

Alla L Lapidus

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.

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	The lineage of coronavirus SARS-CoV-2 of Russian origin: Genetic characteristics and correlations with clinical parameters and severity of coronavirus infection. <i>Sibirskij žurnal Kliničeskoj i Eksperimental'noj Mediciny</i> , 2022 , 36, 132-143	0.3	0
348	Metagenomic Data Assembly - The Way of Decoding Unknown Microorganisms. <i>Frontiers in Microbiology</i> , 2021 , 12, 613791	5.7	20
347	Elemental and Molecular Composition of Humic Acids Isolated from Soils of Tallgrass Temperate Rainforests (Chernevaya taiga) by 1H-13C HECTCOR NMR Spectroscopy. <i>Agronomy</i> , 2021 , 11, 1998	3.6	3
346	Using SPAdes De Novo Assembler. <i>Current Protocols in Bioinformatics</i> , 2020 , 70, e102	24.2	182
345	A New Thioalkalivibrio sp. Strain Isolated from Petroleum-Contaminated Brackish Estuary Sediments: A New Candidate for Bio-Based Application for Sulfide Oxidation in Halo-Alkaline Conditions. <i>Water (Switzerland)</i> , 2020 , 12, 1385	3	1
344	Metaviral SPAdes: assembly of viruses from metagenomic data. <i>Bioinformatics</i> , 2020 , 36, 4126-4129	7.2	44
343	MGnify: the microbiome analysis resource in 2020. <i>Nucleic Acids Research</i> , 2020 , 48, D570-D578	20.1	127
342	Mixotrophic Iron-Oxidizing Isolates from an Acid Mine Drainage-Affected Creek. <i>Applied and Environmental Microbiology</i> , 2020 , 86,	4.8	2
341	CDSnake: Snakemake pipeline for retrieval of annotated OTUs from paired-end reads using CD-HIT utilities. <i>BMC Bioinformatics</i> , 2020 , 21, 303	3.6	0
340	Extending rnaSPAdes functionality for hybrid transcriptome assembly. <i>BMC Bioinformatics</i> , 2020 , 21, 302	3.6	8
339	rnaSPAdes: a de novo transcriptome assembler and its application to RNA-Seq data. <i>GigaScience</i> , 2019 , 8,	7.6	170
338	Plasmid detection and assembly in genomic and metagenomic data sets. <i>Genome Research</i> , 2019 , 29, 961-968	9.7	48
337	Sequence Analysis 2019 , 292-322		3
336	IonHammer: Homopolymer-Space Hamming Clustering for IonTorrent Read Error Correction. <i>Journal of Computational Biology</i> , 2019 , 26, 124-127	1.7	2
335	Autoprotobiotics as an Approach for Restoration of Personalised Microbiota. <i>Frontiers in Microbiology</i> , 2018 , 9, 1869	5.7	16
334	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus <i>Aspergillus</i> . <i>Genome Biology</i> , 2017 , 18, 28	18.3	261
333	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

332	Permanent Draft Genome Sequence of Strain Z-533, a Peptide and Starch Degradator Isolated from Thermal Springs in the Kamchatka Peninsula and Kunashir Island, Russia. <i>Genome Announcements</i> , 2017 , 5,		2
331	Draft genome sequence of strain AHT1, a gram-positive sulfidogenic polyextremophile. <i>Standards in Genomic Sciences</i> , 2017 , 12, 57		7
330	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
329	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
328	Complete Mitochondrial Genomes of Baikal Oilfishes (Perciformes: Cottoidei), Earth's Deepest-Swimming Freshwater Fishes. <i>Mitochondrial DNA Part B: Resources</i> , 2017 , 2, 773-775	0.5	1
327	Comparative genomics of biotechnologically important yeasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 9882-7	11.5	212
326	Complete Genome Sequence of <i>Alkaliphilus metalliredigens</i> Strain QYMF, an Alkaliphilic and Metal-Reducing Bacterium Isolated from Borax-Contaminated Leachate Ponds. <i>Genome Announcements</i> , 2016 , 4,		5
325	Complete genome sequence of the Antarctic <i>Halorubrum lacusprofundi</i> type strain ACAM 34. <i>Standards in Genomic Sciences</i> , 2016 , 11, 70		15
324	Complete genome sequence of the haloalkaliphilic, obligately chemolithoautotrophic thiosulfate and sulfide-oxidizing β proteobacterium <i>Thioalkalimicrobium cyclicum</i> type strain ALM 1 (DSM 14477(T)). <i>Standards in Genomic Sciences</i> , 2016 , 11, 38		5
323	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
322	Draft genome of CCAP 1490/1 (CALU1027), the chlorophyll containing filamentous cyanobacterium. <i>Standards in Genomic Sciences</i> , 2016 , 11, 82		
321	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
320	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
319	Complete genome sequence of <i>Methanospirillum hungatei</i> type strain JF1. <i>Standards in Genomic Sciences</i> , 2016 , 11, 2		23
318	High quality permanent draft genome sequence of <i>Phaseolibacter flectens</i> ATCC 12775(T), a plant pathogen of French bean pods. <i>Standards in Genomic Sciences</i> , 2016 , 11, 4		1
317	Fungi Contribute Critical but Spatially Varying Roles in Nitrogen and Carbon Cycling in Acid Mine Drainage. <i>Frontiers in Microbiology</i> , 2016 , 7, 238	5.7	40
316	Transposable Elements versus the Fungal Genome: Impact on Whole-Genome Architecture and Transcriptional Profiles. <i>PLoS Genetics</i> , 2016 , 12, e1006108	6	103
315	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

314	rnaQUAST: a quality assessment tool for de novo transcriptome assemblies. <i>Bioinformatics</i> , 2016 , 32, 2210-2	7.2	65
313	plasmidSPAdes: assembling plasmids from whole genome sequencing data. <i>Bioinformatics</i> , 2016 , 32, 3380-3387	7.2	233
312	IgRepertoireConstructor: a novel algorithm for antibody repertoire construction and immunoproteogenomics analysis. <i>Bioinformatics</i> , 2015 , 31, i53-61	7.2	27
311	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
310	Consortium of the Dichlorophyllous Cyanobacterium <i>Prochlorothrix hollandica</i> and chemoheterotrophic partner bacteria: culture and metagenome-based description. <i>Environmental Microbiology Reports</i> , 2015 , 7, 623-33	3.7	5
309	Complete Genome Sequence of <i>Anaeromyxobacter</i> sp. Fw109-5, an Anaerobic, Metal-Reducing Bacterium Isolated from a Contaminated Subsurface Environment. <i>Genome Announcements</i> , 2015 , 3,		10
308	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
307	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
306	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
305	Sequencing, biochemical characterization, crystal structure and molecular dynamics of cellobiohydrolase Cel7A from <i>Geotrichum candidum</i> 3C. <i>FEBS Journal</i> , 2015 , 282, 4515-37	5.7	27
304	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
303	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
302	High-quality permanent draft genome sequence of the extremely osmotolerant diphenol degrading bacterium <i>Halotalea alkalilenta</i> AW-7(T), and emended description of the genus <i>Halotalea</i> . <i>Standards in Genomic Sciences</i> , 2015 , 10, 52		4
301	Genome Sequence of the Atypical Symbiotic <i>Frankia</i> R43 Strain, a Nitrogen-Fixing and Hydrogen-Producing Actinobacterium. <i>Genome Announcements</i> , 2015 , 3,		18
300	High quality draft genome sequence of <i>Flavobacterium rivuli</i> 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
299	High quality draft genome sequence of <i>Corynebacterium ulceribovis</i> type strain IMMIB-L1395(T) (DSM 45146(T)). <i>Standards in Genomic Sciences</i> , 2015 , 10, 50		1
298	Complete genome sequence of the phenanthrene-degrading soil bacterium <i>Delftia acidovorans</i> Cs1-4. <i>Standards in Genomic Sciences</i> , 2015 , 10, 55		17
297	IgSimulator: a versatile immunosequencing simulator. <i>Bioinformatics</i> , 2015 , 31, 3213-5	7.2	21

296	High quality draft genome sequence of <i>Leucobacter chironomi</i> strain MM2LB(T) (DSM 19883(T)) isolated from a <i>Chironomus</i> sp. egg mass. <i>Standards in Genomic Sciences</i> , 2015 , 10, 21		6
295	High-Quality Draft Genome Sequence of <i>Desulfovibrio carbinoliphilus</i> FW-101-2B, an Organic Acid-Oxidizing Sulfate-Reducing Bacterium Isolated from Uranium(VI)-Contaminated Groundwater. <i>Genome Announcements</i> , 2015 , 3,		1
294	Genome-wide <i>Mycobacterium tuberculosis</i> variation (GMTV) database: a new tool for integrating sequence variations and epidemiology. <i>BMC Genomics</i> , 2014 , 15, 308	4.5	61
293	Complete genome sequence of <i>Planctomyces brasiliensis</i> type strain (DSM 5305(T)), phylogenomic analysis and reclassification of Planctomycetes including the descriptions of <i>Gimesia</i> gen. nov., <i>Planctopirus</i> gen. nov. and <i>Rubinisphaera</i> gen. nov. and emended descriptions of the order Planctomycetales and the family Planctomycetaceae. <i>Standards in Genomic Sciences</i> , 2014 , 9, 10		39
292	Genome sequence and emended description of <i>Leisingera nanhaiensis</i> strain DSM 24252(T) isolated from marine sediment. <i>Standards in Genomic Sciences</i> , 2014 , 9, 687-703		5
291	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
290	Genome analyses of the carboxydrotrophic sulfate-reducers <i>Desulfotomaculum nigrificans</i> and <i>Desulfotomaculum carboxydivorans</i> and reclassification of <i>Desulfotomaculum caboxydivorans</i> as a later synonym of <i>Desulfotomaculum nigrificans</i> . <i>Standards in Genomic Sciences</i> , 2014 , 9, 655-75		17
289	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> , 2014 , 9, 783-93		8
288	Genome sequence of the mud-dwelling archaeon <i>Methanoplanus limicola</i> type strain (DSM 2279(T)), reclassification of <i>Methanoplanus petrolearius</i> as <i>Methanolacinia petrolearia</i> and emended descriptions of the genera <i>Methanoplanus</i> and <i>Methanolacinia</i> . <i>Standards in Genomic Sciences</i> , 2014 , 9, 1076-88		10
287	High quality draft genome sequence of the slightly halophilic bacterium <i>Halomonas zhanjiangensis</i> 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
286	Characterization of cyanobacterial hydrocarbon composition and distribution of biosynthetic pathways. <i>PLoS ONE</i> , 2014 , 9, e85140	3.7	114
285	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , 2014 , 12, e1001920	9.7	146
284	ExSPAnDer: a universal repeat resolver for DNA fragment assembly. <i>Bioinformatics</i> , 2014 , 30, i293-301	7.2	80
283	Assembling Genomes and Mini-metagenomes from Highly Chimeric Reads. <i>Lecture Notes in Computer Science</i> , 2013 , 158-170	0.9	288
282	Assembling single-cell genomes and mini-metagenomes from chimeric MDA products. <i>Journal of Computational Biology</i> , 2013 , 20, 714-37	1.7	815
281	Genome Sequence of the Obligate Gammaproteobacterial Methanotroph <i>Methylomicrobium album</i> Strain BG8. <i>Genome Announcements</i> , 2013 , 1, e0017013		16
280	Complete Genome Sequence of the Hyperthermophilic Sulfate-Reducing Bacterium <i>Thermodesulfobacterium geofontis</i> OPF15T. <i>Genome Announcements</i> , 2013 , 1, e0016213		4
279	Correction for Morin et al., 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> , 2013 , 110, 4146-4146	11.5	4

278	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	
277	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	
276	High-quality-draft genome sequence of the yellow-pigmented flavobacterium <i>Joostella marina</i> type strain (En5(T)). <i>Standards in Genomic Sciences</i> , 2013 , 8, 37-46	4	
275	Complete genome sequence of the moderate thermophile <i>Anaerobaculum mobile</i> type strain (NGA(T)). <i>Standards in Genomic Sciences</i> , 2013 , 8, 47-57	10	
274	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	
273	Complete genome sequence of <i>Halorhodospira halophila</i> SL1. <i>Standards in Genomic Sciences</i> , 2013 , 8, 206-14	13	
272	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	
271	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	
270	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	
269	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	
268	Genome sequence of the thermophilic fresh-water bacterium <i>Spirochaeta caldaria</i> type strain (H1(T)), reclassification of <i>Spirochaeta caldaria</i> , <i>Spirochaeta stenostrepta</i> , and <i>Spirochaeta zuelzeri</i> in the genus <i>Treponema</i> as <i>Treponema caldaria</i> comb. nov., <i>Treponema stenostrepta</i> comb. nov., and <i>Treponema zuelzeri</i> comb. nov., and emendation of the genus <i>Treponema</i> .	24	
267	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	
266	Genome sequence of the phylogenetically isolated spirochete <i>Leptonema illini</i> type strain (3055(T)). <i>Standards in Genomic Sciences</i> , 2013 , 8, 177-87	4	
265	Genome sequence of <i>Phaeobacter daeponensis</i> type strain (DSM 23529(T)), a facultatively anaerobic bacterium isolated from marine sediment, and emendation of <i>Phaeobacter daeponensis</i> . <i>Standards in Genomic Sciences</i> , 2013 , 9, 142-59	10	
264	Complete genome sequence of the marine methyl-halide oxidizing <i>Leisingera methylohalidivorans</i> type strain (DSM 14336(T)), a representative of the <i>Roseobacter</i> clade. <i>Standards in Genomic Sciences</i> , 2013 , 9, 128-41	13	
263	Genome sequence of <i>Phaeobacter caeruleus</i> type strain (DSM 24564(T)), a surface-associated member of the marine <i>Roseobacter</i> clade. <i>Standards in Genomic Sciences</i> , 2013 , 8, 403-19	12	
262	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> , 2012 , 109, 17501-6	11.5	277
261	CD45-deficient severe combined immunodeficiency caused by uniparental disomy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 10456-61	11.5	33

260	The genome of the xerotolerant mold <i>Walleimia sebi</i> reveals adaptations to osmotic stress and suggests cryptic sexual reproduction. <i>Fungal Genetics and Biology</i> , 2012 , 49, 217-26	3.9	83
259	Comparative genomics of the white-rot fungi, <i>Phanerochaete carnososa</i> and <i>P. chrysosporium</i> , to elucidate the genetic basis of the distinct wood types they colonize. <i>BMC Genomics</i> , 2012 , 13, 444	4.5	97
258	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
257	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> , 2012 , 109, 5458-63	11.5	225
256	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
255	The genomes of the fungal plant pathogens <i>Cladosporium fulvum</i> and <i>Dothistroma septosporium</i> reveal adaptation to different hosts and lifestyles but also signatures of common ancestry. <i>PLoS Genetics</i> , 2012 , 8, e1003088	6	189
254	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
253	Complete genome sequence of the thermophilic, piezophilic, heterotrophic bacterium <i>Marinitoga piezophila</i> KA3. <i>Journal of Bacteriology</i> , 2012 , 194, 5974-5	3.5	18
252	Complete genome sequence of <i>Desulfurococcus fermentans</i> , a hyperthermophilic cellulolytic crenarchaeon isolated from a freshwater hot spring in Kamchatka, Russia. <i>Journal of Bacteriology</i> , 2012 , 194, 5703-4	3.5	11
251	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
250	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
249	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
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	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
246	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
245	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
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 <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

242	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
241	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
240	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
239	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
238	Complete genome sequence of the thermophilic sulfate-reducing ocean bacterium <i>Thermodesulfator indicus</i> type strain (CIR29812(T)). <i>Standards in Genomic Sciences</i> , 2012 , 6, 155-64	9
237	Complete genome sequence of <i>Thauera aminoaromatica</i> strain MZ1T. <i>Standards in Genomic Sciences</i> , 2012 , 6, 325-35	47
236	Complete genome sequence of <i>Serratia plymuthica</i> strain AS12. <i>Standards in Genomic Sciences</i> , 2012 , 6, 165-73	15
235	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
234	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
233	Complete genome sequence of the plant-associated <i>Serratia plymuthica</i> strain AS13. <i>Standards in Genomic Sciences</i> , 2012 , 7, 22-30	16
232	Complete genome sequence of <i>Syntrophobacter fumaroxidans</i> strain (MPOB(T)). <i>Standards in Genomic Sciences</i> , 2012 , 7, 91-106	42
231	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
230	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
229	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
228	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
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