

Hilary G Morrison

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

102 papers	13,550 citations	48 h-index	109 g-index
109 ext. papers	16,227 ext. citations	7.6 avg, IF	6.2 L-index

#	Paper	IF	Citations
102	Microbial diversity in the deep sea and the underexplored "rare biosphere". <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 12115-20	11.5	2773
101	Ironing out the wrinkles in the rare biosphere through improved OTU clustering. <i>Environmental Microbiology</i> , 2010 , 12, 1889-98	5.2	1036
100	Accuracy and quality of massively parallel DNA pyrosequencing. <i>Genome Biology</i> , 2007 , 8, R143	18.3	958
99	AnviO: an advanced analysis and visualization platform for omics data. <i>PeerJ</i> , 2015 , 3, e1319	3.1	809
98	Microbial population structures in the deep marine biosphere. <i>Science</i> , 2007 , 318, 97-100	33.3	732
97	Genomic minimalism in the early diverging intestinal parasite <i>Giardia lamblia</i> . <i>Science</i> , 2007 , 317, 1921-6	33.3	613
96	Reproducible community dynamics of the gastrointestinal microbiota following antibiotic perturbation. <i>Infection and Immunity</i> , 2009 , 77, 2367-75	3.7	418
95	Oligotyping: Differentiating between closely related microbial taxa using 16S rRNA gene data. <i>Methods in Ecology and Evolution</i> , 2013 , 4, 1111	7.7	407
94	Rapid, low-input, low-bias construction of shotgun fragment libraries by high-density in vitro transposition. <i>Genome Biology</i> , 2010 , 11, R119	18.3	377
93	Minimum entropy decomposition: unsupervised oligotyping for sensitive partitioning of high-throughput marker gene sequences. <i>ISME Journal</i> , 2015 , 9, 968-79	11.9	355
92	Analysis, optimization and verification of Illumina-generated 16S rRNA gene amplicon surveys. <i>PLoS ONE</i> , 2014 , 9, e94249	3.7	237
91	Broadly sampled multigene analyses yield a well-resolved eukaryotic tree of life. <i>Systematic Biology</i> , 2010 , 59, 518-33	8.4	191
90	<i>GiardiaDB</i> and <i>TrichDB</i> : integrated genomic resources for the eukaryotic protist pathogens <i>Giardia lamblia</i> and <i>Trichomonas vaginalis</i> . <i>Nucleic Acids Research</i> , 2009 , 37, D526-30	20.1	179
89	A filtering method to generate high quality short reads using Illumina paired-end technology. <i>PLoS ONE</i> , 2013 , 8, e66643	3.7	176
88	Association of Cesarean Delivery and Formula Supplementation With the Intestinal Microbiome of 6-Week-Old Infants. <i>JAMA Pediatrics</i> , 2016 , 170, 212-9	8.3	170
87	A microbial signature approach to identify fecal pollution in the waters off an urbanized coast of Lake Michigan. <i>Microbial Ecology</i> , 2013 , 65, 1011-23	4.4	162
86	Microplastic bacterial communities in the Bay of Brest: Influence of polymer type and size. <i>Environmental Pollution</i> , 2018 , 242, 614-625	9.3	156

85	Sewage reflects the microbiomes of human populations. <i>MBio</i> , 2015 , 6, e02574	7.8	153
84	The Giardia genome project database. <i>FEMS Microbiology Letters</i> , 2000 , 189, 271-3	2.9	153
83	VAMPS: a website for visualization and analysis of microbial population structures. <i>BMC Bioinformatics</i> , 2014 , 15, 41	3.6	138
82	A spliceosomal intron in Giardia lamblia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 3701-5	11.5	137
81	Prevalence of streptococci and increased polymicrobial diversity associated with cystic fibrosis patient stability. <i>Journal of Bacteriology</i> , 2012 , 194, 4709-17	3.5	134
80	Effect of PCR amplicon size on assessments of clone library microbial diversity and community structure. <i>Environmental Microbiology</i> , 2009 , 11, 1292-302	5.2	122
79	Acinetobacter, Aeromonas and Trichococcus populations dominate the microbial community within urban sewer infrastructure. <i>Environmental Microbiology</i> , 2012 , 14, 2538-52	5.2	113
78	Evidence for lateral transfer of genes encoding ferredoxins, nitroreductases, NADH oxidase, and alcohol dehydrogenase 3 from anaerobic prokaryotes to Giardia lamblia and Entamoeba histolytica. <i>Eukaryotic Cell</i> , 2002 , 1, 181-90		112
77	Maternal diet during pregnancy is related with the infant stool microbiome in a delivery mode-dependent manner. <i>Microbiome</i> , 2018 , 6, 109	16.6	106
76	A single genus in the gut microbiome reflects host preference and specificity. <i>ISME Journal</i> , 2015 , 9, 90-100	10.9	105
75	Genomic survey of the non-cultivable opportunistic human pathogen, Enterocytozoon bienersi. <i>PLoS Pathogens</i> , 2009 , 5, e1000261	7.6	105
74	Characterization and quantification of the fungal microbiome in serial samples from individuals with cystic fibrosis. <i>Microbiome</i> , 2014 , 2, 40	16.6	103
73	Unique microbial communities persist in individual cystic fibrosis patients throughout a clinical exacerbation. <i>Microbiome</i> , 2013 , 1, 27	16.6	102
72	Microbial community composition in sediments resists perturbation by nutrient enrichment. <i>ISME Journal</i> , 2011 , 5, 1540-8	11.9	98
71	The reduced genome of the parasitic microsporidian Enterocytozoon bienersi lacks genes for core carbon metabolism. <i>Genome Biology and Evolution</i> , 2010 , 2, 304-9	3.9	95
70	Genetic code supports targeted insertion of two amino acids by one codon. <i>Science</i> , 2009 , 323, 259-61	33.3	95
69	A gene-targeted approach to investigate the intestinal butyrate-producing bacterial community. <i>Microbiome</i> , 2013 , 1, 8	16.6	94
68	Associations between Gut Microbial Colonization in Early Life and Respiratory Outcomes in Cystic Fibrosis. <i>Journal of Pediatrics</i> , 2015 , 167, 138-47.e1-3	3.6	88

67	Analysis of Lung Microbiota in Bronchoalveolar Lavage, Protected Brush and Sputum Samples from Subjects with Mild-To-Moderate Cystic Fibrosis Lung Disease. <i>PLoS ONE</i> , 2016 , 11, e0149998	3.7	80
66	Evolution of eukaryotic transcription: insights from the genome of <i>Giardia lamblia</i> . <i>Genome Research</i> , 2004 , 14, 1537-47	9.7	78
65	Annexin-like alpha giardins: a new cytoskeletal gene family in <i>Giardia lamblia</i> . <i>International Journal for Parasitology</i> , 2005 , 35, 617-26	4.3	74
64	Comparison of brush and biopsy sampling methods of the ileal pouch for assessment of mucosa-associated microbiota of human subjects. <i>Microbiome</i> , 2014 , 2, 5	16.6	72
63	Protection of guinea pigs from Lassa fever by vaccinia virus recombinants expressing the nucleoprotein or the envelope glycoproteins of Lassa virus. <i>Virology</i> , 1989 , 171, 179-88	3.6	67
62	Salt marsh sediment diversity: a test of the variability of the rare biosphere among environmental replicates. <i>ISME Journal</i> , 2012 , 6, 2014-23	11.9	66
61	The premature infant gut microbiome during the first 6 weeks of life differs based on gestational maturity at birth. <i>Pediatric Research</i> , 2018 , 84, 71-79	3.2	61
60	Shifts in the microbial community composition of Gulf Coast beaches following beach oiling. <i>PLoS ONE</i> , 2013 , 8, e74265	3.7	60
59	The transcriptional response to encystation stimuli in <i>Giardia lamblia</i> is restricted to a small set of genes. <i>Eukaryotic Cell</i> , 2010 , 9, 1566-76		59
58	The <i>Giardia lamblia</i> vsp gene repertoire: characteristics, genomic organization, and evolution. <i>BMC Genomics</i> , 2010 , 11, 424	4.5	57
57	Genomic and metabolic diversity of Marine Group I Thaumarchaeota in the mesopelagic of two subtropical gyres. <i>PLoS ONE</i> , 2014 , 9, e95380	3.7	54
56	Tracking microbial colonization in fecal microbiota transplantation experiments via genome-resolved metagenomics. <i>Microbiome</i> , 2017 , 5, 50	16.6	51
55	Microbial communities in the subglacial waters of the Vatnajökull ice cap, Iceland. <i>ISME Journal</i> , 2013 , 7, 427-37	11.9	49
54	Comparison of Sewage and Animal Fecal Microbiomes by Using Oligotyping Reveals Potential Human Fecal Indicators in Multiple Taxonomic Groups. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 7023-33	4.8	45
53	Sequence and phylogenetic position of a class II aldolase gene in the amitochondriate protist, <i>Giardia lamblia</i> . <i>Gene</i> , 1998 , 222, 163-8	3.8	45
52	<i>Giardia lamblia</i> expresses a proteobacterial-like DnaK homolog. <i>Molecular Biology and Evolution</i> , 2001 , 18, 530-41	8.3	45
51	Evidence for the cooperation of gp120 amino acids 322 and 448 in SIVmac entry. <i>Virology</i> , 1993 , 195, 167-74	3.6	45
50	Patterns of genome evolution among the microsporidian parasites <i>Encephalitozoon cuniculi</i> , <i>Antonospora locustae</i> and <i>Enterocytozoon bieneusi</i> . <i>PLoS ONE</i> , 2007 , 2, e1277	3.7	44

49	The microbiome in pediatric cystic fibrosis patients: the role of shared environment suggests a window of intervention. <i>Microbiome</i> , 2014 , 2, 14	16.6	37
48	Fetal exposures and perinatal influences on the stool microbiota of premature infants. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , 2016 , 29, 99-105	2	36
47	Sex-specific associations of infants' gut microbiome with arsenic exposure in a US population. <i>Scientific Reports</i> , 2018 , 8, 12627	4.9	32
46	Molecular cloning of CYP1A from the estuarine fish <i>Fundulus heteroclitus</i> and phylogenetic analysis of CYP1 genes: update with new sequences. <i>Comparative Biochemistry and Physiology C, Comparative Pharmacology and Toxicology</i> , 1998 , 121, 231-40		32
45	Calcium signaling in excystation of the early diverging eukaryote, <i>Giardia lamblia</i> . <i>Journal of Biological Chemistry</i> , 2003 , 278, 2533-40	5.4	32
44	Functional and genetic markers of niche partitioning among enigmatic members of the human oral microbiome. <i>Genome Biology</i> , 2020 , 21, 292	18.3	30
43	Multiphasic analysis of the temporal development of the distal gut microbiota in patients following ileal pouch anal anastomosis. <i>Microbiome</i> , 2013 , 1, 9	16.6	29
42	Exploring the relationship between sequence similarity and accurate phylogenetic trees. <i>Molecular Biology and Evolution</i> , 2006 , 23, 2090-100	8.3	27
41	Primary structure and phylogenetic relationships of a malate dehydrogenase gene from <i>Giardia lamblia</i> . <i>Journal of Molecular Evolution</i> , 1999 , 48, 750-5	3.1	27
40	Cloning and sequencing of an acetyl-CoA synthetase (ADP-forming) gene from the amitochondriate protist, <i>Giardia lamblia</i> . <i>Gene</i> , 1999 , 233, 225-31	3.8	27
39	The microbiota regulates susceptibility to Fas-mediated acute hepatic injury. <i>Laboratory Investigation</i> , 2014 , 94, 938-49	5.9	26
38	Altered Stool Microbiota of Infants with Cystic Fibrosis Shows a Reduction in Genera Associated with Immune Programming from Birth. <i>Journal of Bacteriology</i> , 2019 , 201,	3.5	25
37	Hydrogen Limitation and Syntrophic Growth among Natural Assemblages of Thermophilic Methanogens at Deep-sea Hydrothermal Vents. <i>Frontiers in Microbiology</i> , 2016 , 7, 1240	5.7	25
36	Patient-Specific <i>Bacteroides</i> Genome Variants in Pouchitis. <i>MBio</i> , 2016 , 7,	7.8	22
35	Microbiome-based body fluid identification of samples exposed to indoor conditions. <i>Forensic Science International: Genetics</i> , 2019 , 40, 105-113	4.3	21
34	Characterisation of the subtelomeric regions of <i>Giardia lamblia</i> genome isolate WBC6. <i>International Journal for Parasitology</i> , 2007 , 37, 503-13	4.3	21
33	Metagenomic analysis of the medicinal leech gut microbiota. <i>Frontiers in Microbiology</i> , 2014 , 5, 151	5.7	20
32	Cloning and analysis of the CYP1A promoter from the atlantic killifish (<i>Fundulus heteroclitus</i>). <i>Marine Environmental Research</i> , 2004 , 58, 119-24	3.3	19

31	Effects of mutations in constant regions 3 and 4 of envelope of simian immunodeficiency virus. <i>Virology</i> , 1995 , 210, 448-55	3.6	19
30	Microbial Communities in Human Milk Relate to Measures of Maternal Weight. <i>Frontiers in Microbiology</i> , 2019 , 10, 2886	5.7	17
29	Simultaneous expression of the Lassa virus N and GPC genes from a single recombinant vaccinia virus. <i>Virus Research</i> , 1991 , 18, 231-41	6.4	15
28	Profiling of Bacterial and Fungal Microbial Communities in Cystic Fibrosis Sputum Using RNA. <i>MSphere</i> , 2018 , 3,	5	14
27	Optical map of the genotype A1 WB C6 Giardia lamblia genome isolate. <i>Molecular and Biochemical Parasitology</i> , 2011 , 180, 112-4	1.9	11
26	Electroactive Bacteria Associated With Stainless Steel Ennoblement in Seawater. <i>Frontiers in Microbiology</i> , 2019 , 10, 170	5.7	9
25	A common garden experiment with Porphyra umbilicalis (Rhodophyta) evaluates methods to study spatial differences in the macroalgal microbiome. <i>Journal of Phycology</i> , 2018 , 54, 653-664	3	9
24	Inferring protein function from genomic sequence: Giardia lamblia expresses a phosphatidylinositol kinase-related kinase similar to yeast and mammalian TOR. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2002 , 133, 477-91	2.3	9
23	SIVmac expressing hybrid envelope proteins containing HIV-1 V3 and/or C4 sequences is not competent for replication. <i>AIDS Research and Human Retroviruses</i> , 1994 , 10, 309-13	1.6	8
22	Infant Feeding Alters the Longitudinal Impact of Birth Mode on the Development of the Gut Microbiota in the First Year of Life. <i>Frontiers in Microbiology</i> , 2021 , 12, 642197	5.7	8
21	Marine Oxygen-Deficient Zones Harbor Depauperate Denitrifying Communities Compared to Novel Genetic Diversity in Coastal Sediments. <i>Microbial Ecology</i> , 2015 , 70, 311-21	4.4	7
20	Adaptive ecological processes and metabolic independence drive microbial colonization and resilience in the human gut		7
19	Microbiome profiling in extremely acidic soils affected by hydrothermal fluids: the case of the Solfatara Crater (Campi Flegrei, southern Italy). <i>FEMS Microbiology Ecology</i> , 2018 , 94,	4.3	7
18	Bacterial Communities Show Algal Host (spp.)/Zone Differentiation Across the Stress Gradient of the Intertidal Zone. <i>Frontiers in Microbiology</i> , 2020 , 11, 563118	5.7	5
17	Reliability of stool microbiome methods for DNA yields and sequencing among infants and young children. <i>MicrobiologyOpen</i> , 2020 , 9, e1018	3.4	5
16	Identification of V3 mutations that can compensate for inactivating mutations in C4 of simian immunodeficiency virus. <i>Virology</i> , 1995 , 213, 179-89	3.6	5
15	Functional and genetic markers of niche partitioning among enigmatic members of the human oral microbiome		4
14	DRISSEE overestimates errors in metagenomic sequencing data. <i>Briefings in Bioinformatics</i> , 2014 , 15, 783-7	3.4	3

13	The rare biosphere: sorting out fact from fiction 2010 , 11, 119		3
12	The microbiome of the habitat-forming brown alga <i>Fucus vesiculosus</i> (Phaeophyceae) has similar cross-Atlantic structure that reflects past and present drivers. <i>Journal of Phycology</i> , 2021 , 57, 1681-1698 ³		3
11	Associations between the gut microbiome and metabolome in early life. <i>BMC Microbiology</i> , 2021 , 21, 238	4.5	3
10	Linking Spatial and Temporal Dynamic of Bacterioplankton Communities With Ecological Strategies Across a Coastal Frontal Area. <i>Frontiers in Marine Science</i> , 2020 , 7,	4.5	2
9	Influence of dissolved oxygen content on the bacteria-induced ennoblement of stainless steels in seawater and its consequence on the localized corrosion risk. <i>Materials and Corrosion - Werkstoffe Und Korrosion</i> , 2019 , 70, 2238-2246	1.6	2
8	High-resolution tracking of microbial colonization in Fecal Microbiota Transplantation experiments via metagenome-assembled genomes		2
7	Time outweighs the effect of host developmental stage on microbial community composition. <i>FEMS Microbiology Ecology</i> , 2021 , 97,	4.3	2
6	Assessment of bacterial diversity in western Accra, Ghana, drinking water samples. <i>Journal of Water Sanitation and Hygiene for Development</i> , 2019 , 9, 644-661	1.5	1
5	Profiling of bacterial and fungal microbial communities in cystic fibrosis sputum using RNA		1
4	High molecular weight DNA extraction strategies for long-read sequencing of complex metagenomes		1
3	Soil Microsite Outweighs Cultivar Genotype Contribution to Rhizobacterial Community Structure. <i>Frontiers in Microbiology</i> , 2021 , 12, 645784	5.7	1
2	Genomics of <i>Giardia</i> 2011 , 95-101		
1	Spatiotemporal Heterogeneity and Intragenus Variability in Rhizobacterial Associations with Growth.. <i>MSystems</i> , 2022 , e0006022	7.6	