

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 | The Impact of the Gut Microbiota on Human Health: An Integrative View. <i>Cell</i> , 2012, 148, 1258-1270. | 28.9 | 2,920 |
| 2 | The SILVA and "All-species Living Tree Project (LTP)" taxonomic frameworks. <i>Nucleic Acids Research</i> , 2014, 42, D643-D648. | 14.5 | 2,667 |
| 3 | Decoupling function and taxonomy in the global ocean microbiome. <i>Science</i> , 2016, 353, 1272-1277. | 12.6 | 2,001 |
| 4 | The Revised Classification of Eukaryotes. <i>Journal of Eukaryotic Microbiology</i> , 2012, 59, 429-514. | 1.7 | 1,340 |
| 5 | Function and functional redundancy in microbial systems. <i>Nature Ecology and Evolution</i> , 2018, 2, 936-943. | 7.8 | 912 |
| 6 | Defining the human microbiome. <i>Nutrition Reviews</i> , 2012, 70, S38-S44. | 5.8 | 789 |
| 7 | 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 |
| 8 | Experimental and analytical tools for studying the human microbiome. <i>Nature Reviews Genetics</i> , 2012, 13, 47-58. | 16.3 | 601 |
| 9 | 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 |
| 10 | Correcting for 16S rRNA gene copy numbers in microbiome surveys remains an unsolved problem. <i>Microbiome</i> , 2018, 6, 41. | 11.1 | 514 |
| 11 | Global biogeography of highly diverse protistan communities in soil. <i>ISME Journal</i> , 2013, 7, 652-659. | 9.8 | 412 |
| 12 | High taxonomic variability despite stable functional structure across microbial communities. <i>Nature Ecology and Evolution</i> , 2017, 1, 15. | 7.8 | 378 |
| 13 | The amphibian skin-associated microbiome across species, space and life history stages. <i>Molecular Ecology</i> , 2014, 23, 1238-1250. | 3.9 | 360 |
| 14 | 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 |
| 15 | Convergence of gut microbiomes in myrmecophagous mammals. <i>Molecular Ecology</i> , 2014, 23, 1301-1317. | 3.9 | 311 |
| 16 | A microbial clock provides an accurate estimate of the postmortem interval in a mouse model system. <i>ELife</i> , 2013, 2, e011104. | 6.0 | 270 |
| 17 | Broadly Sampled Multigene Analyses Yield a Well-Resolved Eukaryotic Tree of Life. <i>Systematic Biology</i> , 2010, 59, 518-533. | 5.6 | 212 |
| 18 | Microbial Eukaryotes in the Human Microbiome: Ecology, Evolution, and Future Directions. <i>Frontiers in Microbiology</i> , 2011, 2, 153. | 3.5 | 186 |

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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 | Evaluating Support for the Current Classification of Eukaryotic Diversity. <i>PLoS Genetics</i> , 2006, 2, e220. | 3.5 | 148 |
| 21 | 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 |
| 22 | Are Human Intestinal Eukaryotes Beneficial or Commensals?. <i>PLoS Pathogens</i> , 2015, 11, e1005039. | 4.7 | 146 |
| 23 | A census-based estimate of Earth's bacterial and archaeal diversity. <i>PLoS Biology</i> , 2019, 17, e3000106. | 5.6 | 139 |
| 24 | Human-Associated Microbial Signatures: Examining Their Predictive Value. <i>Cell Host and Microbe</i> , 2011, 10, 292-296. | 11.0 | 134 |
| 25 | 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 |
| 26 | The Dynamic Nature of Eukaryotic Genomes. <i>Molecular Biology and Evolution</i> , 2008, 25, 787-794. | 8.9 | 127 |
| 27 | 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 |
| 28 | Is Host Filtering the Main Driver of Phyllosymbiosis across the Tree of Life?. <i>MSystems</i> , 2018, 3, . | 3.8 | 119 |
| 29 | 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 |
| 30 | EukRef: Phylogenetic curation of ribosomal RNA to enhance understanding of eukaryotic diversity and distribution. <i>PLoS Biology</i> , 2018, 16, e2005849. | 5.6 | 101 |
| 31 | Deconstructing the Bat Skin Microbiome: Influences of the Host and the Environment. <i>Frontiers in Microbiology</i> , 2016, 7, 1753. | 3.5 | 81 |
| 32 | Bacterial diversification through geological time. <i>Nature Ecology and Evolution</i> , 2018, 2, 1458-1467. | 7.8 | 81 |
| 33 | 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 |
| 34 | <i>UniEuk</i>: Time to Speak a Common Language in Protistology!. <i>Journal of Eukaryotic Microbiology</i> , 2017, 64, 407-411. | 1.7 | 74 |
| 35 | 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 |
| 36 | Sympatric kelp species share a large portion of their surface bacterial communities. <i>Environmental Microbiology</i> , 2018, 20, 658-670. | 3.8 | 65 |

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|----|--|------|-----------|
| 37 | Multicellularity arose several times in the evolution of eukaryotes (Response to DOI) Tj ETQq1 1 0.784314 rgBT /Overlock 10 If 50 742 | 2.5 | 57 |
| 38 | 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 |
| 39 | Changes in bacterial and eukaryotic communities during sewage decomposition in Mississippi river water. <i>Water Research</i> , 2015, 69, 30-39. | 11.3 | 49 |
| 40 | Introduction: The host-associated microbiome: Pattern, process and function. <i>Molecular Ecology</i> , 2018, 27, 1749-1765. | 3.9 | 46 |
| 41 | Alternate life history phases of a common seaweed have distinct microbial surface communities. <i>Molecular Ecology</i> , 2018, 27, 3555-3568. | 3.9 | 41 |
| 42 | 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 |
| 43 | 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 |
| 44 | Meeting Report: Fungal ITS Workshop (October 2012). <i>Standards in Genomic Sciences</i> , 2013, 8, 118-123. | 1.5 | 34 |
| 45 | Biodiversity of protists and nematodes in the wild nonhuman primate gut. <i>ISME Journal</i> , 2020, 14, 609-622. | 9.8 | 32 |
| 46 | 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 |
| 47 | Molecular Data Are Transforming Hypotheses on the Origin and Diversification of Eukaryotes. <i>BioScience</i> , 2009, 59, 471-481. | 4.9 | 29 |
| 48 | <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 |
| 49 | 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 |
| 50 | Kelp-associated Microbiota are Structured by Host Anatomy. <i>Journal of Phycology</i> , 2021, 57, 1119-1130. | 2.3 | 22 |
| 51 | 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 |
| 52 | 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 |
| 53 | Morphological complexity affects the diversity of marine microbiomes. <i>ISME Journal</i> , 2021, 15, 1372-1386. | 9.8 | 18 |
| 54 | Dynamic Genomes of Eukaryotes and the Maintenance of Genomic Integrity. <i>Microbe Magazine</i> , 2010, 5, 156-163. | 0.4 | 15 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 55 | 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 |
| 56 | 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 |
| 57 | 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 |
| 58 | Evaluating rodent experimental models for studies of Blastocystis ST1. <i>Experimental Parasitology</i> , 2018, 191, 55-61. | 1.2 | 11 |
| 59 | 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 |
| 60 | 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 |
| 61 | 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 |
| 62 | Wildcards in climate change biology. <i>Ecological Monographs</i> , 2021, 91, e01471. | 5.4 | 9 |
| 63 | 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 |
| 64 | 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 |
| 65 | 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 |
| 66 | Mock communities highlight the diversity of host-associated eukaryotes. <i>Molecular Ecology</i> , 2015, 24, 4337-4339. | 3.9 | 4 |
| 67 | Response to "Vast (but avoidable) underestimation of global biodiversity". <i>PLoS Biology</i> , 2021, 19, e3001362. | 5.6 | 2 |
| 68 | II.12. Origin and Diversification of Eukaryotes. , 2013, , 136-142. | | 0 |
| 69 | Putting Animals in their Place Within a Context of Eukaryotic Innovations. , 2010, , 3-14. | | 0 |