

Jonathan A Eisen

List of Publications by Year in descending order

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Version: 2024-02-01

430
papers

70,550
citations

2696

98
h-index

804

253
g-index

529
all docs

529
docs citations

529
times ranked

66923
citing authors

#	ARTICLE	IF	CITATIONS
1	Metagenomic methylation patterns resolve bacterial genomes of unusual size and structural complexity. ISME Journal, 2022, 16, 1921-1931.	4.4	11
2	Teredinibacter haidensis sp. nov., Teredinibacter purpureus sp. nov. and Teredinibacter franksiae sp. nov., marine, cellulolytic endosymbiotic bacteria isolated from the gills of the wood-boring mollusc <i>Bankia setacea</i> (Bivalvia: Teredinidae) and emended description of the genus <i>Teredinibacter</i> . International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	20
3	Global Diversity and Biogeography of the <i>Zostera marina</i> Mycobiome. Applied and Environmental Microbiology, 2021, 87, e0279520.	1.4	19
4	SARS-CoV-2 detection and genomic sequencing from hospital surface samples collected at UC Davis. PLoS ONE, 2021, 16, e0253578.	1.1	37
5	A global metagenomic map of urban microbiomes and antimicrobial resistance. Cell, 2021, 184, 3376-3393.e17.	13.5	164
6	Global biogeography of chemosynthetic symbionts reveals both localized and globally distributed symbiont groups. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	15
7	Natural experiments and long-term monitoring are critical to understand and predict marine hostâ€microbe ecology and evolution. PLoS Biology, 2021, 19, e3001322.	2.6	17
8	Reconstruction of Metagenome-Assembled Genomes from Aquaria. Microbiology Resource Announcements, 2021, 10, e0055721.	0.3	1
9	Draft Genome Sequences and Genomic Analysis for Pigment Production in Bacteria Isolated from Blue Discolored Soymilk and Tofu. Journal of Genomics, 2021, 9, 55-67.	0.6	2
10	Energetic and Environmental Constraints on the Community Structure of Benthic Microbial Mats in Lake Fryxell, Antarctica. FEMS Microbiology Ecology, 2020, 96, .	1.3	13
11	The emergence of microbiome centres. Nature Microbiology, 2020, 5, 2-3.	5.9	13
12	Combining Microbial Culturing With Mathematical Modeling in an Introductory Course-Based Undergraduate Research Experience. Frontiers in Microbiology, 2020, 11, 581903.	1.5	1
13	Fungi, bacteria and oomycota opportunistically isolated from the seagrass, <i>Zostera marina</i> . PLoS ONE, 2020, 15, e0236135.	1.1	35
14	Ancestral Absence of Electron Transport Chains in Patescibacteria and DPANN. Frontiers in Microbiology, 2020, 11, 1848.	1.5	62
15	A phylogenetically novel cyanobacterium most closely related to <i>Gloeobacter</i>. ISME Journal, 2020, 14, 2142-2152.	4.4	45
16	Roadmap for naming uncultivated Archaea and Bacteria. Nature Microbiology, 2020, 5, 987-994.	5.9	115
17	Draft Genome Analysis of <i>Christensenella minuta</i> DSM 22607, exhibiting an unusual expansion of transporter homologs of unknown function. Journal of Genomics, 2020, 8, 25-29.	0.6	5
18	Reply to McDonald, â€œProtections against the Risk of Airborne SARS-CoV-2 Infectionâ€• MSystems, 2020, 5, .	1.7	0

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19	Whole genome sequence analysis reveals the broad distribution of the RtxA type 1 secretion system and four novel putative type 1 secretion systems throughout the Legionella genus. PLoS ONE, 2020, 15, e0223033.	1.1	5
20	2019 Novel Coronavirus (COVID-19) Pandemic: Built Environment Considerations To Reduce Transmission. MSystems, 2020, 5, .	1.7	302
21	Bacterial Community Sequences of Submerged Aquatic Vegetation in the Potomac River. Microbiology Resource Announcements, 2020, 9, .	0.3	0
22	Environmental control on the distribution of metabolic strategies of benthic microbial mats in Lake Fryxell, Antarctica. PLoS ONE, 2020, 15, e0231053.	1.1	13
23	Teredinibacter waterburyi sp. nov., a marine, cellulolytic endosymbiotic bacterium isolated from the gills of the wood-boring mollusc Bankia setacea (Bivalvia: Teredinidae) and emended description of the genus Teredinibacter. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2388-2394.	0.8	18
24	Bacterial communities associated with cell phones and shoes. PeerJ, 2020, 8, e9235.	0.9	6
25	Isolation and sequence-based characterization of a koala symbiont: <i>Lonepinella koalarum</i> . PeerJ, 2020, 8, e10177.	0.9	5
26	Title is missing!. , 2020, 15, e0223033.		0
27	Title is missing!. , 2020, 15, e0223033.		0
28	Title is missing!. , 2020, 15, e0223033.		0
29	Title is missing!. , 2020, 15, e0223033.		0
30	Fungi, bacteria and oomycota opportunistically isolated from the seagrass, Zostera marina. , 2020, 15, e0236135.		0
31	Fungi, bacteria and oomycota opportunistically isolated from the seagrass, Zostera marina. , 2020, 15, e0236135.		0
32	Fungi, bacteria and oomycota opportunistically isolated from the seagrass, Zostera marina. , 2020, 15, e0236135.		0
33	Fungi, bacteria and oomycota opportunistically isolated from the seagrass, Zostera marina. , 2020, 15, e0236135.		0
34	Comparison of Whole-Genome Sequences of <i>Legionella pneumophila</i> in Tap Water and in Clinical Strains, Flint, Michigan, USA, 2016. Emerging Infectious Diseases, 2019, 25, 2013-2020.	2.0	14
35	Prospecting Microbial Strains for Bioremediation and Probiotics Development for Metaorganism Research and Preservation. Journal of Visualized Experiments, 2019, , .	0.2	7
36	Host-associated microbiomes drive structure and function of marine ecosystems. PLoS Biology, 2019, 17, e3000533.	2.6	103

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37	Bacteria isolated from Bengal cat (<i>Felis catus</i> Æ <i>Prionailurus bengalensis</i>) anal sac secretions produce volatile compounds potentially associated with animal signaling. <i>PLoS ONE</i> , 2019, 14, e0216846.	1.1	11
38	Genomes from bacteria associated with the canine oral cavity: A test case for automated genome-based taxonomic assignment. <i>PLoS ONE</i> , 2019, 14, e0214354.	1.1	7
39	Microbial Community Succession and Nutrient Cycling Responses following Perturbations of Experimental Saltwater Aquaria. <i>MSphere</i> , 2019, 4, .	1.3	14
40	Metagenome-assembled genomes provide new insight into the microbial diversity of two thermal pools in Kamchatka, Russia. <i>Scientific Reports</i> , 2019, 9, 3059.	1.6	63
41	Characterization of the Mycobiome of the Seagrass, <i>Zostera marina</i> , Reveals Putative Associations With Marine Chytrids. <i>Frontiers in Microbiology</i> , 2019, 10, 2476.	1.5	34
42	Marine probiotics: increasing coral resistance to bleaching through microbiome manipulation. <i>ISME Journal</i> , 2019, 13, 921-936.	4.4	269
43	The Cloacal Microbiome of Five Wild Duck Species Varies by Species and Influenza A Virus Infection Status. <i>MSphere</i> , 2018, 3, .	1.3	28
44	Nitrogen fixation in a landrace of maize is supported by a mucilage-associated diazotrophic microbiota. <i>PLoS Biology</i> , 2018, 16, e2006352.	2.6	236
45	Characterization of shifts of koala (<i>Phascolarctos cinereus</i>) intestinal microbial communities associated with antibiotic treatment. <i>PeerJ</i> , 2018, 6, e4452.	0.9	30
46	Effects of preservation method on canine (<i>Canis lupus familiaris</i>) fecal microbiota. <i>PeerJ</i> , 2018, 6, e4827.	0.9	18
47	Genomic attributes of extended-spectrum β -lactamase-producing <i>Escherichia coli</i> isolated from patients in Lebanon. <i>Future Microbiology</i> , 2017, 12, 213-226.	1.0	10
48	Complete genome sequence of <i>Jiangella gansuensis</i> strain YIM 002T (DSM 44835T), the type species of the genus <i>Jiangella</i> and source of new antibiotic compounds. <i>Standards in Genomic Sciences</i> , 2017, 12, 21.	1.5	9
49	Global-Scale Structure of the Eelgrass Microbiome. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	147
50	Complete Genome Sequence of a <i>Paenacaligenes hominis</i> Strain Isolated from a Paraplegic Patient with Neurogenic Bladder Using Single-Molecule Real-Time Sequencing Technology. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
51	Draft Genome Sequences of <i>Dermacoccus nishinomiyaensis</i> Strains UCD-KPL2534 and UCD-KPL2528 Isolated from an Indoor Track Facility. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
52	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. <i>Nature Biotechnology</i> , 2017, 35, 676-683.	9.4	222
53	Community-Level Differences in the Microbiome of Healthy Wild Mallards and Those Infected by Influenza A Viruses. <i>MSystems</i> , 2017, 2, .	1.7	41
54	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017, 35, 725-731.	9.4	1,512

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55	Complete Genome Sequence of <i>Dolosigranulum pigrum</i> from a Patient with Interstitial Lung Disease Using Single-Molecule Real-Time Sequencing Technology. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
56	Draft genome sequences of eight bacteria isolated from the indoor environment: <i>Staphylococcus capitis</i> strain H36, <i>S. capitis</i> strain H65, <i>S. cohnii</i> strain H62, <i>S. hominis</i> strain H69, <i>Microbacterium</i> sp. strain H83, <i>Mycobacterium iranicum</i> strain H39, <i>Plantibacter</i> sp. strain H53, and <i>Pseudomonas oryzihabitans</i> strain H72. <i>Standards in Genomic Sciences</i> , 2017, 12, 17.	1.5	9
57	Draft Genome Sequence of <i>Propionibacterium avidum</i> Strain UCD-PD2 Isolated from a Feline Anal Sac. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
58	The Green Berry Consortia of the Sippewissett Salt Marsh: Millimeter-Sized Aggregates of Diazotrophic Unicellular Cyanobacteria. <i>Frontiers in Microbiology</i> , 2017, 8, 1623.	1.5	7
59	Rokubacteria: Genomic Giants among the Uncultured Bacterial Phyla. <i>Frontiers in Microbiology</i> , 2017, 8, 2264.	1.5	142
60	Research priorities for harnessing plant microbiomes in sustainable agriculture. <i>PLoS Biology</i> , 2017, 15, e2001793.	2.6	640
61	Draft Genome Sequence of <i>Arthrobacter</i> sp. Strain UCD-GKA (Phylum Actinobacteria). <i>Genome Announcements</i> , 2017, 5, .	0.8	3
62	Microbial communities in sediment from <i>Zostera marina</i> patches, but not the <i>Z. Âmarina</i> leaf or root microbiomes, vary in relation to distance from patch edge. <i>PeerJ</i> , 2017, 5, e3246.	0.9	115
63	Draft Genome Sequences of <i>Pseudomonas moraviensis</i> UCD-KL30, <i>Vibrio ostreicida</i> UCD-KL16, <i>Colwellia</i> sp. Strain UCD-KL20, <i>Shewanella</i> sp. Strain UCD-KL12, and <i>Shewanella</i> sp. Strain UCD-KL21, Isolated from Seagrass. <i>Genome Announcements</i> , 2017, 5, .	0.8	10
64	Gut Check: The evolution of an educational board game. <i>PLoS Biology</i> , 2017, 15, e2001984.	2.6	31
65	Microbiome succession during ammonification in eelgrass bed sediments. <i>PeerJ</i> , 2017, 5, e3674.	0.9	24
66	A microbial survey of the International Space Station (ISS). <i>PeerJ</i> , 2017, 5, e4029.	0.9	52
67	Draft Genome Sequence of <i>Enterococcus faecalis</i> Strain UCD-PD3. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
68	Draft Genome Sequence of <i>Tenacibaculum soleae</i> UCD-KL19. <i>Genome Announcements</i> , 2016, 4, .	0.8	18
69	Draft Genome Sequence of <i>Curtobacterium</i> sp. Strain UCD-KPL2560 (Phylum) Tj ETQq1 1 0.784314 rgBT /Oyerlock 1Q Tf 50 182		
70	Genes Required for the Anti-fungal Activity of a Bacterial Endophyte Isolated from a Corn Landrace Grown Continuously by Subsistence Farmers Since 1000 BC. <i>Frontiers in Microbiology</i> , 2016, 7, 1548.	1.5	22
71	Additional Draft Genome Sequences of <i>Escherichia coli</i> Strains Isolated from Septic Patients. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
72	Draft Genome Sequence of <i>Cobetia</i> sp. UCD-24C, Isolated from Roots and Leaves of the Seagrass <i>Zostera marina</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	5

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73	Draft Genome Sequences of <i>Acinetobacter baumannii</i> Strains Harboring the <i>bla</i> _{NDM-1} Gene Isolated in Lebanon from Civilians Wounded during the Syrian Civil War. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
74	Recent Outbreaks of Shigellosis in California Caused by Two Distinct Populations of <i>Shigella sonnei</i> with either Increased Virulence or Fluoroquinolone Resistance. <i>MSphere</i> , 2016, 1, .	1.3	40
75	Draft Genome Sequence of <i>Klebsiella pneumoniae</i> UCD-JA29 Isolated from a Patient with Sepsis. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
76	Ten questions concerning the microbiomes of buildings. <i>Building and Environment</i> , 2016, 109, 224-234.	3.0	143
77	Root-hair endophyte stacking in finger millet creates a physicochemical barrier to trap the fungal pathogen <i>Fusarium graminearum</i> . <i>Nature Microbiology</i> , 2016, 1, 16167.	5.9	113
78	Draft Genome Sequence of <i>Gordonia</i> sp. Strain UCD-TK1 (Phylum Actinobacteria). <i>Genome Announcements</i> , 2016, 4, .	0.8	4
79	Genome Sequence of a Multidrug-Resistant Strain of <i>Bacillus pumilus</i> , CB01, Isolated from the Feces of an American Crow, <i>Corvus brachyrhynchos</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	1
80	Draft Genome Sequences of Two <i>Pseudoalteromonas</i> Strains Isolated from Roots and Leaf Blades of the Seagrass <i>Zostera marina</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	3
81	Draft Genome Sequences of Two <i>Pseudoalteromonas porphyrae</i> Strains Isolated from Seagrass Sediment. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
82	Draft Genome Sequences of Two <i>Vibrio splendidus</i> Strains, Isolated from Seagrass Sediment. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
83	Draft Genome Sequence of <i>Klebsiella pneumoniae</i> KGM-IMP216 Harboring <i>bla</i> _{CTX-M-15} , <i>bla</i> _{DHA-1} , <i>bla</i> _{TEM-1B} , <i>bla</i> _{NDM-1} , <i>bla</i> _{SHV-28} , and <i>bla</i> _{OXA-1} , Isolated from a Patient in Lebanon. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
84	Microbial Mat Communities along an Oxygen Gradient in a Perennially Ice-Covered Antarctic Lake. <i>Applied and Environmental Microbiology</i> , 2016, 82, 620-630.	1.4	69
85	Genome Analysis of <i>Streptococcus pyogenes</i> Associated with Pharyngitis and Skin Infections. <i>PLoS ONE</i> , 2016, 11, e0168177.	1.1	20
86	Growth of 48 built environment bacterial isolates on board the International Space Station (ISS). <i>PeerJ</i> , 2016, 4, e1842.	0.9	37
87	PHYLOGENETIC DIVERSITY OF THE MICROBIAL MATS IN LAKE FRYXELL, ANTARCTICA. , 2016, , .		0
88	Draft Genome Sequence of <i>Porphyrobacter mercurialis</i> (sp. nov.) Strain Coronado. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
89	Transcriptomes of post-mitotic neurons identify the usage of alternative pathways during adult and embryonic neuronal differentiation. <i>BMC Genomics</i> , 2015, 16, 1100.	1.2	21
90	Draft Genome Sequence of <i>Planomicrobium glaciei</i> UCD-HAM (Phylum <i>Firmicutes</i>). <i>Genome Announcements</i> , 2015, 3, .	0.8	2

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91	Draft Genome Sequence of <i>Pseudoalteromonas tetraodonis</i> Strain UCD-SED8 (Phylum Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.8	4
92	Draft Genome Sequence of <i>Bacillus safensis</i> JPL-MERTA-8-2, Isolated from a Mars-Bound Spacecraft. Genome Announcements, 2015, 3, .	0.8	8
93	Draft Genome Sequence of <i>Bacillus vietnamensis</i> Strain UCD-SED5 (Phylum Firmicutes). Genome Announcements, 2015, 3, .	0.8	4
94	Whole genome sequencing of extended-spectrum β -lactamase producing <i>Klebsiella pneumoniae</i> isolated from a patient in Lebanon. <i>Frontiers in Cellular and Infection Microbiology</i> , 2015, 5, 32.	1.8	20
95	Comparative Genomics of the Genus <i>Porphyromonas</i> Identifies Adaptations for Heme Synthesis within the Prevalent Canine Oral Species <i>Porphyromonas gingivalis</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 3397-3413.	1.1	23
96	Draft Genome Sequences of 26 <i>Porphyromonas</i> Strains Isolated from the Canine Oral Microbiome. <i>Genome Announcements</i> , 2015, 3, .	0.8	9
97	Draft Genome Sequence of <i>Burkholderia gladioli</i> Strain UCD-UG_CHAPALOTE (Phylum Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.8	6
98	Genome Sequence of the Sulfate-Reducing Thermophilic Bacterium <i>Thermodesulfovibrio yellowstonii</i> Strain DSM 11347 T (Phylum Nitrospirae). <i>Genome Announcements</i> , 2015, 3, .	0.8	17
99	Genome Sequence of a Sulfate-Reducing Thermophilic Bacterium, <i>Thermodesulfobacterium commune</i> DSM 2178 T (Phylum Thermodesulfobacteria). <i>Genome Announcements</i> , 2015, 3, .	0.8	4
100	Structure, variation, and assembly of the root-associated microbiomes of rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E911-20.	3.3	2,016
101	The United States Culture Collection Network (USCCN): Enhancing Microbial Genomics Research through Living Microbe Culture Collections. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5671-5674.	1.4	33
102	Forensic analysis of the microbiome of phones and shoes. <i>Microbiome</i> , 2015, 3, 21.	4.9	140
103	Genomic Encyclopedia of Bacterial and Archaeal Type Strains, Phase III: the genomes of soil and plant-associated and newly described type strains. <i>Standards in Genomic Sciences</i> , 2015, 10, 26.	1.5	74
104	Deep-sea hydrothermal vent bacteria related to human pathogenic <i>Vibrio</i> species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2813-9.	3.3	63
105	Draft Genome Sequence of <i>Enterobacter</i> sp. Strain UCD-UG_FMILLET (Phylum Proteobacteria). <i>Genome Announcements</i> , 2015, 3, .	0.8	1
106	Automated and Accurate Estimation of Gene Family Abundance from Shotgun Metagenomes. <i>PLoS Computational Biology</i> , 2015, 11, e1004573.	1.5	55
107	What does the term microbiome mean? And where did it come from? A bit of a surprise ... <i>The Winnower</i> , 2015, . .	0.0	10
108	<i>Porphyrobacter mercurialis</i> sp. nov., isolated from a stadium seat and emended description of the genus <i>Porphyrobacter</i> . <i>PeerJ</i> , 2015, 3, e1400.	0.9	16

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109	Swabs to genomes: a comprehensive workflow. PeerJ, 2015, 3, e960.	0.9	37
110	Methylisothiazolinone in household items - a growing (or well, killing) problem #germophobia. The Winnower, 2015, , .	0.0	0
111	11+ things everyone needs to know about microbes. The Winnower, 2015, , .	0.0	0
112	MixS-BE: a MixS extension defining a minimum information standard for sequence data from the built environment. ISME Journal, 2014, 8, 1-3.	4.4	127
113	Phylogenetically Driven Sequencing of Extremely Halophilic Archaea Reveals Strategies for Static and Dynamic Osmo-response. PLoS Genetics, 2014, 10, e1004784.	1.5	136
114	Open Science and Reporting Animal Studies: Who's Accountable?. PLoS Biology, 2014, 12, e1001757.	2.6	21
115	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. PLoS Biology, 2014, 12, e1001920.	2.6	190
116	Draft Genome Sequences of Streptococcus pyogenes Strains Associated with Throat and Skin Infections in Lebanon. Genome Announcements, 2014, 2, .	0.8	5
117	microBEnet: Lessons Learned from Building an Interdisciplinary Scientific Community in the Online Sphere. PLoS Biology, 2014, 12, e1001884.	2.6	4
118	Complete Genome Sequence of the Extreme Thermophile Dictyoglomus thermophilum H-6-12. Genome Announcements, 2014, 2, .	0.8	16
119	Draft Genome Sequences of Extended-Spectrum Î²-Lactamase-Producing Escherichia coli Strains Isolated from Patients in Lebanon. Genome Announcements, 2014, 2, .	0.8	0
120	Draft Genome Sequence of the Endosymbiont <i>Candidatus</i> Ruthia magnifica UCD-CM (Phylum Tj ETQ q0 0 0 rgBT /Overlo	0.8	0
121	Draft Genome Sequence of the Pyridinediol-Fermenting Bacterium Synergistes jonesii 78-1. Genome Announcements, 2014, 2, .	0.8	1
122	Draft Genome Sequence of <i>Tatumella</i> sp. Strain UCD-D_suzukii (Phylum <i>Proteobacteria</i>) Isolated from <i>Drosophila suzukii</i> Larvae. Genome Announcements, 2014, 2, .	0.8	4
123	Draft Genome Sequences of Escherichia coli Strains Isolated from Septic Patients. Genome Announcements, 2014, 2, .	0.8	4
124	Microscale sulfur cycling in the phototrophic pink berry consortia of the <i>S</i> spp. Environmental Microbiology, 2014, 16, 3398-3415.	1.8	106
125	The genome of the intracellular bacterium of the coastal bivalve, Solemya velum: a blueprint for thriving in and out of symbiosis. BMC Genomics, 2014, 15, 924.	1.2	26
126	Complete genome sequence of Planctomyces brasiliensis type strain (DSM 5305T), phylogenomic analysis and reclassification of Planctomycetes including the descriptions of Gimesia gen. nov., Planctopirus gen. nov. and Rubinisphaera gen. nov. and emended descriptions of the order Planctomycetales and the family Planctomycetaceae. Standards in Genomic Sciences, 2014, 9, 10.	1.5	76

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127	Draft Genome Sequence of Extended-Spectrum β -Lactamase-Producing <i>Klebsiella pneumoniae</i> Isolated from a Patient in Lebanon. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
128	Genome sequence of the <i>Thermotoga thermarum</i> type strain (LA3T) from an African solfataric spring. <i>Standards in Genomic Sciences</i> , 2014, 9, 1105-1117.	1.5	7
129	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
130	Complete Genome Sequence of <i>Coprothermobacter proteolyticus</i> DSM 5265. <i>Genome Announcements</i> , 2014, 2, .	0.8	8
131	PhyloSift: phylogenetic analysis of genomes and metagenomes. <i>PeerJ</i> , 2014, 2, e243.	0.9	633
132	Strain- and plasmid-level deconvolution of a synthetic metagenome by sequencing proximity ligation products. <i>PeerJ</i> , 2014, 2, e415.	0.9	111
133	The microbes we eat: abundance and taxonomy of microbes consumed in a day's worth of meals for three diet types. <i>PeerJ</i> , 2014, 2, e659.	0.9	85
134	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013, 499, 431-437.	13.7	2,239
135	Insights into the evolution of Darwin's finches from comparative analysis of the <i>Geospiza magnirostris</i> genome sequence. <i>BMC Genomics</i> , 2013, 14, 95.	1.2	38
136	Extraordinary phylogenetic diversity and metabolic versatility in aquifer sediment. <i>Nature Communications</i> , 2013, 4, 2120.	5.8	201
137	Improving the coverage of the cyanobacterial phylum using diversity-driven genome sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1053-1058.	3.3	769
138	Draft Genome Sequence of an Actinobacterium, <i>Brachybacterium muris</i> Strain UCD-AY4. <i>Genome Announcements</i> , 2013, 1, e0008613.	0.8	9
139	Draft Genome Sequence of <i>Microbacterium</i> sp. Strain UCD-TDU (Phylum <i>Actinobacteria</i>). <i>Genome Announcements</i> , 2013, 1, e0012013.	0.8	5
140	Draft Genome Sequence of <i>Kocuria</i> sp. Strain UCD-OTCP (Phylum <i>Actinobacteria</i>). <i>Genome Announcements</i> , 2013, 1, .	0.8	5
141	Draft Genome Sequence of <i>Curtobacterium flaccumfaciens</i> Strain UCD-AKU (Phylum) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 182		
142	Expert Failure: Re-evaluating Research Assessment. <i>PLoS Biology</i> , 2013, 11, e1001677.	2.6	11
143	Gene Conservation among Endospore-Forming Bacteria Reveals Additional Sporulation Genes in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2013, 195, 253-260.	1.0	57
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428	The phylogenetic relationships of <i>Chlorobium tepidum</i> and <i>Chloroflexus aurantiacus</i> based upon their RecA sequences. , 0, .		1
429	Even Superheroes Need Help Sometimes: Three Incredible Tales of Microbial Symbiosis. <i>Frontiers for Young Minds</i> , 0, 6, .	0.8	0
430	An Incredible Invisible World: How Microorganisms Could Take Care of Corals in Difficult Times. <i>Frontiers for Young Minds</i> , 0, 8, .	0.8	0