

# Carly P Rosewarne

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4906211/publications.pdf>

Version: 2024-02-01

16  
papers

1,433  
citations

623734

14  
h-index

940533

16  
g-index

16  
all docs

16  
docs citations

16  
times ranked

2345  
citing authors

#	ARTICLE	IF	CITATIONS
1	Effect of Fecal Microbiota Transplantation on 8-Week Remission in Patients With Ulcerative Colitis. JAMA - Journal of the American Medical Association, 2019, 321, 156.	7.4	548
2	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. Nature Biotechnology, 2018, 36, 359-367.	17.5	414
3	Class 1 integrons in benthic bacterial communities: abundance, association with Tn <i>402</i> -like transposition modules and evidence for coselection with heavy-metal resistance. FEMS Microbiology Ecology, 2010, 72, 35-46.	2.7	130
4	Genomic Structure of the Salmonella enterica Serovar Typhimurium DT 64 Bacteriophage ST64T: Evidence for Modular Genetic Architecture. Journal of Bacteriology, 2003, 185, 3473-3475.	2.2	47
5	In Vitro Response of Rumen Microbiota to the Antimethanogenic Red Macroalga Asparagopsis taxiformis. Microbial Ecology, 2018, 75, 811-818.	2.8	42
6	Analysis of the bovine rumen microbiome reveals a diversity of Sus-like polysaccharide utilization loci from the bacterial phylum <i>Bacteroidetes</i> . Journal of Industrial Microbiology and Biotechnology, 2014, 41, 601-606.	3.0	41
7	High-Yield and Phylogenetically Robust Methods of DNA Recovery for Analysis of Microbial Biofilms Adherent to Plant Biomass in the Herbivore Gut. Microbial Ecology, 2011, 61, 448-454.	2.8	33
8	Draft Genome Sequence of Treponema sp. Strain JC4, a Novel Spirochete Isolated from the Bovine Rumen. Journal of Bacteriology, 2012, 194, 4130-4130.	2.2	33
9	Fiber Supplements Derived From Sugarcane Stem, Wheat Dextrin and Psyllium Husk Have Different In Vitro Effects on the Human Gut Microbiota. Frontiers in Microbiology, 2018, 9, 1618.	3.5	25
10	Culture- and metagenomics-enabled analyses of the <i>Methanosphaera</i> genus reveals their monophyletic origin and differentiation according to genome size. ISME Journal, 2018, 12, 2942-2953.	9.8	24
11	Enhancing biogenic methane generation from a brown coal by combining different microbial communities. International Journal of Coal Geology, 2016, 154-155, 107-110.	5.0	23
12	Cytotoxic G-rich oligodeoxynucleotides: putative protein targets and required sequence motif. Nucleic Acids Research, 2007, 35, 4562-4572.	14.5	21
13	Genomic insights into the carbohydrate catabolism of Cairneyella variabilis gen. nov. sp. nov., the first reports from a genome of an ericoid mycorrhizal fungus from the southern hemisphere. Mycorrhiza, 2016, 26, 345-352.	2.8	18
14	ST64B is a defective bacteriophage in Salmonella enterica serovar Typhimurium DT64 that encodes a functional immunity region capable of mediating phage-type conversion. International Journal of Medical Microbiology, 2004, 294, 59-63.	3.6	15
15	Draft Genome Sequence of <i>Methanobacterium</i> sp. Maddingley, Reconstructed from Metagenomic Sequencing of a Methanogenic Microbial Consortium Enriched from Coal-Seam Gas Formation Water. Genome Announcements, 2013, 1, .	0.8	10
16	Draft Genome Sequence of <i>Clostridium</i> sp. Maddingley, Isolated from Coal-Seam Gas Formation Water. Genome Announcements, 2013, 1, .	0.8	9