

Hans-Peter Klenk

List of Publications by Year in descending order

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406
papers

31,039
citations

22099

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7136

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413
docs citations

413
times ranked

23864
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence-based species delimitation with confidence intervals and improved distance functions. <i>BMC Bioinformatics</i> , 2013, 14, 60.	1.2	5,139
2	Genome-Based Taxonomic Classification of the Phylum Actinobacteria. <i>Frontiers in Microbiology</i> , 2018, 9, 2007.	1.5	2,599
3	The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon <i>Archaeoglobus fulgidus</i> . <i>Nature</i> , 1997, 390, 364-370.	13.7	1,460
4	Digital DNA-DNA hybridization for microbial species delineation by means of genome-to-genome sequence comparison. <i>Standards in Genomic Sciences</i> , 2010, 2, 117-134.	1.5	1,442
5	Taxonomy, Physiology, and Natural Products of Actinobacteria. <i>Microbiology and Molecular Biology Reviews</i> , 2016, 80, 1-43.	2.9	1,395
6	A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea. <i>Nature</i> , 2009, 462, 1056-1060.	13.7	924
7	Novel genes for nitrite reductase and Amo-related proteins indicate a role of uncultivated mesophilic crenarchaeota in nitrogen cycling. <i>Environmental Microbiology</i> , 2005, 7, 1985-1995.	1.8	758
8	Critical Assessment of Metagenome Interpretation – a benchmark of metagenomics software. <i>Nature Methods</i> , 2017, 14, 1063-1071.	9.0	635
9	Standard operating procedure for calculating genome-to-genome distances based on high-scoring segment pairs. <i>Standards in Genomic Sciences</i> , 2010, 2, 142-148.	1.5	509
10	Genome-Based Taxonomic Classification of Bacteroidetes. <i>Frontiers in Microbiology</i> , 2016, 7, 2003.	1.5	493
11	When should a DDH experiment be mandatory in microbial taxonomy?. <i>Archives of Microbiology</i> , 2013, 195, 413-418.	1.0	490
12	Complete genome sequence of DSM 30083T, the type strain (U5/41T) of <i>Escherichia coli</i> , and a proposal for delineating subspecies in microbial taxonomy. <i>Standards in Genomic Sciences</i> , 2014, 9, 2.	1.5	454
13	The genome sequence of the extreme thermophile <i>Thermus thermophilus</i> . <i>Nature Biotechnology</i> , 2004, 22, 547-553.	9.4	345
14	Comparative genomics of biotechnologically important yeasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9882-9887.	3.3	302
15	<i>Bacillus amyloliquefaciens</i> , <i>Bacillus velezensis</i> , and <i>Bacillus siamensis</i> Form an ‘Operational Group B. amyloliquefaciens’ within the <i>B. subtilis</i> Species Complex. <i>Frontiers in Microbiology</i> , 2017, 8, 22.	1.5	296
16	Phylogenomics of <i>Rhodobacteraceae</i> reveals evolutionary adaptation to marine and non-marine habitats. <i>ISME Journal</i> , 2017, 11, 1483-1499.	4.4	283
17	The revisited genome of <i>Pseudomonas putida</i> KT2440 enlightens its value as a robust metabolic chassis. <i>Environmental Microbiology</i> , 2016, 18, 3403-3424.	1.8	270
18	Relationship of <i>Bacillus amyloliquefaciens</i> clades associated with strains DSM 7T and FZB42T: a proposal for <i>Bacillus amyloliquefaciens</i> subsp. <i>amyloliquefaciens</i> subsp. nov. and <i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> subsp. nov. based on complete genome sequence comparisons. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 1786-1801.	0.8	265

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19	The Genome of <i>Sulfolobus acidocaldarius</i> , a Model Organism of the Crenarchaeota. <i>Journal of Bacteriology</i> , 2005, 187, 4992-4999.	1.0	262
20	The complete genome sequence of the algal symbiont <i>Dinoroseobacter shibae</i> : a hitchhiker's guide to life in the sea. <i>ISME Journal</i> , 2010, 4, 61-77.	4.4	244
21	High-resolution phylogenetic microbial community profiling. <i>ISME Journal</i> , 2016, 10, 2020-2032.	4.4	232
22	A blueprint of ectoine metabolism from the genome of the industrial producer <i>Halomonas elongata</i> DSM 2581. <i>Environmental Microbiology</i> , 2011, 13, 1973-1994.	1.8	224
23	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. <i>Nature Biotechnology</i> , 2017, 35, 676-683.	9.4	222
24	opm: an R package for analysing OmniLog [®] phenotype microarray data. <i>Bioinformatics</i> , 2013, 29, 1823-1824.	1.8	214
25	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. <i>PLoS Biology</i> , 2014, 12, e1001920.	2.6	190
26	<i>Chryseobacterium hispalense</i> sp. nov., a plant-growth-promoting bacterium isolated from a rainwater pond in an olive plant nursery, and emended descriptions of <i>Chryseobacterium defluvii</i> , <i>Chryseobacterium indologenes</i> , <i>Chryseobacterium wanjuese</i> and <i>Chryseobacterium gregarium</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 4386-4395.	0.8	187
27	The Genomic Standards Consortium. <i>PLoS Biology</i> , 2011, 9, e1001088.	2.6	180
28	The Earth Microbiome Project: Meeting report of the 1st EMP meeting on sample selection and acquisition at Argonne National Laboratory October 6th 2010. <i>Standards in Genomic Sciences</i> , 2010, 3, 249-253.	1.5	176
29	Visualization and Curve-Parameter Estimation Strategies for Efficient Exploration of Phenotype Microarray Kinetics. <i>PLoS ONE</i> , 2012, 7, e34846.	1.1	173
30	Characterization of the first cultured representative of <i>Verrucomicrobia</i> subdivision 5 indicates the proposal of a novel phylum. <i>ISME Journal</i> , 2016, 10, 2801-2816.	4.4	173
31	A taxonomic framework for emerging groups of ecologically important marine gammaproteobacteria based on the reconstruction of evolutionary relationships using genome-scale data. <i>Frontiers in Microbiology</i> , 2015, 6, 281.	1.5	168
32	Database Resources of the National Genomics Data Center in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D24-D33.	6.5	165
33	First insight into the genome of an uncultivated crenarchaeote from soil. <i>Environmental Microbiology</i> , 2002, 4, 603-611.	1.8	161
34	An Archaeobacterial ATPase, Homologous to ATPases in the Eukaryotic 26 S Proteasome, Activates Protein Breakdown by 20 S Proteasomes. <i>Journal of Biological Chemistry</i> , 1999, 274, 26008-26014.	1.6	154
35	Homologues of nitrite reductases in ammonia-oxidizing archaea: diversity and genomic context. <i>Environmental Microbiology</i> , 2010, 12, 1075-1088.	1.8	137
36	The DNA Bank Network: The Start from a German Initiative. <i>Biopreservation and Biobanking</i> , 2011, 9, 51-55.	0.5	137

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37	Harnessing the landscape of microbial culture media to predict new organism-media pairings. <i>Nature Communications</i> , 2015, 6, 8493.	5.8	119
38	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
39	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.	5.9	115
40	Comparative evaluation of gene expression in archaeobacteria. <i>FEBS Journal</i> , 1988, 173, 473-482.	0.2	111
41	Genome-based classification of micromonosporae with a focus on their biotechnological and ecological potential. <i>Scientific Reports</i> , 2018, 8, 525.	1.6	102
42	Genome sequence of <i>Desulfobacterium autotrophicum</i> HRM2, a marine sulfate reducer oxidizing organic carbon completely to carbon dioxide. <i>Environmental Microbiology</i> , 2009, 11, 1038-1055.	1.8	100
43	Complete genome sequence of <i>Kytococcus sedentarius</i> type strain (541T). <i>Standards in Genomic Sciences</i> , 2009, 1, 12-20.	1.5	100
44	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
45	Genomics of Aerobic Cellulose Utilization Systems in Actinobacteria. <i>PLoS ONE</i> , 2012, 7, e39331.	1.1	92
46	Genome-scale data suggest reclassifications in the <i>Leisingera</i> - <i>Phaeobacter</i> cluster including proposals for <i>Sedimentitalea</i> gen. nov. and <i>Pseudophaeobacter</i> gen. nov.. <i>Frontiers in Microbiology</i> , 2014, 5, 416.	1.5	88
47	PP _i -Dependent Phosphofructokinase from <i>Thermoproteus tenax</i> , an Archaeal Descendant of an Ancient Line in Phosphofructokinase Evolution. <i>Journal of Bacteriology</i> , 1998, 180, 2137-2143.	1.0	85
48	Genomic Encyclopedia of Type Strains, Phase I: The one thousand microbial genomes (KMG-I) project. <i>Standards in Genomic Sciences</i> , 2013, 9, 1278-1284.	1.5	79
49	Comparative Genomics of the Bacterial Genus <i>Streptococcus</i> Illuminates Evolutionary Implications of Species Groups. <i>PLoS ONE</i> , 2014, 9, e101229.	1.1	76
50	Complete genome sequence of <i>Chitinophaga pinensis</i> type strain (UQM 2034T). <i>Standards in Genomic Sciences</i> , 2010, 2, 87-95.	1.5	74
51	Genomic Encyclopedia of Bacterial and Archaeal Type Strains, Phase III: the genomes of soil and plant-associated and newly described type strains. <i>Standards in Genomic Sciences</i> , 2015, 10, 26.	1.5	74
52	Complete Genome Sequences of <i>Desulfosporosinus orientis</i> DSM765 ^T , <i>Desulfosporosinus youngiae</i> DSM17734 ^T , <i>Desulfosporosinus meridiei</i> DSM13257 ^T , and <i>Desulfosporosinus acidiphilus</i> DSM22704 ^T . <i>Journal of Bacteriology</i> , 2012, 194, 6300-6301.	1.0	73
53	Novel Insights into the Diversity of Catabolic Metabolism from Ten Haloarchaeal Genomes. <i>PLoS ONE</i> , 2011, 6, e20237.	1.1	72
54	Stone-dwelling actinobacteria <i>Blastococcus saxobsidens</i> , <i>Modestobacter marinus</i> and <i>Geodermatophilus obscurus</i> proteogenomes. <i>ISME Journal</i> , 2016, 10, 21-29.	4.4	71

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55	Complete genome sequence of <i>Haliangium ochraceum</i> type strain (SMP-2T). <i>Standards in Genomic Sciences</i> , 2010, 2, 96-106.	1.5	70
56	The phylogenetic relations of DNA-dependent RNA polymerases of archaeobacteria, eukaryotes, and eubacteria. <i>Canadian Journal of Microbiology</i> , 1989, 35, 73-80.	0.8	69
57	Proposal of a type strain for <i>Frankia alni</i> (Woronin 1866) Von Tubeuf 1895, emended description of <i>Frankia alni</i> , and recognition of <i>Frankia casuarinae</i> sp. nov. and <i>Frankia elaeagni</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 5201-5210.	0.8	68
58	Reconstruction of the Central Carbohydrate Metabolism of <i>Thermoproteus tenax</i> by Use of Genomic and Biochemical Data. <i>Journal of Bacteriology</i> , 2004, 186, 2179-2194.	1.0	66
59	Metabolic traits of an uncultured archaeal lineage -MSBL1- from brine pools of the Red Sea. <i>Scientific Reports</i> , 2016, 6, 19181.	1.6	66
60	Genomic Analysis of <i>Caldithrix abyssi</i> , the Thermophilic Anaerobic Bacterium of the Novel Bacterial Phylum <i>Calditrichaeota</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 195.	1.5	66
61	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
62	Dissecting the taxonomic heterogeneity within <i>Propionibacterium acnes</i> : proposal for <i>Propionibacterium acnes</i> subsp. <i>acnes</i> subsp. nov. and <i>Propionibacterium acnes</i> subsp. <i>elongatum</i> subsp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 4776-4787.	0.8	64
63	Complete Nucleotide Sequence of the <i>Sulfolobus islandicus</i> Multicopy Plasmid pRN1. <i>Plasmid</i> , 1996, 35, 141-144.	0.4	63
64	Highly parallelized inference of large genome-based phylogenies. <i>Concurrency Computation Practice and Experience</i> , 2014, 26, 1715-1729.	1.4	63
65	Complete genome sequence of the first endornavirus from the ascocarp of the ectomycorrhizal fungus <i>Tuber aestivum</i> Vittad.. <i>Archives of Virology</i> , 2011, 156, 343-345.	0.9	60
66	RNA Polymerase of <i>Aquifex pyrophilus</i> : Implications for the Evolution of the Bacterial rpoBC Operon and Extremely Thermophilic Bacteria. <i>Journal of Molecular Evolution</i> , 1999, 48, 528-541.	0.8	59
67	Genome biology of a novel lineage of planctomycetes widespread in anoxic aquatic environments. <i>Environmental Microbiology</i> , 2018, 20, 2438-2455.	1.8	57
68	DNA-dependent RNA polymerase subunit B as a tool for phylogenetic reconstructions: Branching topology of the archaeal domain. <i>Journal of Molecular Evolution</i> , 1994, 38, 420-432.	0.8	56
69	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
70	Hot standards for the thermoacidophilic archaeon <i>Sulfolobus solfataricus</i> . <i>Extremophiles</i> , 2010, 14, 119-142.	0.9	55
71	<i>Geodermatophilus africanus</i> sp. nov., a halotolerant actinomycete isolated from Saharan desert sand. <i>Antonie Van Leeuwenhoek</i> , 2013, 104, 207-216.	0.7	52
72	The Complete Genome Sequence of <i>Thermoproteus tenax</i> : A Physiologically Versatile Member of the Crenarchaeota. <i>PLoS ONE</i> , 2011, 6, e24222.	1.1	51

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73	Complete genome sequence of <i>Desulfobulbus propionicus</i> type strain (1pr3T). <i>Standards in Genomic Sciences</i> , 2011, 4, 100-110.	1.5	51
74	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 <i>Alicyclobacillaceae</i> da Costa and Rainey, 2010.. <i>Standards in Genomic Sciences</i> , 2011, 5, 121-134.	1.5	51
75	Characterization of the first cultured representative of a <i>Bacteroidetes</i> clade specialized on the scavenging of cyanobacteria. <i>Environmental Microbiology</i> , 2017, 19, 1134-1148.	1.8	50
76	<i>Fuerstia marisgermanicae</i> gen. nov., sp. nov., an Unusual Member of the Phylum Planctomycetes from the German Wadden Sea. <i>Frontiers in Microbiology</i> , 2016, 7, 2079.	1.5	49
77	<i>Geodermatophilus siccatus</i> sp. nov., isolated from arid sand of the Saharan desert in Chad. <i>Antonie Van Leeuwenhoek</i> , 2013, 103, 449-456.	0.7	48
78	<i>Frankia inefficax</i> sp. nov., an actinobacterial endophyte inducing ineffective, non nitrogen-fixing, root nodules on its actinorhizal host plants. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 313-320.	0.7	48
79	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
80	Codivergence of Mycoviruses with Their Hosts. <i>PLoS ONE</i> , 2011, 6, e22252.	1.1	46
81	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
82	Complete genome sequence of <i>Isosphaera pallida</i> type strain (IS1BT). <i>Standards in Genomic Sciences</i> , 2011, 4, 63-71.	1.5	46
83	Phylogeny-driven target selection for large-scale genome-sequencing (and other) projects. <i>Standards in Genomic Sciences</i> , 2013, 8, 360-374.	1.5	46
84	High Diversity of Culturable Prokaryotes in a Lithifying Hypersaline Microbial Mat. <i>Geomicrobiology Journal</i> , 2015, 32, 332-346.	1.0	46
85	Genomic Insights Into Plant-Growth-Promoting Potentialities of the Genus <i>Frankia</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1457.	1.5	46
86	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
87	Toward unrestricted use of public genomic data. <i>Science</i> , 2019, 363, 350-352.	6.0	45
88	Complete genome sequence of <i>Veillonella parvula</i> type strain (Te3T). <i>Standards in Genomic Sciences</i> , 2010, 2, 57-65.	1.5	44
89	Complete genome sequence of <i>Rhodospirillum rubrum</i> type strain (S1T). <i>Standards in Genomic Sciences</i> , 2011, 4, 293-302.	1.5	44
90	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 zuelzerae</i> in the genus <i>Treponema</i> as <i>Treponema caldaria</i> comb. nov., <i>Treponema stenostrepta</i> comb. nov., and <i>Treponema zuelzerae</i> comb. nov., and emendation of the genus <i>Treponema</i> . <i>Standards in Genomic Sciences</i> , 2013, 8, 88-105.	1.5	44

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91	454 Pyrosequencing-based assessment of bacterial diversity and community structure in termite guts, mounds and surrounding soils. SpringerPlus, 2015, 4, 471.	1.2	44
92	Complete genome sequence of <i>Olsenella uli</i> type strain (VPI D76D-27CT). Standards in Genomic Sciences, 2010, 3, 76-84.	1.5	43
93	Genome analysis of <i>Desulfotomaculum kuznetsovii</i> strain 17T reveals a physiological similarity with <i>Pelotomaculum thermopropionicum</i> strain SIT.. Standards in Genomic Sciences, 2013, 8, 69-87.	1.5	42
94	Chapter 12 Transcription in archaea. New Comprehensive Biochemistry, 1993, 26, 367-391.	0.1	41
95	The genome of <i>Hyperthermus butylicus</i> : a sulfur-reducing, peptide fermenting, neutrophilic Crenarchaeote growing up to 108 Å°C. Archaea, 2007, 2, 127-135.	2.3	41
96	Oxidation of aliphatic, branched chain, and aromatic hydrocarbons by <i>Nocardia cyriacigeorgica</i> isolated from oil-polluted sand samples collected in the Saudi Arabian Desert. Journal of Basic Microbiology, 2010, 50, 241-253.	1.8	41
97	Complete genome sequence of <i>Treponema succinifaciens</i> type strain (6091T). Standards in Genomic Sciences, 2011, 4, 361-370.	1.5	41
98	Complete genome sequence of <i>Spirosoma linguale</i> type strain (1T). Standards in Genomic Sciences, 2010, 2, 176-184.	1.5	40
99	Complete genome sequence of <i>Arcobacter nitrofigilis</i> type strain (CIT). Standards in Genomic Sciences, 2010, 2, 300-308.	1.5	40
100	A novel <i>Tuber aestivum</i> (Vittad.) mitovirus. Archives of Virology, 2011, 156, 1107-1110.	0.9	39
101	<i>Blastococcus capsensis</i> sp. nov., isolated from an archaeological Roman pool and emended description of the genus <i>Blastococcus</i> , <i>B. aggregatus</i> , <i>B. saxobsidens</i> , <i>B. jejuensis</i> and <i>B. endophyticus</i> . International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4864-4872.	0.8	39
102	Complete genome sequence of <i>Actinosynnema mirum</i> type strain (101T). Standards in Genomic Sciences, 2009, 1, 46-53.	1.5	38
103	Complete genome sequence of <i>Cellulomonas flavigena</i> type strain (134T). Standards in Genomic Sciences, 2010, 3, 15-25.	1.5	38
104	Complete genome sequence and description of <i>Salinispira pacifica</i> gen. nov., sp. nov., a novel spirochaete isolated from a hypersaline microbial mat. Standards in Genomic Sciences, 2015, 10, 7.	1.5	38
105	Complete genome sequence of <i>Eggerthella lenta</i> type strain (VPI 0255T). Standards in Genomic Sciences, 2009, 1, 174-182.	1.5	37
106	Complete genome sequence of <i>Desulfarculus baarsii</i> type strain (2st14T). Standards in Genomic Sciences, 2010, 3, 276-284.	1.5	37
107	Complete genome sequence of the sulfur compounds oxidizing chemolithoautotroph <i>Sulfuricurvum kujijense</i> type strain (YK-1T). Standards in Genomic Sciences, 2012, 6, 94-103.	1.5	37
108	Description of <i>Streptomonospora sediminis</i> sp. nov. and <i>Streptomonospora nanhaiensis</i> sp. nov., and reclassification of <i>Nocardiopsis arabia</i> Hozzein & Goodfellow 2008 as <i>Streptomonospora arabica</i> comb. nov. and emended description of the genus <i>Streptomonospora</i> . International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 4447-4455.	0.8	37

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109	<i>Frankia coriariae</i> sp. nov., an infective and effective microsymbiont isolated from <i>Coriaria japonica</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 1266-1270.	0.8	37
110	Complete genome sequence of <i>Sulfurimonas autotrophica</i> type strain (OK10T). <i>Standards in Genomic Sciences</i> , 2010, 3, 194-202.	1.5	37
111	Biochemical and Phylogenetic Characterization of the dUTPase from the Archaeal Virus SIRV. <i>Journal of Biological Chemistry</i> , 1998, 273, 6024-6029.	1.6	36
112	Complete genome sequence of <i>Desulfomicrobium baculatum</i> type strain (XT). <i>Standards in Genomic Sciences</i> , 2009, 1, 29-37.	1.5	36
113	Complete genome sequence of the extremely halophilic <i>Halanaerobium praevalens</i> type strain (GSLT). <i>Standards in Genomic Sciences</i> , 2011, 4, 312-321.	1.5	36
114	Isolation, characterization and analysis of bacteriophages from the haloalkaline lake Elmenteita, Kenya. <i>PLoS ONE</i> , 2019, 14, e0215734.	1.1	36
115	Degradation of the multiple branched alkane 2,6,10,14-tetramethyl-pentadecane (pristane) in <i>Rhodococcus ruber</i> and <i>Mycobacterium neoaurum</i> . <i>International Biodeterioration and Biodegradation</i> , 2009, 63, 201-207.	1.9	35
116	Complete genome sequence of <i>Desulfotomaculum acetoxidans</i> type strain (5575T). <i>Standards in Genomic Sciences</i> , 2009, 1, 242-253.	1.5	35
117	Complete genome sequence of <i>Nakamurella multipartita</i> type strain (Y-104T). <i>Standards in Genomic Sciences</i> , 2010, 2, 168-175.	1.5	35
118	Complete genome sequence of the halophilic and highly halotolerant <i>Chromohalobacter salexigens</i> type strain (1H11T). <i>Standards in Genomic Sciences</i> , 2011, 5, 379-388.	1.5	35
119	Complete genome sequence of <i>Thermomonospora curvata</i> type strain (B9T). <i>Standards in Genomic Sciences</i> , 2011, 4, 13-22.	1.5	35
120	<i>Kibdelosporangium phytohabitans</i> sp. nov., a novel endophytic actinomycete isolated from oil-seed plant <i>Jatropha curcas</i> L. containing 1-aminocyclopropane-1-carboxylic acid deaminase. <i>Antonie Van Leeuwenhoek</i> , 2012, 101, 433-441.	0.7	35
121	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
122	Complete genome sequence of <i>Sebaldella termitidis</i> type strain (NCTC 11300T). <i>Standards in Genomic Sciences</i> , 2010, 2, 220-227.	1.5	34
123	<i>Geodermatophilus pulveris</i> sp. nov., a gamma-radiation-resistant actinobacterium isolated from the Sahara desert. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 3828-3834.	0.8	34
124	<i>Frankia asymbiotica</i> sp. nov., a non-infective actinobacterium isolated from <i>Morella californica</i> root nodule. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 4897-4901.	0.8	34
125	<i>Nonomuraea antimicrobica</i> sp. nov., an endophytic actinomycete isolated from a leaf of <i>Maytenus austroyunnanensis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 2747-2751.	0.8	33
126	Complete genome sequence of <i>Meiothermus ruber</i> type strain (21T). <i>Standards in Genomic Sciences</i> , 2010, 3, 26-36.	1.5	33

#	ARTICLE	IF	CITATIONS
127	Complete genome sequence of <i>Cellulophaga lytica</i> type strain (LIM-21T). <i>Standards in Genomic Sciences</i> , 2011, 4, 221-232.	1.5	33
128	Complete genome sequence of <i>Polynucleobacter necessarius</i> subsp. <i>asymbioticus</i> type strain (QLW-P1DMWA-1T). <i>Standards in Genomic Sciences</i> , 2012, 6, 74-83.	1.5	33
129	A novel mitovirus from the hypogeous ectomycorrhizal fungus <i>Tuber excavatum</i> . <i>Archives of Virology</i> , 2012, 157, 787-790.	0.9	33
130	<i>Actinopolyspora mزابensis</i> sp. nov., a halophilic actinomycete isolated from an Algerian Saharan soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 3787-3792.	0.8	33
131	Comparative Genomic Analysis of the Genus <i>Nocardiopsis</i> Provides New Insights into Its Genetic Mechanisms of Environmental Adaptability. <i>PLoS ONE</i> , 2013, 8, e61528.	1.1	33
132	<i>Frankia discariae</i> sp. nov.: an infective and effective microsymbiont isolated from the root nodule of <i>Discaria trinervis</i> . <i>Archives of Microbiology</i> , 2017, 199, 641-647.	1.0	33
133	Complete genome sequence of <i>Acidimicrobium ferrooxidans</i> type strain (ICPT). <i>Standards in Genomic Sciences</i> , 2009, 1, 38-45.	1.5	32
134	Complete genome sequence of <i>Nocardiopsis dassonvillei</i> type strain (IMRU 509T). <i>Standards in Genomic Sciences</i> , 2010, 3, 325-336.	1.5	32
135	Complete genome sequence of <i>Haloterrigena turkmenica</i> type strain (4kT). <i>Standards in Genomic Sciences</i> , 2010, 2, 107-116.	1.5	32
136	Complete genome sequence of <i>Aminobacterium colombiense</i> type strain (ALA-1T). <i>Standards in Genomic Sciences</i> , 2010, 2, 280-289.	1.5	32
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138	Species Delimitation in Taxonomically Difficult Fungi: The Case of <i>Hymenogaster</i> . <i>PLoS ONE</i> , 2011, 6, e15614.	1.1	32
139	Location of Protist Lineages in a Phylogenetic Tree Inferred from Sequences of DNA-dependent RNA Polymerases. <i>Archiv für Protistenkunde</i> , 1995, 145, 221-230.	0.8	31
140	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
141	Complete genome sequence of <i>Planctomyces limnophilus</i> type strain (MÄ¼ 290T). <i>Standards in Genomic Sciences</i> , 2010, 3, 47-56.	1.5	31
142	Complete genome sequence of <i>Acidaminococcus fermentans</i> type strain (VR4T). <i>Standards in Genomic Sciences</i> , 2010, 3, 1-14.	1.5	31
143	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
144	Complete genome sequence of <i>Paludibacter propionicigenes</i> type strain (WB4T). <i>Standards in Genomic Sciences</i> , 2011, 4, 36-44.	1.5	30

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145	High quality draft genome sequences of <i>Pseudomonas fulva</i> DSM 17717T, <i>Pseudomonas parafulva</i> DSM 17004T and <i>Pseudomonas cremoricolorata</i> DSM 17059T type strains. <i>Standards in Genomic Sciences</i> , 2016, 11, 55.	1.5	30
146	Complete genome sequence of <i>Sulfurospirillum deleyianum</i> type strain (5175T). <i>Standards in Genomic Sciences</i> , 2010, 2, 149-157.	1.5	29
147	<i>Actinopolyspora saharensis</i> sp. nov., a novel halophilic actinomycete isolated from a Saharan soil of Algeria. <i>Antonie Van Leeuwenhoek</i> , 2013, 103, 771-776.	0.7	29
148	<i>Frankia torreyi</i> sp. nov., the first actinobacterium of the genus <i>Frankia</i> Brunchorst 1886, 174AL isolated in axenic culture. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 57-65.	0.7	29
149	An update on the taxonomy of the genus <i>Frankia</i> Brunchorst, 1886, 174AL. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 5-21.	0.7	29
150	<i>Labrenzia salina</i> sp. nov., isolated from the rhizosphere of the halophyte <i>Arthrocnemum macrostachyum</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 5173-5180.	0.8	29
151	Genomic Standards Consortium Projects. <i>Standards in Genomic Sciences</i> , 2014, 9, 599-601.	1.5	29
152	Characterization and phylogeny of <i>mcrII</i> , a gene cluster encoding an isoenzyme of methyl coenzyme M reductase from hyperthermophilic <i>Methanothermus fervidus</i> . <i>Molecular Genetics and Genomics</i> , 1994, 243, 198-206.	2.4	28
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154	Complete genome sequence of <i>Kangiella koreensis</i> type strain (SW-125T). <i>Standards in Genomic Sciences</i> , 2009, 1, 226-233.	1.5	28
155	Complete genome sequence of <i>Coralimargarita akajimensis</i> type strain (04OKA010-24T). <i>Standards in Genomic Sciences</i> , 2010, 2, 290-299.	1.5	28
156	Complete genome sequence of <i>Cellulophaga algicola</i> type strain (IC166T). <i>Standards in Genomic Sciences</i> , 2011, 4, 72-80.	1.5	28
157	<i>Actinopolyspora righensis</i> sp. nov., a novel halophilic actinomycete isolated from Saharan soil in Algeria. <i>Antonie Van Leeuwenhoek</i> , 2013, 104, 301-307.	0.7	28
158	16S-rRNA-based analysis of bacterial diversity in the gut of fungus-cultivating termites (<i>Microtermes</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.7	28
159	Pathways and substrate-specific regulation of amino acid degradation in <i>Pseudomonas</i> <i>inhibens</i> DSM 17395 (archetype of the marine <i>Roseobacter</i> clade). <i>Environmental Microbiology</i> , 2014, 16, 218-238.	1.8	28
160	<i>Nocardia vulneris</i> sp. nov., isolated from wounds of human patients in North America. <i>Antonie Van Leeuwenhoek</i> , 2014, 106, 543-553.	0.7	28
161	Description of gamma radiation-resistant <i>Geodermatophilus dictyosporus</i> sp. nov. to accommodate the not validly named <i>Geodermatophilus obscurus</i> subsp. <i>dictyosporus</i> (Luedemann, 1968). <i>Extremophiles</i> , 2015, 19, 77-85.	0.9	28
162	Complete genome sequence of <i>Sphaerobacter thermophilus</i> type strain (S 6022T). <i>Standards in Genomic Sciences</i> , 2010, 2, 49-56.	1.5	27

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164	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.	1.5	27
165	Genome analysis of <i>Desulfotomaculum gibsoniae</i> strain GrollT a highly versatile Gram-positive sulfate-reducing bacterium. <i>Standards in Genomic Sciences</i> , 2014, 9, 821-839.	1.5	27
166	<i>Nocardiopsis algeriensis</i> sp. nov., an alkalitolerant actinomycete isolated from Saharan soil. <i>Antonie Van Leeuwenhoek</i> , 2015, 107, 313-320.	0.7	27
167	Comparing polysaccharide decomposition between the type strains <i>Gramella echinicola</i> KMM 6050T (DSM 19838T) and <i>Gramella portivictoriae</i> UST040801-001T (DSM 23547T), 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.	1.5	27
168	Characterization and sequence comparison of temperature-regulated chaperonins from the hyperthermophilic archaeon <i>Archaeoglobus fulgidus</i> . <i>Gene</i> , 1998, 215, 431-438.	1.0	26
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170	Complete genome sequence of <i>Gordonia bronchialis</i> type strain (3410T). <i>Standards in Genomic Sciences</i> , 2010, 2, 19-28.	1.5	26
171	Complete genome sequence of <i>Haliscomenobacter hydrossis</i> type strain (OT). <i>Standards in Genomic Sciences</i> , 2011, 4, 352-360.	1.5	26
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174	<i>Saccharothrix hoggarensis</i> sp. nov., an actinomycete isolated from Saharan soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 549-553.	0.8	26
175	Non-contiguous finished genome sequence of plant-growth promoting <i>Serratia proteamaculans</i> S4. <i>Standards in Genomic Sciences</i> , 2013, 8, 441-449.	1.5	26
176	Genome sequence of <i>Phaeobacter inhibens</i> type strain (T5T), a secondary metabolite producing representative of the marine <i>Roseobacter</i> clade, and emendation of the species description of <i>Phaeobacter inhibens</i> . <i>Standards in Genomic Sciences</i> , 2013, 9, 334-350.	1.5	26
177	<i>Mzabimyces algeriensis</i> gen. nov., sp. nov., a halophilic filamentous actinobacterium isolated from a Saharan soil, and proposal of <i>Mzabimycetaceae</i> fam. nov.. <i>Antonie Van Leeuwenhoek</i> , 2014, 106, 1021-1030.	0.7	26
178	SulfoSYS (Sulfolobus Systems Biology): towards a silicon cell model for the central carbohydrate metabolism of the archaeon <i>Sulfolobus solfataricus</i> under temperature variation. <i>Biochemical Society Transactions</i> , 2009, 37, 58-64.	1.6	25
179	Complete genome sequence of <i>Pedobacter heparinus</i> type strain (HIM 762-3T). <i>Standards in Genomic Sciences</i> , 2009, 1, 54-62.	1.5	25
180	Complete genome sequence of <i>Anaerococcus prevotii</i> type strain (PC1T). <i>Standards in Genomic Sciences</i> , 2009, 1, 159-165.	1.5	25

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182	Complete genome sequence of <i>Dyadobacter fermentans</i> type strain (NS114T). <i>Standards in Genomic Sciences</i> , 2009, 1, 133-140.	1.5	25
183	<i>Streptomyces iranensis</i> sp. nov., isolated from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010, 60, 1504-1509.	0.8	25
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185	<i>Actinopolyspora algeriensis</i> sp. nov., a novel halophilic actinomycete isolated from a Saharan soil. <i>Extremophiles</i> , 2012, 16, 771-776.	0.9	25
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187	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
188	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
189	Complete genome sequence of <i>Saccharomonospora viridis</i> type strain (P101T). <i>Standards in Genomic Sciences</i> , 2009, 1, 141-149.	1.5	24
190	Complete genome sequence of <i>Conexibacter woesei</i> type strain (ID131577T). <i>Standards in Genomic Sciences</i> , 2010, 2, 212-219.	1.5	24
191	Complete genome sequence of <i>Acetohalobium arabaticum</i> type strain (Z-7288T). <i>Standards in Genomic Sciences</i> , 2010, 3, 57-65.	1.5	24
192	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
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197	Complete genome sequence of <i>Halogeometricum borinquense</i> type strain (PR3T). <i>Standards in Genomic Sciences</i> , 2009, 1, 150-158.	1.5	23
198	Complete genome sequence of <i>Thermanaerovibrio acidaminovorans</i> type strain (Su883T). <i>Standards in Genomic Sciences</i> , 2009, 1, 254-261.	1.5	23

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200	Complete genome sequence of <i>Thermobispora bispora</i> type strain (R51T). <i>Standards in Genomic Sciences</i> , 2010, 2, 318-326.	1.5	23
201	Complete genome sequence of the gliding freshwater bacterium <i>Fluviicola taffensis</i> type strain (RW262T). <i>Standards in Genomic Sciences</i> , 2011, 5, 21-29.	1.5	23
202	<i>Streptomyces sediminis</i> sp. nov. isolated from crater lake sediment. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 493-500.	0.7	23
203	Revisiting the Taxonomic Status of the Biomedically and Industrially Important Genus <i>Amycolatopsis</i> , Using a Phylogenomic Approach. <i>Frontiers in Microbiology</i> , 2018, 9, 2281.	1.5	23
204	<i>Micromonospora profundus</i> sp. nov., isolated from deep marine sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 4735-4743.	0.8	23
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206	Complete genome sequence of <i>Desulfohalobium retbaense</i> type strain (HR100T). <i>Standards in Genomic Sciences</i> , 2010, 2, 38-48.	1.5	22
207	Complete genome sequence of <i>Leadbetterella byssophila</i> type strain (4M15T). <i>Standards in Genomic Sciences</i> , 2011, 4, 2-12.	1.5	22
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209	Complete genome sequence of the plant-associated <i>Serratia plymuthica</i> strain AS13. <i>Standards in Genomic Sciences</i> , 2012, 7, 22-30.	1.5	22
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211	<i>Saccharopolyspora ghardaiensis</i> sp. nov., an extremely halophilic actinomycete isolated from Algerian Saharan soil. <i>Journal of Antibiotics</i> , 2014, 67, 299-303.	1.0	22
212	Identification of novel biomass-degrading enzymes from genomic dark matter: Populating genomic sequence space with functional annotation. <i>Biotechnology and Bioengineering</i> , 2014, 111, 1550-1565.	1.7	22
213	Genome sequence of the mud-dwelling archaeon <i>Methanoplanus limicola</i> type strain (DSM 2279T), 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, 1076-1088.	1.5	22
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215	<i>Actinokineospora mzabensis</i> sp. nov., a novel actinomycete isolated from Saharan soil. <i>Antonie Van Leeuwenhoek</i> , 2015, 107, 291-296.	0.7	22
216	<i>Streptosporangium becharensis</i> sp. nov., an actinobacterium isolated from desert soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2484-2490.	0.8	22

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218	Complete genome sequence of <i>Streptobacillus moniliformis</i> type strain (9901T). <i>Standards in Genomic Sciences</i> , 2009, 1, 300-307.	1.5	21
219	Complete genome sequence of the <i>Phaeobacter gallaeciensis</i> type strain CIP 105210T (= DSM 26640T =) Tj ETQq1_1_0.784314 rgBT	1.5	21
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221	<i>Pseudomonas khazarica</i> sp. nov., a polycyclic aromatic hydrocarbon-degrading bacterium isolated from Khazar Sea sediments. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 521-532.	0.7	21
222	<i>Prauserella isguenensis</i> sp. nov., a halophilic actinomycete isolated from desert soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 1598-1603.	0.8	21
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226	<i>Saccharothrix tamanrassetensis</i> sp. nov., an actinomycete isolated from Saharan soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 1316-1320.	0.8	20
227	<i>Actinomadura algeriensis</i> sp. nov., an actinobacterium isolated from Saharan soil. <i>Antonie Van Leeuwenhoek</i> , 2016, 109, 159-165.	0.7	20
228	Editorial: Actinobacteria in Special and Extreme Habitats: Diversity, Function Roles and Environmental Adaptations, Second Edition. <i>Frontiers in Microbiology</i> , 2019, 10, 944.	1.5	20
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231	Complete genome sequence of <i>Meiothermus silvanus</i> type strain (VI-R2T). <i>Standards in Genomic Sciences</i> , 2010, 3, 37-46.	1.5	19
232	Description of <i>Geodermatophilus bullaregiensis</i> sp. nov.. <i>Antonie Van Leeuwenhoek</i> , 2015, 108, 415-425.	0.7	19
233	<i>Microbulbifer rhizosphaerae</i> sp. nov., isolated from the rhizosphere of the halophyte <i>Arthrocnemum macrostachyum</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 1844-1850.	0.8	19
234	<i>Actinophytocola algeriensis</i> sp. nov., an actinobacterium isolated from Saharan soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2760-2765.	0.8	19

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236	Complete genome sequence of <i>Thermocrinis albus</i> type strain (HI 11/12T). <i>Standards in Genomic Sciences</i> , 2010, 2, 194-202.	1.5	18
237	Complete genome sequence of <i>Spirochaeta smaragdinae</i> type strain (SEBR 4228T). <i>Standards in Genomic Sciences</i> , 2010, 3, 1-9.	1.5	18
238	Complete genome sequence of <i>Marivirga tractuosa</i> type strain (H-43T). <i>Standards in Genomic Sciences</i> , 2011, 4, 154-162.	1.5	18
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240	<i>Nonomuraea jabiensis</i> sp. nov., isolated from arid soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 212-218.	0.8	18
241	<i>Streptomonospora algeriensis</i> sp. nov., a halophilic actinomycete isolated from soil in Algeria. <i>Antonie Van Leeuwenhoek</i> , 2014, 106, 287-292.	0.7	18
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243	<i>Blastococcus colisei</i> sp. nov, isolated from an archaeological amphitheatre. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 339-346.	0.7	18
244	Complete genome sequence of <i>Cryptobacterium curtum</i> type strain (12-3T). <i>Standards in Genomic Sciences</i> , 2009, 1, 93-100.	1.5	17
245	Complete genome sequence of <i>Methanothermus fervidus</i> type strain (V24ST). <i>Standards in Genomic Sciences</i> , 2010, 3, 315-324.	1.5	17
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248	<i>Actinomadura adrarensis</i> sp. nov., an actinobacterium isolated from Saharan soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2724-2729.	0.8	17
249	Nucleotide sequence of the genes encoding the L30, S12 and S7 equivalent ribosomal proteins from the archaeum <i>Thermococcus celer</i> . <i>Nucleic Acids Research</i> , 1991, 19, 6047-6047.	6.5	16
250	Nucleotide sequence of the genes encoding the subunits H, B, A α ² and A α ³ of te DNA-dependent RNA polymerase and the initiator tRNA from <i>Thermoplasma acidophilum</i> . <i>Nucleic Acids Research</i> , 1992, 20, 5226-5226.	6.5	16
251	Complete genome sequence of <i>Sanguibacter keddieii</i> type strain (ST-74T). <i>Standards in Genomic Sciences</i> , 2009, 1, 110-118.	1.5	16
252	Complete genome sequence of <i>Denitrovibrio acetiphilus</i> type strain (N2460T). <i>Standards in Genomic Sciences</i> , 2010, 2, 270-279.	1.5	16

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253	Complete genome sequence of the gliding, heparinolytic <i>Pedobacter saltans</i> type strain (113T). <i>Standards in Genomic Sciences</i> , 2011, 5, 30-40.	1.5	16
254	Genome sequence of the Antarctic rhodopsins-containing flavobacterium <i>Gillisia limnaea</i> type strain (R-8282T). <i>Standards in Genomic Sciences</i> , 2012, 7, 107-119.	1.5	16
255	Complete genome sequence of <i>Enterobacter</i> sp. IIT-BT 08: A potential microbial strain for high rate hydrogen production. <i>Standards in Genomic Sciences</i> , 2013, 9, 359-369.	1.5	16
256	High quality draft genome sequence of <i>Flavobacterium rivuli</i> type strain WB 3.3-2T (DSM 21788T), a valuable source of polysaccharide decomposing enzymes. <i>Standards in Genomic Sciences</i> , 2015, 10, 46.	1.5	16
257	<i>Streptomyces alkaliphilus</i> sp. nov., isolated from sediments of Lake Elmenteita in the Kenyan Rift Valley. <i>Antonie Van Leeuwenhoek</i> , 2015, 107, 1249-1259.	0.7	16
258	<i>Saccharothrix ghardaiensis</i> sp. nov., an actinobacterium isolated from Saharan soil. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 399-405.	0.7	16
259	<i>Micromonospora orduensis</i> sp. nov., isolated from deep marine sediment. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 397-405.	0.7	16
260	pIT3, a cryptic plasmid isolated from the hyperthermophilic crenarchaeon <i>Sulfolobus solfataricus</i> IT3. <i>Plasmid</i> , 2006, 56, 35-45.	0.4	15
261	Complete genome sequence of <i>Ignisphaera aggregans</i> type strain (AQ1.S1T). <i>Standards in Genomic Sciences</i> , 2010, 3, 66-75.	1.5	15
262	Complete genome sequence of <i>Weeksella virosa</i> type strain (9751T). <i>Standards in Genomic Sciences</i> , 2011, 4, 81-90.	1.5	15
263	Complete genome sequence of the marine methyl-halide oxidizing <i>Leisingera methylohalidivorans</i> type strain (DSM 14336T), a representative of the <i>Roseobacter</i> clade. <i>Standards in Genomic Sciences</i> , 2013, 9, 128-141.	1.5	15
264	<i>Actinoalloteichus hoggarensis</i> sp. nov., an actinomycete isolated from Saharan soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 2006-2010.	0.8	15
265	<i>Belliella kenyensis</i> sp. nov., isolated from an alkaline lake. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 457-462.	0.8	15
266	High quality draft genome sequence of <i>Meganema perideroedes</i> str. Gr1T and a proposal for its reclassification to the family <i>Meganemaceae</i> fam. nov.. <i>Standards in Genomic Sciences</i> , 2015, 10, 23.	1.5	15
267	<i>Nocardia donostiensis</i> sp. nov., isolated from human respiratory specimens. <i>Antonie Van Leeuwenhoek</i> , 2016, 109, 653-660.	0.7	15
268	<i>Kribbella soli</i> sp. nov., isolated from soil. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 641-649.	0.7	15
269	<i>Planomonospora algeriensis</i> sp. nov., an actinobacterium isolated from a Saharan soil of Algeria. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 245-252.	0.7	15
270	<i>Kocuria salina</i> sp. nov., an actinobacterium isolated from the rhizosphere of the halophyte <i>Arthrocnemum macrostachyum</i> and emended description of <i>Kocuria turfaniensis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 5006-5012.	0.8	15

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272	<i>Pseudoalteromonas rhizosphaerae</i> sp. nov., a novel plant growth-promoting bacterium with potential use in phytoremediation. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3287-3294.	0.8	15
273	Complete genome sequence of <i>Capnocytophaga ochracea</i> type strain (VPI 2845T). <i>Standards in Genomic Sciences</i> , 2009, 1, 101-109.	1.5	14
274	Complete genome sequence of <i>Jonesia denitrificans</i> type strain (Prevot 55134T). <i>Standards in Genomic Sciences</i> , 2009, 1, 262-269.	1.5	14
275	Complete genome sequence of <i>Ferrimonas balearica</i> type strain (PATT). <i>Standards in Genomic Sciences</i> , 2010, 3, 174-182.	1.5	14
276	Complete genome sequence of <i>Thermosphaera aggregans</i> type strain (M11TLT). <i>Standards in Genomic Sciences</i> , 2010, 2, 245-259.	1.5	14
277	Complete genome sequence of <i>Bacteroides helcogenes</i> type strain (P 36-108T). <i>Standards in Genomic Sciences</i> , 2011, 4, 45-53.	1.5	14
278	Complete genome sequence of <i>Deinococcus maricopenis</i> type strain (LB-34T). <i>Standards in Genomic Sciences</i> , 2011, 4, 163-172.	1.5	14
279	Complete genome sequence of the thermophilic sulfate-reducing ocean bacterium <i>Thermodesulfator indicus</i> type strain (CIR29812T). <i>Standards in Genomic Sciences</i> , 2012, 6, 155-164.	1.5	14
280	Complete genome sequence of the orange-red pigmented, radioresistant <i>Deinococcus proteolyticus</i> type strain (MRPT). <i>Standards in Genomic Sciences</i> , 2012, 6, 240-250.	1.5	14
281	Charcoal filter paper improves the viability of cryopreserved filamentous ectomycorrhizal and saprotrophic Basidiomycota and Ascomycota. <i>Mycologia</i> , 2012, 104, 324-330.	0.8	14
282	<i>Hoffmannoscypha</i> , a novel genus of brightly coloured, cupulate Pyrenomataceae closely related to <i>Tricharina</i> and <i>Geopora</i> . <i>Mycological Progress</i> , 2013, 12, 675-686.	0.5	14
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284	Hunting for cultivable <i>Micromonospora</i> strains in soils of the Atacama Desert. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 1375-1387.	0.7	14
285	<i>Brevundimonas canariensis</i> sp. nov., isolated from roots of <i>Triticum aestivum</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 969-973.	0.8	14
286	Complete genome sequence of <i>Methanoplanus petrolearius</i> type strain (SEBR 4847T). <i>Standards in Genomic Sciences</i> , 2010, 3, 203-211.	1.5	14
287	Complete genome sequence of <i>Nitratifactor salsuginis</i> type strain (E9137-1T). <i>Standards in Genomic Sciences</i> , 2011, 4, 322-330.	1.5	13
288	Complete genome sequence of the hyperthermophilic chemolithoautotroph <i>Pyrolobus fumarii</i> type strain (1AT). <i>Standards in Genomic Sciences</i> , 2011, 4, 381-392.	1.5	13

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289	Genome sequence of the soil bacterium <i>Saccharomonospora azurea</i> type strain (NA-128T). <i>Standards in Genomic Sciences</i> , 2012, 6, 220-229.	1.5	13
290	<i>Actinopolyspora biskrensis</i> sp. nov., a Novel Halophilic Actinomycete Isolated from Northern Sahara. <i>Current Microbiology</i> , 2015, 70, 423-428.	1.0	13
291	Draft Genome Sequence of <i>Frankia</i> Strain G2, a Nitrogen-Fixing Actinobacterium Isolated from <i>Casuarina equisetifolia</i> and Able To Nodulate Actinorhizal Plants of the Order <i>Rhamales</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	13
292	<i>Micromonospora yasonensis</i> sp. nov., isolated from a Black Sea sediment. <i>Antonie Van Leeuwenhoek</i> , 2016, 109, 1019-1028.	0.7	13
293	<i>Streptosporangium algeriense</i> sp. nov., an actinobacterium isolated from desert soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 1034-1038.	0.8	13
294	<i>Saccharothrix isguenensis</i> sp. nov., an actinobacterium isolated from desert soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 4785-4790.	0.8	13
295	<i>Nakamurella silvestris</i> sp. nov., an actinobacterium isolated from alpine forest soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 5460-5464.	0.8	13
296	<i>Mycobacterium eburneum</i> sp. nov., a non-chromogenic, fast-growing strain isolated from sputum. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 3174-3181.	0.8	13
297	Complete genome sequence of <i>Beutenbergia cavernae</i> type strain (HKI 0122T). <i>Standards in Genomic Sciences</i> , 2009, 1, 21-28.	1.5	12
298	Complete genome sequence of <i>Thermosediminibacter oceani</i> type strain (JW/IW-1228PT). <i>Standards in Genomic Sciences</i> , 2010, 3, 108-116.	1.5	12
299	Complete genome sequence of <i>Hydrogenobacter thermophilus</i> type strain (TK-6T). <i>Standards in Genomic Sciences</i> , 2011, 4, 131-143.	1.5	12
300	Complete genome sequence of <i>Hirschia baltica</i> type strain (IFAM 1418T). <i>Standards in Genomic Sciences</i> , 2011, 5, 287-297.	1.5	12
301	Genome sequence of the moderately thermophilic halophile <i>Flexistipes sinusarabici</i> strain (MAS10T). <i>Standards in Genomic Sciences</i> , 2011, 5, 86-96.	1.5	12
302	Complete genome sequence of the bile-resistant pigment-producing anaerobe <i>Alistipes finegoldii</i> type strain (AHN2437T). <i>Standards in Genomic Sciences</i> , 2013, 8, 26-36.	1.5	12
303	Genome sequence of <i>Phaeobacter daeponensis</i> type strain (DSM 23529T), a facultatively anaerobic bacterium isolated from marine sediment, and emendation of <i>Phaeobacter daeponensis</i> . <i>Standards in Genomic Sciences</i> , 2013, 9, 142-159.	1.5	12
304	Genome sequence of the pink to light reddish-pigmented <i>Rubellimicrobium mesophilum</i> type strain (DSM 19309T), a representative of the <i>Roseobacter</i> group isolated from soil, and emended description of the species. <i>Standards in Genomic Sciences</i> , 2014, 9, 902-913.	1.5	12
305	<i>Caldisaliniibacter kiritimatiensis</i> gen. nov., sp. nov., a Moderately Thermohalophilic Thiosulfate-Reducing Bacterium from a Hypersaline Microbial Mat. <i>Geomicrobiology Journal</i> , 2015, 32, 347-354.	1.0	12
306	<i>Kroppenstedtia pulmonis</i> sp. nov. and <i>Kroppenstedtia sanguinis</i> sp. nov., isolated from human patients. <i>Antonie Van Leeuwenhoek</i> , 2016, 109, 603-610.	0.7	12

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308	<i>Actinomadura alkaliterrae</i> sp. nov., isolated from an alkaline soil. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 787-794.	0.7	12
309	Formal description of <i>Mycobacterium neglectum</i> sp. nov. and <i>Mycobacterium palauense</i> sp. nov., rapidly growing actinobacteria. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 1209-1223.	0.7	12
310	Reclassification of <i>Mzabimyces algeriensis</i> Saker et al. 2015 as <i>Halopolyspora algeriensis</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 2787-2790.	0.8	12
311	Two novel species of rapidly growing mycobacteria: <i>Mycobacterium lehmannii</i> sp. nov. and <i>Mycobacterium neumannii</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 4948-4955.	0.8	12
312	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.	1.5	12
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314	Complete genome sequence of <i>Kribbella flavida</i> type strain (IFO 14399T). <i>Standards in Genomic Sciences</i> , 2010, 2, 185-192.	1.5	11
315	Complete genome sequence of <i>Thermobaculum terrenum</i> ™ type strain (YNP1T). <i>Standards in Genomic Sciences</i> , 2010, 3, 153-162.	1.5	11
316	Complete genome sequence of the thermophilic sulfur-reducer <i>Desulfurobacterium thermolithotrophum</i> type strain (BSAT) from a deep-sea hydrothermal vent. <i>Standards in Genomic Sciences</i> , 2011, 5, 407-415.	1.5	11
317	Complete genome sequence of <i>Bacteroides salanitronis</i> type strain (BL78T). <i>Standards in Genomic Sciences</i> , 2011, 4, 191-199.	1.5	11
318	Genome sequence of the orange-pigmented seawater bacterium <i>Owenweeksia hongkongensis</i> type strain (UST20020801T). <i>Standards in Genomic Sciences</i> , 2012, 7, 120-130.	1.5	11
319	High-quality-draft genome sequence of the yellow-pigmented flavobacterium <i>Joostella marina</i> type strain (En5T). <i>Standards in Genomic Sciences</i> , 2013, 8, 37-46.	1.5	11
320	Complete genome sequence of the moderate thermophile <i>Anaerobaculum mobile</i> type strain (NGAT). <i>Standards in Genomic Sciences</i> , 2013, 8, 47-57.	1.5	11
321	Genome sequence of the free-living aerobic spirochete <i>Turneriella parva</i> type strain (HT), and emendation of the species <i>Turneriella parva</i> . <i>Standards in Genomic Sciences</i> , 2013, 8, 228-238.	1.5	11
322	Genome sequence of the exopolysaccharide-producing <i>Salipiger mucosus</i> type strain (DSM 16094T), a moderately halophilic member of the <i>Roseobacter</i> clade. <i>Standards in Genomic Sciences</i> , 2014, 9, 1333-1345.	1.5	11
323	<i>Nocardia arizonensis</i> sp. nov., obtained from human respiratory specimens. <i>Antonie Van Leeuwenhoek</i> , 2015, 108, 1129-1137.	0.7	11
324	<i>Nocardiopsis mwathae</i> sp. nov., isolated from the haloalkaline Lake Elmenteita in the African Rift Valley. <i>Antonie Van Leeuwenhoek</i> , 2016, 109, 421-430.	0.7	11

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326	Genome-based classification of <i>Micromonospora craterilacus</i> sp. nov., a novel actinobacterium isolated from Nemrut Lake. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 791-801.	0.7	11
327	<i>Promicromonospora kermanensis</i> sp. nov., an actinobacterium isolated from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 262-267.	0.8	11
328	<i>Streptomyces harenosi</i> sp. nov., a home for a gifted strain isolated from Indonesian sand dune soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4874-4882.	0.8	11
329	Complete genome sequence of <i>Ilyobacter polytropus</i> type strain (CuHbu1T). <i>Standards in Genomic Sciences</i> , 2010, 3, 304-314.	1.5	10
330	Complete genome sequence of <i>Vulcanisaeta distributa</i> type strain (IC-017T). <i>Standards in Genomic Sciences</i> , 2010, 3, 117-125.	1.5	10
331	Complete genome sequence of <i>Thermaerobacter marianensis</i> type strain (7p75aT). <i>Standards in Genomic Sciences</i> , 2010, 3, 337-345.	1.5	10
332	Complete genome sequence of <i>Xylanimonas cellulositytica</i> type strain (XIL07T). <i>Standards in Genomic Sciences</i> , 2010, 2, 1-8.	1.5	10
333	Complete genome sequence of <i>Segniliparus rotundus</i> type strain (CDC 1076T). <i>Standards in Genomic Sciences</i> , 2010, 2, 203-211.	1.5	10
334	Complete genome sequence of <i>Desulfurococcus mucosus</i> type strain (O7/1T). <i>Standards in Genomic Sciences</i> , 2011, 4, 173-182.	1.5	10
335	Complete genome sequence of <i>Calditerrivibrio nitroreducens</i> type strain (Yu37-1T). <i>Standards in Genomic Sciences</i> , 2011, 4, 54-62.	1.5	10
336	Complete genome sequence of <i>Tsukamurella paurometabola</i> type strain (no. 33T). <i>Standards in Genomic Sciences</i> , 2011, 4, 342-351.	1.5	10
337	Complete genome sequence of the facultatively anaerobic, appendaged bacterium <i>Muricauda ruestringensis</i> type strain (B1T). <i>Standards in Genomic Sciences</i> , 2012, 6, 185-193.	1.5	10
338	Genome of the R-body producing marine alphaproteobacterium <i>Labrenzia alexandrii</i> type strain (DFL-11T). <i>Standards in Genomic Sciences</i> , 2013, 7, 413-426.	1.5	10
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340	<i>Nonomuraea insulae</i> sp. nov., isolated from forest soil. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 2051-2059.	0.7	10
341	High-quality draft genome sequences of <i>Pseudomonas monteilii</i> DSM 14164T, <i>Pseudomonas mosselii</i> DSM 17497T, <i>Pseudomonas plecoglossicida</i> DSM 15088T, <i>Pseudomonas taiwanensis</i> DSM 21245T and <i>Pseudomonas vranovensis</i> DSM 16006T: taxonomic considerations. <i>Access Microbiology</i> , 2019, 1, e000067.	0.2	10
342	Permanent draft genome sequence of <i>Dethiosulfovibrio peptidovorans</i> type strain (SEBR 4207T). <i>Standards in Genomic Sciences</i> , 2010, 3, 85-92.	1.5	9

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344	Non-contiguous finished genome sequence of <i>Bacteroides coprosuis</i> type strain (PC139T). Standards in Genomic Sciences, 2011, 4, 233-243.	1.5	9
345	Complete genome sequence of <i>Halopiger xanaduensis</i> type strain (SH-6T). Standards in Genomic Sciences, 2012, 6, 31-42.	1.5	9
346	<i>Microclunatus cavernae</i> sp. nov., a novel actinobacterium isolated from Alu ancient cave, Yunnan, south-west China. Antonie Van Leeuwenhoek, 2013, 104, 95-101.	0.7	9
347	Genome sequence of the phage-gene rich marine <i>Phaeobacter arcticus</i> type strain DSM 23566T. Standards in Genomic Sciences, 2013, 8, 450-464.	1.5	9
348	High quality draft genome sequence of the slightly halophilic bacterium <i>Halomonas zhanjiangensis</i> type strain JSM 078169T (DSM 21076T) from a sea urchin in southern China. Standards in Genomic Sciences, 2014, 9, 1020-1030.	1.5	9
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356	Complete genome sequence of the aerobic, heterotroph <i>Marinithermus hydrothermalis</i> type strain (T1T) from a deep-sea hydrothermal vent chimney. Standards in Genomic Sciences, 2012, 6, 21-30.	1.5	8
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358	Genome of the marine alphaproteobacterium <i>Hoeflea phototrophica</i> type strain (DFL-43T). Standards in Genomic Sciences, 2013, 7, 440-448.	1.5	8
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360	Genome sequence of the moderately thermophilic sulfur-reducing bacterium <i>Thermanaerovibrio velox</i> type strain (Z-9701T) and emended description of the genus <i>Thermanaerovibrio</i> . Standards in Genomic Sciences, 2013, 9, 57-70.	1.5	8

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362	Genome sequence and emended description of <i>Leisingera nanhaiensis</i> strain DSM 24252T isolated from marine sediment. <i>Standards in Genomic Sciences</i> , 2014, 9, 585-601.	1.5	8
363	<i>Phytomonospora cypria</i> sp. nov., isolated from soil. <i>Antonie Van Leeuwenhoek</i> , 2015, 108, 1425-1432.	0.7	8
364	<i>Nocardia zapadnayensis</i> sp. nov., isolated from soil. <i>Antonie Van Leeuwenhoek</i> , 2016, 109, 95-103.	0.7	8
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367	Complete genome sequence of <i>Mahella australiensis</i> type strain (50-1 BONT). <i>Standards in Genomic Sciences</i> , 2011, 4, 331-341.	1.5	7
368	Complete genome sequence of <i>Staphylothermus hellenicus</i> P8T. <i>Standards in Genomic Sciences</i> , 2011, 5, 12-20.	1.5	7
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372	<i>Actinoalloteichus fjordicus</i> sp. nov. isolated from marine sponges: phenotypic, chemotaxonomic and genomic characterisation. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 1705-1717.	0.7	7
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374	Complete genome sequence of <i>Tolomonas auensis</i> type strain (TA 4T). <i>Standards in Genomic Sciences</i> , 2011, 5, 112-120.	1.5	6
375	Genome sequence of the reddish-pigmented <i>Rubellimicrobium thermophilum</i> type strain (DSM 16684T), a member of the Roseobacter clade. <i>Standards in Genomic Sciences</i> , 2013, 8, 480-490.	1.5	6
376	<i>Jonesia luteola</i> sp. nov., a bacterium isolated from Xinjiang Province, China. <i>Antonie Van Leeuwenhoek</i> , 2015, 108, 611-618.	0.7	6
377	Complete genome sequence of the haloalkaliphilic, obligately chemolithoautotrophic thiosulfate and sulfide-oxidizing Γ^3 -proteobacterium <i>Thioalkalimicrobium cyclicum</i> type strain ALM 1 (DSM 14477T). <i>Standards in Genomic Sciences</i> , 2016, 11, 38.	1.5	6
378	<i>Jiangella anatolica</i> sp. nov. isolated from coastal lake soil. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 887-895.	0.7	6

#	ARTICLE	IF	CITATIONS
379	Isolation, Classification and Antagonistic Properties of Alkalitolerant Actinobacteria from Algerian Saharan Soils. <i>Geomicrobiology Journal</i> , 2020, 37, 826-836.	1.0	6
380	DNA-rRNA hybridization studies on <i>Halococcus saccharolyticus</i> and other halobacteria. <i>FEMS Microbiology Letters</i> , 1993, 111, 69-72.	0.7	5
381	Genome sequence of the ocean sediment bacterium <i>Saccharomonospora marina</i> type strain (XMU15T). <i>Standards in Genomic Sciences</i> , 2012, 6, 265-275.	1.5	5
382	Genome sequence of the phylogenetically isolated spirochete <i>Leptonema illini</i> type strain (3055T). <i>Standards in Genomic Sciences</i> , 2013, 8, 177-187.	1.5	5
383	High-quality draft genome sequence of <i>Sedimenticola selenatireducens</i> strain AK4OH1T, a gammaproteobacterium isolated from estuarine sediment. <i>Standards in Genomic Sciences</i> , 2016, 11, 66.	1.5	5
384	Consent insufficient for data release – Response. <i>Science</i> , 2019, 364, 446-446.	6.0	5
385	Draft genome sequence of <i>Promicromonospora panici</i> sp. nov., a novel ionizing-radiation-resistant actinobacterium isolated from roots of the desert plant <i>Panicum turgidum</i> . <i>Extremophiles</i> , 2021, 25, 25-38.	0.9	5
386	Complete genome sequence of <i>Oceanithermus profundus</i> type strain (506T). <i>Standards in Genomic Sciences</i> , 2011, 4, 210-220.	1.5	4
387	Genome sequence of the chemoheterotrophic soil bacterium <i>Saccharomonospora cyanea</i> type strain (NA-134T). <i>Standards in Genomic Sciences</i> , 2013, 9, 28-41.	1.5	4
388	Complete genome sequence of the bacteriochlorophyll a-containing <i>Roseibacterium elongatum</i> type strain (DSM 19469T), a representative of the <i>Roseobacter</i> group isolated from Australian coast sand. <i>Standards in Genomic Sciences</i> , 2014, 9, 840-854.	1.5	4
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390	Complete genome sequence of <i>Syntrophobotulus glycolicus</i> type strain (FIGlyR). <i>Standards in Genomic Sciences</i> , 2011, 4, 371-80.	1.5	4
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393	Genome sequence of <i>Frateuria aurantia</i> type strain (KondÅ´ 67T), a xanthomonade isolated from <i>Lilium auratum</i> Lindl.. <i>Standards in Genomic Sciences</i> , 2013, 9, 83-92.	1.5	3
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396	High-quality draft genome sequence of <i>Gracilimonas tropica</i> CL-CB462T (DSM 19535T), isolated from a <i>Synechococcus</i> culture. <i>Standards in Genomic Sciences</i> , 2015, 10, 98.	1.5	3

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398	Genomic Encyclopedia of Bacteria and Archaea (GEBA) VI: learning from type strains. <i>Microbiology Australia</i> , 2019, 40, 125.	0.1	3
399	Genome sequence of the flexirubin-pigmented soil bacterium <i>Niabella soli</i> type strain (JS13-8T). <i>Standards in Genomic Sciences</i> , 2012, 7, 210-220.	1.5	2
400	High quality permanent draft genome sequence of <i>Chryseobacterium bovis</i> DSM 19482T, isolated from raw cow milk. <i>Standards in Genomic Sciences</i> , 2017, 12, 31.	1.5	2
401	High quality permanent draft genome sequence of <i>Phaseolibacter flectens</i> ATCC 12775T, a plant pathogen of French bean pods. <i>Standards in Genomic Sciences</i> , 2016, 11, 4.	1.5	1
402	Draft genome sequence of <i>Marinobacterium rhizophilum</i> CL-YJ9T (DSM 18822T), isolated from the rhizosphere of the coastal tidal-flat plant <i>Suaeda japonica</i> . <i>Standards in Genomic Sciences</i> , 2017, 12, 65.	1.5	1
403	Genome sequence and comparative analysis of <i>Jiangella alba</i> YIM 61503T isolated from a medicinal plant <i>Maytenus austroyunnanensis</i> . <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 667-678.	0.7	1
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405	Genome-based reclassification of <i>Actinopolyspora righensis</i> Meklat et al. 2013 as a later heterotypic synonym of <i>Actinopolyspora lacussalsi</i> Guan et al. 2013 and description of <i>Actinopolyspora lacussalsi</i> subsp. <i>lacussalsi</i> subsp. nov. and <i>Actinopolyspora lacussalsi</i> subsp. <i>righensis</i> subsp. nov.. <i>Archives of Microbiology</i> , 2022, 204, .	1.0	1
406	Draft Genome Sequence of <i>Bordetella</i> sp. Strain FB-8, Isolated from a Former Uranium Mining Area in Germany. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0