

# Daniel Wibberg

## List of Publications by Year in Descending Order

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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.

151  
papers

2,792  
citations

31  
h-index

43  
g-index

161  
ext. papers

3,767  
ext. citations

4.5  
avg. IF

5.13  
L-index

| #   | Paper   | IF   | Citations |
|-----|---|------|-----------|
| 151 | Biosynthetic potential of the endophytic fungus <i>Helotiales</i> sp. BL73 revealed via compound identification and genome mining.. <i>Applied and Environmental Microbiology</i> , <b>2022</b> , aem0251021  | 4.8  | 0         |
| 150 | Seventeen Ustilaginaceae High-Quality Genome Sequences Allow Phylogenomic Analysis and Provide Insights into Secondary Metabolite Synthesis.. <i>Journal of Fungi (Basel, Switzerland)</i> , <b>2022</b> , 8,   | 5.6  | 1         |
| 149 | <i>Ustilago maydis</i> Metabolic Characterization and Growth Quantification with a Genome-Scale Metabolic Model. <i>Journal of Fungi (Basel, Switzerland)</i> , <b>2022</b> , 8, 524  | 5.6  | 0         |
| 148 | Activity-Based Protein Profiling for the Identification of Novel Carbohydrate-Active Enzymes Involved in Xylan Degradation in the Hyperthermophilic Euryarchaeon sp. Strain 2319x1E.. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 734039                         | 5.7  | 1         |
| 147 | Establishment of a near-contiguous genome sequence of the citric acid producing yeast DSM 3286 with resolution of rDNA clusters and telomeres. <i>NAR Genomics and Bioinformatics</i> , <b>2021</b> , 3, lqab085  | 3.7  | 0         |
| 146 | Genome Analyses of the Less Aggressive AG1-IB Isolates 1/2/21 and O8/2 Compared to the Reference AG1-IB Isolate 7/3/14. <i>Journal of Fungi (Basel, Switzerland)</i> , <b>2021</b> , 7,   | 5.6  | 2         |
| 145 | Genomic and Transcriptomic Investigation of the Physiological Response of the Methylophilium to 5-Aminovalerate. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 664598  | 5.7  | 2         |
| 144 | Genomic and proteomic profiles of biofilms on microplastics are decoupled from artificial surface properties. <i>Environmental Microbiology</i> , <b>2021</b> , 23, 3099-3115   | 5.2  | 7         |
| 143 | High quality genome sequences of thirteen Hypoxylaceae (Ascomycota) strengthen the phylogenetic family backbone and enable the discovery of new taxa. <i>Fungal Diversity</i> , <b>2021</b> , 106, 7-28   | 17.6 | 32        |
| 142 | Phytoplankton consortia as a blueprint for mutually beneficial eukaryote-bacteria ecosystems based on the biocoenosis of Botryococcus consortia. <i>Scientific Reports</i> , <b>2021</b> , 11, 1726   | 4.9  | 3         |
| 141 | Implementing FAIR data management within the German Network for Bioinformatics Infrastructure (de.NBI) exemplified by selected use cases. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,  | 13.4 | 4         |
| 140 | A Regulator Based "Semi-Targeted" Approach to Activate Silent Biosynthetic Gene Clusters. <i>International Journal of Molecular Sciences</i> , <b>2021</b> , 22,  | 6.3  | 1         |
| 139 | A novel plant-fungal association reveals fundamental sRNA and gene expression reprogramming at the onset of symbiosis. <i>BMC Biology</i> , <b>2021</b> , 19, 171   | 7.3  | 2         |
| 138 | Draft genome sequence of <i>Streptomyces tunisialis</i> DSM 105760. <i>Archives of Microbiology</i> , <b>2020</b> , 202, 2013-2017  | 3    | 1         |
| 137 | Impact of process temperature and organic loading rate on cellulolytic / hydrolytic biofilm microbiomes during biomethanation of ryegrass silage revealed by genome-centered metagenomics and metatranscriptomics. <i>Environmental Microbiomes</i> , <b>2020</b> , 15, 7 | 5.6  | 6         |
| 136 | The colonic mucosa-associated microbiome in SIV infection: shift towards Bacteroidetes coincides with mucosal CD4 T cell depletion and enterocyte damage. <i>Scientific Reports</i> , <b>2020</b> , 10, 10887   | 4.9  | 6         |
| 135 | Intragenomic polymorphisms in the ITS region of high-quality genomes of the Hypoxylaceae (Xylariales, Ascomycota). <i>Mycological Progress</i> , <b>2020</b> , 19, 235-245  | 1.9  | 33        |

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|-----|--|------|----|
| 134 | Comparative Transcriptome Analysis Provides Molecular Insights into the Interaction of and with Their Host Sugar Beet. <i>Viruses</i> , <b>2020</b> , 12,  | 6.2  | 7  |
| 133 | The Peptidoglycan Biosynthesis Gene in Actinorhizal vs. Plant Type. <i>Genes</i> , <b>2020</b> , 11,   | 4.2  | 2  |
| 132 | Complete Genome Sequence of Ovine subsp. Strain JIII-386 (MAP-S/type III) and Its Comparison to MAP-S/type I, MAP-C, and Complex Genomes. <i>Microorganisms</i> , <b>2020</b> , 9,   | 4.9  | 4  |
| 131 | sp. nov., isolated from beef. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2020</b> , 70, 292-301   | 2.2  | 1  |
| 130 | sp. nov., isolated from meat. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2020</b> , 70, 1528-1540   | 2.2  | 4  |
| 129 | Candidatus Frankia nodulisporulans sp. nov., an Alnus glutinosa-infective Frankia species unable to grow in pure culture and able to sporulate in-planta. <i>Systematic and Applied Microbiology</i> , <b>2020</b> , 43, 1261-1274 | 4.2  | 4  |
| 128 | The sporothriolides. A new biosynthetic family of fungal secondary metabolites. <i>Chemical Science</i> , <b>2020</b> , 11, 12477-12484  | 9.4  | 6  |
| 127 | Multi-omic Directed Discovery of Cellulosomes, Polysaccharide Utilization Loci, and Lignocellulases from an Enriched Rumen Anaerobic Consortium. <i>Applied and Environmental Microbiology</i> , <b>2020</b> , 86,                 | 4.8  | 7  |
| 126 | Synthetisch biologisch getriebene Biosynthese von unnatürlichen Tropolon-Sesquiterpenoiden. <i>Angewandte Chemie</i> , <b>2020</b> , 132, 24079-24087  | 3.6  | 3  |
| 125 | Necrotrophic lifestyle of Rhizoctonia solani AG3-PT during interaction with its host plant potato as revealed by transcriptome analysis. <i>Scientific Reports</i> , <b>2020</b> , 10, 12574                                       | 4.9  | 7  |
| 124 | Synthetic Biology Driven Biosynthesis of Unnatural Tropolone Sesquiterpenoids. <i>Angewandte Chemie - International Edition</i> , <b>2020</b> , 59, 23870-23878  | 16.4 | 19 |
| 123 | A framework to assess the quality and impact of bioinformatics training across ELIXIR. <i>PLoS Computational Biology</i> , <b>2020</b> , 16, e1007976  | 5    | 3  |
| 122 | The Role of ING2-E5A in Mesophilic Biogas Reactor Systems as Deduced from Multiomics Analyses. <i>Microorganisms</i> , <b>2020</b> , 8,  | 4.9  | 6  |
| 121 | A comprehensive analysis of the Lactuca sativa, L. transcriptome during different stages of the compatible interaction with Rhizoctonia solani. <i>Scientific Reports</i> , <b>2019</b> , 9, 7221                                  | 4.9  | 10 |
| 120 | Biosynthetic reconstitution of deoxysugar phosphoramidate metalloprotease inhibitors using an N-P-bond-forming kinase. <i>Chemical Science</i> , <b>2019</b> , 10, 4486-4490   | 9.4  | 4  |
| 119 | Insight into the structure, function and conjugative transfer of pLPU83a, an accessory plasmid of Rhizobium favelukesii LPU83. <i>Plasmid</i> , <b>2019</b> , 103, 9-16  | 3.3  | 7  |
| 118 | Frankia-Enriched Metagenomes from the Earliest Diverging Symbiotic Frankia Cluster: They Come in Teams. <i>Genome Biology and Evolution</i> , <b>2019</b> , 11, 2273-2291  | 3.9  | 18 |
| 117 | Assessing genetic diversity and similarity of 435 KPC-carrying plasmids. <i>Scientific Reports</i> , <b>2019</b> , 9, 112234.9   | 4.9  | 12 |

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|-----|---|------|----|
| 116 | Bioactive secondary metabolites from new endophytic fungus <i>Curvularia</i> . sp isolated from <i>Rauwolfia macrophylla</i> . <i>PLoS ONE</i> , <b>2019</b> , 14, e0217627   | 3.7  | 32 |
| 115 | The de.NBI / ELIXIR-DE training platform - Bioinformatics training in Germany and across Europe within ELIXIR. <i>F1000Research</i> , <b>2019</b> , 8,  | 3.6  | 1  |
| 114 | The de.NBI / ELIXIR-DE training platform - Bioinformatics training in Germany and across Europe within ELIXIR. <i>F1000Research</i> , <b>2019</b> , 8, 1877   | 3.6  | 2  |
| 113 | Genome Analyses and Genome-Centered Metatranscriptomics of Strain SIV6, Isolated from a Thermophilic Production-Scale Biogas Fermenter. <i>Microorganisms</i> , <b>2019</b> , 8,  | 4.9  | 4  |
| 112 | The secreted metabolome of and implications for bacterial chemistry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, 2490-2495  | 11.5 | 48 |
| 111 | Complete Genome Sequencing of <i>Acinetobacter baumannii</i> Strain K50 Discloses the Large Conjugative Plasmid pK50a Encoding Carbapenemase OXA-23 and Extended-Spectrum $\beta$ -Lactamase GES-11. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2018</b> , 62, | 5.9  | 17 |
| 110 | Identification of a novel aminopolycarboxylic acid siderophore gene cluster encoding the biosynthesis of ethylenediaminesuccinic acid hydroxyarginine (EDHA). <i>Metallomics</i> , <b>2018</b> , 10, 722-734  | 4.5  | 3  |
| 109 | Characterization of the Actinonin Biosynthetic Gene Cluster. <i>ChemBioChem</i> , <b>2018</b> , 19, 1189  | 3.8  | 7  |
| 108 | Single-bacterial genomics validates rich and varied specialized metabolism of uncultivated sponge symbionts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, 1718-1723                                    | 11.5 | 45 |
| 107 | Assembly of the <i>Lactuca sativa</i> , L. cv. Tizian draft genome sequence reveals differences within major resistance complex 1 as compared to the cv. Salinas reference genome. <i>Journal of Biotechnology</i> , <b>2018</b> , 267, 12-18                         | 3.7  | 11 |
| 106 | Individual- and Species-Specific Skin Microbiomes in Three Different Estrildid Finch Species Revealed by 16S Amplicon Sequencing. <i>Microbial Ecology</i> , <b>2018</b> , 76, 518-529  | 4.4  | 19 |
| 105 | Genome Sequence of the Bile Salt-Degrading Bacterium sp. Strain Chol11, a Model Organism for Bacterial Steroid Catabolism. <i>Genome Announcements</i> , <b>2018</b> , 6,   |      | 4  |
| 104 | Optimization of Tetrahydrocannabinolic acid synthase production in <i>Komagataella phaffii</i> via post-translational bottleneck identification. <i>Journal of Biotechnology</i> , <b>2018</b> , 272-273, 40-47   | 3.7  | 17 |
| 103 | N-Acetylborrelidin B: a new bioactive metabolite from <i>Streptomyces mutabilis</i> sp. M11. <i>Zeitschrift Fur Naturforschung - Section C Journal of Biosciences</i> , <b>2018</b> , 73, 49-57   | 1.7  | 13 |
| 102 | Isolation and whole genome analysis of endospore-forming bacteria from heroin. <i>Forensic Science International: Genetics</i> , <b>2018</b> , 32, 1-6  | 4.3  | 3  |
| 101 | Fungal community profiles in agricultural soils of a long-term field trial under different tillage, fertilization and crop rotation conditions analyzed by high-throughput ITS-amplicon sequencing. <i>PLoS ONE</i> , <b>2018</b> , 13, e0195345                      | 3.7  | 42 |
| 100 | Comparative genomics reveals phylogenetic distribution patterns of secondary metabolites in <i>Amycolatopsis</i> species. <i>BMC Genomics</i> , <b>2018</b> , 19, 426   | 4.5  | 66 |
| 99  | Petroleum hydrocarbon and microbial community structure successions in marine oil-related aggregates associated with diatoms relevant for Arctic conditions. <i>Marine Pollution Bulletin</i> , <b>2018</b> , 135, 759-768  | 6.7  | 9  |

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|----|---|------|----|
| 98 | Microbiome-Triggered Transformations of Trace Organic Chemicals in the Presence of Effluent Organic Matter in Managed Aquifer Recharge (MAR) Systems. <i>Environmental Science &amp; Technology</i> , <b>2018</b> , 52, 14342-14351                       | 10.3 | 11 |
| 97 | The genus <i>Borrelia</i> reloaded. <i>PLoS ONE</i> , <b>2018</b> , 13, e0208432  | 3.7  | 50 |
| 96 | Harvest of the Oleaginous Microalgae by Flocculation From Culture Based on Natural Water Sources. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2018</b> , 6, 200   | 5.8  | 12 |
| 95 | Binning enables efficient host genome reconstruction in cnidarian holobionts. <i>GigaScience</i> , <b>2018</b> , 7,   | 7.6  | 8  |
| 94 | str. M3/6 isolated from a laboratory biogas reactor is versatile in polysaccharide and oligopeptide utilization as deduced from genome-based metabolic reconstructions. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , <b>2018</b> , 18, e00254  | 5.3  | 14 |
| 93 | Three previously unrecognised classes of biosynthetic enzymes revealed during the production of xenovulene A. <i>Nature Communications</i> , <b>2018</b> , 9, 1963  | 17.4 | 48 |
| 92 | Comparative genomic analysis of <i>Acinetobacter</i> spp. plasmids originating from clinical settings and environmental habitats. <i>Scientific Reports</i> , <b>2018</b> , 8, 7783   | 4.9  | 27 |
| 91 | A flavin-dependent halogenase from metagenomic analysis prefers bromination over chlorination. <i>PLoS ONE</i> , <b>2018</b> , 13, e0196797   | 3.7  | 40 |
| 90 | Genome sequence of <i>Methanobacterium congolense</i> strain Buetzberg, a hydrogenotrophic, methanogenic archaeon, isolated from a mesophilic industrial-scale biogas plant utilizing bio-waste. <i>Journal of Biotechnology</i> , <b>2017</b> , 247, 1-5 | 3.7  | 38 |
| 89 | Comparative genomics of host adaptive traits in <i>Xanthomonas translucens</i> pv. <i>graminis</i> . <i>BMC Genomics</i> , <b>2017</b> , 18, 35   | 4.5  | 16 |
| 88 | Transcriptome profiling of the Australian arid-land plant <i>Eremophila serrulata</i> (A.DC.) Druce (Scrophulariaceae) for the identification of monoterpene synthases. <i>Phytochemistry</i> , <b>2017</b> , 136, 15-22                                  | 4    | 6  |
| 87 | Genome improvement of the acarbose producer <i>Actinoplanes</i> sp. SE50/110 and annotation refinement based on RNA-seq analysis. <i>Journal of Biotechnology</i> , <b>2017</b> , 251, 112-123  | 3.7  | 9  |
| 86 | Refined annotation of the complete genome of the phytopathogenic and xanthan producing <i>Xanthomonas campestris</i> pv. <i>campestris</i> strain B100 based on RNA sequence data. <i>Journal of Biotechnology</i> , <b>2017</b> , 253, 55-61             | 3.7  | 6  |
| 85 | The completely annotated genome and comparative genomics of the Peptoniphilaceae bacterium str. ING2-D1G, a novel acidogenic bacterium isolated from a mesophilic biogas reactor. <i>Journal of Biotechnology</i> , <b>2017</b> , 257, 178-186            | 3.7  | 1  |
| 84 | Draft genome sequence of the potato pathogen <i>Rhizoctonia solani</i> AG3-PT isolate Ben3. <i>Archives of Microbiology</i> , <b>2017</b> , 199, 1065-1068  | 3    | 8  |
| 83 | The <i>Rhizoctonia solani</i> AG1-IB (isolate 7/3/14) transcriptome during interaction with the host plant lettuce ( <i>Lactuca sativa</i> L.). <i>PLoS ONE</i> , <b>2017</b> , 12, e0177278  | 3.7  | 20 |
| 82 | Whole transcriptome RNA-Seq analysis reveals extensive cell type-specific compartmentalization in <i>Volvox carteri</i> . <i>BMC Biology</i> , <b>2017</b> , 15, 111  | 7.3  | 16 |
| 81 | Highly efficient methane generation from untreated microalgae biomass. <i>Biotechnology for Biofuels</i> , <b>2017</b> , 10, 186  | 7.8  | 46 |

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|----|---|-----|----|
| 80 | Draft Genome Sequence of sp. Strain KarMa, a Model Organism for Monomethylamine-Degrading Nonmethylophilic Bacteria. <i>Genome Announcements</i> , <b>2017</b> , 5,   |     | 3  |
| 79 | Lifestyle-determining extrachromosomal replicon pAMV1 and its contribution to the carbon metabolism of the methylotrophic bacterium <i>Paracoccus aminovorans</i> JCM 7685. <i>Environmental Microbiology</i> , <b>2017</b> , 19, 4536-4550                                 | 5.2 | 12 |
| 78 | Genome content, metabolic pathways and biotechnological potential of the psychrophilic Arctic bacterium <i>Psychrobacter</i> sp. DAB_AL43B, a source and a host of novel <i>Psychrobacter</i> -specific vectors. <i>Journal of Biotechnology</i> , <b>2017</b> , 263, 64-74 | 3.7 | 7  |
| 77 | Linking secondary metabolites to biosynthesis genes in the fungal endophyte <i>Cyanoderma asteris</i> : The anti-cancer bisanthraquinone skyrin. <i>Journal of Biotechnology</i> , <b>2017</b> , 257, 233-239   | 3.7 | 25 |
| 76 | Identification of a novel mycovirus isolated from <i>Rhizoctonia solani</i> (AG 2-2 IV) provides further information about genome plasticity within the order Tymovirales. <i>Archives of Virology</i> , <b>2017</b> , 162, 555-559   | 2.6 | 7  |
| 75 | Genomics and prevalence of bacterial and archaeal isolates from biogas-producing microbiomes. <i>Biotechnology for Biofuels</i> , <b>2017</b> , 10, 264   | 7.8 | 26 |
| 74 | A Mitochondrial Autonomously Replicating Sequence from for Uniform High Level Recombinant Protein Production. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 780   | 5.7 | 16 |
| 73 | Evolutionary and biogeographical implications of degraded LAGLIDADG endonuclease functionality and group I intron occurrence in stony corals (Scleractinia) and mushroom corals (Corallimorpharia). <i>PLoS ONE</i> , <b>2017</b> , 12, e0173734                            | 3.7 | 10 |
| 72 | Biphasic Study to Characterize Agricultural Biogas Plants by High-Throughput 16S rRNA Gene Amplicon Sequencing and Microscopic Analysis. <i>Journal of Microbiology and Biotechnology</i> , <b>2017</b> , 27, 321-334   | 3.3 | 25 |
| 71 | Draft Genome Sequence of <i>Propionispora</i> sp. Strain 2/2-37, a New Xylan-Degrading Bacterium Isolated from a Mesophilic Biogas Reactor. <i>Genome Announcements</i> , <b>2016</b> , 4,  |     | 1  |
| 70 | Complete Genome Sequence of <i>Herbinix luporum</i> SD1D, a New Cellulose-Degrading Bacterium Isolated from a Thermophilic Biogas Reactor. <i>Genome Announcements</i> , <b>2016</b> , 4,   |     | 6  |
| 69 | Draft Genome Sequence of the <i>Xanthomonas bromi</i> Type Strain LMG 947. <i>Genome Announcements</i> , <b>2016</b> , 4,   |     | 1  |
| 68 | Genomics of high molecular weight plasmids isolated from an on-farm biopurification system. <i>Scientific Reports</i> , <b>2016</b> , 6, 28284  | 4.9 | 12 |
| 67 | An assemblage of <i>Frankia</i> Cluster II strains from California contains the canonical nod genes and also the sulfotransferase gene nodH. <i>BMC Genomics</i> , <b>2016</b> , 17, 796  | 4.5 | 41 |
| 66 | Complete Genome Sequence of the Barley Pathogen <i>Xanthomonas translucens</i> pv. <i>translucens</i> DSM 18974T (ATCC 19319T). <i>Genome Announcements</i> , <b>2016</b> , 4,  |     | 15 |
| 65 | Draft Genome Sequence of <i>Streptococcus anginosus</i> BVI, a New Vaginal Pathogen Candidate. <i>Genome Announcements</i> , <b>2016</b> , 4,   |     | 2  |
| 64 | Complete Draft Genome Sequence of <i>Escherichia coli</i> JF733. <i>Genome Announcements</i> , <b>2016</b> , 4,   |     | 1  |
| 63 | Comparative transcriptome analysis of the biocontrol strain <i>Bacillus amyloliquefaciens</i> FZB42 as response to biofilm formation analyzed by RNA sequencing. <i>Journal of Biotechnology</i> , <b>2016</b> , 231, 212-223   | 3.7 | 29 |

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|----|--|-----|----|
| 62 | Targeted genome editing in the rare actinomycete <i>Actinoplanes</i> sp. SE50/110 by using the CRISPR/Cas9 System. <i>Journal of Biotechnology</i> , <b>2016</b> , 231, 122-128  | 3.7 | 31 |
| 61 | Complete Chloroplast and Mitochondrial Genome Sequences of the Hydrocarbon Oil-Producing Green Microalga <i>Botryococcus braunii</i> Race B (Showa). <i>Genome Announcements</i> , <b>2016</b> , 4,  |     | 4  |
| 60 | Genome wide transcription start sites analysis of <i>Xanthomonas campestris</i> pv. <i>campestris</i> B100 with insights into the gum gene cluster directing the biosynthesis of the exopolysaccharide xanthan. <i>Journal of Biotechnology</i> , <b>2016</b> , 225, 18-28 | 3.7 | 31 |
| 59 | Complete mitochondrial genome of the scleractinian coral <i>Porites rus</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , <b>2016</b> , 27, 3695-6  | 1.3 | 1  |
| 58 | Complete genome sequence of <i>Streptomyces reticuli</i> , an efficient degrader of crystalline cellulose. <i>Journal of Biotechnology</i> , <b>2016</b> , 222, 13-4   | 3.7 | 13 |
| 57 | Draft genome sequence of the sugar beet pathogen <i>Rhizoctonia solani</i> AG2-2IIIB strain BBA69670. <i>Journal of Biotechnology</i> , <b>2016</b> , 222, 11-2  | 3.7 | 13 |
| 56 | Intraspecies Transfer of the Chromosomal <i>Acinetobacter baumannii</i> blaNDM-1 Carbapenemase Gene. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2016</b> , 60, 3032-40  | 5.9 | 49 |
| 55 | Taxonomic analysis of the microbial community in stored sugar beets using high-throughput sequencing of different marker genes. <i>FEMS Microbiology Ecology</i> , <b>2016</b> , 92,   | 4.3 | 25 |
| 54 | Complete genome analysis of <i>Clostridium bornimense</i> strain M2/40(T): A new acidogenic <i>Clostridium</i> species isolated from a mesophilic two-phase laboratory-scale biogas reactor. <i>Journal of Biotechnology</i> , <b>2016</b> , 232, 38-49                    | 3.7 | 13 |
| 53 | Deep Sequencing Analysis Reveals the Mycoviral Diversity of the Virome of an Avirulent Isolate of <i>Rhizoctonia solani</i> AG-2-2 IV. <i>PLoS ONE</i> , <b>2016</b> , 11, e0165965  | 3.7 | 37 |
| 52 | Complete Genome Sequence of the Methanogen <i>Methanoculleus bourgensis</i> BA1 Isolated from a Biogas Reactor. <i>Genome Announcements</i> , <b>2016</b> , 4,   |     | 7  |
| 51 | Draft genome sequences of three <i>Xanthomonas translucens</i> pathovar reference strains (pv. <i>arrhenatheri</i> , pv. <i>poae</i> and pv. <i>phlei</i> ) with different specificities for forage grasses. <i>Standards in Genomic Sciences</i> , <b>2016</b> , 11, 50   |     | 5  |
| 50 | Finished genome sequence and methylome of the cyanide-degrading <i>Pseudomonas pseudoalcaligenes</i> strain CECT5344 as resolved by single-molecule real-time sequencing. <i>Journal of Biotechnology</i> , <b>2016</b> , 232, 61-8  | 3.7 | 11 |
| 49 | Genome analysis of the sugar beet pathogen <i>Rhizoctonia solani</i> AG2-2IIIB revealed high numbers in secreted proteins and cell wall degrading enzymes. <i>BMC Genomics</i> , <b>2016</b> , 17, 245   | 4.5 | 52 |
| 48 | Genomic characterization of <i>DeFluviitoga tunisiensis</i> L3, a key hydrolytic bacterium in a thermophilic biogas plant and its abundance as determined by metagenome fragment recruitment. <i>Journal of Biotechnology</i> , <b>2016</b> , 232, 50-60                   | 3.7 | 38 |
| 47 | Genetic engineering in <i>Actinoplanes</i> sp. SE50/110 - development of an intergeneric conjugation system for the introduction of actinophage-based integrative vectors. <i>Journal of Biotechnology</i> , <b>2016</b> , 232, 79-88                                      | 3.7 | 13 |
| 46 | Diversity and role of plasmids in adaptation of bacteria inhabiting the Lubin copper mine in Poland, an environment rich in heavy metals. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 152  | 5.7 | 38 |
| 45 | Improved genome sequence of the phytopathogenic fungus <i>Rhizoctonia solani</i> AG1-IB 7/3/14 as established by deep mate-pair sequencing on the MiSeq (Illumina) system. <i>Journal of Biotechnology</i> , <b>2015</b> , 203, 19-21                                      | 3.7 | 20 |

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|----|---|-----|----|
| 44 | Genome Sequence of the Urethral Catheter Isolate <i>Pseudomonas aeruginosa</i> MH19. <i>Genome Announcements</i> , <b>2015</b> , 3,   |     | 2  |
| 43 | Complete genome sequence of the strain <i>DeFluviitoga tunisiensis</i> L3, isolated from a thermophilic, production-scale biogas plant. <i>Journal of Biotechnology</i> , <b>2015</b> , 203, 17-8   | 3-7 | 35 |
| 42 | Draft genome of the xanthan producer <i>Xanthomonas campestris</i> NRRL B-1459 (ATCC 13951). <i>Journal of Biotechnology</i> , <b>2015</b> , 204, 45-6  | 3-7 | 17 |
| 41 | Complete Genome Sequence of the Clinical Strain <i>Acinetobacter baumannii</i> R2090 Carrying the Chromosomally Encoded Metallo- $\beta$ -Lactamase Gene blaNDM-1. <i>Genome Announcements</i> , <b>2015</b> , 3,   |     | 1  |
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| 31 | Draft Genome Sequence of <i>Pseudomonas aeruginosa</i> Strain WS136, a Highly Cytotoxic ExoS-Positive Wound Isolate Recovered from Pyoderma Gangrenosum. <i>Genome Announcements</i> , <b>2015</b> , 3,   |     | 2  |
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| 24 | Complete genome sequence of the cellulolytic thermophile <i>Ruminoclostridium cellulosi</i> wild-type strain DG5 isolated from a thermophilic biogas plant. <i>Journal of Biotechnology</i> , <b>2014</b> , 188, 136-7   | 3.7 | 26 |
| 23 | Transcriptome analysis of the phytopathogenic fungus <i>Rhizoctonia solani</i> AG1-IB 7/3/14 applying high-throughput sequencing of expressed sequence tags (ESTs). <i>Fungal Biology</i> , <b>2014</b> , 118, 800-13  | 2.8 | 27 |
| 22 | Genome sequence of the acid-tolerant strain <i>Rhizobium</i> sp. LPU83. <i>Journal of Biotechnology</i> , <b>2014</b> , 176, 40-1  | 3.7 | 8  |
| 21 | IncH-type plasmid harboring bla CTX-M-15, bla DHA-1, and qnrB4 genes recovered from animal isolates. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2014</b> , 58, 3768-73  | 5.9 | 18 |
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| 18 | Effect of the strain <i>Bacillus amyloliquefaciens</i> FZB42 on the microbial community in the rhizosphere of lettuce under field conditions analyzed by whole metagenome sequencing. <i>Frontiers in Microbiology</i> , <b>2014</b> , 5, 252  | 5.7 | 70 |
| 17 | Rhizobial plasmid pLPU83a is able to switch between different transfer machineries depending on its genomic background. <i>FEMS Microbiology Ecology</i> , <b>2014</b> , 88, 565-78  | 4.3 | 17 |
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| 12 | Establishment and interpretation of the genome sequence of the phytopathogenic fungus <i>Rhizoctonia solani</i> AG1-IB isolate 7/3/14. <i>Journal of Biotechnology</i> , <b>2013</b> , 167, 142-55   | 3.7 | 68 |
| 11 | Complete genome sequence of the hydrogenotrophic Archaeon <i>Methanobacterium</i> sp. Mb1 isolated from a production-scale biogas plant. <i>Journal of Biotechnology</i> , <b>2013</b> , 168, 734-6  | 3.7 | 37 |
| 10 | The IncF plasmid pRSB225 isolated from a municipal wastewater treatment plant's on-site prefloder combining antibiotic resistance and putative virulence functions is highly related to virulence plasmids identified in pathogenic <i>E. coli</i> isolates. <i>Plasmid</i> , <b>2013</b> , 69, 127-37 | 3.3 | 30 |
| 9  | Complete sequence of broad-host-range plasmid pNOR-2000 harbouring the metallo- $\beta$ -lactamase gene blaVIM-2 from <i>Pseudomonas aeruginosa</i> . <i>Journal of Antimicrobial Chemotherapy</i> , <b>2013</b> , 68, 1060-5  | 5.1 | 28 |

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| 8 | The complete genome sequences of four new IncN plasmids from wastewater treatment plant effluent provide new insights into IncN plasmid diversity and evolution. <i>Plasmid</i> , <b>2012</b> , 68, 13-24   | 3.3 | 52  |
| 7 | Insights into the completely annotated genome of <i>Lactobacillus buchneri</i> CD034, a strain isolated from stable grass silage. <i>Journal of Biotechnology</i> , <b>2012</b> , 161, 153-66   | 3.7 | 73  |
| 6 | IncP-1 $\alpha$ plasmids of <i>Comamonas</i> sp. and <i>Delftia</i> sp. strains isolated from a wastewater treatment plant mediate resistance to and decolorization of the triphenylmethane dye crystal violet. <i>Microbiology (United Kingdom)</i> , <b>2012</b> , 158, 2060-2072                               | 2.9 | 16  |
| 5 | Complete genome sequence of the hydrogenotrophic, methanogenic archaeon <i>Methanoculleus bourgensis</i> strain MS2(T), isolated from a sewage sludge digester. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 5487-8  | 3.5 | 32  |
| 4 | The complete genome sequence of the dominant <i>Sinorhizobium meliloti</i> field isolate SM11 extends the <i>S. meliloti</i> pan-genome. <i>Journal of Biotechnology</i> , <b>2011</b> , 155, 20-33   | 3.7 | 52  |
| 3 | Complete genome sequencing of <i>Agrobacterium</i> sp. H13-3, the former <i>Rhizobium lupini</i> H13-3, reveals a tripartite genome consisting of a circular and a linear chromosome and an accessory plasmid but lacking a tumor-inducing Ti-plasmid. <i>Journal of Biotechnology</i> , <b>2011</b> , 155, 50-62 | 3.7 | 90  |
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| 1 | High-quality genome sequence of <i>Pichia pastoris</i> CBS7435. <i>Journal of Biotechnology</i> , <b>2011</b> , 154, 312-20   | 3.7 | 123 |