# Markus Gker

## List of Publications by Year in Descending Order

**Source:** https://exaly.com/author-pdf/4858659/markus-goker-publications-by-year.pdf
**Version:** 2024-04-27

| | | | |
|---|---|---|---|
| 325<br>papers | 16,479<br>citations | 52<br>h-index | 119<br>g-index |
| 338<br>ext. papers | 27,306<br>ext. citations | 5.3<br>avg, IF | 6.97<br>L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 325 | The Evolution of Ecological Diversity in .. *Frontiers in Microbiology*, **2022**, 13, 715637 | 5.7 | 4 |
| 324 | ICSP response to ‘Science depends on nomenclature, but nomenclature is not science’. *Nature Reviews Microbiology*, **2022**, 20, 249-250 | 22.2 | 3 |
| 323 | TYGS and LPSN: a database tandem for fast and reliable genome-based classification and nomenclature of prokaryotes. *Nucleic Acids Research*, **2021**, | 20.1 | 108 |
| 322 | Analysis of 1,000+ Type-Strain Genomes Substantially Improves Taxonomic Classification of. *Frontiers in Microbiology*, **2020**, 11, 468 | 5.7 | 101 |
| 321 | Draft Genome Sequences of Six Type Strains of the Genus. *Microbiology Resource Announcements*, **2020**, 9, | 1.3 | 2 |
| 320 | List of Prokaryotic names with Standing in Nomenclature (LPSN) moves to the DSMZ. *International Journal of Systematic and Evolutionary Microbiology*, **2020**, 70, 5607-5612 | 2.2 | 291 |
| 319 | A publicly accessible database for genome sequences supports tracing of transmission chains and epidemics. *Microbial Genomics*, **2020**, 6, | 4.4 | 11 |
| 318 | 100-year-old enigma solved: identification, genomic characterization and biogeography of the yet uncultured Planctomyces bekefii. *Environmental Microbiology*, **2020**, 22, 198-211 | 5.2 | 16 |
| 317 | Genome-guided analysis allows the identification of novel physiological traits in Trichococcus species. *BMC Genomics*, **2020**, 21, 24 | 4.5 | 6 |
| 316 | 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 | 3 | 3 |
| 315 | 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 | 11.5 | 7 |
| 314 | TYGS is an automated high-throughput platform for state-of-the-art genome-based taxonomy. *Nature Communications*, **2019**, 10, 2182 | 17.4 | 590 |
| 313 | Haloplasma **2019**, 1-8 | | |
| 312 | Cobaviruses – a new globally distributed phage group infecting Rhodobacteraceae in marine ecosystems. *ISME Journal*, **2019**, 13, 1404-1421 | 11.9 | 16 |
| 311 | Analysis of 1,000 Type-Strain Genomes Improves Taxonomic Classification of. *Frontiers in Microbiology*, **2019**, 10, 2083 | 5.7 | 66 |
| 310 | High-quality draft genome sequences of DSM 14164, DSM 17497, DSM 15088, DSM 21245 and DSM 16006: taxonomic considerations. *Access Microbiology*, **2019**, 1, e000067 | 1 | 2 |
| 309 | Shotgun metagenome data of a defined mock community using Oxford Nanopore, PacBio and Illumina technologies. *Scientific Data*, **2019**, 6, 285 | 8.2 | 36 |

| | | | |
|---|---|---|---|
| 308 | Genome-based classification of micromonosporae with a focus on their biotechnological and ecological potential. *Scientific Reports*, **2018**, 8, 525 | 4.9 | 63 |
| 307 | Genome-Based Taxonomic Classification of the Phylum. *Frontiers in Microbiology*, **2018**, 9, 2007 | 5.7 | 297 |
| 306 | Horizontal operon transfer, plasmids, and the evolution of photosynthesis in Rhodobacteraceae. *ISME Journal*, **2018**, 12, 1994-2010 | 11.9 | 33 |
| 305 | Phylogenomics of Rhodobacteraceae reveals evolutionary adaptation to marine and non-marine habitats. *ISME Journal*, **2017**, 11, 1483-1499 | 11.9 | 167 |
| 304 | Complete genome sequence of strain YIM 002 (DSM 44835), the type species of the genus and source of new antibiotic compounds. *Standards in Genomic Sciences*, **2017**, 12, 21 | | 5 |
| 303 | High quality draft genome of type strain a rock actinobacterium, and emended description of. *Standards in Genomic Sciences*, **2017**, 12, 4 | | 6 |
| 302 | High quality permanent draft genome sequence of DSM 19482, isolated from raw cow milk. *Standards in Genomic Sciences*, **2017**, 12, 31 | | 2 |
| 301 | 1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. *Nature Biotechnology*, **2017**, 35, 676-683 | 44.5 | 161 |
| 300 | VICTOR: genome-based phylogeny and classification of prokaryotic viruses. *Bioinformatics*, **2017**, 33, 3396-3404 | 7.2 | 191 |
| 299 | Critical Assessment of Metagenome Interpretation-a benchmark of metagenomics software. *Nature Methods*, **2017**, 14, 1063-1071 | 21.6 | 412 |
| 298 | Draft genome sequence of CL-YJ9 (DSM 18822), isolated from the rhizosphere of the coastal tidal-flat plant. *Standards in Genomic Sciences*, **2017**, 12, 65 | | 1 |
| 297 | 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 | 4.9 | 35 |
| 296 | Toward a Novel Multilocus Phylogenetic Taxonomy for the Dermatophytes. *Mycopathologia*, **2017**, 182, 5-31 | 2.9 | 287 |
| 295 | Genomic Analysis of , the Thermophilic Anaerobic Bacterium of the Novel Bacterial Phylum. *Frontiers in Microbiology*, **2017**, 8, 195 | 5.7 | 30 |
| 294 | The Composite 259-kb Plasmid of DSM 17316-A Natural Replicon with Functional RepABC Modules from and. *Frontiers in Microbiology*, **2017**, 8, 1787 | 5.7 | 7 |
| 293 | Genome-Scale Data Call for a Taxonomic Rearrangement of. *Frontiers in Microbiology*, **2017**, 8, 2501 | 5.7 | 33 |
| 292 | Comparative genomics of biotechnologically important yeasts. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 9882-7 | 11.5 | 212 |
| 291 | Choosing one name for pleomorphic fungi: The example of Aspergillus versus Eurotium, Neosartorya and Emericella. *Taxon*, **2016**, 65, 593-601 | 0.8 | 12 |

| | | | |
|---|---|---|---|
| 290 | Biofilm plasmids with a rhamnose operon are widely distributed determinants of the Ɽswim-or-stickP lifestyle in roseobacters. *ISME Journal*, **2016**, 10, 2498-513 | 11.9 | 37 |
| 289 | Metabolic traits of an uncultured archaeal lineage--MSBL1--from brine pools of the Red Sea. *Scientific Reports*, **2016**, 6, 19181 | 4.9 | 51 |
| 288 | High quality draft genome sequences of Pseudomonas fulva DSM 17717(T), Pseudomonas parafulva DSM 17004(T) and Pseudomonas cremoricolorata DSM 17059(T) type strains. *Standards in Genomic Sciences*, **2016**, 11, 55 | | 9 |
| 287 | High-quality draft genome sequence of strain AK4OH1, a gammaproteobacterium isolated from estuarine sediment. *Standards in Genomic Sciences*, **2016**, 11, 66 | | 4 |
| 286 | Complete genome sequence of the haloalkaliphilic, obligately chemolithoautotrophic thiosulfate and sulfide-oxidizing □proteobacterium Thioalkalimicrobium cyclicum type strain ALM 1 (DSM 14477(T)). *Standards in Genomic Sciences*, **2016**, 11, 38 | | 5 |
| 285 | Comparing polysaccharide decomposition between the type strains Gramella echinicola KMM 6050(T) (DSM 19838(T)) and Gramella portivictoriae UST040801-001(T) (DSM 23547(T)), 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 | | 14 |
| 284 | High-quality draft genome sequence of Flavobacterium suncheonense GH29-5(T) (DSM 17707(T)) isolated from greenhouse soil in South Korea, and emended description of Flavobacterium suncheonense GH29-5(T). *Standards in Genomic Sciences*, **2016**, 11, 42 | | 1 |
| 283 | Genome sequence of Shimia str. SK013, a representative of the Roseobacter group isolated from marine sediment. *Standards in Genomic Sciences*, **2016**, 11, 25 | | 4 |
| 282 | High quality permanent draft genome sequence of Phaseolibacter flectens ATCC 12775(T), a plant pathogen of French bean pods. *Standards in Genomic Sciences*, **2016**, 11, 4 | | 1 |
| 281 | Improving Phylogeny Reconstruction at the Strain Level Using Peptidome Datasets. *PLoS Computational Biology*, **2016**, 12, e1005271 | 5 | 3 |
| 280 | Genomic and Genetic Diversity within the Pseudomonas fluorescens Complex. *PLoS ONE*, **2016**, 11, e0150183 | 9.7 | 109 |
| 279 | 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 | 2.2 | 18 |
| 278 | 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 | 2.2 | 42 |
| 277 | Genome-Based Taxonomic Classification of. *Frontiers in Microbiology*, **2016**, 7, 2003 | 5.7 | 114 |
| 276 | Draft Genome Sequence of Frankia Strain G2, a Nitrogen-Fixing Actinobacterium Isolated from Casuarina equisetifolia and Able To Nodulate Actinorhizal Plants of the Order Rhamnales. *Genome Announcements*, **2016**, 4, | | 10 |
| 275 | Nocardiopsis mwathae sp. nov., isolated from the haloalkaline Lake Elmenteita in the African Rift Valley. *Antonie Van Leeuwenhoek*, **2016**, 109, 421-30 | 2.1 | 4 |
| 274 | Streptomyces alkaliphilus sp. nov., isolated from sediments of Lake Elmenteita in the Kenyan Rift Valley. *Antonie Van Leeuwenhoek*, **2015**, 107, 1249-59 | 2.1 | 10 |
| 273 | Controlling false discoveries in high-dimensional situations: boosting with stability selection. *BMC Bioinformatics*, **2015**, 16, 144 | 3.6 | 53 |

| | | | |
|---|---|---|---|
| 272 | 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 | 3 | 18 |
| 271 | Towards an integrated phylogenetic classification of the Tremellomycetes. *Studies in Mycology*, **2015**, 81, 85-147 | 22.2 | 280 |
| 270 | Genomic insights into the taxonomic status of the Bacillus cereus group. *Scientific Reports*, **2015**, 5, 14082 | 4.9 | 152 |
| 269 | High-quality draft genome sequence of Gracilimonas tropica CL-CB462(T) (DSM 19535(T)), isolated from a Synechococcus culture. *Standards in Genomic Sciences*, **2015**, 10, 98 | | 1 |
| 268 | Phylogenetic classification of yeasts and related taxa within Pucciniomycotina. *Studies in Mycology*, **2015**, 81, 149-89 | 22.2 | 158 |
| 267 | Genome sequence of the Roseovarius mucosus type strain (DSM 17069(T)), a bacteriochlorophyll a-containing representative of the marine Roseobacter group isolated from the dinoflagellate Alexandrium ostenfeldii. *Standards in Genomic Sciences*, **2015**, 10, 17 | | 8 |
| 266 | High quality draft genome sequence and analysis of Pontibacter roseus type strain SRC-1(T) (DSM 17521(T)) isolated from muddy waters of a drainage system in Chandigarh, India. *Standards in Genomic Sciences*, **2015**, 10, 8 | | 4 |
| 265 | Genome sequence of the pink-pigmented marine bacterium Loktanella hongkongensis type strain (UST950701-009P(T)), a representative of the Roseobacter group. *Standards in Genomic Sciences*, **2015**, 10, 51 | | 1 |
| 264 | Ocean Twelve: flagellar and biofilm chromids in the multipartite genome of Marinovum algicola DG898 exemplify functional compartmentalization. *Environmental Microbiology*, **2015**, 17, 4019-34 | 5.2 | 19 |
| 263 | 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 | 5.7 | 88 |
| 262 | High quality draft genome sequence of Flavobacterium rivuli type strain WB 3.3-2(T) (DSM 21788(T)), a valuable source of polysaccharide decomposing enzymes. *Standards in Genomic Sciences*, **2015**, 10, 46 | | 11 |
| 261 | Belliella kenyensis sp. nov., isolated from an alkaline lake. *International Journal of Systematic and Evolutionary Microbiology*, **2015**, 65, 457-462 | 2.2 | 8 |
| 260 | 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 | 2.2 | 337 |
| 259 | Description of Geodermatophilus amargosae sp. nov., to accommodate the not validly named Geodermatophilus obscurus subsp. amargosae (Luedemann, 1968). *Current Microbiology*, **2014**, 68, 365-71 | 2.4 | 16 |
| 258 | Genomik: Grundlage zum Verständnis des Erfolgs von Roseobacter-Gruppe. *BioSpektrum*, **2014**, 20, 279-282 | 0.1 | |
| 257 | 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. ursilacticum and C. vrystaatense. *Systematic and Applied Microbiology*, **2014**, 37, 342-50 | 4.2 | 47 |
| 256 | Complete genome sequence of Planctomyces brasiliensis type strain (DSM 5305(T)), 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 | | 39 |
| 255 | 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. *Standards in Genomic Sciences*, **2014**, 9, 2 | | 267 |

| | | | |
|---|---|---|---|
| 254 | Genome sequence and emended description of Leisingera nanhaiensis strain DSM 24252(T) isolated from marine sediment. *Standards in Genomic Sciences*, **2014**, 9, 687-703 | | 5 |
| 253 | Complete genome sequence of the Phaeobacter gallaeciensis type strain CIP 105210(T) (= DSM 26640(T) = BS107(T)). *Standards in Genomic Sciences*, **2014**, 9, 914-32 | | 13 |
| 252 | Genome sequence of the Thermotoga thermarum type strain (LA3(T)) from an African solfataric spring. *Standards in Genomic Sciences*, **2014**, 9, 1105-17 | | 4 |
| 251 | Genome sequence of the exopolysaccharide-producing Salipiger mucosus type strain (DSM 16094(T)), a moderately halophilic member of the Roseobacter clade. *Standards in Genomic Sciences* , **2014**, 9, 1331-43 | | 10 |
| 250 | Genome sequence of the mud-dwelling archaeon Methanoplanus limicola type strain (DSM 2279(T)), reclassification of Methanoplanus petrolearius as Methanolacinia petrolearia and emended descriptions of the genera Methanoplanus and Methanolacinia. *Standards in Genomic Sciences*, **2014**, 9, 1076-88 | | 10 |
| 249 | Complete genome sequence of the bacteriochlorophyll a-containing Roseibacterium elongatum type strain (DSM 19469(T)), a representative of the Roseobacter group isolated from Australian coast sand. *Standards in Genomic Sciences*, **2014**, 9, 840-54 | | 3 |
| 248 | Genome sequence of the Wenxinia marina type strain (DSM 24838(T)), a representative of the Roseobacter group isolated from oilfield sediments. *Standards in Genomic Sciences*, **2014**, 9, 855-65 | | 2 |
| 247 | Genome sequence of the pink to light reddish-pigmented Rubellimicrobium mesophilum type strain (DSM 19309(T)), a representative of the Roseobacter group isolated from soil, and emended description of the species. *Standards in Genomic Sciences*, **2014**, 9, 902-13 | | 6 |
| 246 | 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 | 5.7 | 38 |
| 245 | Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. *PLoS Biology*, **2014**, 12, e1001920 | 9.7 | 146 |
| 244 | Geodermatophilus poikilotrophi sp. nov.: a multitolerant actinomycete isolated from dolomitic marble. *BioMed Research International*, **2014**, 2014, 914767 | 3 | 23 |
| 243 | Genome Sequence of Gammaproteobacterial Pseudohaliea rubra Type Strain DSM 19751, Isolated from Coastal Seawater of the Mediterranean Sea. *Genome Announcements*, **2014**, 2, | | 3 |
| 242 | Highly parallelized inference of large genome-based phylogenies. *Concurrency Computation Practice and Experience*, **2014**, 26, 1715-1729 | 1.4 | 39 |
| 241 | Pathways and substrate-specific regulation of amino acid degradation in Phaeobacter inhibens DSM 17395 (archetype of the marine Roseobacter clade). *Environmental Microbiology*, **2014**, 16, 218-38 | 5.2 | 24 |
| 240 | Novel genera and species of coniothyrium-like fungi in Montagnulaceae (Ascomycota). *Persoonia: Molecular Phylogeny and Evolution of Fungi*, **2014**, 32, 25-51 | 9 | 73 |
| 239 | The Families Erysipelotrichaceae emend., Coprobacillaceae fam. nov., and Turicibacteraceae fam. nov. **2014**, 79-105 | | 3 |
| 238 | The Family Intrasporangiaceae **2014**, 397-424 | | 0 |
| 237 | Geodermatophilus saharensis sp. nov., isolated from sand of the Saharan desert in Chad. *Archives of Microbiology*, **2013**, 195, 153-9 | 3 | 27 |

| | | | |
|---|---|---|---|
| 236 | When should a DDH experiment be mandatory in microbial taxonomy?. *Archives of Microbiology*, **2013**, 195, 413-8 | 3 | 377 |
| 235 | Genome sequence-based species delimitation with confidence intervals and improved distance functions. *BMC Bioinformatics*, **2013**, 14, 60 | 3.6 | 3251 |
| 234 | Hoffmannoscypha, a novel genus of brightly coloured, cupulate Pyronemataceae closely related to Tricharina and Geopora. *Mycological Progress*, **2013**, 12, 675-686 | 1.9 | 12 |
| 233 | Geodermatophilus africanus sp. nov., a halotolerant actinomycete isolated from Saharan desert sand. *Antonie Van Leeuwenhoek*, **2013**, 104, 207-16 | 2.1 | 36 |
| 232 | Kribbella shirazensis sp. nov., isolated from Iranian soil. *International Journal of Systematic and Evolutionary Microbiology*, **2013**, 63, 3369-3374 | 2.2 | 11 |
| 231 | 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 | 2.2 | 156 |
| 230 | Extrachromosomal, extraordinary and essential--the plasmids of the Roseobacter clade. *Applied Microbiology and Biotechnology*, **2013**, 97, 2805-15 | 5.7 | 69 |
| 229 | Geodermatophilus telluris sp. nov., an actinomycete isolated from Saharan desert sand. *International Journal of Systematic and Evolutionary Microbiology*, **2013**, 63, 2254-2259 | 2.2 | 26 |
| 228 | Geodermatophilus normandii sp. nov., isolated from Saharan desert sand. *International Journal of Systematic and Evolutionary Microbiology*, **2013**, 63, 3437-3443 | 2.2 | 21 |
| 227 | Geodermatophilus siccatus sp. nov., isolated from arid sand of the Saharan desert in Chad. *Antonie Van Leeuwenhoek*, **2013**, 103, 449-56 | 2.1 | 35 |
| 226 | Geodermatophilus tzadiensis sp. nov., a UV radiation-resistant bacterium isolated from sand of the Saharan desert. *Systematic and Applied Microbiology*, **2013**, 36, 177-82 | 4.2 | 29 |
| 225 | 16S-rRNA-based analysis of bacterial diversity in the gut of fungus-cultivating termites (Microtermes and Odontotermes species). *Antonie Van Leeuwenhoek*, **2013**, 104, 869-83 | 2.1 | 24 |
| 224 | opm: an R package for analysing OmniLog(R) phenotype microarray data. *Bioinformatics*, **2013**, 29, 1823-4 | 7.2 | 153 |
| 223 | Impacts of pr-10a overexpression at the molecular and the phenotypic level. *International Journal of Molecular Sciences*, **2013**, 14, 15141-66 | 6.3 | 7 |
| 222 | 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 | 2.2 | 48 |
| 221 | Phylogeny-driven target selection for large-scale genome-sequencing (and other) projects. *Standards in Genomic Sciences*, **2013**, 8, 360-74 | | 42 |
| 220 | Genome of the marine alphaproteobacterium Hoeflea phototrophica type strain (DFL-43(T)). *Standards in Genomic Sciences*, **2013**, 7, 440-8 | | 7 |
| 219 | Complete genome sequence of Coriobacterium glomerans type strain (PW2(T)) from the midgut of Pyrrhocoris apterus L. (red soldier bug). *Standards in Genomic Sciences*, **2013**, 8, 15-25 | | 5 |

| | | |
|---|---|---|
| 218 | Complete genome sequence of the bile-resistant pigment-producing anaerobe Alistipes finegoldii type strain (AHN2437(T)). *Standards in Genomic Sciences*, **2013**, 8, 26-36 | 6 |
| 217 | High-quality-draft genome sequence of the yellow-pigmented flavobacterium Joostella marina type strain (En5(T)). *Standards in Genomic Sciences*, **2013**, 8, 37-46 | 4 |
| 216 | Complete genome sequence of the moderate thermophile Anaerobaculum mobile type strain (NGA(T)). *Standards in Genomic Sciences*, **2013**, 8, 47-57 | 10 |
| 215 | Genome sequence of the free-living aerobic spirochete Turneriella parva type strain (H(T)), and emendation of the species Turneriella parva. *Standards in Genomic Sciences*, **2013**, 8, 228-38 | 8 |
| 214 | Genome sequence of the phage-gene rich marine Phaeobacter arcticus type strain DSM 23566(T.). *Standards in Genomic Sciences*, **2013**, 8, 450-64 | 9 |
| 213 | Genome sequence of the Leisingera aquimarina type strain (DSM 24565(T)), a member of the marine Roseobacter clade rich in extrachromosomal elements. *Standards in Genomic Sciences*, **2013**, 8, 389-402 | 16 |
| 212 | 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 | 12 |
| 211 | Genome sequence of the chemoheterotrophic soil bacterium Saccharomonospora cyanea type strain (NA-134(T)). *Standards in Genomic Sciences*, **2013**, 9, 28-41 | 1 |
| 210 | Genome sequence of the moderately thermophilic sulfur-reducing bacterium Thermanaerovibrio velox type strain (Z-9701(T)) and emended description of the genus Thermanaerovibrio. *Standards in Genomic Sciences*, **2013**, 9, 57-70 | 4 |
| 209 | Genome sequence of the Litoreibacter arenae type strain (DSM 19593(T)), a member of the Roseobacter clade isolated from sea sand. *Standards in Genomic Sciences*, **2013**, 9, 117-27 | 6 |
| 208 | Genome sequence of Frateuria aurantia type strain (Kond[illegible]67(T)), a xanthomonade isolated from Lilium auratium Lindl. *Standards in Genomic Sciences*, **2013**, 9, 83-92 | 1 |
| 207 | Genome of the R-body producing marine alphaproteobacterium Labrenzia alexandrii type strain (DFL-11(T)). *Standards in Genomic Sciences*, **2013**, 7, 413-26 | 8 |
| 206 | Genome sequence of the thermophilic fresh-water bacterium Spirochaeta caldaria type strain (H1(T)), 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 | 24 |
| 205 | Complete genome sequence of the halophilic bacterium Spirochaeta africana type strain (Z-7692(T)) from the alkaline Lake Magadi in the East African Rift. *Standards in Genomic Sciences*, **2013**, 8, 165-76 | 2 |
| 204 | Genome sequence of the phylogenetically isolated spirochete Leptonema illini type strain (3055(T)). *Standards in Genomic Sciences*, **2013**, 8, 177-87 | 4 |
| 203 | Genome sequence of the reddish-pigmented Rubellimicrobium thermophilum type strain (DSM 16684(T)), a member of the Roseobacter clade. *Standards in Genomic Sciences*, **2013**, 8, 480-90 | 3 |
| 202 | Genome sequence of Phaeobacter daeponensis type strain (DSM 23529(T)), a facultatively anaerobic bacterium isolated from marine sediment, and emendation of Phaeobacter daeponensis. *Standards in Genomic Sciences*, **2013**, 9, 142-59 | 10 |
| 201 | Complete genome sequence of the marine methyl-halide oxidizing Leisingera methylohalidivorans type strain (DSM 14336(T)), a representative of the Roseobacter clade. *Standards in Genomic Sciences*, **2013**, 9, 128-41 | 13 |

| | | | |
|---|---|---|---|
| 200 | Genome sequence of Phaeobacter inhibens type strain (T5(T)), 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, 334-50 | | 19 |
| 199 | Genomics and physiology of a marine flavobacterium encoding a proteorhodopsin and a xanthorhodopsin-like protein. *PLoS ONE*, **2013**, 8, e57487 | 3.7 | 38 |
| 198 | Diversity of Termitomyces associated with fungus-farming termites assessed by cultural and culture-independent methods. *PLoS ONE*, **2013**, 8, e56464 | 3.7 | 18 |
| 197 | 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 | | 12 |
| 196 | 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 | 3.4 | 19 |
| 195 | Charcoal filter paper improves the viability of cryopreserved filamentous ectomycorrhizal and saprotrophic Basidiomycota and Ascomycota. *Mycologia*, **2012**, 104, 324-30 | 2.4 | 12 |
| 194 | Geodermatophilus arenarius sp. nov., a xerophilic actinomycete isolated from Saharan desert sand in Chad. *Extremophiles*, **2012**, 16, 903-9 | 3 | 44 |
| 193 | Visualization and curve-parameter estimation strategies for efficient exploration of phenotype microarray kinetics. *PLoS ONE*, **2012**, 7, e34846 | 3.7 | 139 |
| 192 | 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 | 1.9 | 9 |
| 191 | Genome sequence of the moderately thermophilic, amino-acid-degrading and sulfur-reducing bacterium Thermovirga lienii type strain (Cas60314(T)). *Standards in Genomic Sciences*, **2012**, 6, 230-9 | | 21 |
| 190 | Genome sequence of the orange-pigmented seawater bacterium Owenweeksia hongkongensis type strain (UST20020801(T)). *Standards in Genomic Sciences*, **2012**, 7, 120-30 | | 11 |
| 189 | Complete genome sequence of the moderately thermophilic mineral-sulfide-oxidizing firmicute Sulfobacillus acidophilus type strain (NAL(T)). *Standards in Genomic Sciences*, **2012**, 6, 1-13 | | 20 |
| 188 | Complete genome sequence of the termite hindgut bacterium Spirochaeta coccoides type strain (SPN1(T)), 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 | | 46 |
| 187 | Permanent draft genome sequence of the gliding predator Saprospira grandis strain Sa g1 (= HR1). *Standards in Genomic Sciences*, **2012**, 6, 210-9 | | 1 |
| 186 | Genome sequence of the soil bacterium Saccharomonospora azurea type strain (NA-128(T)). *Standards in Genomic Sciences*, **2012**, 6, 220-9 | | 10 |
| 185 | Complete genome sequence of the facultatively anaerobic, appendaged bacterium Muricauda ruestringensis type strain (B1(T)). *Standards in Genomic Sciences*, **2012**, 6, 185-93 | | 8 |
| 184 | Complete genome sequence of Polynucleobacter necessarius subsp. asymbioticus type strain (QLW-P1DMWA-1(T)). *Standards in Genomic Sciences*, **2012**, 6, 74-83 | | 27 |
| 183 | Complete genome sequence of the aerobic, heterotroph Marinithermus hydrothermalis type strain (T1(T)) from a deep-sea hydrothermal vent chimney. *Standards in Genomic Sciences*, **2012**, 6, 21-30 | | 6 |

| | | | |
|---|---|---|---|
| 182 | Complete genome sequence of the aquatic bacterium Runella slithyformis type strain (LSU 4(T)). *Standards in Genomic Sciences*, **2012**, 6, 145-54 | | 16 |
| 181 | Genome sequence of the ocean sediment bacterium Saccharomonospora marina type strain (XMU15(T)). *Standards in Genomic Sciences*, **2012**, 6, 265-75 | | 3 |
| 180 | Complete genome sequence of the thermophilic sulfate-reducing ocean bacterium Thermodesulfatator indicus type strain (CIR29812(T)). *Standards in Genomic Sciences*, **2012**, 6, 155-64 | | 9 |
| 179 | Genome sequence of the homoacetogenic bacterium Holophaga foetida type strain (TMBS4(T)). *Standards in Genomic Sciences*, **2012**, 6, 174-84 | | 23 |
| 178 | Complete genome sequence of the orange-red pigmented, radioresistant Deinococcus proteolyticus type strain (MRP(T)). *Standards in Genomic Sciences*, **2012**, 6, 240-50 | | 7 |
| 177 | Genome sequence of the flexirubin-pigmented soil bacterium Niabella soli type strain (JS13-8(T)). *Standards in Genomic Sciences*, **2012**, 7, 210-20 | | 0 |
| 176 | Genome sequence of the Antarctic rhodopsins-containing flavobacterium Gillisia limnaea type strain (R-8282(T)). *Standards in Genomic Sciences*, **2012**, 7, 107-19 | | 9 |
| 175 | Complete genome sequence of the sulfate-reducing firmicute Desulfotomaculum ruminis type strain (DL(T)). *Standards in Genomic Sciences*, **2012**, 7, 304-19 | | 18 |
| 174 | Complete genome sequencing and analysis of Saprospira grandis str. Lewin, a predatory marine bacterium. *Standards in Genomic Sciences*, **2012**, 6, 84-93 | | 19 |
| 173 | Complete genome sequence of the facultatively chemolithoautotrophic and methylotrophic alpha Proteobacterium Starkeya novella type strain (ATCC 8093(T)). *Standards in Genomic Sciences*, **2012**, 7, 44-58 | | 12 |
| 172 | Complete genome sequence of the sulfur compounds oxidizing chemolithoautotroph Sulfuricurvum kujiense type strain (YK-1(T)). *Standards in Genomic Sciences*, **2012**, 6, 94-103 | | 31 |
| 171 | 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 | | 15 |
| 170 | Molecular Phylogenetic Reconstruction **2011**, 159-174 | | 5 |
| 169 | Complete genome sequence of the filamentous gliding predatory bacterium Herpetosiphon aurantiacus type strain (114-95(T)). *Standards in Genomic Sciences*, **2011**, 5, 356-70 | | 35 |
| 168 | Novel insights into the diversity of catabolic metabolism from ten haloarchaeal genomes. *PLoS ONE* , **2011**, 6, e20237 | 3.7 | 60 |
| 167 | Codivergence of mycoviruses with their hosts. *PLoS ONE*, **2011**, 6, e22252 | 3.7 | 37 |
| 166 | Complete genome sequence of Leadbetterella byssophila type strain (4M15). *Standards in Genomic Sciences*, **2011**, 4, 2-12 | | 15 |
| 165 | Complete genome sequence of Hydrogenobacter thermophilus type strain (TK-6). *Standards in Genomic Sciences*, **2011**, 4, 131-43 | | 8 |

| | | |
|---|---|---|
| 164 | Complete genome sequence of Paludibacter propionicigenes type strain (WB4). *Standards in Genomic Sciences*, **2011**, 4, 36-44 | 24 |
| 163 | Complete genome sequence of Bacteroides helcogenes type strain (P 36-108). *Standards in Genomic Sciences*, **2011**, 4, 45-53 | 7 |
| 162 | Complete genome sequence of Weeksella virosa type strain (9751). *Standards in Genomic Sciences*, **2011**, 4, 81-90 | 8 |
| 161 | Complete genome sequence of Desulfobulbus propionicus type strain (1pr3). *Standards in Genomic Sciences*, **2011**, 4, 100-10 | 39 |
| 160 | Complete genome sequence of Marivirga tractuosa type strain (H-43). *Standards in Genomic Sciences*, **2011**, 4, 154-62 | 15 |
| 159 | Complete genome sequence of Desulfurococcus mucosus type strain (O7/1). *Standards in Genomic Sciences*, **2011**, 4, 173-82 | 9 |
| 158 | Complete genome sequence of Cellulophaga lytica type strain (LIM-21). *Standards in Genomic Sciences*, **2011**, 4, 221-32 | 23 |
| 157 | Non-contiguous finished genome sequence of Bacteroides coprosuis type strain (PC139). *Standards in Genomic Sciences*, **2011**, 4, 233-43 | 4 |
| 156 | Complete genome sequence of Rhodospirillum rubrum type strain (S1). *Standards in Genomic Sciences*, **2011**, 4, 293-302 | 31 |
| 155 | Complete genome sequence of the extremely halophilic Halanaerobium praevalens type strain (GSL). *Standards in Genomic Sciences*, **2011**, 4, 312-21 | 24 |
| 154 | Complete genome sequence of Nitratifractor salsuginis type strain (E9I37-1). *Standards in Genomic Sciences*, **2011**, 4, 322-30 | 10 |
| 153 | Complete genome sequence of Mahella australiensis type strain (50-1 BON). *Standards in Genomic Sciences*, **2011**, 4, 331-41 | 6 |
| 152 | Complete genome sequence of Treponema succinifaciens type strain (6091). *Standards in Genomic Sciences*, **2011**, 4, 361-70 | 20 |
| 151 | Complete genome sequence of Syntrophobotulus glycolicus type strain (FlGlyRT). *Standards in Genomic Sciences*, **2011**, 4, 371-380 | 9 |
| 150 | Complete genome sequence of the hyperthermophilic chemolithoautotroph Pyrolobus fumarii type strain (1A). *Standards in Genomic Sciences*, **2011**, 4, 381-92 | 10 |
| 149 | Complete genome sequence of the acetate-degrading sulfate reducer Desulfobacca acetoxidans type strain (ASRB2). *Standards in Genomic Sciences*, **2011**, 4, 393-401 | 19 |
| 148 | Complete genome sequence of the thermophilic, hydrogen-oxidizing Bacillus tusciae type strain (T2) 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, 121-34 | 35 |
| 147 | Complete genome sequence of the gliding, heparinolytic Pedobacter saltans type strain (113). *Standards in Genomic Sciences*, **2011**, 5, 30-40 | 11 |

| | | |
|---|---|---|
| 146 | Non-contiguous finished genome sequence of the opportunistic oral pathogen Prevotella multisaccharivorax type strain (PPPA20). *Standards in Genomic Sciences*, **2011**, 5, 41-9 | 2 |
| 145 | Complete genome sequence of Tolumonas auensis type strain (TA 4). *Standards in Genomic Sciences* , **2011**, 5, 112-20 | 4 |
| 144 | Complete genome sequence of Hirschia baltica type strain (IFAM 1418(T)). *Standards in Genomic Sciences*, **2011**, 5, 287-97 | 8 |
| 143 | Complete genome sequence of the halophilic and highly halotolerant Chromohalobacter salexigens type strain (1H11(T)). *Standards in Genomic Sciences*, **2011**, 5, 379-88 | 28 |
| 142 | Genome sequence of the filamentous, gliding Thiothrix nivea neotype strain (JP2(T)). *Standards in Genomic Sciences*, **2011**, 5, 398-406 | 9 |
| 141 | Complete genome sequence of the thermophilic sulfur-reducer Desulfurobacterium thermolithotrophum type strain (BSA(T)) from a deep-sea hydrothermal vent. *Standards in Genomic Sciences*, **2011**, 5, 407-15 | 10 |
| 140 | Complete genome sequence of Calditerrivibrio nitroreducens type strain (Yu37-1). *Standards in Genomic Sciences*, **2011**, 4, 54-62 | 9 |
| 139 | Complete genome sequence of Truepera radiovictrix type strain (RQ-24). *Standards in Genomic Sciences*, **2011**, 4, 91-9 | 37 |
| 138 | Complete genome sequence of Bacteroides salanitronis type strain (BL78). *Standards in Genomic Sciences*, **2011**, 4, 191-9 | 8 |
| 137 | Complete genome sequence of Odoribacter splanchnicus type strain (1651/6). *Standards in Genomic Sciences*, **2011**, 4, 200-9 | 62 |
| 136 | Complete genome sequence of Oceanithermus profundus type strain (506). *Standards in Genomic Sciences*, **2011**, 4, 210-20 | 3 |
| 135 | Complete genome sequence of Tsukamurella paurometabola type strain (no. 33). *Standards in Genomic Sciences*, **2011**, 4, 342-51 | 8 |
| 134 | Non-contiguous finished genome sequence and contextual data of the filamentous soil bacterium Ktedonobacter racemifer type strain (SOSP1-21). *Standards in Genomic Sciences*, **2011**, 5, 97-111 | 72 |
| 133 | Complete genome sequence of Isosphaera pallida type strain (IS1B). *Standards in Genomic Sciences*, **2011**, 4, 63-71 | 40 |
| 132 | Complete genome sequence of Cellulophaga algicola type strain (IC166). *Standards in Genomic Sciences*, **2011**, 4, 72-80 | 22 |
| 131 | Complete genome sequence of Riemerella anatipestifer type strain (ATCC 11845T). *Standards in Genomic Sciences*, **2011**, 4, 144-153 | 26 |
| 130 | Complete genome sequence of the thermophilic sulfur-reducer Hippea maritima type strain (MH(2)). *Standards in Genomic Sciences*, **2011**, 4, 303-11 | 6 |
| 129 | Complete genome sequence of Haliscomenobacter hydrossis type strain (O). *Standards in Genomic Sciences*, **2011**, 4, 352-60 | 17 |

| | | | |
|---|---|---|---|
| 128 | Complete genome sequence of the gliding freshwater bacterium Fluviicola taffensis type strain (RW262). *Standards in Genomic Sciences*, **2011**, 5, 21-9 | | 19 |
| 127 | Genome sequence of the moderately thermophilic halophile Flexistipes sinusarabici strain (MAS10). *Standards in Genomic Sciences*, **2011**, 5, 86-96 | | 8 |
| 126 | Complete genome sequence of Deinococcus maricopensis type strain (LB-34). *Standards in Genomic Sciences*, **2011**, 4, 163-72 | | 11 |
| 125 | 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 | 2.2 | 9 |
| 124 | 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 | 1.9 | 14 |
| 123 | Nocardiopsis arvandica sp. nov., isolated from sandy soil. *International Journal of Systematic and Evolutionary Microbiology*, **2011**, 61, 1189-1194 | 2.2 | 24 |
| 122 | Quantifying the phylodynamic forces driving papillomavirus evolution. *Molecular Biology and Evolution*, **2011**, 28, 2101-13 | 8.3 | 99 |
| 121 | Complete genome sequence of Thermomonospora curvata type strain (B9). *Standards in Genomic Sciences*, **2011**, 4, 13-22 | | 24 |
| 120 | Species delimitation in taxonomically difficult fungi: the case of Hymenogaster. *PLoS ONE*, **2011**, 6, e15614 | 3.7 | 25 |
| 119 | Complete genome sequence of Syntrophobotulus glycolicus type strain (FlGlyR). *Standards in Genomic Sciences*, **2011**, 4, 371-80 | | 3 |
| 118 | Complete genome sequence of Riemerella anatipestifer type strain (ATCC 11845). *Standards in Genomic Sciences*, **2011**, 4, 144-53 | | 16 |
| 117 | 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, 690737 | 2 | 31 |
| 116 | A Clustering Optimization Strategy for Molecular Taxonomy Applied to Planktonic Foraminifera SSU rDNA. *Evolutionary Bioinformatics*, **2010**, 6, 97-112 | 1.9 | 27 |
| 115 | Maximum Likelihood Analyses of 3,490 rbcL Sequences: Scalability of Comprehensive Inference versus Group-Specific Taxon Sampling. *Evolutionary Bioinformatics*, **2010**, 6, 73-90 | 1.9 | 5 |
| 114 | Complete genome sequence of Cellulomonas flavigena type strain (134). *Standards in Genomic Sciences*, **2010**, 3, 15-25 | | 31 |
| 113 | Digital DNA-DNA hybridization for microbial species delineation by means of genome-to-genome sequence comparison. *Standards in Genomic Sciences*, **2010**, 2, 117-34 | | 972 |
| 112 | Complete genome sequence of Planctomyces limnophilus type strain (M□290). *Standards in Genomic Sciences*, **2010**, 3, 47-56 | | 28 |
| 111 | Permanent draft genome sequence of Dethiosulfovibrio peptidovorans type strain (SEBR 4207). *Standards in Genomic Sciences*, **2010**, 3, 85-92 | | 8 |

| | | |
|---|---|---|
| 110 | Complete genome sequence of Ferrimonas balearica type strain (PAT). *Standards in Genomic Sciences*, **2010**, 3, 174-82 | 9 |
| 109 | Non-contiguous finished genome sequence of Aminomonas paucivorans type strain (GLU-3). *Standards in Genomic Sciences*, **2010**, 3, 285-93 | 8 |
| 108 | Complete genome sequence of Ilyobacter polytropus type strain (CuHbu1). *Standards in Genomic Sciences*, **2010**, 3, 304-14 | 7 |
| 107 | Complete genome sequence of Nocardiopsis dassonvillei type strain (IMRU 509). *Standards in Genomic Sciences*, **2010**, 3, 325-36 | 27 |
| 106 | Complete genome sequence of Veillonella parvula type strain (Te3). *Standards in Genomic Sciences*, **2010**, 2, 57-65 | 29 |
| 105 | Complete genome sequence of Kribbella flavida type strain (IFO 14399). *Standards in Genomic Sciences*, **2010**, 2, 186-93 | 10 |
| 104 | Complete genome sequence of Conexibacter woesei type strain (ID131577). *Standards in Genomic Sciences*, **2010**, 2, 212-9 | 15 |
| 103 | Complete genome sequence of Thermocrinis albus type strain (HI 11/12). *Standards in Genomic Sciences*, **2010**, 2, 194-202 | 14 |
| 102 | Complete genome sequence of Meiothermus silvanus type strain (VI-R2). *Standards in Genomic Sciences*, **2010**, 3, 37-46 | 16 |
| 101 | Complete genome sequence of Olsenella uli type strain (VPI D76D-27C). *Standards in Genomic Sciences*, **2010**, 3, 76-84 | 27 |
| 100 | Complete genome sequence of Acidaminococcus fermentans type strain (VR4). *Standards in Genomic Sciences*, **2010**, 3, 1-14 | 19 |
| 99 | Complete genome sequence of Meiothermus ruber type strain (21). *Standards in Genomic Sciences*, **2010**, 3, 26-36 | 28 |
| 98 | Complete genome sequence of Acetohalobium arabaticum type strain (Z-7288). *Standards in Genomic Sciences*, **2010**, 3, 57-65 | 16 |
| 97 | Complete genome sequence of Ignisphaera aggregans type strain (AQ1.S1). *Standards in Genomic Sciences*, **2010**, 3, 66-75 | 13 |
| 96 | Complete genome sequence of Vulcanisaeta distributa type strain (IC-017). *Standards in Genomic Sciences*, **2010**, 3, 117-25 | 8 |
| 95 | Complete genome sequence of Arcanobacterium haemolyticum type strain (11018). *Standards in Genomic Sciences*, **2010**, 3, 126-35 | 7 |
| 94 | Complete genome sequence of Thermosediminibacter oceani type strain (JW/IW-1228P). *Standards in Genomic Sciences*, **2010**, 3, 108-16 | 10 |
| 93 | Complete genome sequence of Spirochaeta smaragdinae type strain (SEBR 4228). *Standards in Genomic Sciences*, **2010**, 3, 136-44 | 15 |

| | | |
|---|---|---|
| 92 | Complete genome sequence of PThermobaculum terrenumPtype strain (YNP1). *Standards in Genomic Sciences*, **2010**, 3, 153-62 | 9 |
| 91 | Complete genome sequence of Syntrophothermus lipocalidus type strain (TGB-C1). *Standards in Genomic Sciences*, **2010**, 3, 268-75 | 10 |
| 90 | Complete genome sequence of Desulfarculus baarsii type strain (2st14). *Standards in Genomic Sciences*, **2010**, 3, 276-84 | 27 |
| 89 | Complete genome sequence of Intrasporangium calvum type strain (7 KIP). *Standards in Genomic Sciences*, **2010**, 3, 294-303 | 4 |
| 88 | Complete genome sequence of Methanothermus fervidus type strain (V24S). *Standards in Genomic Sciences*, **2010**, 3, 315-24 | 14 |
| 87 | Complete genome sequence of Thermaerobacter marianensis type strain (7p75a). *Standards in Genomic Sciences*, **2010**, 3, 337-45 | 7 |
| 86 | Standard operating procedure for calculating genome-to-genome distances based on high-scoring segment pairs. *Standards in Genomic Sciences*, **2010**, 2, 142-8 | 384 |
| 85 | Complete genome sequence of Xylanimonas cellulosilytica type strain (XIL07). *Standards in Genomic Sciences*, **2010**, 2, 1-8 | 8 |
| 84 | Complete genome sequence of Alicyclobacillus acidocaldarius type strain (104-IA). *Standards in Genomic Sciences*, **2010**, 2, 9-18 | 20 |
| 83 | Complete genome sequence of Sphaerobacter thermophilus type strain (S 6022). *Standards in Genomic Sciences*, **2010**, 2, 49-56 | 20 |
| 82 | Complete genome sequence of Streptosporangium roseum type strain (NI 9100). *Standards in Genomic Sciences*, **2010**, 2, 29-37 | 25 |
| 81 | Complete genome sequence of Chitinophaga pinensis type strain (UQM 2034). *Standards in Genomic Sciences*, **2010**, 2, 87-95 | 57 |
| 80 | Complete genome sequence of Sulfurospirillum deleyianum type strain (5175). *Standards in Genomic Sciences*, **2010**, 2, 149-57 | 24 |
| 79 | Complete genome sequence of Haloterrigena turkmenica type strain (4k). *Standards in Genomic Sciences*, **2010**, 2, 107-16 | 28 |
| 78 | Complete genome sequence of Haliangium ochraceum type strain (SMP-2). *Standards in Genomic Sciences*, **2010**, 2, 96-106 | 53 |
| 77 | Complete genome sequence of Geodermatophilus obscurus type strain (G-20). *Standards in Genomic Sciences*, **2010**, 2, 158-67 | 49 |
| 76 | Complete genome sequence of Nakamurella multipartita type strain (Y-104). *Standards in Genomic Sciences*, **2010**, 2, 168-75 | 28 |
| 75 | Complete genome sequence of Spirosoma linguale type strain (1). *Standards in Genomic Sciences,* **2010**, 2, 176-85 | 35 |

| | | | |
|---|---|---|---|
| 74 | Complete genome sequence of Segniliparus rotundus type strain (CDC 1076). *Standards in Genomic Sciences*, **2010**, 2, 203-11 | | 9 |
| 73 | Complete genome sequence of Sebaldella termitidis type strain (NCTC 11300). *Standards in Genomic Sciences*, **2010**, 2, 220-7 | | 16 |
| 72 | Complete genome sequence of Thermosphaera aggregans type strain (M11TL). *Standards in Genomic Sciences*, **2010**, 2, 245-59 | | 12 |
| 71 | Complete genome sequence of Brachyspira murdochii type strain (56-150). *Standards in Genomic Sciences*, **2010**, 2, 260-9 | | 18 |
| 70 | Complete genome sequence of Aminobacterium colombiense type strain (ALA-1). *Standards in Genomic Sciences*, **2010**, 2, 280-9 | | 27 |
| 69 | Complete genome sequence of Arcobacter nitrofigilis type strain (CI). *Standards in Genomic Sciences*, **2010**, 2, 300-8 | | 32 |
| 68 | Complete genome sequence of Coraliomargarita akajimensis type strain (04OKA010-24). *Standards in Genomic Sciences*, **2010**, 2, 290-9 | | 18 |
| 67 | Complete genome sequence of Thermobispora bispora type strain (R51). *Standards in Genomic Sciences*, **2010**, 2, 318-26 | | 18 |
| 66 | Complete genome sequence of Desulfohalobium retbaense type strain (HR(100)). *Standards in Genomic Sciences*, **2010**, 2, 38-48 | | 17 |
| 65 | Complete genome sequence of Archaeoglobus profundus type strain (AV18). *Standards in Genomic Sciences*, **2010**, 2, 327-46 | | 20 |
| 64 | Complete genome sequence of Denitrovibrio acetiphilus type strain (N2460). *Standards in Genomic Sciences*, **2010**, 2, 270-9 | | 11 |
| 63 | Complete genome sequence of Gordonia bronchialis type strain (3410). *Standards in Genomic Sciences*, **2010**, 2, 19-28 | | 19 |
| 62 | 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 | 1.9 | 16 |
| 61 | En route to a genome-based classification of Archaea and Bacteria?. *Systematic and Applied Microbiology*, **2010**, 33, 175-82 | 4.2 | 251 |
| 60 | Complete genome sequence of Sulfurimonas autotrophica type strain (OK10). *Standards in Genomic Sciences*, **2010**, 3, 194-202 | | 32 |
| 59 | Complete genome sequence of Methanoplanus petrolearius type strain (SEBR 4847). *Standards in Genomic Sciences*, **2010**, 3, 203-11 | | 12 |
| 58 | Relicts Within the Genus Complex Astragalus/Oxytropis (Fabaceae), and the Comparison of Diversity by Objective Means **2010**, 105-117 | | 3 |
| 57 | Large-Scale Co-Phylogenetic Analysis on the Grid. *International Journal of Grid and High Performance Computing*, **2009**, 1, 39-54 | 0.7 | 2 |

| | | | |
|---|---|---|---|
| 56 | Complete genome sequence of Capnocytophaga ochracea type strain (VPI 2845). *Standards in Genomic Sciences*, **2009**, 1, 101-9 | | 12 |
| 55 | Species delimitation in downy mildews: the case of Hyaloperonospora in the light of nuclear ribosomal ITS and LSU sequences. *Mycological Research*, **2009**, 113, 308-25 | | 68 |
| 54 | Fine-structured multi-scaling long-range correlations in completely sequenced genomes--features, origin, and classification. *European Biophysics Journal*, **2009**, 38, 757-79 | 1.9 | 16 |
| 53 | Cutaneotropic human beta-/gamma-papillomaviruses are rarely shared between family members. *Journal of Investigative Dermatology*, **2009**, 129, 2427-34 | 4.3 | 17 |
| 52 | Hidden diversity in the non-caryophyllaceous plant-parasitic members of Microbotryum (Pucciniomycotina: Microbotryales). *Systematics and Biodiversity*, **2009**, 7, 297-306 | 1.7 | 31 |
| 51 | 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, 155-77 | 5.3 | 25 |
| 50 | Complete genome sequence of Halorhabdus utahensis type strain (AX-2). *Standards in Genomic Sciences*, **2009**, 1, 218-25 | | 21 |
| 49 | Complete genome sequence of Beutenbergia cavernae type strain (HKI 0122). *Standards in Genomic Sciences*, **2009**, 1, 21-8 | | 11 |
| 48 | Complete genome sequence of Cryptobacterium curtum type strain (12-3). *Standards in Genomic Sciences*, **2009**, 1, 93-100 | | 13 |
| 47 | Complete genome sequence of Desulfomicrobium baculatum type strain (X). *Standards in Genomic Sciences*, **2009**, 1, 29-37 | | 30 |
| 46 | Complete genome sequence of Acidimicrobium ferrooxidans type strain (ICP). *Standards in Genomic Sciences*, **2009**, 1, 38-45 | | 27 |
| 45 | Complete genome sequence of Sanguibacter keddieii type strain (ST-74). *Standards in Genomic Sciences*, **2009**, 1, 110-8 | | 10 |
| 44 | Complete genome sequence of Catenulispora acidiphila type strain (ID 139908). *Standards in Genomic Sciences*, **2009**, 1, 119-25 | | 19 |
| 43 | Complete genome sequence of Leptotrichia buccalis type strain (C-1013-b). *Standards in Genomic Sciences*, **2009**, 1, 126-32 | | 17 |
| 42 | Complete genome sequence of Saccharomonospora viridis type strain (P101). *Standards in Genomic Sciences*, **2009**, 1, 141-9 | | 21 |
| 41 | Complete genome sequence of Actinosynnema mirum type strain (101). *Standards in Genomic Sciences*, **2009**, 1, 46-53 | | 32 |
| 40 | Complete genome sequence of Pedobacter heparinus type strain (HIM 762-3). *Standards in Genomic Sciences*, **2009**, 1, 54-62 | | 19 |
| 39 | Complete genome sequence of Halogeometricum borinquense type strain (PR3). *Standards in Genomic Sciences*, **2009**, 1, 150-9 | | 22 |

| | | | |
|---|---|---|---|
| 38 | Complete genome sequence of Anaerococcus prevotii type strain (PC1). *Standards in Genomic Sciences*, **2009**, 1, 159-65 | | 18 |
| 37 | Complete genome sequence of Atopobium parvulum type strain (IPP 1246). *Standards in Genomic Sciences*, **2009**, 1, 166-73 | | 21 |
| 36 | Complete genome sequence of Eggerthella lenta type strain (IPP VPI 0255). *Standards in Genomic Sciences*, **2009**, 1, 174-82 | | 31 |
| 35 | Complete genome sequence of Kangiella koreensis type strain (SW-125). *Standards in Genomic Sciences*, **2009**, 1, 226-33 | | 10 |
| 34 | Complete genome sequence of Jonesia denitrificans type strain (Prevot 55134). *Standards in Genomic Sciences*, **2009**, 1, 262-9 | | 10 |
| 33 | Complete genome sequence of Halomicrobium mukohataei type strain (arg-2). *Standards in Genomic Sciences*, **2009**, 1, 270-7 | | 30 |
| 32 | Complete genome sequence of Rhodothermus marinus type strain (R-10). *Standards in Genomic Sciences*, **2009**, 1, 283-90 | | 20 |
| 31 | Complete genome sequence of Streptobacillus moniliformis type strain (9901). *Standards in Genomic Sciences*, **2009**, 1, 300-7 | | 16 |
| 30 | Complete genome sequence of Brachybacterium faecium type strain (Schefferle 6-10). *Standards in Genomic Sciences*, **2009**, 1, 3-11 | | 19 |
| 29 | Complete genome sequence of Pirellula staleyi type strain (ATCC 27377). *Standards in Genomic Sciences*, **2009**, 1, 308-16 | | 26 |
| 28 | Complete genome sequence of Kytococcus sedentarius type strain (541). *Standards in Genomic Sciences*, **2009**, 1, 12-20 | | 94 |
| 27 | Complete genome sequence of Dyadobacter fermentans type strain (NS114). *Standards in Genomic Sciences*, **2009**, 1, 133-40 | | 19 |
| 26 | Complete genome sequence of Thermanaerovibrio acidaminovorans type strain (Su883). *Standards in Genomic Sciences*, **2009**, 1, 254-61 | | 19 |
| 25 | Complete genome sequence of Slackia heliotrinireducens type strain (RHS 1). *Standards in Genomic Sciences*, **2009**, 1, 234-41 | | 16 |
| 24 | Complete genome sequence of Desulfotomaculum acetoxidans type strain (5575). *Standards in Genomic Sciences*, **2009**, 1, 242-53 | | 33 |
| 23 | Complete genome sequence of Stackebrandtia nassauensis type strain (LLR-40K-21). *Standards in Genomic Sciences*, **2009**, 1, 234-41 | | 16 |
| 22 | Molecular taxonomy of phytopathogenic fungi: a case study in Peronospora. *PLoS ONE*, **2009**, 4, e6319 | 3.7 | 127 |
| 21 | 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 | 39 |

# (-2008)

| | | | |
|---|---|---|---|
| 20 | Phylogeny of Peronospora, parasitic on Fabaceae, based on ITS sequences. *Mycological Research*, **2008**, 112, 502-12 | | 52 |
| 19 | Phylogenetic relationships of graminicolous downy mildews based on cox2 sequence data. *Mycological Research*, **2008**, 112, 345-51 | | 43 |
| 18 | AxPcoords & parallel AxParafit: statistical co-phylogenetic analyses on thousands of taxa. *BMC Bioinformatics*, **2007**, 8, 405 | 3.6 | 37 |
| 17 | A revision of Plasmopara penniseti, with implications for the host range of the downy mildews with pyriform haustoria. *Mycological Research*, **2007**, 111, 1377-85 | | 27 |
| 16 | COPYCAT: cophylogenetic analysis tool. *Bioinformatics*, **2007**, 23, 898-900 | 7.2 | 84 |
| 15 | How do obligate parasites evolve? A multi-gene phylogenetic analysis of downy mildews. *Fungal Genetics and Biology*, **2007**, 44, 105-22 | 3.9 | 114 |
| 14 | A revision of Bremia graminicola. *Mycological Research*, **2006**, 110, 646-56 | | 31 |
| 13 | Genome BLAST distance phylogenies inferred from whole plastid and whole mitochondrion genome sequences. *BMC Bioinformatics*, **2006**, 7, 350 | 3.6 | 54 |
| 12 | Implications of molecular characters for the phylogeny of the Microbotryaceae (Basidiomycota: Urediniomycetes). *BMC Evolutionary Biology*, **2006**, 6, 35 | 3 | 63 |
| 11 | 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 | 2.1 | 41 |
| 10 | Anther smuts of Caryophyllaceae: Molecular characters indicate host-dependent species delimitation. *Mycological Progress*, **2005**, 4, 225-238 | 1.9 | 64 |
| 9 | 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, 1011-24 | | 88 |
| 8 | Phylogeny of Hyaloperonospora based on nuclear ribosomal internal transcribed spacer sequences. *Mycological Progress*, **2004**, 3, 83-94 | 1.9 | 77 |
| 7 | Taxonomic aspects of Peronosporaceae inferred from Bayesian molecular phylogenetics. *Canadian Journal of Botany*, **2003**, 81, 672-683 | | 70 |
| 6 | Phylogenetic Relationships of the Downy Mildews (Peronosporales) and Related Groups Based on Nuclear Large Subunit Ribosomal DNA Sequences. *Mycologia*, **2002**, 94, 834 | 2.4 | 114 |
| 5 | Taxonomy and Phylogeny of the Downy Mildews (Peronosporaceae)47-75 | | 25 |
| 4 | Large-Scale Co-Phylogenetic Analysis on the Grid222-237 | | |
| 3 | Critical Assessment of Metagenome Interpretation □a benchmark of computational metagenomics software | | 17 |

| | | |
|---|---|---|
| 2 | Global genomic population structure of Clostridioides difficile | 3 |
| 1 | VICTOR: Genome-based Phylogeny and Classification of Prokaryotic Viruses | 3 |