

Daniel Wibberg

List of Publications by Citations

Source: <https://exaly.com/author-pdf/3032775/daniel-wibberg-publications-by-citations.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	High-quality genome sequence of <i>Pichia pastoris</i> CBS7435. <i>Journal of Biotechnology</i> , 2011 , 154, 312-20	3.7	123
150	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> , 2011 , 155, 50-62	3.7	90
149	Insights into the completely annotated genome of <i>Lactobacillus buchneri</i> CD034, a strain isolated from stable grass silage. <i>Journal of Biotechnology</i> , 2012 , 161, 153-66	3.7	73
148	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> , 2014 , 5, 252	5.7	70
147	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> , 2013 , 167, 142-55	3.7	68
146	Comparative genomics reveals phylogenetic distribution patterns of secondary metabolites in <i>Amycolatopsis</i> species. <i>BMC Genomics</i> , 2018 , 19, 426	4.5	66
145	Complete genome sequence of the novel Porphyromonadaceae bacterium strain ING2-E5B isolated from a mesophilic lab-scale biogas reactor. <i>Journal of Biotechnology</i> , 2015 , 193, 34-6	3.7	53
144	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> , 2012 , 68, 13-24	3.3	52
143	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> , 2011 , 155, 20-33	3.7	52
142	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> , 2016 , 17, 245	4.5	52
141	The genus <i>Borrelia</i> reloaded. <i>PLoS ONE</i> , 2018 , 13, e0208432	3.7	50
140	Intraspecies Transfer of the Chromosomal <i>Acinetobacter baumannii</i> blaNDM-1 Carbapenemase Gene. <i>Antimicrobial Agents and Chemotherapy</i> , 2016 , 60, 3032-40	5.9	49
139	Community shifts in a well-operating agricultural biogas plant: how process variations are handled by the microbiome. <i>Applied Microbiology and Biotechnology</i> , 2015 , 99, 7791-803	5.7	48
138	The secreted metabolome of and implications for bacterial chemistry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 2490-2495	11.5	48
137	Three previously unrecognised classes of biosynthetic enzymes revealed during the production of xenovulene A. <i>Nature Communications</i> , 2018 , 9, 1963	17.4	48
136	Highly efficient methane generation from untreated microalgae biomass. <i>Biotechnology for Biofuels</i> , 2017 , 10, 186	7.8	46
135	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> , 2018 , 115, 1718-1723	11.5	45

134	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> , 2018 , 13, e0195345	3.7	42
133	An assemblage of Frankia Cluster II strains from California contains the canonical nod genes and also the sulfotransferase gene nodH. <i>BMC Genomics</i> , 2016 , 17, 796	4.5	41
132	A flavin-dependent halogenase from metagenomic analysis prefers bromination over chlorination. <i>PLoS ONE</i> , 2018 , 13, e0196797	3.7	40
131	Genome sequence of Methanobacterium congolense strain Buetzberg, a hydrogenotrophic, methanogenic archaeon, isolated from a mesophilic industrial-scale biogas plant utilizing bio-waste. <i>Journal of Biotechnology</i> , 2017 , 247, 1-5	3.7	38
130	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> , 2015 , 6, 152	5.7	38
129	Genomic characterization of Defluviitoga tunisiensis L3, a key hydrolytic bacterium in a thermophilic biogas plant and its abundance as determined by metagenome fragment recruitment. <i>Journal of Biotechnology</i> , 2016 , 232, 50-60	3.7	38
128	Complete genome sequence of the hydrogenotrophic Archaeon Methanobacterium sp. Mb1 isolated from a production-scale biogas plant. <i>Journal of Biotechnology</i> , 2013 , 168, 734-6	3.7	37
127	Deep Sequencing Analysis Reveals the Mycoviral Diversity of the Virome of an Avirulent Isolate of Rhizoctonia solani AG-2-2 IV. <i>PLoS ONE</i> , 2016 , 11, e0165965	3.7	37
126	Complete genome sequence of the strain Defluviitoga tunisiensis L3, isolated from a thermophilic, production-scale biogas plant. <i>Journal of Biotechnology</i> , 2015 , 203, 17-8	3.7	35
125	Intragenomic polymorphisms in the ITS region of high-quality genomes of the Hypoxylaceae (Xylariales, Ascomycota). <i>Mycological Progress</i> , 2020 , 19, 235-245	1.9	33
124	Bioactive secondary metabolites from new endophytic fungus Curvularia. sp isolated from Rauwolfia macrophylla. <i>PLoS ONE</i> , 2019 , 14, e0217627	3.7	32
123	Complete genome sequence of the hydrogenotrophic, methanogenic archaeon Methanoculleus bourgensis strain MS2(T), Isolated from a sewage sludge digester. <i>Journal of Bacteriology</i> , 2012 , 194, 5487-8	3.5	32
122	High quality genome sequences of thirteen Hypoxylaceae (Ascomycota) strengthen the phylogenetic family backbone and enable the discovery of new taxa. <i>Fungal Diversity</i> , 2021 , 106, 7-28	17.6	32
121	Targeted genome editing in the rare actinomycete Actinoplanes sp. SE50/110 by using the CRISPR/Cas9 System. <i>Journal of Biotechnology</i> , 2016 , 231, 122-128	3.7	31
120	Genome wide transcription start sites analysis of Xanthomonas campestris pv. campestris B100 with insights into the gum gene cluster directing the biosynthesis of the exopolysaccharide xanthan. <i>Journal of Biotechnology</i> , 2016 , 225, 18-28	3.7	31
119	The IncF plasmid pRSB225 isolated from a municipal wastewater treatment plant's on-site preflooder combining antibiotic resistance and putative virulence functions is highly related to virulence plasmids identified in pathogenic E. coli isolates. <i>Plasmid</i> , 2013 , 69, 127-37	3.3	30
118	Comparative transcriptome analysis of the biocontrol strain Bacillus amyloliquefaciens FZB42 as response to biofilm formation analyzed by RNA sequencing. <i>Journal of Biotechnology</i> , 2016 , 231, 212-223	3.7	29
117	Development of a Rhizoctonia solani AG1-IB Specific Gene Model Enables Comparative Genome Analyses between Phytopathogenic R. solani AG1-IA, AG1-IB, AG3 and AG8 Isolates. <i>PLoS ONE</i> , 2015 , 10, e0144769	3.7	28

116	Complete sequence of broad-host-range plasmid pNOR-2000 harbouring the metallo-β-lactamase gene blaVIM-2 from <i>Pseudomonas aeruginosa</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2013 , 68, 1060-5	5.1	28
115	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> , 2014 , 118, 800-13	2.8	27
114	Draft whole genome sequence of the cyanide-degrading bacterium <i>Pseudomonas pseudoalcaligenes</i> CECT5344. <i>Environmental Microbiology</i> , 2013 , 15, 253-70	5.2	27
113	Comparative genomic analysis of <i>Acinetobacter</i> spp. plasmids originating from clinical settings and environmental habitats. <i>Scientific Reports</i> , 2018 , 8, 7783	4.9	27
112	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> , 2014 , 188, 136-7	3.7	26
111	Genomics and prevalence of bacterial and archaeal isolates from biogas-producing microbiomes. <i>Biotechnology for Biofuels</i> , 2017 , 10, 264	7.8	26
110	Taxonomic analysis of the microbial community in stored sugar beets using high-throughput sequencing of different marker genes. <i>FEMS Microbiology Ecology</i> , 2016 , 92,	4.3	25
109	Linking secondary metabolites to biosynthesis genes in the fungal endophyte <i>Cyanoderma asteris</i> : The anti-cancer bisanthraquinone skyrin. <i>Journal of Biotechnology</i> , 2017 , 257, 233-239	3.7	25
108	Insights into the annotated genome sequence of <i>Methanoculleus bourgensis</i> MS2(T), related to dominant methanogens in biogas-producing plants. <i>Journal of Biotechnology</i> , 2015 , 201, 43-53	3.7	25
107	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> , 2017 , 27, 321-334	3.3	25
106	Genome-guided insight into the methylotrophy of <i>Paracoccus aminophilus</i> JCM 7686. <i>Frontiers in Microbiology</i> , 2015 , 6, 852	5.7	24
105	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> , 2015 , 203, 19-21	3.7	20
104	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> , 2017 , 12, e0177278	3.7	20
103	Draft genome sequence of the cellulolytic <i>Clostridium thermocellum</i> wild-type strain BC1 playing a role in cellulosic biomass degradation. <i>Journal of Biotechnology</i> , 2013 , 168, 62-3	3.7	20
102	Individual- and Species-Specific Skin Microbiomes in Three Different Estrildid Finch Species Revealed by 16S Amplicon Sequencing. <i>Microbial Ecology</i> , 2018 , 76, 518-529	4.4	19
101	Synthetic Biology Driven Biosynthesis of Unnatural Tropolone Sesquiterpenoids. <i>Angewandte Chemie - International Edition</i> , 2020 , 59, 23870-23878	16.4	19
100	Draft genome sequence of <i>Herbinix hemicellulosilytica</i> T3/55 T, a new thermophilic cellulose degrading bacterium isolated from a thermophilic biogas reactor. <i>Journal of Biotechnology</i> , 2015 , 214, 59-60	3.7	18
99	Frankia-Enriched Metagenomes from the Earliest Diverging Symbiotic Frankia Cluster: They Come in Teams. <i>Genome Biology and Evolution</i> , 2019 , 11, 2273-2291	3.9	18

98	Complete genome sequence of the cyanide-degrading bacterium <i>Pseudomonas pseudoalcaligenes</i> CECT5344. <i>Journal of Biotechnology</i> , 2014 , 175, 67-8	3.7	18
97	IncH-type plasmid harboring bla CTX-M-15, bla DHA-1, and qnrB4 genes recovered from animal isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2014 , 58, 3768-73	5.9	18
96	Draft genome of the xanthan producer <i>Xanthomonas campestris</i> NRRL B-1459 (ATCC 13951). <i>Journal of Biotechnology</i> , 2015 , 204, 45-6	3.7	17
95	Complete Genome Sequencing of <i>Acinetobacter baumannii</i> Strain K50 Discloses the Large Conjugative Plasmid pK50a Encoding Carbapenemase OXA-23 and Extended-Spectrum β -Lactamase GES-11. <i>Antimicrobial Agents and Chemotherapy</i> , 2018 , 62,	5.9	17
94	Optimization of β -tetrahydrocannabinolic acid synthase production in <i>Komagataella phaffii</i> via post-translational bottleneck identification. <i>Journal of Biotechnology</i> , 2018 , 272-273, 40-47	3.7	17
93	Complete genome sequence of the methanogenic neotype strain <i>Methanobacterium formicicum</i> MF(T.). <i>Journal of Biotechnology</i> , 2014 , 192 Pt A, 40-1	3.7	17
92	Rhizobial plasmid pLPU83a is able to switch between different transfer machineries depending on its genomic background. <i>FEMS Microbiology Ecology</i> , 2014 , 88, 565-78	4.3	17
91	Comparative genomics of host adaptive traits in <i>Xanthomonas translucens</i> pv. <i>graminis</i> . <i>BMC Genomics</i> , 2017 , 18, 35	4.5	16
90	Whole transcriptome RNA-Seq analysis reveals extensive cell type-specific compartmentalization in <i>Volvox carteri</i> . <i>BMC Biology</i> , 2017 , 15, 111	7.3	16
89	A Mitochondrial Autonomously Replicating Sequence from for Uniform High Level Recombinant Protein Production. <i>Frontiers in Microbiology</i> , 2017 , 8, 780	5.7	16
88	IncP-1 β 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> , 2012 , 158, 2060-2072	2.9	16
87	Complete Genome Sequence of the Barley Pathogen <i>Xanthomonas translucens</i> pv. <i>translucens</i> DSM 18974T (ATCC 19319T). <i>Genome Announcements</i> , 2016 , 4,		15
86	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> , 2018 , 18, e00254	5.3	14
85	N-Acetylborrelidin B: a new bioactive metabolite from <i>Streptomyces mutabilis</i> sp. M11. <i>Zeitschrift Fur Naturforschung - Section C Journal of Biosciences</i> , 2018 , 73, 49-57	1.7	13
84	Complete genome sequence of <i>Streptomyces reticuli</i> , an efficient degrader of crystalline cellulose. <i>Journal of Biotechnology</i> , 2016 , 222, 13-4	3.7	13
83	Draft genome sequence of the sugar beet pathogen <i>Rhizoctonia solani</i> AG2-2IIIB strain BBA69670. <i>Journal of Biotechnology</i> , 2016 , 222, 11-2	3.7	13
82	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> , 2016 , 232, 38-49	3.7	13
81	Complete genome sequence of <i>Peptoniphilus</i> sp. strain ING2-D1G isolated from a mesophilic lab-scale completely stirred tank reactor utilizing maize silage in co-digestion with pig and cattle manure for biomethanation. <i>Journal of Biotechnology</i> , 2014 , 192 Pt A, 59-61	3.7	13

80	First genomic analysis of the broad-host-range Rhizobium sp. LPU83 strain, a member of the low-genetic diversity Oregon-like Rhizobium sp. group. <i>Journal of Biotechnology</i> , 2011 , 155, 3-10	3.7	13
79	Genetic engineering in Actinoplanes sp. SE50/110 - development of an intergeneric conjugation system for the introduction of actinophage-based integrative vectors. <i>Journal of Biotechnology</i> , 2016 , 232, 79-88	3.7	13
78	Genomics of high molecular weight plasmids isolated from an on-farm biopurification system. <i>Scientific Reports</i> , 2016 , 6, 28284	4.9	12
77	Assessing genetic diversity and similarity of 435 KPC-carrying plasmids. <i>Scientific Reports</i> , 2019 , 9, 11223	4.9	12
76	Lifestyle-determining extrachromosomal replicon pAMV1 and its contribution to the carbon metabolism of the methylotrophic bacterium Paracoccus aminovorans JCM 7685. <i>Environmental Microbiology</i> , 2017 , 19, 4536-4550	5.2	12
75	Harvest of the Oleaginous Microalgae by Flocculation From Culture Based on Natural Water Sources. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018 , 6, 200	5.8	12
74	Draft genome sequence of Talaromyces islandicus ("Penicillium islandicum") WF-38-12, a neglected mold with significant biotechnological potential. <i>Journal of Biotechnology</i> , 2015 , 211, 101-2	3.7	11
73	Assembly of the Lactuca sativa, 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> , 2018 , 267, 12-18	3.7	11
72	Taxonomic profiling and metagenome analysis of a microbial community from a habitat contaminated with industrial discharges. <i>Microbial Ecology</i> , 2013 , 66, 533-50	4.4	11
71	Finished genome sequence and methylome of the cyanide-degrading Pseudomonas pseudoalcaligenes strain CECT5344 as resolved by single-molecule real-time sequencing. <i>Journal of Biotechnology</i> , 2016 , 232, 61-8	3.7	11
70	Microbiome-Triggered Transformations of Trace Organic Chemicals in the Presence of Effluent Organic Matter in Managed Aquifer Recharge (MAR) Systems. <i>Environmental Science & Technology</i> , 2018 , 52, 14342-14351	10.3	11
69	A comprehensive analysis of the Lactuca sativa, L. transcriptome during different stages of the compatible interaction with Rhizoctonia solani. <i>Scientific Reports</i> , 2019 , 9, 7221	4.9	10
68	New FeFe-hydrogenase genes identified in a metagenomic fosmid library from a municipal wastewater treatment plant as revealed by high-throughput sequencing. <i>Research in Microbiology</i> , 2015 , 166, 9-19	4	10
67	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> , 2017 , 12, e0173734	3.7	10
66	Genome improvement of the acarbose producer Actinoplanes sp. SE50/110 and annotation refinement based on RNA-seq analysis. <i>Journal of Biotechnology</i> , 2017 , 251, 112-123	3.7	9
65	Complete Genome Sequence of Acinetobacter baumannii CIP 70.10, a Susceptible Reference Strain for Comparative Genome Analyses. <i>Genome Announcements</i> , 2015 , 3,		9
64	Petroleum hydrocarbon and microbial community structure successions in marine oil-related aggregates associated with diatoms relevant for Arctic conditions. <i>Marine Pollution Bulletin</i> , 2018 , 135, 759-768	6.7	9
63	Complete genome sequence of Paenibacillus riograndensis SBR5(T), a Gram-positive diazotrophic rhizobacterium. <i>Journal of Biotechnology</i> , 2015 , 207, 30-1	3.7	9

62	Draft genome sequence of the potato pathogen <i>Rhizoctonia solani</i> AG3-PT isolate Ben3. <i>Archives of Microbiology</i> , 2017 , 199, 1065-1068	3	8
61	First draft genome sequence of the amylolytic <i>Bacillus thermoamylovorans</i> wild-type strain 1A1 isolated from a thermophilic biogas plant. <i>Journal of Biotechnology</i> , 2014 , 192 Pt A, 154-5	3.7	8
60	Genome sequence of the acid-tolerant strain <i>Rhizobium</i> sp. LPU83. <i>Journal of Biotechnology</i> , 2014 , 176, 40-1	3.7	8
59	Whole genome sequence of <i>Clostridium bornimense</i> strain M2/40 isolated from a lab-scale mesophilic two-phase biogas reactor digesting maize silage and wheat straw. <i>Journal of Biotechnology</i> , 2014 , 184, 199-200	3.7	8
58	Draft genome sequence of <i>Sinorhizobium meliloti</i> RU11/001, a model organism for flagellum structure, motility and chemotaxis. <i>Journal of Biotechnology</i> , 2013 , 168, 731-3	3.7	8
57	Binning enables efficient host genome reconstruction in cnidarian holobionts. <i>GigaScience</i> , 2018 , 7,	7.6	8
56	Insight into the structure, function and conjugative transfer of pLPU83a, an accessory plasmid of <i>Rhizobium favelukesii</i> LPU83. <i>Plasmid</i> , 2019 , 103, 9-16	3.3	7
55	Comparative Transcriptome Analysis Provides Molecular Insights into the Interaction of and with Their Host Sugar Beet. <i>Viruses</i> , 2020 , 12,	6.2	7
54	Characterization of the Actinonin Biosynthetic Gene Cluster. <i>ChemBioChem</i> , 2018 , 19, 1189	3.8	7
53	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> , 2017 , 263, 64-74	3.7	7
52	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> , 2017 , 162, 555-559	2.6	7
51	Multi-omic Directed Discovery of Cellulosomes, Polysaccharide Utilization Loci, and Lignocellulases from an Enriched Rumen Anaerobic Consortium. <i>Applied and Environmental Microbiology</i> , 2020 , 86,	4.8	7
50	Necrotrophic lifestyle of <i>Rhizoctonia solani</i> AG3-PT during interaction with its host plant potato as revealed by transcriptome analysis. <i>Scientific Reports</i> , 2020 , 10, 12574	4.9	7
49	Genomic and proteomic profiles of biofilms on microplastics are decoupled from artificial surface properties. <i>Environmental Microbiology</i> , 2021 , 23, 3099-3115	5.2	7
48	Complete Genome Sequence of the Methanogen <i>Methanoculleus bourgensis</i> BA1 Isolated from a Biogas Reactor. <i>Genome Announcements</i> , 2016 , 4,		7
47	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> , 2017 , 136, 15-22	4	6
46	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> , 2017 , 253, 55-61	3.7	6
45	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> , 2020 , 15, 7	5.6	6

44	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> , 2020 , 10, 10887	4-9	6
43	Complete Genome Sequence of <i>Herbinix luporum</i> SD1D, a New Cellulose-Degrading Bacterium Isolated from a Thermophilic Biogas Reactor. <i>Genome Announcements</i> , 2016 , 4,		6
42	The sporothriolides. A new biosynthetic family of fungal secondary metabolites. <i>Chemical Science</i> , 2020 , 11, 12477-12484	9-4	6
41	The Role of ING2-E5A in Mesophilic Biogas Reactor Systems as Deduced from Multiomics Analyses. <i>Microorganisms</i> , 2020 , 8,	4-9	6
40	Draft genome sequences of three <i>Xanthomonas translucens</i> pathovar reference strains (pv. arrhenatheri, pv. poae and pv. phlei) with different specificities for forage grasses. <i>Standards in Genomic Sciences</i> , 2016 , 11, 50		5
39	Biosynthetic reconstitution of deoxysugar phosphoramidate metalloprotease inhibitors using an N-P-bond-forming kinase. <i>Chemical Science</i> , 2019 , 10, 4486-4490	9-4	4
38	Genome Sequence of the Bile Salt-Degrading Bacterium sp. Strain Chol11, a Model Organism for Bacterial Steroid Catabolism. <i>Genome Announcements</i> , 2018 , 6,		4
37	Complete Chloroplast and Mitochondrial Genome Sequences of the Hydrocarbon Oil-Producing Green Microalga <i>Botryococcus braunii</i> Race B (Showa). <i>Genome Announcements</i> , 2016 , 4,		4
36	Complete Genome Sequence of <i>Ovine</i> subsp. Strain JIII-386 (MAP-S/type III) and Its Comparison to MAP-S/type I, MAP-C, and Complex Genomes. <i>Microorganisms</i> , 2020 , 9,	4-9	4
35	sp. nov., isolated from meat. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020 , 70, 1528-1540	2-2	4
34	Genome Analyses and Genome-Centered Metatranscriptomics of Strain SIV6, Isolated from a Thermophilic Production-Scale Biogas Fermenter. <i>Microorganisms</i> , 2019 , 8,	4-9	4
33	Candidatus <i>Frankia nodulisporulans</i> sp. nov., an <i>Alnus glutinosa</i> -infective <i>Frankia</i> species unable to grow in pure culture and able to sporulate in-planta. <i>Systematic and Applied Microbiology</i> , 2020 , 43, 1261-1274	4-2	4
32	Implementing FAIR data management within the German Network for Bioinformatics Infrastructure (de.NBI) exemplified by selected use cases. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13-4	4
31	Draft Genome Sequence of sp. Strain KarMa, a Model Organism for Monomethylamine-Degrading Nonmethylophilic Bacteria. <i>Genome Announcements</i> , 2017 , 5,		3
30	Identification of a novel aminopolycarboxylic acid siderophore gene cluster encoding the biosynthesis of ethylenediaminesuccinic acid hydroxyarginine (EDHA). <i>Metallomics</i> , 2018 , 10, 722-734	4-5	3
29	Isolation and whole genome analysis of endospore-forming bacteria from heroin. <i>Forensic Science International: Genetics</i> , 2018 , 32, 1-6	4-3	3
28	Synthetisch biologisch getriebene Biosynthese von unnatürlichen Tropolon-Sesquiterpenoiden. <i>Angewandte Chemie</i> , 2020 , 132, 24079-24087	3-6	3
27	A framework to assess the quality and impact of bioinformatics training across ELIXIR. <i>PLoS Computational Biology</i> , 2020 , 16, e1007976	5	3

26	Phytoplankton consortia as a blueprint for mutually beneficial eukaryote-bacteria ecosystems based on the biocoenosis of Botryococcus consortia. <i>Scientific Reports</i> , 2021 , 11, 1726	4.9	3
25	Genome Sequence of the Urethral Catheter Isolate <i>Pseudomonas aeruginosa</i> MH19. <i>Genome Announcements</i> , 2015 , 3,		2
24	The Peptidoglycan Biosynthesis Gene in Actinorhizal vs. Plant Type. <i>Genes</i> , 2020 , 11,	4.2	2
23	Draft Genome Sequence of <i>Streptococcus anginosus</i> BVI, a New Vaginal Pathogen Candidate. <i>Genome Announcements</i> , 2016 , 4,		2
22	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> , 2015 , 3,		2
21	Genome Sequence of the Urethral Isolate <i>Pseudomonas aeruginosa</i> RN21. <i>Genome Announcements</i> , 2015 , 3,		2
20	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> , 2021 , 7,	5.6	2
19	The de.NBI / ELIXIR-DE training platform - Bioinformatics training in Germany and across Europe within ELIXIR. <i>F1000Research</i> , 2019 , 8, 1877	3.6	2
18	Genomic and Transcriptomic Investigation of the Physiological Response of the Methylophile to 5-Aminovalerate. <i>Frontiers in Microbiology</i> , 2021 , 12, 664598	5.7	2
17	A novel plant-fungal association reveals fundamental sRNA and gene expression reprogramming at the onset of symbiosis. <i>BMC Biology</i> , 2021 , 19, 171	7.3	2
16	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> , 2017 , 257, 178-186	3.7	1
15	Complete Genome Sequence of the Clinical Strain <i>Acinetobacter baumannii</i> R2090 Carrying the Chromosomally Encoded Metallo- β -Lactamase Gene blaNDM-1. <i>Genome Announcements</i> , 2015 , 3,		1
14	Draft genome sequence of <i>Streptomyces tunisialis</i> DSM 105760. <i>Archives of Microbiology</i> , 2020 , 202, 2013-2017	3	1
13	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> , 2016 , 4,		1
12	Draft Genome Sequence of the <i>Xanthomonas bromi</i> Type Strain LMG 947. <i>Genome Announcements</i> , 2016 , 4,		1
11	Complete Draft Genome Sequence of <i>Escherichia coli</i> JF733. <i>Genome Announcements</i> , 2016 , 4,		1
10	Complete mitochondrial genome of the scleractinian coral <i>Porites rus</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 3695-6	1.3	1
9	Draft Genome Sequence of <i>Pseudomonas aeruginosa</i> Strain WS394, a Multidrug-Resistant and Highly Cytotoxic Wound Isolate from Chronic Ulcus Cruris. <i>Genome Announcements</i> , 2014 , 2,		1

8	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> , 2021 , 12, 734039	5.7	1
7	The de.NBI / ELIXIR-DE training platform - Bioinformatics training in Germany and across Europe within ELIXIR. <i>F1000Research</i> , 2019 , 8,	3.6	1
6	sp. nov., isolated from beef. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020 , 70, 292-301	2.2	1
5	A Regulator Based "Semi-Targeted" Approach to Activate Silent Biosynthetic Gene Clusters. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	1
4	Seventeen Ustilaginaceae High-Quality Genome Sequences Allow Phylogenomic Analysis and Provide Insights into Secondary Metabolite Synthesis.. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022 , 8,	5.6	1
3	Biosynthetic potential of the endophytic fungus Helotiales sp. BL73 revealed via compound identification and genome mining.. <i>Applied and Environmental Microbiology</i> , 2022 , aem0251021	4.8	0
2	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> , 2021 , 3, lqab085	3.7	0
1	<i>Ustilago maydis</i> Metabolic Characterization and Growth Quantification with a Genome-Scale Metabolic Model. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022 , 8, 524	5.6	0