

Patrick S Chain

List of Publications by Year in descending order

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245
papers

18,949
citations

16411

64
h-index

14156

128
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266
all docs

266
docs citations

266
times ranked

23143
citing authors

#	ARTICLE	IF	CITATIONS
1	The Composite Genome of the Legume Symbiont <i>Sinorhizobium meliloti</i> . <i>Science</i> , 2001, 293, 668-672.	6.0	1,098
2	Genome divergence in two <i>Prochlorococcus</i> ecotypes reflects oceanic niche differentiation. <i>Nature</i> , 2003, 424, 1042-1047.	13.7	1,086
3	A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea. <i>Nature</i> , 2009, 462, 1056-1060.	13.7	924
4	Complete genome sequence of the metabolically versatile photosynthetic bacterium <i>Rhodospseudomonas palustris</i> . <i>Nature Biotechnology</i> , 2004, 22, 55-61.	9.4	675
5	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MlxS) specifications. <i>Nature Biotechnology</i> , 2011, 29, 415-420.	9.4	608
6	Metagenome, metatranscriptome and single-cell sequencing reveal microbial response to Deepwater Horizon oil spill. <i>ISME Journal</i> , 2012, 6, 1715-1727.	4.4	547
7	Complete Genome Sequence of the Ammonia-Oxidizing Bacterium and Obligate Chemolithoautotroph <i>Nitrosomonas europaea</i> . <i>Journal of Bacteriology</i> , 2003, 185, 2759-2773.	1.0	510
8	The complete genome sequence of <i>Francisella tularensis</i> , the causative agent of tularemia. <i>Nature Genetics</i> , 2005, 37, 153-159.	9.4	436
9	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.	3.3	399
10	Genome Project Standards in a New Era of Sequencing. <i>Science</i> , 2009, 326, 236-237.	6.0	382
11	<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, 15280-15287.	3.3	339
12	The Genome of <i>Akkermansia muciniphila</i> , a Dedicated Intestinal Mucin Degradar, and Its Use in Exploring Intestinal Metagenomes. <i>PLoS ONE</i> , 2011, 6, e16876.	1.1	328
13	Saliva microbiomes distinguish caries-active from healthy human populations. <i>ISME Journal</i> , 2012, 6, 1-10.	4.4	320
14	The Genome Sequence of the Obligately Chemolithoautotrophic, Facultatively Anaerobic Bacterium <i>Thiobacillus denitrificans</i> . <i>Journal of Bacteriology</i> , 2006, 188, 1473-1488.	1.0	306
15	Next generation sequencing and bioinformatic bottlenecks: the current state of metagenomic data analysis. <i>Current Opinion in Biotechnology</i> , 2012, 23, 9-15.	3.3	296
16	Advances and Challenges in Metatranscriptomic Analysis. <i>Frontiers in Genetics</i> , 2019, 10, 904.	1.1	253
17	Capturing Single Cell Genomes of Active Polysaccharide Degradars: An Unexpected Contribution of <i>Verrucomicrobia</i> . <i>PLoS ONE</i> , 2012, 7, e35314.	1.1	236
18	Genome of the Epsilonproteobacterial Chemolithoautotroph <i>Sulfurimonas denitrificans</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 1145-1156.	1.4	228

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19	A programmable droplet-based microfluidic device applied to multiparameter analysis of single microbes and microbial communities. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7665-7670.	3.3	222
20	Comparative genome analysis of Burkholderia phytofirmans PsjN reveals a wide spectrum of endophytic lifestyles based on interaction strategies with host plants. Frontiers in Plant Science, 2013, 4, 120.	1.7	219
21	Complete Genome Sequence of <i>Nitrosospira multiformis</i> , an Ammonia-Oxidizing Bacterium from the Soil Environment. Applied and Environmental Microbiology, 2008, 74, 3559-3572.	1.4	212
22	Ecological roles of dominant and rare prokaryotes in acid mine drainage revealed by metagenomics and metatranscriptomics. ISME Journal, 2015, 9, 1280-1294.	4.4	207
23	Single-cell and metagenomic analyses indicate a fermentative and saccharolytic lifestyle for members of the OP9 lineage. Nature Communications, 2013, 4, 1854.	5.8	199
24	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. PLoS Biology, 2014, 12, e1001920.	2.6	190
25	The Genome Sequence of <i>Psychrobacter arcticus</i> 273-4, a Psychroactive Siberian Permafrost Bacterium, Reveals Mechanisms for Adaptation to Low-Temperature Growth. Applied and Environmental Microbiology, 2010, 76, 2304-2312.	1.4	184
26	Whole-Genome Analyses of Speciation Events in Pathogenic Brucellae. Infection and Immunity, 2005, 73, 8353-8361.	1.0	179
27	Rapid evaluation and quality control of next generation sequencing data with FaQCs. BMC Bioinformatics, 2014, 15, 366.	1.2	176
28	Complete Genome Sequence of Yersinia pestis Strains Antiqua and Nepal516: Evidence of Gene Reduction in an Emerging Pathogen. Journal of Bacteriology, 2006, 188, 4453-4463.	1.0	174
29	Contrasting elevational diversity patterns between eukaryotic soil microbes and plants. Ecology, 2014, 95, 3190-3202.	1.5	174
30	Genome Sequence of the Chemolithoautotrophic Nitrite-Oxidizing Bacterium Nitrobacter winogradskyi Nb-255. Applied and Environmental Microbiology, 2006, 72, 2050-2063.	1.4	169
31	Identification of MglA-Regulated Genes Reveals Novel Virulence Factors in Francisella tularensis. Infection and Immunity, 2006, 74, 6642-6655.	1.0	165
32	The Impact of Genome Analyses on Our Understanding of Ammonia-Oxidizing Bacteria. Annual Review of Microbiology, 2007, 61, 503-528.	2.9	165
33	A novel metatranscriptomic approach to identify gene expression dynamics during extracellular electron transfer. Nature Communications, 2013, 4, 1601.	5.8	162
34	Whole-Genome-Based Phylogeny and Divergence of the Genus <i>Brucella</i> . Journal of Bacteriology, 2009, 191, 2864-2870.	1.0	157
35	Whole-genome analysis of the ammonia-oxidizing bacterium, <i>Nitrosomonas eutropha</i> C91: implications for niche adaptation. Environmental Microbiology, 2007, 9, 2993-3007.	1.8	150
36	Enabling the democratization of the genomics revolution with a fully integrated web-based bioinformatics platform. Nucleic Acids Research, 2017, 45, 67-80.	6.5	147

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37	The Genome of Deep-Sea Vent Chemolithoautotroph <i>Thiomicrospira crunogena</i> XCL-2. <i>PLoS Biology</i> , 2006, 4, e383.	2.6	144
38	Complete Genome Sequence of the Plant Growth-Promoting Endophyte <i>Burkholderia phytofirmans</i> Strain PsJN. <i>Journal of Bacteriology</i> , 2011, 193, 3383-3384.	1.0	144
39	Accurate read-based metagenome characterization using a hierarchical suite of unique signatures. <i>Nucleic Acids Research</i> , 2015, 43, e69-e69.	6.5	141
40	Complete Genome Sequence of the Marine, Chemolithoautotrophic, Ammonia-Oxidizing Bacterium <i>Nitrosococcus oceani</i> ATCC 19707. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6299-6315.	1.4	139
41	Whole-Genome Analysis of the Methyl tert -Butyl Ether-Degrading Beta-Proteobacterium <i>Methylibium petroleiphilum</i> PM1. <i>Journal of Bacteriology</i> , 2007, 189, 1931-1945.	1.0	139
42	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, 18543-18548.	3.3	131
43	Soil Microbial Community Responses to a Decade of Warming as Revealed by Comparative Metagenomics. <i>Applied and Environmental Microbiology</i> , 2014, 80, 1777-1786.	1.4	131
44	Genomic Comparison of <i>Escherichia coli</i> O104:H4 Isolates from 2009 and 2011 Reveals Plasmid, and Prophage Heterogeneity, Including Shiga Toxin Encoding Phage stx2. <i>PLoS ONE</i> , 2012, 7, e48228.	1.1	118
45	Complete Genome Sequence of <i>Nitrobacter hamburgensis</i> X14 and Comparative Genomic Analysis of Species within the Genus <i>Nitrobacter</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 2852-2863.	1.4	115
46	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.	5.9	115
47	Complete genome sequence of <i>Kytococcus sedentarius</i> type strain (541T). <i>Standards in Genomic Sciences</i> , 2009, 1, 12-20.	1.5	100
48	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
49	The Genome Sequence of <i>Yersinia pestis</i> Bacteriophage Ψ A1122 Reveals an Intimate History with the Coliphage T3 and T7 Genomes. <i>Journal of Bacteriology</i> , 2003, 185, 5248-5262.	1.0	95
50	Genomic and Metabolic Diversity of Marine Group I Thaumarchaeota in the Mesopelagic of Two Subtropical Gyres. <i>PLoS ONE</i> , 2014, 9, e95380.	1.1	95
51	Standards for Sequencing Viral Genomes in the Era of High-Throughput Sequencing. <i>MBio</i> , 2014, 5, e01360-14.	1.8	89
52	Under-detection of endospore-forming Firmicutes in metagenomic data. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 299-306.	1.9	88
53	Comparative genomics of enterohemorrhagic <i>Escherichia coli</i> O145:H28 demonstrates a common evolutionary lineage with <i>Escherichia coli</i> O157:H7. <i>BMC Genomics</i> , 2014, 15, 17.	1.2	84
54	Microbial community adaptation to quaternary ammonium biocides as revealed by metagenomics. <i>Environmental Microbiology</i> , 2013, 15, 2850-2864.	1.8	82

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55	Complete Genome Sequences for 59 <i>Burkholderia</i> Isolates, Both Pathogenic and Near Neighbor. Genome Announcements, 2015, 3, .	0.8	82
56	MicroRNA in Pancreatic Cancer: From Biology to Therapeutic Potential. Genes, 2019, 10, 752.	1.0	81
57	<i>Polynucleobacter necessarius</i> , a model for genome reduction in both free-living and symbiotic bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18590-18595.	3.3	80
58	Oxalic acid, a molecule at the crossroads of bacterial-fungal interactions. Advances in Applied Microbiology, 2019, 106, 49-77.	1.3	79
59	Community and gene composition of a human dental plaque microbiota obtained by metagenomic sequencing. Molecular Oral Microbiology, 2010, 25, 391-405.	1.3	78
60	Comparative metagenomics reveals impact of contaminants on groundwater microbiomes. Frontiers in Microbiology, 2015, 6, 1205.	1.5	77
61	Complete genome sequence of <i>Chitinophaga pinensis</i> type strain (UQM 2034T). Standards in Genomic Sciences, 2010, 2, 87-95.	1.5	74
62	<i>Nitrosococcus watsonii</i> sp. nov., a new species of marine obligate ammonia-oxidizing bacteria that is not omnipresent in the world's oceans: calls to validate the names "Nitrosococcus halophilus" and "Nitrosomonas mobilis". FEMS Microbiology Ecology, 2011, 76, 39-48.	1.3	74
63	Complete Genome Sequences of <i>Desulfosporosinus orientis</i> DSM765, <i>Desulfosporosinus youngiae</i> DSM17734, <i>Desulfosporosinus meridiei</i> DSM13257, and <i>Desulfosporosinus acidiphilus</i> DSM22704. Journal of Bacteriology, 2012, 194, 6300-6301.	1.0	73
64	Complete Genome sequence of <i>Burkholderia phymatum</i> STM815T, a broad host range and efficient nitrogen-fixing symbiont of Mimosa species. Standards in Genomic Sciences, 2014, 9, 763-774.	1.5	71
65	The Complete Plastid Genome Sequence of the Secondarily Nonphotosynthetic Alga <i>Cryptomonas paramecium</i> : Reduction, Compaction, and Accelerated Evolutionary Rate. Genome Biology and Evolution, 2009, 1, 439-448.	1.1	70
66	Standardized phylogenetic and molecular evolutionary analysis applied to species across the microbial tree of life. Scientific Reports, 2020, 10, 1723.	1.6	65
67	Metagenomic reconstruction of nitrogen cycling pathways in a CO ₂ -enriched grassland ecosystem. Soil Biology and Biochemistry, 2017, 106, 99-108.	4.2	63
68	Proteogenomic Analysis of a Thermophilic Bacterial Consortium Adapted to Deconstruct Switchgrass. PLoS ONE, 2013, 8, e68465.	1.1	62
69	Complete genome sequence of <i>Rhizobium leguminosarum</i> bv. trifolii strain WSM2304, an effective microsymbiont of the South American clover <i>Trifolium polymorphum</i> . Standards in Genomic Sciences, 2010, 2, 66-76.	1.5	60
70	An applications-focused review of comparative genomics tools: Capabilities, limitations and future challenges. Briefings in Bioinformatics, 2003, 4, 105-123.	3.2	59
71	Targeted and shotgun metagenomic approaches provide different descriptions of dryland soil microbial communities in a manipulated field study. Environmental Microbiology Reports, 2012, 4, 248-256.	1.0	58
72	Complete genome sequence of <i>Rhizobium leguminosarum</i> bv. trifolii strain WSM1325, an effective microsymbiont of annual Mediterranean clovers. Standards in Genomic Sciences, 2010, 2, 347-356.	1.5	53

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73	Genome of the Cyanobacterium <i>Microcoleus vaginatus</i> FGP-2, a Photosynthetic Ecosystem Engineer of Arid Land Soil Biocrusts Worldwide. <i>Journal of Bacteriology</i> , 2011, 193, 4569-4570.	1.0	53
74	Nearly finished genomes produced using gel microdroplet culturing reveal substantial intraspecies genomic diversity within the human microbiome. <i>Genome Research</i> , 2013, 23, 878-888.	2.4	53
75	Complete Genome Sequences for 35 Biothreat Assay-Relevant <i>Bacillus</i> Species. <i>Genome Announcements</i> , 2015, 3, .	0.8	52
76	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.	0.8	51
77	Genome of <i>Ochrobactrum anthropi</i> ATCC 49188 ^T , a Versatile Opportunistic Pathogen and Symbiont of Several Eukaryotic Hosts. <i>Journal of Bacteriology</i> , 2011, 193, 4274-4275.	1.0	46
78	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
79	Toward unrestricted use of public genomic data. <i>Science</i> , 2019, 363, 350-352.	6.0	45
80	Complete genome sequence of <i>Veillonella parvula</i> type strain (Te3T). <i>Standards in Genomic Sciences</i> , 2010, 2, 57-65.	1.5	44
81	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
82	Genomic, Proteomic, and Biochemical Analysis of the Organohalide Respiratory Pathway in <i>Desulfotobacterium dehalogenans</i> . <i>Journal of Bacteriology</i> , 2015, 197, 893-904.	1.0	43
83	Genome analysis of <i>Desulfotomaculum kuznetsovii</i> strain 17T reveals a physiological similarity with <i>Pelotomaculum thermopropionicum</i> strain SIT.. <i>Standards in Genomic Sciences</i> , 2013, 8, 69-87.	1.5	42
84	The National Microbiome Data Collaborative: enabling microbiome science. <i>Nature Reviews Microbiology</i> , 2020, 18, 313-314.	13.6	42
85	Pathogen comparative genomics in the next-generation sequencing era: genome alignments, pangenomics and metagenomics. <i>Briefings in Functional Genomics</i> , 2011, 10, 322-333.	1.3	41
86	Complete genome sequence of <i>Spirosoma linguale</i> type strain (1T). <i>Standards in Genomic Sciences</i> , 2010, 2, 176-184.	1.5	40
87	Comparative Transcriptome Analysis of <i>Methylobium petroleiphilum</i> PM1 Exposed to the Fuel Oxygenates Methyl <i>tert</i> -Butyl Ether and Ethanol. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7347-7357.	1.4	39
88	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.	0.8	39
89	Improved Assemblies Using a Source-Agnostic Pipeline for MetaGenomic Assembly by Merging (MeGAMerge) of Contigs. <i>Scientific Reports</i> , 2015, 4, 6480.	1.6	39
90	CRP-Mediated Carbon Catabolite Regulation of <i>Yersinia pestis</i> Biofilm Formation Is Enhanced by the Carbon Storage Regulator Protein, CsrA. <i>PLoS ONE</i> , 2015, 10, e0135481.	1.1	39

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91	Complete genome sequence of <i>Actinosynnema mirum</i> type strain (101T). <i>Standards in Genomic Sciences</i> , 2009, 1, 46-53.	1.5	38
92	Whole-Genome Sequences of 80 Environmental and Clinical Isolates of <i>Burkholderia pseudomallei</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	38
93	Adaptation Genomics of a Small-Colony Variant in a <i>Pseudomonas chlororaphis</i> 30-84 Biofilm. <i>Applied and Environmental Microbiology</i> , 2015, 81, 890-899.	1.4	38
94	Complete genome sequence of <i>Eggerthella lenta</i> type strain (VPI 0255T). <i>Standards in Genomic Sciences</i> , 2009, 1, 174-182.	1.5	37
95	Metagenomic investigation of the geologically unique <i>Hellenic Volcanic Arc</i> reveals a distinctive ecosystem with unexpected physiology. <i>Environmental Microbiology</i> , 2016, 18, 1122-1136.	1.8	37
96	Pestoides F, an Atypical <i>Yersinia pestis</i> Strain from the Former Soviet Union. <i>Advances in Experimental Medicine and Biology</i> , 2007, 603, 17-22.	0.8	37
97	Complete genome sequence of <i>Desulfomicrobium baculatum</i> type strain (XT). <i>Standards in Genomic Sciences</i> , 2009, 1, 29-37.	1.5	36
98	Draft Genome Sequence of <i>Methylobacterium buryatense</i> Strain 5G, a Haloalkaline-Tolerant Methanotrophic Bacterium. <i>Genome Announcements</i> , 2013, 1, .	0.8	36
99	<i>Candidatus Nitrosotenuis aquarius</i> , an Ammonia-Oxidizing Archaeon from a Freshwater Aquarium Biofilter. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	36
100	Complete genome sequence of <i>Desulfotomaculum acetoxidans</i> type strain (5575T). <i>Standards in Genomic Sciences</i> , 2009, 1, 242-253.	1.5	35
101	Complete genome sequence of <i>Pirellula staleyi</i> type strain (ATCC 27377T). <i>Standards in Genomic Sciences</i> , 2009, 1, 308-316.	1.5	34
102	Complete genome sequence of <i>Acidimicrobium ferrooxidans</i> type strain (ICPT). <i>Standards in Genomic Sciences</i> , 2009, 1, 38-45.	1.5	32
103	Complete genome sequence of <i>Haloterrigena turkmenica</i> type strain (4kT). <i>Standards in Genomic Sciences</i> , 2010, 2, 107-116.	1.5	32
104	Complete genome sequence of <i>Halomicrobium mukohataei</i> type strain (arg-2T). <i>Standards in Genomic Sciences</i> , 2009, 1, 270-277.	1.5	31
105	Thirty-Two Complete Genome Assemblies of Nine <i>Yersinia</i> Species, Including <i>Y. pestis</i> , <i>Y. pseudotuberculosis</i> , and <i>Y. enterocolitica</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	31
106	Culture-Independent Diagnostics for Health Security. <i>Health Security</i> , 2016, 14, 122-142.	0.9	31
107	Molecular characterization of L-413C, a P2-related plague diagnostic bacteriophage. <i>Virology</i> , 2008, 372, 85-96.	1.1	30
108	Complete genome sequence of <i>Atopobium parvulum</i> type strain (IPP 1246T). <i>Standards in Genomic Sciences</i> , 2009, 1, 166-173.	1.5	30

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109	The United States of America and Scientific Research. PLoS ONE, 2010, 5, e12203.	1.1	30
110	Complete genome sequence of <i>Sulfurospirillum deleyianum</i> type strain (5175T). Standards in Genomic Sciences, 2010, 2, 149-157.	1.5	29
111	Complete genome sequence of <i>Kangiella koreensis</i> type strain (SW-125T). Standards in Genomic Sciences, 2009, 1, 226-233.	1.5	28
112	Challenges and opportunities in understanding microbial communities with metagenome assembly (accompanied by IPython Notebook tutorial). Frontiers in Microbiology, 2015, 6, 678.	1.5	28
113	Whole-Genome Comparative Analysis of Two Carbapenem-Resistant ST-258 <i>Klebsiella pneumoniae</i> Strains Isolated during a North-Eastern Ohio Outbreak: Differences within the High Heterogeneity Zones. Genome Biology and Evolution, 2016, 8, 2036-2043.	1.1	28
114	Microbiome Metadata Standards: Report of the National Microbiome Data Collaborative's Workshop and Follow-On Activities. MSystems, 2021, 6, .	1.7	28
115	Complete genome sequence of <i>Sphaerobacter thermophilus</i> type strain (S 6022T). Standards in Genomic Sciences, 2010, 2, 49-56.	1.5	27
116	Complete genome sequence of <i>Streptosporangium roseum</i> type strain (NI 9100T). Standards in Genomic Sciences, 2010, 2, 29-37.	1.5	27
117	Whole-Genome Assemblies of 56 Burkholderia Species. Genome Announcements, 2014, 2, .	0.8	27
118	Genome analysis of <i>Desulfotomaculum gibsoniae</i> strain GrollT a highly versatile Gram-positive sulfate-reducing bacterium. Standards in Genomic Sciences, 2014, 9, 821-839.	1.5	27
119	Complete genome sequence of <i>Archaeoglobus profundus</i> type strain (AV18T). Standards in Genomic Sciences, 2010, 2, 327-346.	1.5	26
120	Complete genome sequence of <i>Gordonia bronchialis</i> type strain (3410T). Standards in Genomic Sciences, 2010, 2, 19-28.	1.5	26
121	Non-contiguous finished genome sequence of plant-growth promoting <i>Serratia proteamaculans</i> S4. Standards in Genomic Sciences, 2013, 8, 441-449.	1.5	26
122	Genome sequence of <i>Phaeobacter inhibens</i> type strain (T5T), a secondary metabolite producing representative of the marine Roseobacter clade, and emendation of the species description of <i>Phaeobacter inhibens</i> . Standards in Genomic Sciences, 2013, 9, 334-350.	1.5	26
123	Bacterial spores, from ecology to biotechnology. Advances in Applied Microbiology, 2019, 106, 79-111.	1.3	26
124	Complete genome sequence of <i>Anaerococcus prevotii</i> type strain (PC1T). Standards in Genomic Sciences, 2009, 1, 159-165.	1.5	25
125	Complete genome sequence of <i>Brachybacterium faecium</i> type strain (Schefferle 6-10T). Standards in Genomic Sciences, 2009, 1, 3-11.	1.5	25
126	Complete genome sequence of <i>Dyadobacter fermentans</i> type strain (NS114T). Standards in Genomic Sciences, 2009, 1, 133-140.	1.5	25

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127	Genome analyses of the carboxydrotrophic sulfate-reducers <i>Desulfotomaculum nigrificans</i> and <i>Desulfotomaculum carboxydvorans</i> and reclassification of <i>Desulfotomaculum carboxydvorans</i> as a later synonym of <i>Desulfotomaculum nigrificans</i> . <i>Standards in Genomic Sciences</i> , 2014, 9, 655-675.	1.5	25
128	Complete Genome Sequences of Two <i>Escherichia coli</i> O145:H28 Outbreak Strains of Food Origin. <i>Genome Announcements</i> , 2014, 2, .	0.8	25
129	Complete genome sequence of <i>Catenulispora acidiphila</i> type strain (ID 139908T). <i>Standards in Genomic Sciences</i> , 2009, 1, 119-125.	1.5	24
130	Complete genome sequence of <i>Leptotrichia buccalis</i> type strain (C-1013-bT). <i>Standards in Genomic Sciences</i> , 2009, 1, 126-132.	1.5	24
131	Complete genome sequence of <i>Saccharomonospora viridis</i> type strain (P101T). <i>Standards in Genomic Sciences</i> , 2009, 1, 141-149.	1.5	24
132	Complete genome sequence of <i>Conexibacter woesei</i> type strain (ID131577T). <i>Standards in Genomic Sciences</i> , 2010, 2, 212-219.	1.5	24
133	Complete genome sequence of <i>Alicyclobacillus acidocaldarius</i> type strain (104-IAT). <i>Standards in Genomic Sciences</i> , 2010, 2, 9-18.	1.5	24
134	oriT-Directed Cloning of Defined Large Regions from Bacterial Genomes: Identification of the <i>Sinorhizobium meliloti</i> pExo Megaplasmid Replicator Region. <i>Journal of Bacteriology</i> , 2000, 182, 5486-5494.	1.0	23
135	Complete genome sequence of <i>Halogeometricum borinquense</i> type strain (PR3T). <i>Standards in Genomic Sciences</i> , 2009, 1, 150-158.	1.5	23
136	Complete genome sequence of <i>Thermanaerovibrio acidaminovorans</i> type strain (Su883T). <i>Standards in Genomic Sciences</i> , 2009, 1, 254-261.	1.5	23
137	Complete genome sequence of <i>Stackebrandtia nassauensis</i> type strain (LLR-40K-21T). <i>Standards in Genomic Sciences</i> , 2009, 1, 292-299.	1.5	23
138	Phylogenetic and metagenomic analysis of <i>Verrucomicrobia</i> in former agricultural grassland soil. <i>FEMS Microbiology Ecology</i> , 2010, 71, 23-33.	1.3	23
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