

Nur A Hasan

List of Publications by Year in Descending Order

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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.

94
papers

4,793
citations

30
h-index

68
g-index

104
ext. papers

6,382
ext. citations

6.4
avg, IF

4.98
L-index

#	Paper	IF	Citations
94	Aging-Induced Dysbiosis of Gut Microbiota as a Risk Factor for Increased Infection. <i>Frontiers in Immunology</i> , 2021 , 12, 672353	8.4	7
93	Dynamics, Diversity, and Virulence of . in Homestead Pond Water in Coastal Bangladesh. <i>Frontiers in Public Health</i> , 2021 , 9, 692166	6	0
92	Microbiome signatures of progression toward celiac disease onset in at-risk children in a longitudinal prospective cohort study. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	18
91	Evaluation of a Combined Multilocus Sequence Typing and Whole-Genome Sequencing Two-Step Algorithm for Routine Typing of. <i>Journal of Clinical Microbiology</i> , 2021 , 59,	9.7	2
90	Metagenomic Sequencing and Quantitative Real-Time PCR for Fecal Pollution Assessment in an Urban Watershed. <i>Frontiers in Water</i> , 2021 , 3, 626849	2.6	2
89	Nanopore-based metagenomics analysis reveals prevalence of mobile antibiotic and heavy metal resistome in wastewater. <i>Ecotoxicology</i> , 2021 , 30, 1572-1585	2.9	3
88	Treatment of fresh produce with a Salmonella-targeted bacteriophage cocktail is compatible with chlorine or peracetic acid and more consistently preserves the microbial community on produce. <i>Journal of Food Safety</i> , 2020 , 40, e12763	2	5
87	SYN-007, an Orally Administered Beta-Lactamase Enzyme, Protects the Gut Microbiome from Oral Amoxicillin/Clavulanate without Adversely Affecting Antibiotic Systemic Absorption in Dogs. <i>Microorganisms</i> , 2020 , 8,	4.9	4
86	A comparative analysis of drinking water employing metagenomics. <i>PLoS ONE</i> , 2020 , 15, e0231210	3.7	14
85	A New Whole Genome Culture-Independent Diagnostic Test (WG-CIDT) for Rapid Detection of in Lettuce. <i>Frontiers in Microbiology</i> , 2020 , 11, 602	5.7	3
84	Multiple NDM-5-Expressing Isolates From an Immunocompromised Pediatric Host. <i>Open Forum Infectious Diseases</i> , 2020 , 7, ofaa018	1	4
83	Multi-omics analysis reveals the influence of genetic and environmental risk factors on developing gut microbiota in infants at risk of celiac disease. <i>Microbiome</i> , 2020 , 8, 130	16.6	28
82	Temporal Resistome and Microbial Community Dynamics in an Intensive Aquaculture Facility with Prophylactic Antimicrobial Treatment. <i>Microorganisms</i> , 2020 , 8,	4.9	5
81	Metagenome sequencing-based strain-level and functional characterization of supragingival microbiome associated with dental caries in children. <i>Journal of Oral Microbiology</i> , 2019 , 11, 1557986	6.3	33
80	Oral Beta-Lactamase Protects the Canine Gut Microbiome from Oral Amoxicillin-Mediated Damage. <i>Microorganisms</i> , 2019 , 7,	4.9	5
79	Metagenomic Profiling of Microbial Pathogens in the Little Bighorn River, Montana. <i>International Journal of Environmental Research and Public Health</i> , 2019 , 16,	4.6	34
78	Low dose oral beta-lactamase protects the gut microbiome from oral beta-lactam-mediated damage in dogs. <i>AIMS Public Health</i> , 2019 , 6, 477-487	1.9	4

77	Prosthetic joint infections present diverse and unique microbial communities using combined whole-genome shotgun sequencing and culturing methods. <i>Journal of Medical Microbiology</i> , 2019 , 68, 1507-1516	3.2	8
76	Oral Metallo-Beta-Lactamase Protects the Gut Microbiome From Carbapenem-Mediated Damage and Reduces Propagation of Antibiotic Resistance in Pigs. <i>Frontiers in Microbiology</i> , 2019 , 10, 101	5.7	22
75	673. Novel Delayed-Release Formulation of an Oral β -Lactamase Prevents Gut Microbiome Damage and Attenuates Antibiotic Resistance Caused by Oral Amoxicillin/Clavulanate without Interfering with Amoxicillin Systemic Absorption in Dogs. <i>Open Forum Infectious Diseases</i> , 2019 , 6, S307-S307	1	78
74	T6SS and ExoA of flesh-eating in peritonitis and necrotizing fasciitis during mono- and polymicrobial infections. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 24084-24092	11.5	10
73	Biofilms Comprise a Component of the Annual Cycle of <i>Vibrio cholerae</i> in the Bay of Bengal Estuary. <i>MBio</i> , 2018 , 9,	7.8	16
72	Microbial diversity changes with rhizosphere and hydrocarbons in contrasting soils. <i>Ecotoxicology and Environmental Safety</i> , 2018 , 156, 434-442	7	20
71	Distinct consequences of amoxicillin and ertapenem exposure in the porcine gut microbiome. <i>Anaerobe</i> , 2018 , 53, 82-93	2.8	21
70	Comparison of Infant Gut and Skin Microbiota, Resistome and Virulome Between Neonatal Intensive Care Unit (NICU) Environments. <i>Frontiers in Microbiology</i> , 2018 , 9, 1361	5.7	24
69	620. Oral β -Lactamase Therapies Prevent Microbiome Damage and Attenuate Antibiotic Resistance From IV and Oral Antibiotics in Large Animal Models of Antibiotic-Mediated Gut Dysbiosis. <i>Open Forum Infectious Diseases</i> , 2018 , 5, S226-S226	1	1
68	Characterization of the Microbiome at the World's Largest Potable Water Reuse Facility. <i>Frontiers in Microbiology</i> , 2018 , 9, 2435	5.7	28
67	A Metagenomic Approach to Evaluating Surface Water Quality in Haiti. <i>International Journal of Environmental Research and Public Health</i> , 2018 , 15,	4.6	20
66	Sa1839 - Orally Delivered Beta-Lactamase Prevents Gut Microbiome Dysbiosis Caused by IV and Oral Antibiotics and Mitigates Propagation of Antibiotic Resistance in Porcine and Canine Models. <i>Gastroenterology</i> , 2018 , 154, S-415	13.3	2
65	SYN-004 (ribaxamase), an oral beta-lactamase, mitigates antibiotic-mediated dysbiosis in a porcine gut microbiome model. <i>Journal of Applied Microbiology</i> , 2017 , 123, 66-79	4.7	22
64	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017 , 551, 457-463	50.4	1076
63	Gut Antibiotic Inactivation by β -Lactamases Is Intended to Prevent Microbiome Damage and Attenuate Antibiotic Resistance in Large Animal Models. <i>Open Forum Infectious Diseases</i> , 2017 , 4, S232-S233	1	1
62	Comprehensive benchmarking and ensemble approaches for metagenomic classifiers. <i>Genome Biology</i> , 2017 , 18, 182	18.3	152
61	Differences in the Stool and Skin Microbiome, Virulence Factor and Antimicrobial Resistance Genes in a Private Room Versus a Shared Space Neonatal Intensive Care Unit. <i>Gastroenterology</i> , 2017 , 152, S213-S214	13.3	14 ²
60	The microbiomes of blowflies and houseflies as bacterial transmission reservoirs. <i>Scientific Reports</i> , 2017 , 7, 16324	4.9	63

59	Characterization of Microbial Signatures From Advanced Treated Wastewater Biofilms. <i>Journal - American Water Works Association</i> , 2017 , 109, E503-E512	0.5	18
58	Comparative genomic analysis and characterization of incompatibility group FIB plasmid encoded virulence factors of <i>Salmonella enterica</i> isolated from food sources. <i>BMC Genomics</i> , 2017 , 18, 570	4.5	16
57	Membrane Bioreactor-Based Wastewater Treatment Plant in Saudi Arabia: Reduction of Viral Diversity, Load, and Infectious Capacity. <i>Water (Switzerland)</i> , 2017 , 9, 534	3	22
56	O1 with Reduced Susceptibility to Ciprofloxacin and Azithromycin Isolated from a Rural Coastal Area of Bangladesh. <i>Frontiers in Microbiology</i> , 2017 , 8, 252	5.7	14
55	Characterization of Two Cryptic Plasmids Isolated in Haiti from Clinical Non-O1/Non-O139. <i>Frontiers in Microbiology</i> , 2017 , 8, 2283	5.7	5
54	Characterization of Pathogenic from the Chesapeake Bay, Maryland. <i>Frontiers in Microbiology</i> , 2017 , 8, 2460	5.7	15
53	Genotypic and phenotypic characterization of multidrug resistant <i>Salmonella</i> Typhimurium and <i>Salmonella</i> Kentucky strains recovered from chicken carcasses. <i>PLoS ONE</i> , 2017 , 12, e0176938	3.7	9
52	Development of SYN-004, an oral beta-lactamase treatment to protect the gut microbiome from antibiotic-mediated damage and prevent <i>Clostridium difficile</i> infection. <i>Anaerobe</i> , 2016 , 41, 58-67	2.8	42
51	Phylogenetic Diversity of <i>Vibrio cholerae</i> Associated with Endemic Cholera in Mexico from 1991 to 2008. <i>MBio</i> , 2016 , 7, e02160	7.8	20
50	Cross-talk among flesh-eating <i>Aeromonas hydrophila</i> strains in mixed infection leading to necrotizing fasciitis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 722-7	11.5	65
49	Enrichment dynamics of <i>Listeria monocytogenes</i> and the associated microbiome from naturally contaminated ice cream linked to a listeriosis outbreak. <i>BMC Microbiology</i> , 2016 , 16, 275	4.5	83
48	Nontoxicogenic <i>Vibrio cholerae</i> non-O1/O139 isolate from a case of human gastroenteritis in the U.S. Gulf Coast. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 9-14	9.7	10
47	Deep-sea hydrothermal vent bacteria related to human pathogenic <i>Vibrio</i> species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E2813-9	11.5	38
46	Hybrid <i>Vibrio cholerae</i> El Tor lacking SXT identified as the cause of a cholera outbreak in the Philippines. <i>MBio</i> , 2015 , 6,	7.8	8
45	Non-O1/non-O139 <i>Vibrio cholerae</i> carrying multiple virulence factors and <i>V. cholerae</i> O1 in the Chesapeake Bay, Maryland. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 1909-18	4.8	51
44	Concordance and discordance of sequence survey methods for molecular epidemiology. <i>PeerJ</i> , 2015 , 3, e761	3.1	5
43	Longitudinal analysis of microbial interaction between humans and the indoor environment. <i>Science</i> , 2014 , 345, 1048-52	33.3	543
42	Occurrence in Mexico, 1998-2008, of <i>Vibrio cholerae</i> CTX+ El Tor carrying an additional truncated CTX prophage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 9917-22	11.5	17

41	How community ecology can improve our understanding of cholera dynamics. <i>Frontiers in Microbiology</i> , 2014 , 5, 137	5.7	4
40	Microbial community profiling of human saliva using shotgun metagenomic sequencing. <i>PLoS ONE</i> , 2014 , 9, e97699	3.7	102
39	Genomic and phenotypic characterization of <i>Vibrio cholerae</i> non-O1 isolates from a US Gulf Coast cholera outbreak. <i>PLoS ONE</i> , 2014 , 9, e86264	3.7	26
38	GENOTYPE AND DRUG RESISTANCE OF CLINICAL AND ENVIRONMENTAL VIBRIO CHOLERAЕ NON-O1/NON-O139 IN NORTHEASTERN THAILAND. <i>Southeast Asian Journal of Tropical Medicine and Public Health</i> , 2014 , 45, 1354-64	1	2
37	A new integrative conjugative element detected in Haitian isolates of <i>Vibrio cholerae</i> non-O1/non-O139. <i>Research in Microbiology</i> , 2013 , 164, 891-893	4	11
36	Drug response and genetic properties of <i>Vibrio cholerae</i> associated with endemic cholera in north-eastern Thailand, 2003-2011. <i>Journal of Medical Microbiology</i> , 2013 , 62, 599-609	3.2	10
35	Genome Sequences of Clinical <i>Vibrio cholerae</i> Isolates from an Oyster-Borne Cholera Outbreak in Florida. <i>Genome Announcements</i> , 2013 , 1,		5
34	In response. <i>American Journal of Tropical Medicine and Hygiene</i> , 2013 , 89, 1231-1232	3.2	1
33	<i>Vibrio cholerae</i> O1 El Tor and O139 Bengal strains carrying ctxB(ET), Bangladesh. <i>Emerging Infectious Diseases</i> , 2013 , 19, 1713-5	10.2	15
32	Environmental factors influencing epidemic cholera. <i>American Journal of Tropical Medicine and Hygiene</i> , 2013 , 89, 597-607	3.2	93
31	Distribution of virulence genes in clinical and environmental <i>Vibrio cholerae</i> strains in Bangladesh. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 5782-5	4.8	25
30	Distribution and dynamics of epidemic and pandemic <i>Vibrio parahaemolyticus</i> virulence factors. <i>Frontiers in Cellular and Infection Microbiology</i> , 2013 , 3, 97	5.9	121
29	<i>Vibrio cholerae</i> in an Historically Cholera-Free Country. <i>Environmental Microbiology Reports</i> , 2012 , 4, 381-389	3.7	23
28	Detection, isolation, and identification of <i>Vibrio cholerae</i> from the environment. <i>Current Protocols in Microbiology</i> , 2012 , Chapter 6, Unit6A.5	7.1	52
27	<i>Vibrio cholerae</i> classical biotype strains reveal distinct signatures in Mexico. <i>Journal of Clinical Microbiology</i> , 2012 , 50, 2212-6	9.7	25
26	Genomic diversity of 2010 Haitian cholera outbreak strains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, E2010-7	11.5	143
25	Genomic analysis of ICEVchBan8: An atypical genetic element in <i>Vibrio cholerae</i> . <i>FEBS Letters</i> , 2012 , 586, 1617-21	3.8	14
24	Temperature regulation of virulence factors in the pathogen <i>Vibrio coralliilyticus</i> . <i>ISME Journal</i> , 2012 , 6, 835-46	11.9	149

23	Ecology of <i>Vibrio parahaemolyticus</i> and <i>Vibrio vulnificus</i> in the coastal and estuarine waters of Louisiana, Maryland, Mississippi, and Washington (United States). <i>Applied and Environmental Microbiology</i> , 2012 , 78, 7249-57	4.8	140
22	Reply to Mekalanos et al.: Genomic diversity of <i>Vibrio cholerae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, E3207-E3207	11.5	78
21	Reply to Frerichs et al.: Chasing the genetic diversity, not source attribution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, E3209-E3209	11.5	2
20	Role of Shrimp Chitin in the Ecology of Toxigenic <i>Vibrio cholerae</i> and Cholera Transmission. <i>Frontiers in Microbiology</i> , 2011 , 2, 260	5.7	27
19	Metagenomic 16S rDNA Targeted PCR-DGGE in Determining Bacterial Diversity in Aquatic Ecosystem. <i>Bangladesh Journal of Microbiology</i> , 2011 , 27, 46-50	0.6	4
18	Role of zooplankton diversity in <i>Vibrio cholerae</i> population dynamics and in the incidence of cholera in the Bangladesh Sundarbans. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 6125-32	4.8	48
17	Discovery of novel <i>Vibrio cholerae</i> VSP-II genomic islands using comparative genomic analysis. <i>FEMS Microbiology Letters</i> , 2010 , 308, 130-7	2.9	44
16	Diagnostic limitations to accurate diagnosis of cholera. <i>Journal of Clinical Microbiology</i> , 2010 , 48, 3918-23	7	64
15	Comparative genomics of clinical and environmental <i>Vibrio mimicus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 21134-9	11.5	40
14	Genome sequence of hybrid <i>Vibrio cholerae</i> O1 MJ-1236, B-33, and CIRS101 and comparative genomics with <i>V. cholerae</i> . <i>Journal of Bacteriology</i> , 2010 , 192, 3524-33	3.5	87
13	The pre-seventh pandemic <i>Vibrio cholerae</i> BX 330286 El Tor genome: evidence for the environment as a genome reservoir. <i>Environmental Microbiology Reports</i> , 2010 , 2, 208-16	3.7	3
12	Occurrence of the <i>Vibrio cholerae</i> seventh pandemic VSP-I island and a new variant. <i>OMICS A Journal of Integrative Biology</i> , 2010 , 14, 1-7	3.8	30
11	Comparative genomic analysis reveals evidence of two novel <i>Vibrio</i> species closely related to <i>V. cholerae</i> . <i>BMC Microbiology</i> , 2010 , 10, 154	4.5	44
10	RNA colony blot hybridization method for enumeration of culturable <i>Vibrio cholerae</i> and <i>Vibrio mimicus</i> bacteria. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 5439-44	4.8	6
9	Comparative genomics reveals mechanism for short-term and long-term clonal transitions in pandemic <i>Vibrio cholerae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 15442-7	11.5	297
8	Serogroup, virulence, and genetic traits of <i>Vibrio parahaemolyticus</i> in the estuarine ecosystem of Bangladesh. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 6268-74	4.8	27
7	Viable but nonculturable <i>Vibrio cholerae</i> O1 in biofilms in the aquatic environment and their role in cholera transmission. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 17801-6	11.5	169
6	Seasonal cholera caused by <i>Vibrio cholerae</i> serogroups O1 and O139 in the coastal aquatic environment of Bangladesh. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 4096-104	4.8	99

5	Proteolytic activation of <i>Vibrio mimicus</i> (Vm) major outer membrane protein haemagglutinin (HA) with Vm-HA/protease: Implication for understanding bacterial adherence. <i>Microbiology and Immunology</i> , 2006 , 50, 845-50	2.7	3
4	Phenotypic and molecular characteristics of <i>Escherichia coli</i> isolated from aquatic environment of Bangladesh. <i>Microbiology and Immunology</i> , 2006 , 50, 359-70	2.7	10
3	Effect of transport at ambient temperature on detection and isolation of <i>Vibrio cholerae</i> from environmental samples. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 2185-90	4.8	21
2	Comprehensive Benchmarking and Ensemble Approaches for Metagenomic Classifiers		3
1	Metagenomic sequencing to replace semi-quantitative urine culture for detection of urinary tract infections: a proof of concept		3