

# Alla L Lapidus

## List of Publications by Citations

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349  
papers

20,563  
citations

69  
h-index

133  
g-index

360  
ext. papers

25,631  
ext. citations

7.8  
avg, IF

5.98  
L-index

#	Paper	IF	Citations
349	Assembling single-cell genomes and mini-metagenomes from chimeric MDA products. <i>Journal of Computational Biology</i> , <b>2013</b> , 20, 714-37	1.7	815
348	A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea. <i>Nature</i> , <b>2009</b> , 462, 1056-60	50.4	803
347	Genome sequence of <i>Bacillus cereus</i> and comparative analysis with <i>Bacillus anthracis</i> . <i>Nature</i> , <b>2003</b> , 423, 87-91	50.4	670
346	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 725-731	44.5	648
345	The genomic basis of trophic strategy in marine bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 15527-33	11.5	472
344	The <i>Wolbachia</i> genome of <i>Brugia malayi</i> : endosymbiont evolution within a human pathogenic nematode. <i>PLoS Biology</i> , <b>2005</b> , 3, e121	9.7	452
343	Genome sequencing reveals complex secondary metabolome in the marine actinomycete <i>Salinispora tropica</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 10376-81	11.5	443
342	The plant cell wall-decomposing machinery underlies the functional diversity of forest fungi. <i>Science</i> , <b>2011</b> , 333, 762-5	33.3	417
341	Patterns and implications of gene gain and loss in the evolution of <i>Prochlorococcus</i> . <i>PLoS Genetics</i> , <b>2007</b> , 3, e231	6	397
340	Complete sequence and comparative genome analysis of the dairy bacterium <i>Streptococcus thermophilus</i> . <i>Nature Biotechnology</i> , <b>2004</b> , 22, 1554-8	44.5	397
339	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> , <b>2005</b> , 102, 11064-9	11.5	354
338	Environmental genomics reveals a single-species ecosystem deep within Earth. <i>Science</i> , <b>2008</b> , 322, 275-833.3	33.3	344
337	Genome characteristics of facultatively symbiotic <i>Frankia</i> sp. strains reflect host range and host plant biogeography. <i>Genome Research</i> , <b>2007</b> , 17, 7-15	9.7	296
336	A bioinformatician's guide to metagenomics. <i>Microbiology and Molecular Biology Reviews</i> , <b>2008</b> , 72, 557-78, Table of Contents	13.2	292
335	Assembling Genomes and Mini-metagenomes from Highly Chimeric Reads. <i>Lecture Notes in Computer Science</i> , <b>2013</b> , 158-170	0.9	288
334	Living with genome instability: the adaptation of phytoplasmas to diverse environments of their insect and plant hosts. <i>Journal of Bacteriology</i> , <b>2006</b> , 188, 3682-96	3.5	284
333	Genome sequence of the button mushroom <i>Agaricus bisporus</i> reveals mechanisms governing adaptation to a humic-rich ecological niche. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 17501-6	11.5	277

332	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus <i>Aspergillus</i> . <i>Genome Biology</i> , <b>2017</b> , 18, 28	18.3	261
331	Complete genome sequence of the industrial bacterium <i>Bacillus licheniformis</i> and comparisons with closely related <i>Bacillus</i> species. <i>Genome Biology</i> , <b>2004</b> , 5, R77	18.3	261
330	Use of simulated data sets to evaluate the fidelity of metagenomic processing methods. <i>Nature Methods</i> , <b>2007</b> , 4, 495-500	21.6	257
329	plasmidSPAdes: assembling plasmids from whole genome sequencing data. <i>Bioinformatics</i> , <b>2016</b> , 32, 3380-3387	7.2	233
328	High-resolution metagenomics targets specific functional types in complex microbial communities. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 1029-34	44.5	226
327	Comparative genomics of <i>Ceriporiopsis subvermispora</i> and <i>Phanerochaete chrysosporium</i> provide insight into selective ligninolysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 5458-63	11.5	225
326	Methylotrophy in <i>Methylobacterium extorquens</i> AM1 from a genomic point of view. <i>Journal of Bacteriology</i> , <b>2003</b> , 185, 2980-7	3.5	223
325	A korarchaeal genome reveals insights into the evolution of the Archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 8102-7	11.5	214
324	Comparative genomics of biotechnologically important yeasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 9882-7	11.5	212
323	The complete genome sequence of <i>Cupriavidus metallidurans</i> strain CH34, a master survivalist in harsh and anthropogenic environments. <i>PLoS ONE</i> , <b>2010</b> , 5, e10433	3.7	208
322	The evolution of host specialization in the vertebrate gut symbiont <i>Lactobacillus reuteri</i> . <i>PLoS Genetics</i> , <b>2011</b> , 7, e1001314	6	203
321	Genome of the epsilonproteobacterial chemolithoautotroph <i>Sulfurimonas denitrificans</i> . <i>Applied and Environmental Microbiology</i> , <b>2008</b> , 74, 1145-56	4.8	191
320	The genomes of the fungal plant pathogens <i>Cladosporium fulvum</i> and <i>Dothistroma septosporum</i> reveal adaptation to different hosts and lifestyles but also signatures of common ancestry. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1003088	6	189
319	One bacterial cell, one complete genome. <i>PLoS ONE</i> , <b>2010</b> , 5, e10314	3.7	184
318	Using SPAdes De Novo Assembler. <i>Current Protocols in Bioinformatics</i> , <b>2020</b> , 70, e102	24.2	182
317	<i>Deinococcus geothermalis</i> : the pool of extreme radiation resistance genes shrinks. <i>PLoS ONE</i> , <b>2007</b> , 2, e955	3.7	179
316	Novel features of the polysaccharide-digesting gliding bacterium <i>Flavobacterium johnsoniae</i> as revealed by genome sequence analysis. <i>Applied and Environmental Microbiology</i> , <b>2009</b> , 75, 6864-75	4.8	177
315	rnaSPAdes: a de novo transcriptome assembler and its application to RNA-Seq data. <i>GigaScience</i> , <b>2019</b> , 8,	7.6	170

314	Genome sequence and analysis of the soil cellulolytic actinomycete <i>Thermobifida fusca</i> YX. <i>Journal of Bacteriology</i> , <b>2007</b> , 189, 2477-86	3.5	167
313	Genomic islands link secondary metabolism to functional adaptation in marine Actinobacteria. <i>ISME Journal</i> , <b>2009</b> , 3, 1193-203	11.9	153
312	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , <b>2014</b> , 12, e1001920	9.7	146
311	Metabolic analysis of the soil microbe <i>Dechloromonas aromatica</i> str. RCB: indications of a surprisingly complex life-style and cryptic anaerobic pathways for aromatic degradation. <i>BMC Genomics</i> , <b>2009</b> , 10, 351	4.5	136
310	The <i>Methanosarcina barkeri</i> genome: comparative analysis with <i>Methanosarcina acetivorans</i> and <i>Methanosarcina mazei</i> reveals extensive rearrangement within methanosarcinal genomes. <i>Journal of Bacteriology</i> , <b>2006</b> , 188, 7922-31	3.5	136
309	Localized plasticity in the streamlined genomes of vinyl chloride respiring <i>Dehalococcoides</i> . <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000714	6	135
308	Comparative genomics of xylose-fermenting fungi for enhanced biofuel production. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 13212-7	11.5	131
307	The genome sequence of the psychrophilic archaeon, <i>Methanococcoides burtonii</i> : the role of genome evolution in cold adaptation. <i>ISME Journal</i> , <b>2009</b> , 3, 1012-35	11.9	128
306	Extending the <i>Bacillus cereus</i> group genomics to putative food-borne pathogens of different toxicity. <i>Chemico-Biological Interactions</i> , <b>2008</b> , 171, 236-49	5	128
305	MGnify: the microbiome analysis resource in 2020. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, D570-D578	20.1	127
304	Genome erosion in a nitrogen-fixing vertically transmitted endosymbiotic multicellular cyanobacterium. <i>PLoS ONE</i> , <b>2010</b> , 5, e11486	3.7	125
303	The genome of <i>Syntrophomonas wolfei</i> : new insights into syntrophic metabolism and biohydrogen production. <i>Environmental Microbiology</i> , <b>2010</b> , 12, 2289-301	5.2	120
302	Characterization of cyanobacterial hydrocarbon composition and distribution of biosynthetic pathways. <i>PLoS ONE</i> , <b>2014</b> , 9, e85140	3.7	114
301	The fast changing landscape of sequencing technologies and their impact on microbial genome assemblies and annotation. <i>PLoS ONE</i> , <b>2012</b> , 7, e48837	3.7	112
300	The genome of deep-sea vent chemolithoautotroph <i>Thiomicrospira crunogena</i> XCL-2. <i>PLoS Biology</i> , <b>2006</b> , 4, e383	9.7	112
299	The enigmatic planctomycetes may hold a key to the origins of methanogenesis and methylotrophy. <i>Molecular Biology and Evolution</i> , <b>2004</b> , 21, 1234-41	8.3	106
298	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> , <b>2009</b> , 9, 109	4.5	104
297	Transposable Elements versus the Fungal Genome: Impact on Whole-Genome Architecture and Transcriptional Profiles. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1006108	6	103

296	Complete genome of the cellulolytic thermophile <i>Acidothermus cellulolyticus</i> 11B provides insights into its ecophysiological and evolutionary adaptations. <i>Genome Research</i> , <b>2009</b> , 19, 1033-43	9.7	98
295	Comparative genomics of the white-rot fungi, <i>Phanerochaete carnosus</i> and <i>P. chrysosporium</i> , to elucidate the genetic basis of the distinct wood types they colonize. <i>BMC Genomics</i> , <b>2012</b> , 13, 444	4.5	97
294	Complete genome sequence of <i>Kytococcus sedentarius</i> type strain (541). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 12-20		94
293	A genomic analysis of the archaeal system <i>Ignicoccus hospitalis</i> - <i>Nanoarchaeum equitans</i> . <i>Genome Biology</i> , <b>2008</b> , 9, R158	18.3	92
292	A genomic perspective on the potential of <i>Actinobacillus succinogenes</i> for industrial succinate production. <i>BMC Genomics</i> , <b>2010</b> , 11, 680	4.5	85
291	Genomic characterization of methanomicrobiales reveals three classes of methanogens. <i>PLoS ONE</i> , <b>2009</b> , 4, e5797	3.7	85
290	The complete multipartite genome sequence of <i>Cupriavidus necator</i> JMP134, a versatile pollutant degrader. <i>PLoS ONE</i> , <b>2010</b> , 5, e9729	3.7	84
289	The genome of the xerotolerant mold <i>Wallemia sebi</i> reveals adaptations to osmotic stress and suggests cryptic sexual reproduction. <i>Fungal Genetics and Biology</i> , <b>2012</b> , 49, 217-26	3.9	83
288	Exploring the symbiotic pangenome of the nitrogen-fixing bacterium <i>Sinorhizobium meliloti</i> . <i>BMC Genomics</i> , <b>2011</b> , 12, 235	4.5	83
287	Genome of <i>Methylobacillus flagellatus</i> , molecular basis for obligate methylotrophy, and polyphyletic origin of methylotrophy. <i>Journal of Bacteriology</i> , <b>2007</b> , 189, 4020-7	3.5	83
286	ExSPAnDer: a universal repeat resolver for DNA fragment assembly. <i>Bioinformatics</i> , <b>2014</b> , 30, i293-301	7.2	80
285	Complete genome sequence of the <i>Medicago</i> microsymbiont <i>Ensifer</i> ( <i>Sinorhizobium</i> ) <i>medicagae</i> strain WSM419. <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 77-86		80
284	Complete genome sequence of the filamentous anoxygenic phototrophic bacterium <i>Chloroflexus aurantiacus</i> . <i>BMC Genomics</i> , <b>2011</b> , 12, 334	4.5	77
283	Complete genome sequence of the photosynthetic purple nonsulfur bacterium <i>Rhodobacter capsulatus</i> SB 1003. <i>Journal of Bacteriology</i> , <b>2010</b> , 192, 3545-6	3.5	77
282	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> , <b>2011</b> , 5, 97-111		72
281	Sequencing of multiple clostridial genomes related to biomass conversion and biofuel production. <i>Journal of Bacteriology</i> , <b>2010</b> , 192, 6494-6	3.5	71
280	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> , <b>2003</b> , 13, 1180-9	9.7	67
279	rnaQUAST: a quality assessment tool for de novo transcriptome assemblies. <i>Bioinformatics</i> , <b>2016</b> , 32, 2210-2	7.2	65

278	Comparative genome analysis of <i>Bacillus cereus</i> group genomes with <i>Bacillus subtilis</i> . <i>FEMS Microbiology Letters</i> , <b>2005</b> , 250, 175-84	2.9	64
277	Complete genome sequence of the cellulolytic thermophile <i>Clostridium thermocellum</i> DSM1313. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 2906-7	3.5	63
276	Complete genome sequence of <i>Odoribacter splanchnicus</i> type strain (1651/6). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 200-9		62
275	Genome-wide <i>Mycobacterium tuberculosis</i> variation (GMTV) database: a new tool for integrating sequence variations and epidemiology. <i>BMC Genomics</i> , <b>2014</b> , 15, 308	4.5	61
274	Complete genome of the cellulolytic ruminal bacterium <i>Ruminococcus albus</i> 7. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 5574-5	3.5	61
273	Massive changes in genome architecture accompany the transition to self-fertility in the filamentous fungus <i>Neurospora tetrasperma</i> . <i>Genetics</i> , <b>2011</b> , 189, 55-69	4	61
272	How to be moderately halophilic with broad salt tolerance: clues from the genome of <i>Chromohalobacter salexigens</i> . <i>Extremophiles</i> , <b>2005</b> , 9, 275-9	3	60
271	Whole-genome shotgun optical mapping of <i>Rhodospirillum rubrum</i> . <i>Applied and Environmental Microbiology</i> , <b>2005</b> , 71, 5511-22	4.8	59
270	Complete genome sequence of the aerobic marine methanotroph <i>Methylomonas methanica</i> MC09. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 7001-2	3.5	57
269	Complete genome sequence of <i>Chitinophaga pinensis</i> type strain (UQM 2034). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 87-95		57
268	Genome sequence of the Fleming strain of <i>Micrococcus luteus</i> , a simple free-living actinobacterium. <i>Journal of Bacteriology</i> , <b>2010</b> , 192, 841-60	3.5	55
267	Genome analysis of the anaerobic thermohalophilic bacterium <i>Halothermothrix orenii</i> . <i>PLoS ONE</i> , <b>2009</b> , 4, e4192	3.7	54
266	Complete genome sequence of <i>Haliangium ochraceum</i> type strain (SMP-2). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 96-106		53
265	Complete genome sequence of " <i>Thioalkalivibrio sulfidophilus</i> " HL-EbGr7. <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 23-35		51
264	Genome sequence of the 1,4-dioxane-degrading <i>Pseudonocardia dioxanivorans</i> strain CB1190. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 4549-50	3.5	51
263	Genome sequence of the Arctic methanotroph <i>Methylobacter tundripaludum</i> SV96. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 6418-9	3.5	50
262	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> , <b>2011</b> , 193, 1483-4	3.5	49
261	Complete genome sequence of <i>Geodermatophilus obscurus</i> type strain (G-20). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 158-67		49

260	Genome sequence of <i>Thermofilum pendens</i> reveals an exceptional loss of biosynthetic pathways without genome reduction. <i>Journal of Bacteriology</i> , <b>2008</b> , 190, 2957-65	3.5	49
259	Plasmid detection and assembly in genomic and metagenomic data sets. <i>Genome Research</i> , <b>2019</b> , 29, 961-968	9.7	48
258	Complete genome sequence of <i>Thauera aminoaromatica</i> strain MZ1T. <i>Standards in Genomic Sciences</i> , <b>2012</b> , 6, 325-35		47
257	Complete genome sequence and updated annotation of <i>Desulfovibrio alaskensis</i> G20. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 4268-9	3.5	46
256	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> , <b>2012</b> , 194, 6300-1	3.5	46
255	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> , <b>2012</b> , 6, 181-200		46
254	Genome sequence of the methanotrophic alphaproteobacterium <i>Methylocystis</i> sp. strain Rockwell (ATCC 49242). <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 2668-9	3.5	45
253	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> , <b>2012</b> , 6, 251-64		45
252	Metaviral SPAdes: assembly of viruses from metagenomic data. <i>Bioinformatics</i> , <b>2020</b> , 36, 4126-4129	7.2	44
251	Genomes of three methylotrophs from a single niche reveal the genetic and metabolic divergence of the methylphilaceae. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 3757-64	3.5	42
250	Complete genome sequence of <i>Syntrophobacter fumaroxidans</i> strain (MPOB(T)). <i>Standards in Genomic Sciences</i> , <b>2012</b> , 7, 91-106		42
249	Complete genome sequence of <i>Isosphaera pallida</i> type strain (IS1B). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 63-71		40
248	Genome sequence of <i>Chthoniobacter flavus</i> Ellin428, an aerobic heterotrophic soil bacterium. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 2902-3	3.5	40
247	Fungi Contribute Critical but Spatially Varying Roles in Nitrogen and Carbon Cycling in Acid Mine Drainage. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 238	5.7	40
246	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> , <b>2014</b> , 9, 10		39
245	Complete genome sequence of <i>Desulfobulbus propionicus</i> type strain (1pr3). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 100-10		39
244	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> , <b>2010</b> , 2, 66-76		39
243	Facile recovery of individual high-molecular-weight, low-copy-number natural plasmids for genomic sequencing. <i>Applied and Environmental Microbiology</i> , <b>2006</b> , 72, 4899-906	4.8	39

242	The genetically remote pathogenic strain NVH391-98 of the <i>Bacillus cereus</i> group is representative of a cluster of thermophilic strains. <i>Applied and Environmental Microbiology</i> , <b>2008</b> , 74, 1276-80	4.8	38
241	Complete genome sequence of <i>Truepera radiovictrix</i> type strain (RQ-24). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 91-9		37
240	Complete genome sequence of the filamentous gliding predatory bacterium <i>Herpetosiphon aurantiacus</i> type strain (114-95(T)). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 5, 356-70		35
239	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> , <b>2011</b> , 5, 121-34		35
238	Complete genome sequence of <i>Spirosoma linguale</i> type strain (1). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 176-85		35
237	Complete genome sequence of <i>Thioalkalivibrio</i> sp. K90mix. <i>Standards in Genomic Sciences</i> , <b>2011</b> , 5, 341-55		34
236	Genome sequence of the verrucomicrobium <i>Opitutus terrae</i> PB90-1, an abundant inhabitant of rice paddy soil ecosystems. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 2367-8	3.5	34
235	CD45-deficient severe combined immunodeficiency caused by uniparental disomy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 10456-61	11.5	33
234	Complete genome sequence of the Thermophilic Bacterium <i>Exiguobacterium</i> sp. AT1b. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 2880-1	3.5	33
233	Genome sequence of the mercury-methylating strain <i>Desulfovibrio desulfuricans</i> ND132. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 2078-9	3.5	33
232	Complete genome sequence of <i>Desulfotomaculum acetoxidans</i> type strain (5575). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 242-53		33
231	Complete genome sequence of <i>Actinosynnema mirum</i> type strain (101). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 46-53		32
230	Complete genome sequence of <i>Arcobacter nitrofigilis</i> type strain (CI). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 300-8		32
229	The <i>Rhodobacter capsulatus</i> genome. <i>Photosynthesis Research</i> , <b>2001</b> , 70, 43-52	3.7	32
228	Complete genome sequence of <i>Sulfurimonas autotrophica</i> type strain (OK10). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 194-202		32
227	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> , <b>2015</b> , 10, 1		31
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222	Complete genome sequence of <i>Eggerthella lenta</i> type strain (IPP VPI 0255). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 174-82		31
221	Complete genome sequence of <i>Desulfomicrobium baculatum</i> type strain (X). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 29-37		30
220	Complete genome sequence of <i>Halomicrobium mukohataei</i> type strain (arg-2). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 270-7		30
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204	Complete genome sequence of <i>Desulfarculus baarsii</i> type strain (2st14). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 276-84		27
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91	Complete genome sequence of <i>Syntrophothermus lipocalidus</i> type strain (TGB-C1). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 268-75	10
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79	High quality draft genome sequence of <i>Olivibacter sitiensis</i> type strain (AW-6(T)), a diphenol degrader with genes involved in the catechol pathway. <i>Standards in Genomic Sciences</i> , <b>2014</b> , 9, 783-93		8
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74	Complete genome sequence of <i>Hirschia baltica</i> type strain (IFAM 1418(T)). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 5, 287-97		8
73	Complete genome sequence of <i>Bacteroides salanitronis</i> type strain (BL78). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 191-9		8
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62	Complete genome sequence of <i>Bacteroides helcogenes</i> type strain (P 36-108). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 45-53		7
61	Complete genome sequence of the orange-red pigmented, radioresistant <i>Deinococcus proteolyticus</i> type strain (MRP(T)). <i>Standards in Genomic Sciences</i> , <b>2012</b> , 6, 240-50		7
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59	Complete genome sequence of <i>Staphylothermus marinus</i> Stetter and Fiala 1986 type strain F1. <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 183-8		7
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