

# Laura Wegener Parfrey

## List of Publications by Year in descending order

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Version: 2024-02-01

69  
papers

18,290  
citations

81900

39  
h-index

98798

67  
g-index

70  
all docs

70  
docs citations

70  
times ranked

25656  
citing authors

#	ARTICLE	IF	CITATIONS
1	Evidence for long-lasting alterations in the fecal microbiota following prenatal alcohol exposure. <i>Alcoholism: Clinical and Experimental Research</i> , 2022, 46, 542-555.	2.4	11
2	A reciprocal transplant experiment sheds new light on a classic marine seagrass-algal symbiosis and suggests influence of epiphytic symbiont on seagrass microbiota. <i>Aquatic Botany</i> , 2022, 179, 103511.	1.6	7
3	Beyond specialization: re-examining routes of host influence on symbiont evolution. <i>Trends in Ecology and Evolution</i> , 2022, 37, 590-598.	8.7	10
4	Microeukaryotic Communities Associated With the Seagrass <i>Zostera marina</i> Are Spatially Structured. <i>Journal of Eukaryotic Microbiology</i> , 2021, 68, e12827.	1.7	12
5	Morphological complexity affects the diversity of marine microbiomes. <i>ISME Journal</i> , 2021, 15, 1372-1386.	9.8	18
6	The microbiota of intertidal macroalgae <i>Fucus distichus</i> is site-specific and resistant to change following transplant. <i>Environmental Microbiology</i> , 2021, 23, 2617-2631.	3.8	6
7	Blastocystis Colonization Alters the Gut Microbiome and, in Some Cases, Promotes Faster Recovery From Induced Colitis. <i>Frontiers in Microbiology</i> , 2021, 12, 641483.	3.5	31
8	Kelp-associated Microbiota are Structured by Host Anatomy <sup>1</sup> . <i>Journal of Phycology</i> , 2021, 57, 1119-1130.	2.3	22
9	Wildcards in climate change biology. <i>Ecological Monographs</i> , 2021, 91, e01471.	5.4	9
10	Response to "Vast (but avoidable) underestimation of global biodiversity". <i>PLoS Biology</i> , 2021, 19, e3001362.	5.6	2
11	Biodiversity of protists and nematodes in the wild nonhuman primate gut. <i>ISME Journal</i> , 2020, 14, 609-622.	9.8	32
12	Host-Specificity and Core Taxa of Seagrass Leaf Microbiome Identified Across Tissue Age and Geographical Regions. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	2.2	12
13	Effects of forced taxonomic transitions on metabolic composition and function in microbial microcosms. <i>Environmental Microbiology Reports</i> , 2020, 12, 514-524.	2.4	10
14	A census-based estimate of Earth's bacterial and archaeal diversity. <i>PLoS Biology</i> , 2019, 17, e3000106.	5.6	139
15	Function and functional redundancy in microbial systems. <i>Nature Ecology and Evolution</i> , 2018, 2, 936-943.	7.8	912
16	Correcting for 16S rRNA gene copy numbers in microbiome surveys remains an unsolved problem. <i>Microbiome</i> , 2018, 6, 41.	11.1	514
17	Introduction: The host-associated microbiome: Pattern, process and function. <i>Molecular Ecology</i> , 2018, 27, 1749-1765.	3.9	46
18	Incubation with macroalgae induces large shifts in water column microbiota, but minor changes to the epibiota of co-occurring macroalgae. <i>Molecular Ecology</i> , 2018, 27, 1966-1979.	3.9	50

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19	Associations between infant fungal and bacterial dysbiosis and childhood atopic wheeze in a nonindustrialized setting. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 142, 424-434.e10.	2.9	181
20	Sympatric kelp species share a large portion of their surface bacterial communities. <i>Environmental Microbiology</i> , 2018, 20, 658-670.	3.8	65
21	Is Host Filtering the Main Driver of Phylosymbiosis across the Tree of Life?. <i>MSystems</i> , 2018, 3, .	3.8	119
22	EukRef: Phylogenetic curation of ribosomal RNA to enhance understanding of eukaryotic diversity and distribution. <i>PLoS Biology</i> , 2018, 16, e2005849.	5.6	101
23	Diverse Bacteria Utilize Alginate Within the Microbiome of the Giant Kelp <i>Macrocystis pyrifera</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1914.	3.5	38
24	Evaluating rodent experimental models for studies of <i>Blastocystis</i> ST1. <i>Experimental Parasitology</i> , 2018, 191, 55-61.	1.2	11
25	Bacterial diversification through geological time. <i>Nature Ecology and Evolution</i> , 2018, 2, 1458-1467.	7.8	81
26	Alternate life history phases of a common seaweed have distinct microbial surface communities. <i>Molecular Ecology</i> , 2018, 27, 3555-3568.	3.9	41
27	Stunted childhood growth is associated with decompartmentalization of the gastrointestinal tract and overgrowth of oropharyngeal taxa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8489-E8498.	7.1	119
28	The benign helminth <i>Hymenolepis diminuta</i> ameliorates chemically induced colitis in a rat model system. <i>Parasitology</i> , 2018, 145, 1324-1335.	1.5	13
29	<i>UniEuk</i> : Time to Speak a Common Language in Protistology!. <i>Journal of Eukaryotic Microbiology</i> , 2017, 64, 407-411.	1.7	74
30	High taxonomic variability despite stable functional structure across microbial communities. <i>Nature Ecology and Evolution</i> , 2017, 1, 15.	7.8	378
31	A benign helminth alters the host immune system and the gut microbiota in a rat model system. <i>PLoS ONE</i> , 2017, 12, e0182205.	2.5	36
32	Vertebrate Hosts as Islands: Dynamics of Selection, Immigration, Loss, Persistence, and Potential Function of Bacteria on Salamander Skin. <i>Frontiers in Microbiology</i> , 2016, 7, 333.	3.5	65
33	Deconstructing the Bat Skin Microbiome: Influences of the Host and the Environment. <i>Frontiers in Microbiology</i> , 2016, 7, 1753.	3.5	81
34	Decoupling function and taxonomy in the global ocean microbiome. <i>Science</i> , 2016, 353, 1272-1277.	12.6	2,001
35	Mock communities highlight the diversity of host-associated eukaryotes. <i>Molecular Ecology</i> , 2015, 24, 4337-4339.	3.9	4
36	Are Human Intestinal Eukaryotes Beneficial or Commensals?. <i>PLoS Pathogens</i> , 2015, 11, e1005039.	4.7	146

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37	Changes in bacterial and eukaryotic communities during sewage decomposition in Mississippi river water. <i>Water Research</i> , 2015, 69, 30-39.	11.3	49
38	Communities of microbial eukaryotes in the mammalian gut within the context of environmental eukaryotic diversity. <i>Frontiers in Microbiology</i> , 2014, 5, 298.	3.5	130
39	The amphibian skin-associated microbiome across species, space and life history stages. <i>Molecular Ecology</i> , 2014, 23, 1238-1250.	3.9	360
40	Convergence of gut microbiomes in myrmecophagous mammals. <i>Molecular Ecology</i> , 2014, 23, 1301-1317.	3.9	311
41	Microbial community dynamics and effect of environmental microbial reservoirs on red-backed salamanders ( <i>Plethodon cinereus</i> ). <i>ISME Journal</i> , 2014, 8, 830-840.	9.8	316
42	The SILVA and "All-species Living Tree Project (LTP)" taxonomic frameworks. <i>Nucleic Acids Research</i> , 2014, 42, D643-D648.	14.5	2,667
43	Global biogeography of highly diverse protistan communities in soil. <i>ISME Journal</i> , 2013, 7, 652-659.	9.8	412
44	Multicellularity arose several times in the evolution of eukaryotes (Response to DOI) <a href="#">Tj ETQq0 0 0 rgBT /Overlock 10 If 50 462 Td (10.1093</a>	2.5	57
45	Meeting Report: Fungal ITS Workshop (October 2012). <i>Standards in Genomic Sciences</i> , 2013, 8, 118-123.	1.5	34
46	A microbial clock provides an accurate estimate of the postmortem interval in a mouse model system. <i>ELife</i> , 2013, 2, e01104.	6.0	270
47	II.12. Origin and Diversification of Eukaryotes. , 2013, , 136-142.		0
48	A Modular Organization of the Human Intestinal Mucosal Microbiota and Its Association with Inflammatory Bowel Disease. <i>PLoS ONE</i> , 2013, 8, e80702.	2.5	147
49	The Revised Classification of Eukaryotes. <i>Journal of Eukaryotic Microbiology</i> , 2012, 59, 429-514.	1.7	1,340
50	Defining the human microbiome. <i>Nutrition Reviews</i> , 2012, 70, S38-S44.	5.8	789
51	RIBOSOMAL DNA IS DIFFERENTIALLY AMPLIFIED ACROSS LIFE-CYCLE STAGES IN THE FORAMINIFER ALLOGROMIA LATICOLLARIS STRAIN CSH. <i>Journal of Foraminiferal Research</i> , 2012, 42, 151-155.	0.5	8
52	The Impact of the Gut Microbiota on Human Health: An Integrative View. <i>Cell</i> , 2012, 148, 1258-1270.	28.9	2,920
53	Turning the Crown Upside Down: Gene Tree Parsimony Roots the Eukaryotic Tree of Life. <i>Systematic Biology</i> , 2012, 61, 653-660.	5.6	80
54	Experimental and analytical tools for studying the human microbiome. <i>Nature Reviews Genetics</i> , 2012, 13, 47-58.	16.3	601

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55	Human-Associated Microbial Signatures: Examining Their Predictive Value. <i>Cell Host and Microbe</i> , 2011, 10, 292-296.	11.0	134
56	Combined phylogenetic and genomic approaches for the high-throughput study of microbial habitat adaptation. <i>Trends in Microbiology</i> , 2011, 19, 472-482.	7.7	23
57	Microbial Eukaryotes in the Human Microbiome: Ecology, Evolution, and Future Directions. <i>Frontiers in Microbiology</i> , 2011, 2, 153.	3.5	186
58	<i>Subulatomonas tetraspora</i> nov. gen. nov. sp. is a Member of a Previously Unrecognized Major Clade of Eukaryotes. <i>Protist</i> , 2011, 162, 762-773.	1.5	27
59	Estimating the timing of early eukaryotic diversification with multigene molecular clocks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13624-13629.	7.1	747
60	The chastity of amoebae: re-evaluating evidence for sex in amoeboid organisms. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 2081-2090.	2.6	122
61	Genome Dynamics Are Influenced by Food Source in <i>Allogromia laticollaris</i> Strain CSH (Foraminifera). <i>Genome Biology and Evolution</i> , 2010, 2, 678-685.	2.5	18
62	Broadly Sampled Multigene Analyses Yield a Well-Resolved Eukaryotic Tree of Life. <i>Systematic Biology</i> , 2010, 59, 518-533.	5.6	212
63	Dynamic Genomes of Eukaryotes and the Maintenance of Genomic Integrity. <i>Microbe Magazine</i> , 2010, 5, 156-163.	0.4	15
64	Putting Animals in their Place Within a Context of Eukaryotic Innovations. , 2010, , 3-14.		0
65	Molecular Data Are Transforming Hypotheses on the Origin and Diversification of Eukaryotes. <i>BioScience</i> , 2009, 59, 471-481.	4.9	29
66	The Dynamic Nature of Eukaryotic Genomes. <i>Molecular Biology and Evolution</i> , 2008, 25, 787-794.	8.9	127
67	Genome-wide analysis of transcriptional dependence and probable target sites for Abf1 and Rap1 in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2007, 35, 193-202.	14.5	592
68	Evaluating Support for the Current Classification of Eukaryotic Diversity. <i>PLoS Genetics</i> , 2006, 2, e220.	3.5	148
69	Phylogeny and Ultrastructure of <i>Miliammina fusca</i> : Evidence for Secondary Loss of Calcification in a Miliolid Foraminifer. <i>Journal of Eukaryotic Microbiology</i> , 2006, 53, 204-210.	1.7	20