

# Boyke Bunk

## List of Publications by Year in descending order

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97  
papers

5,262  
citations

101384

36  
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110170

64  
g-index

100  
all docs

100  
docs citations

100  
times ranked

7796  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative genome and phenotypic analysis of three <i>Clostridioides difficile</i> strains isolated from a single patient provide insight into multiple infection of <i>C. difficile</i> . <i>BMC Genomics</i> , 2018, 19, 1.	1.2	725
2	Genome-guided design of a defined mouse microbiota that confers colonization resistance against <i>Salmonella enterica</i> serovar Typhimurium. <i>Nature Microbiology</i> , 2017, 2, 16215.	5.9	313
3	A collection of bacterial isolates from the pig intestine reveals functional and taxonomic diversity. <i>Nature Communications</i> , 2020, 11, 6389.	5.8	269
4	The complete genome sequence of the algal symbiont <i>Dinoroseobacter shibae</i> : a hitchhiker's guide to life in the sea. <i>ISME Journal</i> , 2010, 4, 61-77.	4.4	244
5	Global outbreak of severe <i>Mycobacterium chimaera</i> disease after cardiac surgery: a molecular epidemiological study. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 1033-1041.	4.6	198
6	Characterization of the first cultured representative of <i>Verrucomicrobia</i> subdivision 5 indicates the proposal of a novel phylum. <i>ISME Journal</i> , 2016, 10, 2801-2816.	4.4	173
7	Cultivation and functional characterization of 79 planctomycetes uncovers their unique biology. <i>Nature Microbiology</i> , 2020, 5, 126-140.	5.9	164
8	Genome Sequences of the Biotechnologically Important <i>Bacillus megaterium</i> Strains QM B1551 and DSM319. <i>Journal of Bacteriology</i> , 2011, 193, 4199-4213.	1.0	155
9	The complex methylome of the human gastric pathogen <i>Helicobacter pylori</i> . <i>Nucleic Acids Research</i> , 2014, 42, 2415-2432.	6.5	132
10	Manual curation and reannotation of the genomes of <i>Clostridium difficile</i> 630 <sup>erm</sup> and <i>C. difficile</i> 630. <i>Journal of Medical Microbiology</i> , 2017, 66, 286-293.	0.7	117
11	Long-read DNA metabarcoding of ribosomal RNA in the analysis of fungi from aquatic environments. <i>Molecular Ecology Resources</i> , 2018, 18, 1500-1514.	2.2	103
12	<i>Chromera velia</i> , Endosymbioses and the Rhodoplex Hypothesis—Plastid Evolution in Cryptophytes, Alveolates, Stramenopiles, and Haptophytes (CASH Lineages). <i>Genome Biology and Evolution</i> , 2014, 6, 666-684.	1.1	93
13	Transcriptional response of the photoheterotrophic marine bacterium <i>Dinoroseobacter shibae</i> to changing light regimes. <i>ISME Journal</i> , 2011, 5, 1957-1968.	4.4	88
14	PRODORIC (release 2009): a database and tool platform for the analysis of gene regulation in prokaryotes. <i>Nucleic Acids Research</i> , 2009, 37, D61-D65.	6.5	83
15	Characterization of JG024, a <i>Pseudomonas aeruginosa</i> PB1-like broad host range phage under simulated infection conditions. <i>BMC Microbiology</i> , 2010, 10, 301.	1.3	81
16	Metabolic engineering of cobalamin (vitamin B <sub>12</sub> ) production in <i>Bacillus megaterium</i> . <i>Microbial Biotechnology</i> , 2010, 3, 24-37.	2.0	75
17	Global occurrence and heterogeneity of the <i>Roseobacter</i> -clade species <i>Ruegeria mobilis</i> . <i>ISME Journal</i> , 2017, 11, 569-583.	4.4	75
18	Chromosomal Locations of <i>mcr-1</i> and <i>bla</i> <sub>CTX-M-15</sub> in Fluoroquinolone-Resistant <i>Escherichia coli</i> ST410. <i>Emerging Infectious Diseases</i> , 2016, 22, 1689-1691.	2.0	70

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19	MetaQuant: a tool for the automatic quantification of GC/MS-based metabolome data. <i>Bioinformatics</i> , 2006, 22, 2962-2965.	1.8	67
20	High metabolic versatility of different toxigenic and non-toxigenic <i>Clostridioides difficile</i> isolates. <i>International Journal of Medical Microbiology</i> , 2017, 307, 311-320.	1.5	67
21	Systems Biology of Recombinant Protein Production Using <i>Bacillus megaterium</i> . <i>Methods in Enzymology</i> , 2011, 500, 165-195.	0.4	60
22	Sequencing and Characterization of <i>Pseudomonas aeruginosa</i> phage JG004. <i>BMC Microbiology</i> , 2011, 11, 102.	1.3	60
23	First genome sequences of <i>Achromobacter</i> phages reveal new members of the N4 family. <i>Virology Journal</i> , 2014, 11, 14.	1.4	59
24	Genome biology of a novel lineage of planctomycetes widespread in anoxic aquatic environments. <i>Environmental Microbiology</i> , 2018, 20, 2438-2455.	1.8	57
25	The Global Genome Biodiversity Network (GGBN) Data Standard specification. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw125.	1.4	55
26	Packaging of <i>Dinoroseobacter shibae</i> DNA into Gene Transfer Agent Particles Is Not Random. <i>Genome Biology and Evolution</i> , 2018, 10, 359-369.	1.1	55
27	A short story about a big magic bug. <i>Bioengineered Bugs</i> , 2010, 1, 85-91.	2.0	53
28	Think pink: photosynthesis, plasmids and the <i>Roseobacter</i> clade. <i>Environmental Microbiology</i> , 2012, 14, 2661-2672.	1.8	52
29	Diversity of Prokaryotic Community at a Shallow Marine Hydrothermal Site Elucidated by Illumina Sequencing Technology. <i>Current Microbiology</i> , 2014, 69, 457-466.	1.0	52
30	BacDive – The Bacterial Diversity Metadatabase in 2016. <i>Nucleic Acids Research</i> , 2016, 44, D581-D585.	6.5	51
31	SYSTEMONAS – an integrated database for systems biology analysis of <i>Pseudomonas</i> . <i>Nucleic Acids Research</i> , 2007, 35, D533-D537.	6.5	50
32	A <i>Clostridioides difficile</i> bacteriophage genome encodes functional binary toxin-associated genes. <i>Journal of Biotechnology</i> , 2017, 250, 23-28.	1.9	50
33	Characterization of the first cultured representative of a <i>Bacteroidetes</i> clade specialized on the scavenging of cyanobacteria. <i>Environmental Microbiology</i> , 2017, 19, 1134-1148.	1.8	50
34	<i>Fuerstia marisgermanicae</i> gen. nov., sp. nov., an Unusual Member of the Phylum Planctomycetes from the German Wadden Sea. <i>Frontiers in Microbiology</i> , 2016, 7, 2079.	1.5	49
35	High-Quality Whole-Genome Sequences of the Oligo-Mouse-Microbiota Bacterial Community. <i>Genome Announcements</i> , 2017, 5, .	0.8	49
36	Discovery of <i>Paenibacillus larvae</i> ERIC V: Phenotypic and genomic comparison to genotypes ERIC I-IV reveal different inventories of virulence factors which correlate with epidemiological prevalences of American Foulbrood. <i>International Journal of Medical Microbiology</i> , 2020, 310, 151394.	1.5	47

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37	Paenibacillus larvae-Directed Bacteriophage HB10c2 and Its Application in American Foulbrood-Affected Honey Bee Larvae. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5411-5419.	1.4	42
38	Genome and Methylome Variation in <i>Helicobacter pylori</i> With a <i>cag</i> Pathogenicity Island During Early Stages of Human Infection. <i>Gastroenterology</i> , 2018, 154, 612-623.e7.	0.6	40
39	Comparative Genomics Reveal a Flagellar System, a Type VI Secretion System and Plant Growth-Promoting Gene Clusters Unique to the Endophytic Bacterium <i>Kosakonia radicincitans</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1997.	1.5	39
40	Complete genome sequence and description of <i>Salinispira pacifica</i> gen. nov., sp. nov., a novel spirochaete isolated from a hypersaline microbial mat. <i>Standards in Genomic Sciences</i> , 2015, 10, 7.	1.5	38
41	Genome Analysis of the Fruiting Body-Forming Myxobacterium <i>Chondromyces crocatus</i> Reveals High Potential for Natural Product Biosynthesis. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1945-1957.	1.4	37
42	Genome Resequencing of the Virulent and Multidrug-Resistant Reference Strain <i>Clostridium difficile</i> 630. <i>Genome Announcements</i> , 2015, 3, .	0.8	36
43	BacDive—the Bacterial Diversity Metadatabase. <i>Nucleic Acids Research</i> , 2014, 42, D592-D599.	6.5	35
44	OxyR-dependent formation of DNA methylation patterns in <i>OpvAB</i> cell lineages of <i>Salmonella enterica</i> . <i>Nucleic Acids Research</i> , 2016, 44, 3595-3609.	6.5	35
45	Identification of a <i>Pseudomonas aeruginosa</i> PAO1 DNA Methyltransferase, Its Targets, and Physiological Roles. <i>MBio</i> , 2017, 8, .	1.8	32
46	Monitoring microevolution of OXA-48-producing <i>Klebsiella pneumoniae</i> ST147 in a hospital setting by SMRT sequencing. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 2737-2744.	1.3	30
47	Convergent Loss of ABC Transporter Genes From <i>Clostridioides difficile</i> Genomes Is Associated With Impaired Tyrosine Uptake and <i>p</i> -Cresol Production. <i>Frontiers in Microbiology</i> , 2018, 9, 901.	1.5	30
48	Tripartite species interaction: eukaryotic hosts suffer more from phage susceptible than from phage resistant bacteria. <i>BMC Evolutionary Biology</i> , 2017, 17, 98.	3.2	27
49	Construction and characterization of nitrate and nitrite respiring <i>Pseudomonas putida</i> KT2440 strains for anoxic biotechnical applications. <i>Journal of Biotechnology</i> , 2013, 163, 155-165.	1.9	26
50	A transferable plasticity region in <i>Campylobacter coli</i> allows isolates of an otherwise non-glycolytic food-borne pathogen to catabolize glucose. <i>Molecular Microbiology</i> , 2015, 98, 809-830.	1.2	26
51	Cobaviruses—a new globally distributed phage group infecting <i>Rhodobacteraceae</i> in marine ecosystems. <i>ISME Journal</i> , 2019, 13, 1404-1421.	4.4	26
52	New insights into the energy metabolism and taxonomy of <i>Deferribacteres</i> revealed by the characterization of a new isolate from a hypersaline microbial mat. <i>Environmental Microbiology</i> , 2022, 24, 2543-2575.	1.8	26
53	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
54	<i>Vibrio anguillarum</i> Is Genetically and Phenotypically Unaffected by Long-Term Continuous Exposure to the Antibacterial Compound Tropodithietic Acid. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4802-4810.	1.4	24

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55	Changes in prokaryotic community composition accompanying a pronounced temperature shift of a shallow marine thermal brine pool (Panarea Island, Italy). <i>Extremophiles</i> , 2015, 19, 547-559.	0.9	23
56	Trophic networks improve the performance of microbial anodes treating wastewater. <i>Npj Biofilms and Microbiomes</i> , 2019, 5, 27.	2.9	23
57	Identification and Targeted Cultivation of Abundant Novel Freshwater Sphingomonads and Analysis of Their Population Substructure. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7355-7364.	1.4	22
58	Genome sequence of the mud-dwelling archaeon <i>Methanoplanus limicola</i> type strain (DSM 2279T), reclassification of <i>Methanoplanus petrolearius</i> as <i>Methanolacinia petrolearia</i> and emended descriptions of the genera <i>Methanoplanus</i> and <i>Methanolacinia</i> . <i>Standards in Genomic Sciences</i> , 2014, 9, 1076-1088.	1.5	22
59	Complete Genome Sequence of the Novel Temperate <i>Clostridium difficile</i> Phage phiCDIF1296T. <i>Genome Announcements</i> , 2015, 3, .	0.8	22
60	<i>Streptomyces bathyalis</i> sp. nov., an actinobacterium isolated from the sponge in a deep sea. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 425-435.	0.7	22
61	A publicly accessible database for <i>Clostridioides difficile</i> genome sequences supports tracing of transmission chains and epidemics. <i>Microbial Genomics</i> , 2020, 6, .	1.0	22
62	Optimization of antibody fragment production in <i>Bacillus megaterium</i> : The role of metal ions on protein secretion. <i>Journal of Biotechnology</i> , 2010, 150, 115-124.	1.9	21
63	Successive Conditioning in Complex Artificial Wastewater Increases the Performance of Electrochemically Active Biofilms Treating Real Wastewater. <i>ChemElectroChem</i> , 2017, 4, 3081-3090.	1.7	20
64	Transcriptional adaptations during long-term persistence of <i>Staphylococcus aureus</i> in the airways of a cystic fibrosis patient. <i>International Journal of Medical Microbiology</i> , 2015, 305, 38-46.	1.5	19
65	Production of the Bioactive Compounds Violacein and Indolmycin Is Conditional in a <i>maeA</i> Mutant of <i>Pseudoalteromonas luteoviolacea</i> S4054 Lacking the Malic Enzyme. <i>Frontiers in Microbiology</i> , 2016, 7, 1461.	1.5	18
66	The Composite 259-kb Plasmid of <i>Marteella mediterranea</i> DSM 17316T—A Natural Replicon with Functional RepABC Modules from Rhodobacteraceae and Rhizobiaceae. <i>Frontiers in Microbiology</i> , 2017, 8, 1787.	1.5	18
67	Complete genome sequence of the bioleaching bacterium <i>Leptospirillum</i> sp. group II strain CF-1. <i>Journal of Biotechnology</i> , 2016, 222, 21-22.	1.9	16
68	Characterization and genome comparisons of three <i>Achromobacter</i> phages of the family Siphoviridae. <i>Archives of Virology</i> , 2017, 162, 2191-2201.	0.9	16
69	Whole-genome comparison of high and low virulent <i>Staphylococcus aureus</i> isolates inducing implant-associated bone infections. <i>International Journal of Medical Microbiology</i> , 2018, 308, 505-513.	1.5	15
70	Molecular basis of a bacterial-amphibian symbiosis revealed by comparative genomics, modeling, and functional testing. <i>ISME Journal</i> , 2022, 16, 788-800.	4.4	15
71	First Complete Genome Sequence of a Subdivision 6 <i>Acidobacterium</i> Strain. <i>Genome Announcements</i> , 2016, 4, .	0.8	14
72	<i>In Vivo</i> Genome and Methylome Adaptation of <i>cagA</i> -Negative <i>Helicobacter pylori</i> during Experimental Human Infection. <i>MBio</i> , 2020, 11, .	1.8	14

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73	Genomic analysis of three <i>Clostridioides difficile</i> isolates from urban water sources. <i>Anaerobe</i> , 2019, 56, 22-26.	1.0	13
74	The <i>Mycobacterium avium</i> ssp. <i>paratuberculosis</i> specific <i>mptD</i> gene is required for maintenance of the metabolic homeostasis necessary for full virulence in mouse infections. <i>Frontiers in Cellular and Infection Microbiology</i> , 2014, 4, 110.	1.8	12
75	<i>Caldisalibacter kiritimatiensis</i> gen. nov., sp. nov., a Moderately Thermohalophilic Thiosulfate-Reducing Bacterium from a Hypersaline Microbial Mat. <i>Geomicrobiology Journal</i> , 2015, 32, 347-354.	1.0	12
76	<i>Natronoglycomyces albus</i> gen. nov., sp. nov, a haloalkaliphilic actinobacterium from a soda solonchak soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	12
77	The importance of biofilm formation for cultivation of a Micrarchaeon and its interactions with its <i>Thermoplasmatales</i> host. <i>Nature Communications</i> , 2022, 13, 1735.	5.8	12
78	Complete Genome Sequence of the <i>Clostridium difficile</i> Type Strain DSM 1296 T. <i>Genome Announcements</i> , 2015, 3, .	0.8	11
79	Simultaneous Presence of Bacteriochlorophyll and Xanthorhodopsin Genes in a Freshwater Bacterium. <i>MSystems</i> , 2020, 5, .	1.7	11
80	Complete Genome Sequence of the Urethral Catheter Isolate <i>Myroides</i> sp. A21. <i>Genome Announcements</i> , 2015, 3, .	0.8	10
81	First Report of <i>Kosakonia radincitans</i> Bacteraemia from Europe (Austria) - Identification and Whole-Genome Sequencing of Strain DSM 107547. <i>Scientific Reports</i> , 2020, 10, 1948.	1.6	10
82	Systems Biology of Recombinant Protein Production in <i>Bacillus megaterium</i> . , 2010, 120, 133-161.		9
83	Complete Genome Sequence of a CTX-M-15-Producing <i>Klebsiella pneumoniae</i> Outbreak Strain from Multilocus Sequence Type 514. <i>Genome Announcements</i> , 2015, 3, .	0.8	9
84	Detection of translocatable units in a blaCTX-M-15 extended-spectrum $\beta$ -lactamase-producing ST131 <i>Escherichia coli</i> isolate using a hybrid sequencing approach. <i>International Journal of Antimicrobial Agents</i> , 2016, 47, 245-247.	1.1	9
85	Genome Analysis of the Carbapenem- and Colistin-Resistant <i>Escherichia coli</i> Isolate NRZ14408 Reveals Horizontal Gene Transfer Pathways towards Panresistance and Enhanced Virulence. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	9
86	Impact of rare codons and the functional coproduction of rate-limiting tRNAs on recombinant protein production in <i>Bacillus megaterium</i> . <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 8999-9010.	1.7	8
87	Enhanced whole exome sequencing by higher DNA insert lengths. <i>BMC Genomics</i> , 2016, 17, 399.	1.2	8
88	Amphibian skin-associated Pigmentiphaga: Genome sequence and occurrence across geography and hosts. <i>PLoS ONE</i> , 2019, 14, e0223747.	1.1	8
89	GeneReporter™ sequence-based document retrieval and annotation. <i>Bioinformatics</i> , 2011, 27, 1034-1035.	1.8	5
90	Filling the Gaps in the Cyanobacterial Tree of Life™ Metagenome Analysis of <i>Stigonema ocellatum</i> DSM 106950, <i>Chlorogloea purpurea</i> SAG 13.99 and <i>Gomphosphaeria aponina</i> DSM 107014. <i>Genes</i> , 2021, 12, 389.	1.0	5

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91	Complete Genome Sequences of Three Multidrug-Resistant Clinical Isolates of <i>Streptococcus pneumoniae</i> Serotype 19A with Different Susceptibilities to the Myxobacterial Metabolite Carolacton. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
92	Complete Genome Sequencing of <i>Leptospira interrogans</i> Isolates from Malaysia Reveals Massive Genome Rearrangement but High Conservation of Virulence-Associated Genes. <i>Pathogens</i> , 2021, 10, 1198.	1.2	4
93	Genome Sequence of <i>Prosthecochloris</i> sp. Strain CIB 2401 of the Phylum Chlorobi. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
94	ROSY--a flexible and universal database and bioinformatics tool platform for <i>Roseobacter</i> related species. <i>In Silico Biology</i> , 2008, 8, 177-86.	0.4	3
95	Complete Genome and Plasmid Sequences of <i>Staphylococcus aureus</i> EDCC 5055 (DSM 28763), Used To Study Implant-Associated Infections. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
96	Construction and Application of a Plasmid-Based Signal Peptide Library for Improved Secretion of Recombinant Proteins with <i>Priestia megaterium</i> . <i>Microorganisms</i> , 2022, 10, 777.	1.6	2
97	<i>Natronosporangium hydrolyticum</i> gen. nov., sp. nov., a haloalkaliphilic polyhydrolytic actinobacterium from a soda solonchak soil in Central Asia. <i>Systematic and Applied Microbiology</i> , 2022, 45, 126307.	1.2	2