

# Markus Gker

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

325  
papers

16,479  
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27,306  
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| #   | Paper                                                                                                                                                                                                                | IF   | Citations |
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| 325 | Genome sequence-based species delimitation with confidence intervals and improved distance functions. <i>BMC Bioinformatics</i> , <b>2013</b> , 14, 60                                                               | 3.6  | 3251      |
| 324 | Digital DNA-DNA hybridization for microbial species delineation by means of genome-to-genome sequence comparison. <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 117-34                                     |      | 972       |
| 323 | TYGS is an automated high-throughput platform for state-of-the-art genome-based taxonomy. <i>Nature Communications</i> , <b>2019</b> , 10, 2182                                                                      | 17.4 | 590       |
| 322 | Critical Assessment of Metagenome Interpretation-a benchmark of metagenomics software. <i>Nature Methods</i> , <b>2017</b> , 14, 1063-1071                                                                           | 21.6 | 412       |
| 321 | Standard operating procedure for calculating genome-to-genome distances based on high-scoring segment pairs. <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 142-8                                           |      | 384       |
| 320 | When should a DDH experiment be mandatory in microbial taxonomy?. <i>Archives of Microbiology</i> , <b>2013</b> , 195, 413-8                                                                                         | 3    | 377       |
| 319 | Taxonomic use of DNA G+C content and DNA-DNA hybridization in the genomic age. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2014</b> , 64, 352-356                                  | 2.2  | 337       |
| 318 | Genome-Based Taxonomic Classification of the Phylum. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 2007                                                                                                        | 5.7  | 297       |
| 317 | List of Prokaryotic names with Standing in Nomenclature (LPSN) moves to the DSMZ. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2020</b> , 70, 5607-5612                             | 2.2  | 291       |
| 316 | Toward a Novel Multilocus Phylogenetic Taxonomy for the Dermatophytes. <i>Mycopathologia</i> , <b>2017</b> , 182, 5-31                                                                                               | 2.9  | 287       |
| 315 | Towards an integrated phylogenetic classification of the Tremellomycetes. <i>Studies in Mycology</i> , <b>2015</b> , 81, 85-147                                                                                      | 22.2 | 280       |
| 314 | Complete genome sequence of DSM 30083(T), the type strain (U5/41(T)) of Escherichia coli, and a proposal for delineating subspecies in microbial taxonomy. <i>Standards in Genomic Sciences</i> , <b>2014</b> , 9, 2 |      | 267       |
| 313 | En route to a genome-based classification of Archaea and Bacteria?. <i>Systematic and Applied Microbiology</i> , <b>2010</b> , 33, 175-82                                                                            | 4.2  | 251       |
| 312 | Comparative genomics of biotechnologically important yeasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 9882-7                                      | 11.5 | 212       |
| 311 | VICTOR: genome-based phylogeny and classification of prokaryotic viruses. <i>Bioinformatics</i> , <b>2017</b> , 33, 3396-3404                                                                                        | 7.2  | 191       |
| 310 | Phylogenomics of Rhodobacteraceae reveals evolutionary adaptation to marine and non-marine habitats. <i>ISME Journal</i> , <b>2017</b> , 11, 1483-1499                                                               | 11.9 | 167       |
| 309 | 1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 676-683                                                              | 44.5 | 161       |

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| 308 | Phylogenetic classification of yeasts and related taxa within Pucciniomycotina. <i>Studies in Mycology</i> , <b>2015</b> , 81, 149-89                                                                                                                                                                                                                                                                                           | 22.2 | 158 |
| 307 | <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 wanjuense</i> and <i>Chryseobacterium gregarium</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2013</b> , 63, 4386-4395 | 2.2  | 156 |
| 306 | opm: an R package for analysing OmniLog(R) phenotype microarray data. <i>Bioinformatics</i> , <b>2013</b> , 29, 1823-4                                                                                                                                                                                                                                                                                                          | 4.2  | 153 |
| 305 | Genomic insights into the taxonomic status of the <i>Bacillus cereus</i> group. <i>Scientific Reports</i> , <b>2015</b> , 5, 14082                                                                                                                                                                                                                                                                                              | 4.9  | 152 |
| 304 | Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , <b>2014</b> , 12, e1001920                                                                                                                                                                                                                                                                                             | 9.7  | 146 |
| 303 | Visualization and curve-parameter estimation strategies for efficient exploration of phenotype microarray kinetics. <i>PLoS ONE</i> , <b>2012</b> , 7, e34846                                                                                                                                                                                                                                                                   | 3.7  | 139 |
| 302 | Molecular taxonomy of phytopathogenic fungi: a case study in <i>Peronospora</i> . <i>PLoS ONE</i> , <b>2009</b> , 4, e6319                                                                                                                                                                                                                                                                                                      | 3.7  | 127 |
| 301 | How do obligate parasites evolve? A multi-gene phylogenetic analysis of downy mildews. <i>Fungal Genetics and Biology</i> , <b>2007</b> , 44, 105-22                                                                                                                                                                                                                                                                            | 3.9  | 114 |
| 300 | Phylogenetic Relationships of the Downy Mildews (Peronosporales) and Related Groups Based on Nuclear Large Subunit Ribosomal DNA Sequences. <i>Mycologia</i> , <b>2002</b> , 94, 834                                                                                                                                                                                                                                            | 2.4  | 114 |
| 299 | Genome-Based Taxonomic Classification of. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 2003                                                                                                                                                                                                                                                                                                                              | 5.7  | 114 |
| 298 | Genomic and Genetic Diversity within the <i>Pseudomonas fluorescens</i> Complex. <i>PLoS ONE</i> , <b>2016</b> , 11, e0159183                                                                                                                                                                                                                                                                                                   | 5.83 | 109 |
| 297 | TYGS and LPSN: a database tandem for fast and reliable genome-based classification and nomenclature of prokaryotes. <i>Nucleic Acids Research</i> , <b>2021</b> ,                                                                                                                                                                                                                                                               | 20.1 | 108 |
| 296 | Analysis of 1,000+ Type-Strain Genomes Substantially Improves Taxonomic Classification of. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 468                                                                                                                                                                                                                                                                             | 5.7  | 101 |
| 295 | Quantifying the phylodynamic forces driving papillomavirus evolution. <i>Molecular Biology and Evolution</i> , <b>2011</b> , 28, 2101-13                                                                                                                                                                                                                                                                                        | 8.3  | 99  |
| 294 | Complete genome sequence of <i>Kytococcus sedentarius</i> type strain (541). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 12-20                                                                                                                                                                                                                                                                                      |      | 94  |
| 293 | 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> , <b>2015</b> , 6, 281                                                                                                                                                                                       | 5.7  | 88  |
| 292 | Phylogenetic relationships of <i>Plasmopara</i> , <i>Bremia</i> and other genera of downy mildew pathogens with pyriform haustoria based on Bayesian analysis of partial LSU rDNA sequence data. <i>Mycological Research</i> , <b>2004</b> , 108, 1011-24                                                                                                                                                                       |      | 88  |
| 291 | COPYCAT: cophylogenetic analysis tool. <i>Bioinformatics</i> , <b>2007</b> , 23, 898-900                                                                                                                                                                                                                                                                                                                                        | 7.2  | 84  |

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| 290 | Phylogeny of Hyaloperonospora based on nuclear ribosomal internal transcribed spacer sequences. <i>Mycological Progress</i> , <b>2004</b> , 3, 83-94                                                         | 1.9 | 77 |
| 289 | Novel genera and species of coniothyrium-like fungi in Montagnulaceae (Ascomycota). <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , <b>2014</b> , 32, 25-51                                   | 9   | 73 |
| 288 | Non-contiguous finished genome sequence and contextual data of the filamentous soil bacterium Ktedonobacter racemifer type strain (SOSP1-21). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 5, 97-111 |     | 72 |
| 287 | Taxonomic aspects of Peronosporaceae inferred from Bayesian molecular phylogenetics. <i>Canadian Journal of Botany</i> , <b>2003</b> , 81, 672-683                                                           |     | 70 |
| 286 | Extrachromosomal, extraordinary and essential--the plasmids of the Roseobacter clade. <i>Applied Microbiology and Biotechnology</i> , <b>2013</b> , 97, 2805-15                                              | 5.7 | 69 |
| 285 | Species delimitation in downy mildews: the case of Hyaloperonospora in the light of nuclear ribosomal ITS and LSU sequences. <i>Mycological Research</i> , <b>2009</b> , 113, 308-25                         |     | 68 |
| 284 | Analysis of 1,000 Type-Strain Genomes Improves Taxonomic Classification of. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 2083                                                                        | 5.7 | 66 |
| 283 | Anther smuts of Caryophyllaceae: Molecular characters indicate host-dependent species delimitation. <i>Mycological Progress</i> , <b>2005</b> , 4, 225-238                                                   | 1.9 | 64 |
| 282 | Genome-based classification of micromonosporae with a focus on their biotechnological and ecological potential. <i>Scientific Reports</i> , <b>2018</b> , 8, 525                                             | 4.9 | 63 |
| 281 | Implications of molecular characters for the phylogeny of the Microbotryaceae (Basidiomycota: Urediniomycetes). <i>BMC Evolutionary Biology</i> , <b>2006</b> , 6, 35                                        | 3   | 63 |
| 280 | Complete genome sequence of Odoribacter splanchnicus type strain (1651/6). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 200-9                                                                     |     | 62 |
| 279 | Novel insights into the diversity of catabolic metabolism from ten haloarchaeal genomes. <i>PLoS ONE</i> , <b>2011</b> , 6, e20237                                                                           | 3.7 | 60 |
| 278 | Complete genome sequence of Chitinophaga pinensis type strain (UQM 2034). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 87-95                                                                      |     | 57 |
| 277 | Genome BLAST distance phylogenies inferred from whole plastid and whole mitochondrion genome sequences. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 350                                                     | 3.6 | 54 |
| 276 | Controlling false discoveries in high-dimensional situations: boosting with stability selection. <i>BMC Bioinformatics</i> , <b>2015</b> , 16, 144                                                           | 3.6 | 53 |
| 275 | Complete genome sequence of Haliangium ochraceum type strain (SMP-2). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 96-106                                                                         |     | 53 |
| 274 | Phylogeny of Peronospora, parasitic on Fabaceae, based on ITS sequences. <i>Mycological Research</i> , <b>2008</b> , 112, 502-12                                                                             |     | 52 |
| 273 | Metabolic traits of an uncultured archaeal lineage--MSBL1--from brine pools of the Red Sea. <i>Scientific Reports</i> , <b>2016</b> , 6, 19181                                                               | 4.9 | 51 |

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| 272 | Complete genome sequence of <i>Geodermatophilus obscurus</i> type strain (G-20). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 158-67                                                                                                                                                                                                                                                                                                                                                                                     |      | 49 |
| 271 | Molecular and phenotypic analyses reveal the non-identity of the <i>Phaeobacter gallaeciensis</i> type strain deposits CIP 105210T and DSM 17395. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2013</b> , 63, 4340-4349                                                                                                                                                                                                                                                                            | 2.2  | 48 |
| 270 | <i>Chryseobacterium oleae</i> sp. nov., an efficient plant growth promoting bacterium in the rooting induction of olive tree ( <i>Olea europaea</i> L.) cuttings and emended descriptions of the genus <i>Chryseobacterium</i> , <i>C. daecheongense</i> , <i>C. gambrini</i> , <i>C. gleum</i> , <i>C. joostei</i> , <i>C. jejuense</i> , <i>C. luteum</i> , <i>C. tigrisense</i> , <i>C. taiwanense</i> , <i>C. urugaiticum</i> and <i>C. vryssabense</i> . <i>Systematic and Applied Microbiology</i> , <b>2014</b> , 38, 342-50 | 4.2  | 47 |
| 269 | Complete genome sequence of the termite hindgut bacterium <i>Spirochaeta coccoides</i> type strain (SPN1(T)), reclassification in the genus <i>Sphaerochaeta</i> as <i>Sphaerochaeta coccoides</i> comb. nov. and emendations of the family Spirochaetaceae and the genus <i>Sphaerochaeta</i> . <i>Standards in Genomic Sciences</i> , <b>2012</b> , 6, 194-209                                                                                                                                                                    |      | 46 |
| 268 | <i>Geodermatophilus arenarius</i> sp. nov., a xerophilic actinomycete isolated from Saharan desert sand in Chad. <i>Extremophiles</i> , <b>2012</b> , 16, 903-9                                                                                                                                                                                                                                                                                                                                                                     | 3    | 44 |
| 267 | Phylogenetic relationships of graminicolous downy mildews based on <i>cox2</i> sequence data. <i>Mycological Research</i> , <b>2008</b> , 112, 345-51                                                                                                                                                                                                                                                                                                                                                                               |      | 43 |
| 266 | Phylogeny-driven target selection for large-scale genome-sequencing (and other) projects. <i>Standards in Genomic Sciences</i> , <b>2013</b> , 8, 360-74                                                                                                                                                                                                                                                                                                                                                                            |      | 42 |
| 265 | 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> , <b>2016</b> , 66, 5201-5210                                                                                                                                                                                                    | 2.2  | 42 |
| 264 | Intraspecific Relationship of <i>Plasmopara halstedii</i> Isolates Differing in Pathogenicity and Geographic Origin Based on ITS Sequence Data. <i>European Journal of Plant Pathology</i> , <b>2006</b> , 114, 309-315 <sup>2.1</sup>                                                                                                                                                                                                                                                                                              |      | 41 |
| 263 | Complete genome sequence of <i>Isosphaera pallida</i> type strain (IS1B). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 63-71                                                                                                                                                                                                                                                                                                                                                                                             |      | 40 |
| 262 | Complete genome sequence of <i>Planctomyces brasiliensis</i> type strain (DSM 5305(T)), phylogenomic analysis and reclassification of Planctomycetes including the descriptions of <i>Gimesia</i> gen. nov., <i>Planctopirus</i> gen. nov. and <i>Rubinisphaera</i> gen. nov. and emended descriptions of the order Planctomycetales and the family Planctomycetaceae. <i>Standards in Genomic Sciences</i> , <b>2014</b> , 9, 10                                                                                                   |      | 39 |
| 261 | Highly parallelized inference of large genome-based phylogenies. <i>Concurrency Computation Practice and Experience</i> , <b>2014</b> , 26, 1715-1729                                                                                                                                                                                                                                                                                                                                                                               | 1.4  | 39 |
| 260 | Complete genome sequence of <i>Desulfobulbus propionicus</i> type strain (1pr3). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 100-10                                                                                                                                                                                                                                                                                                                                                                                     |      | 39 |
| 259 | General functions to transform associate data to host data, and their use in phylogenetic inference from sequences with intra-individual variability. <i>BMC Evolutionary Biology</i> , <b>2008</b> , 8, 86                                                                                                                                                                                                                                                                                                                         | 3    | 39 |
| 258 | Genome-scale data suggest reclassifications in the Leisingera-Phaeobacter cluster including proposals for <i>Sedimentitalea</i> gen. nov. and <i>Pseudophaeobacter</i> gen. nov. <i>Frontiers in Microbiology</i> , <b>2014</b> , 5, 416                                                                                                                                                                                                                                                                                            | 5.7  | 38 |
| 257 | Genomics and physiology of a marine flavobacterium encoding a proteorhodopsin and a xanthorhodopsin-like protein. <i>PLoS ONE</i> , <b>2013</b> , 8, e57487                                                                                                                                                                                                                                                                                                                                                                         | 3.7  | 38 |
| 256 | Biofilm plasmids with a rhamnose operon are widely distributed determinants of the $\beta$ wim-or-stickP lifestyle in roseobacters. <i>ISME Journal</i> , <b>2016</b> , 10, 2498-513                                                                                                                                                                                                                                                                                                                                                | 11.9 | 37 |
| 255 | Codivergence of mycoviruses with their hosts. <i>PLoS ONE</i> , <b>2011</b> , 6, e22252                                                                                                                                                                                                                                                                                                                                                                                                                                             | 3.7  | 37 |

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| 254 | Complete genome sequence of <i>Truepera radiovictrix</i> type strain (RQ-24). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 91-9                                                                                                                                                                                                                  |      | 37 |
| 253 | AxPcoords & parallel AxParafit: statistical co-phylogenetic analyses on thousands of taxa. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 405                                                                                                                                                                                                                 | 3.6  | 37 |
| 252 | <i>Geodermatophilus africanus</i> sp. nov., a halotolerant actinomycete isolated from Saharan desert sand. <i>Antonie Van Leeuwenhoek</i> , <b>2013</b> , 104, 207-16                                                                                                                                                                                       | 2.1  | 36 |
| 251 | Shotgun metagenome data of a defined mock community using Oxford Nanopore, PacBio and Illumina technologies. <i>Scientific Data</i> , <b>2019</b> , 6, 285                                                                                                                                                                                                  | 8.2  | 36 |
| 250 | Dual function of tropodithietic acid as antibiotic and signaling molecule in global gene regulation of the probiotic bacterium <i>Phaeobacter inhibens</i> . <i>Scientific Reports</i> , <b>2017</b> , 7, 730                                                                                                                                               | 4.9  | 35 |
| 249 | <i>Geodermatophilus siccatus</i> sp. nov., isolated from arid sand of the Saharan desert in Chad. <i>Antonie Van Leeuwenhoek</i> , <b>2013</b> , 103, 449-56                                                                                                                                                                                                | 2.1  | 35 |
| 248 | Complete genome sequence of the filamentous gliding predatory bacterium <i>Herpetosiphon aurantiacus</i> type strain (114-95(T)). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 5, 356-70                                                                                                                                                            |      | 35 |
| 247 | Complete genome sequence of the thermophilic, hydrogen-oxidizing <i>Bacillus tusciae</i> type strain (T2) and reclassification in the new genus, <i>Kyrpidia</i> gen. nov. as <i>Kyrpidia tusciae</i> comb. nov. and emendation of the family Alicyclobacillaceae da Costa and Rainey, 2010. <i>Standards in Genomic Sciences</i> , <b>2011</b> , 5, 121-34 |      | 35 |
| 246 | Complete genome sequence of <i>Spirosoma linguale</i> type strain (1). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 176-85                                                                                                                                                                                                                       |      | 35 |
| 245 | Genome-Scale Data Call for a Taxonomic Rearrangement of. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 2501                                                                                                                                                                                                                                           | 5.7  | 33 |
| 244 | Complete genome sequence of <i>Desulfotomaculum acetoxidans</i> type strain (5575). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 242-53                                                                                                                                                                                                          |      | 33 |
| 243 | Horizontal operon transfer, plasmids, and the evolution of photosynthesis in Rhodobacteraceae. <i>ISME Journal</i> , <b>2018</b> , 12, 1994-2010                                                                                                                                                                                                            | 11.9 | 33 |
| 242 | Complete genome sequence of <i>Actinosynnema mirum</i> type strain (101). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 46-53                                                                                                                                                                                                                     |      | 32 |
| 241 | Complete genome sequence of <i>Arcobacter nitrofigilis</i> type strain (CI). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 300-8                                                                                                                                                                                                                  |      | 32 |
| 240 | Complete genome sequence of <i>Sulfurimonas autotrophica</i> type strain (OK10). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 194-202                                                                                                                                                                                                            |      | 32 |
| 239 | Complete genome sequence of <i>Rhodospirillum rubrum</i> type strain (S1). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 293-302                                                                                                                                                                                                                  |      | 31 |
| 238 | The genome sequence of <i>Methanohalophilus mahii</i> SLP(T) reveals differences in the energy metabolism among members of the Methanosarcinaceae inhabiting freshwater and saline environments. <i>Archaea</i> , <b>2010</b> , 2010, 690737                                                                                                                | 2    | 31 |
| 237 | Complete genome sequence of <i>Cellulomonas flavigena</i> type strain (134). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 15-25                                                                                                                                                                                                                  |      | 31 |

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| 236 | Complete genome sequence of the sulfur compounds oxidizing chemolithoautotroph <i>Sulfuricurvum kujiense</i> type strain (YK-1(T)). <i>Standards in Genomic Sciences</i> , <b>2012</b> , 6, 94-103 |     | 31 |
| 235 | Hidden diversity in the non-caryophyllaceous plant-parasitic members of <i>Microbotryum</i> (Pucciniomycotina: Microbotryales). <i>Systematics and Biodiversity</i> , <b>2009</b> , 7, 297-306     | 1.7 | 31 |
| 234 | Complete genome sequence of <i>Eggerthella lenta</i> type strain (IPP VPI 0255). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 174-82                                                    |     | 31 |
| 233 | A revision of <i>Bremia graminicola</i> . <i>Mycological Research</i> , <b>2006</b> , 110, 646-56                                                                                                  |     | 31 |
| 232 | Genomic Analysis of , the Thermophilic Anaerobic Bacterium of the Novel Bacterial Phylum. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 195                                                  | 5.7 | 30 |
| 231 | Complete genome sequence of <i>Desulfomicrobium baculatum</i> type strain (X). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 29-37                                                       |     | 30 |
| 230 | Complete genome sequence of <i>Halomicrobium mukohataei</i> type strain (arg-2). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 270-7                                                     |     | 30 |
| 229 | <i>Geodermatophilus tzadiensis</i> sp. nov., a UV radiation-resistant bacterium isolated from sand of the Saharan desert. <i>Systematic and Applied Microbiology</i> , <b>2013</b> , 36, 177-82    | 4.2 | 29 |
| 228 | Complete genome sequence of <i>Veillonella parvula</i> type strain (Te3). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 57-65                                                            |     | 29 |
| 227 | Complete genome sequence of the halophilic and highly halotolerant <i>Chromohalobacter salexigens</i> type strain (1H11(T)). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 5, 379-88        |     | 28 |
| 226 | Complete genome sequence of <i>Planctomyces limnophilus</i> type strain (M290). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 47-56                                                      |     | 28 |
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| 223 | Complete genome sequence of <i>Nakamurella multipartita</i> type strain (Y-104). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 168-75                                                    |     | 28 |
| 222 | <i>Geodermatophilus saharensis</i> sp. nov., isolated from sand of the Saharan desert in Chad. <i>Archives of Microbiology</i> , <b>2013</b> , 195, 153-9                                          | 3   | 27 |
| 221 | A Clustering Optimization Strategy for Molecular Taxonomy Applied to Planktonic Foraminifera SSU rDNA. <i>Evolutionary Bioinformatics</i> , <b>2010</b> , 6, 97-112                                | 1.9 | 27 |
| 220 | Complete genome sequence of <i>Polynucleobacter necessarius</i> subsp. <i>asymbioticus</i> type strain (QLW-P1DMWA-1(T)). <i>Standards in Genomic Sciences</i> , <b>2012</b> , 6, 74-83            |     | 27 |
| 219 | Complete genome sequence of <i>Acidimicrobium ferrooxidans</i> type strain (ICP). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 38-45                                                    |     | 27 |

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| 217 | Complete genome sequence of <i>Olsenella uli</i> type strain (VPI D76D-27C). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 76-84                                                                                                                                                                                                                                                                                             |     | 27 |
| 216 | Complete genome sequence of <i>Desulfarculus baarsii</i> type strain (2st14). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 276-84                                                                                                                                                                                                                                                                                           |     | 27 |
| 215 | Complete genome sequence of <i>Aminobacterium colombiense</i> type strain (ALA-1). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 280-9                                                                                                                                                                                                                                                                                       |     | 27 |
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| 213 | <i>Geodermatophilus telluris</i> sp. nov., an actinomycete isolated from Saharan desert sand. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2013</b> , 63, 2254-2259                                                                                                                                                                                                                                   | 2.2 | 26 |
| 212 | Complete genome sequence of <i>Riemerella anatipestifer</i> type strain (ATCC 11845T). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 144-153                                                                                                                                                                                                                                                                                 |     | 26 |
| 211 | Complete genome sequence of <i>Pirellula staley</i> type strain (ATCC 27377). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 308-16                                                                                                                                                                                                                                                                                           |     | 26 |
| 210 | Taxonomy and Phylogeny of the Downy Mildews (Peronosporaceae)47-75                                                                                                                                                                                                                                                                                                                                                                     |     | 25 |
| 209 | Using the Multiple Analysis Approach to Reconstruct Phylogenetic Relationships among Planktonic Foraminifera from Highly Divergent and Length-polymorphic SSU rDNA Sequences. <i>Bioinformatics and Biology Insights</i> , <b>2009</b> , 3, 155-77                                                                                                                                                                                     | 5.3 | 25 |
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| 207 | Species delimitation in taxonomically difficult fungi: the case of <i>Hymenogaster</i> . <i>PLoS ONE</i> , <b>2011</b> , 6, e15634                                                                                                                                                                                                                                                                                                     | 3.4 | 25 |
| 206 | Pathways and substrate-specific regulation of amino acid degradation in <i>Phaeobacter inhibens</i> DSM 17395 (archetype of the marine <i>Roseobacter</i> clade). <i>Environmental Microbiology</i> , <b>2014</b> , 16, 218-38                                                                                                                                                                                                         | 5.2 | 24 |
| 205 | 16S-rRNA-based analysis of bacterial diversity in the gut of fungus-cultivating termites ( <i>Microtermes</i> and <i>Odontotermes</i> species). <i>Antonie Van Leeuwenhoek</i> , <b>2013</b> , 104, 869-83                                                                                                                                                                                                                             | 2.1 | 24 |
| 204 | Genome sequence of the thermophilic fresh-water bacterium <i>Spirochaeta caldaria</i> type strain (H1(T)), reclassification of <i>Spirochaeta caldaria</i> , <i>Spirochaeta stenostrepta</i> , and <i>Spirochaeta zuelzer</i> in the genus <i>Treponema</i> as <i>Treponema caldaria</i> comb. nov., <i>Treponema stenostrepta</i> comb. nov., and <i>Treponema zuelzer</i> comb. nov., and emendation of the genus <i>Treponema</i> . |     | 24 |
| 203 | Complete genome sequence of <i>Paludibacter propionigenes</i> type strain (WB4). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 36-44                                                                                                                                                                                                                                                                                         |     | 24 |
| 202 | Complete genome sequence of the extremely halophilic <i>Halanaerobium praevalens</i> type strain (GSL). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 312-21                                                                                                                                                                                                                                                                 |     | 24 |
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| 200 | Complete genome sequence of <i>Thermomonospora curvata</i> type strain (B9). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 13-22                                                                            |     | 24 |
| 199 | Complete genome sequence of <i>Sulfurospirillum deleyianum</i> type strain (5175). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 149-57                                                                     |     | 24 |
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| 197 | Complete genome sequence of <i>Cellulophaga lytica</i> type strain (LIM-21). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 221-32                                                                           |     | 23 |
| 196 | Genome sequence of the homoacetogenic bacterium <i>Holophaga foetida</i> type strain (TMBS4(T)). <i>Standards in Genomic Sciences</i> , <b>2012</b> , 6, 174-84                                                       |     | 23 |
| 195 | Complete genome sequence of <i>Cellulophaga algicola</i> type strain (IC166). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 72-80                                                                           |     | 22 |
| 194 | Complete genome sequence of <i>Halogeometricum borinquense</i> type strain (PR3). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 150-9                                                                       |     | 22 |
| 193 | <i>Geodermatophilus normandii</i> sp. nov., isolated from Saharan desert sand. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2013</b> , 63, 3437-3443                                 | 2.2 | 21 |
| 192 | Genome sequence of the moderately thermophilic, amino-acid-degrading and sulfur-reducing bacterium <i>Thermovirga lienii</i> type strain (Cas60314(T)). <i>Standards in Genomic Sciences</i> , <b>2012</b> , 6, 230-9 |     | 21 |
| 191 | Complete genome sequence of <i>Halorhabdus utahensis</i> type strain (AX-2). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 218-25                                                                           |     | 21 |
| 190 | Complete genome sequence of <i>Saccharomonospora viridis</i> type strain (P101). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 141-9                                                                        |     | 21 |
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| 187 | Complete genome sequence of the moderately thermophilic mineral-sulfide-oxidizing firmicute <i>Sulfobacillus acidophilus</i> type strain (NAL(T)). <i>Standards in Genomic Sciences</i> , <b>2012</b> , 6, 1-13       |     | 20 |
| 186 | Complete genome sequence of <i>Rhodothermus marinus</i> type strain (R-10). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 283-90                                                                            |     | 20 |
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| 184 | Complete genome sequence of <i>Sphaerobacter thermophilus</i> type strain (S 6022). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 49-56                                                                     |     | 20 |
| 183 | Complete genome sequence of <i>Archaeoglobus profundus</i> type strain (AV18). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 327-46                                                                         |     | 20 |

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| 180 | Genome sequence of <i>Phaeobacter inhibens</i> type strain (T5(T)), a secondary metabolite producing representative of the marine Roseobacter clade, and emendation of the species description of <i>Phaeobacter inhibens</i> . <i>Standards in Genomic Sciences</i> , <b>2013</b> , 9, 334-50 |     | 19 |
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| 175 | Complete genome sequence of <i>Pedobacter heparinus</i> type strain (HIM 762-3). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 54-62                                                                                                                                                 |     | 19 |
| 174 | Complete genome sequence of <i>Brachybacterium faecium</i> type strain (Schefferle 6-10). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 3-11                                                                                                                                         |     | 19 |
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| 172 | Complete genome sequence of <i>Thermanaerovibrio acidaminovorans</i> type strain (Su883). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 254-61                                                                                                                                       |     | 19 |
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| 170 | Complete genome sequence of <i>Gordonia bronchialis</i> type strain (3410). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 19-28                                                                                                                                                      |     | 19 |
| 169 | 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> , <b>2015</b> , 19, 77-85                                      | 3   | 18 |
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| 167 | Complete genome sequence of <i>Anaerococcus prevotii</i> type strain (PC1). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 159-65                                                                                                                                                     |     | 18 |
| 166 | Complete genome sequence of <i>Brachyspira murdochii</i> type strain (56-150). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 260-9                                                                                                                                                   |     | 18 |
| 165 | Complete genome sequence of <i>Coralimargarita akajimensis</i> type strain (04OKA010-24). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 290-9                                                                                                                                        |     | 18 |

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| 162 | Description of <i>Trichococcus ilyis</i> sp. nov. by combined physiological and in silico genome hybridization analyses. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2016</b> , 66, 3957-3963     | 3-3  | 18 |
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| 160 | Cutaneotropic human beta-/gamma-papillomaviruses are rarely shared between family members. <i>Journal of Investigative Dermatology</i> , <b>2009</b> , 129, 2427-34                                                                 | 4-3  | 17 |
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| 157 | Critical Assessment of Metagenome Interpretation $\square$ benchmark of computational metagenomics software                                                                                                                         |      | 17 |
| 156 | Cobaviruses $\square$ a new globally distributed phage group infecting Rhodobacteraceae in marine ecosystems. <i>ISME Journal</i> , <b>2019</b> , 13, 1404-1421                                                                     | 11.9 | 16 |
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| 149 | Complete genome sequence of <i>Stackebrandtia nassauensis</i> type strain (LLR-40K-21). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 234-41                                                                              |      | 16 |
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| 146 | Complete genome sequence of <i>Sebaldella termitidis</i> type strain (NCTC 11300). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 220-7                                                                                                                                                                                                                                                                      |     | 16 |
| 145 | The neglected hypogeous fungus <i>Hydnotrya bailii</i> Soehner (1959) is a widespread sister taxon of <i>Hydnotrya tulasnei</i> (Berk.) Berk. & Broome (1846). <i>Mycological Progress</i> , <b>2010</b> , 9, 195-203                                                                                                                                                                                                 | 1.9 | 16 |
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| 139 | Complete genome sequence of <i>Spirochaeta smaragdinae</i> type strain (SEBR 4228). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 136-44                                                                                                                                                                                                                                                                    |     | 15 |
| 138 | Complete genome sequence of the facultatively chemolithoautotrophic and methylotrophic alpha Proteobacterium <i>Starkeya novella</i> type strain (ATCC 8093T). <i>Standards in Genomic Sciences</i> , <b>2012</b> , 7, 44-58                                                                                                                                                                                          |     | 15 |
| 137 | Comparing polysaccharide decomposition between the type strains <i>Gramella echinicola</i> KMM 6050(T) (DSM 19838(T)) and <i>Gramella portivictoriae</i> UST040801-001(T) (DSM 23547(T)), and emended description of <i>Gramella echinicola</i> Nedashkovskaya et al. 2005 emend. Shahina et al. 2014 and <i>Gramella portivictoriae</i> Lau et al. 2005. <i>Standards in Genomic Sciences</i> , <b>2016</b> , 11, 37 |     | 14 |
| 136 | Morphology and phylogeny of <i>Hyaloperonospora erophilae</i> and <i>H. praecox</i> sp. nov., two downy mildew species co-occurring on <i>Draba verna</i> sensu lato. <i>Mycological Progress</i> , <b>2011</b> , 10, 283-292                                                                                                                                                                                         | 1.9 | 14 |
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| 133 | Complete genome sequence of the <i>Phaeobacter gallaeciensis</i> type strain CIP 105210(T) (= DSM 26640(T) = BS107(T)). <i>Standards in Genomic Sciences</i> , <b>2014</b> , 9, 914-32                                                                                                                                                                                                                                |     | 13 |
| 132 | Complete genome sequence of the marine methyl-halide oxidizing <i>Leisingera methylohalidivorans</i> type strain (DSM 14336(T)), a representative of the <i>Roseobacter</i> clade. <i>Standards in Genomic Sciences</i> , <b>2013</b> , 9, 128-41                                                                                                                                                                     |     | 13 |
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| 130 | Complete genome sequence of <i>Ignisphaera aggregans</i> type strain (AQ1.S1). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 66-75                                                                                                                                                                                                                                                                          |     | 13 |
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| 125 | Complete genome sequence of Capnocytophaga ochracea type strain (VPI 2845). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 101-9                                                                                 |     | 12 |
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| 123 | Complete genome sequence of Thermosphaera aggregans type strain (M11TL). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 245-59                                                                                   |     | 12 |
| 122 | Complete genome sequence of Methanoplanus petrolearius type strain (SEBR 4847). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 203-11                                                                            |     | 12 |
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| 117 | Complete genome sequence of Deinococcus maricopensis type strain (LB-34). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 163-72                                                                                  |     | 11 |
| 116 | Genome sequence of the orange-pigmented seawater bacterium Owenweeksia hongkongensis type strain (UST20020801(T)). <i>Standards in Genomic Sciences</i> , <b>2012</b> , 7, 120-30                                         |     | 11 |
| 115 | Complete genome sequence of Beutenbergia cavernae type strain (HKI 0122). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 21-8                                                                                    |     | 11 |
| 114 | Complete genome sequence of Denitrovibrio acetiphilus type strain (N2460). <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 270-9                                                                                  |     | 11 |
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| 110 | Genome sequence of the mud-dwelling archaeon <i>Methanoplanus limicola</i> type strain (DSM 2279(T)), reclassification of <i>Methanoplanus petrolearius</i> as <i>Methanolacinia petrolearia</i> and emended descriptions of the genera <i>Methanoplanus</i> and <i>Methanolacinia</i> . <i>Standards in Genomic Sciences</i> , <b>2014</b> , 9, 1076-88 | 10    |
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| 108 | Genome sequence of <i>Phaeobacter daeponensis</i> type strain (DSM 23529(T)), a facultatively anaerobic bacterium isolated from marine sediment, and emendation of <i>Phaeobacter daeponensis</i> . <i>Standards in Genomic Sciences</i> , <b>2013</b> , 9, 142-59                                                                                       | 10    |
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| 103 | Complete genome sequence of <i>Sanguibacter keddieii</i> type strain (ST-74). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 110-8                                                                                                                                                                                                              | 10    |
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| 97  | 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 Rhamnales. <i>Genome Announcements</i> , <b>2016</b> , 4,                                                                                                        | 10    |
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| 83 | Genome sequence of the <i>Roseovarius mucosus</i> type strain (DSM 17069(T)), a bacteriochlorophyll <i>a</i> -containing representative of the marine <i>Roseobacter</i> group isolated from the dinoflagellate <i>Alexandrium ostenfeldii</i> . <i>Standards in Genomic Sciences</i> , <b>2015</b> , 10, 17 |     | 8 |
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| 25 | The Families <i>Erysipelotrichaceae</i> emend., <i>Coprobaclaceae</i> fam. nov., and <i>Turicibacteraceae</i> fam. nov. <b>2014</b> , 79-105                                                                                                                                      |      | 3 |
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