

Natalia N Ivanova

List of Publications by Year in Descending Order

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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	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	0
459	Sodalis ligni Strain 159R Isolated from an Anaerobic Lignin-Degrading Consortium.. <i>Microbiology Spectrum</i> , 2022 , e0234621	8.9	
458	Genomics, Exometabolomics, and Metabolic Probing Reveal Conserved Proteolytic Metabolism of and Three Candidate Species From China and Japan. <i>Frontiers in Microbiology</i> , 2021 , 12, 632731	5.7	2
457	High-Quality Draft Genome Sequence of the Siderophilic and Thermophilic Cyanobacterium JSC-12. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0049521	1.3	0
456	Metagenomic compendium of 189,680 DNA viruses from the human gut microbiome. <i>Nature Microbiology</i> , 2021 , 6, 960-970	26.6	36
455	DOE JGI Metagenome Workflow. <i>MSystems</i> , 2021 , 6,	7.6	12
454	Genome Analysis of a Verrucomicrobial Endosymbiont With a Tiny Genome Discovered in an Antarctic Lake. <i>Frontiers in Microbiology</i> , 2021 , 12, 674758	5.7	5
453	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021 , 39, 499-509	44.5	120
452	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
451	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
450	VPF-Class: Taxonomic assignment and host prediction of uncultivated viruses based on viral protein families. <i>Bioinformatics</i> , 2021 ,	7.2	9
449	The biogeographic differentiation of algal microbiomes in the upper ocean from pole to pole. <i>Nature Communications</i> , 2021 , 12, 5483	17.4	3
448	Ecological and genomic analyses of candidate phylum WPS-2 bacteria in an unvegetated soil. <i>Environmental Microbiology</i> , 2020 , 22, 3143-3157	5.2	16
447	Novel heavy metal resistance gene clusters are present in the genome of Cupriavidus neocaledonicus STM 6070, a new species of Mimosa pudica microsymbiont isolated from heavy-metal-rich mining site soil. <i>BMC Genomics</i> , 2020 , 21, 214	4.5	5
446	Metabolic dependencies govern microbial syntrophies during methanogenesis in an anaerobic digestion ecosystem. <i>Microbiome</i> , 2020 , 8, 22	16.6	42
445	One Complete and Seven Draft Genome Sequences of Subdivision 1 and 3 Isolated from Soil. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	4
444	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

443	Metagenomes and Metatranscriptomes of a Glucose-Amended Agricultural Soil. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	1
442	Function-driven single-cell genomics uncovers cellulose-degrading bacteria from the rare biosphere. <i>ISME Journal</i> , 2020 , 14, 659-675	11.9	29
441	Insights into the dynamics between viruses and their hosts in a hot spring microbial mat. <i>ISME Journal</i> , 2020 , 14, 2527-2541	11.9	13
440	Molecular Dialogues between Early Divergent Fungi and Bacteria in an Antagonism versus a Mutualism. <i>MBio</i> , 2020 , 11,	7.8	5
439	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> , 2019 , 8,	1.3	1
438	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> , 2019 , 76, 566-574	2.4	3
437	A Comparison of Microbial Genome Web Portals. <i>Frontiers in Microbiology</i> , 2019 , 10, 208	5.7	10
436	Microbiomes of Velloziaceae from phosphorus-impooverished soils of the campos rupestres, a biodiversity hotspot. <i>Scientific Data</i> , 2019 , 6, 140	8.2	3
435	Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes. <i>Nature Microbiology</i> , 2019 , 4, 1895-1906	26.6	99
434	Microbial metagenomes and metatranscriptomes during a coastal phytoplankton bloom. <i>Scientific Data</i> , 2019 , 6, 129	8.2	13
433	Metagenomes and metatranscriptomes from boreal potential and actual acid sulfate soil materials. <i>Scientific Data</i> , 2019 , 6, 207	8.2	3
432	High-quality draft genome sequences of DSM 14164, DSM 17497, DSM 15088, DSM 21245 and DSM 16006: taxonomic considerations. <i>Access Microbiology</i> , 2019 , 1, e000067	1	2
431	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> , 2019 , 8,	1.3	3
430	Diversity, evolution, and classification of virophages uncovered through global metagenomics. <i>Microbiome</i> , 2019 , 7, 157	16.6	21
429	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019 , 37, 29-37	44.5	180
428	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
427	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
426	Genomes of ubiquitous marine and hypersaline <i>Hydrogenovibrio</i> , <i>Thiomicrothrix</i> and <i>Thiomicrospira</i> spp. encode a diversity of mechanisms to sustain chemolithoautotrophy in heterogeneous environments. <i>Environmental Microbiology</i> , 2018 , 20, 2686-2708	5.2	14

425	Complete Genome Sequence of sp. Strain RBITD, a Butyrate- and Butanol-Producing Thermophile. <i>Genome Announcements</i> , 2018 , 6,		1
424	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , 2018 , 36, 359-367	44.5	207
423	High-Quality Draft Genome Sequences of Eight Bacteria Isolated from Fungus Gardens Grown by <i>Trachymyrmex septentrionalis</i> Ants. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1.3	3
422	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
421	Single-cell genomics of co-sorted Nanoarchaeota suggests novel putative host associations and diversification of proteins involved in symbiosis. <i>Microbiome</i> , 2018 , 6, 161	16.6	24
420	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> , 2017 , 12, 21		5
419	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
418	Permanent draft genome of DSM 505, an obligately chemolithoautotrophic member of the. <i>Standards in Genomic Sciences</i> , 2017 , 12, 10		23
417	RNA-Dependent Cysteine Biosynthesis in Bacteria and Archaea. <i>MBio</i> , 2017 , 8,	7.8	16
416	High quality permanent draft genome sequence of DSM 19482, isolated from raw cow milk. <i>Standards in Genomic Sciences</i> , 2017 , 12, 31		2
415	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
414	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> , 2017 , 5,		2
413	Complete Genome Sequence of ATCC 49181, a Phylogenetically Distinct Ammonia-Oxidizing Bacterium Isolated from Arctic Waters. <i>Genome Announcements</i> , 2017 , 5,		2
412	Giant viruses with an expanded complement of translation system components. <i>Science</i> , 2017 , 356, 82-85,	33.3	148
411	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
410	High-quality genome sequence of the radioresistant bacterium KS 0460. <i>Standards in Genomic Sciences</i> , 2017 , 12, 46		7
409	Draft genome sequence of strain AHT1, a gram-positive sulfidogenic polyextremophile. <i>Standards in Genomic Sciences</i> , 2017 , 12, 57		7
408	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		

407	Draft genome sequence of CL-YJ9 (DSM 18822), isolated from the rhizosphere of the coastal tidal-flat plant. <i>Standards in Genomic Sciences</i> , 2017 , 12, 65		1
406	Draft genome of TNe-841, a free-living, nitrogen-fixing, tomato plant-associated bacterium. <i>Standards in Genomic Sciences</i> , 2017 , 12, 80		7
405	Genome Sequence of sp. Strain MCTG156(1a), Isolated from a Scottish Coastal Phytoplankton Net Sample. <i>Genome Announcements</i> , 2017 , 5,		2
404	Draft Genome Sequence of NE2, an Obligate Methanotroph from Subarctic Soil. <i>Genome Announcements</i> , 2017 , 5,		10
403	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2017 , 45, D457-D465	20.1	115
402	Nontargeted virus sequence discovery pipeline and virus clustering for metagenomic data. <i>Nature Protocols</i> , 2017 , 12, 1673-1682	18.8	71
401	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
400	High-quality draft genome sequence of strain STM6155, a microsymbiont from New Caledonia. <i>Standards in Genomic Sciences</i> , 2017 , 12, 7		1
399	High-quality-draft genome sequence of the fermenting bacterium type strain GluBS11 (DSM 29698). <i>Standards in Genomic Sciences</i> , 2017 , 12, 24		4
398	High-quality permanent draft genome sequence of the type strain USDA 76, isolated from (L.) Merr. <i>Standards in Genomic Sciences</i> , 2017 , 12, 26		4
397	IMG/M: integrated genome and metagenome comparative data analysis system. <i>Nucleic Acids Research</i> , 2017 , 45, D507-D516	20.1	317
396	Towards a balanced view of the bacterial tree of life. <i>Microbiome</i> , 2017 , 5, 140	16.6	44
395	Genomic Analysis of , the Thermophilic Anaerobic Bacterium of the Novel Bacterial Phylum. <i>Frontiers in Microbiology</i> , 2017 , 8, 195	5.7	30
394	Genome Data Provides High Support for Generic Boundaries in Sensu Lato. <i>Frontiers in Microbiology</i> , 2017 , 8, 1154	5.7	66
393	Rokubacteria: Genomic Giants among the Uncultured Bacterial Phyla. <i>Frontiers in Microbiology</i> , 2017 , 8, 2264	5.7	55
392	Absence of genome reduction in diverse, facultative endohyphal bacteria. <i>Microbial Genomics</i> , 2017 , 3, e000101	4.4	23
391	Transfer RNAs with novel cloverleaf structures. <i>Nucleic Acids Research</i> , 2017 , 45, 2776-2785	20.1	16
390	ProDeGe: a computational protocol for fully automated decontamination of genomes. <i>ISME Journal</i> , 2016 , 10, 269-72	11.9	48

389	Uncovering Earth's virome. <i>Nature</i> , 2016 , 536, 425-30	50.4	551
388	Permanent Draft Genome Sequence of <i>Nocardia</i> sp. BMG111209, an Actinobacterium Isolated from Nodules of <i>Casuarina glauca</i> . <i>Genome Announcements</i> , 2016 , 4,		3
387	Complete genome of <i>Nitrosospira briensis</i> C-128, an ammonia-oxidizing bacterium from agricultural soil. <i>Standards in Genomic Sciences</i> , 2016 , 11, 46		17
386	Metagenomics uncovers gaps in amplicon-based detection of microbial diversity. <i>Nature Microbiology</i> , 2016 , 1, 15032	26.6	132
385	Draft Genome Sequence of Heavy Metal-Resistant <i>Cupriavidus alkaliphilus</i> ASC-732T, Isolated from Agave Rhizosphere in the Northeast of Mexico. <i>Genome Announcements</i> , 2016 , 4,		6
384	High quality draft genome sequences of <i>Pseudomonas fulva</i> DSM 17717(T), <i>Pseudomonas parafulva</i> DSM 17004(T) and <i>Pseudomonas cremoricolorata</i> DSM 17059(T) type strains. <i>Standards in Genomic Sciences</i> , 2016 , 11, 55		9
383	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> , 2016 , 11, 65		2
382	Complete genome sequence of the Antarctic <i>Halorubrum lacusprofundi</i> type strain ACAM 34. <i>Standards in Genomic Sciences</i> , 2016 , 11, 70		15
381	High-quality permanent draft genome sequence of <i>Ensifer</i> sp. PC2, isolated from a nitrogen-fixing root nodule of the legume tree (Khejri) native to the Thar Desert of India. <i>Standards in Genomic Sciences</i> , 2016 , 11, 43		6
380	Complete genome sequence of the haloalkaliphilic, obligately chemolithoautotrophic thiosulfate and sulfide-oxidizing <i>Proteobacterium</i> <i>Thioalkalimicrobium cyclicum</i> type strain ALM 1 (DSM 14477(T)). <i>Standards in Genomic Sciences</i> , 2016 , 11, 38		5
379	Comparing polysaccharide decomposition between the type strains <i>Gramella echinicola</i> KMM 6050(T) (DSM 19838(T)) and <i>Gramella portivictoriae</i> UST040801-001(T) (DSM 23547(T)), and emended description of <i>Gramella echinicola</i> Nedashkovskaya et al. 2005 emend. Shahina et al. 2014 and <i>Gramella portivictoriae</i> Lau et al. 2005. <i>Standards in Genomic Sciences</i> , 2016 , 11, 37		14
378	Permanent draft genome sequence of <i>Desulfurococcus mobilis</i> type strain DSM 2161, a thermoacidophilic sulfur-reducing crenarchaeon isolated from acidic hot springs of Hveravellir, Iceland. <i>Standards in Genomic Sciences</i> , 2016 , 11, 3		2
377	The standard operating procedure of the DOE-JGI Metagenome Annotation Pipeline (MAP v.4). <i>Standards in Genomic Sciences</i> , 2016 , 11, 17		81
376	High-quality draft genome sequence of <i>Flavobacterium suncheonense</i> GH29-5(T) (DSM 17707(T)) isolated from greenhouse soil in South Korea, and emended description of <i>Flavobacterium suncheonense</i> GH29-5(T). <i>Standards in Genomic Sciences</i> , 2016 , 11, 42		1
375	Supporting community annotation and user collaboration in the integrated microbial genomes (IMG) system. <i>BMC Genomics</i> , 2016 , 17, 307	4.5	38
374	Complete genome sequence of <i>Methanospirillum hungatei</i> type strain JF1. <i>Standards in Genomic Sciences</i> , 2016 , 11, 2		23
373	High-quality draft genome sequence of the <i>Thermus amyloliquefaciens</i> type strain YIM 77409(T) with an incomplete denitrification pathway. <i>Standards in Genomic Sciences</i> , 2016 , 11, 20		5
372	Facile Recoding of Selenocysteine in Nature. <i>Angewandte Chemie - International Edition</i> , 2016 , 55, 5337-41	46.4	43

371	Metagenomic investigation of the geologically unique Hellenic Volcanic Arc reveals a distinctive ecosystem with unexpected physiology. <i>Environmental Microbiology</i> , 2016 , 18, 1122-36	5.2	24
370	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. <i>Nature Communications</i> , 2016 , 7, 10476	17.4	90
369	Permanent Improved High-Quality Draft Genome Sequence of <i>Nocardia casuarinae</i> Strain BMG51109, an Endophyte of Actinorhizal Root Nodules of <i>Casuarina glauca</i> . <i>Genome Announcements</i> , 2016 , 4,		4
368	Genome Sequence of <i>Arenibacter algicola</i> Strain TG409, a Hydrocarbon-Degrading Bacterium Associated with Marine Eukaryotic Phytoplankton. <i>Genome Announcements</i> , 2016 , 4,		6
367	Functional Metagenomics of Spacecraft Assembly Cleanrooms: Presence of Virulence Factors Associated with Human Pathogens. <i>Frontiers in Microbiology</i> , 2016 , 7, 1321	5.7	15
366	Genome-Based Taxonomic Classification of. <i>Frontiers in Microbiology</i> , 2016 , 7, 2003	5.7	114
365	Draft Genome Sequence of <i>Frankia</i> Strain G2, a Nitrogen-Fixing Actinobacterium Isolated from <i>Casuarina equisetifolia</i> and Able To Nodulate Actinorhizal Plants of the Order Rhamnales. <i>Genome Announcements</i> , 2016 , 4,		10
364	Complete genome sequence of <i>Desulfurivibrio alkaliphilus</i> strain AHT2(T), a haloalkaliphilic sulfidogen from Egyptian hypersaline alkaline lakes. <i>Standards in Genomic Sciences</i> , 2016 , 11, 67		22
363	Microbiome Data Science: Understanding Our Microbial Planet. <i>Trends in Microbiology</i> , 2016 , 24, 425-427	12.4	33
362	High-Quality Draft Genomes from <i>Thermus caliditerrae</i> YIM 77777 and <i>T. tengchongensis</i> YIM 77401, Isolates from Tengchong, China. <i>Genome Announcements</i> , 2016 , 4,		3
361	Application of Long Sequence Reads To Improve Genomes for <i>Clostridium thermocellum</i> AD2, <i>Clostridium thermocellum</i> LQRI, and <i>Pelosinus fermentans</i> R7. <i>Genome Announcements</i> , 2016 , 4,		2
360	Permanent draft genome of DSM 3134, a moderately thermophilic, obligately chemolithoautotrophic member of the. <i>Standards in Genomic Sciences</i> , 2016 , 11, 74		12
359	Uncultivated thermophiles: current status and spotlight on 'Aigarchaeota'. <i>Current Opinion in Microbiology</i> , 2015 , 25, 136-45	7.9	32
358	Complete Genome Sequence of the Oritutaceae Bacterium Strain TAV5, a Potential Facultative Methylophile of the Wood-Feeding Termite <i>Reticulitermes flavipes</i> . <i>Genome Announcements</i> , 2015 , 3,		15
357	Microbial species delineation using whole genome sequences. <i>Nucleic Acids Research</i> , 2015 , 43, 6761-71	20.1	433
356	High quality draft genome sequence of <i>Meganema perideroedes</i> str. Gr1(T) and a proposal for its reclassification to the family Meganemaceae fam. nov. <i>Standards in Genomic Sciences</i> , 2015 , 10, 23		9
355	High-quality permanent draft genome sequence of <i>Bradyrhizobium</i> sp. Tv2a.2, a microsymbiont of <i>Tachigali versicolor</i> discovered in Barro Colorado Island of Panama. <i>Standards in Genomic Sciences</i> , 2015 , 10, 27		3
354	Ten years of maintaining and expanding a microbial genome and metagenome analysis system. <i>Trends in Microbiology</i> , 2015 , 23, 730-741	12.4	18

353	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
352	The Genome Sequence of the Novel Rhizobial Species <i>Microvirga lotononidis</i> Strain WSM3557T 2015 , 235-244		
351	Discovery of Novel Plant Interaction Determinants from the Genomes of 163 Root Nodule Bacteria. <i>Scientific Reports</i> , 2015 , 5, 16825	4.9	26
350	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		0
349	High-quality permanent draft genome sequence of the <i>Parapiptadenia rigida</i> -nodulating <i>Burkholderia</i> sp. strain UYPR1.413. <i>Standards in Genomic Sciences</i> , 2015 , 10, 31		2
348	High quality draft genome sequence of <i>Bacteroides barnesiae</i> type strain BL2(T) (DSM 18169(T)) from chicken caecum. <i>Standards in Genomic Sciences</i> , 2015 , 10, 48		2
347	High-quality permanent draft genome sequence of the <i>Lebeckia</i> - nodulating <i>Burkholderia</i> <i>dilworthii</i> strain WSM3556(T). <i>Standards in Genomic Sciences</i> , 2015 , 10, 64		1
346	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
345	High-quality permanent draft genome sequence of the <i>Lebeckia</i> <i>ambigua</i> -nodulating <i>Burkholderia</i> sp. strain WSM4176. <i>Standards in Genomic Sciences</i> , 2015 , 10, 79		5
344	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
343	Partial genome sequence of <i>Thioalkalivibrio thiocyanodenitrificans</i> ARhD 1(T), a chemolithoautotrophic haloalkaliphilic sulfur-oxidizing bacterium capable of complete denitrification. <i>Standards in Genomic Sciences</i> , 2015 , 10, 84		2
342	High-quality permanent draft genome sequence of the <i>Parapiptadenia rigida</i> -nodulating <i>Cupriavidus</i> sp. strain UYPR2.512. <i>Standards in Genomic Sciences</i> , 2015 , 10, 13		2
341	Large-scale contamination of microbial isolate genomes by Illumina PhiX control. <i>Standards in Genomic Sciences</i> , 2015 , 10, 18		85
340	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
339	Draft genome sequence of <i>Halomonas lutea</i> 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
338	High quality draft genome sequence and analysis of <i>Pontibacter roseus</i> type strain SRC-1(T) (DSM 17521(T)) isolated from muddy waters of a drainage system in Chandigarh, India. <i>Standards in Genomic Sciences</i> , 2015 , 10, 8		4
337	A viability-linked metagenomic analysis of cleanroom environments: eukarya, prokaryotes, and viruses. <i>Microbiome</i> , 2015 , 3, 62	16.6	38
336	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

335	Genome sequence of the pink-pigmented marine bacterium Loktanella hongkongensis type strain (UST950701-009P(T)), a representative of the Roseobacter group. <i>Standards in Genomic Sciences</i> , 2015 , 10, 51	1
334	High-quality permanent draft genome sequence of the extremely osmotolerant diphenol degrading bacterium Halotalea alkalilenta AW-7(T), and emended description of the genus Halotalea. <i>Standards in Genomic Sciences</i> , 2015 , 10, 52	4
333	High-quality permanent draft genome sequence of the Mimosa asperata - nodulating Cupriavidus sp. strain AMP6. <i>Standards in Genomic Sciences</i> , 2015 , 10, 80	1
332	Genome sequence and description of the anaerobic lignin-degrading bacterium Tolumonas lignolytica sp. nov. <i>Standards in Genomic Sciences</i> , 2015 , 10, 106	28
331	Draft Genome Sequence of the Cellulolytic and Xylanolytic Thermophile Clostridium clariflavum Strain 4-2a. <i>Genome Announcements</i> , 2015 , 3,	2
330	High-Quality Draft Genome Sequence of Kallotenue papyrolyticum JKG1T Reveals Broad Heterotrophic Capacity Focused on Carbohydrate and Amino Acid Metabolism. <i>Genome Announcements</i> , 2015 , 3,	3
329	High-quality permanent draft genome sequence of Rhizobium leguminosarum bv. viciae strain GB30; an effective microsymbiont of Pisum sativum growing in Poland. <i>Standards in Genomic Sciences</i> , 2015 , 10, 36	3
328	High quality draft genome sequence of Flavobacterium rivuli type strain WB 3.3-2(T) (DSM 21788(T)), a valuable source of polysaccharide decomposing enzymes. <i>Standards in Genomic Sciences</i> , 2015 , 10, 46	11
327	Toward a standard in structural genome annotation for prokaryotes. <i>Standards in Genomic Sciences</i> , 2015 , 10, 45	12
326	High quality draft genome sequence of Corynebacterium ulceribovis type strain IMMIB-L1395(T) (DSM 45146(T)). <i>Standards in Genomic Sciences</i> , 2015 , 10, 50	1
325	Complete genome sequence of the phenanthrene-degrading soil bacterium Delftia acidovorans Cs1-4. <i>Standards in Genomic Sciences</i> , 2015 , 10, 55	17
324	Genome and Transcriptome of Clostridium phytofermentans, Catalyst for the Direct Conversion of Plant Feedstocks to Fuels. <i>PLoS ONE</i> , 2015 , 10, e0118285	3.7 16
323	High-quality permanent draft genome sequence of Bradyrhizobium sp. Th.b2, a microsymbiont of Amphicarpaea bracteata collected in Johnson City, New York. <i>Standards in Genomic Sciences</i> , 2015 , 10, 24	1
322	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
321	High quality draft genome sequence of Leucobacter chironomi strain MM2LB(T) (DSM 19883(T)) isolated from a Chironomus sp. egg mass. <i>Standards in Genomic Sciences</i> , 2015 , 10, 21	6
320	Genome Sequence of Polycyclovorans algicola Strain TG408, an Obligate Polycyclic Aromatic Hydrocarbon-Degrading Bacterium Associated with Marine Eukaryotic Phytoplankton. <i>Genome Announcements</i> , 2015 , 3,	4
319	High-quality permanent draft genome sequence of Rhizobium sullae strain WSM1592; a Hedysarum coronarium microsymbiont from Sassari, Italy. <i>Standards in Genomic Sciences</i> , 2015 , 10, 44	7
318	Complete Genome Sequences of Caldicellulosiruptor sp. Strain Rt8.B8, Caldicellulosiruptor sp. Strain Wai35.B1, and "Thermoanaerobacter cellulolyticus". <i>Genome Announcements</i> , 2015 , 3,	12

317	Genome Sequence of Porticoccus hydrocarbonoclasticus Strain MCTG13d, an Obligate Polycyclic Aromatic Hydrocarbon-Degrading Bacterium Associated with Marine Eukaryotic Phytoplankton. <i>Genome Announcements</i> , 2015 , 3,	8
316	Genome Sequence of Halomonas sp. Strain MCTG39a, a Hydrocarbon-Degrading and Exopolymeric Substance-Producing Bacterium. <i>Genome Announcements</i> , 2015 , 3,	6
315	Draft Genome Sequence of Frankia sp. Strain DC12, an Atypical, Noninfective, Ineffective Isolate from Datisca cannabina. <i>Genome Announcements</i> , 2015 , 3,	19
314	Partial genome sequence of the haloalkaliphilic soda lake bacterium Thioalkalivibrio thiocyanoxidans ARh 2(T). <i>Standards in Genomic Sciences</i> , 2015 , 10, 85	3
313	Complete genome sequence of Thioalkalivibrio paradoxus type strain ARh 1(T), an obligately chemolithoautotrophic haloalkaliphilic sulfur-oxidizing bacterium isolated from a Kenyan soda lake. <i>Standards in Genomic Sciences</i> , 2015 , 10, 105	5
312	High-quality permanent draft genome sequence of Ensifer meliloti strain 4H41, an effective salt- and drought-tolerant microsymbiont of Phaseolus vulgaris. <i>Standards in Genomic Sciences</i> , 2015 , 10, 34	3
311	High-quality permanent draft genome sequence of Ensifer medicae strain WSM244, a microsymbiont isolated from Medicago polymorpha growing in alkaline soil. <i>Standards in Genomic Sciences</i> , 2015 , 10, 126	0
310	Genome sequence of Bradyrhizobium sp. WSM1253; a microsymbiont of Ornithopus compressus from the Greek Island of Sifnos. <i>Standards in Genomic Sciences</i> , 2015 , 10, 113	3
309	Stop codon reassignments in the wild. <i>Science</i> , 2014 , 344, 909-13	33-3 83
308	Complete genome sequence of Planctomyces brasiliensis type strain (DSM 5305(T)), phylogenomic analysis and reclassification of Planctomycetes including the descriptions of Gimesia gen. nov., Planctopirus gen. nov. and Rubinisphaera gen. nov. and emended descriptions of the order Planctomycetales and the family Planctomycetaceae. <i>Standards in Genomic Sciences</i> , 2014 , 9, 10	39
307	Complete genome sequence of DSM 30083(T), the type strain (U5/41(T)) of Escherichia coli, and a proposal for delineating subspecies in microbial taxonomy. <i>Standards in Genomic Sciences</i> , 2014 , 9, 2	267
306	Genome sequence of the Lotus corniculatus microsymbiont Mesorhizobium loti strain R88B. <i>Standards in Genomic Sciences</i> , 2014 , 9, 3	7
305	Genome sequence of Ensifer medicae Di28; an effective N ₂ -fixing microsymbiont of Medicago murex and M. polymorpha. <i>Standards in Genomic Sciences</i> , 2014 , 9, 4	
304	Genome sequence of the dark pink pigmented Listia bainesii microsymbiont Methylobacterium sp. WSM2598. <i>Standards in Genomic Sciences</i> , 2014 , 9, 5	3
303	Genome sequence of the Lotus spp. microsymbiont Mesorhizobium loti strain NZP2037. <i>Standards in Genomic Sciences</i> , 2014 , 9, 7	4
302	Genome sequence of the Lotus spp. microsymbiont Mesorhizobium loti strain R7A. <i>Standards in Genomic Sciences</i> , 2014 , 9, 6	16
301	Genome sequence and emended description of Leisingera nanhaiensis strain DSM 24252(T) isolated from marine sediment. <i>Standards in Genomic Sciences</i> , 2014 , 9, 687-703	5
300	Genome sequence of the Thermotoga thermarum type strain (LA3(T)) from an African solfataric spring. <i>Standards in Genomic Sciences</i> , 2014 , 9, 1105-17	4

299	Genome sequence of the Medicago-nodulating Ensifer meliloti commercial inoculant strain RRI128. <i>Standards in Genomic Sciences</i> , 2014 , 9, 602-13			3
298	Genome sequence of the mud-dwelling archaeon Methanoplanus limicola type strain (DSM 2279(T)), reclassification of Methanoplanus petrolearius as Methanolacinia petrolearia and emended descriptions of the genera Methanoplanus and Methanolacinia. <i>Standards in Genomic Sciences</i> , 2014 , 9, 1076-88			10
297	The complete genome sequence of Clostridium indolis DSM 755(T.). <i>Standards in Genomic Sciences</i> , 2014 , 9, 1089-104			11
296	High quality draft genome sequence of the slightly halophilic bacterium Halomonas zhanjiangensis type strain JSM 078169(T) (DSM 21076(T)) from a sea urchin in southern China. <i>Standards in Genomic Sciences</i> , 2014 , 9, 1020-30			8
295	Genome sequence of the Wenxinia marina type strain (DSM 24838(T)), a representative of the Roseobacter group isolated from oilfield sediments. <i>Standards in Genomic Sciences</i> , 2014 , 9, 855-65			2
294	Genome sequence of Microvirga lupini strain LUT6(T), a novel Lupinus alphaproteobacterial microsymbiont from Texas. <i>Standards in Genomic Sciences</i> , 2014 , 9, 1159-67			5
293	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
292	IMG/M 4 version of the integrated metagenome comparative analysis system. <i>Nucleic Acids Research</i> , 2014 , 42, D568-73		20.1	212
291	Draft genome sequences of 10 strains of the genus exiguobacterium. <i>Genome Announcements</i> , 2014 , 2,			15
290	Complete genome sequence of the lignin-degrading bacterium Klebsiella sp. strain BRL6-2. <i>Standards in Genomic Sciences</i> , 2014 , 9, 19			27
289	IMG 4 version of the integrated microbial genomes comparative analysis system. <i>Nucleic Acids Research</i> , 2014 , 42, D560-7		20.1	444
288	Genome sequence of the Listia angolensis microsymbiont Microvirga lotononidis strain WSM3557(T.). <i>Standards in Genomic Sciences</i> , 2014 , 9, 540-50			4
287	Genome sequence of Burkholderia mimosarum strain LMG 23256(T), a Mimosa pigra microsymbiont from Anso, Taiwan. <i>Standards in Genomic Sciences</i> , 2014 , 9, 484-94			2
286	Genome sequence of Ensifer medicae strain WSM1115; an acid-tolerant Medicago-nodulating microsymbiont from Samothraki, Greece. <i>Standards in Genomic Sciences</i> , 2014 , 9, 514-26			1
285	Genome sequence of Ensifer arboris strain LMG 14919(T); a microsymbiont of the legume Prosopis chilensis growing in Kosti, Sudan. <i>Standards in Genomic Sciences</i> , 2014 , 9, 473-83			4
284	Genome sequence of Rhizobium leguminosarum bv trifolii strain WSM1689, the microsymbiont of the one flowered clover Trifolium uniflorum. <i>Standards in Genomic Sciences</i> , 2014 , 9, 527-39			11
283	Genome sequence of the acid-tolerant Burkholderia sp. strain WSM2230 from Karijini National Park, Australia. <i>Standards in Genomic Sciences</i> , 2014 , 9, 551-61			3
282	Genome sequence of the acid-tolerant Burkholderia sp. strain WSM2232 from Karijini National Park, Australia. <i>Standards in Genomic Sciences</i> , 2014 , 9, 1168-80			2

281	Complete genome sequence of Mesorhizobium ciceri bv. biserrulae type strain (WSM1271(T)). <i>Standards in Genomic Sciences</i> , 2014 , 9, 462-72		16
280	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
279	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013 , 499, 431-7	50.4	1484
278	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
277	Draft genome sequence of Frankia sp. strain QA3, a nitrogen-fixing actinobacterium isolated from the root nodule of Alnus nitida. <i>Genome Announcements</i> , 2013 , 1, e0010313		35
276	Draft Genome Sequence of Frankia sp. Strain BMG5.12, a Nitrogen-Fixing Actinobacterium Isolated from Tunisian Soils. <i>Genome Announcements</i> , 2013 , 1,		33
275	Draft Genome Sequence of Pseudomonas azotifigens Strain DSM 17556T (6H33bT), a Nitrogen Fixer Strain Isolated from a Compost Pile. <i>Genome Announcements</i> , 2013 , 1,		3
274	Draft Genome Sequence of Frankia sp. Strain BCU110501, a Nitrogen-Fixing Actinobacterium Isolated from Nodules of Discaria trinevis. <i>Genome Announcements</i> , 2013 , 1,		34
273	Draft genome sequence of Frankia sp. strain CN3, an atypical, noninfective (Nod-) ineffective (Fix-) isolate from Coriaria nepalensis. <i>Genome Announcements</i> , 2013 , 1, e0008513		46
272	Complete Genome Sequence of the Hyperthermophilic Sulfate-Reducing Bacterium Thermodesulfobacterium geofontis OPF15T. <i>Genome Announcements</i> , 2013 , 1, e0016213		4
271	Genome Sequence of Streptomyces viridosporus Strain T7A ATCC 39115, a Lignin-Degrading Actinomycete. <i>Genome Announcements</i> , 2013 , 1,		15
270	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
269	Genome sequence of the Trifolium rueppellianum -nodulating Rhizobium leguminosarum bv. trifolii strain WSM2012. <i>Standards in Genomic Sciences</i> , 2013 , 9, 283-93		3
268	Genome sequence of Ensifer medicae strain WSM1369; an effective microsymbiont of the annual legume Medicago sphaerocarpos. <i>Standards in Genomic Sciences</i> , 2013 , 9, 420-30		1
267	Complete genome sequence of Coriobacterium glomerans type strain (PW2(T)) from the midgut of Pyrrhocoris apterus L. (red soldier bug). <i>Standards in Genomic Sciences</i> , 2013 , 8, 15-25		5
266	Complete genome sequence of the bile-resistant pigment-producing anaerobe Alistipes finegoldii type strain (AHN2437(T)). <i>Standards in Genomic Sciences</i> , 2013 , 8, 26-36		6
265	High-quality-draft genome sequence of the yellow-pigmented flavobacterium Joostella marina type strain (En5(T)). <i>Standards in Genomic Sciences</i> , 2013 , 8, 37-46		4
264	Complete genome sequence of the moderate thermophile Anaerobaculum mobile type strain (NGA(T)). <i>Standards in Genomic Sciences</i> , 2013 , 8, 47-57		10

263	Genome sequence of the free-living aerobic spirochete <i>Turneriella parva</i> type strain (H(T)), and emendation of the species <i>Turneriella parva</i> . <i>Standards in Genomic Sciences</i> , 2013 , 8, 228-38	8
262	<i>Thermus oshimai</i> JL-2 and <i>T. thermophilus</i> JL-18 genome analysis illuminates pathways for carbon, nitrogen, and sulfur cycling. <i>Standards in Genomic Sciences</i> , 2013 , 7, 449-68	22
261	Complete genome sequence of <i>Halorhodospira halophila</i> SL1. <i>Standards in Genomic Sciences</i> , 2013 , 8, 206-14	13
260	Complete genome sequence of <i>Dehalobacter restrictus</i> PER-K23(T.). <i>Standards in Genomic Sciences</i> , 2013 , 8, 375-88	34
259	Permanent draft genome sequences of the symbiotic nitrogen fixing <i>Ensifer meliloti</i> strains BO21CC and AK58. <i>Standards in Genomic Sciences</i> , 2013 , 9, 325-33	4
258	Genome sequence of the phage-gene rich marine <i>Phaeobacter arcticus</i> type strain DSM 23566(T.). <i>Standards in Genomic Sciences</i> , 2013 , 8, 450-64	9
257	Genome sequence of the <i>Leisingera aquimarina</i> type strain (DSM 24565(T)), a member of the marine <i>Roseobacter</i> clade rich in extrachromosomal elements. <i>Standards in Genomic Sciences</i> , 2013 , 8, 389-402	16
256	Genome sequence of <i>Phaeobacter caeruleus</i> type strain (DSM 24564T), a surface-associated member of the marine <i>Roseobacter</i> clade. <i>Standards in Genomic Sciences</i> , 2013 , 8, 403-419	12
255	Non-contiguous finished genome sequence of plant-growth promoting <i>Serratia proteamaculans</i> S4. <i>Standards in Genomic Sciences</i> , 2013 , 8, 441-9	9
254	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
253	Genome sequence of the moderately thermophilic sulfur-reducing bacterium <i>Thermanaerovibrio velox</i> type strain (Z-9701(T)) and emended description of the genus <i>Thermanaerovibrio</i> . <i>Standards in Genomic Sciences</i> , 2013 , 9, 57-70	4
252	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
251	Genome sequence of the clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain SRDI565. <i>Standards in Genomic Sciences</i> , 2013 , 9, 220-31	3
250	Genome sequence of the clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain TA1. <i>Standards in Genomic Sciences</i> , 2013 , 9, 243-53	8
249	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	
248	Genome sequence of the South American clover-nodulating <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM597. <i>Standards in Genomic Sciences</i> , 2013 , 9, 264-72	3
247	Genome sequence of the lupin-nodulating <i>Bradyrhizobium</i> sp. strain WSM1417. <i>Standards in Genomic Sciences</i> , 2013 , 9, 273-82	2
246	Complete genome sequence of <i>Mesorhizobium opportunistum</i> type strain WSM2075(T.). <i>Standards in Genomic Sciences</i> , 2013 , 9, 294-303	10

245	Genome sequence of Ensifer sp. TW10; a Tephrosia wallichii (Biyani) microsymbiont native to the Indian Thar Desert. <i>Standards in Genomic Sciences</i> , 2013 , 9, 304-14		11
244	Genome sequence of Ensifer meliloti strain WSM1022; a highly effective microsymbiont of the model legume Medicago truncatula A17. <i>Standards in Genomic Sciences</i> , 2013 , 9, 315-24		9
243	Complete genome sequence of Mesorhizobium australicum type strain (WSM2073(T)). <i>Standards in Genomic Sciences</i> , 2013 , 9, 410-9		9
242	Genome sequence of the thermophilic fresh-water bacterium Spirochaeta caldaria type strain (H1(T)), reclassification of Spirochaeta caldaria, Spirochaeta stenostrepta, and Spirochaeta zuelzeriae in the genus Treponema as Treponema caldaria comb. nov., Treponema stenostrepta		24
241	Complete genome sequence of the halophilic bacterium Spirochaeta africana type strain (Z-7692(T)) from the alkaline Lake Magadi in the East African Rift. <i>Standards in Genomic Sciences</i> , 2013 , 8, 165-76		2
240	Genome sequence of the phylogenetically isolated spirochete Leptonema illini type strain (3055(T)). <i>Standards in Genomic Sciences</i> , 2013 , 8, 177-87		4
239	Genome sequence of Phaeobacter daeponensis type strain (DSM 23529(T)), a facultatively anaerobic bacterium isolated from marine sediment, and emendation of Phaeobacter daeponensis. <i>Standards in Genomic Sciences</i> , 2013 , 9, 142-59		10
238	Complete genome sequence of the marine methyl-halide oxidizing Leisingera methylohalidivorans type strain (DSM 14336(T)), a representative of the Roseobacter clade. <i>Standards in Genomic Sciences</i> , 2013 , 9, 128-41		13
237	Complete genome sequence of Enterobacter sp. IIT-BT 08: A potential microbial strain for high rate hydrogen production. <i>Standards in Genomic Sciences</i> , 2013 , 9, 359-69		13
236	Genome sequence of Phaeobacter inhibens type strain (T5(T)), a secondary metabolite producing representative of the marine Roseobacter clade, and emendation of the species description of Phaeobacter inhibens. <i>Standards in Genomic Sciences</i> , 2013 , 9, 334-50		19
235	Genome sequence of the Lebeckia ambigua-nodulating "Burkholderia spreintiae" strain WSM5005(T.). <i>Standards in Genomic Sciences</i> , 2013 , 9, 385-94		6
234	Functional genomics of novel secondary metabolites from diverse cyanobacteria using untargeted metabolomics. <i>Marine Drugs</i> , 2013 , 11, 3617-31	6	45
233	Improving microbial genome annotations in an integrated database context. <i>PLoS ONE</i> , 2013 , 8, e54859	3,7	49
232	Complete genome sequence of Nitrosomonas sp. Is79, an ammonia oxidizing bacterium adapted to low ammonium concentrations. <i>Standards in Genomic Sciences</i> , 2013 , 7, 469-82		27
231	Genome sequence of Phaeobacter caeruleus type strain (DSM 24564(T)), a surface-associated member of the marine Roseobacter clade. <i>Standards in Genomic Sciences</i> , 2013 , 8, 403-19		12
230	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
229	Complete genome sequence of Mesorhizobium australicum type strain (WSM2073T). <i>Standards in Genomic Sciences</i> , 2013 , 9, 1-15		
228	Revised sequence and annotation of the Rhodobacter sphaeroides 2.4.1 genome. <i>Journal of Bacteriology</i> , 2012 , 194, 7016-7	3,5	32

227	Complete genome sequence of the rapeseed plant-growth promoting <i>Serratia plymuthica</i> strain AS9. <i>Standards in Genomic Sciences</i> , 2012 , 6, 54-62		25
226	IMG/M-HMP: a metagenome comparative analysis system for the Human Microbiome Project. <i>PLoS ONE</i> , 2012 , 7, e40151	3.7	36
225	High-quality draft genome sequence of the Opitutaceae bacterium strain TAV1, a symbiont of the wood-feeding termite <i>Reticulitermes flavipes</i> . <i>Journal of Bacteriology</i> , 2012 , 194, 2744-5	3.5	18
224	Genome sequences for six Rhodanobacter strains, isolated from soils and the terrestrial subsurface, with variable denitrification capabilities. <i>Journal of Bacteriology</i> , 2012 , 194, 4461-2	3.5	47
223	Complete genome sequences of six strains of the genus <i>Methylobacterium</i> . <i>Journal of Bacteriology</i> , 2012 , 194, 4746-8	3.5	70
222	IMG/M: the integrated metagenome data management and comparative analysis system. <i>Nucleic Acids Research</i> , 2012 , 40, D123-9	20.1	207
221	IMG: the Integrated Microbial Genomes database and comparative analysis system. <i>Nucleic Acids Research</i> , 2012 , 40, D115-22	20.1	953
220	Genome sequence of the moderately thermophilic, amino-acid-degrading and sulfur-reducing bacterium <i>Thermovirga lienii</i> type strain (Cas60314(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 230-9		21
219	Genome sequence of the orange-pigmented seawater bacterium <i>Owenweeksia hongkongensis</i> type strain (UST20020801(T)). <i>Standards in Genomic Sciences</i> , 2012 , 7, 120-30		11
218	Complete genome sequence of the moderately thermophilic mineral-sulfide-oxidizing firmicute <i>Sulfobacillus acidophilus</i> type strain (NAL(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 1-13		20
217	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
216	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
215	Complete genome sequence of the melanogenic marine bacterium <i>Marinomonas mediterranea</i> type strain (MMB-1(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 63-73		18
214	Genome sequence of the soil bacterium <i>Saccharomonospora azurea</i> type strain (NA-128(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 220-9		10
213	Complete genome sequence of the facultatively anaerobic, appendaged bacterium <i>Muricauda ruestringensis</i> type strain (B1(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 185-93		8
212	Complete genome sequence of <i>Polynucleobacter necessarius</i> subsp. <i>asymbioticus</i> type strain (QLW-P1DMWA-1(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 74-83		27
211	Complete genome sequence of the aerobic, heterotroph <i>Marinithermus hydrothermalis</i> type strain (T1(T)) from a deep-sea hydrothermal vent chimney. <i>Standards in Genomic Sciences</i> , 2012 , 6, 21-30		6
210	Complete genome sequence of the aquatic bacterium <i>Runella slithyformis</i> type strain (LSU 4(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 145-54		16

209	Genome sequence of the ocean sediment bacterium <i>Saccharomonospora marina</i> type strain (XMU15(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 265-75	3
208	Complete genome sequence of the thermophilic sulfate-reducing ocean bacterium <i>Thermodesulfatator indicus</i> type strain (CIR29812(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 155-64	9
207	Complete genome sequence of <i>Serratia plymuthica</i> strain AS12. <i>Standards in Genomic Sciences</i> , 2012 , 6, 165-73	15
206	Genome sequence of the homoacetogenic bacterium <i>Holophaga foetida</i> type strain (TMBS4(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 174-84	23
205	Complete genome sequence of the orange-red pigmented, radioresistant <i>Deinococcus proteolyticus</i> type strain (MRP(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 240-50	7
204	Complete genome sequence of <i>Thermovibrio ammonificans</i> HB-1(T), a thermophilic, chemolithoautotrophic bacterium isolated from a deep-sea hydrothermal vent. <i>Standards in Genomic Sciences</i> , 2012 , 7, 82-90	8
203	Complete genome sequence of the plant-associated <i>Serratia plymuthica</i> strain AS13. <i>Standards in Genomic Sciences</i> , 2012 , 7, 22-30	16
202	Complete genome sequence of <i>Marinomonas posidonica</i> type strain (IVIA-Po-181(T)). <i>Standards in Genomic Sciences</i> , 2012 , 7, 31-43	5
201	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	0
200	Genome sequence of the Antarctic rhodopsins-containing flavobacterium <i>Gillisia limnaea</i> type strain (R-8282(T)). <i>Standards in Genomic Sciences</i> , 2012 , 7, 107-19	9
199	Complete genome sequence of the sulfate-reducing firmicute <i>Desulfotomaculum ruminis</i> type strain (DL(T)). <i>Standards in Genomic Sciences</i> , 2012 , 7, 304-19	18
198	Complete genome sequencing and analysis of <i>Saprospira grandis</i> str. Lewin, a predatory marine bacterium. <i>Standards in Genomic Sciences</i> , 2012 , 6, 84-93	19
197	Complete genome sequence of <i>Halopiger xanaduensis</i> type strain (SH-6(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 31-42	7
196	Complete genome sequence of the facultatively chemolithoautotrophic and methylotrophic alpha Proteobacterium <i>Starkeya novella</i> type strain (ATCC 8093(T)). <i>Standards in Genomic Sciences</i> , 2012 , 7, 44-58	12
195	Complete genome sequence of the sulfur compounds oxidizing chemolithoautotroph <i>Sulfuricurvum kujiense</i> type strain (YK-1(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 94-103	31
194	Genomics of aerobic cellulose utilization systems in actinobacteria. <i>PLoS ONE</i> , 2012 , 7, e39331	3-7 73
193	Complete genome sequence of the facultatively chemolithoautotrophic and methylotrophic alpha Proteobacterium <i>Starkeya novella</i> type strain (ATCC 8093T). <i>Standards in Genomic Sciences</i> , 2012 , 7, 44-58	15
192	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

191	Novel insights into the diversity of catabolic metabolism from ten haloarchaeal genomes. <i>PLoS ONE</i> , 2011 , 6, e20237	3.7	60
190	Complete genome sequence of <i>Leadbetterella byssophila</i> type strain (4M15). <i>Standards in Genomic Sciences</i> , 2011 , 4, 2-12		15
189	Complete genome sequence of <i>Hydrogenobacter thermophilus</i> type strain (TK-6). <i>Standards in Genomic Sciences</i> , 2011 , 4, 131-43		8
188	Complete genome sequence of <i>Paludibacter propionigenes</i> type strain (WB4). <i>Standards in Genomic Sciences</i> , 2011 , 4, 36-44		24
187	Complete genome sequence of <i>Bacteroides helcogenes</i> type strain (P 36-108). <i>Standards in Genomic Sciences</i> , 2011 , 4, 45-53		7
186	Complete genome sequence of <i>Weeksella virosa</i> type strain (9751). <i>Standards in Genomic Sciences</i> , 2011 , 4, 81-90		8
185	Complete genome sequence of <i>Desulfobulbus propionicus</i> type strain (1pr3). <i>Standards in Genomic Sciences</i> , 2011 , 4, 100-10		39
184	Complete genome sequence of <i>Marivirga tractuosa</i> type strain (H-43). <i>Standards in Genomic Sciences</i> , 2011 , 4, 154-62		15
183	Complete genome sequence of <i>Desulfurococcus mucosus</i> type strain (O7/1). <i>Standards in Genomic Sciences</i> , 2011 , 4, 173-82		9
182	Complete genome sequence of <i>Cellulophaga lytica</i> type strain (LIM-21). <i>Standards in Genomic Sciences</i> , 2011 , 4, 221-32		23
181	Non-contiguous finished genome sequence of <i>Bacteroides coprosuis</i> type strain (PC139). <i>Standards in Genomic Sciences</i> , 2011 , 4, 233-43		4
180	Complete genome sequence of the extremely halophilic <i>Halanaerobium praevalens</i> type strain (GSL). <i>Standards in Genomic Sciences</i> , 2011 , 4, 312-21		24
179	Complete genome sequence of <i>Nitratifractor salsuginis</i> type strain (E9I37-1). <i>Standards in Genomic Sciences</i> , 2011 , 4, 322-30		10
178	Complete genome sequence of <i>Mahella australiensis</i> type strain (50-1 BON). <i>Standards in Genomic Sciences</i> , 2011 , 4, 331-41		6
177	Complete genome sequence of <i>Treponema succinifaciens</i> type strain (6091). <i>Standards in Genomic Sciences</i> , 2011 , 4, 361-70		20
176	Complete genome sequence of <i>Syntrophobotulus glycolicus</i> type strain (FlGlyRT). <i>Standards in Genomic Sciences</i> , 2011 , 4, 371-380		9
175	Complete genome sequence of the hyperthermophilic chemolithoautotroph <i>Pyrolobus fumarii</i> type strain (1A). <i>Standards in Genomic Sciences</i> , 2011 , 4, 381-92		10
174	Complete genome sequence of <i>Staphylothermus hellenicus</i> P8. <i>Standards in Genomic Sciences</i> , 2011 , 5, 12-20		5

173	Complete genome sequence of the acetate-degrading sulfate reducer <i>Desulfobacca acetoxidans</i> type strain (ASRB2). <i>Standards in Genomic Sciences</i> , 2011 , 4, 393-401	19
172	Complete genome sequence of " <i>Enterobacter lignolyticus</i> " SCF1. <i>Standards in Genomic Sciences</i> , 2011 , 5, 69-85	60
171	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
170	Complete genome sequence of the gliding, heparinolytic <i>Pedobacter saltans</i> type strain (113). <i>Standards in Genomic Sciences</i> , 2011 , 5, 30-40	11
169	Non-contiguous finished genome sequence of the opportunistic oral pathogen <i>Prevotella multisaccharivorax</i> type strain (PPPA20). <i>Standards in Genomic Sciences</i> , 2011 , 5, 41-9	2
168	Complete genome sequence of <i>Tolomonas auensis</i> type strain (TA 4). <i>Standards in Genomic Sciences</i> , 2011 , 5, 112-20	4
167	Complete genome sequence of <i>Hirschia baltica</i> type strain (IFAM 1418(T)). <i>Standards in Genomic Sciences</i> , 2011 , 5, 287-97	8
166	Complete genome sequence of <i>Ferroglobus placidus</i> AEDII12DO. <i>Standards in Genomic Sciences</i> , 2011 , 5, 50-60	27
165	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
164	Genome sequence of the filamentous, gliding <i>Thiothrix nivea</i> neotype strain (JP2(T)). <i>Standards in Genomic Sciences</i> , 2011 , 5, 398-406	9
163	Complete genome sequence of <i>Desulfurispirillum indicum</i> strain S5(T). <i>Standards in Genomic Sciences</i> , 2011 , 5, 371-8	8
162	Complete genome sequence of the thermophilic sulfur-reducer <i>Desulfurobacterium thermolithotrophum</i> type strain (BSA(T)) from a deep-sea hydrothermal vent. <i>Standards in Genomic Sciences</i> , 2011 , 5, 407-15	10
161	Complete genome sequence of " <i>Thioalkalivibrio sulfidophilus</i> " HL-EbGr7. <i>Standards in Genomic Sciences</i> , 2011 , 4, 23-35	51
160	Complete genome sequence of <i>Calditerrivibrio nitroreducens</i> type strain (Yu37-1). <i>Standards in Genomic Sciences</i> , 2011 , 4, 54-62	9
159	Complete genome sequence of <i>Truepera radiovictrix</i> type strain (RQ-24). <i>Standards in Genomic Sciences</i> , 2011 , 4, 91-9	37
158	Complete genome sequence of <i>Bacteroides salanitronis</i> type strain (BL78). <i>Standards in Genomic Sciences</i> , 2011 , 4, 191-9	8
157	Complete genome sequence of <i>Odoribacter splanchnicus</i> type strain (1651/6). <i>Standards in Genomic Sciences</i> , 2011 , 4, 200-9	62
156	Complete genome sequence of <i>Oceanithermus profundus</i> type strain (506). <i>Standards in Genomic Sciences</i> , 2011 , 4, 210-20	3

155	Complete genome sequence of Tsukamurella paurometabola type strain (no. 33). <i>Standards in Genomic Sciences</i> , 2011 , 4, 342-51		8
154	Complete genome sequence of Mycobacterium sp. strain (Spyr1) and reclassification to Mycobacterium gilvum Spyr1. <i>Standards in Genomic Sciences</i> , 2011 , 5, 144-53		19
153	Complete genome sequence of Thioalkalivibrio sp. K90mix. <i>Standards in Genomic Sciences</i> , 2011 , 5, 341-55		34
152	Complete genome sequence of Arthrobacter phenanthrenivorans type strain (Sphe3). <i>Standards in Genomic Sciences</i> , 2011 , 4, 123-30		23
151	ClAMS: A Classifier for Metagenomic Sequences. <i>Standards in Genomic Sciences</i> , 2011 , 5, 248-53		34
150	Non-contiguous finished genome sequence and contextual data of the filamentous soil bacterium Ktedonobacter racemifer type strain (SOSP1-21). <i>Standards in Genomic Sciences</i> , 2011 , 5, 97-111		72
149	Complete genome sequence of Isosphaera pallida type strain (IS1B). <i>Standards in Genomic Sciences</i> , 2011 , 4, 63-71		40
148	Complete genome sequence of Cellulophaga algicola type strain (IC166). <i>Standards in Genomic Sciences</i> , 2011 , 4, 72-80		22
147	Complete genome sequence of Riemerella anatipestifer type strain (ATCC 11845T). <i>Standards in Genomic Sciences</i> , 2011 , 4, 144-153		26
146	Complete genome sequence of the thermophilic sulfur-reducer Hippea maritima type strain (MH(2)). <i>Standards in Genomic Sciences</i> , 2011 , 4, 303-11		6
145	Complete genome sequence of Haliscomenobacter hydrossis type strain (O). <i>Standards in Genomic Sciences</i> , 2011 , 4, 352-60		17
144	Complete genome sequence of the gliding freshwater bacterium Fluviicola taffensis type strain (RW262). <i>Standards in Genomic Sciences</i> , 2011 , 5, 21-9		19
143	Genome sequence of the moderately thermophilic halophile Flexistipes sinusarabici strain (MAS10). <i>Standards in Genomic Sciences</i> , 2011 , 5, 86-96		8
142	Complete genome sequence of Deinococcus maricopensis type strain (LB-34). <i>Standards in Genomic Sciences</i> , 2011 , 4, 163-72		11
141	Exploring the symbiotic pangenome of the nitrogen-fixing bacterium Sinorhizobium meliloti. <i>BMC Genomics</i> , 2011 , 12, 235	4.5	83
140	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
139	Genome sequence of the Arctic methanotroph Methylobacter tundripaludum SV96. <i>Journal of Bacteriology</i> , 2011 , 193, 6418-9	3.5	50
138	The evolution of host specialization in the vertebrate gut symbiont Lactobacillus reuteri. <i>PLoS Genetics</i> , 2011 , 7, e1001314	6	203

137	Genomic potential of <i>Marinobacter aquaeolei</i> , a biogeochemical "opportunotroph". <i>Applied and Environmental Microbiology</i> , 2011 , 77, 2763-71	4.8	85
136	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
135	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
134	Complete genome sequence of the cellulolytic thermophile <i>Clostridium thermocellum</i> DSM1313. <i>Journal of Bacteriology</i> , 2011 , 193, 2906-7	3.5	63
133	Genome sequence of "Candidatus Frankia daticae" 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
132	Genome sequence of the mercury-methylating strain <i>Desulfovibrio desulfuricans</i> ND132. <i>Journal of Bacteriology</i> , 2011 , 193, 2078-9	3.5	33
131	Complete genome sequence of <i>Thermomonospora curvata</i> type strain (B9). <i>Standards in Genomic Sciences</i> , 2011 , 4, 13-22		24
130	SOP for pathway inference in Integrated Microbial Genomes (IMG). <i>Standards in Genomic Sciences</i> , 2011 , 5, 420-3		1
129	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
128	Complete genome sequence of <i>Syntrophobotulus glycolicus</i> type strain (FLGlyR). <i>Standards in Genomic Sciences</i> , 2011 , 4, 371-80		3
127	Complete genome sequence of <i>Riemerella anatipestifer</i> type strain (ATCC 11845). <i>Standards in Genomic Sciences</i> , 2011 , 4, 144-53		16
126	GenePRIMP: a gene prediction improvement pipeline for prokaryotic genomes. <i>Nature Methods</i> , 2010 , 7, 455-7	21.6	441
125	Metatranscriptomic array analysis of 'Candidatus Accumulibacter phosphatis'-enriched enhanced biological phosphorus removal sludge. <i>Environmental Microbiology</i> , 2010 , 12, 1205-17	5.2	67
124	A call for standardized classification of metagenome projects. <i>Environmental Microbiology</i> , 2010 , 12, 1803-5	5.2	23
123	The genome sequence of <i>Methanohalophilus mahii</i> 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
122	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
121	Estimating DNA coverage and abundance in metagenomes using a gamma approximation. <i>Bioinformatics</i> , 2010 , 26, 295-301	7.2	26
120	The integrated microbial genomes system: an expanding comparative analysis resource. <i>Nucleic Acids Research</i> , 2010 , 38, D382-90	20.1	210

119	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
118	Complete genome sequence of <i>Cellulomonas flavigena</i> type strain (134). <i>Standards in Genomic Sciences</i> , 2010 , 3, 15-25	31
117	Complete genome sequence of <i>Planctomyces limnophilus</i> type strain (M290). <i>Standards in Genomic Sciences</i> , 2010 , 3, 47-56	28
116	Permanent draft genome sequence of <i>Dethiosulfovibrio peptidovorans</i> type strain (SEBR 4207). <i>Standards in Genomic Sciences</i> , 2010 , 3, 85-92	8
115	Complete genome sequence of <i>Ferrimonas balearica</i> type strain (PAT). <i>Standards in Genomic Sciences</i> , 2010 , 3, 174-82	9
114	Non-contiguous finished genome sequence of <i>Aminomonas paucivorans</i> type strain (GLU-3). <i>Standards in Genomic Sciences</i> , 2010 , 3, 285-93	8
113	Complete genome sequence of <i>Ilyobacter polytropus</i> type strain (CuHbu1). <i>Standards in Genomic Sciences</i> , 2010 , 3, 304-14	7
112	Complete genome sequence of <i>Nocardiopsis dassonvillei</i> type strain (IMRU 509). <i>Standards in Genomic Sciences</i> , 2010 , 3, 325-36	27
111	Complete genome sequence of <i>Veillonella parvula</i> type strain (Te3). <i>Standards in Genomic Sciences</i> , 2010 , 2, 57-65	29
110	Complete genome sequence of <i>Kribbella flavida</i> type strain (IFO 14399). <i>Standards in Genomic Sciences</i> , 2010 , 2, 186-93	10
109	Complete genome sequence of <i>Conexibacter woesei</i> type strain (ID131577). <i>Standards in Genomic Sciences</i> , 2010 , 2, 212-9	15
108	Complete genome sequence of <i>Thermocrinis albus</i> type strain (HI 11/12). <i>Standards in Genomic Sciences</i> , 2010 , 2, 194-202	14
107	Complete genome sequence of <i>Meiothermus silvanus</i> type strain (VI-R2). <i>Standards in Genomic Sciences</i> , 2010 , 3, 37-46	16
106	Complete genome sequence of <i>Olsenella uli</i> type strain (VPI D76D-27C). <i>Standards in Genomic Sciences</i> , 2010 , 3, 76-84	27
105	Complete genome sequence of <i>Acidaminococcus fermentans</i> type strain (VR4). <i>Standards in Genomic Sciences</i> , 2010 , 3, 1-14	19
104	Complete genome sequence of <i>Meiothermus ruber</i> type strain (21). <i>Standards in Genomic Sciences</i> , 2010 , 3, 26-36	28
103	Complete genome sequence of <i>Acetohalobium arabaticum</i> type strain (Z-7288). <i>Standards in Genomic Sciences</i> , 2010 , 3, 57-65	16
102	Complete genome sequence of <i>Ignisphaera aggregans</i> type strain (AQ1.S1). <i>Standards in Genomic Sciences</i> , 2010 , 3, 66-75	13

101	Complete genome sequence of <i>Vulcanisaeta distributa</i> type strain (IC-017). <i>Standards in Genomic Sciences</i> , 2010 , 3, 117-25	8
100	Complete genome sequence of <i>Arcanobacterium haemolyticum</i> type strain (11018). <i>Standards in Genomic Sciences</i> , 2010 , 3, 126-35	7
99	Complete genome sequence of <i>Thermosediminibacter oceani</i> type strain (JW/IW-1228P). <i>Standards in Genomic Sciences</i> , 2010 , 3, 108-16	10
98	Complete genome sequence of <i>Spirochaeta smaragdinae</i> type strain (SEBR 4228). <i>Standards in Genomic Sciences</i> , 2010 , 3, 136-44	15
97	Complete genome sequence of 'Thermobaculum terrenum' type strain (YNP1). <i>Standards in Genomic Sciences</i> , 2010 , 3, 153-62	9
96	Complete genome sequence of <i>Syntrophothermus lipocalidus</i> type strain (TGB-C1). <i>Standards in Genomic Sciences</i> , 2010 , 3, 268-75	10
95	Complete genome sequence of <i>Desulfarculus baarsii</i> type strain (2st14). <i>Standards in Genomic Sciences</i> , 2010 , 3, 276-84	27
94	Complete genome sequence of <i>Intrasporangium calvum</i> type strain (7 KIP). <i>Standards in Genomic Sciences</i> , 2010 , 3, 294-303	4
93	Complete genome sequence of <i>Methanothermus fervidus</i> type strain (V24S). <i>Standards in Genomic Sciences</i> , 2010 , 3, 315-24	14
92	Complete genome sequence of <i>Thermaerobacter marianensis</i> type strain (7p75a). <i>Standards in Genomic Sciences</i> , 2010 , 3, 337-45	7
91	Complete genome sequence of the <i>Medicago</i> microsymbiont Ensifer (<i>Sinorhizobium</i>) <i>medicae</i> strain WSM419. <i>Standards in Genomic Sciences</i> , 2010 , 2, 77-86	80
90	Complete genome sequence of <i>Rhizobium leguminosarum</i> bv <i>trifolii</i> 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
89	Complete genome sequence of <i>Xylanimonas cellulolytica</i> type strain (XIL07). <i>Standards in Genomic Sciences</i> , 2010 , 2, 1-8	8
88	Complete genome sequence of <i>Alicyclobacillus acidocaldarius</i> type strain (104-IA). <i>Standards in Genomic Sciences</i> , 2010 , 2, 9-18	20
87	Complete genome sequence of <i>Sphaerobacter thermophilus</i> type strain (S 6022). <i>Standards in Genomic Sciences</i> , 2010 , 2, 49-56	20
86	Complete genome sequence of <i>Streptosporangium roseum</i> type strain (NI 9100). <i>Standards in Genomic Sciences</i> , 2010 , 2, 29-37	25
85	Complete genome sequence of <i>Chitinophaga pinensis</i> type strain (UQM 2034). <i>Standards in Genomic Sciences</i> , 2010 , 2, 87-95	57
84	Complete genome sequence of <i>Sulfurospirillum deleyianum</i> type strain (5175). <i>Standards in Genomic Sciences</i> , 2010 , 2, 149-57	24

83	Complete genome sequence of <i>Haloterrigena turkmenica</i> type strain (4k). <i>Standards in Genomic Sciences</i> , 2010 , 2, 107-16	28
82	Complete genome sequence of <i>Haliangium ochraceum</i> type strain (SMP-2). <i>Standards in Genomic Sciences</i> , 2010 , 2, 96-106	53
81	Complete genome sequence of <i>Geodermatophilus obscurus</i> type strain (G-20). <i>Standards in Genomic Sciences</i> , 2010 , 2, 158-67	49
80	Complete genome sequence of <i>Nakamurella multipartita</i> type strain (Y-104). <i>Standards in Genomic Sciences</i> , 2010 , 2, 168-75	28
79	Complete genome sequence of <i>Spirosoma linguale</i> type strain (1). <i>Standards in Genomic Sciences</i> , 2010 , 2, 176-85	35
78	Complete genome sequence of <i>Segniliparus rotundus</i> type strain (CDC 1076). <i>Standards in Genomic Sciences</i> , 2010 , 2, 203-11	9
77	Complete genome sequence of <i>Sebaldella termitidis</i> type strain (NCTC 11300). <i>Standards in Genomic Sciences</i> , 2010 , 2, 220-7	16
76	Complete genome sequence of <i>Thermosphaera aggregans</i> type strain (M11TL). <i>Standards in Genomic Sciences</i> , 2010 , 2, 245-59	12
75	Complete genome sequence of <i>Brachyspira murdochii</i> type strain (56-150). <i>Standards in Genomic Sciences</i> , 2010 , 2, 260-9	18
74	Complete genome sequence of <i>Aminobacterium colombiense</i> type strain (ALA-1). <i>Standards in Genomic Sciences</i> , 2010 , 2, 280-9	27
73	Complete genome sequence of <i>Arcobacter nitrofigilis</i> type strain (CI). <i>Standards in Genomic Sciences</i> , 2010 , 2, 300-8	32
72	Complete genome sequence of <i>Coralimargarita akajimensis</i> type strain (04OKA010-24). <i>Standards in Genomic Sciences</i> , 2010 , 2, 290-9	18
71	Complete genome sequence of <i>Thermobispora bispora</i> type strain (R51). <i>Standards in Genomic Sciences</i> , 2010 , 2, 318-26	18
70	Complete genome sequence of <i>Desulfohalobium retbaense</i> type strain (HR(100)). <i>Standards in Genomic Sciences</i> , 2010 , 2, 38-48	17
69	Complete genome sequence of <i>Archaeoglobus profundus</i> type strain (AV18). <i>Standards in Genomic Sciences</i> , 2010 , 2, 327-46	20
68	Complete genome sequence of <i>Denitrovibrio acetiphilus</i> type strain (N2460). <i>Standards in Genomic Sciences</i> , 2010 , 2, 270-9	11
67	Complete genome sequence of <i>Gordonia bronchialis</i> type strain (3410). <i>Standards in Genomic Sciences</i> , 2010 , 2, 19-28	19
66	Targeted discovery of glycoside hydrolases from a switchgrass-adapted compost community. <i>PLoS ONE</i> , 2010 , 5, e8812	3.7 154

65	Complete genome sequence of <i>Sulfurimonas autotrophica</i> type strain (OK10). <i>Standards in Genomic Sciences</i> , 2010 , 3, 194-202		32
64	Complete genome sequence of <i>Methanoplanus petrolearius</i> type strain (SEBR 4847). <i>Standards in Genomic Sciences</i> , 2010 , 3, 203-11		12
63	Genome analysis of the anaerobic thermohalophilic bacterium <i>Halothermothrix orenii</i> . <i>PLoS ONE</i> , 2009 , 4, e4192	3.7	54
62	IMG ER: a system for microbial genome annotation expert review and curation. <i>Bioinformatics</i> , 2009 , 25, 2271-8	7.2	742
61	Complete genome sequence of <i>Capnocytophaga ochracea</i> type strain (VPI 2845). <i>Standards in Genomic Sciences</i> , 2009 , 1, 101-9		12
60	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
59	A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea. <i>Nature</i> , 2009 , 462, 1056-60	50.4	803
58	Complete genome sequence of <i>Halorhabdus utahensis</i> type strain (AX-2). <i>Standards in Genomic Sciences</i> , 2009 , 1, 218-25		21
57	Complete genome sequence of <i>Beutenbergia cavernae</i> type strain (HKI 0122). <i>Standards in Genomic Sciences</i> , 2009 , 1, 21-8		11
56	Complete genome sequence of <i>Cryptobacterium curtum</i> type strain (12-3). <i>Standards in Genomic Sciences</i> , 2009 , 1, 93-100		13
55	Complete genome sequence of <i>Desulfomicrobium baculatum</i> type strain (X). <i>Standards in Genomic Sciences</i> , 2009 , 1, 29-37		30
54	Complete genome sequence of <i>Acidimicrobium ferrooxidans</i> type strain (ICP). <i>Standards in Genomic Sciences</i> , 2009 , 1, 38-45		27
53	Complete genome sequence of <i>Sanguibacter keddii</i> type strain (ST-74). <i>Standards in Genomic Sciences</i> , 2009 , 1, 110-8		10
52	Complete genome sequence of <i>Catenulispora acidiphila</i> type strain (ID 139908). <i>Standards in Genomic Sciences</i> , 2009 , 1, 119-25		19
51	Complete genome sequence of <i>Leptotrichia buccalis</i> type strain (C-1013-b). <i>Standards in Genomic Sciences</i> , 2009 , 1, 126-32		17
50	Complete genome sequence of <i>Saccharomonospora viridis</i> type strain (P101). <i>Standards in Genomic Sciences</i> , 2009 , 1, 141-9		21
49	Complete genome sequence of <i>Actinosynnema mirum</i> type strain (101). <i>Standards in Genomic Sciences</i> , 2009 , 1, 46-53		32
48	Complete genome sequence of <i>Pedobacter heparinus</i> type strain (HIM 762-3). <i>Standards in Genomic Sciences</i> , 2009 , 1, 54-62		19

47	Complete genome sequence of Halogeometricum borinquense type strain (PR3). <i>Standards in Genomic Sciences</i> , 2009 , 1, 150-9	22
46	Complete genome sequence of Anaerococcus prevotii type strain (PC1). <i>Standards in Genomic Sciences</i> , 2009 , 1, 159-65	18
45	Complete genome sequence of Atopobium parvulum type strain (IPP 1246). <i>Standards in Genomic Sciences</i> , 2009 , 1, 166-73	21
44	Complete genome sequence of Eggerthella lenta type strain (IPP VPI 0255). <i>Standards in Genomic Sciences</i> , 2009 , 1, 174-82	31
43	Complete genome sequence of Kangiella koreensis type strain (SW-125). <i>Standards in Genomic Sciences</i> , 2009 , 1, 226-33	10
42	Complete genome sequence of Jonesia denitrificans type strain (Prevot 55134). <i>Standards in Genomic Sciences</i> , 2009 , 1, 262-9	10
41	Complete genome sequence of Halomicrobium mukohataei type strain (arg-2). <i>Standards in Genomic Sciences</i> , 2009 , 1, 270-7	30
40	Complete genome sequence of Rhodothermus marinus type strain (R-10). <i>Standards in Genomic Sciences</i> , 2009 , 1, 283-90	20
39	Complete genome sequence of Streptobacillus moniliformis type strain (9901). <i>Standards in Genomic Sciences</i> , 2009 , 1, 300-7	16
38	Complete genome sequence of Pirellula staleyi type strain (ATCC 27377). <i>Standards in Genomic Sciences</i> , 2009 , 1, 308-16	26
37	Complete genome sequence of Kytococcus sedentarius type strain (541). <i>Standards in Genomic Sciences</i> , 2009 , 1, 12-20	94
36	Complete genome sequence of Dyadobacter fermentans type strain (NS114). <i>Standards in Genomic Sciences</i> , 2009 , 1, 133-40	19
35	Complete genome sequence of Thermanaerovibrio acidaminovorans type strain (Su883). <i>Standards in Genomic Sciences</i> , 2009 , 1, 254-61	19
34	The DOE-JGI Standard Operating Procedure for the Annotations of Microbial Genomes. <i>Standards in Genomic Sciences</i> , 2009 , 1, 63-7	177
33	Complete genome sequence of Slackia heliotrinireducens type strain (RHS 1). <i>Standards in Genomic Sciences</i> , 2009 , 1, 234-41	16
32	Complete genome sequence of Desulfotomaculum acetoxidans type strain (5575). <i>Standards in Genomic Sciences</i> , 2009 , 1, 242-53	33
31	Complete genome sequence of Stackebrandtia nassauensis type strain (LLR-40K-21). <i>Standards in Genomic Sciences</i> , 2009 , 1, 234-41	16
30	Gene context analysis in the Integrated Microbial Genomes (IMG) data management system. <i>PLoS ONE</i> , 2009 , 4, e7979	3.7 51

29	High-resolution metagenomics targets specific functional types in complex microbial communities. <i>Nature Biotechnology</i> , 2008 , 26, 1029-34	44.5	226
28	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
27	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
26	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
25	A bacterial metapopulation adapts locally to phage predation despite global dispersal. <i>Genome Research</i> , 2008 , 18, 293-7	9.7	119
24	Annotation of metagenome short reads using proxygenes. <i>Bioinformatics</i> , 2008 , 24, i7-13	7.2	35
23	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
22	IMG/M: a data management and analysis system for metagenomes. <i>Nucleic Acids Research</i> , 2008 , 36, D534-8	20.1	268
21	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
20	Use of simulated data sets to evaluate the fidelity of metagenomic processing methods. <i>Nature Methods</i> , 2007 , 4, 495-500	21.6	257
19	Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. <i>Nature</i> , 2007 , 450, 560-5	50.4	990
18	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
17	An experimental metagenome data management and analysis system. <i>Bioinformatics</i> , 2006 , 22, e359-67	7.2	72
16	The integrated microbial genomes (IMG) system. <i>Nucleic Acids Research</i> , 2006 , 34, D344-8	20.1	306
15	Metagenomic analysis of two enhanced biological phosphorus removal (EBPR) sludge communities. <i>Nature Biotechnology</i> , 2006 , 24, 1263-9	44.5	541
14	Symbiosis insights through metagenomic analysis of a microbial consortium. <i>Nature</i> , 2006 , 443, 950-5	50.4	339
13	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
12	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

11	The ERGO genome analysis and discovery system. <i>Nucleic Acids Research</i> , 2003 , 31, 164-71	20.1	173
10	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
9	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
8	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
7	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
6	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
5	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
4	Genomic Prospecting for Microbial Biodiesel Production405-418		4
3	The DOE JGI Metagenome Workflow		1
2	Cryptic inoviruses are pervasive in bacteria and archaea across Earth's biomes		2
1	A centimeter-long bacterium with DNA compartmentalized in membrane-bound organelles		1