## Hein M Tun

## List of Publications by Year in descending order

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136950 149698 3,645 81 32 56 citations h-index g-index papers 5101 87 87 87 citing authors all docs docs citations times ranked

#	Article	IF	CITATIONS
1	Comparison of virus concentration methods and RNA extraction methods for SARS-CoV-2 wastewater surveillance. Science of the Total Environment, 2022, 824, 153687.	8.0	49
2	Gut microbiota composition is associated with SARS-CoV-2 vaccine immunogenicity and adverse events. Gut, 2022, 71, 1106-1116.	12.1	84
3	Alleviation of Hepatic Steatosis: Dithizone-Related Gut Microbiome Restoration During Paneth Cell Dysfunction. Frontiers in Microbiology, 2022, 13, 813783.	3.5	6
4	Gut microbiota insights into human adaption to highâ€plateau diet. , 2022, 1, .		3
5	Use of Sewage Surveillance for COVID-19: A Large-Scale Evidence-Based Program in Hong Kong. Environmental Health Perspectives, 2022, 130, 57008.	6.0	20
6	Evaluation of RT-qPCR Primer-Probe Sets to Inform Public Health Interventions Based on COVID-19 Sewage Tests. Environmental Science & Environmental Sc	10.0	11
7	A Universal LC-MS/MS Method for Simultaneous Detection of Antibiotic Residues in Animal and Environmental Samples. Antibiotics, 2022, 11, 845.	3.7	13
8	Quantification of SARS-CoV-2 RNA in wastewater treatment plants mirrors the pandemic trend in Hong Kong. Science of the Total Environment, 2022, 844, 157121.	8.0	22
9	From Birth to Overweight and Atopic Disease: Multiple and Common Pathways of the Infant Gut Microbiome. Gastroenterology, 2021, 160, 128-144.e10.	1.3	31
10	The New Foe and Old Friends: Are We Ready for Microbiota-Based Therapeutics in Treating COVID-19 Patients?. Gastroenterology, 2021, 160, 2192-2193.	1.3	4
11	Bacteroides-dominant gut microbiome of late infancy is associated with enhanced neurodevelopment. Gut Microbes, 2021, 13, 1-17.	9.8	74
12	Efficacy of metformin and fermentable fiber combination therapy in adolescents with severe obesity and insulin resistance: study protocol for a double-blind randomized controlled trial. Trials, 2021, 22, 148.	1.6	4
13	Role of gut microbiota in travel-related acquisition of extended spectrum $\hat{I}^2$ -lactamase-producing Enterobacteriaceae. Journal of Travel Medicine, 2021, 28, .	3.0	14
14	Multi-platform omics analysis reveals molecular signature for COVID-19 pathogenesis, prognosis and drug target discovery. Signal Transduction and Targeted Therapy, 2021, 6, 155.	17.1	49
15	Characterization of respiratory microbial dysbiosis in hospitalized COVID-19 patients. Cell Discovery, 2021, 7, 23.	6.7	34
16	Coronavirus seroprevalence among villagers exposed to bats in Thailand. Zoonoses and Public Health, 2021, 68, 464-473.	2.2	7
17	Gut microbiome and resistome changes during the first wave of the COVID-19 pandemic in comparison with pre-pandemic travel-related changes. Journal of Travel Medicine, 2021, 28, .	3.0	14
18	Gestational diabetes mellitus is associated with the neonatal gut microbiota and metabolome. BMC Medicine, 2021, 19, 120.	5.5	44

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19	Probiotics, prebiotics, synbiotics, and fecal microbiota transplantation in the treatment of behavioral symptoms of autism spectrum disorder: A systematic review. Autism Research, 2021, 14, 1820-1836.	3.8	57
20	Ethnicity Associations With Food Sensitization Are Mediated by Gut Microbiota Development in the First Year of Life. Gastroenterology, 2021, 161, 94-106.	1.3	16
21	Composition and Functions of the Gut Microbiome in Pediatric Obesity: Relationships with Markers of Insulin Resistance. Microorganisms, 2021, 9, 1490.	3.6	15
22	Prenatal Depression, Breastfeeding, and Infant Gut Microbiota. Frontiers in Microbiology, 2021, 12, 664257.	3.5	15
23	Metagenomic Survey Reveals More Diverse and Abundant Antibiotic Resistance Genes in Municipal Wastewater Than Hospital Wastewater. Frontiers in Microbiology, 2021, 12, 712843.	3.5	6
24	Impact of Maternal Intrapartum Antibiotics, and Caesarean Section with and without Labour on Bifidobacterium and Other Infant Gut Microbiota. Microorganisms, 2021, 9, 1847.	3.6	15
25	Veterinary Experiences can Inform One Health Strategies for Animal Coronaviruses. EcoHealth, 2021, 18, 301-314.	2.0	1
26	The first case study of wastewater-based epidemiology of COVID-19 in Hong Kong. Science of the Total Environment, 2021, 790, 148000.	8.0	50
27	Upholding veterinary services as a pillar of one health in Myanmar. One Health, 2021, 13, 100329.	3.4	0
28	Current and emerging therapies for managing hyperphagia and obesity in Praderâ€Willi syndrome: A narrative review. Obesity Reviews, 2020, 21, e12992.	<b>6.</b> 5	56
29	Saccharomyces cerevisiae fermentation products (SCFP) stabilize the ruminal microbiota of lactating dairy cows during periods of a depressed rumen pH. BMC Veterinary Research, 2020, 16, 237.	1.9	22
30	Vitamin D supplementation in pregnancy and early infancy in relation to gut microbiota composition and <i>C. difficile</i> colonization: implications for viral respiratory infections. Gut Microbes, 2020, 12, 1799734.	9.8	16
31	The Gut Microbiota Profile in Children with Prader–Willi Syndrome. Genes, 2020, 11, 904.	2.4	18
32	Impact of outdoor nature-related activities on gut microbiota, fecal serotonin, and perceived stress in preschool children: the Play&Grow randomized controlled trial. Scientific Reports, 2020, 10, 21993.	3.3	58
33	Increased risk of gestational diabetes mellitus in women with higher prepregnancy ambient PM2.5 exposure. Science of the Total Environment, 2020, 730, 138982.	8.0	26
34	Natural environments in the urban context and gut microbiota in infants. Environment International, 2020, 142, 105881.	10.0	30
35	Early-Life Social and Economic Adversities on Health. , 2020, , 181-193.		0
36	Clostridioides Difficile Colonization Is Differentially Associated with Gut Microbiota Composition in Breastfed versus Formula Fed Infants (OR01-02-19). Current Developments in Nutrition, 2019, 3, nzz040.OR01-02-19.	0.3	0

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37	Clostridioides difficile Colonization Is Differentially Associated With Gut Microbiome Profiles by Infant Feeding Modality at 3–4 Months of Age. Frontiers in Immunology, 2019, 10, 2866.	4.8	22
38	Dietary supplementation with flaxseed meal and oat hulls modulates intestinal histomorphometric characteristics, digesta- and mucosa-associated microbiota in pigs. Scientific Reports, 2018, 8, 5880.	3.3	30
39	Interaction of genotype and diet on small intestine microbiota of Japanese quail fed a cholesterol enriched diet. Scientific Reports, 2018, 8, 2381.	3.3	14
40	Roles of Birth Mode and Infant Gut Microbiota in Intergenerational Transmission of Overweight and Obesity From Mother to Offspring. JAMA Pediatrics, 2018, 172, 368.	6.2	235
41	Commentary: The Influence of Proton Pump Inhibitors on the Fecal Microbiome of Infants with Gastroesophageal Reflux-A Prospective Longitudinal Interventional Study. Frontiers in Cellular and Infection Microbiology, 2018, 8, 430.	3.9	1
42	Meta-analysis of effects of exclusive breastfeeding on infant gut microbiota across populations. Nature Communications, 2018, 9, 4169.	12.8	283
43	Postnatal exposure to household disinfectants, infant gut microbiota and subsequent risk of overweight in children. Cmaj, 2018, 190, E1097-E1107.	2.0	46
44	The association between early life antibiotic use and allergic disease in young children: recent insights and their implications. Expert Review of Clinical Immunology, 2018, 14, 841-855.	3.0	25
45	Impact of xylanases on gut microbiota of growing pigs fed corn- or wheat-based diets. Animal Nutrition, 2018, 4, 339-350.	5.1	41
46	Association of Exposure to Formula in the Hospital and Subsequent Infant Feeding Practices With Gut Microbiota and Risk of Overweight in the First Year of Life. JAMA Pediatrics, 2018, 172, e181161.	6.2	218
47	Selective Induction of Homeostatic Th17 Cells in the Murine Intestine by Cholera Toxin Interacting with the Microbiota. Journal of Immunology, 2017, 199, 312-322.	0.8	18
48	Exposure to household furry pets influences the gut microbiota of infants at 3–4Âmonths following various birth scenarios. Microbiome, 2017, 5, 40.	11.1	197
49	Comparison of DNA-, PMA-, and RNA-based 16S rRNA Illumina sequencing for detection of live bacteria in water. Scientific Reports, 2017, 7, 5752.	3.3	116
50	Bacteria in drinking water sources of a First Nation reserve in Canada. Science of the Total Environment, 2017, 575, 813-819.	8.0	32
51	Linking Peripartal Dynamics of Ruminal Microbiota to Dietary Changes and Production Parameters. Frontiers in Microbiology, 2017, 7, 2143.	3.5	58
52	Common Distribution of gad Operon in Lactobacillus brevis and its GadA Contributes to Efficient GABA Synthesis toward Cytosolic Near-Neutral pH. Frontiers in Microbiology, 2017, 8, 206.	3.5	61
53	Cesarean Section, Formula Feeding, and Infant Antibiotic Exposure: Separate and Combined Impacts on Gut Microbial Changes in Later Infancy. Frontiers in Pediatrics, 2017, 5, 200.	1.9	69
54	Sex-specific impact of asthma during pregnancy on infant gut microbiota. European Respiratory Journal, 2017, 50, 1700280.	6.7	20

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55	0501 Comparative genomics of Lactobacillus brevis uncovers its common capability for efficiently synthesizing neuroactive Î <sup>3</sup> -aminobutyric acid. Journal of Animal Science, 2016, 94, 241-241.	0.5	О
56	High Molecular Weight Barley $\hat{I}^2$ -Glucan Alters Gut Microbiota Toward Reduced Cardiovascular Disease Risk. Frontiers in Microbiology, 2016, 7, 129.	3.5	133
57	Monitoring Survivability and Infectivity of Porcine Epidemic Diarrhea Virus (PEDv) in the Infected On-Farm Earthen Manure Storages (EMS). Frontiers in Microbiology, 2016, 7, 265.	3.5	23
58	Effects of grain feeding on microbiota in the digestive tract of cattle. Animal Frontiers, 2016, 6, 13-19.	1.7	97
59	Detection of Antibiotic Resistance Genes in Source and Drinking Water Samples from a First Nations Community in Canada. Applied and Environmental Microbiology, 2016, 82, 4767-4775.	3.1	103
60	An extended singleâ€index multiplexed 16S rRNA sequencing for microbial community analysis on MiSeq illumina platforms. Journal of Basic Microbiology, 2016, 56, 321-326.	3.3	93
61	Nutritional Models of Experimentally-Induced Subacute Ruminal Acidosis (SARA) Differ in Their Impact on Rumen and Hindgut Bacterial Communities in Dairy Cows. Frontiers in Microbiology, 2016, 7, 2128.	3.5	97
62	Deletion of the Toll-Like Receptor 5 Gene Per Se Does Not Determine the Gut Microbiome Profile That Induces Metabolic Syndrome: Environment Trumps Genotype. PLoS ONE, 2016, 11, e0150943.	2.5	20
63	The effect of diet and host genotype on ceca microbiota of Japanese quail fed a cholesterol enriched diet. Frontiers in Microbiology, 2015, 6, 1092.	3.5	20
64	Pyrosequencing of the bacteria associated with Platygyra carnosus corals with skeletal growth anomalies reveals differences in bacterial community composition in apparently healthy and diseased tissues. Frontiers in Microbiology, 2015, 6, 1142.	3.5	35
65	Re-emerging of porcine respiratory and reproductive syndrome virus (lineage 3) and increased pathogenicity after genomic recombination with vaccine variant. Veterinary Microbiology, 2015, 175, 332-340.	1.9	78
66	Complete Genome Sequence of Staphylococcus xylosus HKUOPL8, a Potential Opportunistic Pathogen of Mammals. Genome Announcements, 2014, 2, .	0.8	8
67	Complete genome sequence and comparative genome analysis of Klebsiella oxytoca HKOPL1 isolated from giant panda feces. BMC Research Notes, 2014, 7, 827.	1.4	14
68	Risk factors for H7 and H9 infection in commercial poultry farm workers in provinces within Pakistan. Preventive Veterinary Medicine, 2014, 117, 610-614.	1.9	16
69	A survey of gastro-intestinal parasitic infection in domestic and wild birds in Chittagong and Greater Sylhet, Bangladesh. Preventive Veterinary Medicine, 2014, 117, 305-312.	1.9	14
70	Microbial community in microbial fuel cell (MFC) medium and effluent enriched with purple photosynthetic bacterium (Rhodopseudomonas sp.). AMB Express, 2014, 4, 22.	3.0	43
71	Genomic insights into high exopolysaccharide-producing dairy starter bacterium Streptococcus thermophilus ASCC 1275. Scientific Reports, 2014, 4, 4974.	3.3	109
72	Microbial Diversity and Evidence of Novel Homoacetogens in the Gut of Both Geriatric and Adult Giant Pandas (Ailuropoda melanoleuca). PLoS ONE, 2014, 9, e79902.	2.5	53

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73	Towards a metagenomic understanding on enhanced biomethane production from waste activated sludge after pH 10 pretreatment. Biotechnology for Biofuels, 2013, 6, 38.	6.2	108
74	Molecular epidemiology of influenza A (H5N1) viruses, Bangladesh, 2007–2011. Preventive Veterinary Medicine, 2013, 111, 314-318.	1.9	8
75	Characterization of cecal microbiota of the emu (Dromaius novaehollandiae). Veterinary Microbiology, 2013, 166, 304-310.	1.9	35
76	Gene-centric metagenomics analysis of feline intestinal microbiome using 454 junior pyrosequencing. Journal of Microbiological Methods, 2012, 88, 369-376.	1.6	93
77	Phylodynamics of H5N1 avian influenza virus in Indonesia. Molecular Ecology, 2012, 21, 3062-3077.	3.9	33
78	Genetic diversity and multiple introductions of porcine reproductive and respiratory syndrome viruses in Thailand. Virology Journal, 2011, 8, 164.	3.4	16
79	Role of Gut Microbiota in Cardiovascular Disease that Links to Host Genotype and Diet., 0,,.		1
80	Gut microbial-induced inflammation: normal aging or lifestyle changes?. Journal of Laboratory and Precision Medicine, 0, 2, 48-48.	1.1	0
81	Unpacking Multi-Level Governance of Antimicrobial Resistance Policies: the Case of Guangdong, China. Health Policy and Planning, 0, , .	2.7	1