

Alla L Lapidus

List of Publications by Year in descending order

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349
papers

28,592
citations

9264

74
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7518

151
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360
docs citations

360
times ranked

30100
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	17.5	1,512
2	Assembling Single-Cell Genomes and Mini-Metagenomes From Chimeric MDA Products. <i>Journal of Computational Biology</i> , 2013, 20, 714-737.	1.6	1,235
3	Using SPAdes De Novo Assembler. <i>Current Protocols in Bioinformatics</i> , 2020, 70, e102.	25.8	1,113
4	A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea. <i>Nature</i> , 2009, 462, 1056-1060.	27.8	924
5	Genome sequence of <i>Bacillus cereus</i> and comparative analysis with <i>Bacillus anthracis</i> . <i>Nature</i> , 2003, 423, 87-91.	27.8	740
6	The genomic basis of trophic strategy in marine bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15527-15533.	7.1	685
7	The <i>Wolbachia</i> Genome of <i>Brugia malayi</i> : Endosymbiont Evolution within a Human Pathogenic Nematode. <i>PLoS Biology</i> , 2005, 3, e121.	5.6	529
8	The Plant Cell Wall—Decomposing Machinery Underlies the Functional Diversity of Forest Fungi. <i>Science</i> , 2011, 333, 762-765.	12.6	512
9	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> , 2007, 104, 10376-10381.	7.1	502
10	Complete sequence and comparative genome analysis of the dairy bacterium <i>Streptococcus thermophilus</i> . <i>Nature Biotechnology</i> , 2004, 22, 1554-1558.	17.5	485
11	Environmental Genomics Reveals a Single-Species Ecosystem Deep Within Earth. <i>Science</i> , 2008, 322, 275-278.	12.6	474
12	Patterns and Implications of Gene Gain and Loss in the Evolution of <i>Prochlorococcus</i> . <i>PLoS Genetics</i> , 2007, 3, e231.	3.5	469
13	plasmidSPAdes: assembling plasmids from whole genome sequencing data. <i>Bioinformatics</i> , 2016, 32, 3380-3387.	4.1	468
14	Assembling Genomes and Mini-metagenomes from Highly Chimeric Reads. <i>Lecture Notes in Computer Science</i> , 2013, , 158-170.	1.3	439
15	rnaSPAdes: a de novo transcriptome assembler and its application to RNA-Seq data. <i>GigaScience</i> , 2019, 8, .	6.4	428
16	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.	8.8	417
17	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, 11064-11069.	7.1	399
18	A Bioinformatician's Guide to Metagenomics. <i>Microbiology and Molecular Biology Reviews</i> , 2008, 72, 557-578.	6.6	361

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19	Genome sequence of the button mushroom <i>Agaricus bisporus</i> reveals mechanisms governing adaptation to a humic-rich ecological niche. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17501-17506.	7.1	359
20	Living with Genome Instability: the Adaptation of Phytoplasmas to Diverse Environments of Their Insect and Plant Hosts. Journal of Bacteriology, 2006, 188, 3682-3696.	2.2	356
21	Genome characteristics of facultatively symbiotic Frankia sp. strains reflect host range and host plant biogeography. Genome Research, 2006, 17, 7-15.	5.5	352
22	Use of simulated data sets to evaluate the fidelity of metagenomic processing methods. Nature Methods, 2007, 4, 495-500.	19.0	322
23	Complete genome sequence of the industrial bacterium <i>Bacillus licheniformis</i> and comparisons with closely related <i>Bacillus</i> species. Genome Biology, 2004, 5, r77.	9.6	319
24	Comparative genomics of biotechnologically important yeasts. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9882-9887.	7.1	302
25	MGnify: the microbiome analysis resource in 2020. Nucleic Acids Research, 2020, 48, D570-D578.	14.5	296
26	The Complete Genome Sequence of <i>Cupriavidus metallidurans</i> Strain CH34, a Master Survivalist in Harsh and Anthropogenic Environments. PLoS ONE, 2010, 5, e10433.	2.5	275
27	The Evolution of Host Specialization in the Vertebrate Gut Symbiont <i>Lactobacillus reuteri</i> . PLoS Genetics, 2011, 7, e1001314.	3.5	270
28	Methylotrophy in <i>Methylobacterium extorquens</i> AM1 from a Genomic Point of View. Journal of Bacteriology, 2003, 185, 2980-2987.	2.2	262
29	Comparative genomics of <i>Ceriporiopsis subvermispora</i> and <i>Phanerochaete chrysosporium</i> provide insight into selective ligninolysis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5458-5463.	7.1	259
30	High-resolution metagenomics targets specific functional types in complex microbial communities. Nature Biotechnology, 2008, 26, 1029-1034.	17.5	254
31	A korarchaeal genome reveals insights into the evolution of the Archaea. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8102-8107.	7.1	253
32	Genome of the Epsilonproteobacterial Chemolithoautotroph <i>Sulfurimonas denitrificans</i> . Applied and Environmental Microbiology, 2008, 74, 1145-1156.	3.1	228
33	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. PLoS Genetics, 2012, 8, e1003088.	3.5	226
34	One Bacterial Cell, One Complete Genome. PLoS ONE, 2010, 5, e10314.	2.5	215
35	Novel Features of the Polysaccharide-Digesting Gliding Bacterium <i>Flavobacterium johnsoniae</i> as Revealed by Genome Sequence Analysis. Applied and Environmental Microbiology, 2009, 75, 6864-6875.	3.1	212
36	<i>Deinococcus geothermalis</i> : The Pool of Extreme Radiation Resistance Genes Shrinks. PLoS ONE, 2007, 2, e955.	2.5	212

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37	Genome Sequence and Analysis of the Soil Cellulolytic Actinomycete <i>Thermobifida fusca</i> YX. <i>Journal of Bacteriology</i> , 2007, 189, 2477-2486.	2.2	194
38	Characterization of Cyanobacterial Hydrocarbon Composition and Distribution of Biosynthetic Pathways. <i>PLoS ONE</i> , 2014, 9, e85140.	2.5	190
39	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. <i>PLoS Biology</i> , 2014, 12, e1001920.	5.6	190
40	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, 1012-1035.	9.8	178
41	Genome Erosion in a Nitrogen-Fixing Vertically Transmitted Endosymbiotic Multicellular Cyanobacterium. <i>PLoS ONE</i> , 2010, 5, e11486.	2.5	178
42	Transposable Elements versus the Fungal Genome: Impact on Whole-Genome Architecture and Transcriptional Profiles. <i>PLoS Genetics</i> , 2016, 12, e1006108.	3.5	177
43	Genomic islands link secondary metabolism to functional adaptation in marine Actinobacteria. <i>ISME Journal</i> , 2009, 3, 1193-1203.	9.8	175
44	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> , 2011, 108, 13212-13217.	7.1	163
45	Localized Plasticity in the Streamlined Genomes of Vinyl Chloride Respiring <i>Dehalococcoides</i> . <i>PLoS Genetics</i> , 2009, 5, e1000714.	3.5	162
46	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> , 2006, 188, 7922-7931.	2.2	158
47	The genome of <i>Syntrophomonas wolfei</i> : new insights into syntrophic metabolism and biohydrogen production. <i>Environmental Microbiology</i> , 2010, 12, 2289-2301.	3.8	158
48	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> , 2009, 10, 351.	2.8	155
49	<i>Metaviral</i> <i>SPAdes</i> : assembly of viruses from metagenomic data. <i>Bioinformatics</i> , 2020, 36, 4126-4129.	4.1	149
50	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.	3.3	145
51	The Fast Changing Landscape of Sequencing Technologies and Their Impact on Microbial Genome Assemblies and Annotation. <i>PLoS ONE</i> , 2012, 7, e48837.	2.5	145
52	The Genome of Deep-Sea Vent Chemolithoautotroph <i>Thiomicrospira crunogena</i> XCL-2. <i>PLoS Biology</i> , 2006, 4, e383.	5.6	144
53	Extending the <i>Bacillus cereus</i> group genomics to putative food-borne pathogens of different toxicity. <i>Chemico-Biological Interactions</i> , 2008, 171, 236-249.	4.0	140
54	Comparative genomics of the white-rot fungi, <i>Phanerochaete carnosa</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.	2.8	125

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55	The Enigmatic Planctomycetes May Hold a Key to the Origins of Methanogenesis and Methylo trophy. <i>Molecular Biology and Evolution</i> , 2004, 21, 1234-1241.	8.9	123
56	Non-contiguous finished genome sequence and contextual data of the filamentous soil bacterium <i>Ktedonobacter racemifer</i> type strain (SOSP1-21T). <i>Standards in Genomic Sciences</i> , 2011, 5, 97-111.	1.5	115
57	The Complete Multipartite Genome Sequence of <i>Cupriavidus necator</i> JMP134, a Versatile Pollutant Degrader. <i>PLoS ONE</i> , 2010, 5, e9729.	2.5	112
58	Complete genome of the cellulolytic thermophile <i>Acidothermus cellulolyticus</i> 11B provides insights into its ecophysiological and evolutionary adaptations. <i>Genome Research</i> , 2009, 19, 1033-1043.	5.5	109
59	Plasmid detection and assembly in genomic and metagenomic data sets. <i>Genome Research</i> , 2019, 29, 961-968.	5.5	108
60	Genome of <i>Methylobacillus flagellatus</i> , Molecular Basis for Obligate Methylo trophy, and Polyphyletic Origin of Methylo trophy. <i>Journal of Bacteriology</i> , 2007, 189, 4020-4027.	2.2	107
61	rnaQUAST: a quality assessment tool for <i>de novo</i> transcriptome assemblies. <i>Bioinformatics</i> , 2016, 32, 2210-2212.	4.1	106
62	A genomic analysis of the archaeal system <i>Ignicoccus hospitalis</i> - <i>Nanoarchaeum equitans</i> . <i>Genome Biology</i> , 2008, 9, R158.	8.8	104
63	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> , 2012, 49, 217-226.	2.1	103
64	ExSPAnDer: a universal repeat resolver for DNA fragment assembly. <i>Bioinformatics</i> , 2014, 30, i293-i301.	4.1	103
65	Genomic Characterization of Methanomicrobiales Reveals Three Classes of Methanogens. <i>PLoS ONE</i> , 2009, 4, e5797.	2.5	103
66	Complete genome sequence of <i>Kytococcus sedentarius</i> type strain (541T). <i>Standards in Genomic Sciences</i> , 2009, 1, 12-20.	1.5	100
67	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.	1.5	100
68	A genomic perspective on the potential of <i>Actinobacillus succinogenes</i> for industrial succinate production. <i>BMC Genomics</i> , 2010, 11, 680.	2.8	100
69	Exploring the symbiotic pangenome of the nitrogen-fixing bacterium <i>Sinorhizobium meliloti</i> . <i>BMC Genomics</i> , 2011, 12, 235.	2.8	97
70	Complete genome sequence of <i>Odoribacter splanchnicus</i> type strain (1651/6T). <i>Standards in Genomic Sciences</i> , 2011, 4, 200-209.	1.5	96
71	Complete Genome Sequence of the Photosynthetic Purple Nonsulfur Bacterium <i>Rhodobacter capsulatus</i> SB 1003. <i>Journal of Bacteriology</i> , 2010, 192, 3545-3546.	2.2	90
72	Complete genome sequence of the filamentous anoxygenic phototrophic bacterium <i>Chloroflexus aurantiacus</i> . <i>BMC Genomics</i> , 2011, 12, 334.	2.8	90

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73	Genome-wide Mycobacterium tuberculosis variation (GMTV) database: a new tool for integrating sequence variations and epidemiology. BMC Genomics, 2014, 15, 308.	2.8	89
74	Complete Genome of the Cellulolytic Ruminal Bacterium Ruminococcus albus 7. Journal of Bacteriology, 2011, 193, 5574-5575.	2.2	87
75	Sequencing of Multiple Clostridial Genomes Related to Biomass Conversion and Biofuel Production. Journal of Bacteriology, 2010, 192, 6494-6496.	2.2	81
76	Genome Sequence of the Arctic Methanotroph Methylobacter tundripaludum SV96. Journal of Bacteriology, 2011, 193, 6418-6419.	2.2	78
77	Complete genome sequence of Planctomyces brasiliensis type strain (DSM 5305T), 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. Standards in Genomic Sciences, 2014, 9, 10.	1.5	76
78	Complete genome sequence of Chitinophaga pinensis type strain (UQM 2034T). Standards in Genomic Sciences, 2010, 2, 87-95.	1.5	74
79	Comparative genome analysis of Bacillus cereus group genomes with Bacillus subtilis. FEMS Microbiology Letters, 2005, 250, 175-184.	1.8	73
80	Complete Genome Sequences of Desulfosporosinus orientis DSM765 ^T , Desulfosporosinus youngiae DSM17734 ^T , Desulfosporosinus meridiei DSM13257 ^T , and Desulfosporosinus acidiphilus DSM22704 ^T . Journal of Bacteriology, 2012, 194, 6300-6301.	2.2	73
81	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. Genome Research, 2003, 13, 1180-1189.	5.5	72
82	Complete genome sequence of Thioalkalivibrio <i>œsulfidophilus</i> HL-EbGr7. Standards in Genomic Sciences, 2011, 4, 23-35.	1.5	72
83	Complete Genome Sequence of the Aerobic Marine Methanotroph Methylomonas methanica MC09. Journal of Bacteriology, 2011, 193, 7001-7002.	2.2	72
84	Complete genome sequence of Haliangium ochraceum type strain (SMP-2T). Standards in Genomic Sciences, 2010, 2, 96-106.	1.5	70
85	How to be moderately halophilic with broad salt tolerance: clues from the genome of Chromohalobacter salexigens. Extremophiles, 2005, 9, 275-279.	2.3	69
86	Massive Changes in Genome Architecture Accompany the Transition to Self-Fertility in the Filamentous Fungus <i>Neurospora tetrasperma</i> . Genetics, 2011, 189, 55-69.	2.9	69
87	Genome Sequence of the Fleming Strain of <i>Micrococcus luteus</i> , a Simple Free-Living Actinobacterium. Journal of Bacteriology, 2010, 192, 841-860.	2.2	68
88	Metagenomic Data Assembly <i>œ</i> The Way of Decoding Unknown Microorganisms. Frontiers in Microbiology, 2021, 12, 613791.	3.5	67
89	Genomes of Three Methylophilids from a Single Niche Reveal the Genetic and Metabolic Divergence of the Methylophilaceae. Journal of Bacteriology, 2011, 193, 3757-3764.	2.2	66
90	Complete Genome Sequence of the Cellulolytic Thermophile Clostridium thermocellum DSM1313. Journal of Bacteriology, 2011, 193, 2906-2907.	2.2	66

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91	Fungi Contribute Critical but Spatially Varying Roles in Nitrogen and Carbon Cycling in Acid Mine Drainage. <i>Frontiers in Microbiology</i> , 2016, 7, 238.	3.5	66
92	Draft genome sequence of <i>Halomonas lutea</i> strain YIM 91125T (DSM 23508T) isolated from the alkaline Lake Ebinur in Northwest China. <i>Standards in Genomic Sciences</i> , 2015, 10, 1.	1.5	65
93	Whole-Genome Shotgun Optical Mapping of <i>Rhodospirillum rubrum</i> . <i>Applied and Environmental Microbiology</i> , 2005, 71, 5511-5522.	3.1	62
94	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.	1.5	60
95	Genome Analysis of the Anaerobic Thermophilic Bacterium <i>Halothermothrix orenii</i> . <i>PLoS ONE</i> , 2009, 4, e4192.	2.5	58
96	Complete genome sequence of the termite hindgut bacterium <i>Spirochaeta coccoides</i> type strain (SPN1T), 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.	1.5	58
97	Complete genome sequence of <i>Geodermatophilus obscurus</i> type strain (G-20T). <i>Standards in Genomic Sciences</i> , 2010, 2, 158-167.	1.5	56
98	Genome Sequence of the 1,4-Dioxane-Degrading <i>Pseudonocardia dioxanivorans</i> Strain CB1190. <i>Journal of Bacteriology</i> , 2011, 193, 4549-4550.	2.2	56
99	Complete Genome Sequence and Updated Annotation of <i>Desulfovibrio alaskensis</i> G20. <i>Journal of Bacteriology</i> , 2011, 193, 4268-4269.	2.2	56
100	Genome Sequence of the Methanotrophic Alphaproteobacterium <i>Methylocystis</i> sp. Strain Rockwell (ATCC 49242). <i>Journal of Bacteriology</i> , 2011, 193, 2668-2669.	2.2	55
101	Complete genome sequence of <i>Syntrophobacter fumaroxidans</i> strain (MPOBT). <i>Standards in Genomic Sciences</i> , 2012, 7, 91-106.	1.5	55
102	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, 1483-1484.	2.2	54
103	Genome Sequence of <i>Thermophilum pendens</i> Reveals an Exceptional Loss of Biosynthetic Pathways without Genome Reduction. <i>Journal of Bacteriology</i> , 2008, 190, 2957-2965.	2.2	53
104	Complete genome sequence of <i>Thauera aminoaromatica</i> strain MZ1T. <i>Standards in Genomic Sciences</i> , 2012, 6, 325-335.	1.5	53
105	Genome Sequence of <i>Chthoniobacter flavus</i> Ellin428, an Aerobic Heterotrophic Soil Bacterium. <i>Journal of Bacteriology</i> , 2011, 193, 2902-2903.	2.2	52
106	Complete genome sequence of <i>Desulfobulbus propionicus</i> type strain (1pr3T). <i>Standards in Genomic Sciences</i> , 2011, 4, 100-110.	1.5	51
107	Complete genome sequence of the thermophilic, hydrogen-oxidizing <i>Bacillus tusciae</i> type strain (T2T) 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, 121-134.	1.5	51
108	Complete genome sequence of <i>Dehalogenimonas lykanthroporepellens</i> type strain (BL-DC-9T) and comparison to "Dehalococcoides" strains. <i>Standards in Genomic Sciences</i> , 2012, 6, 251-264.	1.5	51

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109	Complete genome sequence of the filamentous gliding predatory bacterium <i>Herpetosiphon aurantiacus</i> type strain (114-95T). <i>Standards in Genomic Sciences</i> , 2011, 5, 356-370.	1.5	47
110	Complete Genome Sequence of the Thermophilic Bacterium <i>Exiguobacterium</i> sp. AT1b. <i>Journal of Bacteriology</i> , 2011, 193, 2880-2881.	2.2	47
111	Complete genome sequence of <i>Truepera radiovictrix</i> type strain (RQ-24T). <i>Standards in Genomic Sciences</i> , 2011, 4, 91-99.	1.5	46
112	Complete genome sequence of <i>Isosphaera pallida</i> type strain (IS1BT). <i>Standards in Genomic Sciences</i> , 2011, 4, 63-71.	1.5	46
113	Complete genome sequence of <i>Rhodothermus marinus</i> type strain (R-10T). <i>Standards in Genomic Sciences</i> , 2009, 1, 283-290.	1.5	45
114	Complete genome sequence of <i>Thioalkalivibrio</i> sp. K90mix. <i>Standards in Genomic Sciences</i> , 2011, 5, 341-355.	1.5	45
115	Facile Recovery of Individual High-Molecular-Weight, Low-Copy-Number Natural Plasmids for Genomic Sequencing. <i>Applied and Environmental Microbiology</i> , 2006, 72, 4899-4906.	3.1	44
116	Complete genome sequence of <i>Veillonella parvula</i> type strain (Te3T). <i>Standards in Genomic Sciences</i> , 2010, 2, 57-65.	1.5	44
117	Complete genome sequence of <i>Rhodospirillum rubrum</i> type strain (S1T). <i>Standards in Genomic Sciences</i> , 2011, 4, 293-302.	1.5	44
118	Genome Sequence of the Verrucomicrobium <i>Opitutus terrae</i> PB90-1, an Abundant Inhabitant of Rice Paddy Soil Ecosystems. <i>Journal of Bacteriology</i> , 2011, 193, 2367-2368.	2.2	44
119	Genome sequence of the thermophilic fresh-water bacterium <i>Spirochaeta caldaria</i> type strain (H1T), 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> . <i>Standards in Genomic Sciences</i> , 2013, 8, 88-105.	1.5	44
120	Complete genome sequence of <i>Olsenella uli</i> type strain (VPI D76D-27CT). <i>Standards in Genomic Sciences</i> , 2010, 3, 76-84.	1.5	43
121	Complete genome sequence of the phenanthrene-degrading soil bacterium <i>Delftia acidovorans</i> Cs1-4. <i>Standards in Genomic Sciences</i> , 2015, 10, 55.	1.5	43
122	IgRepertoireConstructor: a novel algorithm for antibody repertoire construction and immunoproteogenomics analysis. <i>Bioinformatics</i> , 2015, 31, i53-i61.	4.1	42
123	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> , 2008, 74, 1276-1280.	3.1	41
124	Complete genome sequence of <i>Treponema succinifaciens</i> type strain (6091T). <i>Standards in Genomic Sciences</i> , 2011, 4, 361-370.	1.5	41
125	Genome Sequence of the Mercury-Methylating Strain <i>Desulfovibrio desulfuricans</i> ND132. <i>Journal of Bacteriology</i> , 2011, 193, 2078-2079.	2.2	41
126	Complete genome sequence of <i>Spirosoma linguale</i> type strain (1T). <i>Standards in Genomic Sciences</i> , 2010, 2, 176-184.	1.5	40

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127	Complete genome sequence of <i>Arcobacter nitrofigilis</i> type strain (CIT). Standards in Genomic Sciences, 2010, 2, 300-308.	1.5	40
128	CD45-deficient severe combined immunodeficiency caused by uniparental disomy. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10456-10461.	7.1	39
129	Complete genome sequence of <i>Actinosynnema mirum</i> type strain (101T). Standards in Genomic Sciences, 2009, 1, 46-53.	1.5	38
130	Complete genome sequence of <i>Cellulomonas flavigena</i> type strain (134T). Standards in Genomic Sciences, 2010, 3, 15-25.	1.5	38
131	Complete genome sequence of <i>Eggerthella lenta</i> type strain (VPI 0255T). Standards in Genomic Sciences, 2009, 1, 174-182.	1.5	37
132	Complete genome sequence of <i>Desulfarculus baarsii</i> type strain (2st14T). Standards in Genomic Sciences, 2010, 3, 276-284.	1.5	37
133	Complete genome sequence of the sulfur compounds oxidizing chemolithoautotroph <i>Sulfuricurvum kujiense</i> type strain (YK-1T). Standards in Genomic Sciences, 2012, 6, 94-103.	1.5	37
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266	Genome sequence of the moderately thermophilic halophile <i>Flexistipes sinuarabici</i> strain (MAS10T). <i>Standards in Genomic Sciences</i> , 2011, 5, 86-96.	1.5	12
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