

# The human gut and groundwater harbor non-photosynthetic candidate phylum sibling to Cyanobacteria

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Genomes from Metagenomics. <i>Science</i> , 2013, 342, 1057-1058.	6.0	149
2	Getting to the bottom of Cyanobacteria. <i>Nature Reviews Microbiology</i> , 2013, 11, 818-819.	13.6	8
4	IM-TORNADO: A Tool for Comparison of 16S Reads from Paired-End Libraries. <i>PLoS ONE</i> , 2014, 9, e114804.	1.1	110
5	An Expanded Genomic Representation of the Phylum Cyanobacteria. <i>Genome Biology and Evolution</i> , 2014, 6, 1031-1045.	1.1	326
6	Inter-species interconnections in acid mine drainage microbial communities. <i>Frontiers in Microbiology</i> , 2014, 5, 367.	1.5	56
7	Diversity and genomic insights into the uncultured <i>Cycloflexi</i> from the human microbiota. <i>Environmental Microbiology</i> , 2014, 16, 2635-2643.	1.8	55
8	High-grain feeding alters caecal bacterial microbiota composition and fermentation and results in caecal mucosal injury in goats. <i>British Journal of Nutrition</i> , 2014, 112, 416-427.	1.2	95
9	Single-cell genomics reveals metabolic strategies for microbial growth and survival in an oligotrophic aquifer. <i>Microbiology (United Kingdom)</i> , 2014, 160, 362-372.	0.7	10
10	The first 1000 cultured species of the human gastrointestinal microbiota. <i>FEMS Microbiology Reviews</i> , 2014, 38, 996-1047.	3.9	923
11	Human Genetics Shape the Gut Microbiome. <i>Cell</i> , 2014, 159, 789-799.	13.5	2,523
12	STAMP: statistical analysis of taxonomic and functional profiles. <i>Bioinformatics</i> , 2014, 30, 3123-3124.	1.8	3,456
13	Conducting a Microbiome Study. <i>Cell</i> , 2014, 158, 250-262.	13.5	625
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17	Metagenome-assembled genomes uncover a global brackish microbiome. <i>Genome Biology</i> , 2015, 16, 279.	3.8	186
18	Evolutionary Ecology of Microorganisms: From the Tamed to the Wild. , 0, , 4.1.2-1-4.1.2-12.		4
19	Improved taxonomic assignment of human intestinal 16S rRNA sequences by a dedicated reference database. <i>BMC Genomics</i> , 2015, 16, 1056.	1.2	127

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20	Advances in Understanding Carboxysome Assembly in <i>Prochlorococcus</i> and <i>Synechococcus</i> Implicate CsoS2 as a Critical Component. <i>Life</i> , 2015, 5, 1141-1171.	1.1	82
21	Comparison of Fecal Microbiota in Children with Autism Spectrum Disorders and Neurotypical Siblings in the Simons Simplex Collection. <i>PLoS ONE</i> , 2015, 10, e0137725.	1.1	173
22	Molecular analysis of single room humidifier bacteriology. <i>Water Research</i> , 2015, 69, 318-327.	5.3	9
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32	Structure, mineralogy, and microbial diversity of geothermal spring microbialites associated with a deep oil drilling in Romania. <i>Frontiers in Microbiology</i> , 2015, 6, 253.	1.5	24
33	Sequencing and beyond: integrating molecular 'omics' for microbial community profiling. <i>Nature Reviews Microbiology</i> , 2015, 13, 360-372.	13.6	544
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39	Fecal microbiota analysis: an overview of sample collection methods and sequencing strategies. <i>Future Microbiology</i> , 2015, 10, 1485-1504.	1.0	90
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41	Assessing the global phylum level diversity within the bacterial domain: A review. <i>Journal of Advanced Research</i> , 2015, 6, 269-282.	4.4	57
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43	Exploration of Microbial Diversity and Community Structure of Lonar Lake: The Only Hypersaline Meteorite Crater Lake within Basalt Rock. <i>Frontiers in Microbiology</i> , 2015, 6, 1553.	1.5	100
44	<i>Mycobacterium avium</i> Subspecies paratuberculosis Infection Modifies Gut Microbiota under Different Dietary Conditions in a Rabbit Model. <i>Frontiers in Microbiology</i> , 2016, 7, 446.	1.5	56
45	Reconstruction of Bacterial and Viral Genomes from Multiple Metagenomes. <i>Frontiers in Microbiology</i> , 2016, 7, 469.	1.5	13
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53	How did life survive Earth's great oxygenation?. <i>Current Opinion in Chemical Biology</i> , 2016, 31, 166-178.	2.8	92
54	Evolution of Oxygenic Photosynthesis. <i>Annual Review of Earth and Planetary Sciences</i> , 2016, 44, 647-683.	4.6	334
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57	Next-generation sequencing characterization of the gut bacterial community of gilthead sea bream ( <i>Sparus aurata</i> , L.) fed low fishmeal based diets with increasing soybean meal levels. <i>Animal Feed Science and Technology</i> , 2016, 222, 204-216.	1.1	72
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63	Marine microbial community structure assessed from combined metagenomic analysis and ribosomal amplicon deep-sequencing. <i>Marine Biology Research</i> , 2016, 12, 30-42.	0.3	3
64	Core-satellite populations and seasonality of water meter biofilms in a metropolitan drinking water distribution system. <i>ISME Journal</i> , 2016, 10, 582-595.	4.4	91
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75	How Cyanobacteria went green. <i>Science</i> , 2017, 355, 1372-1373.	6.0	20
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150	Evidence of viable <i>Helicobacter pylori</i> and other bacteria of public health interest associated with free-living amoebae in lettuce samples by next generation sequencing and other molecular techniques. <i>International Journal of Food Microbiology</i> , 2020, 318, 108477.	2.1	18
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153	Seasonal and Nutrient Supplement Responses in Rumen Microbiota Structure and Metabolites of Tropical Rangeland Cattle. <i>Microorganisms</i> , 2020, 8, 1550.	1.6	19
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