

Jochen Blom

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/696204/publications.pdf>

Version: 2024-02-01

177
papers

6,192
citations

94269

37
h-index

98622

67
g-index

188
all docs

188
docs citations

188
times ranked

7056
citing authors

#	ARTICLE	IF	CITATIONS
1	EDGAR: A software framework for the comparative analysis of prokaryotic genomes. BMC Bioinformatics, 2009, 10, 154.	1.2	401
2	EDGAR 2.0: an enhanced software platform for comparative gene content analyses. Nucleic Acids Research, 2016, 44, W22-W28.	6.5	398
3	Bacillus amyloliquefaciens, Bacillus velezensis, and Bacillus siamensis Form an "Operational Group B. amyloliquefaciens" within the B. subtilis Species Complex. Frontiers in Microbiology, 2017, 8, 22.	1.5	296
4	Relationship of Bacillus amyloliquefaciens clades associated with strains DSM 7T and FZB42T: a proposal for Bacillus amyloliquefaciens subsp. amyloliquefaciens subsp. nov. and Bacillus amyloliquefaciens subsp. plantarum subsp. nov. based on complete genome sequence comparisons. International Journal of Systematic and Evolutionary Microbiology, 2011, 61, 1786-1801.	0.8	265
5	Bakta: rapid and standardized annotation of bacterial genomes via alignment-free sequence identification. Microbial Genomics, 2021, 7, .	1.0	168
6	Whole-genome comparison of disease and carriage strains provides insights into virulence evolution in <i>Neisseria meningitidis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3473-3478.	3.3	159
7	Brucella vulpis sp. nov., isolated from mandibular lymph nodes of red foxes (Vulpes vulpes). International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 2090-2098.	0.8	155
8	Pangenomic Study of Corynebacterium diphtheriae That Provides Insights into the Genomic Diversity of Pathogenic Isolates from Cases of Classical Diphtheria, Endocarditis, and Pneumonia. Journal of Bacteriology, 2012, 194, 3199-3215.	1.0	142
9	Insect pathogenicity in plant-beneficial pseudomonads: phylogenetic distribution and comparative genomics. ISME Journal, 2016, 10, 2527-2542.	4.4	127
10	Genome Data Provides High Support for Generic Boundaries in Burkholderia Sensu Lato. Frontiers in Microbiology, 2017, 8, 1154.	1.5	122
11	Phylogenomic re-assessment of the thermophilic genus Geobacillus. Systematic and Applied Microbiology, 2016, 39, 527-533.	1.2	116
12	An assemblage of Frankia Cluster II strains from California contains the canonical nod genes and also the sulfotransferase gene nodH. BMC Genomics, 2016, 17, 796.	1.2	97
13	Non-pathogenic <i>Rhizobium radiobacter</i> F4 deploys plant beneficial activity independent of its host <i>Piriformospora indica</i> . ISME Journal, 2016, 10, 871-884.	4.4	93
14	Experimental Evaluation of Host Adaptation of Lactobacillus reuteri to Different Vertebrate Species. Applied and Environmental Microbiology, 2017, 83, .	1.4	87
15	Diversification and niche adaptations of <i>Nitrospina</i> -like bacteria in the polyextreme interfaces of Red Sea brines. ISME Journal, 2016, 10, 1383-1399.	4.4	85
16	Isolation of a novel "atypical" Brucella strain from a bluespotted ribbontail ray (Taeniura lymma). Antonie Van Leeuwenhoek, 2017, 110, 221-234.	0.7	74
17	Genome analysis of the sugar beet pathogen Rhizoctonia solani AG2-2IIIB revealed high numbers in secreted proteins and cell wall degrading enzymes. BMC Genomics, 2016, 17, 245.	1.2	69
18	Diversity of phytobeneficial traits revealed by whole-genome analysis of worldwide-isolated phenazine-producing <i>Pseudomonas</i> spp.. Environmental Microbiology, 2019, 21, 437-455.	1.8	66

#	ARTICLE	IF	CITATIONS
19	EDGAR3.0: comparative genomics and phylogenomics on a scalable infrastructure. <i>Nucleic Acids Research</i> , 2021, 49, W185-W192.	6.5	65
20	Genomic diversification of giant enteric symbionts reflects host dietary lifestyles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7592-E7601.	3.3	64
21	Genome-informed <i>Bradyrhizobium</i> taxonomy: where to from here?. <i>Systematic and Applied Microbiology</i> , 2019, 42, 427-439.	1.2	62
22	Metagenomic binning reveals versatile nutrient cycling and distinct adaptive features in alphaproteobacterial symbionts of marine sponges. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	61
23	Comparative genomics reveals adaptations of a halotolerant thaumarchaeon in the interfaces of brine pools in the Red Sea. <i>ISME Journal</i> , 2015, 9, 396-411.	4.4	60
24	Genomic Avenue to Avian Colisepticemia. <i>MBio</i> , 2015, 6, .	1.8	59
25	Pan-genome analysis of <i>Aeromonas hydrophila</i> , <i>Aeromonas veronii</i> and <i>Aeromonas caviae</i> indicates phylogenomic diversity and greater pathogenic potential for <i>Aeromonas hydrophila</i> . <i>Antonie Van Leeuwenhoek</i> , 2016, 109, 945-956.	0.7	58
26	Whole genome sequence and manual annotation of <i>Clostridium autoethanogenum</i> , an industrially relevant bacterium. <i>BMC Genomics</i> , 2015, 16, 1085.	1.2	56
27	The Change of a Medically Important Genus: Worldwide Occurrence of Genetically Diverse Novel <i>Brucella</i> Species in Exotic Frogs. <i>PLoS ONE</i> , 2016, 11, e0168872.	1.1	56
28	Mixta gen. nov., a new genus in the Erwiniaceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1396-1407.	0.8	53
29	Genomic, Physiologic, and Symbiotic Characterization of <i>Serratia marcescens</i> Strains Isolated from the Mosquito <i>Anopheles stephensi</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1483.	1.5	52
30	All ANIs are not created equal: implications for prokaryotic species boundaries and integration of ANIs into polyphasic taxonomy. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2937-2948.	0.8	51
31	Comparative genomics of <i>Aeromonas veronii</i> : Identification of a pathotype impacting aquaculture globally. <i>PLoS ONE</i> , 2019, 14, e0221018.	1.1	50
32	Phylogenomic resolution of the bacterial genus <i>Pantoea</i> and its relationship with <i>Erwinia</i> and <i>Tatumella</i> . <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 1287-1309.	0.7	48
33	<i>Parendozoicomonas haliclona</i> gen. nov. sp. nov. isolated from a marine sponge of the genus <i>Haliclona</i> and description of the family <i>Endozoicomonadaceae</i> fam. nov. comprising the genera <i>Endozoicomonas</i> , <i>Parendozoicomonas</i> , and <i>Kistimonas</i> . <i>Systematic and Applied Microbiology</i> , 2018, 41, 73-84.	1.2	48
34	Adherence and invasive properties of <i>Corynebacterium diphtheriae</i> strains correlates with the predicted membrane-associated and secreted proteome. <i>BMC Genomics</i> , 2015, 16, 765.	1.2	47
35	A lack of genetic basis for biovar differentiation in clinically important <i>Corynebacterium diphtheriae</i> from whole genome sequencing. <i>Infection, Genetics and Evolution</i> , 2014, 21, 54-57.	1.0	43
36	Cold-adapted <i>Bacilli</i> isolated from the Qinghai-Tibetan Plateau are able to promote plant growth in extreme environments. <i>Environmental Microbiology</i> , 2019, 21, 3505-3526.	1.8	42

#	ARTICLE	IF	CITATIONS
37	Whole genome analysis calls for a taxonomic rearrangement of the genus <i>Colwellia</i> . Antonie Van Leeuwenhoek, 2020, 113, 919-931.	0.7	42
38	Genomic analysis of endemic clones of toxigenic and non-toxigenic <i>Corynebacterium diphtheriae</i> in Belarus during and after the major epidemic in 1990s. BMC Genomics, 2017, 18, 873.	1.2	41
39	Genomic Analysis of <i>Bacillus</i> sp. Strain B25, a Biocontrol Agent of Maize Pathogen <i>Fusarium verticillioides</i> . Current Microbiology, 2018, 75, 247-255.	1.0	40
40	Analysis of the Genome and Metabolome of Marine Myxobacteria Reveals High Potential for Biosynthesis of Novel Specialized Metabolites. Scientific Reports, 2018, 8, 16600.	1.6	40
41	The Complete Genome of <i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> CAU B946 Contains a Gene Cluster for Nonribosomal Synthesis of Iturin A. Journal of Bacteriology, 2012, 194, 1845-1846.	1.0	39
42	Comparative Genomics of <i>Streptococcus thermophilus</i> Support Important Traits Concerning the Evolution, Biology and Technological Properties of the Species. Frontiers in Microbiology, 2019, 10, 2916.	1.5	39
43	Comparative functional pan-genome analyses to build connections between genomic dynamics and phenotypic evolution in polycyclic aromatic hydrocarbon metabolism in the genus <i>Mycobacterium</i> . BMC Evolutionary Biology, 2015, 15, 21.	3.2	38
44	Large genomic differences between <i>Moraxella bovoculi</i> isolates acquired from the eyes of cattle with infectious bovine keratoconjunctivitis versus the deep nasopharynx of asymptomatic cattle. Veterinary Research, 2016, 47, 31.	1.1	38
45	Characterization of <i>Bathyarchaeota</i> genomes assembled from metagenomes of biofilms residing in mesophilic and thermophilic biogas reactors. Biotechnology for Biofuels, 2018, 11, 167.	6.2	38
46	Comprehensive Genomic Analyses of the OM43 Clade, Including a Novel Species from the Red Sea, Indicate Ecotype Differentiation among Marine Methylotrophs. Applied and Environmental Microbiology, 2016, 82, 1215-1226.	1.4	37
47	Emended description of the genus <i>Phytobacter</i> , its type species <i>Phytobacter diazotrophicus</i> (Zhang) Tj ETQq1 1 0.784314 rgBT /Over Evolutionary Microbiology, 2018, 68, 176-184.	0.8	37
48	Genome-based reclassification of <i>Lactobacillus casei</i> : emended classification and description of the species <i>Lactobacillus zeae</i> . International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3755-3762.	0.8	36
49	Genomic insights into the virulence and salt tolerance of <i>Staphylococcus equorum</i> . Scientific Reports, 2017, 7, 5383.	1.6	34
50	Comprehensive molecular, genomic and phenotypic analysis of a major clone of <i>Enterococcus faecalis</i> MLST ST40. BMC Genomics, 2015, 16, 175.	1.2	33
51	Frankia-Enriched Metagenomes from the Earliest Diverging Symbiotic Frankia Cluster: They Come in Teams. Genome Biology and Evolution, 2019, 11, 2273-2291.	1.1	33
52	Pantocin A, a peptide-derived antibiotic involved in biological control by plant-associated <i>Pantoea</i> species. Archives of Microbiology, 2019, 201, 713-722.	1.0	33
53	<i>Erwinia gerundensis</i> sp. nov., a cosmopolitan epiphyte originally isolated from pome fruit trees. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 1583-1592.	0.8	33
54	Development of a <i>Rhizoctonia solani</i> AG1-IB Specific Gene Model Enables Comparative Genome Analyses between Phytopathogenic <i>R. solani</i> AG1-IA, AG1-IB, AG3 and AG8 Isolates. PLoS ONE, 2015, 10, e0144769.	1.1	32

#	ARTICLE	IF	CITATIONS
55	The Emerging Fish Pathogen <i>Flavobacterium spartansii</i> Isolated from Chinook Salmon: Comparative Genome Analysis and Molecular Manipulation. <i>Frontiers in Microbiology</i> , 2017, 8, 2339.	1.5	32
56	Defining the Species <i>Micromonospora saelicesensis</i> and <i>Micromonospora noduli</i> Under the Framework of Genomics. <i>Frontiers in Microbiology</i> , 2018, 9, 1360.	1.5	32
57	The complete genome sequence of the yogurt isolate <i>Streptococcus thermophilus</i> ACA-DC 2. <i>Standards in Genomic Sciences</i> , 2017, 12, 18.	1.5	31
58	Genome analysis reveals insights of the endophytic <i>Bacillus toyonensis</i> BAC3151 as a potentially novel agent for biocontrol of plant pathogens. <i>World Journal of Microbiology and Biotechnology</i> , 2017, 33, 185.	1.7	30
59	Genome sequence of the endophytic strain <i>Enterobacter</i> sp. J49, a potential biofertilizer for peanut and maize. <i>Genomics</i> , 2019, 111, 913-920.	1.3	30
60	Comparative genomics and pathogenicity potential of members of the <i>Pseudomonas syringae</i> species complex on <i>Prunus</i> spp. <i>BMC Genomics</i> , 2019, 20, 172.	1.2	30
61	Identification of Antimicrobial Resistance Determinants in <i>Aeromonas veronii</i> Strain MS-17-88 Recovered From Channel Catfish (<i>Ictalurus punctatus</i>). <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 348.	1.8	30
62	Draft Genome Sequence of the Commercial Biocontrol Strain <i>Pantoea agglomerans</i> P10c. <i>Genome Announcements</i> , 2015, 3, .	0.8	29
63	Strain <i>Serratia</i> sp. S119: A potential biofertilizer for peanut and maize and a model bacterium to study phosphate solubilization mechanisms. <i>Applied Soil Ecology</i> , 2018, 126, 107-112.	2.1	28
64	Complete Genome Sequence of <i>Weissella hellenica</i> 0916-4-2 and Its Comparative Genomic Analysis. <i>Frontiers in Microbiology</i> , 2019, 10, 1619.	1.5	28
65	Metagenomics-Guided Survey, Isolation, and Characterization of Uranium Resistant Microbiota from the Savannah River Site, USA. <i>Genes</i> , 2019, 10, 325.	1.0	28
66	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.	1.9	27
67	Gene Loss and Lineage-Specific Restriction-Modification Systems Associated with Niche Differentiation in the <i>Campylobacter jejuni</i> Sequence Type 403 Clonal Complex. <i>Applied and Environmental Microbiology</i> , 2015, 81, 3641-3647.	1.4	27
68	Comparative genomics reveals complex natural product biosynthesis capacities and carbon metabolism across host-associated and free-living <i>Aquimarina</i> (<i>Bacteroidetes</i>). <i>Frontiers in Microbiology</i> , 2017, 8, 1750.	1.5	27
69	Complete genome sequence and comparative genomic analysis of <i>Enterococcus faecalis</i> EF-2001, a probiotic bacterium. <i>Genomics</i> , 2021, 113, 1534-1542.	1.3	27
70	Evolution of Anabaenopeptin Peptide Structural Variability in the Cyanobacterium <i>Planktothrix</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 219.	1.5	26
71	Comparative Genome Sequencing Reveals Within-Host Genetic Changes in <i>Neisseria meningitidis</i> during Invasive Disease. <i>PLoS ONE</i> , 2017, 12, e0169892.	1.1	26
72	<i>Xanthomonas euroxanthea</i> sp. nov., a new xanthomonad species including pathogenic and non-pathogenic strains of walnut. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 6024-6031.	0.8	25

#	ARTICLE	IF	CITATIONS
73	<i>Corynebacterium pseudotuberculosis</i> Pneumonia in a Veterinary Student Infected During Laboratory Work. <i>Open Forum Infectious Diseases</i> , 2015, 2, ofv053.	0.4	24
74	Complete Genome Sequence of the Barley Pathogen <i>Xanthomonas translucens</i> pv. <i>translucens</i> DSM 18974 ^T (ATCC 19319 ^T). <i>Genome Announcements</i> , 2016, 4, .	0.8	24
75	Comparative genomics of host adaptive traits in <i>Xanthomonas translucens</i> pv. <i>graminis</i> . <i>BMC Genomics</i> , 2017, 18, 35.	1.2	24
76	Revisiting the Taxonomic Status of the Biomedically and Industrially Important Genus <i>Amycolatopsis</i> , Using a Phylogenomic Approach. <i>Frontiers in Microbiology</i> , 2018, 9, 2281.	1.5	23
77	Comparative Genomics of <i>Lactobacillus acidipiscis</i> ACA-DC 1533 Isolated From Traditional Greek Kopanisti Cheese Against Species Within the <i>Lactobacillus salivarius</i> Clade. <i>Frontiers in Microbiology</i> , 2018, 9, 1244.	1.5	22
78	Comparative Genomics and Metabolic Analysis Reveals Peculiar Characteristics of <i>Rhodococcus opacus</i> Strain M213 Particularly for Naphthalene Degradation. <i>PLoS ONE</i> , 2016, 11, e0161032.	1.1	21
79	Phylogenomic, Pan-genomic, Pathogenomic and Evolutionary Genomic Insights into the Agronomically Relevant Enterobacteria <i>Pantoea ananatis</i> and <i>Pantoea stewartii</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1755.	1.5	20
80	Comparative Genomics of <i>Aeromonas hydrophila</i> Secretion Systems and Mutational Analysis of <i>hcp1</i> and <i>vgrG1</i> Genes From T6SS. <i>Frontiers in Microbiology</i> , 2018, 9, 3216.	1.5	20
81	<i>Erysipelothrix anatis</i> sp. nov., <i>Erysipelothrix aquatica</i> sp. nov. and <i>Erysipelothrix urinaevulpis</i> sp. nov., three novel species of the genus, and emended description of <i>Erysipelothrix</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	20
82	Specific surface glycan decorations enable antimicrobial peptide resistance in plantâ€beneficial pseudomonads with insectâ€pathogenic properties. <i>Environmental Microbiology</i> , 2016, 18, 4265-4281.	1.8	19
83	<i>Acinetobacter baumannii</i> in manure and anaerobic digestates of German biogas plants. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	19
84	<i>Phytobacter palmae</i> sp. nov., a novel endophytic, N2 fixing, plant growth promoting Gammaproteobacterium isolated from oil palm (<i>Elaeis guineensis</i> Jacq.). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 841-848.	0.8	19
85	<i>Pseudomonas carnis</i> sp. nov., isolated from meat. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1528-1540.	0.8	19
86	Whole Genome Sequencing of 39 Invasive <i>Streptococcus pneumoniae</i> Sequence Type 199 Isolates Revealed Switches from Serotype 19A to 15B. <i>PLoS ONE</i> , 2017, 12, e0169370.	1.1	19
87	<i>Mycoplasma miroungirhinis</i> sp. nov. and <i>Mycoplasma miroungigenitalium</i> sp. nov., isolated from northern elephant seals (<i>Mirounga angustirostris</i>), <i>Mycoplasma phocoenae</i> sp. nov., isolated from harbour porpoise (<i>Phocoena phocoena</i>), and <i>Mycoplasma phocoeninasale</i> sp. nov., isolated from harbour porpoise and California sea lions (<i>Zalophus californianus</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	19
88	Complete Genome Sequence of the Plant Growth-Promoting Bacterium <i>Hartmannibacter diazotrophicus</i> Strain E19^T. <i>International Journal of Genomics</i> , 2019, 2019, 1-12.	0.8	17
89	Subspecies Typing of <i>Streptococcus agalactiae</i> Based on Ribosomal Subunit Protein Mass Variation by MALDI-TOF MS. <i>Frontiers in Microbiology</i> , 2019, 10, 471.	1.5	17
90	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, 126134.	1.2	17

#	ARTICLE	IF	CITATIONS
91	<i>Pseudomonas abyssi</i> sp. nov., isolated from the abyssopelagic water of the Mariana Trench. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2462-2467.	0.8	17
92	Reclassification of <i>Micrococcus aloeverae</i> and <i>Micrococcus yunnanensis</i> as later heterotypic synonyms of <i>Micrococcus luteus</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3512-3518.	0.8	17
93	<i>Sneathia vaginalis</i> sp. nov. (Fusobacteriales, Leptotrichiaceae) as a replacement of the species <i>Sneathia amnii</i> ™ Harwich et al. 2012 and <i>Leptotrichia amnionii</i> ™ Shukla et al. 2002, and emended description of <i>Sneathia</i> Collins et al. 2001. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	17
94	Complete Genome Sequence of the Porcine Isolate <i>Enterococcus faecalis</i> D32. <i>Journal of Bacteriology</i> , 2012, 194, 5490-5491.	1.0	16
95	Comparative analysis of the Hrp pathogenicity island of <i>Rubus</i> - and <i>Spiraeoideae</i> -infecting <i>Erwinia amylovora</i> strains identifies the IT region as a remnant of an integrative conjugative element. <i>Gene</i> , 2012, 504, 6-12.	1.0	16
96	<i>Streptococcus vicugnae</i> sp. nov., isolated from faeces of alpacas (<i>Vicugna pacos</i>) and cattle (<i>Bos</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 respiratory tract of California sea lions (<i>Zalophus californianus</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	16
97	Evolutionary and biogeographical implications of degraded LAGLIDADG endonuclease functionality and group I intron occurrence in stony corals (<i>Scleractinia</i>) and mushroom corals (<i>Corallimorpharia</i>). <i>PLoS ONE</i> , 2017, 12, e0173734.	1.1	16
98	Genomic characterization of two novel SAR11 isolates from the Red Sea, including the first strain of the SAR11 Ib clade. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	15
99	Comparative genomic analyses reveal diverse virulence factors and antimicrobial resistance mechanisms in clinical <i>Elizabethkingia meningoseptica</i> strains. <i>PLoS ONE</i> , 2019, 14, e0222648.	1.1	15
100	<i>Xanthomonas hydrangeae</i> sp. nov., a novel plant pathogen isolated from <i>Hydrangea arborescens</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	15
101	Genome-Based Characterization of Biological Processes That Differentiate Closely Related Bacteria. <i>Frontiers in Microbiology</i> , 2018, 9, 113.	1.5	14
102	High diversity of <i>Vibrio</i> spp. associated with different ecological niches in a marine aquaria system and description of <i>Vibrio aquimaris</i> sp. nov. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126123.	1.2	14
103	Expanding the host range: infection of a reptilian host (<i>Furcifer pardalis</i>) by an atypical <i>Brucella</i> strain. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1531-1537.	0.7	14
104	Genomic diversity in flavobacterial pathogens of aquatic origin. <i>Microbial Pathogenesis</i> , 2020, 142, 104053.	1.3	14
105	Taxonomic reassessment of the genus <i>Pseudocitrobacter</i> using whole genome sequencing: <i>Pseudocitrobacter anthropi</i> is a later heterotypic synonym of <i>Pseudocitrobacter faecalis</i> and description of <i>Pseudocitrobacter vendiensis</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1315-1320.	0.8	14
106	<i>Streptobacillus canis</i> sp. nov. isolated from a dog. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2648-2656.	0.8	14
107	<i>Streptococcus catagoni</i> sp. nov., isolated from the respiratory tract of diseased Chacoan peccaries (<i>Catagonus wagneri</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5734-5739.	0.8	14
108	Comparative genomics of the fish pathogens <i>Edwardsiella ictaluri</i> 93-146 and <i>Edwardsiella piscicida</i> C07-087. <i>Microbial Genomics</i> , 2020, 6, .	1.0	14

#	ARTICLE	IF	CITATIONS
109	Integrative conjugative elements of the ICEPan family play a potential role in <i>Pantoea ananatis</i> ecological diversification and antibiosis. <i>Frontiers in Microbiology</i> , 2015, 6, 576.	1.5	13
110	Complete Sequence of Probiotic Symbioflor 2 <i>Escherichia coli</i> Strain G3/10 and Draft Sequences of Symbioflor 2 <i>E. coli</i> Strains G1/2, G4/9, G5, G6/7, and G8. <i>Genome Announcements</i> , 2015, 3, .	0.8	13
111	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> , 2018, 267, 12-18.	1.9	13
112	<i>Prevotella hominis</i> sp. nov., isolated from human faeces. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4767-4773.	0.8	13
113	Complete Genome Sequence of Ovine <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> Strain JIII-386 (MAP-S/type III) and Its Comparison to MAP-S/type I, MAP-C, and <i>M. avium</i> Complex Genomes. <i>Microorganisms</i> , 2021, 9, 70.	1.6	13
114	Phylogenomic grouping of <i>Listeria monocytogenes</i> . <i>Canadian Journal of Microbiology</i> , 2015, 61, 637-646.	0.8	12
115	Draft genome sequence of the potato pathogen <i>Rhizoctonia solani</i> AG3-PT isolate Ben3. <i>Archives of Microbiology</i> , 2017, 199, 1065-1068.	1.0	12
116	Complete Genome Sequences of Three Isolates of <i>Xanthomonas fragariae</i> , the Bacterium Responsible for Angular Leaf Spots on Strawberry Plants. <i>Genome Announcements</i> , 2017, 5, .	0.8	12
117	Phytoplankton consortia as a blueprint for mutually beneficial eukaryote-bacteria ecosystems based on the biocoenosis of <i>Botryococcus</i> consortia. <i>Scientific Reports</i> , 2021, 11, 1726.	1.6	12
118	<i>Acinetobacter stercoris</i> sp. nov. isolated from output source of a mesophilic german biogas plant with anaerobic operating conditions. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 235-251.	0.7	12
119	Proposal to reclassify <i>Streptobacillus hongkongensis</i> into a novel genus as <i>Pseudostreptobacillus hongkongensis</i> gen. nov., comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2366-2368.	0.8	12
120	<i>Pseudomonas piscis</i> sp. nov., isolated from the profound head ulcers of farmed Murray cod (<i>Maccullochella peelii peelii</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2732-2739.	0.8	12
121	Comparative Genomics of Potato Common Scab-Causing <i>Streptomyces</i> spp. Displaying Varying Virulence. <i>Frontiers in Microbiology</i> , 2021, 12, 716522.	1.5	11
122	Proposal to reclassify <i>Leptotrichia goodfellowii</i> into a novel genus as <i>Pseudoleptotrichia goodfellowii</i> gen. nov., comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2084-2088.	0.8	11
123	The synergistic effect of concatenation in phylogenomics: the case in <i>Pantoea</i> . <i>PeerJ</i> , 2019, 7, e6698.	0.9	11
124	Comparison of clinical and immunological findings in gnotobiotic piglets infected with <i>Escherichia coli</i> O104:H4 outbreak strain and EHEC O157:H7. <i>Gut Pathogens</i> , 2017, 9, 30.	1.6	10
125	Comparative Genomics of <i>Xanthomonas euroxanthea</i> and <i>Xanthomonas arboricola</i> pv. <i>juglandis</i> Strains Isolated from a Single Walnut Host Tree. <i>Microorganisms</i> , 2021, 9, 624.	1.6	10
126	<i>Lactobacillus suantsaii</i> sp. nov., isolated from suan-tsai, a traditional Taiwanese fermented mustard green. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1484-1489.	0.8	10

#	ARTICLE	IF	CITATIONS
127	<i>Cochlodiniinecator piscidefendens</i> gen. nov., sp. nov., an algicidal bacterium against the ichthyotoxic dinoflagellate <i>Cochlodinium polykrikoides</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	10
128	Differences between predicted outer membrane proteins of genotype 1 and <i>Mannheimia haemolytica</i> . <i>BMC Microbiology</i> , 2020, 20, 250.	1.3	9
129	<i>Pseudomonas bubulae</i> sp. nov., isolated from beef. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 292-301.	0.8	9
130	<i>Oceanivirga miroungae</i> sp. nov., isolated from oral cavity of northern elephant seal (<i>Mirounga</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622 3037-3048.	0.8	9
131	Comparative genomics of <i>Xanthomonas fragariae</i> and <i>Xanthomonas arboricola</i> pv. <i>fragariae</i> reveals intra- and interspecies variations. <i>Phytopathology Research</i> , 2020, 2, .	0.9	8
132	<i>Pseudomonas paracarnis</i> sp. nov., isolated from refrigerated beef. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	8
133	Satellite-Like W-Elements: Repetitive, Transcribed, and Putative Mobile Genetic Factors with Potential Roles for Biology and Evolution of <i>Schistosoma mansoni</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	8
134	The status of the genus <i>Prolinoborus</i> (Pot et al. 1992) and the species <i>Prolinoborus fasciculus</i> (Pot et) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622	0.8	8
135	Analysis of the complete genome sequence of the archaeon <i>Pyrococcus chitonophagus</i> DSM 10152 (formerly <i>Thermococcus chitonophagus</i>). <i>Extremophiles</i> , 2016, 20, 351-361.	0.9	7
136	High-Quality Draft Genome Sequence of <i>Xanthomonas</i> sp. Strain CPBF 424, a Walnut-Pathogenic Strain with Atypical Features. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	7
137	<i>Pseudomonas paraversuta</i> sp. nov. isolated from refrigerated dry-aged beef. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	7
138	Systems and synthetic biology perspective of the versatile plant-pathogenic and polysaccharide-producing bacterium <i>Xanthomonas campestris</i> . <i>Microbiology (United Kingdom)</i> , 2017, 163, 1117-1144.	0.7	7
139	First complete genome sequence of <i>Bacillus glycinifermentans</i> B-27. <i>Journal of Biotechnology</i> , 2017, 257, 187-191.	1.9	6
140	High-Quality Draft Genome Sequences of Five <i>Xanthomonas arboricola</i> pv. <i>fragariae</i> Isolates. <i>Genome Announcements</i> , 2018, 6, .	0.8	6
141	Genomic and phenotypic analysis of siderophore-producing <i>Rhodococcus qingshengii</i> strain S10 isolated from an arid weathered serpentine rock environment. <i>Archives of Microbiology</i> , 2021, 203, 855-860.	1.0	6
142	Genome-wide comparison of four MRSA clinical isolates from Germany and Hungary. <i>PeerJ</i> , 2021, 9, e10185.	0.9	6
143	Comparative Methylome Analysis of the Occasional Ruminant Respiratory Pathogen <i>Bibersteinia trehalosi</i> . <i>PLoS ONE</i> , 2016, 11, e0161499.	1.1	6
144	<i>Streptomyces dysideae</i> sp. nov., isolated from a marine Mediterranean sponge <i>Dysidea tupha</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	6

#	ARTICLE	IF	CITATIONS
145	Rapid protein alignment in the cloud: HAMOND combines fast DIAMOND alignments with Hadoop parallelism. <i>Journal of Biotechnology</i> , 2017, 257, 58-60.	1.9	5
146	High-Quality Draft Genome Sequence of <i>Xanthomonas arboricola</i> pv. <i>juglandis</i> CPBF 1521, Isolated from Leaves of a Symptomatic Walnut Tree in Portugal without a Past of Phytosanitary Treatment. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	5
147	High-Quality Draft Genome Sequence of <i>Pseudomonas wadenswilerensis</i> CCOS 864 T. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	5
148	The genome of a novel isolate of <i>Prochlorococcus</i> from the Red Sea contains transcribed genes for compatible solute biosynthesis. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	5
149	Updated Genome Sequence and Annotation for the Full Genome of <i>Pseudomonas protegens</i> CHA0. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
150	Estimation of pathogenic potential of an environmental <i>Pseudomonas aeruginosa</i> isolate using comparative genomics. <i>Scientific Reports</i> , 2021, 11, 1370.	1.6	5
151	<i>Streptomyces phaeopurpureus</i> Shinobu 1957 (Approved Lists 1980) and <i>Streptomyces griseorubiginosus</i> (Ryabova and Preobrazhenskaya 1957) Pridham et al. 1958 (Approved Lists 1980) are heterotypic subjective synonyms. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 3111-3116.	0.8	5
152	Genome Analyses of the Less Aggressive <i>Rhizoctonia solani</i> AG1-IB Isolates 1/2/21 and O8/2 Compared to the Reference AG1-IB Isolate 7/3/14. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 832.	1.5	5
153	Draft genome of formaldehyde-degrading strain, <i>Pseudomonas montellii</i> IOFA19. <i>Marine Genomics</i> , 2014, 15, 1-2.	0.4	4
154	Complete Genome Sequence of the Cyanogenic Phosphate-Solubilizing <i>Pseudomonas</i> sp. Strain CCOS 191, a Close Relative of <i>Pseudomonas mosselii</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	4
155	Genomic analysis of a novel <i>Rhodococcus</i> (<i>Prescottella</i>) <i>equi</i> isolate from a bovine host. <i>Archives of Microbiology</i> , 2019, 201, 1317-1321.	1.0	4
156	<i>Streptomyces ciscaucasicus</i> Sveshnikova et al. 1983 is a later subjective synonym of <i>Streptomyces canus</i> Heinemann et al. 1953. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 42-46.	0.8	4
157	Genome sequence data of <i>Bacillus velezensis</i> BP1.2A and BT2.4. <i>Data in Brief</i> , 2022, 41, 107978.	0.5	4
158	Draft Genome Sequence of <i>Pseudomonas aeruginosa</i> Strain WS136, a Highly Cytotoxic ExoS-Positive Wound Isolate Recovered from <i>Pyoderma Gangrenosum</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	3
159	Draft Genome Sequence of the <i>Xanthomonas bromi</i> Type Strain LMG 947. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
160	Comparative Genomic Analysis of the Biotechnological Potential of the Novel Species <i>Pseudomonas wadenswilerensis</i> CCOS 864T and <i>Pseudomonas reidholzensis</i> CCOS 865T. <i>Diversity</i> , 2019, 11, 204.	0.7	3
161	Complete Genome Sequence of the Corallopyronin A-Producing <i>Myxobacterium Corallococcus coralloides</i> B035. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
162	The de.NBI / ELIXIR-DE training platform - Bioinformatics training in Germany and across Europe within ELIXIR. <i>F1000Research</i> , 2019, 8, 1877.	0.8	3

#	ARTICLE	IF	CITATIONS
163	A dominant clonal lineage of <i>Streptococcus uberis</i> in cattle in Germany. <i>Antonie Van Leeuwenhoek</i> , 2022, , 1.	0.7	3
164	Differentiation of the <i>Xanthomonas hortorum</i> “ <i>Xanthomonas hydrangeae</i> Species Complex Using Sensitive and Selective LAMP Assays. <i>Frontiers in Agronomy</i> , 2022, 4, .	1.5	3
165	Genome Sequence of the Urethral Isolate <i>Pseudomonas aeruginosa</i> RN21. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
166	Genome Sequence of the Urethral Catheter Isolate <i>Pseudomonas aeruginosa</i> MH19. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
167	High-Quality Draft Genome Sequence of <i>Pseudomonas reidholzensis</i> Strain CCOS 865 T. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
168	A simple, rapid typing method for <i>Streptococcus agalactiae</i> based on ribosomal subunit proteins by MALDI-TOF MS. <i>Scientific Reports</i> , 2020, 10, 8788.	1.6	2
169	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, .	0.8	1
170	Whole genome sequences of a free-living <i>Pseudomonas</i> sp. strain ML96 isolated from a freshwater Maar Lake. <i>Marine Genomics</i> , 2015, 24, 219-221.	0.4	1
171	Detection and Characterization of Endobacteria in the Fungal Endophyte <i>Piriformospora indica</i> . , 2017, , 237-250.		1
172	Genome Analysis of the Marine Bacterium <i>Labrenzia</i> sp. Strain 011, a Potential Protective Agent of Mollusks. <i>Data</i> , 2019, 4, 33.	1.2	1
173	<i>Streptobacillus felis</i> , a member of the oropharynx microbiota of the Felidae, isolated from a tropical rusty-spotted cat. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 1455-1465.	0.7	1
174	The de.NBI / ELIXIR-DE training platform - Bioinformatics training in Germany and across Europe within ELIXIR. <i>F1000Research</i> , 2019, 8, 1877.	0.8	1
175	Feed Insects as a Reservoir of Granadaene-Producing Lactococci. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	1
176	Metabolism of the Genus <i>Guyparkeria</i> Revealed by Pangenome Analysis. <i>Microorganisms</i> , 2022, 10, 724.	1.6	0
177	Comparative Genomics of <i>Prunus</i> -Associated Members of the <i>Pseudomonas syringae</i> Species Complex Reveals Traits Supporting Co-evolution and Host Adaptation. <i>Frontiers in Microbiology</i> , 2022, 13, 804681.	1.5	0