

Emily B Hollister

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

21,842
citations

196777

29
h-index

286692

43
g-index

47
all docs

47
docs citations

47
times ranked

32674
citing authors

#	ARTICLE	IF	CITATIONS
1	Fecal Microbiota Transplantation Commonly Failed in Children With Co-morbidities. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2022, 74, 227-235.	0.9	4
2	Probiotic VSL#3 Treatment Reduces Colonic Permeability and Abdominal Pain Symptoms in Patients With Irritable Bowel Syndrome. <i>Frontiers in Pain Research</i> , 2021, 2, 691689.	0.9	9
3	Multi-omic data integration: A review of concepts, considerations, and approaches. <i>Seminars in Perinatology</i> , 2021, 45, 151456.	1.1	37
4	Can prescribed fires restore C ₄ grasslands invaded by a C ₃ woody species and a dominant C ₃ grass species?. <i>Ecosphere</i> , 2021, 12, .	1.0	6
5	Potential Applications of Human Viral Metagenomics and Reference Materials: Considerations for Current and Future Viruses. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	13
6	Human Virome and Disease: High-Throughput Sequencing for Virus Discovery, Identification of Phage-Bacteria Dysbiosis and Development of Therapeutic Approaches with Emphasis on the Human Gut. <i>Viruses</i> , 2019, 11, 656.	1.5	111
7	Leveraging Human Microbiome Features to Diagnose and Stratify Children with Irritable Bowel Syndrome. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 449-461.	1.2	59
8	Fungal Community Structural and Microbial Functional Pattern Changes After Soil Amendments by Oilseed Meals of <i>Jatropha curcas</i> and <i>Camelina sativa</i> : A Microcosm Study. <i>Frontiers in Microbiology</i> , 2019, 10, 537.	1.5	10
9	<p>Biochemical but not compositional recovery of skin mucosal microbiome communities after disruption</p>. <i>Infection and Drug Resistance</i> , 2019, Volume 12, 399-416.	1.1	5
10	Considering the Supraorganism: Harnessing the Gut Microbiome for Cancer Prevention, Detection, and Treatment. <i>American Journal of Gastroenterology</i> , 2019, 114, 1030-1031.	0.2	0
11	Airway Microbiome and Development of Bronchopulmonary Dysplasia in Preterm Infants: A Systematic Review. <i>Journal of Pediatrics</i> , 2019, 204, 126-133.e2.	0.9	81
12	Leveraging sequence-based faecal microbial community survey data to identify a composite biomarker for colorectal cancer. <i>Gut</i> , 2018, 67, 882-891.	6.1	159
13	Characterization of the Stool Microbiome in Hispanic Preschool Children by Weight Status and Time. <i>Childhood Obesity</i> , 2018, 14, 122-130.	0.8	21
14	Re-purposing 16S rRNA gene sequence data from within case paired tumor biopsy and tumor-adjacent biopsy or fecal samples to identify microbial markers for colorectal cancer. <i>PLoS ONE</i> , 2018, 13, e0207002.	1.1	25
15	Psyllium Fiber Reduces Abdominal Pain in Children With Irritable Bowel Syndrome in a Randomized, Double-Blind Trial. <i>Clinical Gastroenterology and Hepatology</i> , 2017, 15, 712-719.e4.	2.4	77
16	Differences in gut microbial composition correlate with regional brain volumes in irritable bowel syndrome. <i>Microbiome</i> , 2017, 5, 49.	4.9	228
17	Microbial markers in the diagnosis of colorectal cancer: the promise, reality and challenge. <i>Future Microbiology</i> , 2017, 12, 1341-1344.	1.0	8
18	The Microbiome, Intestinal Function, and Arginine Metabolism of Healthy Indian Women Are Different from Those of American and Jamaican Women. <i>Journal of Nutrition</i> , 2016, 146, 706-713.	1.3	40

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19	Colonic Mucosal Epigenome and Microbiome Development in Children and Adolescents. <i>Journal of Immunology Research</i> , 2016, 2016, 1-7.	0.9	36
20	The mucosal microbiota in a young child with severe non-Helicobacter gastritis. <i>Therapeutic Advances in Gastroenterology</i> , 2016, 9, 749-751.	1.4	0
21	Composition and function of the pediatric colonic mucosal microbiome in untreated patients with ulcerative colitis. <i>Gut Microbes</i> , 2016, 7, 384-396.	4.3	84
22	Reply. <i>Clinical Gastroenterology and Hepatology</i> , 2016, 14, 1667-1668.	2.4	0
23	Transfer of Viral Communities between Human Individuals during Fecal Microbiota Transplantation. <i>MBio</i> , 2016, 7, e00322.	1.8	90
24	The Fecal Microbiome in Pediatric Patients With Short Bowel Syndrome. <i>Journal of Parenteral and Enteral Nutrition</i> , 2016, 40, 1106-1113.	1.3	57
25	Role of the Gut Microbiome in Obstructive Sleep Apnea-Induced Hypertension. <i>Hypertension</i> , 2016, 67, 469-474.	1.3	252
26	Bioinformation and -Omic Approaches for Characterization of Environmental Microorganisms. , 2015, , 483-505.		4
27	Serial Fecal Microbiota Transplantation Alters Mucosal Gene Expression in Pediatric Ulcerative Colitis. <i>American Journal of Gastroenterology</i> , 2015, 110, 604-606.	0.2	61
28	Structure and function of the healthy pre-adolescent pediatric gut microbiome. <i>Microbiome</i> , 2015, 3, 36.	4.9	283
29	Gut microbiota influences low fermentable substrate diet efficacy in children with irritable bowel syndrome. <i>Gut Microbes</i> , 2014, 5, 165-175.	4.3	121
30	The airway microbiome of intubated premature infants: characteristics and changes that predict the development of bronchopulmonary dysplasia. <i>Pediatric Research</i> , 2014, 76, 294-301.	1.1	112
31	From Prediction to Function Using Evolutionary Genomics: Human-Specific Ecotypes of <i>Lactobacillus reuteri</i> Have Diverse Probiotic Functions. <i>Genome Biology and Evolution</i> , 2014, 6, 1772-1789.	1.1	83
32	Compositional and Functional Features of the Gastrointestinal Microbiome and Their Effects on Human Health. <i>Gastroenterology</i> , 2014, 146, 1449-1458.	0.6	386
33	Evaluating the performance of carboxylate platform fermentations across diverse inocula originating as sediments from extreme environments. <i>Bioresource Technology</i> , 2014, 155, 388-394.	4.8	11
34	Soil bacterial and fungal communities respond differently to various isothiocyanates added for biofumigation. <i>Frontiers in Microbiology</i> , 2014, 5, 729.	1.5	56
35	Differential impacts of brassicaceous and nonbrassicaceous oilseed meals on soil bacterial and fungal communities. <i>FEMS Microbiology Ecology</i> , 2013, 83, 632-641.	1.3	71
36	Comparison of mixed-acid fermentations inoculated with six different mixed cultures. <i>Bioresource Technology</i> , 2012, 118, 343-349.	4.8	11

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37	Impact of Indian Mustard (<i>Brassica juncea</i>) and Flax (<i>Linum usitatissimum</i>) Seed Meal Applications on Soil Carbon, Nitrogen, and Microbial Dynamics. <i>Applied and Environmental Soil Science</i> , 2012, 2012, 1-14.	0.8	26
38	Mesophilic and Thermophilic Conditions Select for Unique but Highly Parallel Microbial Communities to Perform Carboxylate Platform Biomass Conversion. <i>PLoS ONE</i> , 2012, 7, e39689.	1.1	30
39	Impacts of Cropping Systems and Long-Term Tillage on Soil Microbial Population Levels and Community Composition in Dryland Agricultural Setting. <i>ISRN Ecology</i> , 2012, 2012, 1-11.	1.0	16
40	Water Management Impacts on Arsenic Speciation and Iron-Reducing Bacteria in Contrasting Rice-Rhizosphere Compartments. <i>Environmental Science & Technology</i> , 2011, 45, 8328-8335.	4.6	122
41	Microbial communities in rice rhizosphere altered by intermittent and continuous flooding in fields with long-term arsenic application. <i>Soil Biology and Biochemistry</i> , 2011, 43, 1220-1228.	4.2	71
42	Investigation of intermittent air exposure on four-stage and one-stage anaerobic semi-continuous mixed-acid fermentations. <i>Bioresource Technology</i> , 2011, 102, 5066-5075.	4.8	18
43	Structure and dynamics of the microbial communities underlying the carboxylate platform for biofuel production. <i>Applied Microbiology and Biotechnology</i> , 2010, 88, 389-399.	1.7	32
44	Structural and functional diversity of soil bacterial and fungal communities following woody plant encroachment in the southern Great Plains. <i>Soil Biology and Biochemistry</i> , 2010, 42, 1816-1824.	4.2	72
45	Shifts in microbial community structure along an ecological gradient of hypersaline soils and sediments. <i>ISME Journal</i> , 2010, 4, 829-838.	4.4	289
46	Black Box Chimera Check (B2C2): a Windows-Based Software for Batch Depletion of Chimeras from Bacterial 16S rRNA Gene Datasets. <i>Open Microbiology Journal</i> , 2010, 4, 47-52.	0.2	165
47	Introducing mothur: Open-Source, Platform-Independent, Community-Supported Software for Describing and Comparing Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7537-7541.	1.4	18,390