

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	Gut Microbiome Signatures in Health and Diseases. , 2022, , 344-353.		0
2	Genetic and mutational analysis of virulence traits and their modulation in an environmental toxigenic <i>Vibrio cholerae</i> non-O1/non-O139 strain, VCE232. <i>Microbiology (United Kingdom)</i> , 2022, 168, .	1.8	1
3	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
4	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
5	Editorial: Systems Biology and Omics Approaches for Understanding Complex Disease Biology. <i>Frontiers in Genetics</i> , 2022, 13, 896818.	2.3	4
6	<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
7	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
8	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
9	Trans-ethnic gut microbial signatures of prediabetic subjects from India and Denmark. <i>Genome Medicine</i> , 2021, 13, 36.	8.2	31
10	Trans-ethnic gut microbiota signatures of type 2 diabetes in Denmark and India. <i>Genome Medicine</i> , 2021, 13, 37.	8.2	34
11	Spatiotemporal persistence of multiple, diverse clades and toxins of <i>Corynebacterium diphtheriae</i> . <i>Nature Communications</i> , 2021, 12, 1500.	12.8	22
12	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
13	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
14	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
15	Human Milk Microbiome of Healthy Indian Mothers is Dominated by Genus <i>Pseudomonas</i> . <i>Journal of Human Lactation</i> , 2021, , 089033442110484.	1.6	1
16	Antimicrobial resistance and virulence in <i>Helicobacter pylori</i> : Genomic insights. <i>Genomics</i> , 2021, 113, 3951-3966.	2.9	11
17	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
18	Diagnostic techniques for rapid detection of <i>Vibrio cholerae</i> O1/O139. <i>Vaccine</i> , 2020, 38, A73-A82.	3.8	36

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19	Antibiotic resistance in <i>Vibrio cholerae</i> : Understanding the ecology of resistance genes and mechanisms. <i>Vaccine</i> , 2020, 38, A83-A92.	3.8	127
20	CTX phage of <i>Vibrio cholerae</i> : Genomics and applications. <i>Vaccine</i> , 2020, 38, A7-A12.	3.8	25
21	<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
22	(p)ppGpp Metabolism and Antimicrobial Resistance in Bacterial Pathogens. <i>Frontiers in Microbiology</i> , 2020, 11, 563944.	3.5	23
23	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
24	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
25	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
26	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
27	The 2019 novel coronavirus disease (COVID-19) pandemic: A review of the current evidence. <i>Indian Journal of Medical Research</i> , 2020, 151, 147.	1.0	173
28	Molecular Insights into Antimicrobial Resistance Traits of Commensal Human Gut Microbiota. <i>Microbial Ecology</i> , 2019, 77, 546-557.	2.8	49
29	Commentary: Functionality of Two Origins of Replication in <i>Vibrio cholerae</i> Strains With a Single Chromosome. <i>Frontiers in Microbiology</i> , 2019, 10, 1314.	3.5	0
30	Revisiting the Global Epidemiology of Cholera in Conjunction With the Genomics of <i>Vibrio cholerae</i> . <i>Frontiers in Public Health</i> , 2019, 7, 203.	2.7	56
31	Homeostasis and dysbiosis of the gut microbiome in health and disease. <i>Journal of Biosciences</i> , 2019, 44, 1.	1.1	107
32	Insights into the gastrointestinal tract microbiomes of Indian population. <i>Journal of Biosciences</i> , 2019, 44, 1.	1.1	3
33	Serum protein signature of coronary artery disease in type 2 diabetes mellitus. <i>Journal of Translational Medicine</i> , 2019, 17, 17.	4.4	30
34	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
35	Genomic plasticity associated with antimicrobial resistance in <i>Vibrio cholerae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 6226-6231.	7.1	90
36	Insights into λ 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

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37	Comparison of Japanese and Indian intestinal microbiota shows diet-dependent interaction between bacteria and fungi. <i>Npj Biofilms and Microbiomes</i> , 2019, 5, 37.	6.4	60
38	Diphtheria. <i>Nature Reviews Disease Primers</i> , 2019, 5, 81.	30.5	117
39	Insights into the gastrointestinal tract microbiomes of Indian population. <i>Journal of Biosciences</i> , 2019, 44, .	1.1	0
40	Homeostasis and dysbiosis of the gut microbiome in health and disease. <i>Journal of Biosciences</i> , 2019, 44, .	1.1	29
41	1113. Real-Time Evolution of Extensively Drug-Resistant <i>Vibrio cholerae</i> . <i>Open Forum Infectious Diseases</i> , 2018, 5, S334-S334.	0.9	1
42	IDDF2018-ABS-0255â€¦Impact of commensal human gut microbiota in the emergence of extensive drug-resistant pathogens. , 2018, , .		0
43	Analysis of the Gut Microbiome of Rural and Urban Healthy Indians Living in Sea Level and High Altitude Areas. <i>Scientific Reports</i> , 2018, 8, 10104.	3.3	104
44	Novel Genetic Tool to Study the Stability of Genomic Islands. <i>Recent Patents on Biotechnology</i> , 2018, 12, 200-207.	0.8	3
45	Insights into the human gut microbiome and cardiovascular diseases. <i>Journal of the Practice of Cardiovascular Sciences</i> , 2018, 4, 10.	0.1	8
46	<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
47	Whole-Genome Sequence of <i>Bifidobacterium longum</i> Strain Indica, Isolated from the Gut of a Healthy Indian Adult. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
48	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
49	Gastric microbiome of Indian patients with <i>Helicobacter pylori</i> infection, and their interaction networks. <i>Scientific Reports</i> , 2017, 7, 15438.	3.3	51
50	Molecular Insights into Antimicrobial Resistance Traits of Multidrug Resistant Enteric Pathogens isolated from India. <i>Scientific Reports</i> , 2017, 7, 14468.	3.3	30
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	Fostering research into antimicrobial resistance in India. <i>BMJ: British Medical Journal</i> , 2017, 358, j3535.	2.3	17
53	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
54	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

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55	Editorial: Filamentous Bacteriophage in Bio/Nano/Technology, Bacterial Pathogenesis and Ecology. <i>Frontiers in Microbiology</i> , 2016, 7, 2109.	3.5	5
56	Molecular evolution and functional divergence of <i>Vibrio cholerae</i> . <i>Current Opinion in Infectious Diseases</i> , 2016, 29, 520-527.	3.1	29
57	An Improved Method for High Quality Metagenomics DNA Extraction from Human and Environmental Samples. <i>Scientific Reports</i> , 2016, 6, 26775.	3.3	164
58	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
59	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
60	Gut Microbiomes of Indian Children of Varying Nutritional Status. <i>PLoS ONE</i> , 2014, 9, e95547.	2.5	154
61	Mechanistic insights into filamentous phage integration in <i>Vibrio cholerae</i> . <i>Frontiers in Microbiology</i> , 2014, 5, 650.	3.5	18
62	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
63	XerD-mediated FtsK-independent integration of TLC ϕ 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
64	Dynamics in genome evolution of <i>Vibrio cholerae</i> . <i>Infection, Genetics and Evolution</i> , 2014, 23, 32-41.	2.3	44
65	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
66	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
67	Acquisition and dissemination mechanisms of CTX ϕ in <i>Vibrio cholerae</i> : New paradigm for dif residents. <i>World Journal of Medical Genetics</i> , 2014, 4, 27.	1.0	0
68	Integrative mobile elements exploiting Xer recombination. <i>Trends in Microbiology</i> , 2013, 21, 23-30.	7.7	83
69	Functional Characterization of the Stringent Response Regulatory Gene <i>dksA</i> of <i>Vibrio cholerae</i> and Its Role in Modulation of Virulence Phenotypes. <i>Journal of Bacteriology</i> , 2012, 194, 5638-5648.	2.2	48
70	The Genomics of Cholera. <i>Advances in Microbial Ecology</i> , 2012, , 21-38.	0.1	0
71	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
72	VCJ ϕ integration and excision mechanisms contribute to the genetic diversity of <i>Vibrio cholerae</i> epidemic strains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 2516-2521.	7.1	62

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73	Small Molecule Signaling Systems in <i>Vibrio cholerae</i> . , 2011, , 185-201.		1
74	Molecular mechanism of acquisition of the cholera toxin genes. Indian Journal of Medical Research, 2011, 133, 195-200.	1.0	12
75	Genetic components of stringent response in <i>Vibrio cholerae</i> . Indian Journal of Medical Research, 2011, 133, 212-7.	1.0	6
76	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
77	Molecular evidence favouring step-wise evolution of Mozambique <i>Vibrio cholerae</i> O1 El Tor hybrid strain. Microbiology (United Kingdom), 2010, 156, 99-107.	1.8	22
78	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
79	Molecular characterization of <i>Vibrio cholerae</i> Δ relA Δ spoT double mutants. Archives of Microbiology, 2008, 189, 227-238.	2.2	27
80	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
81	Functional Analysis of the Essential GTP-Binding-Protein-Coding Gene <i>cgtA</i> of <i>Vibrio cholerae</i> . Journal of Bacteriology, 2008, 190, 4764-4771.	2.2	24
82	Small chromosomal integration site of classical CTX prophage in Mozambique <i>Vibrio cholerae</i> O1 biotype El Tor strain. Archives of Microbiology, 2007, 188, 677-683.	2.2	26
83	Genetic organization of pre-CTX and CTX prophages in the genome of an environmental <i>Vibrio cholerae</i> non-O1, non-O139 strain. Microbiology (United Kingdom), 2006, 152, 3633-3641.	1.8	47