# Ryan J Newton

## List of Publications by Citations



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|---|---|---|---|
| 45 papers | 4,178 citations | 29 h-index | 49 g-index |
| 49 ext. papers | 5,468 ext. citations | 6.5 avg, IF | 5.5 L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 45 | A guide to the natural history of freshwater lake bacteria. *Microbiology and Molecular Biology Reviews*, **2011**, 75, 14-49 | 13.2 | 914 |
| 44 | Microbes as Engines of Ecosystem Function: When Does Community Structure Enhance Predictions of Ecosystem Processes?. *Frontiers in Microbiology*, **2016**, 7, 214 | 5.7 | 321 |
| 43 | Genome characteristics of a generalist marine bacterial lineage. *ISME Journal*, **2010**, 4, 784-98 | 11.9 | 275 |
| 42 | Community structures of fecal bacteria in cattle from different animal feeding operations. *Applied and Environmental Microbiology*, **2011**, 77, 2992-3001 | 4.8 | 230 |
| 41 | A microbial signature approach to identify fecal pollution in the waters off an urbanized coast of Lake Michigan. *Microbial Ecology*, **2013**, 65, 1011-23 | 4.4 | 162 |
| 40 | Phylogenetic ecology of the freshwater Actinobacteria acI lineage. *Applied and Environmental Microbiology*, **2007**, 73, 7169-76 | 4.8 | 157 |
| 39 | Sewage reflects the microbiomes of human populations. *MBio*, **2015**, 6, e02574 | 7.8 | 153 |
| 38 | Genome-wide selective sweeps and gene-specific sweeps in natural bacterial populations. *ISME Journal*, **2016**, 10, 1589-601 | 11.9 | 146 |
| 37 | Interannual dynamics and phenology of bacterial communities in a eutrophic lake. *Limnology and Oceanography*, **2007**, 52, 487-494 | 4.8 | 128 |
| 36 | Comparison of the microbial community structures of untreated wastewaters from different geographic locales. *Applied and Environmental Microbiology*, **2013**, 79, 2906-13 | 4.8 | 119 |
| 35 | Freshwater Recirculating Aquaculture System Operations Drive Biofilter Bacterial Community Shifts around a Stable Nitrifying Consortium of Ammonia-Oxidizing and Comammox. *Frontiers in Microbiology*, **2017**, 8, 101 | 5.7 | 113 |
| 34 | A single genus in the gut microbiome reflects host preference and specificity. *ISME Journal*, **2015**, 9, 90-100 | 11.9 | 105 |
| 33 | Evidence for structuring of bacterial community composition by organic carbon source in temperate lakes. *Environmental Microbiology*, **2009**, 11, 2463-72 | 5.2 | 103 |
| 32 | Microbial community dynamics in a humic lake: differential persistence of common freshwater phylotypes. *Environmental Microbiology*, **2006**, 8, 956-70 | 5.2 | 99 |
| 31 | Lachnospiraceae and Bacteroidales alternative fecal indicators reveal chronic human sewage contamination in an urban harbor. *Applied and Environmental Microbiology*, **2011**, 77, 6972-81 | 4.8 | 93 |
| 30 | Occurrence of tetracycline resistance genes in aquaculture facilities with varying use of oxytetracycline. *Microbial Ecology*, **2010**, 59, 799-807 | 4.4 | 91 |
| 29 | Sewage reflects the distribution of human faecal Lachnospiraceae. *Environmental Microbiology*, **2013**, 15, 2213-27 | 5.2 | 75 |

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| 28 | The polycyclic aromatic hydrocarbon degradation potential of Gulf of Mexico native coastal microbial communities after the Deepwater Horizon oil spill. *Frontiers in Microbiology*, **2014**, 5, 205 | 5.7 | 67 |
| 27 | Seasonal differences in bacterial community composition following nutrient additions in a eutrophic lake. *Environmental Microbiology*, **2011**, 13, 887-99 | 5.2 | 66 |
| 26 | A unique assemblage of cosmopolitan freshwater bacteria and higher community diversity differentiate an urbanized estuary from oligotrophic Lake Michigan. *Frontiers in Microbiology*, **2015**, 6, 1028 | 5.7 | 60 |
| 25 | Shifts in the microbial community composition of Gulf Coast beaches following beach oiling. *PLoS ONE*, **2013**, 8, e74265 | 3.7 | 60 |
| 24 | Fecal source identification using random forest. *Microbiome*, **2018**, 6, 185 | 16.6 | 51 |
| 23 | Spatial and temporal scales of aquatic bacterial beta diversity. *Frontiers in Microbiology*, **2012**, 3, 318 | 5.7 | 50 |
| 22 | Stripping Away the Soil: Plant Growth Promoting Microbiology Opportunities in Aquaponics. *Frontiers in Microbiology*, **2018**, 9, 8 | 5.7 | 40 |
| 21 | Experimental manipulations of microbial food web interactions in a humic lake: shifting biological drivers of bacterial community structure. *Environmental Microbiology*, **2006**, 8, 1448-59 | 5.2 | 40 |
| 20 | Evaluation of Sampling, Analysis, and Normalization Methods for SARS-CoV-2 Concentrations in Wastewater to Assess COVID-19 Burdens in Wisconsin Communities. *ACS ES&T Water*, **2021**, 1, 1955-1965 | | 39 |
| 19 | TaxAss: Leveraging a Custom Freshwater Database Achieves Fine-Scale Taxonomic Resolution. *MSphere*, **2018**, 3, | 5 | 37 |
| 18 | Potential for atmospheric deposition of bacteria to influence bacterioplankton communities. *FEMS Microbiology Ecology*, **2008**, 64, 388-94 | 4.3 | 32 |
| 17 | Detection of multi-drug resistant Escherichia coli in the urban waterways of Milwaukee, WI. *Frontiers in Microbiology*, **2015**, 6, 336 | 5.7 | 24 |
| 16 | Component Microenvironments and System Biogeography Structure Microorganism Distributions in Recirculating Aquaculture and Aquaponic Systems. *MSphere*, **2019**, 4, | 5 | 21 |
| 15 | Analysis of the gull fecal microbial community reveals the dominance of Catellicoccus marimammalium in relation to culturable Enterococci. *Applied and Environmental Microbiology*, **2014**, 80, 757-65 | 4.8 | 21 |
| 14 | The flux and impact of wastewater infrastructure microorganisms on human and ecosystem health. *Current Opinion in Biotechnology*, **2019**, 57, 145-150 | 11.4 | 19 |
| 13 | Transcriptional changes underlying elemental stoichiometry shifts in a marine heterotrophic bacterium. *Frontiers in Microbiology*, **2012**, 3, 159 | 5.7 | 17 |
| 12 | Microbial communities of the Laurentian Great Lakes reflect connectivity and local biogeochemistry. *Environmental Microbiology*, **2020**, 22, 433-446 | 5.2 | 14 |
| 11 | FORENSIC: an Online Platform for Fecal Source Identification. *MSystems*, **2020**, 5, | 7.6 | 10 |

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| 10 | Evaluation of sampling frequency and normalization of SARS-CoV-2 wastewater concentrations for capturing COVID-19 burdens in the community | | 9 |
| 9 | Urban wastewater bacterial communities assemble into seasonal steady states. *Microbiome*, **2021**, 9, 116 | 16.6 | 6 |
| 8 | Nutritional quality of different starches in feed fed to juvenile yellow perch, Perca flavescens. *Aquaculture Nutrition*, **2020**, 26, 671-682 | 3.2 | 4 |
| 7 | Causal relationship between alkaline phosphatase activities and phosphorus dynamics in a eutrophic coastal lagoon in Lake Michigan. *Science of the Total Environment*, **2021**, 787, 147681 | 10.2 | 4 |
| 6 | Cast iron drinking water pipe biofilms support diverse microbial communities containing antibiotic resistance genes, metal resistance genes, and class 1 integrons. *Environmental Science: Water Research and Technology*, **2021**, 7, 584-598 | 4.2 | 3 |
| 5 | Chronic exposure to high-density polyethylene microplastic through feeding alters the nutrient metabolism of juvenile yellow perch ().. *Animal Nutrition*, **2022**, 9, 143-158 | 4.8 | 0 |
| 4 | Human Fecal Contamination Corresponds to Changes in the Freshwater Bacterial Communities of a Large River Basin. *Microbiology Spectrum*, **2021**, 9, e0120021 | 8.9 | 0 |
| 3 | Disproportionate Changes in Composition and Molecular Size Spectra of Dissolved Organic Matter between Influent and Effluent from a Major Metropolitan Wastewater Treatment Plant. *ACS ES&T Water*, **2022**, 2, 216-225 | | 0 |
| 2 | AQUACULTURE FACILITIES AS A POTENTIAL SOURCE OF ANTIBIOTIC RESISTANCE TO THE AQUATIC ENVIRONMENT. *Proceedings of the Water Environment Federation*, **2007**, 2007, 3132-3143 | | |
| 1 | Shifts in Vaginal Bacterial Community Composition Are Associated With Vaginal Mesh Exposure. *Female Pelvic Medicine and Reconstructive Surgery*, **2021**, 27, e681-e686 | 1.9 | |