

Patrick S Chain

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9071858/publications.pdf>

Version: 2024-02-01

245
papers

18,949
citations

16411

64
h-index

14156

128
g-index

266
all docs

266
docs citations

266
times ranked

23143
citing authors

#	ARTICLE	IF	CITATIONS
1	Challenges in Bioinformatics Workflows for Processing Microbiome Omics Data at Scale. <i>Frontiers in Bioinformatics</i> , 2022, 1, .	1.0	6
2	EDGE COVID-19: a web platform to generate submission-ready genomes from SARS-CoV-2 sequencing efforts. <i>Bioinformatics</i> , 2022, 38, 2700-2704.	1.8	12
3	Comparative Genomics Applied to Systematically Assess Pathogenicity Potential in Shiga Toxin-Producing <i>Escherichia coli</i> O145:H28. <i>Microorganisms</i> , 2022, 10, 866.	1.6	7
4	Advances and Challenges in Fluorescence in situ Hybridization for Visualizing Fungal Endobacteria. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	4
5	A public website for the automated assessment and validation of SARS-CoV-2 diagnostic PCR assays. <i>Bioinformatics</i> , 2021, 37, 1024-1025.	1.8	7
6	Democratization of fungal highway columns as a tool to investigate bacteria associated with soil fungi. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	15
7	Microbiome Metadata Standards: Report of the National Microbiome Data Collaborative's Workshop and Follow-On Activities. <i>MSystems</i> , 2021, 6, .	1.7	28
8	Comparative genomic and phenotypic characterization of invasive non-typhoidal <i>Salmonella</i> isolates from Siaya, Kenya. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0008991.	1.3	3
9	Epigenetic regulation of gene expression in Shiga toxin-producing <i>Escherichia coli</i> : Transcriptomic data. <i>Data in Brief</i> , 2021, 36, 107065.	0.5	0
10	DNA adenine methylase, not the PstI restriction-modification system, regulates virulence gene expression in Shiga toxin-producing <i>Escherichia coli</i> . <i>Food Microbiology</i> , 2021, 96, 103722.	2.1	7
11	The Gut Microbiome and Alcoholic Liver Disease: Ethanol Consumption Drives Consistent and Reproducible Alteration in Gut Microbiota in Mice. <i>Life</i> , 2021, 11, 7.	1.1	15
12	Widespread bacterial diversity within the bacteriome of fungi. <i>Communications Biology</i> , 2021, 4, 1168.	2.0	19
13	Discovery of an Antarctic Ascidian-Associated Uncultivated <i>Verrucomicrobia</i> with Antimelanoma Palmerolide Biosynthetic Potential. <i>MSphere</i> , 2021, 6, e0075921.	1.3	7
14	Multiple Cases of Bacterial Sequence Erroneously Incorporated Into Publicly Available Chloroplast Genomes. <i>Frontiers in Genetics</i> , 2021, 12, 821715.	1.1	4
15	Bioinformatic and Mechanistic Analysis of the Palmerolide PKS-NRPS Biosynthetic Pathway From the Microbiome of an Antarctic Ascidian. <i>Frontiers in Chemistry</i> , 2021, 9, 802574.	1.8	7
16	Active Targeted Surveillance to Identify Sites of Emergence of Hantavirus. <i>Clinical Infectious Diseases</i> , 2020, 70, 464-473.	2.9	22
17	Precision Medicine and Precision Public Health in the Era of Pathogen Next-Generation Sequencing. <i>Journal of Infectious Diseases</i> , 2020, 221, S289-S291.	1.9	8
18	Genomic Analysis of Diverse Members of the Fungal Genus <i>Monosporascus</i> Reveals Novel Lineages, Unique Genome Content and a Potential Bacterial Associate. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2573-2583.	0.8	5

#	ARTICLE	IF	CITATIONS
19	A Gene Cluster That Encodes Histone Deacetylase Inhibitors Contributes to Bacterial Persistence and Antibiotic Tolerance in <i>Burkholderia thailandensis</i> . <i>MSystems</i> , 2020, 5, .	1.7	6
20	Uncovering the Core Microbiome and Distribution of Palmerolide in <i>Synocicum adareanum</i> Across the Anvers Island Archipelago, Antarctica. <i>Marine Drugs</i> , 2020, 18, 298.	2.2	12
21	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.	5.9	115
22	Standardized phylogenetic and molecular evolutionary analysis applied to species across the microbial tree of life. <i>Scientific Reports</i> , 2020, 10, 1723.	1.6	65
23	The National Microbiome Data Collaborative: enabling microbiome science. <i>Nature Reviews Microbiology</i> , 2020, 18, 313-314.	13.6	42
24	Investigating intestinal permeability and gut microbiota roles in acute coronary syndrome patients. <i>Human Microbiome Journal</i> , 2019, 13, 100059.	3.8	20
25	Advances and Challenges in Metatranscriptomic Analysis. <i>Frontiers in Genetics</i> , 2019, 10, 904.	1.1	253
26	Novel Insights Into the Spread of Enteric Pathogens Using Genomics. <i>Journal of Infectious Diseases</i> , 2019, 221, S319-S330.	1.9	2
27	MicroRNA in Pancreatic Cancer: From Biology to Therapeutic Potential. <i>Genes</i> , 2019, 10, 752.	1.0	81
28	Toward unrestricted use of public genomic data. <i>Science</i> , 2019, 363, 350-352.	6.0	45
29	Whole-genome SNP-based phylogenetic analysis of <i>Yersinia pestis</i> isolates from Georgia and neighboring Caucasian countries. <i>International Journal of Infectious Diseases</i> , 2019, 79, 80.	1.5	0
30	Consent insufficient for data release—Response. <i>Science</i> , 2019, 364, 446-446.	6.0	5
31	The evolution of a super-swarm of foot-and-mouth disease virus in cattle. <i>PLoS ONE</i> , 2019, 14, e0210847.	1.1	14
32	Adaptive Strategies in a Poly-Extreme Environment: Differentiation of Vegetative Cells in <i>Serratia ureilytica</i> and Resistance to Extreme Conditions. <i>Frontiers in Microbiology</i> , 2019, 10, 102.	1.5	19
33	Oxalic acid, a molecule at the crossroads of bacterial-fungal interactions. <i>Advances in Applied Microbiology</i> , 2019, 106, 49-77.	1.3	79
34	Remedial Treatment of Corroded Iron Objects by Environmental <i>Aeromonas</i> Isolates. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	10
35	Bacterial spores, from ecology to biotechnology. <i>Advances in Applied Microbiology</i> , 2019, 106, 79-111.	1.3	26
36	Diagnostic targeted sequencing adjudication (DETEQT). <i>Journal of Molecular Diagnostics</i> , 2019, 21, 99-110.	1.2	5

#	ARTICLE	IF	CITATIONS
37	“Candidatus Nitrosotenuis aquarius,” an Ammonia-Oxidizing Archaeon from a Freshwater Aquarium Biofilter. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	36
38	<i>Rheinheimera salexigens</i> sp. nov., isolated from a fishing hook, and emended description of the genus <i>Rheinheimera</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 35-41.	0.8	17
39	Draft Genome Sequence of Sorghum Grain Mold Fungus <i>Epicoccum sorghinum</i> , a Producer of Tenuazonic Acid. <i>Genome Announcements</i> , 2017, 5, .	0.8	19
40	Ten Genome Sequences of Human and Livestock Isolates of <i>Bacillus anthracis</i> from the Country of Georgia. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
41	High-Quality Draft Genome Sequences of Four Lignocellulose-Degrading Bacteria Isolated from Puerto Rican Forest Soil: <i>Gordonia</i> sp., <i>Paenibacillus</i> sp., <i>Variovorax</i> sp., and <i>Vogesella</i> sp. <i>Genome Announcements</i> , 2017, 5, .	0.8	18
42	Metagenomic reconstruction of nitrogen cycling pathways in a CO ₂ -enriched grassland ecosystem. <i>Soil Biology and Biochemistry</i> , 2017, 106, 99-108.	4.2	63
43	Enabling the democratization of the genomics revolution with a fully integrated web-based bioinformatics platform. <i>Nucleic Acids Research</i> , 2017, 45, 67-80.	6.5	147
44	<i>Streptococcus mutans</i> Displays Altered Stress Responses While Enhancing Biofilm Formation by <i>Lactobacillus casei</i> in Mixed-Species Consortium. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 524.	1.8	23
45	Exception to the Rule: Genomic Characterization of Naturally Occurring Unusual <i>Vibrio cholerae</i> Strains with a Single Chromosome. <i>International Journal of Genomics</i> , 2017, 2017, 1-14.	0.8	18
46	High-quality genome sequence of the radioresistant bacterium <i>Deinococcus ficus</i> KS 0460. <i>Standards in Genomic Sciences</i> , 2017, 12, 46.	1.5	10
47	Brief Protocol for EDGE Bioinformatics: Analyzing Microbial and Metagenomic NGS Data. <i>Bio-protocol</i> , 2017, 7, e2622.	0.2	8
48	Genome Sequence of the Historical Clinical Isolate <i>Burkholderia pseudomallei</i> PHLS 6. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
49	Molecular Dissection of Induced Platinum Resistance through Functional and Gene Expression Analysis in a Cell Culture Model of Bladder Cancer. <i>PLoS ONE</i> , 2016, 11, e0146256.	1.1	13
50	SPIDR-WEB: an NGS biotechnology platform for diagnostic and transcriptomic applications. <i>International Journal of Infectious Diseases</i> , 2016, 45, 194.	1.5	1
51	Culture-Independent Diagnostics for Health Security. <i>Health Security</i> , 2016, 14, 122-142.	0.9	31
52	Whole-Genome Comparative Analysis of Two Carbapenem-Resistant ST-258 <i>Klebsiella pneumoniae</i> Strains Isolated during a North-Eastern Ohio Outbreak: Differences within the High Heterogeneity Zones. <i>Genome Biology and Evolution</i> , 2016, 8, 2036-2043.	1.1	28
53	ADEPT, a dynamic next generation sequencing data error-detection program with trimming. <i>BMC Bioinformatics</i> , 2016, 17, 109.	1.2	4
54	Draft Genomes for Eight <i>Burkholderia mallei</i> Isolates from Turkey. <i>Genome Announcements</i> , 2016, 4, .	0.8	4

#	ARTICLE	IF	CITATIONS
55	Metagenomic investigation of the geologically unique <i>Hellenic Volcanic Arc</i> reveals a distinctive ecosystem with unexpected physiology. <i>Environmental Microbiology</i> , 2016, 18, 1122-1136.	1.8	37
56	<i>Anoxybacillus geothermalis</i> sp. nov., a facultatively anaerobic, endospore-forming bacterium isolated from mineral deposits in a geothermal station. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2944-2951.	0.8	21
57	Functional and Structural Analysis of a Highly-Expressed <i>Yersinia pestis</i> Small RNA following Infection of Cultured Macrophages. <i>PLoS ONE</i> , 2016, 11, e0168915.	1.1	9
58	Finished Genome Assembly of <i>Yersinia pestis</i> EV76D and KIM 10v. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
59	Genome Assemblies for 11 <i>Yersinia pestis</i> Strains Isolated in the Caucasus Region. <i>Genome Announcements</i> , 2015, 3, .	0.8	21
60	Finished Genome Assembly of Warm Spring Isolate <i>Francisella novicida</i> DPG 3A-IS. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
61	First Complete Genome Sequence of <i>Felis catus</i> Gammaherpesvirus 1. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
62	Genome Sequence of <i>Aeribacillus pallidus</i> Strain GS3372, an Endospore-Forming Bacterium Isolated in a Deep Geothermal Reservoir. <i>Genome Announcements</i> , 2015, 3, .	0.8	7
63	Challenges and opportunities in understanding microbial communities with metagenome assembly (accompanied by IPython Notebook tutorial). <i>Frontiers in Microbiology</i> , 2015, 6, 678.	1.5	28
64	Comparative metagenomics reveals impact of contaminants on groundwater microbiomes. <i>Frontiers in Microbiology</i> , 2015, 6, 1205.	1.5	77
65	Complete genome sequence of the phenanthrene-degrading soil bacterium <i>Delftia acidovorans</i> Cs1-4. <i>Standards in Genomic Sciences</i> , 2015, 10, 55.	1.5	43
66	Scanning the Landscape of Genome Architecture of Non-O1 and Non-O139 <i>Vibrio cholerae</i> by Whole Genome Mapping Reveals Extensive Population Genetic Diversity. <i>PLoS ONE</i> , 2015, 10, e0120311.	1.1	19
67	Building International Genomics Collaboration for Global Health Security. <i>Frontiers in Public Health</i> , 2015, 3, 264.	1.3	9
68	Accurate read-based metagenome characterization using a hierarchical suite of unique signatures. <i>Nucleic Acids Research</i> , 2015, 43, e69-e69.	6.5	141
69	Genome Sequence of <i>Kosakonia radicincitans</i> Strain YD4, a Plant Growth-Promoting Rhizobacterium Isolated from Yerba Mate (<i>Ilex paraguariensis</i> St. Hill.). <i>Genome Announcements</i> , 2015, 3, .	0.8	16
70	Draft Genome Sequence of <i>Thauera</i> sp. Strain SWB20, Isolated from a Singapore Wastewater Treatment Facility Using Gel Microdroplets. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
71	Complete Genome Assemblies for Two Single-Chromosome <i>Vibrio cholerae</i> Isolates, Strains 1154-74 (Serogroup O49) and 10432-62 (Serogroup O27). <i>Genome Announcements</i> , 2015, 3, .	0.8	17
72	Genome Sequence of <i>Anoxybacillus geothermalis</i> Strain GSsed3, a Novel Thermophilic Endospore-Forming Species. <i>Genome Announcements</i> , 2015, 3, .	0.8	5

#	ARTICLE	IF	CITATIONS
73	Genome Sequence of <i>Bacillus alveayuensis</i> Strain 24KAM51, a Halotolerant Thermophile Isolated from a Hydrothermal Vent. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
74	Whole-Genome Sequences of 80 Environmental and Clinical Isolates of <i>Burkholderia pseudomallei</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	38
75	Genomic, Proteomic, and Biochemical Analysis of the Organohalide Respiratory Pathway in <i>Desulfitobacterium dehalogenans</i> . <i>Journal of Bacteriology</i> , 2015, 197, 893-904.	1.0	43
76	Genome Sequencing of 18 <i>Francisella</i> Strains To Aid in Assay Development and Testing. <i>Genome Announcements</i> , 2015, 3, .	0.8	16
77	Thirty-Two Complete Genome Assemblies of Nine <i>Yersinia</i> Species, Including <i>Y. pestis</i> , <i>Y. pseudotuberculosis</i> , and <i>Y. enterocolitica</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	31
78	Complete Genome Sequences for 59 <i>Burkholderia</i> Isolates, Both Pathogenic and Near Neighbor. <i>Genome Announcements</i> , 2015, 3, .	0.8	82
79	Finished Genome Sequence of <i>Bacillus cereus</i> Strain O3BB87, a Clinical Isolate with <i>B. anthracis</i> Virulence Genes. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
80	Complete Genome Sequences for 35 Biothreat Assay-Relevant <i>Bacillus</i> Species. <i>Genome Announcements</i> , 2015, 3, .	0.8	52
81	Under-detection of endospore-forming Firmicutes in metagenomic data. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 299-306.	1.9	88
82	Improved Assemblies Using a Source-Agnostic Pipeline for MetaGenomic Assembly by Merging (MeGAMerge) of Contigs. <i>Scientific Reports</i> , 2015, 4, 6480.	1.6	39
83	Adaptation Genomics of a Small-Colony Variant in a <i>Pseudomonas chlororaphis</i> 30-84 Biofilm. <i>Applied and Environmental Microbiology</i> , 2015, 81, 890-899.	1.4	38
84	Ecological roles of dominant and rare prokaryotes in acid mine drainage revealed by metagenomics and metatranscriptomics. <i>ISME Journal</i> , 2015, 9, 1280-1294.	4.4	207
85	CRP-Mediated Carbon Catabolite Regulation of <i>Yersinia pestis</i> Biofilm Formation Is Enhanced by the Carbon Storage Regulator Protein, CsrA. <i>PLoS ONE</i> , 2015, 10, e0135481.	1.1	39
86	Recruiting Human Microbiome Shotgun Data to Site-Specific Reference Genomes. <i>PLoS ONE</i> , 2014, 9, e84963.	1.1	6
87	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. <i>PLoS Biology</i> , 2014, 12, e1001920.	2.6	190
88	Draft Genome Assembly of <i>Acinetobacter baumannii</i> ATCC 19606. <i>Genome Announcements</i> , 2014, 2, .	0.8	20
89	Genome Sequencing of 15 Clinical <i>Vibrio</i> Isolates, Including 13 Non-O1/Non-O139 Serogroup Strains. <i>Genome Announcements</i> , 2014, 2, .	0.8	8
90	Whole-Genome Sequence of <i>Listeria monocytogenes</i> Type Strain 53 XXIII. <i>Genome Announcements</i> , 2014, 2, .	0.8	0

#	ARTICLE	IF	CITATIONS
91	Genome Assembly of <i>Shigella flexneri</i> ATCC 12022, a Quality Control Reference Strain. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
92	Complete Genome Assembly of <i>Staphylococcus epidermidis</i> AmMS 205. <i>Genome Announcements</i> , 2014, 2, .	0.8	3
93	Whole-Genome Assemblies of 56 <i>Burkholderia</i> Species. <i>Genome Announcements</i> , 2014, 2, .	0.8	27
94	Genome Sequences of Two Carbapenemase-Resistant <i>Klebsiella pneumoniae</i> ST258 Isolates. <i>Genome Announcements</i> , 2014, 2, .	0.8	10
95	Rapid evaluation and quality control of next generation sequencing data with FaQCs. <i>BMC Bioinformatics</i> , 2014, 15, 366.	1.2	176
96	Facile, High Quality Sequencing of Bacterial Genomes from Small Amounts of DNA. <i>International Journal of Genomics</i> , 2014, 2014, 1-8.	0.8	1
97	Comparative genomics of enterohemorrhagic <i>Escherichia coli</i> O145:H28 demonstrates a common evolutionary lineage with <i>Escherichia coli</i> O157:H7. <i>BMC Genomics</i> , 2014, 15, 17.	1.2	84
98	Contrasting elevational diversity patterns between eukaryotic soil microbes and plants. <i>Ecology</i> , 2014, 95, 3190-3202.	1.5	174
99	Soil Microbial Community Responses to a Decade of Warming as Revealed by Comparative Metagenomics. <i>Applied and Environmental Microbiology</i> , 2014, 80, 1777-1786.	1.4	131
100	Standards for Sequencing Viral Genomes in the Era of High-Throughput Sequencing. <i>MBio</i> , 2014, 5, e01360-14.	1.8	89
101	Genome sequence of the <i>Lotus corniculatus</i> microsymbiont <i>Mesorhizobium loti</i> strain R88B. <i>Standards in Genomic Sciences</i> , 2014, 9, 3.	1.5	12
102	Genome sequence of the <i>Lotus</i> spp. microsymbiont <i>Mesorhizobium loti</i> strain NZP2037. <i>Standards in Genomic Sciences</i> , 2014, 9, 7.	1.5	5
103	Draft Genome Assembly of <i>Klebsiella pneumoniae</i> Type Strain ATCC 13883. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
104	Genome sequence and emended description of <i>Leisingera nanhaiensis</i> strain DSM 24252T isolated from marine sediment. <i>Standards in Genomic Sciences</i> , 2014, 9, 585-601.	1.5	8
105	Genome analyses of the carboxydophilic sulfate-reducers <i>Desulfotomaculum nigrificans</i> and <i>Desulfotomaculum carboxydvorans</i> and reclassification of <i>Desulfotomaculum carboxydvorans</i> as a later synonym of <i>Desulfotomaculum nigrificans</i> . <i>Standards in Genomic Sciences</i> , 2014, 9, 655-675.	1.5	25
106	Genome analysis of <i>Desulfotomaculum gibsoniae</i> strain GrollT a highly versatile Gram-positive sulfate-reducing bacterium. <i>Standards in Genomic Sciences</i> , 2014, 9, 821-839.	1.5	27
107	Complete Genome sequence of <i>Burkholderia phymatum</i> STM815T, a broad host range and efficient nitrogen-fixing symbiont of <i>Mimosa</i> species. <i>Standards in Genomic Sciences</i> , 2014, 9, 763-774.	1.5	71
108	Complete Genome Sequences of Two <i>Escherichia coli</i> O145:H28 Outbreak Strains of Food Origin. <i>Genome Announcements</i> , 2014, 2, .	0.8	25

#	ARTICLE	IF	CITATIONS
109	Genomic and Metabolic Diversity of Marine Group I Thaumarchaeota in the Mesopelagic of Two Subtropical Gyres. PLoS ONE, 2014, 9, e95380.	1.1	95
110	A novel metatranscriptomic approach to identify gene expression dynamics during extracellular electron transfer. Nature Communications, 2013, 4, 1601.	5.8	162
111	<i>Polynucleobacter necessarius</i> , a model for genome reduction in both free-living and symbiotic bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18590-18595.	3.3	80
112	Single-cell and metagenomic analyses indicate a fermentative and saccharolytic lifestyle for members of the OP9 lineage. Nature Communications, 2013, 4, 1854.	5.8	199
113	Microbial community adaptation to quaternary ammonium biocides as revealed by metagenomics. Environmental Microbiology, 2013, 15, 2850-2864.	1.8	82
114	Draft Genome Sequence of Methylomicrobium buryatense Strain 5G, a Haloalkaline-Tolerant Methanotrophic Bacterium. Genome Announcements, 2013, 1, .	0.8	36
115	Draft Genome Sequence of <i>Frankia</i> sp. Strain QA3, a Nitrogen-Fixing Actinobacterium Isolated from the Root Nodule of <i>Alnus nitida</i> . Genome Announcements, 2013, 1, e0010313.	0.8	39
116	Genome Sequences for Three Denitrifying Bacterial Strains Isolated from a Uranium- and Nitrate-Contaminated Subsurface Environment. Genome Announcements, 2013, 1, .	0.8	12
117	Draft Genome Sequence of Medium-Chain-Length Polyhydroxyalkanoate-Producing Pseudomonas putida Strain LS46. Genome Announcements, 2013, 1, e0015113.	0.8	6
118	Complete Genome of <i>Serratia</i> sp. Strain FGI 94, a Strain Associated with Leaf-Cutter Ant Fungus Gardens. Genome Announcements, 2013, 1, e0023912.	0.8	15
119	Draft Genome Sequence of <i>Frankia</i> sp. Strain CN3, an Atypical, Noninfective (Nod ⁺) Ineffective (Fix ⁻) Isolate from <i>Coriaria nepalensis</i> . Genome Announcements, 2013, 1, e0008513.	0.8	51
120	Genome Sequences of Two Klebsiella pneumoniae Isolates from Different Geographical Regions, Argentina (Strain JHCK1) and the United States (Strain VA360). Genome Announcements, 2013, 1, .	0.8	13
121	Draft Genome Sequence and Description of <i>Janthinobacterium</i> sp. Strain CG3, a Psychrotolerant Antarctic Supraglacial Stream Bacterium. Genome Announcements, 2013, 1, .	0.8	10
122	Comparative genome analysis of Burkholderia phytofirmans PsJN reveals a wide spectrum of endophytic lifestyles based on interaction strategies with host plants. Frontiers in Plant Science, 2013, 4, 120.	1.7	219
123	Nearly finished genomes produced using gel microdroplet culturing reveal substantial intraspecies genomic diversity within the human microbiome. Genome Research, 2013, 23, 878-888.	2.4	53
124	Genome sequence of the clover-nodulating Rhizobium leguminosarum bv. trifolii strain SRDI943.. Standards in Genomic Sciences, 2013, 9, 232-242.	1.5	3
125	Genome sequence of Ensifer medicae strain WSM1115; an acid-tolerant Medicago-nodulating microsymbiont from Samothraki, Greece. Standards in Genomic Sciences, 2013, 9, 514-526.	1.5	2
126	Genome analysis of Desulfotomaculum kuznetsovii strain 17T reveals a physiological similarity with Pelotomaculum thermopropionicum strain SIT.. Standards in Genomic Sciences, 2013, 8, 69-87.	1.5	42

#	ARTICLE	IF	CITATIONS
127	Permanent draft genome sequences of the symbiotic nitrogen fixing Ensifer meliloti strains BO21CC and AK58. Standards in Genomic Sciences, 2013, 9, 352-333.	1.5	7
128	Genome sequence of the phage-gene rich marine Phaeobacter arcticus type strain DSM 23566T. Standards in Genomic Sciences, 2013, 8, 450-464.	1.5	9
129	Genome sequence of the Leisingera aquimarina type strain (DSM 24565T), a member of the marine Roseobacter clade rich in extrachromosomal elements. Standards in Genomic Sciences, 2013, 8, 389-402.	1.5	17
130	Genome sequence of Phaeobacter caeruleus type strain (DSM 24564T), a surface-associated member of the marine Roseobacter clade. Standards in Genomic Sciences, 2013, 8, 403-419.	1.5	12
131	Non-contiguous finished genome sequence of plant-growth promoting Serratia proteamaculans S4. Standards in Genomic Sciences, 2013, 8, 441-449.	1.5	26
132	Genome sequence of the clover-nodulating Rhizobium leguminosarum bv. trifolii strain SRDI565.. Standards in Genomic Sciences, 2013, 9, 220-231.	1.5	4
133	Genome sequence of Phaeobacter daeponensis type strain (DSM 23529T), a facultatively anaerobic bacterium isolated from marine sediment, and emendation of Phaeobacter daeponensis. Standards in Genomic Sciences, 2013, 9, 142-159.	1.5	12
134	Complete genome sequence of the marine methyl-halide oxidizing Leisingera methylohalidivorans type strain (DSM 14336T), a representative of the Roseobacter clade. Standards in Genomic Sciences, 2013, 9, 128-141.	1.5	15
135	Complete genome sequence of Enterobacter sp. IIT-BT 08: A potential microbial strain for high rate hydrogen production. Standards in Genomic Sciences, 2013, 9, 359-369.	1.5	16
136	Genome sequence of Phaeobacter inhibens type strain (T5T), a secondary metabolite producing representative of the marine Roseobacter clade, and emendation of the species description of Phaeobacter inhibens. Standards in Genomic Sciences, 2013, 9, 334-350.	1.5	26
137	Complete Genome of <i>Enterobacteriaceae</i> Bacterium Strain FGI 57, a Strain Associated with Leaf-Cutter Ant Fungus Gardens. Genome Announcements, 2013, 1, .	0.8	4
138	Proteogenomic Analysis of a Thermophilic Bacterial Consortium Adapted to Deconstruct Switchgrass. PLoS ONE, 2013, 8, e68465.	1.1	62
139	Genome sequence of Phaeobacter caeruleus type strain (DSM 24564(T)), a surface-associated member of the marine Roseobacter clade. Standards in Genomic Sciences, 2013, 8, 403-19.	1.5	12
140	Challenge of Metagenome Assembly and Possible Standards. , 2013, , 1-10.		0
141	Complete Genome Sequences of Desulfosporosinus orientis DSM765 ^T , Desulfosporosinus youngiae DSM17734 ^T , Desulfosporosinus meridiei DSM13257 ^T , and Desulfosporosinus acidiphilus DSM22704 ^T . Journal of Bacteriology, 2012, 194, 6300-6301.	1.0	73
142	Genomic Comparison of Escherichia coli O104:H4 Isolates from 2009 and 2011 Reveals Plasmid, and Prophage Heterogeneity, Including Shiga Toxin Encoding Phage stx2. PLoS ONE, 2012, 7, e48228.	1.1	118
143	Complete Genome Sequence of Francisella philomiragia ATCC 25017. Journal of Bacteriology, 2012, 194, 3266-3266.	1.0	18
144	Genome Sequence of Kingella kingae Septic Arthritis Isolate PYKK081. Journal of Bacteriology, 2012, 194, 3017-3017.	1.0	17

#	ARTICLE	IF	CITATIONS
145	Saliva microbiomes distinguish caries-active from healthy human populations. ISME Journal, 2012, 6, 1-10.	4.4	320
146	Multidrug-resistant (MDR) <i>Klebsiella pneumoniae</i> clinical isolates: a zone of high heterogeneity (HHZ) as a tool for epidemiological studies. Clinical Microbiology and Infection, 2012, 18, E254-E258.	2.8	16
147	Metagenome, metatranscriptome and single-cell sequencing reveal microbial response to Deepwater Horizon oil spill. ISME Journal, 2012, 6, 1715-1727.	4.4	547
148	Bacterial Genome Annotation. Methods in Molecular Biology, 2012, 881, 471-503.	0.4	7
149	Capturing Single Cell Genomes of Active Polysaccharide Degradors: An Unexpected Contribution of Verrucomicrobia. PLoS ONE, 2012, 7, e35314.	1.1	236
150	Artificial Polyploidy Improves Bacterial Single Cell Genome Recovery. PLoS ONE, 2012, 7, e37387.	1.1	22
151	A programmable droplet-based microfluidic device applied to multiparameter analysis of single microbes and microbial communities. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7665-7670.	3.3	222
152	Next generation sequencing and bioinformatic bottlenecks: the current state of metagenomic data analysis. Current Opinion in Biotechnology, 2012, 23, 9-15.	3.3	296
153	Targeted and shotgun metagenomic approaches provide different descriptions of dryland soil microbial communities in a manipulated field study. Environmental Microbiology Reports, 2012, 4, 248-256.	1.0	58
154	Pathogen comparative genomics in the next-generation sequencing era: genome alignments, pangenomics and metagenomics. Briefings in Functional Genomics, 2011, 10, 322-333.	1.3	41
155	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MlxS) specifications. Nature Biotechnology, 2011, 29, 415-420.	9.4	608
156	<i>Nitrosococcus watsonii</i> sp. nov., a new species of marine obligate ammonia-oxidizing bacteria that is not omnipresent in the world's oceans: calls to validate the names <i>Nitrosococcus halophilus</i> ™ and <i>Nitrosomonas mobilis</i> ™. FEMS Microbiology Ecology, 2011, 76, 39-48.	1.3	74
157	Genomics for Key Players in the N Cycle. Methods in Enzymology, 2011, 496, 289-318.	0.4	3
158	Complete Genome Sequence of the Plant Growth-Promoting Endophyte <i>Burkholderia phytofirmans</i> Strain PsJN. Journal of Bacteriology, 2011, 193, 3383-3384.	1.0	144
159	Genome of the Cyanobacterium <i>Microcoleus vaginatus</i> FGP-2, a Photosynthetic Ecosystem Engineer of Arid Land Soil Biocrusts Worldwide. Journal of Bacteriology, 2011, 193, 4569-4570.	1.0	53
160	Genome of <i>Ochrobactrum anthropi</i> ATCC 49188 ^T , a Versatile Opportunistic Pathogen and Symbiont of Several Eukaryotic Hosts. Journal of Bacteriology, 2011, 193, 4274-4275.	1.0	46
161	The Genome of <i>Akkermansia muciniphila</i> , a Dedicated Intestinal Mucin Degradator, and Its Use in Exploring Intestinal Metagenomes. PLoS ONE, 2011, 6, e16876.	1.1	328
162	Complete genome sequence of <i>Veillonella parvula</i> type strain (Te3T). Standards in Genomic Sciences, 2010, 2, 57-65.	1.5	44

#	ARTICLE	IF	CITATIONS
163	Complete genome sequence of <i>Kribbella flavida</i> type strain (IFO 14399T). <i>Standards in Genomic Sciences</i> , 2010, 2, 185-192.	1.5	11
164	Complete genome sequence of <i>Conexibacter woesei</i> type strain (ID131577T). <i>Standards in Genomic Sciences</i> , 2010, 2, 212-219.	1.5	24
165	Complete genome sequence of the <i>Medicago</i> microsymbiont <i>Ensifer</i> (<i>Sinorhizobium</i>) <i>medicae</i> strain WSM419. <i>Standards in Genomic Sciences</i> , 2010, 2, 77-86.	1.5	100
166	Complete genome sequence of <i>Rhizobium leguminosarum</i> bv <i>trifolii</i> strain WSM2304, an effective microsymbiont of the South American clover <i>Trifolium polymorphum</i> .. <i>Standards in Genomic Sciences</i> , 2010, 2, 66-76.	1.5	60
167	Complete genome sequence of <i>Xylanimonas cellulositytica</i> type strain (XIL07T). <i>Standards in Genomic Sciences</i> , 2010, 2, 1-8.	1.5	10
168	Complete genome sequence of <i>Alicyclobacillus acidocaldarius</i> type strain (104-IAT). <i>Standards in Genomic Sciences</i> , 2010, 2, 9-18.	1.5	24
169	Complete genome sequence of <i>Sphaerobacter thermophilus</i> type strain (S 6022T). <i>Standards in Genomic Sciences</i> , 2010, 2, 49-56.	1.5	27
170	Complete genome sequence of <i>Streptosporangium roseum</i> type strain (NI 9100T). <i>Standards in Genomic Sciences</i> , 2010, 2, 29-37.	1.5	27
171	Complete genome sequence of <i>Chitinophaga pinensis</i> type strain (UQM 2034T). <i>Standards in Genomic Sciences</i> , 2010, 2, 87-95.	1.5	74
172	Complete genome sequence of <i>Sulfurospirillum deleyianum</i> type strain (5175T). <i>Standards in Genomic Sciences</i> , 2010, 2, 149-157.	1.5	29
173	Complete genome sequence of <i>Haloterrigena turkmenica</i> type strain (4kT). <i>Standards in Genomic Sciences</i> , 2010, 2, 107-116.	1.5	32
174	Complete genome sequence of <i>Spirosoma linguale</i> type strain (1T). <i>Standards in Genomic Sciences</i> , 2010, 2, 176-184.	1.5	40
175	Complete genome sequence of <i>Desulfohalobium retbaense</i> type strain (HR100T). <i>Standards in Genomic Sciences</i> , 2010, 2, 38-48.	1.5	22
176	Complete genome sequence of <i>Archaeoglobus profundus</i> type strain (AV18T). <i>Standards in Genomic Sciences</i> , 2010, 2, 327-346.	1.5	26
177	Complete genome sequence of <i>Gordonia bronchialis</i> type strain (3410T). <i>Standards in Genomic Sciences</i> , 2010, 2, 19-28.	1.5	26
178	Phylogenetic and metagenomic analysis of <i>Verrucomicrobia</i> in former agricultural grassland soil. <i>FEMS Microbiology Ecology</i> , 2010, 71, 23-33.	1.3	23
179	The United States of America and Scientific Research. <i>PLoS ONE</i> , 2010, 5, e12203.	1.1	30
180	The Genome Sequence of <i>Psychrobacter arcticus</i> 273-4, a Psychroactive Siberian Permafrost Bacterium, Reveals Mechanisms for Adaptation to Low-Temperature Growth. <i>Applied and Environmental Microbiology</i> , 2010, 76, 2304-2312.	1.4	184

#	ARTICLE	IF	CITATIONS
181	Complete genome sequence of <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> strain WSM1325, an effective microsymbiont of annual Mediterranean clovers.. <i>Standards in Genomic Sciences</i> , 2010, 2, 347-356.	1.5	53
182	Community and gene composition of a human dental plaque microbiota obtained by metagenomic sequencing. <i>Molecular Oral Microbiology</i> , 2010, 25, 391-405.	1.3	78
183	Whole-Genome-Based Phylogeny and Divergence of the Genus <i>Brucella</i> . <i>Journal of Bacteriology</i> , 2009, 191, 2864-2870.	1.0	157
184	Complete genome sequence of <i>Capnocytophaga ochracea</i> type strain (VPI 2845T). <i>Standards in Genomic Sciences</i> , 2009, 1, 101-109.	1.5	14
185	The Complete Plastid Genome Sequence of the Secondarily Nonphotosynthetic Alga <i>Cryptomonas paramecium</i> : Reduction, Compaction, and Accelerated Evolutionary Rate. <i>Genome Biology and Evolution</i> , 2009, 1, 439-448.	1.1	70
186	A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea. <i>Nature</i> , 2009, 462, 1056-1060.	13.7	924
187	Genome Project Standards in a New Era of Sequencing. <i>Science</i> , 2009, 326, 236-237.	6.0	382
188	Complete genome sequence of <i>Halorhabdus utahensis</i> type strain (AX-2T). <i>Standards in Genomic Sciences</i> , 2009, 1, 218-225.	1.5	22
189	Complete genome sequence of <i>Beutenbergia cavernae</i> type strain (HKI 0122T). <i>Standards in Genomic Sciences</i> , 2009, 1, 21-28.	1.5	12
190	Complete genome sequence of <i>Cryptobacterium curtum</i> type strain (12-3T). <i>Standards in Genomic Sciences</i> , 2009, 1, 93-100.	1.5	17
191	Complete genome sequence of <i>Desulfomicrobium baculatum</i> type strain (XT). <i>Standards in Genomic Sciences</i> , 2009, 1, 29-37.	1.5	36
192	Complete genome sequence of <i>Acidimicrobium ferrooxidans</i> type strain (ICPT). <i>Standards in Genomic Sciences</i> , 2009, 1, 38-45.	1.5	32
193	Complete genome sequence of <i>Sanguibacter keddiei</i> type strain (ST-74T). <i>Standards in Genomic Sciences</i> , 2009, 1, 110-118.	1.5	16
194	Complete genome sequence of <i>Catenulispora acidiphila</i> type strain (ID 139908T). <i>Standards in Genomic Sciences</i> , 2009, 1, 119-125.	1.5	24
195	Complete genome sequence of <i>Leptotrichia buccalis</i> type strain (C-1013-bT). <i>Standards in Genomic Sciences</i> , 2009, 1, 126-132.	1.5	24
196	Complete genome sequence of <i>Saccharomonospora viridis</i> type strain (P101T). <i>Standards in Genomic Sciences</i> , 2009, 1, 141-149.	1.5	24
197	Complete genome sequence of <i>Actinosynnema mirum</i> type strain (101T). <i>Standards in Genomic Sciences</i> , 2009, 1, 46-53.	1.5	38
198	Complete genome sequence of <i>Halogeometricum borinquense</i> type strain (PR3T). <i>Standards in Genomic Sciences</i> , 2009, 1, 150-158.	1.5	23

#	ARTICLE	IF	CITATIONS
199	Complete genome sequence of <i>Anaerococcus prevotii</i> type strain (PC1T). Standards in Genomic Sciences, 2009, 1, 159-165.	1.5	25
200	Complete genome sequence of <i>Atopobium parvulum</i> type strain (IPP 1246T). Standards in Genomic Sciences, 2009, 1, 166-173.	1.5	30
201	Complete genome sequence of <i>Eggerthella lenta</i> type strain (VPI 0255T). Standards in Genomic Sciences, 2009, 1, 174-182.	1.5	37
202	Complete genome sequence of <i>Kangiella koreensis</i> type strain (SW-125T). Standards in Genomic Sciences, 2009, 1, 226-233.	1.5	28
203	Complete genome sequence of <i>Jonesia denitrificans</i> type strain (Prevot 55134T). Standards in Genomic Sciences, 2009, 1, 262-269.	1.5	14
204	Complete genome sequence of <i>Halomicrobium mukohataei</i> type strain (arg-2T). Standards in Genomic Sciences, 2009, 1, 270-277.	1.5	31
205	Complete genome sequence of <i>Rhodothermus marinus</i> type strain (R-10T). Standards in Genomic Sciences, 2009, 1, 283-290.	1.5	45
206	Complete genome sequence of <i>Streptobacillus moniliformis</i> type strain (9901T). Standards in Genomic Sciences, 2009, 1, 300-307.	1.5	21
207	Complete genome sequence of <i>Brachybacterium faecium</i> type strain (Schefferle 6-10T). Standards in Genomic Sciences, 2009, 1, 3-11.	1.5	25
208	Complete genome sequence of <i>Pirellula staleyi</i> type strain (ATCC 27377T). Standards in Genomic Sciences, 2009, 1, 308-316.	1.5	34
209	Complete genome sequence of <i>Kytococcus sedentarius</i> type strain (541T). Standards in Genomic Sciences, 2009, 1, 12-20.	1.5	100
210	Complete genome sequence of <i>Dyadobacter fermentans</i> type strain (NS114T). Standards in Genomic Sciences, 2009, 1, 133-140.	1.5	25
211	Complete genome sequence of <i>Thermanaerovibrio acidaminovorans</i> type strain (Su883T). Standards in Genomic Sciences, 2009, 1, 254-261.	1.5	23
212	Complete genome sequence of <i>Slackia heliotrinireducens</i> type strain (RHS 1T). Standards in Genomic Sciences, 2009, 1, 234-241.	1.5	20
213	Complete genome sequence of <i>Desulfotomaculum acetoxidans</i> type strain (5575T). Standards in Genomic Sciences, 2009, 1, 242-253.	1.5	35
214	Complete genome sequence of <i>Stackebrandtia nassauensis</i> type strain (LLR-40K-21T). Standards in Genomic Sciences, 2009, 1, 292-299.	1.5	23
215	Molecular characterization of L-413C, a P2-related plague diagnostic bacteriophage. Virology, 2008, 372, 85-96.	1.1	30
216	Complete Genome Sequence of <i>Nitrobacter hamburgensis</i> X14 and Comparative Genomic Analysis of Species within the Genus <i>Nitrobacter</i> . Applied and Environmental Microbiology, 2008, 74, 2852-2863.	1.4	115

#	ARTICLE	IF	CITATIONS
217	Multiple genome sequences reveal adaptations of a phototrophic bacterium to sediment microenvironments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 18543-18548.	3.3	131
218	Divergence among Genes Encoding the Elongation Factor Tu of <i>Yersinia</i> Species. <i>Journal of Bacteriology</i> , 2008, 190, 7548-7558.	1.0	22
219	Genome of the Epsilonproteobacterial Chemolithoautotroph <i>Sulfurimonas denitrificans</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 1145-1156.	1.4	228
220	Complete Genome Sequence of <i>Nitrosospira multiformis</i> , an Ammonia-Oxidizing Bacterium from the Soil Environment. <i>Applied and Environmental Microbiology</i> , 2008, 74, 3559-3572.	1.4	212
221	Comparative Transcriptome Analysis of <i>Methylobium petroleiphilum</i> PM1 Exposed to the Fuel Oxygenates Methyl <i>tert</i> -Butyl Ether and Ethanol. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7347-7357.	1.4	39
222	Whole-Genome Analysis of the Methyl <i>tert</i> -Butyl Ether-Degrading Beta-Proteobacterium <i>Methylobium petroleiphilum</i> PM1. <i>Journal of Bacteriology</i> , 2007, 189, 1931-1945.	1.0	139
223	The Impact of Genome Analyses on Our Understanding of Ammonia-Oxidizing Bacteria. <i>Annual Review of Microbiology</i> , 2007, 61, 503-528.	2.9	165
224	Whole-genome analysis of the ammonia-oxidizing bacterium, <i>Nitrosomonas eutropha</i> C91: implications for niche adaptation. <i>Environmental Microbiology</i> , 2007, 9, 2993-3007.	1.8	150
225	Pestoides F, an Atypical <i>Yersinia pestis</i> Strain from the Former Soviet Union. <i>Advances in Experimental Medicine and Biology</i> , 2007, 603, 17-22.	0.8	37
226	Array2BIO: from microarray expression data to functional annotation of co-regulated genes. <i>BMC Bioinformatics</i> , 2006, 7, 307.	1.2	9
227	The Genome of Deep-Sea Vent Chemolithoautotroph <i>Thiomicrospira crunogena</i> XCL-2. <i>PLoS Biology</i> , 2006, 4, e383.	2.6	144
228	Identification of MglA-Regulated Genes Reveals Novel Virulence Factors in <i>Francisella tularensis</i> . <i>Infection and Immunity</i> , 2006, 74, 6642-6655.	1.0	165
229	Complete Genome Sequence of the Marine, Chemolithoautotrophic, Ammonia-Oxidizing Bacterium <i>Nitrosococcus oceani</i> ATCC 19707. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6299-6315.	1.4	139
230	<i>Burkholderia xenovorans</i> LB400 harbors a multi-replicon, 9.73-Mbp genome shaped for versatility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15280-15287.	3.3	339
231	The Genome Sequence of the Obligately Chemolithoautotrophic, Facultatively Anaerobic Bacterium <i>Thiobacillus denitrificans</i> . <i>Journal of Bacteriology</i> , 2006, 188, 1473-1488.	1.0	306
232	Genome Sequence of the Chemolithoautotrophic Nitrite-Oxidizing Bacterium <i>Nitrobacter winogradskyi</i> Nb-255. <i>Applied and Environmental Microbiology</i> , 2006, 72, 2050-2063.	1.4	169
233	Complete Genome Sequence of <i>Yersinia pestis</i> Strains Antiqua and Nepal516: Evidence of Gene Reduction in an Emerging Pathogen. <i>Journal of Bacteriology</i> , 2006, 188, 4453-4463.	1.0	174
234	The complete genome sequence of <i>Francisella tularensis</i> , the causative agent of tularemia. <i>Nature Genetics</i> , 2005, 37, 153-159.	9.4	436

#	ARTICLE	IF	CITATIONS
235	Comparison of the complete genome sequences of <i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a and pv. <i>tomato</i> DC3000. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 11064-11069.	3.3	399
236	Whole-Genome Analyses of Speciation Events in Pathogenic <i>Brucellae</i> . <i>Infection and Immunity</i> , 2005, 73, 8353-8361.	1.0	179
237	Complete genome sequence of the metabolically versatile photosynthetic bacterium <i>Rhodospseudomonas palustris</i> . <i>Nature Biotechnology</i> , 2004, 22, 55-61.	9.4	675
238	Genome divergence in two <i>Prochlorococcus</i> ecotypes reflects oceanic niche differentiation. <i>Nature</i> , 2003, 424, 1042-1047.	13.7	1,086
239	Complete Genome Sequence of the Ammonia-Oxidizing Bacterium and Obligate Chemolithoautotroph <i>Nitrosomonas europaea</i> . <i>Journal of Bacteriology</i> , 2003, 185, 2759-2773.	1.0	510
240	An applications-focused review of comparative genomics tools: Capabilities, limitations and future challenges. <i>Briefings in Bioinformatics</i> , 2003, 4, 105-123.	3.2	59
241	The Genome Sequence of <i>Yersinia pestis</i> Bacteriophage Ψ A1122 Reveals an Intimate History with the Coliphage T3 and T7 Genomes. <i>Journal of Bacteriology</i> , 2003, 185, 5248-5262.	1.0	95
242	The Composite Genome of the Legume Symbiont <i>Sinorhizobium meliloti</i> . <i>Science</i> , 2001, 293, 668-672.	6.0	1,098
243	oriT-Directed Cloning of Defined Large Regions from Bacterial Genomes: Identification of the <i>Sinorhizobium meliloti</i> pExo Megaplasmid Replicator Region. <i>Journal of Bacteriology</i> , 2000, 182, 5486-5494.	1.0	23
244	Cantilevering vertical tow nets to reduce tow-line-induced zooplankton avoidance. <i>Journal of Plankton Research</i> , 1993, 15, 581-587.	0.8	20
245	A 3D-printed microfluidic "bridge" device for active dispersal of flagellated bacteria. , 0, , .		0