

Miriam L Land

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313
papers

18,349
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126
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314
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23,353
ext. citations

6.7
avg, IF

5.87
L-index

#	Paper	IF	Citations
313	Prodigal: prokaryotic gene recognition and translation initiation site identification. <i>BMC Bioinformatics</i> , 2010 , 11, 119	3.6	4667
312	Genome divergence in two Prochlorococcus ecotypes reflects oceanic niche differentiation. <i>Nature</i> , 2003 , 424, 1042-7	50.4	904
311	Complete genome sequence of the metabolically versatile photosynthetic bacterium <i>Rhodospseudomonas palustris</i> . <i>Nature Biotechnology</i> , 2004 , 22, 55-61	44.5	553
310	Complete genome sequence of the ammonia-oxidizing bacterium and obligate chemolithoautotroph <i>Nitrosomonas europaea</i> . <i>Journal of Bacteriology</i> , 2003 , 185, 2759-73	3.5	436
309	KBase: The United States Department of Energy Systems Biology Knowledgebase. <i>Nature Biotechnology</i> , 2018 , 36, 566-569	44.5	419
308	Insights from 20 years of bacterial genome sequencing. <i>Functional and Integrative Genomics</i> , 2015 , 15, 141-61	3.8	391
307	Comparison of the complete genome sequences of <i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a and pv. <i>tomato</i> DC3000. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 11064-9	11.5	354
306	<i>Burkholderia xenovorans</i> LB400 harbors a multi-replicon, 9.73-Mbp genome shaped for versatility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 15280-7	11.5	280
305	Use of simulated data sets to evaluate the fidelity of metagenomic processing methods. <i>Nature Methods</i> , 2007 , 4, 495-500	21.6	257
304	Enigmatic, ultrasmall, uncultivated Archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 8806-11	11.5	231
303	Mechanisms of thermal adaptation revealed from the genomes of the Antarctic Archaea <i>Methanogenium frigidum</i> and <i>Methanococoides burtonii</i> . <i>Genome Research</i> , 2003 , 13, 1580-8	9.7	213
302	The evolution of host specialization in the vertebrate gut symbiont <i>Lactobacillus reuteri</i> . <i>PLoS Genetics</i> , 2011 , 7, e1001314	6	203
301	Genome of the epsilonproteobacterial chemolithoautotroph <i>Sulfurimonas denitrificans</i> . <i>Applied and Environmental Microbiology</i> , 2008 , 74, 1145-56	4.8	191
300	Human chromosome 19 and related regions in mouse: conservative and lineage-specific evolution. <i>Science</i> , 2001 , 293, 104-11	33.3	188
299	<i>Deinococcus geothermalis</i> : the pool of extreme radiation resistance genes shrinks. <i>PLoS ONE</i> , 2007 , 2, e955	3.7	179
298	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
297	Complete genome sequence of <i>Nitrosospora multiformis</i> , an ammonia-oxidizing bacterium from the soil environment. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 3559-72	4.8	158

296	Whole-genome analyses of speciation events in pathogenic Brucellae. <i>Infection and Immunity</i> , 2005 , 73, 8353-61	3.7	152
295	Community genomic and proteomic analyses of chemoautotrophic iron-oxidizing "Leptospirillum rubarum" (Group II) and "Leptospirillum ferrodiazotrophum" (Group III) bacteria in acid mine drainage biofilms. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 4599-615	4.8	149
294	Mutant alcohol dehydrogenase leads to improved ethanol tolerance in <i>Clostridium thermocellum</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 13752-7	11.5	147
293	Genome sequence of the chemolithoautotrophic nitrite-oxidizing bacterium <i>Nitrobacter winogradskyi</i> Nb-255. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 2050-63	4.8	141
292	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
291	Complete genome sequence of the complex carbohydrate-degrading marine bacterium, <i>Saccharophagus degradans</i> strain 2-40 T. <i>PLoS Genetics</i> , 2008 , 4, e1000087	6	132
290	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
289	Extending the <i>Bacillus cereus</i> group genomics to putative food-borne pathogens of different toxicity. <i>Chemico-Biological Interactions</i> , 2008 , 171, 236-49	5	128
288	Twenty-one genome sequences from <i>Pseudomonas</i> species and 19 genome sequences from diverse bacteria isolated from the rhizosphere and endosphere of <i>Populus deltoides</i> . <i>Journal of Bacteriology</i> , 2012 , 194, 5991-3	3.5	117
287	The fast changing landscape of sequencing technologies and their impact on microbial genome assemblies and annotation. <i>PLoS ONE</i> , 2012 , 7, e48837	3.7	112
286	The genome of deep-sea vent chemolithoautotroph <i>Thiomicrospira crunogena</i> XCL-2. <i>PLoS Biology</i> , 2006 , 4, e383	9.7	112
285	Global profiling of <i>Shewanella oneidensis</i> MR-1: expression of hypothetical genes and improved functional annotations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 2099-104	11.5	106
284	Comparison of single-molecule sequencing and hybrid approaches for finishing the genome of <i>Clostridium autoethanogenum</i> and analysis of CRISPR systems in industrial relevant Clostridia. <i>Biotechnology for Biofuels</i> , 2014 , 7, 40	7.8	105
283	The genome sequence of <i>Geobacter metallireducens</i> : features of metabolism, physiology and regulation common and dissimilar to <i>Geobacter sulfurreducens</i> . <i>BMC Microbiology</i> , 2009 , 9, 109	4.5	104
282	Paradigm for industrial strain improvement identifies sodium acetate tolerance loci in <i>Zymomonas mobilis</i> and <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 10395-400	11.5	103
281	Genomics of an extreme psychrophile, <i>Psychromonas ingrahamii</i> . <i>BMC Genomics</i> , 2008 , 9, 210	4.5	101
280	Multiple genome sequences reveal adaptations of a phototrophic bacterium to sediment microenvironments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 18543-8	11.5	100
279	Genome sequence of "Candidatus <i>Frankia datiscae</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

278	Evaluation and validation of de novo and hybrid assembly techniques to derive high-quality genome sequences. <i>Bioinformatics</i> , 2014 , 30, 2709-16	7.2	86
277	Genomic characterization of methanomicrobiales reveals three classes of methanogens. <i>PLoS ONE</i> , 2009 , 4, e5797	3.7	85
276	Improved genome annotation for <i>Zymomonas mobilis</i> . <i>Nature Biotechnology</i> , 2009 , 27, 893-4	44.5	84
275	Exploring the symbiotic pangenome of the nitrogen-fixing bacterium <i>Sinorhizobium meliloti</i> . <i>BMC Genomics</i> , 2011 , 12, 235	4.5	83
274	<i>Caldicellulosiruptor</i> core and pangenomes reveal determinants for noncellulosomal thermophilic deconstruction of plant biomass. <i>Journal of Bacteriology</i> , 2012 , 194, 4015-28	3.5	81
273	Complete genome sequence of the <i>Medicago</i> microsymbiont <i>Ensifer</i> (<i>Sinorhizobium</i>) <i>medicae</i> strain WSM419. <i>Standards in Genomic Sciences</i> , 2010 , 2, 77-86		80
272	Complete genome sequence of the filamentous anoxygenic phototrophic bacterium <i>Chloroflexus aurantiacus</i> . <i>BMC Genomics</i> , 2011 , 12, 334	4.5	77
271	Estimating the mean of data sets with nondetectable values. <i>Environmental Science & Technology</i> , 1990 , 24, 961-962	10.3	76
270	Construction and validation of the <i>Rhodobacter sphaeroides</i> 2.4.1 DNA microarray: transcriptome flexibility at diverse growth modes. <i>Journal of Bacteriology</i> , 2004 , 186, 4748-58	3.5	74
269	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
268	Sequencing of multiple clostridial genomes related to biomass conversion and biofuel production. <i>Journal of Bacteriology</i> , 2010 , 192, 6494-6	3.5	71
267	Complete genome sequences of six strains of the genus <i>Methylobacterium</i> . <i>Journal of Bacteriology</i> , 2012 , 194, 4746-8	3.5	70
266	The whole genome sequence of <i>Sphingobium chlorophenolicum</i> L-1: insights into the evolution of the pentachlorophenol degradation pathway. <i>Genome Biology and Evolution</i> , 2012 , 4, 184-98	3.9	68
265	Complete genome sequence of the cellulolytic thermophile <i>Clostridium thermocellum</i> DSM1313. <i>Journal of Bacteriology</i> , 2011 , 193, 2906-7	3.5	63
264	Complete genome sequence of <i>Odoribacter splanchnicus</i> type strain (1651/6). <i>Standards in Genomic Sciences</i> , 2011 , 4, 200-9		62
263	Complete genome of the cellulolytic ruminal bacterium <i>Ruminococcus albus</i> 7. <i>Journal of Bacteriology</i> , 2011 , 193, 5574-5	3.5	61
262	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
261	Complete genome sequence of <i>Chitinophaga pinensis</i> type strain (UQM 2034). <i>Standards in Genomic Sciences</i> , 2010 , 2, 87-95		57

260	Global transcriptome analysis of <i>Clostridium thermocellum</i> ATCC 27405 during growth on dilute acid pretreated <i>Populus</i> and switchgrass. <i>Biotechnology for Biofuels</i> , 2013 , 6, 179	7.8	53
259	Complete genome sequence of <i>Haliangium ochraceum</i> type strain (SMP-2). <i>Standards in Genomic Sciences</i> , 2010 , 2, 96-106		53
258	Diversity of <i>Pseudomonas</i> Genomes, Including <i>Populus</i> -Associated Isolates, as Revealed by Comparative Genome Analysis. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 375-83	4.8	50
257	Complete genome sequence of <i>Allochromatium vinosum</i> DSM 180(T). <i>Standards in Genomic Sciences</i> , 2011 , 5, 311-30		50
256	Genome sequence of the Arctic methanotroph <i>Methylobacter tundripaludum</i> SV96. <i>Journal of Bacteriology</i> , 2011 , 193, 6418-9	3.5	50
255	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, 4188-4	3.5	49
254	Complete genome sequence of <i>Geodermatophilus obscurus</i> type strain (G-20). <i>Standards in Genomic Sciences</i> , 2010 , 2, 158-67		49
253	Genome sequence of <i>Thermofilum pendens</i> reveals an exceptional loss of biosynthetic pathways without genome reduction. <i>Journal of Bacteriology</i> , 2008 , 190, 2957-65	3.5	49
252	Complete genome sequence of <i>Thauera aminoaromatica</i> strain MZ1T. <i>Standards in Genomic Sciences</i> , 2012 , 6, 325-35		47
251	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
250	Complete genome sequence and updated annotation of <i>Desulfovibrio alaskensis</i> G20. <i>Journal of Bacteriology</i> , 2011 , 193, 4268-9	3.5	46
249	Complete genome sequences of <i>Desulfosporosinus orientis</i> DSM765T, <i>Desulfosporosinus youngiae</i> DSM17734T, <i>Desulfosporosinus meridiei</i> DSM13257T, and <i>Desulfosporosinus acidiphilus</i> DSM22704T. <i>Journal of Bacteriology</i> , 2012 , 194, 6300-1	3.5	46
248	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
247	The genome of <i>Geobacter bemidjiensis</i> , exemplar for the subsurface clade of <i>Geobacter</i> species that predominate in Fe(III)-reducing subsurface environments. <i>BMC Genomics</i> , 2010 , 11, 490	4.5	46
246	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
245	Genome sequence of the methanotrophic alphaproteobacterium <i>Methylocystis</i> sp. strain Rockwell (ATCC 49242). <i>Journal of Bacteriology</i> , 2011 , 193, 2668-9	3.5	45
244	Complete genome sequence of <i>Dehalogenimonas lykanthroporepellens</i> type strain (BL-DC-9(T)) and comparison to "Dehalococcoides" strains. <i>Standards in Genomic Sciences</i> , 2012 , 6, 251-64		45
243	Complete genome sequence of the haloalkaliphilic, hydrogen-producing bacterium <i>Halanaerobium hydrogeniformans</i> . <i>Journal of Bacteriology</i> , 2011 , 193, 3682-3	3.5	41

242	Biological consequences of ancient gene acquisition and duplication in the large genome of <i>Candidatus Solibacter usitatus</i> Ellin6076. <i>PLoS ONE</i> , 2011 , 6, e24882	3.7	41
241	Enrichment of Root Endophytic Bacteria from <i>Populus deltoides</i> and Single-Cell-Genomics Analysis. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 5698-708	4.8	40
240	Complete genome sequence of <i>Isosphaera pallida</i> type strain (IS1B). <i>Standards in Genomic Sciences</i> , 2011 , 4, 63-71		40
239	Genome sequence of <i>Chthoniobacter flavus</i> Ellin428, an aerobic heterotrophic soil bacterium. <i>Journal of Bacteriology</i> , 2011 , 193, 2902-3	3.5	40
238	Complete Genome Sequence of <i>Clostridium clariflavum</i> DSM 19732. <i>Standards in Genomic Sciences</i> , 2012 , 6, 104-15		40
237	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> , 2011 , 4, 10		39
236	Complete genome sequence of <i>Desulfobulbus propionicus</i> type strain (1pr3). <i>Standards in Genomic Sciences</i> , 2011 , 4, 100-10		39
235	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
234	Complete genome sequence of <i>Truepera radiovictrix</i> type strain (RQ-24). <i>Standards in Genomic Sciences</i> , 2011 , 4, 91-9		37
233	Complete Genome sequence of <i>Burkholderia phymatum</i> STM815(T), a broad host range and efficient nitrogen-fixing symbiont of <i>Mimosa</i> species. <i>Standards in Genomic Sciences</i> , 2014 , 9, 763-74		36
232	Complete genome sequence of the cellulolytic thermophile <i>Caldicellulosiruptor obsidiansis</i> OB47T. <i>Journal of Bacteriology</i> , 2010 , 192, 6099-100	3.5	36
231	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
230	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
229	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
228	Complete genome sequence of <i>Spirosoma linguale</i> type strain (1). <i>Standards in Genomic Sciences</i> , 2010 , 2, 176-85		35
227	Ebolavirus comparative genomics. <i>FEMS Microbiology Reviews</i> , 2015 , 39, 764-78	15.1	34
226	Genome sequence of the verrucomicrobium <i>Opiritutus terrae</i> PB90-1, an abundant inhabitant of rice paddy soil ecosystems. <i>Journal of Bacteriology</i> , 2011 , 193, 2367-8	3.5	34
225	Cross-species global proteomics reveals conserved and unique processes in <i>Phytophthora sojae</i> and <i>Phytophthora ramorum</i> . <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 1501-16	7.6	34

224	Evaluation of "shotgun" proteomics for identification of biological threat agents in complex environmental matrixes: experimental simulations. <i>Analytical Chemistry</i> , 2005 , 77, 923-32	7.8	34
223	Quality scores for 32,000 genomes. <i>Standards in Genomic Sciences</i> , 2014 , 9, 20		33
222	Complete genome sequence of the Thermophilic Bacterium Exiguobacterium sp. AT1b. <i>Journal of Bacteriology</i> , 2011 , 193, 2880-1	3.5	33
221	Genome sequence of the mercury-methylating strain <i>Desulfovibrio desulfuricans</i> ND132. <i>Journal of Bacteriology</i> , 2011 , 193, 2078-9	3.5	33
220	Complete genome sequence of <i>Desulfotomaculum acetoxidans</i> type strain (5575). <i>Standards in Genomic Sciences</i> , 2009 , 1, 242-53		33
219	Complete genome sequence of <i>Anabaena variabilis</i> ATCC 29413. <i>Standards in Genomic Sciences</i> , 2014 , 9, 562-73		32
218	Complete genome sequence of <i>Actinosynnema mirum</i> type strain (101). <i>Standards in Genomic Sciences</i> , 2009 , 1, 46-53		32
217	Complete genome sequence of <i>Arcobacter nitrofigilis</i> type strain (CI). <i>Standards in Genomic Sciences</i> , 2010 , 2, 300-8		32
216	Complete genome sequence of <i>Sulfurimonas autotrophica</i> type strain (OK10). <i>Standards in Genomic Sciences</i> , 2010 , 3, 194-202		32
215	<i>Trichodesmium</i> genome maintains abundant, widespread noncoding DNA in situ, despite oligotrophic lifestyle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 4251-6	11.5	31
214	Complete genome sequence of <i>Rhodospirillum rubrum</i> type strain (S1). <i>Standards in Genomic Sciences</i> , 2011 , 4, 293-302		31
213	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
212	Complete genome sequence of <i>Cellulomonas flavigena</i> type strain (134). <i>Standards in Genomic Sciences</i> , 2010 , 3, 15-25		31
211	Genome sequence of <i>Amycolatopsis</i> sp. strain ATCC 39116, a plant biomass-degrading actinomycete. <i>Journal of Bacteriology</i> , 2012 , 194, 2396-7	3.5	31
210	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
209	Complete genome sequence of <i>Eggerthella lenta</i> type strain (IPP VPI 0255). <i>Standards in Genomic Sciences</i> , 2009 , 1, 174-82		31
208	Complete genome sequence of <i>Desulfomicrobium baculatum</i> type strain (X). <i>Standards in Genomic Sciences</i> , 2009 , 1, 29-37		30
207	Complete genome sequence of <i>Halomicrobium mukohataei</i> type strain (arg-2). <i>Standards in Genomic Sciences</i> , 2009 , 1, 270-7		30

206	Complete genome sequence of <i>Parvibaculum lavamentivorans</i> type strain (DS-1(T)). <i>Standards in Genomic Sciences</i> , 2011 , 5, 298-310		29
205	Genome sequences of <i>Alicyclophilus denitrificans</i> strains BC and K601T. <i>Journal of Bacteriology</i> , 2011 , 193, 5028-9	3.5	29
204	Complete genome sequence of <i>Veillonella parvula</i> type strain (Te3). <i>Standards in Genomic Sciences</i> , 2010 , 2, 57-65		29
203	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
202	Complete genome sequence of <i>Methanoculleus marisnigri</i> Romesser et al. 1981 type strain JR1. <i>Standards in Genomic Sciences</i> , 2009 , 1, 189-96		28
201	Complete genome sequence of <i>Planctomyces limnophilus</i> type strain (M290). <i>Standards in Genomic Sciences</i> , 2010 , 3, 47-56		28
200	Complete genome sequence of <i>Meiothermus ruber</i> type strain (21). <i>Standards in Genomic Sciences</i> , 2010 , 3, 26-36		28
199	Complete genome sequence of <i>Haloterrigena turkmenica</i> type strain (4k). <i>Standards in Genomic Sciences</i> , 2010 , 2, 107-16		28
198	Complete genome sequence of <i>Nakamurella multipartita</i> type strain (Y-104). <i>Standards in Genomic Sciences</i> , 2010 , 2, 168-75		28
197	Complete genome sequence of <i>Ferroglobus placidus</i> AEDII12DO. <i>Standards in Genomic Sciences</i> , 2011 , 5, 50-60		27
196	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
195	Complete Genome Sequence of <i>Paenibacillus</i> strain Y4.12MC10, a Novel <i>Paenibacillus lautus</i> strain Isolated from Obsidian Hot Spring in Yellowstone National Park. <i>Standards in Genomic Sciences</i> , 2012 , 6, 381-400		27
194	Complete genome sequence of <i>Acidimicrobium ferrooxidans</i> type strain (ICP). <i>Standards in Genomic Sciences</i> , 2009 , 1, 38-45		27
193	Complete genome sequence of <i>Nocardiopsis dassonvillei</i> type strain (IMRU 509). <i>Standards in Genomic Sciences</i> , 2010 , 3, 325-36		27
192	Complete genome sequence of <i>Olsenella uli</i> type strain (VPI D76D-27C). <i>Standards in Genomic Sciences</i> , 2010 , 3, 76-84		27
191	Complete genome sequence of <i>Desulfarculus baarsii</i> type strain (2st14). <i>Standards in Genomic Sciences</i> , 2010 , 3, 276-84		27
190	Complete genome sequence of <i>Aminobacterium colombiense</i> type strain (ALA-1). <i>Standards in Genomic Sciences</i> , 2010 , 2, 280-9		27
189	Benzene: environmental partitioning and human exposure. <i>Environmental Research</i> , 1990 , 53, 221-32	7.9	27

188	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
187	The genome of Pelobacter carbinolicus reveals surprising metabolic capabilities and physiological features. <i>BMC Genomics</i> , 2012 , 13, 690	4.5	26
186	Complete genome sequence of Riemerella anatipestifer type strain (ATCC 11845T). <i>Standards in Genomic Sciences</i> , 2011 , 4, 144-153		26
185	The complete genome sequence of Staphylothermus marinus reveals differences in sulfur metabolism among heterotrophic Crenarchaeota. <i>BMC Genomics</i> , 2009 , 10, 145	4.5	26
184	Complete genome sequence of the anaerobic, halophilic alkalithermophile Natranaerobius thermophilus JW/NM-WN-LF. <i>Journal of Bacteriology</i> , 2011 , 193, 4023-4	3.5	26
183	Complete genome sequence of Methanococcus labreanus type strain Z. <i>Standards in Genomic Sciences</i> , 2009 , 1, 197-203		26
182	Complete genome sequence of Pirellula staleyi type strain (ATCC 27377). <i>Standards in Genomic Sciences</i> , 2009 , 1, 308-16		26
181	Genome analysis and physiological comparison of Alicyclophilus denitrificans strains BC and K601(T). <i>PLoS ONE</i> , 2013 , 8, e66971	3.7	26
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42	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
41	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
40	Permanent draft genome sequence of <i>Dethiosulfovibrio peptidovorans</i> type strain (SEBR 4207). <i>Standards in Genomic Sciences</i> , 2010 , 3, 85-92	8
39	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
38	Complete genome sequence of <i>Vulcanisaeta distributa</i> type strain (IC-017). <i>Standards in Genomic Sciences</i> , 2010 , 3, 117-25	8
37	Complete genome sequence of <i>Xylanimonas cellulositytica</i> type strain (XIL07). <i>Standards in Genomic Sciences</i> , 2010 , 2, 1-8	8
36	Complete genome sequence of <i>Bacteroides helcogenes</i> type strain (P 36-108). <i>Standards in Genomic Sciences</i> , 2011 , 4, 45-53	7
35	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
34	Complete genome sequence of <i>Halopiger xanaduensis</i> type strain (SH-6(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 31-42	7
33	Complete genome sequence of <i>Staphylothermus marinus</i> Stetter and Fiala 1986 type strain F1. <i>Standards in Genomic Sciences</i> , 2009 , 1, 183-8	7
32	Complete genome sequence of <i>Ilyobacter polytropus</i> type strain (CuHbu1). <i>Standards in Genomic Sciences</i> , 2010 , 3, 304-14	7
31	Complete genome sequence of <i>Arcanobacterium haemolyticum</i> type strain (11018). <i>Standards in Genomic Sciences</i> , 2010 , 3, 126-35	7
30	Complete genome sequence of <i>Thermaerobacter marianensis</i> type strain (7p75a). <i>Standards in Genomic Sciences</i> , 2010 , 3, 337-45	7
29	Complete genome sequence of the bile-resistant pigment-producing anaerobe <i>Alistipes finegoldii</i> type strain (AHN2437(T)). <i>Standards in Genomic Sciences</i> , 2013 , 8, 26-36	6
28	Complete genome sequence of <i>Mahella australiensis</i> type strain (50-1 BON). <i>Standards in Genomic Sciences</i> , 2011 , 4, 331-41	6
27	Complete genome sequence of the thermophilic sulfur-reducer <i>Hippea maritima</i> type strain (MH(2)). <i>Standards in Genomic Sciences</i> , 2011 , 4, 303-11	6

26	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
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23	Complete genome sequence of <i>Coriobacterium glomerans</i> type strain (PW2(T)) from the midgut of <i>Pyrrhocoris apterus</i> L. (red soldier bug). <i>Standards in Genomic Sciences</i> , 2013 , 8, 15-25		5
22	Complete genome sequence of <i>Staphylothermus hellenicus</i> P8. <i>Standards in Genomic Sciences</i> , 2011 , 5, 12-20		5
21	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
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19	Genome sequence of the <i>Thermotoga thermarum</i> type strain (LA3(T)) from an African solfataric spring. <i>Standards in Genomic Sciences</i> , 2014 , 9, 1105-17		4
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16	Non-contiguous finished genome sequence of <i>Bacteroides coprosuis</i> type strain (PC139). <i>Standards in Genomic Sciences</i> , 2011 , 4, 233-43		4
15	Complete genome sequence of <i>Tolomonas auensis</i> type strain (TA 4). <i>Standards in Genomic Sciences</i> , 2011 , 5, 112-20		4
14	Complete genome sequence of <i>Intrasporangium calvum</i> type strain (7 KIP). <i>Standards in Genomic Sciences</i> , 2010 , 3, 294-303		4
13	Analysis and annotation of microbial genome sequences. <i>Genetic Engineering</i> , 2004 , 26, 225-38		4
12	Complete genome sequence of <i>Oceanithermus profundus</i> type strain (506). <i>Standards in Genomic Sciences</i> , 2011 , 4, 210-20		3
11	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
10	Complete genome sequence of <i>Syntrophobotulus glycolicus</i> type strain (FIGlyR). <i>Standards in Genomic Sciences</i> , 2011 , 4, 371-80		3
9	Complete genome sequence of the halophilic bacterium <i>Spirochaeta africana</i> 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

8	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
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