

Bhabatosh Das

List of Publications by Year in descending order

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Version: 2024-02-01

83
papers

2,765
citations

201674

27
h-index

206112

48
g-index

89
all docs

89
docs citations

89
times ranked

3310
citing authors

#	ARTICLE	IF	CITATIONS
1	The 2019 novel coronavirus disease (COVID-19) pandemic: A review of the current evidence. Indian Journal of Medical Research, 2020, 151, 147.	1.0	173
2	An Improved Method for High Quality Metagenomics DNA Extraction from Human and Environmental Samples. Scientific Reports, 2016, 6, 26775.	3.3	164
3	Gut Microbiomes of Indian Children of Varying Nutritional Status. PLoS ONE, 2014, 9, e95547.	2.5	154
4	Antibiotic resistance in <i>Vibrio cholerae</i> : Understanding the ecology of resistance genes and mechanisms. Vaccine, 2020, 38, A83-A92.	3.8	127
5	Intestinal Adherence of <i>Vibrio cholerae</i> Involves a Coordinated Interaction between Colonization Factor GbpA and Mucin. Infection and Immunity, 2008, 76, 4968-4977.	2.2	120
6	Diphtheria. Nature Reviews Disease Primers, 2019, 5, 81.	30.5	117
7	Homeostasis and dysbiosis of the gut microbiome in health and disease. Journal of Biosciences, 2019, 44, 1.	1.1	107
8	Analysis of the Gut Microbiome of Rural and Urban Healthy Indians Living in Sea Level and High Altitude Areas. Scientific Reports, 2018, 8, 10104.	3.3	104
9	Genomic plasticity associated with antimicrobial resistance in <i>Vibrio cholerae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 6226-6231.	7.1	90
10	Integrative mobile elements exploiting Xer recombination. Trends in Microbiology, 2013, 21, 23-30.	7.7	83
11	Stringent response in <i>Vibrio cholerae</i> : genetic analysis of <i>spoT</i> gene function and identification of a novel (p)ppGpp synthetase gene. Molecular Microbiology, 2009, 72, 380-398.	2.5	71
12	VGJÉ, integration and excision mechanisms contribute to the genetic diversity of <i>Vibrio cholerae</i> epidemic strains. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 2516-2521.	7.1	62
13	Comparison of Japanese and Indian intestinal microbiota shows diet-dependent interaction between bacteria and fungi. Npj Biofilms and Microbiomes, 2019, 5, 37.	6.4	60
14	Molecular keys of the tropism of integration of the cholera toxin phage. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 4377-4382.	7.1	58
15	Revisiting the Global Epidemiology of Cholera in Conjunction With the Genomics of <i>Vibrio cholerae</i> . Frontiers in Public Health, 2019, 7, 203.	2.7	56
16	Gastric microbiome of Indian patients with <i>Helicobacter pylori</i> infection, and their interaction networks. Scientific Reports, 2017, 7, 15438.	3.3	51
17	Molecular Insights into Antimicrobial Resistance Traits of Commensal Human Gut Microbiota. Microbial Ecology, 2019, 77, 546-557.	2.8	49
18	Functional Characterization of the Stringent Response Regulatory Gene <i>dksA</i> of <i>Vibrio cholerae</i> and Its Role in Modulation of Virulence Phenotypes. Journal of Bacteriology, 2012, 194, 5638-5648.	2.2	48

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19	Genetic organization of pre-CTX and CTX prophages in the genome of an environmental <i>Vibrio cholerae</i> non-O1, non-O139 strain. <i>Microbiology (United Kingdom)</i> , 2006, 152, 3633-3641.	1.8	47
20	Sub-optimal neutralisation of omicron (B.1.1.529) variant by antibodies induced by vaccine alone or SARS-CoV-2 Infection plus vaccine (hybrid immunity) post 6-months. <i>EBioMedicine</i> , 2022, 78, 103938.	6.1	47
21	Molecular Insights Into the Evolutionary Pathway of <i>Vibrio cholerae</i> O1 Atypical El Tor Variants. <i>PLoS Pathogens</i> , 2014, 10, e1004384.	4.7	45
22	Dynamics in genome evolution of <i>Vibrio cholerae</i> . <i>Infection, Genetics and Evolution</i> , 2014, 23, 32-41.	2.3	44
23	Diagnostic techniques for rapid detection of <i>Vibrio cholerae</i> O1/O139. <i>Vaccine</i> , 2020, 38, A73-A82.	3.8	36
24	Trans-ethnic gut microbiota signatures of type 2 diabetes in Denmark and India. <i>Genome Medicine</i> , 2021, 13, 37.	8.2	34
25	Low <i>Bifidobacterium</i> Abundance in the Lower Gut Microbiota Is Associated With <i>Helicobacter pylori</i> -Related Gastric Ulcer and Gastric Cancer. <i>Frontiers in Microbiology</i> , 2021, 12, 631140.	3.5	32
26	Trans-ethnic gut microbial signatures of prediabetic subjects from India and Denmark. <i>Genome Medicine</i> , 2021, 13, 36.	8.2	31
27	Molecular Insights into Antimicrobial Resistance Traits of Multidrug Resistant Enteric Pathogens isolated from India. <i>Scientific Reports</i> , 2017, 7, 14468.	3.3	30
28	Serum protein signature of coronary artery disease in type 2 diabetes mellitus. <i>Journal of Translational Medicine</i> , 2019, 17, 17.	4.4	30
29	Molecular evolution and functional divergence of <i>Vibrio cholerae</i> . <i>Current Opinion in Infectious Diseases</i> , 2016, 29, 520-527.	3.1	29
30	Complete Genome Sequence of <i>Collinsella aerofaciens</i> Isolated from the Gut of a Healthy Indian Subject. <i>Genome Announcements</i> , 2017, 5, .	0.8	29
31	Homeostasis and dysbiosis of the gut microbiome in health and disease. <i>Journal of Biosciences</i> , 2019, 44, .	1.1	29
32	Molecular characterization of <i>Vibrio cholerae</i> $\hat{\tau}$ relA $\hat{\tau}$ spoT double mutants. <i>Archives of Microbiology</i> , 2008, 189, 227-238.	2.2	27
33	Small chromosomal integration site of classical CTX prophage in Mozambique <i>Vibrio cholerae</i> O1 biotype El Tor strain. <i>Archives of Microbiology</i> , 2007, 188, 677-683.	2.2	26
34	XerD-mediated FtsK-independent integration of TLC $\dot{\cdot}$ into the <i>Vibrio cholerae</i> genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 16848-16853.	7.1	26
35	<i>Aeromonas hydrophila</i> utilizes TLR4 topology for synchronous activation of MyD88 and TRIF to orchestrate anti-inflammatory responses in zebrafish. <i>Cell Death Discovery</i> , 2017, 3, 17067.	4.7	26
36	CTX phage of <i>Vibrio cholerae</i> : Genomics and applications. <i>Vaccine</i> , 2020, 38, A7-A12.	3.8	25

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37	Gut microbiome diversity in acute severe colitis is distinct from mild to moderate ulcerative colitis. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2021, 36, 731-739.	2.8	25
38	Functional Analysis of the Essential GTP-Binding-Protein-Coding Gene <i>cgtA</i> of <i>Vibrio cholerae</i> . <i>Journal of Bacteriology</i> , 2008, 190, 4764-4771.	2.2	24
39	Vaginal Microbiome of Pregnant Indian Women: Insights into the Genome of Dominant <i>Lactobacillus</i> Species. <i>Microbial Ecology</i> , 2020, 80, 487-499.	2.8	24
40	<i>Vibrio</i> Pathogenicity Island-1: The Master Determinant of Cholera Pathogenesis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 561296.	3.9	23
41	(p)ppGpp Metabolism and Antimicrobial Resistance in Bacterial Pathogens. <i>Frontiers in Microbiology</i> , 2020, 11, 563944.	3.5	23
42	The Vaginal Microbial Signatures of Preterm Birth Delivery in Indian Women. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 622474.	3.9	23
43	Molecular evidence favouring step-wise evolution of Mozambique <i>Vibrio cholerae</i> O1 El Tor hybrid strain. <i>Microbiology (United Kingdom)</i> , 2010, 156, 99-107.	1.8	22
44	Complete nucleotide sequence of a quinolone resistance gene (<i>qnrS2</i>) carrying plasmid of <i>Aeromonas hydrophila</i> isolated from fish. <i>Plasmid</i> , 2011, 66, 79-84.	1.4	22
45	Molecular insights into the genome dynamics and interactions between core and acquired genomes of <i>Vibrio cholerae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23762-23773.	7.1	22
46	Spatiotemporal persistence of multiple, diverse clades and toxins of <i>Corynebacterium diphtheriae</i> . <i>Nature Communications</i> , 2021, 12, 1500.	12.8	22
47	Mutational analysis of the (p)ppGpp synthetase activity of the Rel enzyme of <i>Mycobacterium tuberculosis</i> . <i>Archives of Microbiology</i> , 2014, 196, 575-588.	2.2	19
48	Rugose atypical <i>Vibrio cholerae</i> O1 El Tor responsible for 2009 cholera outbreak in India. <i>Journal of Medical Microbiology</i> , 2016, 65, 1130-1136.	1.8	19
49	Mechanistic insights into filamentous phage integration in <i>Vibrio cholerae</i> . <i>Frontiers in Microbiology</i> , 2014, 5, 650.	3.5	18
50	Fostering research into antimicrobial resistance in India. <i>BMJ: British Medical Journal</i> , 2017, 358, j3535.	2.3	17
51	Complete Genome Sequence of <i>Faecalibacterium prausnitzii</i> Isolated from the Gut of a Healthy Indian Adult. <i>Genome Announcements</i> , 2017, 5, .	0.8	14
52	Salivary proteome signatures in the early and middle stages of human pregnancy with term birth outcome. <i>Scientific Reports</i> , 2020, 10, 8022.	3.3	13
53	Molecular mechanism of acquisition of the cholera toxin genes. <i>Indian Journal of Medical Research</i> , 2011, 133, 195-200.	1.0	12
54	Laboratory evaluation of the rapid diagnostic tests for the detection of <i>Vibrio cholerae</i> O1 using diarrheal samples. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009521.	3.0	11

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55	Antimicrobial resistance and virulence in <i>Helicobacter pylori</i> : Genomic insights. <i>Genomics</i> , 2021, 113, 3951-3966.	2.9	11
56	Effect of LexA on Chromosomal Integration of CTX ϕ in <i>Vibrio cholerae</i> . <i>Journal of Bacteriology</i> , 2016, 198, 268-275.	2.2	10
57	Whole-Genome Sequence of a <i>Megasphaera elsdenii</i> Strain Isolated from the Gut of a Healthy Indian Adult Subject. <i>Genome Announcements</i> , 2017, 5, .	0.8	8
58	Insights into the human gut microbiome and cardiovascular diseases. <i>Journal of the Practice of Cardiovascular Sciences</i> , 2018, 4, 10.	0.1	8
59	<i>Vibrio cholerae</i> O139 genomes provide a clue to why it may have failed to usher in the eighth cholera pandemic. <i>Nature Communications</i> , 2022, 13, .	12.8	8
60	A Novel, Broad-Range, CTX ϕ -Derived Stable Integrative Expression Vector for Functional Studies. <i>Journal of Bacteriology</i> , 2014, 196, 4071-4080.	2.2	7
61	TLR2-mediated activation of TNF α -caspase-1/IL-1 β inflammatory axis leads to apoptosis of <i>Aeromonas hydrophila</i> -infected macrophages. <i>Molecular Immunology</i> , 2021, 137, 114-123.	2.2	6
62	Genetic components of stringent response in <i>Vibrio cholerae</i> . <i>Indian Journal of Medical Research</i> , 2011, 133, 212-7.	1.0	6
63	Editorial: Filamentous Bacteriophage in Bio/Nano/Technology, Bacterial Pathogenesis and Ecology. <i>Frontiers in Microbiology</i> , 2016, 7, 2109.	3.5	5
64	Vancomycin-Induced Modulation of Gram-Positive Gut Bacteria and Metabolites Remediate Insulin Resistance in iNOS Knockout Mice. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 795333.	3.9	5
65	Analysis of colistin resistance in carbapenem-resistant <i>Enterobacterales</i> and XDR <i>Klebsiella pneumoniae</i> . <i>Therapeutic Advances in Infectious Disease</i> , 2022, 9, 204993612210806.	1.8	4
66	Editorial: Systems Biology and Omics Approaches for Understanding Complex Disease Biology. <i>Frontiers in Genetics</i> , 2022, 13, 896818.	2.3	4
67	Draft Genome Sequence of <i>Prevotella copri</i> Isolated from the Gut of a Healthy Indian Adult. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
68	Insights into the gastrointestinal tract microbiomes of Indian population. <i>Journal of Biosciences</i> , 2019, 44, 1.	1.1	3
69	Novel Genetic Tool to Study the Stability of Genomic Islands. <i>Recent Patents on Biotechnology</i> , 2018, 12, 200-207.	0.8	3
70	Tu1792 Gut Microbiome Diversity in Acute Severe Colitis is Distinct from Mild to Moderate Ulcerative Colitis. <i>Gastroenterology</i> , 2019, 156, S-1125-S-1126.	1.3	2
71	Insights into TLC ϕ lysogeny: A twist in the mechanism of IMEX integration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 18159-18161.	7.1	2
72	Functional Insights Into the Role of gppA in (p)ppGpp Metabolism of <i>Vibrio cholerae</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 564644.	3.5	2

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73	Whole-Genome Sequence of Bifidobacterium longum Strain Indica, Isolated from the Gut of a Healthy Indian Adult. Genome Announcements, 2017, 5, .	0.8	1
74	1113. Real-Time Evolution of Extensively Drug-Resistant Vibrio cholerae. Open Forum Infectious Diseases, 2018, 5, S334-S334.	0.9	1
75	Human Milk Microbiome of Healthy Indian Mothers is Dominated by Genus Pseudomonas. Journal of Human Lactation, 2021, , 089033442110484.	1.6	1
76	Small Molecule Signaling Systems in Vibrio cholerae. , 2011, , 185-201.		1
77	Genetic and mutational analysis of virulence traits and their modulation in an environmental toxigenic Vibrio cholerae non-O1/non-O139 strain, VCE232. Microbiology (United Kingdom), 2022, 168, .	1.8	1
78	IDDF2018-ABS-0255â€¦Impact of commensal human gut microbiota in the emergence of extensive drug-resistant pathogens. , 2018, , .		0
79	Commentary: Functionality of Two Origins of Replication in Vibrio cholerae Strains With a Single Chromosome. Frontiers in Microbiology, 2019, 10, 1314.	3.5	0
80	Gut Microbiome Signatures in Health and Diseases. , 2022, , 344-353.		0
81	The Genomics of Cholera. Advances in Microbial Ecology, 2012, , 21-38.	0.1	0
82	Acquisition and dissemination mechanisms of CTXÎ inVibrio cholerae: New paradigm fordifresidents. World Journal of Medical Genetics, 2014, 4, 27.	1.0	0
83	Insights into the gastrointestinal tract microbiomes of Indian population. Journal of Biosciences, 2019, 44, .	1.1	0