic Boundaries in Sensu Lato. <i>Frontiers in Microbiology</i> , 2017 , 8, 1154	5.7	66
386	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
385	Complete genome sequence of the cellulolytic thermophile <i>Clostridium thermocellum</i> DSM1313. <i>Journal of Bacteriology</i> , 2011 , 193, 2906-7	3.5	63
384	Complete genome sequence of <i>Odoribacter splanchnicus</i> type strain (1651/6). <i>Standards in Genomic Sciences</i> , 2011 , 4, 200-9		62
383	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
382	Novel insights into the diversity of catabolic metabolism from ten haloarchaeal genomes. <i>PLoS ONE</i> , 2011 , 6, e20237	3.7	60
381	Complete genome sequence of "Enterobacter lignolyticus" SCF1. <i>Standards in Genomic Sciences</i> , 2011 , 5, 69-85		60
380	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
379	The candidate phylum Poribacteria by single-cell genomics: new insights into phylogeny, cell-compartmentation, eukaryote-like repeat proteins, and other genomic features. <i>PLoS ONE</i> , 2014 , 9, e87353	3.7	59
378	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
377	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
376	Complete genome sequence of <i>Chitinophaga pinensis</i> type strain (UQM 2034). <i>Standards in Genomic Sciences</i> , 2010 , 2, 87-95		57
375	Rokubacteria: Genomic Giants among the Uncultured Bacterial Phyla. <i>Frontiers in Microbiology</i> , 2017 , 8, 2264	5.7	55
374	Genome analysis of the anaerobic thermohalophilic bacterium <i>Halothermothrix orenii</i> . <i>PLoS ONE</i> , 2009 , 4, e4192	3.7	54
373	The expanded diversity of methylophilaceae from Lake Washington through cultivation and genomic sequencing of novel ecotypes. <i>PLoS ONE</i> , 2014 , 9, e102458	3.7	53
372	Complete genome sequence of <i>Haliangium ochraceum</i> type strain (SMP-2). <i>Standards in Genomic Sciences</i> , 2010 , 2, 96-106		53

371	Complete genome sequence of "Thioalkalivibrio sulfidophilus" HL-EbGr7. <i>Standards in Genomic Sciences</i> , 2011 , 4, 23-35		51
370	Gene context analysis in the Integrated Microbial Genomes (IMG) data management system. <i>PLoS ONE</i> , 2009 , 4, e7979	3.7	51
369	Genome sequence of the Arctic methanotroph <i>Methylobacter tundripaludum</i> SV96. <i>Journal of Bacteriology</i> , 2011 , 193, 6418-9	3.5	50
368	Improving microbial genome annotations in an integrated database context. <i>PLoS ONE</i> , 2013 , 8, e54859	3.7	49
367	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
366	Complete genome sequence of <i>Geodermatophilus obscurus</i> type strain (G-20). <i>Standards in Genomic Sciences</i> , 2010 , 2, 158-67		49
365	ProDeGe: a computational protocol for fully automated decontamination of genomes. <i>ISME Journal</i> , 2016 , 10, 269-72	11.9	48
364	Genome sequences for six <i>Rhodanobacter</i> strains, isolated from soils and the terrestrial subsurface, with variable denitrification capabilities. <i>Journal of Bacteriology</i> , 2012 , 194, 4461-2	3.5	47
363	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
362	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
361	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
360	Functional genomics of novel secondary metabolites from diverse cyanobacteria using untargeted metabolomics. <i>Marine Drugs</i> , 2013 , 11, 3617-31	6	45
359	Complete genome sequence of <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM1325, an effective microsymbiont of annual Mediterranean clovers. <i>Standards in Genomic Sciences</i> , 2010 , 2, 347-56		45
358	Towards a balanced view of the bacterial tree of life. <i>Microbiome</i> , 2017 , 5, 140	16.6	44
357	Facile Recoding of Selenocysteine in Nature. <i>Angewandte Chemie - International Edition</i> , 2016 , 55, 5337-41	16.4	43
356	Metabolic dependencies govern microbial syntrophies during methanogenesis in an anaerobic digestion ecosystem. <i>Microbiome</i> , 2020 , 8, 22	16.6	42
355	Genomes of three methylotrophs from a single niche reveal the genetic and metabolic divergence of the methylphilaceae. <i>Journal of Bacteriology</i> , 2011 , 193, 3757-64	3.5	42
354	Complete genome sequence of <i>Isosphaera pallida</i> type strain (IS1B). <i>Standards in Genomic Sciences</i> , 2011 , 4, 63-71		40

353	Complete genome sequence of <i>Planctomyces brasiliensis</i> type strain (DSM 5305(T)), phylogenomic analysis and reclassification of Planctomycetes including the descriptions of <i>Gimesia</i> gen. nov., <i>Planctopirus</i> gen. nov. and <i>Rubinisphaera</i> gen. nov. and emended descriptions of the order Planctomycetales and the family Planctomycetaceae. <i>Standards in Genomic Sciences</i> , 2014 , 9, 10		39
352	Complete genome sequence of <i>Desulfohalobium propionicus</i> type strain (1pr3). <i>Standards in Genomic Sciences</i> , 2011 , 4, 100-10		39
351	Complete genome sequence of <i>Rhizobium leguminosarum</i> bv trifolii strain WSM2304, an effective microsymbiont of the South American clover <i>Trifolium polymorphum</i> . <i>Standards in Genomic Sciences</i> , 2010 , 2, 66-76		39
350	Supporting community annotation and user collaboration in the integrated microbial genomes (IMG) system. <i>BMC Genomics</i> , 2016 , 17, 307	4.5	38
349	A viability-linked metagenomic analysis of cleanroom environments: eukarya, prokaryotes, and viruses. <i>Microbiome</i> , 2015 , 3, 62	16.6	38
348	Complete genome sequence of <i>Truepera radiovictrix</i> type strain (RQ-24). <i>Standards in Genomic Sciences</i> , 2011 , 4, 91-9		37
347	IMG/M-HMP: a metagenome comparative analysis system for the Human Microbiome Project. <i>PLoS ONE</i> , 2012 , 7, e40151	3.7	36
346	Metagenomic compendium of 189,680 DNA viruses from the human gut microbiome. <i>Nature Microbiology</i> , 2021 , 6, 960-970	26.6	36
345	Draft genome sequence of <i>Frankia</i> sp. strain QA3, a nitrogen-fixing actinobacterium isolated from the root nodule of <i>Alnus nitida</i> . <i>Genome Announcements</i> , 2013 , 1, e0010313		35
344	Complete genome sequence of the filamentous gliding predatory bacterium <i>Herpetosiphon aurantiacus</i> type strain (114-95(T)). <i>Standards in Genomic Sciences</i> , 2011 , 5, 356-70		35
343	Complete genome sequence of the thermophilic, hydrogen-oxidizing <i>Bacillus tusciae</i> type strain (T2) and reclassification in the new genus, <i>Kyrpidia</i> gen. nov. as <i>Kyrpidia tusciae</i> comb. nov. and emendation of the family Alicyclobacillaceae da Costa and Rainey, 2010. <i>Standards in Genomic Sciences</i> , 2011 , 5, 121-34		35
342	Complete genome sequence of <i>Spirosoma linguale</i> type strain (1). <i>Standards in Genomic Sciences</i> , 2010 , 2, 176-85		35
341	Annotation of metagenome short reads using proxygenes. <i>Bioinformatics</i> , 2008 , 24, i7-13	7.2	35
340	Draft Genome Sequence of <i>Frankia</i> sp. Strain BCU110501, a Nitrogen-Fixing Actinobacterium Isolated from Nodules of <i>Discaria trinevis</i> . <i>Genome Announcements</i> , 2013 , 1,		34
339	Complete genome sequence of <i>Dehalobacter restrictus</i> PER-K23(T.). <i>Standards in Genomic Sciences</i> , 2013 , 8, 375-88		34
338	Complete genome sequence of <i>Thioalkalivibrio</i> sp. K90mix. <i>Standards in Genomic Sciences</i> , 2011 , 5, 341-55		34
337	ClAMS: A Classifier for Metagenomic Sequences. <i>Standards in Genomic Sciences</i> , 2011 , 5, 248-53		34
336	IMG-ABC v.5.0: an update to the IMG/Atlas of Biosynthetic Gene Clusters Knowledgebase. <i>Nucleic Acids Research</i> , 2020 , 48, D422-D430	20.1	33

335	Draft Genome Sequence of Frankia sp. Strain BMG5.12, a Nitrogen-Fixing Actinobacterium Isolated from Tunisian Soils. <i>Genome Announcements</i> , 2013 , 1,		33
334	Genome sequence of the mercury-methylating strain Desulfovibrio desulfuricans ND132. <i>Journal of Bacteriology</i> , 2011 , 193, 2078-9	3.5	33
333	Complete genome sequence of Desulfotomaculum acetoxidans type strain (5575). <i>Standards in Genomic Sciences</i> , 2009 , 1, 242-53		33
332	Microbiome Data Science: Understanding Our Microbial Planet. <i>Trends in Microbiology</i> , 2016 , 24, 425-427	12.4	33
331	Uncultivated thermophiles: current status and spotlight on 'Aigarchaeota'. <i>Current Opinion in Microbiology</i> , 2015 , 25, 136-45	7.9	32
330	Revised sequence and annotation of the Rhodobacter sphaeroides 2.4.1 genome. <i>Journal of Bacteriology</i> , 2012 , 194, 7016-7	3.5	32
329	Complete genome sequence of Actinosynnema mirum type strain (101). <i>Standards in Genomic Sciences</i> , 2009 , 1, 46-53		32
328	Complete genome sequence of Arcobacter nitrofigilis type strain (CI). <i>Standards in Genomic Sciences</i> , 2010 , 2, 300-8		32
327	Complete genome sequence of Sulfurimonas autotrophica type strain (OK10). <i>Standards in Genomic Sciences</i> , 2010 , 3, 194-202		32
326	Draft genome sequence of Halomonas lutea strain YIM 91125(T) (DSM 23508(T)) isolated from the alkaline Lake Ebinur in Northwest China. <i>Standards in Genomic Sciences</i> , 2015 , 10, 1		31
325	The genome sequence of Methanohalophilus mahii SLP(T) reveals differences in the energy metabolism among members of the Methanosarcinaceae inhabiting freshwater and saline environments. <i>Archaea</i> , 2010 , 2010, 690737	2	31
324	Complete genome sequence of Cellulomonas flavigena type strain (134). <i>Standards in Genomic Sciences</i> , 2010 , 3, 15-25		31
323	Complete genome sequence of the sulfur compounds oxidizing chemolithoautotroph Sulfuricurvum kujiense type strain (YK-1(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 94-103		31
322	Complete genome sequence of Eggerthella lenta type strain (IPP VPI 0255). <i>Standards in Genomic Sciences</i> , 2009 , 1, 174-82		31
321	Genomic Analysis of , the Thermophilic Anaerobic Bacterium of the Novel Bacterial Phylum. <i>Frontiers in Microbiology</i> , 2017 , 8, 195	5.7	30
320	Complete genome sequence of Desulfomicrobium baculatum type strain (X). <i>Standards in Genomic Sciences</i> , 2009 , 1, 29-37		30
319	Complete genome sequence of Halomicrobium mukohataei type strain (arg-2). <i>Standards in Genomic Sciences</i> , 2009 , 1, 270-7		30
318	Complete genome sequence of Veillonella parvula type strain (Te3). <i>Standards in Genomic Sciences</i> , 2010 , 2, 57-65		29

3 ¹⁷	Function-driven single-cell genomics uncovers cellulose-degrading bacteria from the rare biosphere. <i>ISME Journal</i> , 2020 , 14, 659-675	11.9	29
3 ¹⁶	Genome sequence and description of the anaerobic lignin-degrading bacterium <i>Tolumonas lignolytica</i> sp. nov. <i>Standards in Genomic Sciences</i> , 2015 , 10, 106		28
3 ¹⁵	Complete genome sequence of the halophilic and highly halotolerant <i>Chromohalobacter salexigens</i> type strain (1H11(T)). <i>Standards in Genomic Sciences</i> , 2011 , 5, 379-88		28
3 ¹⁴	Complete genome sequence of <i>Planctomyces limnophilus</i> type strain (M290). <i>Standards in Genomic Sciences</i> , 2010 , 3, 47-56		28
3 ¹³	Complete genome sequence of <i>Meiothermus ruber</i> type strain (21). <i>Standards in Genomic Sciences</i> , 2010 , 3, 26-36		28
3 ¹²	Complete genome sequence of <i>Haloterrigena turkmenica</i> type strain (4k). <i>Standards in Genomic Sciences</i> , 2010 , 2, 107-16		28
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30	High-quality permanent draft genome sequence of the Lebeckia - nodulating Burkholderia dilworthii strain WSM3556(T). <i>Standards in Genomic Sciences</i> , 2015 , 10, 64		1

29	High-quality draft genome sequence of <i>Gracilimonas tropica</i> CL-CB462(T) (DSM 19535(T)), isolated from a <i>Synechococcus</i> culture. <i>Standards in Genomic Sciences</i> , 2015 , 10, 98		1
28	High-quality permanent draft genome sequence of <i>Bradyrhizobium</i> sp. strain WSM1743 - an effective microsymbiont of an <i>Indigofera</i> sp. growing in Australia. <i>Standards in Genomic Sciences</i> , 2015 , 10, 87		1
27	High-quality permanent draft genome sequence of <i>Bradyrhizobium</i> sp. Ai1a-2; a microsymbiont of <i>Andira inermis</i> discovered in Costa Rica. <i>Standards in Genomic Sciences</i> , 2015 , 10, 33		1
26	Genome sequence of the pink-pigmented marine bacterium <i>Loktanella hongkongensis</i> type strain (UST950701-009P(T)), a representative of the <i>Roseobacter</i> group. <i>Standards in Genomic Sciences</i> , 2015 , 10, 51		1
25	High-quality permanent draft genome sequence of the <i>Mimosa asperata</i> - nodulating <i>Cupriavidus</i> sp. strain AMP6. <i>Standards in Genomic Sciences</i> , 2015 , 10, 50		1
24	High quality draft genome sequence of <i>Corynebacterium ulceribovis</i> type strain IMMIB-L1395(T) (DSM 45146(T)). <i>Standards in Genomic Sciences</i> , 2015 , 10, 50		1
23	High-quality permanent draft genome sequence of <i>Bradyrhizobium</i> sp. Th.b2, a microsymbiont of <i>Amphicarpaea bracteata</i> collected in Johnson City, New York. <i>Standards in Genomic Sciences</i> , 2015 , 10, 24		1
22	Genome sequence of <i>Ensifer medicae</i> strain WSM1369; an effective microsymbiont of the annual legume <i>Medicago sphaerocarpos</i> . <i>Standards in Genomic Sciences</i> , 2013 , 9, 420-30		1
21	Genome sequence of <i>Ensifer medicae</i> strain WSM1115; an acid-tolerant <i>Medicago</i> -nodulating microsymbiont from Samothraki, Greece. <i>Standards in Genomic Sciences</i> , 2014 , 9, 514-26		1
20	Genome sequence of the chemoheterotrophic soil bacterium <i>Saccharomonospora cyanea</i> type strain (NA-134(T)). <i>Standards in Genomic Sciences</i> , 2013 , 9, 28-41		1
19	Genome sequence of <i>Frateuria aurantia</i> type strain (Kond67(T)), a xanthomonade isolated from <i>Lilium auratum</i> Lindl. <i>Standards in Genomic Sciences</i> , 2013 , 9, 83-92		1
18	Permanent draft genome sequence of the gliding predator <i>Saprospira grandis</i> strain Sa g1 (= HR1). <i>Standards in Genomic Sciences</i> , 2012 , 6, 210-9		1
17	SOP for pathway inference in Integrated Microbial Genomes (IMG). <i>Standards in Genomic Sciences</i> , 2011 , 5, 420-3		1
16	Metagenomes and Metatranscriptomes of a Glucose-Amended Agricultural Soil. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	1
15	The DOE JGI Metagenome Workflow		1
14	Draft Genome Sequences of New Isolates and the Known Species of the Family Microbacteriaceae Associated with Plants. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1.3	1
13	A centimeter-long bacterium with DNA compartmentalized in membrane-bound organelles		1
12	Draft genome sequence of <i>Actinotignum schaalii</i> DSM 15541T: Genetic insights into the lifestyle, cell fitness and virulence. <i>PLoS ONE</i> , 2017 , 12, e0188914	3.7	0

11	High quality draft genome sequence of <i>Brachymonas chironomi</i> AIMA4(T) (DSM 19884(T)) isolated from a <i>Chironomus</i> sp. egg mass. <i>Standards in Genomic Sciences</i> , 2015 , 10, 29		o
10	High-quality permanent draft genome sequence of <i>Ensifer medicae</i> strain WSM244, a microsymbiont isolated from <i>Medicago polymorpha</i> growing in alkaline soil. <i>Standards in Genomic Sciences</i> , 2015 , 10, 126		o
9	Genome sequence of the flexirubin-pigmented soil bacterium <i>Niabella soli</i> type strain (JS13-8(T)). <i>Standards in Genomic Sciences</i> , 2012 , 7, 210-20		o
8	High-Quality Draft Genome Sequence of the Siderophilic and Thermophilic Cyanobacterium JSC-12. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0049521	1.3	o
7	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> , 2022 , 13, 735911	5.7	o
6	High-quality draft genome sequence of Mlalz-1, a microsymbiont of (<i>L.</i>) miller collected in Lanzarote, Canary Islands, Spain. <i>Standards in Genomic Sciences</i> , 2017 , 12, 58		
5	Genome sequence of <i>Ensifer medicae</i> Di28; an effective N ₂ -fixing microsymbiont of <i>Medicago murex</i> and <i>M. polymorpha</i> . <i>Standards in Genomic Sciences</i> , 2014 , 9, 4		
4	The Genome Sequence of the Novel Rhizobial Species <i>Microvirga lotononidis</i> Strain WSM3557T 2015 , 235-244		
3	Genome sequence of the <i>Ornithopus/Lupinus</i> -nodulating <i>Bradyrhizobium</i> sp. strain WSM471. <i>Standards in Genomic Sciences</i> , 2013 , 9, 254-63		
2	Complete genome sequence of <i>Mesorhizobium australicum</i> type strain (WSM2073T). <i>Standards in Genomic Sciences</i> , 2013 , 9, 1-15		
1	<i>Sodalis ligni</i> Strain 159R Isolated from an Anaerobic Lignin-Degrading Consortium.. <i>Microbiology Spectrum</i> , 2022 , e0234621	8.9	