

# Jochen Blom

## List of Publications by Year in descending order

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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	<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
2	Metabolism of the Genus <i>Guyarkeria</i> Revealed by Pangenome Analysis. <i>Microorganisms</i> , 2022, 10, 724.	1.6	0
3	Genome sequence data of <i>Bacillus velezensis</i> BP1.2A and BT2.4. <i>Data in Brief</i> , 2022, 41, 107978.	0.5	4
4	A dominant clonal lineage of <i>Streptococcus uberis</i> in cattle in Germany. <i>Antonie Van Leeuwenhoek</i> , 2022, , 1.	0.7	3
5	Feed Insects as a Reservoir of Granadaene-Producing Lactococci. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	1
6	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
7	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
8	<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
9	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
10	Genome-wide comparison of four MRSA clinical isolates from Germany and Hungary. <i>PeerJ</i> , 2021, 9, e10185.	0.9	6
11	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
12	<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
13	<i>Pseudomonas paracarnis</i> sp. nov., isolated from refrigerated beef. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	8
14	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
15	EDGAR3.0: comparative genomics and phylogenomics on a scalable infrastructure. <i>Nucleic Acids Research</i> , 2021, 49, W185-W192.	6.5	65
16	<i>Streptococcus vicugnae</i> sp. nov., isolated from faeces of alpacas ( <i>Vicugna pacos</i> ) and cattle ( <i>Bos Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i> ) respiratory tract of California sea lions ( <i>Zalophus californianus</i> ). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	16
17	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
18	<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

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19	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
20	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
21	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
22	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
23	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 (Basel, Switzerland)</i> , 2021, 7, 832.	1.5	5
24	Bakta: rapid and standardized annotation of bacterial genomes via alignment-free sequence identification. <i>Microbial Genomics</i> , 2021, 7, .	1.0	168
25	<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
26	<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
27	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
28	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
29	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
30	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
31	<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
32	Differences between predicted outer membrane proteins of genotype 1 and <i>Mannheimia haemolytica</i> . <i>BMC Microbiology</i> , 2020, 20, 250.	1.3	9
33	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
34	<i>Acinetobacter baumannii</i> in manure and anaerobic digestates of German biogas plants. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	19
35	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
36	Whole genome analysis calls for a taxonomic rearrangement of the genus <i>Colwellia</i> . <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 919-931.	0.7	42

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37	Genomic diversity in flavobacterial pathogens of aquatic origin. <i>Microbial Pathogenesis</i> , 2020, 142, 104053.	1.3	14
38	<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
39	<i>Phytobacter palmae</i> sp. nov., a novel endophytic, N <sub>2</sub> 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
40	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
41	<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
42	Genome-based reclassification of <i>Lactobacillus casei</i> : emended classification and description of the species <i>Lactobacillus zaeae</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3755-3762.	0.8	36
43	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
44	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
45	<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
46	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
47	<i>Oceanivirga miroungae</i> sp. nov., isolated from oral cavity of northern elephant seal ( <i>Mirounga</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 3037-3048.	0.8	9
48	<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
49	<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
50	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 0.8 8	0.8	8
51	<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
52	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
53	<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
54	Diversity of phytobeneficial traits revealed by whole-genome analysis of worldwide-isolated phenazine-producing <i>Pseudomonas</i> spp.. <i>Environmental Microbiology</i> , 2019, 21, 437-455.	1.8	66

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55	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
56	Frankia-Enriched Metagenomes from the Earliest Diverging Symbiotic Frankia Cluster: They Come in Teams. <i>Genome Biology and Evolution</i> , 2019, 11, 2273-2291.	1.1	33
57	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
58	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> , 2019, 10, 1750-1761.	1.1	17
59	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
60	Complete Genome Sequence of the Plant Growth-Promoting Bacterium <i>Hartmannibacter diazotrophicus</i> Strain E19T. <i>International Journal of Genomics</i> , 2019, 2019, 1-12.	0.8	17
61	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
62	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
63	Comparative genomics of <i>Aeromonas veronii</i> : Identification of a pathotype impacting aquaculture globally. <i>PLoS ONE</i> , 2019, 14, e0221018.	1.1	50
64	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
65	Complete Genome Sequence of the Corallopyronin A-Producing <i>Myxobacterium Corallococcus coralloides</i> B035. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
66	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
67	Genome-informed <i>Bradyrhizobium</i> taxonomy: where to from here?. <i>Systematic and Applied Microbiology</i> , 2019, 42, 427-439.	1.2	62
68	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
69	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
70	Pantocin A, a peptide-derived antibiotic involved in biological control by plant-associated <i>Pantoea</i> species. <i>Archives of Microbiology</i> , 2019, 201, 713-722.	1.0	33
71	High-Quality Draft Genome Sequence of <i>Pseudomonas reidholzensis</i> Strain CCOS 865 T. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
72	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

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73	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
74	Comparative Genomics of <i>Streptococcus thermophilus</i> Support Important Traits Concerning the Evolution, Biology and Technological Properties of the Species. <i>Frontiers in Microbiology</i> , 2019, 10, 2916.	1.5	39
75	<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
76	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
77	<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
78	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
79	The synergistic effect of concatenation in phylogenomics: the case in <i>Pantoea</i> . <i>PeerJ</i> , 2019, 7, e6698.	0.9	11
80	<i>Streptomyces dysideae</i> sp. nov., isolated from a marine Mediterranean sponge <i>Dysidea tupa</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	0.8	6
81	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
82	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
83	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
84	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
85	<i>Parendoziomonas haliclona</i> gen. nov. sp. nov. isolated from a marine sponge of the genus <i>Haliclona</i> and description of the family <i>Endoziomonadaceae</i> fam. nov. comprising the genera <i>Endoziomonas</i> , <i>Parendoziomonas</i> , and <i>Kistimonas</i> . <i>Systematic and Applied Microbiology</i> , 2018, 41, 73-84.	1.2	48
86	Genomic Analysis of <i>Bacillus</i> sp. Strain B25, a Biocontrol Agent of Maize Pathogen <i>Fusarium verticillioides</i> . <i>Current Microbiology</i> , 2018, 75, 247-255.	1.0	40
87	Analysis of the Genome and Metabolome of Marine Myxobacteria Reveals High Potential for Biosynthesis of Novel Specialized Metabolites. <i>Scientific Reports</i> , 2018, 8, 16600.	1.6	40
88	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
89	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
90	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

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91	High-Quality Draft Genome Sequence of <i>Pseudomonas wadenswilerensis</i> CCOS 864 T. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	5
92	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
93	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
94	Characterization of Bathyarchaeota genomes assembled from metagenomes of biofilms residing in mesophilic and thermophilic biogas reactors. <i>Biotechnology for Biofuels</i> , 2018, 11, 167.	6.2	38
95	Genome-Based Characterization of Biological Processes That Differentiate Closely Related Bacteria. <i>Frontiers in Microbiology</i> , 2018, 9, 113.	1.5	14
96	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
97	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
98	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
99	Emended description of the genus <i>Phytobacter</i> , its type species <i>Phytobacter diazotrophicus</i> (Zhang) Tj ETQq1 1 0.784314 rgBT / <i>Open Access Evolutionary Microbiology</i> , 2018, 68, 176-184.	0.8	37
100	<i>Mixta</i> gen. nov., a new genus in the Erwiniaceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1396-1407.	0.8	53
101	<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
102	<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
103	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
104	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
105	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
106	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
107	Experimental Evaluation of Host Adaptation of <i>Lactobacillus reuteri</i> to Different Vertebrate Species. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	87
108	Detection and Characterization of Endobacteria in the Fungal Endophyte <i>Piriformospora indica</i> . , 2017, , 237-250.		1

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109	First complete genome sequence of <i>Bacillus glycinifermentans</i> B-27. <i>Journal of Biotechnology</i> , 2017, 257, 187-191.	1.9	6
110	Genomic characterization of two novel SAR11 isolates from the Red Sea, including the first strain of the SAR11 lb clade. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	15
111	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
112	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
113	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
114	Genomic insights into the virulence and salt tolerance of <i>Staphylococcus equorum</i> . <i>Scientific Reports</i> , 2017, 7, 5383.	1.6	34
115	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
116	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
117	Isolation of a novel "atypical" <i>Brucella</i> strain from a bluespotted ribbontail ray ( <i>Taeniura lymma</i> ). <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 221-234.	0.7	74
118	<i>Bacillus amyloliquefaciens</i> , <i>Bacillus velezensis</i> , and <i>Bacillus siamensis</i> Form an "Operational Group B. amyloliquefaciens" within the <i>B. subtilis</i> Species Complex. <i>Frontiers in Microbiology</i> , 2017, 8, 22.	1.5	296
119	Evolution of Anabaenopeptin Peptide Structural Variability in the Cyanobacterium <i>Planktothrix</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 219.	1.5	26
120	Genome Data Provides High Support for Generic Boundaries in <i>Burkholderia</i> Sensu Lato. <i>Frontiers in Microbiology</i> , 2017, 8, 1154.	1.5	122
121	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
122	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
123	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
124	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
125	Genomic analysis of endemic clones of toxigenic and non-toxigenic <i>Corynebacterium diphtheriae</i> in Belarus during and after the major epidemic in 1990s. <i>BMC Genomics</i> , 2017, 18, 873.	1.2	41
126	<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



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127	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
128	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
129	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.	1.1	16
130	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
131	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.	1.2	69
132	EDGAR 2.0: an enhanced software platform for comparative gene content analyses. <i>Nucleic Acids Research</i> , 2016, 44, W22-W28.	6.5	398
133	Diversification and niche adaptations of <i>Nitrospina</i> -like bacteria in the polyextreme interfaces of Red Sea brines. <i>ISME Journal</i> , 2016, 10, 1383-1399.	4.4	85
134	Phylogenomic re-assessment of the thermophilic genus <i>Geobacillus</i> . <i>Systematic and Applied Microbiology</i> , 2016, 39, 527-533.	1.2	116
135	Draft Genome Sequence of the <i>Xanthomonas bromi</i> Type Strain LMG 947. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
136	Specific surface glycan decorations enable antimicrobial peptide resistance in plant-beneficial pseudomonads with insect-pathogenic properties. <i>Environmental Microbiology</i> , 2016, 18, 4265-4281.	1.8	19
137	An assemblage of <i>Frankia</i> Cluster II strains from California contains the canonical nod genes and also the sulfotransferase gene <i>nodH</i> . <i>BMC Genomics</i> , 2016, 17, 796.	1.2	97
138	Complete Genome Sequence of the Barley Pathogen <i>Xanthomonas translucens</i> pv. <i>translucens</i> DSM 18974 <sup>T</sup> (ATCC 19319 <sup>T</sup> ). <i>Genome Announcements</i> , 2016, 4, .	0.8	24
139	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. <i>Veterinary Research</i> , 2016, 47, 31.	1.1	38
140	Comprehensive Genomic Analyses of the OM43 Clade, Including a Novel Species from the Red Sea, Indicate Ecotype Differentiation among Marine Methylophages. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1215-1226.	1.4	37
141	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
142	Insect pathogenicity in plant-beneficial pseudomonads: phylogenetic distribution and comparative genomics. <i>ISME Journal</i> , 2016, 10, 2527-2542.	4.4	127
143	Non-pathogenic <i>Rhizobium radiobacter</i> F4 deploys plant beneficial activity independent of its host <i>Piriformospora indica</i> . <i>ISME Journal</i> , 2016, 10, 871-884.	4.4	93
144	<i>Erwinia gerundensis</i> sp. nov., a cosmopolitan epiphyte originally isolated from pome fruit trees. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 1583-1592.	0.8	33

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145	<i>Brucella vulpis</i> sp. nov., isolated from mandibular lymph nodes of red foxes ( <i>Vulpes vulpes</i> ). International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 2090-2098.	0.8	155
146	Comparative Genomics and Metabolic Analysis Reveals Peculiar Characteristics of <i>Rhodococcus opacus</i> Strain M213 Particularly for Naphthalene Degradation. PLoS ONE, 2016, 11, e0161032.	1.1	21
147	Comparative Methylome Analysis of the Occasional Ruminant Respiratory Pathogen <i>Bibersteinia trehalosi</i> . PLoS ONE, 2016, 11, e0161499.	1.1	6
148	The Change of a Medically Important Genus: Worldwide Occurrence of Genetically Diverse Novel <i>Brucella</i> Species in Exotic Frogs. PLoS ONE, 2016, 11, e0168872.	1.1	56
149	Whole genome sequence and manual annotation of <i>Clostridium autoethanogenum</i> , an industrially relevant bacterium. BMC Genomics, 2015, 16, 1085.	1.2	56
150	Adherence and invasive properties of <i>Corynebacterium diphtheriae</i> strains correlates with the predicted membrane-associated and secreted proteome. BMC Genomics, 2015, 16, 765.	1.2	47
151	Integrative conjugative elements of the ICEPan family play a potential role in <i>Pantoea ananatis</i> ecological diversification and antibiosis. Frontiers in Microbiology, 2015, 6, 576.	1.5	13
152	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
153	Complete Genome Sequence of the Cyanogenic Phosphate-Solubilizing <i>Pseudomonas</i> sp. Strain CCOS 191, a Close Relative of <i>Pseudomonas mosselii</i> . Genome Announcements, 2015, 3, .	0.8	4
154	Draft Genome Sequence of <i>Pseudomonas aeruginosa</i> Strain WS136, a Highly Cytotoxic ExoS-Positive Wound Isolate Recovered from Pyoderma Gangrenosum. Genome Announcements, 2015, 3, .	0.8	3
155	Genome Sequence of the Urethral Isolate <i>Pseudomonas aeruginosa</i> RN21. Genome Announcements, 2015, 3, .	0.8	2
156	Draft Genome Sequence of the Commercial Biocontrol Strain <i>Pantoea agglomerans</i> P10c. Genome Announcements, 2015, 3, .	0.8	29
157	Whole genome sequences of a free-living <i>Pseudomonas</i> sp. strain ML96 isolated from a freshwater Maar Lake. Marine Genomics, 2015, 24, 219-221.	0.4	1
158	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. Journal of Biotechnology, 2015, 203, 19-21.	1.9	27
159	Genome Sequence of the Urethral Catheter Isolate <i>Pseudomonas aeruginosa</i> MH19. Genome Announcements, 2015, 3, .	0.8	2
160	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. Genome Announcements, 2015, 3, .	0.8	13
161	Genomic Avenue to Avian Colisepticemia. MBio, 2015, 6, .	1.8	59
162	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

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163	Comprehensive molecular, genomic and phenotypic analysis of a major clone of <i>Enterococcus faecalis</i> MLST ST40. <i>BMC Genomics</i> , 2015, 16, 175.	1.2	33
164	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
165	<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
166	Phylogenomic grouping of <i>Listeria monocytogenes</i> . <i>Canadian Journal of Microbiology</i> , 2015, 61, 637-646.	0.8	12
167	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
168	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
169	Draft genome of formaldehyde-degrading strain, <i>Pseudomonas monteilii</i> IOFA19. <i>Marine Genomics</i> , 2014, 15, 1-2.	0.4	4
170	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
171	Pangenomic Study of <i>Corynebacterium diphtheriae</i> That Provides Insights into the Genomic Diversity of Pathogenic Isolates from Cases of Classical Diphtheria, Endocarditis, and Pneumonia. <i>Journal of Bacteriology</i> , 2012, 194, 3199-3215.	1.0	142
172	Complete Genome Sequence of the Porcine Isolate <i>Enterococcus faecalis</i> D32. <i>Journal of Bacteriology</i> , 2012, 194, 5490-5491.	1.0	16
173	The Complete Genome of <i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> CAU B946 Contains a Gene Cluster for Nonribosomal Synthesis of Iturin A. <i>Journal of Bacteriology</i> , 2012, 194, 1845-1846.	1.0	39
174	Comparative analysis of the Hrp pathogenicity island of Rubus- and Spiraeoideae-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
175	Relationship of <i>Bacillus amyloliquefaciens</i> clades associated with strains DSM 7T and FZB42T: a proposal for <i>Bacillus amyloliquefaciens</i> subsp. <i>amyloliquefaciens</i> subsp. nov. and <i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> subsp. nov. based on complete genome sequence comparisons. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 1786-1801.	0.8	265
176	EDGAR: A software framework for the comparative analysis of prokaryotic genomes. <i>BMC Bioinformatics</i> , 2009, 10, 154.	1.2	401
177	Whole-genome comparison of disease and carriage strains provides insights into virulence evolution in <i>Neisseria meningitidis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3473-3478.	3.3	159