Markus Gäßker

List of Publications by Year
in descending order

325 papers	30,802 citations	22153 59 h-index	7518 151 g-index
338 all docs	338 docs citations	338 times ranked	19835 citing authors

#	Article	IF	Citations
1	Genome sequence-based species delimitation with confidence intervals and improved distance functions. BMC Bioinformatics, 2013, 14, 60.	2.6	5,139
2	Genome-Based Taxonomic Classification of the Phylum Actinobacteria. Frontiers in Microbiology, 2018, 9, 2007.	3.5	2,599
3	TYGS is an automated high-throughput platform for state-of-the-art genome-based taxonomy. Nature Communications, 2019, 10, 2182.	12.8	1,588
4	Analysis of 1,000+ Type-Strain Genomes Substantially Improves Taxonomic Classification of Alphaproteobacteria. Frontiers in Microbiology, 2020, 11, 468.	3.5	1,537
5	Digital DNA-DNA hybridization for microbial species delineation by means of genome-to-genome sequence comparison. Standards in Genomic Sciences, 2010, 2, 117-134.	1.5	1,442
6	Analysis of 1,000 Type-Strain Genomes Improves Taxonomic Classification of Bacteroidetes. Frontiers in Microbiology, 2019, 10, 2083.	3.5	1,281
7	List of Prokaryotic names with Standing in Nomenclature (LPSN) moves to the DSMZ. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5607-5612.	1.7	929
8	TYGS and LPSN: a database tandem for fast and reliable genome-based classification and nomenclature of prokaryotes. Nucleic Acids Research, 2022, 50, D801-D807.	14.5	728
9	Critical Assessment of Metagenome Interpretation—a benchmark of metagenomics software. Nature Methods, 2017, 14, 1063-1071.	19.0	635
10	Taxonomic use of DNA G+C content and DNA–DNA hybridization in the genomic age. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 352-356.	1.7	526
11	Standard operating procedure for calculating genome-to-genome distances based on high-scoring segment pairs. Standards in Genomic Sciences, 2010, 2, 142-148.	1.5	509
12	Genome-Based Taxonomic Classification of Bacteroidetes. Frontiers in Microbiology, 2016, 7, 2003.	3.5	493
13	When should a DDH experiment be mandatory in microbial taxonomy?. Archives of Microbiology, 2013, 195, 413-418.	2.2	490
14	Complete genome sequence of DSM 30083T, the type strain (U5/41T) of Escherichia coli, and a proposal for delineating subspecies in microbial taxonomy. Standards in Genomic Sciences, 2014, 9, 2.	1.5	454
15	Toward a Novel Multilocus Phylogenetic Taxonomy for the Dermatophytes. Mycopathologia, 2017, 182, 5-31.	3.1	447
16	VICTOR: genome-based phylogeny and classification of prokaryotic viruses. Bioinformatics, 2017, 33, 3396-3404.	4.1	401
17	Towards an integrated phylogenetic classification of the <i>Tremellomycetes</i>. Studies in Mycology, 2015, 81, 85-147.	7.2	393
18	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

#	Article	IF	Citations
19	Phylogenomics of *Rhodobacteraceae* reveals evolutionary adaptation to marine and non-marine habitats. ISME Journal, 2017, 11, 1483-1499.	9.8	283
20	En route to a genome-based classification of Archaea and Bacteria?. Systematic and Applied Microbiology, 2010, 33, 175-182.	2.8	279
21	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. Nature Biotechnology, 2017, 35, 676-683.	17.5	222
22	Genomic insights into the taxonomic status of the Bacillus cereus group. Scientific Reports, 2015, 5, 14082.	3.3	220
23	opm: an R package for analysing OmniLog® phenotype microarray data. Bioinformatics, 2013, 29, 1823-1824.	4.1	214
24	Phylogenetic classification of yeasts and related taxa within *Pucciniomycotina*. Studies in Mycology, 2015, 81, 149-189.	7.2	202
25	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. PLoS Biology, 2014, 12, e1001920.	5.6	190
26	Chryseobacterium hispalense sp. nov., a plant-growth-promoting bacterium isolated from a rainwater pond in an olive plant nursery, and emended descriptions of Chryseobacterium defluvii, Chryseobacterium indologenes, Chryseobacterium wanjuense and Chryseobacterium gregarium. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 4386-4395.	1.7	187
27	Molecular Taxonomy of Phytopathogenic Fungi: A Case Study in Peronospora. PLoS ONE, 2009, 4, e6319.	2.5	186
28	Visualization and Curve-Parameter Estimation Strategies for Efficient Exploration of Phenotype Microarray Kinetics. PLoS ONE, 2012, 7, e34846.	2.5	173
29	Genomic and Genetic Diversity within the Pseudomonas fluorescens Complex. PLoS ONE, 2016, 11, e0150183.	2.5	171
30	A taxonomic framework for emerging groups of ecologically important marine gammaproteobacteria based on the reconstruction of evolutionary relationships using genome-scale data. Frontiers in Microbiology, 2015, 6, 281.	3.5	168
31	How do obligate parasites evolve? A multi-gene phylogenetic analysis of downy mildews. Fungal Genetics and Biology, 2007, 44, 105-122.	2.1	136
32	Phylogenetic Relationships of the Downy Mildews (Peronosporales) and Related Groups Based on Nuclear Large Subunit Ribosomal DNA Sequences. Mycologia, 2002, 94, 834.	1.9	122
33	Non-contiguous finished genome sequence and contextual data of the filamentous soil bacterium Ktedonobacter racemifer type strain (SOSP1-21T). Standards in Genomic Sciences, 2011, 5, 97-111.	1.5	115
34	Quantifying the Phylodynamic Forces Driving Papillomavirus Evolution. Molecular Biology and Evolution, 2011, 28, 2101-2113.	8.9	114
35	Phylogeny of Hyaloperonospora based on nuclear ribosomal internal transcribed spacer sequences. Mycological Progress, 2004, 3, 83-94.	1.4	106
36	Genome-Scale Data Call for a Taxonomic Rearrangement of Geodermatophilaceae. Frontiers in Microbiology, 2017, 8, 2501.	3.5	105

#	Article	IF	Citations
37	Novel genera and species of coniothyrium-like fungi in *Montagnulaceae* (*Ascomycota*). Persoonia: Molecular Phylogeny and Evolution of Fungi, 2014, 32, 25-51.	4.4	104
38	Genome-based classification of micromonosporae with a focus on their biotechnological and ecological potential. Scientific Reports, 2018, 8, 525.	3.3	102
39	Complete genome sequence of Kytococcus sedentarius type strain (541T). Standards in Genomic Sciences, 2009, 1, 12-20.	1.5	100
40	Phylogenetic relationships of Plasmopara, Bremia and other genera of downy mildew pathogens with pyriform haustoria based on Bayesian analysis of partial LSU rDNA sequence data. Mycological Research, 2004, 108, 1011-1024.	2.5	97
41	Complete genome sequence of Odoribacter splanchnicus type strain (1651/6T). Standards in Genomic Sciences, 2011, 4, 200-209.	1.5	96
42	Controlling false discoveries in high-dimensional situations: boosting with stability selection. BMC Bioinformatics, 2015, 16, 144.	2.6	95
43	COPYCAT : cophylogenetic analysis tool. Bioinformatics, 2007, 23, 898-900.	4.1	92
44	Extrachromosomal, extraordinary and essential—the plasmids of the Roseobacter clade. Applied Microbiology and Biotechnology, 2013, 97, 2805-2815.	3.6	90
45	Chryseobacterium oleae sp. nov., an efficient plant growth promoting bacterium in the rooting induction of olive tree (Olea europaea L.) cuttings and emended descriptions of the genus Chryseobacterium, C. daecheongense, C. gambrini, C. gleum, C. joostei, C. jejuense, C. luteum, C. shigense, C. taiwanense, C. ureilyticum and C. vrystaatense. Systematic and Applied Microbiology, 2014, 37, 342-350.	2.8	89
46	Genome-scale data suggest reclassifications in the Leisingera-Phaeobacter cluster including proposals for Sedimentitalea gen. nov. and Pseudophaeobacter gen. nov.. Frontiers in Microbiology, 2014, 5, 416.	3.5	88
47	Taxonomic aspects of Peronosporaceae inferred from Bayesian molecular phylogenetics. Canadian Journal of Botany, 2003, 81, 672-683.	1.1	82
48	Species delimitation in downy mildews: the case of Hyaloperonospora in the light of nuclear ribosomal ITS and LSU sequences. Mycological Research, 2009, 113, 308-325.	2.5	80
49	Genome BLAST distance phylogenies inferred from whole plastid and whole mitochondrion genome sequences. BMC Bioinformatics, 2006, 7, 350.	2.6	76
50	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
51	Horizontal operon transfer, plasmids, and the evolution of photosynthesis in *Rhodobacteraceae*. ISME Journal, 2018, 12, 1994-2010.	9.8	75
52	Shotgun metagenome data of a defined mock community using Oxford Nanopore, PacBio and Illumina technologies. Scientific Data, 2019, 6, 285.	5.3	75
53	Complete genome sequence of Chitinophaga pinensis type strain (UQM 2034T). Standards in Genomic Sciences, 2010, 2, 87-95.	1.5	74
54	Novel Insights into the Diversity of Catabolic Metabolism from Ten Haloarchaeal Genomes. PLoS ONE, 2011, 6, e20237.	2.5	72

#	Article	IF	Citations
55	Anther smuts of Caryophyllaceae: Molecular characters indicate host-dependent species delimitation. Mycological Progress, 2005, 4, 225-238.	1.4	71
56	Complete genome sequence of Haliangium ochraceum type strain (SMP-2T). Standards in Genomic Sciences, 2010, 2, 96-106.	1.5	70
57	Implications of molecular characters for the phylogeny of the Microbotryaceae (Basidiomycota:) Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.2	68
58	Proposal of a type strain for Frankia alni (Woronin 1866) Von Tubeuf 1895, emended description of Frankia alni, and recognition of Frankia casuarinae sp. nov. and Frankia elaeagni sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 5201-5210.	1.7	68
59	Metabolic traits of an uncultured archaeal lineage -MSBL1- from brine pools of the Red Sea. Scientific Reports, 2016, 6, 19181.	3.3	66
60	Genomic Analysis of Caldithrix abyssi, the Thermophilic Anaerobic Bacterium of the Novel Bacterial Phylum Calditrichaeota. Frontiers in Microbiology, 2017, 8, 195.	3.5	66
61	Highly parallelized inference of large genome‐based phylogenies. Concurrency Computation Practice and Experience, 2014, 26, 1715-1729.	2.2	63
62	Phylogeny of Peronospora, parasitic on Fabaceae, based on ITS sequences. Mycological Research, 2008, 112, 502-512.	2.5	62
63	Complete genome sequence of the termite hindgut bacterium Spirochaeta coccoides type strain (SPN1T), reclassification in the genus Sphaerochaeta as Sphaerochaeta coccoides comb. nov. and emendations of the family Spirochaetaceae and the genus Sphaerochaeta. Standards in Genomic Sciences, 2012, 6, 194-209.	1.5	58
64	Geodermatophilus arenarius sp. nov., a xerophilic actinomycete isolated from Saharan desert sand in Chad. Extremophiles, 2012, 16, 903-909.	2.3	58
65	Dual function of tropodithietic acid as antibiotic and signaling molecule in global gene regulation of the probiotic bacterium Phaeobacter inhibens. Scientific Reports, 2017, 7, 730.	3.3	57
66	Complete genome sequence of Geodermatophilus obscurus type strain (G-20T). Standards in Genomic Sciences, 2010, 2, 158-167.	1.5	56
67	Biofilm plasmids with a rhamnose operon are widely distributed determinants of the 'swim-or-stick' lifestyle in roseobacters. ISME Journal, 2016, 10, 2498-2513.	9.8	56
68	Phylogenetic relationships of graminicolous downy mildews based on cox2 sequence data. Mycological Research, 2008, 112, 345-351.	2.5	53
69	Geodermatophilus africanus sp. nov., a halotolerant actinomycete isolated from Saharan desert sand. Antonie Van Leeuwenhoek, 2013, 104, 207-216.	1.7	52
70	Molecular and phenotypic analyses reveal the non-identity of the Phaeobacter gallaeciensis type strain deposits CIP 105210T and DSM 17395. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 4340-4349.	1.7	52
71	Complete genome sequence of Desulfobulbus propionicus type strain (1pr3T). Standards in Genomic Sciences, 2011, 4, 100-110.	1.5	51
72	Complete genome sequence of the thermophilic, hydrogen-oxidizing Bacillus tusciae type strain (T2T) and reclassification in the new genus, Kyrpidia gen. nov. as Kyrpidia tusciae comb. nov. and emendation of the family Alicyclobacillaceae da Costa and Rainey, 2010.. Standards in Genomic Sciences, 2011, 5, 121-134.	1.5	51

#	Article	IF	Citations
73	Intraspecific Relationship of Plasmopara halstedii Isolates Differing in Pathogenicity and Geographic Origin Based on ITS Sequence Data. European Journal of Plant Pathology, 2006, 114, 309-315.	1.7	50
74	Geodermatophilus siccatus sp. nov., isolated from arid sand of the Saharan desert in Chad. Antonie Van Leeuwenhoek, 2013, 103, 449-456.	1.7	48
75	Complete genome sequence of the filamentous gliding predatory bacterium Herpetosiphon aurantiacus type strain (114-95T). Standards in Genomic Sciences, 2011, 5, 356-370.	1.5	47
76	Codivergence of Mycoviruses with Their Hosts. PLoS ONE, 2011, 6, e22252.	2.5	46
77	Complete genome sequence of Truepera radiovictrix type strain (RQ-24T). Standards in Genomic Sciences, 2011, 4, 91-99.	1.5	46
78	Complete genome sequence of Isosphaera pallida type strain (IS1BT). Standards in Genomic Sciences, 2011, 4, 63-71.	1.5	46
79	Phylogeny-driven target selection for large-scale genome-sequencing (and other) projects. Standards in Genomic Sciences, 2013, 8, 360-374.	1.5	46
80	Complete genome sequence of Rhodothermus marinus type strain (R-10T). Standards in Genomic Sciences, 2009, 1, 283-290.	1.5	45
81	Complete genome sequence of Veillonella parvula type strain (Te3T). Standards in Genomic Sciences, 2010, 2, 57-65.	1.5	44
82	Complete genome sequence of Rhodospirillum rubrum type strain (S1T). Standards in Genomic Sciences, 2011, 4, 293-302.	1.5	44
83	Genome sequence of the thermophilic fresh-water bacterium Spirochaeta caldaria type strain (H1T), reclassification of Spirochaeta caldaria, Spirochaeta stenostrepta, and Spirochaeta zuelzerae in the genus Treponema as Treponema caldaria comb. nov., Treponema stenostrepta comb. nov., and Treponema zuelzerae comb. nov., and emendation of the genus Treponema. Standards in Genomic Sciences, 2013, 8, 88-105.	1.5	44
84	General functions to transform associate data to host data, and their use in phylogenetic inference from sequences with intra-individual variability. BMC Evolutionary Biology, 2008, 8, 86.	3.2	43
85	Complete genome sequence of Olsenella uli type strain (VPI D76D-27CT). Standards in Genomic Sciences, 2010, 3, 76-84.	1.5	43
86	Geodermatophilus tzadiensis sp. nov., a UV radiation-resistant bacterium isolated from sand of the Saharan desert. Systematic and Applied Microbiology, 2013, 36, 177-182.	2.8	43
87	Genomics and Physiology of a Marine Flavobacterium Encoding a Proteorhodopsin and a Xanthorhodopsin-Like Protein. PLoS ONE, 2013, 8, e57487.	2.5	42
88	Complete genome sequence of Treponema succinifaciens type strain (6091T). Standards in Genomic Sciences, 2011, 4, 361-370.	1.5	41
89	Complete genome sequence of Spirosoma linguale type strain (1T). Standards in Genomic Sciences, 2010, 2, 176-184.	1.5	40
90	Complete genome sequence of Arcobacter nitrofigilis type strain (CIT). Standards in Genomic Sciences, 2010, 2, 300-308.	1.5	40

#	Article	IF	Citations
91	AxPcoords & parallel AxParafit: statistical co-phylogenetic analyses on thousands of taxa. BMC Bioinformatics, 2007, 8, 405.	2.6	39
92	Complete genome sequence of Actinosynnema mirum type strain (101T). Standards in Genomic Sciences, 2009, 1, 46-53.	1.5	38
93	Complete genome sequence of Cellulomonas flavigena type strain (134T). Standards in Genomic Sciences, 2010, 3, 15-25.	1.5	38
94	Complete genome sequence of Eggerthella lenta type strain (VPI 0255T). Standards in Genomic Sciences, 2009, 1, 174-182.	1.5	37
95	Complete genome sequence of Desulfarculus baarsii type strain (2st14T). Standards in Genomic Sciences, 2010, 3, 276-284.	1.5	37
96	Complete genome sequence of the sulfur compounds oxidizing chemolithoautotroph Sulfuricurvum kujiense type strain (YK-1T). Standards in Genomic Sciences, 2012, 6, 94-103.	1.5	37
97	Geodermatophilus telluris sp. nov., an actinomycete isolated from Saharan desert sand. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 2254-2259.	1.7	37
98	*Geodermatophilus poikilotrophi* sp. nov.: A Multitolerant Actinomycete Isolated from Dolomitic Marble. BioMed Research International, 2014, 2014, 1-11.	1.9	37
99	Complete genome sequence of Sulfurimonas autotrophica type strain (OK10T). Standards in Genomic Sciences, 2010, 3, 194-202.	1.5	37
100	A revision of Bremia graminicola. Mycological Research, 2006, 110, 646-656.	2.5	36
101	Complete genome sequence of Desulfomicrobium baculatum type strain (XT). Standards in Genomic Sciences, 2009, 1, 29-37.	1.5	36
102	Complete genome sequence of the extremely halophilic Halanaerobium praevalens type strain (GSLT). Standards in Genomic Sciences, 2011, 4, 312-321.	1.5	36
103	Geodermatophilus saharensis sp. nov., isolated from sand of the Saharan desert in Chad. Archives of Microbiology, 2013, 195, 153-159.	2.2	36
104	Hidden diversity in the non–caryophyllaceous plant–parasitic members of *Microbotryum* (Pucciniomycotina: Microbotryales). Systematics and Biodiversity, 2009, 7, 297-306.	1.2	35
105	Complete genome sequence of Desulfotomaculum acetoxidans type strain (5575T). Standards in Genomic Sciences, 2009, 1, 242-253.	1.5	35
106	Complete genome sequence of Nakamurella multipartita type strain (Y-104T). Standards in Genomic Sciences, 2010, 2, 168-175.	1.5	35
107	The Genome Sequence of *Methanohalophilus mahii* SLP^T Reveals Differences in the Energy Metabolism among Members of the *Methanosarcinaceae* Inhabiting Freshwater and Saline Environments. Archaea, 2010, 2010, 1-16.	2.3	35
108	Complete genome sequence of the halophilic and highly halotolerant Chromohalobacter salexigens type strain (1H11T). Standards in Genomic Sciences, 2011, 5, 379-388.	1.5	35

#	Article	IF	Citations
109	Complete genome sequence of Thermomonospora curvata type strain (B9T). Standards in Genomic Sciences, 2011, 4, 13-22.	1.5	35
110	Complete genome sequence of Pirellula staleyi type strain (ATCC 27377T). Standards in Genomic Sciences, 2009, 1, 308-316.	1.5	34
111	Complete genome sequence of Sebaldella termitidis type strain (NCTC 11300T). Standards in Genomic Sciences, 2010, 2, 220-227.	1.5	34
112	Complete genome sequence of Meiothermus ruber type strain (21T). Standards in Genomic Sciences, 2010, 3, 26-36.	1.5	33
113	Complete genome sequence of Cellulophaga lytica type strain (LIM-21T). Standards in Genomic Sciences, 2011, 4, 221-232.	1.5	33
114	Complete genome sequence of Riemerella anatipestifer type strain (ATCC 11845T). Standards in Genomic Sciences, 2011, 4, 144-153.	1.5	33
115	Nocardiopsis arvandica sp. nov., isolated from sandy soil. International Journal of Systematic and Evolutionary Microbiology, 2011, 61, 1189-1194.	1.7	33
116	Complete genome sequence of Polynucleobacter necessarius subsp. asymbioticus type strain (QLW-P1DMWA-1T). Standards in Genomic Sciences, 2012, 6, 74-83.	1.5	33
117	Using the Multiple Analysis Approach to Reconstruct Phylogenetic Relationships among Planktonic Foraminifera from Highly Divergent and Length-polymorphic SSU rDNA Sequences. Bioinformatics and Biology Insights, 2009, 3, BBI.S3334.	2.0	32
118	Complete genome sequence of Acidimicrobium ferrooxidans type strain (ICPT). Standards in Genomic Sciences, 2009, 1, 38-45.	1.5	32
119	Complete genome sequence of Nocardiopsis dassonvillei type strain (IMRU 509T). Standards in Genomic Sciences, 2010, 3, 325-336.	1.5	32
120	Complete genome sequence of Haloterrigena turkmenica type strain (4kT). Standards in Genomic Sciences, 2010, 2, 107-116.	1.5	32
121	Complete genome sequence of Aminobacterium colombiense type strain (ALA-1T). Standards in Genomic Sciences, 2010, 2, 280-289.	1.5	32
122	Species Delimitation in Taxonomically Difficult Fungi: The Case of Hymenogaster. PLoS ONE, 2011, 6, e15614.	2.5	32
123	A revision of Plasmopara penniseti, with implications for the host range of the downy mildews with pyriform haustoria. Mycological Research, 2007, 111, 1377-1385.	2.5	31
124	Complete genome sequence of Halomicrobium mukohataei type strain (arg-2T). Standards in Genomic Sciences, 2009, 1, 270-277.	1.5	31
125	Complete genome sequence of Planctomyces limnophilus type strain (Mü 290T). Standards in Genomic Sciences, 2010, 3, 47-56.	1.5	31
126	Complete genome sequence of Acidaminococcus fermentans type strain (VR4T). Standards in Genomic Sciences, 2010, 3, 1-14.	1.5	31

#	ARTICLE	IF	CITATIONS
127	The Families Erysipelotrichaceae emend., Coprobacillaceae fam. nov., and Turicibacteraceae fam. nov.. , 2014, , 79-105.		31
128	Complete genome sequence of Atopobium parvulum type strain (IPP 1246T). Standards in Genomic Sciences, 2009, 1, 166-173.	1.5	30
129	Complete genome sequence of Paludibacter propionicigenes type strain (WB4T). Standards in Genomic Sciences, 2011, 4, 36-44.	1.5	30
130	Complete genome sequence of Polynucleobacter necessarius subsp. asymbioticus type strain (QLW-P1DMWA-1T). Standards in Genomic Sciences, 2012, 6, 1-14.	1.5	30
131	High quality draft genome sequences of Pseudomonas fulva DSM 17717T, Pseudomonas parafulva DSM 17004T and Pseudomonas cremoricolorata DSM 17059T type strains. Standards in Genomic Sciences, 2016, 11, 55.	1.5	30
132	Complete genome sequence of Sulfurospirillum deleyianum type strain (5175T). Standards in Genomic Sciences, 2010, 2, 149-157.	1.5	29
133	Complete genome sequence of Kangiella koreensis type strain (SW-125T). Standards in Genomic Sciences, 2009, 1, 226-233.	1.5	28
134	Complete genome sequence of Coraliomargarita akajimensis type strain (04OKA010-24T). Standards in Genomic Sciences, 2010, 2, 290-299.	1.5	28
135	Complete genome sequence of Cellulophaga algicola type strain (IC166T). Standards in Genomic Sciences, 2011, 4, 72-80.	1.5	28
136	Geodermatophilus normandii sp. nov., isolated from Saharan desert sand. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 3437-3443.	1.7	28
137	16S-rRNA-based analysis of bacterial diversity in the gut of fungus-cultivating termites (Microtermes) Tj ETQq1 1 0.784314 rgBT /Overlo	1.7	28
138	Pathways and substrate‐specific regulation of amino acid degradation in <i><scp>P</scp>haeobacter inhibens</i>â€...<scp>DSM</scp> 17395 (archetype of the marine <i><scp>R</scp>oseobacter</i> clade). Environmental Microbiology, 2014, 16, 218-238.	3.8	28
139	Ocean's Twelve: flagellar and biofilm chromids in the multipartite genome of <scp><i>M</i></scp><i>arinovum algicola</i>â€...<scp>DG</scp>898 exemplify functional compartmentalization. Environmental Microbiology, 2015, 17, 4019-4034.	3.8	28
140	Description of gamma radiation-resistant Geodermatophilus dictyosporus sp. nov. to accommodate the not validly named Geodermatophilus obscurus subsp. dictyosporus (Luedemann, 1968). Extremophiles, 2015, 19, 77-85.	2.3	28
141	Complete genome sequence of Sphaerobacter thermophilus type strain (S 6022T). Standards in Genomic Sciences, 2010, 2, 49-56.	1.5	27
142	Complete genome sequence of Streptosporangium roseum type strain (NI 9100T). Standards in Genomic Sciences, 2010, 2, 29-37.	1.5	27
143	A Clustering Optimization Strategy for Molecular Taxonomy Applied to Planktonic Foraminifera SSU rDNA. Evolutionary Bioinformatics, 2010, 6, EBO.S5504.	1.2	27
144	Comparing polysaccharide decomposition between the type strains Gramella echinicola KMM 6050T (DSM 19838T) and Gramella portivictoriae UST040801-001T (DSM 23547T), and emended description of Gramella echinicola Nedashkovskaya et al. 2005 emend. Shahina et al. 2014 and Gramella portivictoriae Lau et al. 2005. Standards in Genomic Sciences, 2016, 11, 37.	1.5	27

#	Article	IF	Citations
145	Description of Trichococcus ilyis sp. nov. by combined physiological and in silico genome hybridization analyses. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 3957-3963.	1.7	27
146	Complete genome sequence of Archaeoglobus profundus type strain (AV18T). Standards in Genomic Sciences, 2010, 2, 327-346.	1.5	26
147	Complete genome sequence of Gordonia bronchialis type strain (3410T). Standards in Genomic Sciences, 2010, 2, 19-28.	1.5	26
148	Complete genome sequence of Haliscomenobacter hydrossis type strain (OT). Standards in Genomic Sciences, 2011, 4, 352-360.	1.5	26
149	Genome sequence of the moderately thermophilic, amino-acid-degrading and sulfur-reducing bacterium Thermovirga lienii type strain (Cas60314T). Standards in Genomic Sciences, 2012, 6, 230-239.	1.5	26
150	Genome sequence of the homoacetogenic bacterium Holophaga foetida type strain (TMBS4T). Standards in Genomic Sciences, 2012, 6, 174-184.	1.5	26
151	Genome sequence of Phaeobacter inhibens type strain (T5T), a secondary metabolite producing representative of the marine Roseobacter clade, and emendation of the species description of Phaeobacter inhibens. Standards in Genomic Sciences, 2013, 9, 334-350.	1.5	26
152	Cobaviruses â€" a new globally distributed phage group infecting <i>Rhodobacteraceae</i> in marine ecosystems. ISME Journal, 2019, 13, 1404-1421.	9.8	26
153	Complete genome sequence of Pedobacter heparinus type strain (HIM 762-3T). Standards in Genomic Sciences, 2009, 1, 54-62.	1.5	25
154	Complete genome sequence of Anaerococcus prevotii type strain (PC1T). Standards in Genomic Sciences, 2009, 1, 159-165.	1.5	25
155	Complete genome sequence of Brachybacterium faecium type strain (Schefferle 6-10T). Standards in Genomic Sciences, 2009, 1, 3-11.	1.5	25
156	Complete genome sequence of Dyadobacter fermentans type strain (NS114T). Standards in Genomic Sciences, 2009, 1, 133-140.	1.5	25
157	Complete genome sequence of the acetate-degrading sulfate reducer Desulfobacca acetoxidans type strain (ASRB2T). Standards in Genomic Sciences, 2011, 4, 393-401.	1.5	25
158	100â€year⣠old enigma solved: identification, genomic characterization and biogeography of the yet uncultured <i>Planctomyces bekefii</i>. Environmental Microbiology, 2020, 22, 198-211.	3.8	25
159	Diversity of Termitomyces Associated with Fungus-Farming Termites Assessed by Cultural and Culture-Independent Methods. PLoS ONE, 2013, 8, e56464.	2.5	25
160	Complete genome sequence of Catenulispora acidiphila type strain (ID 139908T). Standards in Genomic Sciences, 2009, 1, 119-125.	1.5	24
161	Complete genome sequence of Leptotrichia buccalis type strain (C-1013-bT). Standards in Genomic Sciences, 2009, 1, 126-132.	1.5	24
162	Complete genome sequence of Saccharomonospora viridis type strain (P101T). Standards in Genomic Sciences, 2009, 1, 141-149.	1.5	24

#	ARTICLE	IF	CITATIONS
163	Complete genome sequence of Conexibacter woesei type strain (ID131577T). Standards in Genomic Sciences, 2010, 2, 212-219.	1.5	24
164	Complete genome sequence of Acetohalobium arabaticum type strain (Z-7288T). Standards in Genomic Sciences, 2010, 3, 57-65.	1.5	24
165	Complete genome sequence of Alicyclobacillus acidocaldarius type strain (104-IAT). Standards in Genomic Sciences, 2010, 2, 9-18.	1.5	24
166	Complete genome sequence of the aquatic bacterium Runella slithyformis type strain (LSU 4T). Standards in Genomic Sciences, 2012, 6, 145-154.	1.5	24
167	Description of Geodermatophilus amargosae sp. nov., to Accommodate the Not Validly Named Geodermatophilus obscurus subsp. amargosae (Luedemann, 1968). Current Microbiology, 2014, 68, 365-371.	2.2	24
168	Complete genome sequence of Halogeometricum borinquense type strain (PR3T). Standards in Genomic Sciences, 2009, 1, 150-158.	1.5	23
169	Complete genome sequence of Thermanaerovibrio acidaminovorans type strain (Su883T). Standards in Genomic Sciences, 2009, 1, 254-261.	1.5	23
170	Complete genome sequence of Stackebrandtia nassauensis type strain (LLR-40K-21T). Standards in Genomic Sciences, 2009, 1, 292-299.	1.5	23
171	Complete genome sequence of Thermobispora bispora type strain (R51T). Standards in Genomic Sciences, 2010, 2, 318-326.	1.5	23
172	Complete genome sequence of the gliding freshwater bacterium Fluviicola taffensis type strain (RW262T). Standards in Genomic Sciences, 2011, 5, 21-29.	1.5	23
173	Complete genome sequence of the moderately thermophilic mineral-sulfide-oxidizing firmicute Sulfobacillus acidophilus type strain (NALT). Standards in Genomic Sciences, 2012, 6, 293-303.	1.5	23
174	A clustering optimization strategy to estimate species richness of Sebacinales in the tropical Andes based on molecular sequences from distinct DNA regions. Biodiversity and Conservation, 2012, 21, 2269-2285.	2.6	23
175	Complete genome sequence of Halorhabdus utahensis type strain (AX-2T). Standards in Genomic Sciences, 2009, 1, 218-225.	1.5	22
176	Complete genome sequence of Desulfohalobium retbaense type strain (HR100T). Standards in Genomic Sciences, 2010, 2, 38-48.	1.5	22
177	Complete genome sequence of Leadbetterella byssophila type strain (4M15T). Standards in Genomic Sciences, 2011, 4, 2-12.	1.5	22
178	Genome sequence of the filamentous, gliding Thiothrix nivea neotype strain (JP2T). Standards in Genomic Sciences, 2011, 5, 398-406.	1.5	22
179	Complete genome sequence of the sulfate-reducing firmicute Desulfotomaculum ruminis type strain (DLT). Standards in Genomic Sciences, 2012, 7, 304-319.	1.5	22
180	Genome sequence of the mud-dwelling archaeon Methanoplanus limicola type strain (DSM 2279T), reclassification of Methanoplanus petrolearius as Methanolacinia petrolearia and emended descriptions of the genera Methanoplanus and Methanolacinia. Standards in Genomic Sciences, 2014, 9, 1076-1088.	1.5	22

#	Article	IF	Citations
181	A publicly accessible database for Clostridioides difficile genome sequences supports tracing of transmission chains and epidemics. Microbial Genomics, 2020, 6, .	2.0	22
182	Complete genome sequence of Streptobacillus moniliformis type strain (9901T). Standards in Genomic Sciences, 2009, 1, 300-307.	1.5	21
183	Complete genome sequence of the Phaeobacter gallaeciensis type strain CIP 105210T (= DSM 26640T =) Tj ETQq1 1 0.784314 rgBT	1.5	21
184	Genome-guided analysis allows the identification of novel physiological traits in Trichococcus species. BMC Genomics, 2020, 21, 24.	2.8	21
185	Ancestral regulatory mechanisms specify conserved midbrain circuitry in arthropods and vertebrates. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 19544-19555.	7.1	21
186	Cutaneotropic Human β-/γ-Papillomaviruses Are Rarely Shared between Family Members. Journal of Investigative Dermatology, 2009, 129, 2427-2434.	0.7	20
187	Complete genome sequence of Slackia heliotrinireducens type strain (RHS 1T). Standards in Genomic Sciences, 2009, 1, 234-241.	1.5	20
188	Complete genome sequence of Brachyspira murdochii type strain (56-150T). Standards in Genomic Sciences, 2010, 2, 260-269.	1.5	20
189	The neglected hypogeous fungus Hydnotrya bailii Soehner (1959) is a widespread sister taxon of Hydnotrya tulasnei (Berk.) Berk. & Broome (1846). Mycological Progress, 2010, 9, 195-203.	1.4	20
190	Complete genome sequence of Riemerella anatipestifer type strain (ATCC 11845). Standards in Genomic Sciences, 2011, 4, 144-53.	1.5	20
191	Complete genome sequence of Meiothermus silvanus type strain (VI-R2T). Standards in Genomic Sciences, 2010, 3, 37-46.	1.5	19
192	Complete genome sequence of the facultatively chemolithoautotrophic and methylotrophic alpha Proteobacterium Starkeya novella type strain (ATCC 8093T). Standards in Genomic Sciences, 2012, 7, 44-58.	1.5	19
193	Fine-structured multi-scaling long-range correlations in completely sequenced genomes—features, origin, and classification. European Biophysics Journal, 2009, 38, 757-779.	2.2	18
194	Complete genome sequence of Thermocrinis albus type strain (HI 11/12T). Standards in Genomic Sciences, 2010, 2, 194-202.	1.5	18
195	Complete genome sequence of Spirochaeta smaragdinae type strain (SEBR 4228T). Standards in Genomic Sciences, 2010, 3, 1-9.	1.5	18
196	Complete genome sequence of Marivirga tractuosa type strain (H-43T). Standards in Genomic Sciences, 2011, 4, 154-162.	1.5	18
197	Choosing one name for pleomorphic fungi: The example of <i>Aspergillus</i> versus <i>Eurotium</i>, <i>Neosartorya</i> and <i>Emericella</i>. Taxon, 2016, 65, 593-601.	0.7	18
198	The Composite 259-kb Plasmid of Martelella mediterranea DSM 17316T—A Natural Replicon with Functional RepABC Modules from Rhodobacteraceae and Rhizobiaceae. Frontiers in Microbiology, 2017, 8, 1787.	3.5	18

#	Article	IF	Citations
199	Complete genome sequence of Cryptobacterium curtum type strain (12-3T). Standards in Genomic Sciences, 2009, 1, 93-100.	1.5	17
200	Complete genome sequence of Methanothermus fervidus type strain (V24ST). Standards in Genomic Sciences, 2010, 3, 315-324.	1.5	17
201	Genome sequence of the Leisingera aquimarina type strain (DSM 24565T), a member of the marine Roseobacter clade rich in extrachromosomal elements. Standards in Genomic Sciences, 2013, 8, 389-402.	1.5	17
202	Complete genome sequence of Sanguibacter keddieii type strain (ST-74T). Standards in Genomic Sciences, 2009, 1, 110-118.	1.5	16
203	Complete genome sequence of Denitrovibrio acetiphilus type strain (N2460T). Standards in Genomic Sciences, 2010, 2, 270-279.	1.5	16
204	Complete genome sequence of the gliding, heparinolytic Pedobacter saltans type strain (113T). Standards in Genomic Sciences, 2011, 5, 30-40.	1.5	16
205	Genome sequence of the Antarctic rhodopsins-containing flavobacterium Gillisia limnaea type strain (R-8282T). Standards in Genomic Sciences, 2012, 7, 107-119.	1.5	16
206	Complete genome sequence of the facultatively chemolithoautotrophic and methylotrophic alpha Proteobacterium Starkeya novella type strain (ATCC 8093T). Standards in Genomic Sciences, 2012, 7, 44-58.	1.5	16
207	Kribbella shirazensis sp. nov., isolated from Iranian soil. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 3369-3374.	1.7	16
208	High quality draft genome sequence of Flavobacterium rivuli type strain WB 3.3-2T (DSM 21788T), a valuable source of polysaccharide decomposing enzymes. Standards in Genomic Sciences, 2015, 10, 46.	1.5	16
209	Streptomyces alkaliphilus sp. nov., isolated from sediments of Lake Elmenteita in the Kenyan Rift Valley. Antonie Van Leeuwenhoek, 2015, 107, 1249-1259.	1.7	16
210	Complete genome sequence of Ignisphaera aggregans type strain (AQ1.S1T). Standards in Genomic Sciences, 2010, 3, 66-75.	1.5	15
211	Complete genome sequence of Weeksella virosa type strain (9751T). Standards in Genomic Sciences, 2011, 4, 81-90.	1.5	15
212	Complete genome sequence of the marine methyl-halide oxidizing Leisingera methylohalidivorans type strain (DSM 14336T), a representative of the Roseobacter clade. Standards in Genomic Sciences, 2013, 9, 128-141.	1.5	15
213	Belliella kenyensis sp. nov., isolated from an alkaline lake. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 457-462.	1.7	15
214	The Evolution of Ecological Diversity in Acidobacteria. Frontiers in Microbiology, 2022, 13, 715637.	3.5	15
215	Complete genome sequence of Capnocytophaga ochracea type strain (VPI 2845T). Standards in Genomic Sciences, 2009, 1, 101-109.	1.5	14
216	Complete genome sequence of Jonesia denitrificans type strain (Prevot 55134T). Standards in Genomic Sciences, 2009, 1, 262-269.	1.5	14

#	Article	IF	Citations
217	Complete genome sequence of Ferrimonas balearica type strain (PATT). Standards in Genomic Sciences, 2010, 3, 174-182.	1.5	14
218	Complete genome sequence of Thermosphaera aggregans type strain (M11TLT). Standards in Genomic Sciences, 2010, 2, 245-259.	1.5	14
219	Complete genome sequence of Bacteroides helcogenes type strain (P 36-108T). Standards in Genomic Sciences, 2011, 4, 45-53.	1.5	14
220	Complete genome sequence of Deinococcus maricopensis type strain (LB-34T). Standards in Genomic Sciences, 2011, 4, 163-172.	1.5	14
221	Morphology and phylogeny of Hyaloperonospora erophilae and H. praecox sp. nov., two downy mildew species co-occurring on Draba verna sensu lato. Mycological Progress, 2011, 10, 283-292.	1.4	14
222	Complete genome sequence of the thermophilic sulfate-reducing ocean bacterium Thermodesulfatator indicus type strain (CIR29812T). Standards in Genomic Sciences, 2012, 6, 155-164.	1.5	14
223	Complete genome sequence of the orange-red pigmented, radioresistant Deinococcus proteolyticus type strain (MRPT). Standards in Genomic Sciences, 2012, 6, 240-250.	1.5	14
224	Charcoal filter paper improves the viability of cryopreserved filamentous ectomycorrhizal and saprotrophic Basidiomycota and Ascomycota. Mycologia, 2012, 104, 324-330.	1.9	14
225	Hoffmannoscypha, a novel genus of brightly coloured, cupulate Pyronemataceae closely related to Tricharina and Geopora. Mycological Progress, 2013, 12, 675-686.	1.4	14
226	High quality draft genome of Nakamurella lactea type strain, a rock actinobacterium, and emended description of Nakamurella lactea. Standards in Genomic Sciences, 2017, 12, 4.	1.5	14
227	Complete genome sequence of Methanoplanus petrolearius type strain (SEBR 4847T). Standards in Genomic Sciences, 2010, 3, 203-211.	1.5	14
228	ICSP response to 'Science depends on nomenclature, but nomenclature is not science'. Nature Reviews Microbiology, 2022, 20, 249-250.	28.6	14
229	Complete genome sequence of Syntrophothermus lipocalidus type strain (TGB-C1T). Standards in Genomic Sciences, 2010, 3, 268-275.	1.5	13
230	Complete genome sequence of Nitratifractor salsuginis type strain (E9I37-1T). Standards in Genomic Sciences, 2011, 4, 322-330.	1.5	13
231	Complete genome sequence of the hyperthermophilic chemolithoautotroph Pyrolobus fumarii type strain (1AT). Standards in Genomic Sciences, 2011, 4, 381-392.	1.5	13
232	Genome sequence of the soil bacterium Saccharomonospora azurea type strain (NA-128T). Standards in Genomic Sciences, 2012, 6, 220-229.	1.5	13
233	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>Rhamnales</i>. Genome Announcements, 2016, 4, .	0.8	13
234	Complete genome sequence of Beutenbergia cavernae type strain (HKI 0122T). Standards in Genomic Sciences, 2009, 1, 21-28.	1.5	12

#	Article	IF	Citations
235	Complete genome sequence of Thermosediminibacter oceani type strain (JW/IW-1228PT). Standards in Genomic Sciences, 2010, 3, 108-116.	1.5	12
236	Complete genome sequence of Hydrogenobacter thermophilus type strain (TK-6T). Standards in Genomic Sciences, 2011, 4, 131-143.	1.5	12
237	Complete genome sequence of Hirschia baltica type strain (IFAM 1418T). Standards in Genomic Sciences, 2011, 5, 287-297.	1.5	12
238	Genome sequence of the moderately thermophilic halophile Flexistipes sinusarabici strain (MAS10T). Standards in Genomic Sciences, 2011, 5, 86-96.	1.5	12
239	Genetic patterns in the Lathyrus pannonicus complex (Fabaceae) reflect ecological differentiation rather than biogeography and traditional subspecific division. Botanical Journal of the Linnean Society, 2011, 165, 402-421.	1.6	12
240	Genea mexicana, sp. nov., and Geopora tolucana, sp. nov., new hypogeous Pyronemataceae from Mexico, and the taxonomy of Geopora reevaluated. Mycological Progress, 2012, 11, 711-724.	1.4	12
241	Complete genome sequence of the bile-resistant pigment-producing anaerobe Alistipes finegoldii type strain (AHN2437T). Standards in Genomic Sciences, 2013, 8, 26-36.	1.5	12
242	Genome sequence of Phaeobacter caeruleus type strain (DSM 24564T), a surface-associated member of the marine Roseobacter clade. Standards in Genomic Sciences, 2013, 8, 403-419.	1.5	12
243	Genome sequence of Phaeobacter daeponensis type strain (DSM 23529T), a facultatively anaerobic bacterium isolated from marine sediment, and emendation of Phaeobacter daeponensis. Standards in Genomic Sciences, 2013, 9, 142-159.	1.5	12
244	Genome sequence of the pink to light reddish-pigmented Rubellimicrobium mesophilum type strain (DSM 19309T), a representative of the Roseobacter group isolated from soil, and emended description of the species. Standards in Genomic Sciences, 2014, 9, 902-913.	1.5	12
245	Genome sequence of the Roseovarius mucosus type strain (DSM 17069T), a bacteriochlorophyll a-containing representative of the marine Roseobacter group isolated from the dinoflagellate Alexandrium ostenfeldii. Standards in Genomic Sciences, 2015, 10, 17.	1.5	12
246	Genome sequence of Phaeobacter caeruleus type strain (DSM 24564(T)), a surface-associated member of the marine Roseobacter clade. Standards in Genomic Sciences, 2013, 8, 403-19.	1.5	12
247	Complete genome sequence of Kribbella flavida type strain (IFO 14399T). Standards in Genomic Sciences, 2010, 2, 185-192.	1.5	11
248	Complete genome sequence of â€˜Thermobaculum terrenumâ€™ type strain (YNP1T). Standards in Genomic Sciences, 2010, 3, 153-162.	1.5	11
249	Molecular Phylogenetic Reconstruction. , 2011, , 159-174.		11
250	Complete genome sequence of Syntrophobotulus glycolicus type strain (FlGlyRT). Standards in Genomic Sciences, 2011, 4, 371-380.	1.5	11
251	Complete genome sequence of the thermophilic sulfur-reducer Desulfurobacterium thermolithotrophum type strain (BSAT) from a deep-sea hydrothermal vent. Standards in Genomic Sciences, 2011, 5, 407-415.	1.5	11
252	Complete genome sequence of Bacteroides salanitronis type strain (BL78T). Standards in Genomic Sciences, 2011, 4, 191-199.	1.5	11

#	ARTICLE	IF	CITATIONS
253	Genome sequence of the orange-pigmented seawater bacterium Owenweeksia hongkongensis type strain (UST20020801T). Standards in Genomic Sciences, 2012, 7, 120-130.	1.5	11
254	High-quality-draft genome sequence of the yellow-pigmented flavobacterium Joostella marina type strain (En5T). Standards in Genomic Sciences, 2013, 8, 37-46.	1.5	11
255	Complete genome sequence of the moderate thermophile Anaerobaculum mobile type strain (NGAT). Standards in Genomic Sciences, 2013, 8, 47-57.	1.5	11
256	Genome sequence of the free-living aerobic spirochete Turneriella parva type strain (HT), and emendation of the species Turneriella parva. Standards in Genomic Sciences, 2013, 8, 228-238.	1.5	11
257	Genome sequence of the exopolysaccharide-producing Salipiger mucosus type strain (DSM 16094T), a moderately halophilic member of the Roseobacter clade. Standards in Genomic Sciences, 2014, 9, 1333-1345.	1.5	11
258	Nocardiopsis mwathae sp. nov., isolated from the haloalkaline Lake Elmenteita in the African Rift Valley. Antonie Van Leeuwenhoek, 2016, 109, 421-430.	1.7	11
259	Genome sequence of Shimia str. SK013, a representative of the Roseobacter group isolated from marine sediment. Standards in Genomic Sciences, 2016, 11, 25.	1.5	11
260	Complete genome sequence of Ilyobacter polytropus type strain (CuHbu1T). Standards in Genomic Sciences, 2010, 3, 304-314.	1.5	10
261	Complete genome sequence of Vulcanisaeta distributa type strain (IC-017T). Standards in Genomic Sciences, 2010, 3, 117-125.	1.5	10
262	Complete genome sequence of Thermaerobacter marianensis type strain (7p75aT). Standards in Genomic Sciences, 2010, 3, 337-345.	1.5	10
263	Complete genome sequence of Xylanimonas cellulosilytica type strain (XIL07T). Standards in Genomic Sciences, 2010, 2, 1-8.	1.5	10
264	Complete genome sequence of Segniliparus rotundus type strain (CDC 1076T). Standards in Genomic Sciences, 2010, 2, 203-211.	1.5	10
265	Complete genome sequence of Desulfurococcus mucosus type strain (O7/1T). Standards in Genomic Sciences, 2011, 4, 173-182.	1.5	10
266	Complete genome sequence of Calditerrivibrio nitroreducens type strain (Yu37-1T). Standards in Genomic Sciences, 2011, 4, 54-62.	1.5	10
267	Complete genome sequence of Tsukamurella paurometabola type strain (no. 33T). Standards in Genomic Sciences, 2011, 4, 342-351.	1.5	10
268	Complete genome sequence of the facultatively anaerobic, appendaged bacterium Muricauda ruestringensis type strain (B1T). Standards in Genomic Sciences, 2012, 6, 185-193.	1.5	10
269	Genome of the R-body producing marine alphaproteobacterium Labrenzia alexandrii type strain (DFL-11T). Standards in Genomic Sciences, 2013, 7, 413-426.	1.5	10
270	High-quality draft genome sequences of Pseudomonas monteilii DSM 14164T, Pseudomonas mosselii DSM 17497T, Pseudomonas plecoglossicida DSM 15088T, Pseudomonas taiwanensis DSM 21245T and Pseudomonas vranovensis DSM 16006T: taxonomic considerations. Access Microbiology, 2019, 1, e000067.	0.5	10

#	Article	IF	Citations
271	Permanent draft genome sequence of Dethiosulfovibrio peptidovorans type strain (SEBR 4207T). Standards in Genomic Sciences, 2010, 3, 85-92.	1.5	9
272	Non-contiguous finished genome sequence of Aminomonas paucivorans type strain (GLU-3T). Standards in Genomic Sciences, 2010, 3, 285-293.	1.5	9
273	Non-contiguous finished genome sequence of Bacteroides coprosuis type strain (PC139T). Standards in Genomic Sciences, 2011, 4, 233-243.	1.5	9
274	Genome sequence of the phage-gene rich marine Phaeobacter arcticus type strain DSM 23566T. Standards in Genomic Sciences, 2013, 8, 450-464.	1.5	9
275	Complete genome sequence of Jiangella gansuensis strain YIM 002T (DSM 44835T), the type species of the genus Jiangella and source of new antibiotic compounds. Standards in Genomic Sciences, 2017, 12, 21.	1.5	9
276	Genome analysis of the marine bacterium Kiloniella laminariae and first insights into comparative genomics with related Kiloniella species. Archives of Microbiology, 2020, 202, 815-824.	2.2	9
277	Complete genome sequence of Arcanobacterium haemolyticum type strain (11018T). Standards in Genomic Sciences, 2010, 3, 126-135.	1.5	8
278	Complete genome sequence of the thermophilic sulfur-reducer Hippea maritima type strain (MH2T). Standards in Genomic Sciences, 2011, 4, 303-311.	1.5	8
279	Complete genome sequence of the aerobic, heterotroph Marinithermus hydrothermalis type strain (T1T) from a deep-sea hydrothermal vent chimney. Standards in Genomic Sciences, 2012, 6, 21-30.	1.5	8
280	Genome of the marine alphaproteobacterium Hoeflea phototrophica type strain (DFL-43T). Standards in Genomic Sciences, 2013, 7, 440-448.	1.5	8
281	Complete genome sequence of Coriobacterium glomerans type strain (PW2T) from the midgut of Pyrrhocoris apterus L. (red soldier bug). Standards in Genomic Sciences, 2013, 8, 15-25.	1.5	8
282	Genome sequence of the moderately thermophilic sulfur-reducing bacterium Thermanaerovibrio velox type strain (Z-9701T) and emended description of the genus Thermanaerovibrio. Standards in Genomic Sciences, 2013, 9, 57-70.	1.5	8
283	Genome sequence of the Litoreibacter arenae type strain (DSM 19593T), a member of the Roseobacter clade isolated from sea sand. Standards in Genomic Sciences, 2013, 9, 117-127.	1.5	8
284	Genome sequence and emended description of Leisingera nanhaiensis strain DSM 24252T isolated from marine sediment. Standards in Genomic Sciences, 2014, 9, 585-601.	1.5	8
285	Judicial Opinions 103–111. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	1.7	8
286	Complete genome sequence of Intrasporangium calvum type strain (7 KIPT). Standards in Genomic Sciences, 2010, 3, 294-303.	1.5	7
287	Complete genome sequence of Mahella australiensis type strain (50-1 BONT). Standards in Genomic Sciences, 2011, 4, 331-341.	1.5	7
288	Non-contiguous finished genome sequence of the opportunistic oral pathogen Prevotella multisaccharivorax type strain (PPPA20T). Standards in Genomic Sciences, 2011, 5, 41-49.	1.5	7

#	Article	IF	Citations
289	Impacts of pr-10a Overexpression at the Molecular and the Phenotypic Level. International Journal of Molecular Sciences, 2013, 14, 15141-15166.	4.1	7
290	Genome sequence of the Thermotoga thermarum type strain (LA3T) from an African solfataric spring. Standards in Genomic Sciences, 2014, 9, 1105-1117.	1.5	7
291	Draft Genome Sequences of Six Type Strains of the Genus <i>Massilia</i>. Microbiology Resource Announcements, 2020, 9, .	0.6	7
292	Evidence of taxonomic bias in public databases: The example of the genus Borrelia. Ticks and Tick-borne Diseases, 2022, 13, 101994.	2.7	7
293	Maximum Likelihood Analyses of 3,490 rbcL Sequences: Scalability of Comprehensive Inference versus Group-Specific Taxon Sampling. Evolutionary Bioinformatics, 2010, 6, EBO.S4528.	1.2	6
294	Complete genome sequence of Tolumonas auensis type strain (TA 4T). Standards in Genomic Sciences, 2011, 5, 112-120.	1.5	6
295	Genome sequence of the reddish-pigmented Rubellimicrobium thermophilum type strain (DSM 16684T), a member of the Roseobacter clade. Standards in Genomic Sciences, 2013, 8, 480-490.	1.5	6
296	High quality draft genome sequence and analysis of Pontibacter roseus type strain SRC-1T (DSM 17521T) isolated from muddy waters of a drainage system in Chandigarh, India. Standards in Genomic Sciences, 2015, 10, 8.	1.5	6
297	Complete genome sequence of the haloalkaliphilic, obligately chemolithoautotrophic thiosulfate and sulfide-oxidizing Î³-proteobacterium Thioalkalimicrobium cyclicum type strain ALM 1 (DSM 14477T). Standards in Genomic Sciences, 2016, 11, 38.	1.5	6
298	Genome sequence of the ocean sediment bacterium Saccharomonospora marina type strain (XMU15T). Standards in Genomic Sciences, 2012, 6, 265-275.	1.5	5
299	Genome sequence of the phylogenetically isolated spirochete Leptonema illini type strain (3055T). Standards in Genomic Sciences, 2013, 8, 177-187.	1.5	5
300	High-quality draft genome sequence of Sedimenticola selenatireducens strain AK4OH1T, a gammaproteobacterium isolated from estuarine sediment. Standards in Genomic Sciences, 2016, 11, 66.	1.5	5
301	Blastococcus tunisiensis sp. nov., isolated from limestone collected in Tunisia. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	1.7	5
302	ICSP response to â€˜Regulating access can restrict participation in reporting new species and taxaâ€™. Nature Microbiology, 2022, 7, 1711-1712.	13.3	5
303	Complete genome sequence of Oceanithermus profundus type strain (506T). Standards in Genomic Sciences, 2011, 4, 210-220.	1.5	4
304	Genome sequence of the chemoheterotrophic soil bacterium Saccharomonospora cyanea type strain (NA-134T). Standards in Genomic Sciences, 2013, 9, 28-41.	1.5	4
305	Complete genome sequence of the bacteriochlorophyll a-containing Roseibacterium elongatum type strain (DSM 19469T), a representative of the Roseobacter group isolated from Australian coast sand. Standards in Genomic Sciences, 2014, 9, 840-854.	1.5	4
306	Improving Phylogeny Reconstruction at the Strain Level Using Peptidome Datasets. PLoS Computational Biology, 2016, 12, e1005271.	3.2	4

#	Article	IF	Citations
307	Complete genome sequence of Syntrophobotulus glycolicus type strain (FlGlyR). Standards in Genomic Sciences, 2011, 4, 371-80.	1.5	4
308	Permanent draft genome sequence of the gliding predator Saprospira grandis strain Sa g1 (= HR1). Standards in Genomic Sciences, 2012, 6, 210-219.	1.5	3
309	Genome sequence of Frateuria aurantia type strain (KondÃ´ 67T), a xanthomonade isolated from Lilium auratium Lindl.. Standards in Genomic Sciences, 2013, 9, 83-92.	1.5	3
310	Complete genome sequence of the halophilic bacterium Spirochaeta africana type strain (Z-7692T) from the alkaline Lake Magadi in the East African Rift. Standards in Genomic Sciences, 2013, 8, 165-176.	1.5	3
311	Genome Sequence of Gammaproteobacterial Pseudohaliea rubra Type Strain DSM 19751, Isolated from Coastal Seawater of the Mediterranean Sea. Genome Announcements, 2014, 2, .	0.8	3
312	Genome sequence of the Wenxinia marina type strain (DSM 24838T), a representative of the Roseobacter group isolated from oilfield sediments. Standards in Genomic Sciences, 2014, 9, 855-865.	1.5	3
313	High-quality draft genome sequence of Gracilimonas tropica CL-CB462T (DSM 19535T), isolated from a Synechococcus culture. Standards in Genomic Sciences, 2015, 10, 98.	1.5	3
314	High-quality draft genome sequence of Flavobacterium suncheonense GH29-5T (DSM 17707T) isolated from greenhouse soil in South Korea, and emended description of Flavobacterium suncheonense GH29-5T. Standards in Genomic Sciences, 2016, 11, 42.	1.5	3
315	Relicts Within the Genus Complex Astragalus/Oxytropis (Fabaceae), and the Comparison of Diversity by Objective Means. , 2010, , 105-117.		3
316	Large-Scale Co-Phylogenetic Analysis on the Grid. International Journal of Grid and High Performance Computing, 2009, 1, 39-54.	0.9	2
317	Genome sequence of the flexirubin-pigmented soil bacterium Niabella soli type strain (JS13-8T). Standards in Genomic Sciences, 2012, 7, 210-220.	1.5	2
318	High quality permanent draft genome sequence of Chryseobacterium bovis DSM 19482T, isolated from raw cow milk. Standards in Genomic Sciences, 2017, 12, 31.	1.5	2
319	Genome sequence of the pinkâ€"pigmented marine bacterium Loktanella hongkongensis type strain (UST950701â€"009PT), a representative of the Roseobacter group. Standards in Genomic Sciences, 2015, 10, 51.	1.5	1
320	High quality permanent draft genome sequence of Phaseolibacter flectens ATCC 12775T, a plant pathogen of French bean pods. Standards in Genomic Sciences, 2016, 11, 4.	1.5	1
321	Draft genome sequence of Marinobacterium rhizophilum CL-YJ9T (DSM 18822T), isolated from the rhizosphere of the coastal tidal-flat plant Suaeda japonica. Standards in Genomic Sciences, 2017, 12, 65.	1.5	1
322	Judicial Commission of the International Committee on Systematics of Prokaryotes: Minutes of the Meeting of 4 August 2021. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	1.7	1
323	The Family Intrasporangiaceae. , 2014, , 397-424.		1
324	Large-Scale Co-Phylogenetic Analysis on the Grid. , 0, , 222-237.		0

#	Article	IF	Citations
325	Judicial Commission of the International Committee on Systematics of Prokaryotes: Minutes of the Meeting on 3 March 2022. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	1.7	0