Suman R Das

List of Publications by Year
in descending order

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51 papers	2,800 citations	201385 27 h-index	189595 50 g-index
52 all docs	52 docs citations	52 times ranked	4739 citing authors

#	ARTICLE	IF	CITATIONS
1	Upper respiratory tract bacterial-immune interactions during respiratory syncytial virus infection in infancy. Journal of Allergy and Clinical Immunology, 2022, 149, 966-976.	1.5	11
2	Exclusive breast-feeding, the early-life microbiome and immune response, and common childhood respiratory illnesses. Journal of Allergy and Clinical Immunology, 2022, 150, 612-621.	1.5	23
3	Nasopharyngeal Haemophilus and local immune response during infant respiratory syncytial virus infection. Journal of Allergy and Clinical Immunology, 2021, 147, 1097-1101.e6.	1.5	12
4	Microbial community structure and composition is associated with host species and sex in Sigmodon cotton rats. Animal Microbiome, 2021, 3, 29.	1.5	3
5	SARS-CoV-2 infection and viral load are associated with the upper respiratory tract microbiome. Journal of Allergy and Clinical Immunology, 2021, 147, 1226-1233.e2.	1.5	58
6	Metatranscriptomics to characterize respiratory virome, microbiome, and host response directly from clinical samples. Cell Reports Methods, 2021, 1, 100091.	1.4	19
7	Severe COVID-19 Is Associated With an Altered Upper Respiratory Tract Microbiome. Frontiers in Cellular and Infection Microbiology, 2021, 11, 781968.	1.8	27
8	Interim analysis of an openâ€label randomized controlled trial evaluating nasal irrigations in nonâ€hospitalized patients with coronavirus disease 2019. International Forum of Allergy and Rhinology, 2020, 10, 1325-1328.	1.5	32
9	Spatial and temporal expansions of Eastern equine encephalitis virus and phylogenetic groups isolated from mosquitoes and mammalian cases in New York State from 2013 to 2019. Emerging Microbes and Infections, 2020, 9, 1638-1650.	3.0	10
10	Evaluation of the upper airway microbiome and immune response with nasal epithelial lining fluid absorption and nasal washes. Scientific Reports, 2020, 10, 20618.	1.6	4
11	Genomic analysis of serologically untypable human enteroviruses in Taiwan. Journal of Biomedical Science, 2019, 26, 49.	2.6	5
12	Lack of selective resistance of influenza A virus in presence of host-targeted antiviral, UV-4B. Scientific Reports, 2019, 9, 7484.	1.6	27
13	Dietary Arginine Regulates Severity of Experimental Colitis and Affects the Colonic Microbiome. Frontiers in Cellular and Infection Microbiology, 2019, 9, 66.	1.8	58
14	Nearly Complete Genome Sequences of 17 Enterovirus D68 Strains from Kansas City, Missouri, 2018. Microbiology Resource Announcements, 2019, 8, .	0.3	6
15	Complex Epidemiological Dynamics of Eastern Equine Encephalitis Virus in Florida. American Journal of Tropical Medicine and Hygiene, 2019, 100, 1266-1274.	0.6	21
16	Poor Immunogenicity, Not Vaccine Strain Egg Adaptation, May Explain the Low H3N2 Influenza Vaccine Effectiveness in 2012â€“2013. Clinical Infectious Diseases, 2018, 67, 327-333.	2.9	53
17	Large-Scale Complete-Genome Sequencing and Phylodynamic Analysis of Eastern Equine Encephalitis Virus Reveals Source-Sink Transmission Dynamics in the United States. Journal of Virology, 2018, 92, .	1.5	31
18	Nasopharyngeal Lactobacillus is associated with a reduced risk of childhood wheezing illnesses following acute respiratory syncytial virus infection in infancy. Journal of Allergy and Clinical Immunology, 2018, 142, 1447-1456.e9.	1.5	74

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19	The transmission dynamics and diversity of human metapneumovirus in Peru. Influenza and Other Respiratory Viruses, 2018, 12, 508-513.	1.5	6
20	Distinct mucosal microbial communities in infants with surgical necrotizing enterocolitis correlate with age and antibiotic exposure. PLoS ONE, 2018, 13, e0206366.	1.1	14
21	Contemporary Circulating Enterovirus D68 Strains Have Acquired the Capacity for Viral Entry and Replication in Human Neuronal Cells. MBio, 2018, 9, .	1.8	79
22	Whole-genome sequencing and analyses identify high genetic heterogeneity, diversity and endemicity of rotavirus genotype P[6] strains circulating in Africa. Infection, Genetics and Evolution, 2018, 63, 79-88.	1.0	26
23	Differing epidemiological dynamics of Chikungunya virus in the Americas during the 2014-2015 epidemic. PLoS Neglected Tropical Diseases, 2018, 12, e0006670.	1.3	23
24	Infant Viral Respiratory Infection Nasal Immune-Response Patterns and Their Association with Subsequent Childhood Recurrent Wheeze. American Journal of Respiratory and Critical Care Medicine, 2018, 198, 1064-1073.	2.5	56
25	Defining B cell immunodominance to viruses. Nature Immunology, 2017, 18, 456-463.	7.0	218
26	The emergence and evolution of influenza A (H1Î±) viruses in swine in Canada and the United States. Journal of General Virology, 2017, 98, 2663-2675.	1.3	23
27	The effective rate of influenza reassortment is limited during human infection. PLoS Pathogens, 2017, 13, e1006203.	2.1	42
28	Differences in the Nasopharyngeal Microbiome During Acute Respiratory Tract Infection With Human Rhinovirus and Respiratory Syncytial Virus in Infancy. Journal of Infectious Diseases, 2016, 214, 1924-1928.	1.9	84
29	Respiratory Syncytial Virus whole-genome sequencing identifies convergent evolution of sequence duplication in the C-terminus of the G gene. Scientific Reports, 2016, 6, 26311.	1.6	77
30	Nasopharyngeal Microbiome in Respiratory Syncytial Virus Resembles Profile Associated with Increased Childhood Asthma Risk. American Journal of Respiratory and Critical Care Medicine, 2016, 193, 1180-1183.	2.5	63
31	Introduction, Evolution, and Dissemination of Influenza A Viruses in Exhibition Swine in the United States during 2009 to 2013. Journal of Virology, 2016, 90, 10963-10971.	1.5	22
32	Deep Sequencing of Influenza A Virus from a Human Challenge Study Reveals a Selective Bottleneck and Only Limited Intrahost Genetic Diversification. Journal of Virology, 2016, 90, 11247-11258.	1.5	97
33	Molecular epidemiology of human enterovirus 71 at the origin of an epidemic of fatal hand, foot and mouth disease cases in Cambodia. Emerging Microbes and Infections, 2016, 5, 1-9.	3.0	54
34	Comprehensive Genome Scale Phylogenetic Study Provides New Insights on the Global Expansion of Chikungunya Virus. Journal of Virology, 2016, 90, 10600-10611.	1.5	72
35	Molecular Evolution and Intraclade Recombination of Enterovirus D68 during the 2014 Outbreak in the United States. Journal of Virology, 2016, 90, 1997-2007.	1.5	59
36	Evolutionary Dynamics of Influenza A Viruses in US Exhibition Swine. Journal of Infectious Diseases, 2016, 213, 173-182.	1.9	28

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37	Minimally Invasive Sampling Method Identifies Differences in Taxonomic Richness of Nasal Microbiomes in Young Infants Associated with Mode of Delivery. Microbial Ecology, 2016, 71, 233-242.	1.4	54
38	Enterovirus D-68 Infection, Prophylaxis, and Vaccination in a Novel Permissive Animal Model, the Cotton Rat (Sigmodon hispidus). PLoS ONE, 2016, 11, e0166336.	1.1	28
39	First Complete Genome Sequences of Two Keystone Viruses from Florida. Genome Announcements, 2015, 3, .	0.8	2
40	Objectives, design and enrollment results from the Infant Susceptibility to Pulmonary Infections and Asthma Following RSV Exposure Study (INSPIRE). BMC Pulmonary Medicine, 2015, 15, 45.	0.8	45
41	Diversifying Selection Analysis Predicts Antigenic Evolution of 2009 Pandemic H1N1 Influenza A Virus in Humans. Journal of Virology, 2015, 89, 5427-5440.	1.5	21
42	The soft palate is an important site of adaptation for transmissible influenza viruses. Nature, 2015, 526, 122-125.	13.7	133
43	Phylodynamics of Enterovirus A71-Associated Hand, Foot, and Mouth Disease in Viet Nam. Journal of Virology, 2015, 89, 8871-8879.	1.5	51
44	Defining Influenza A Virus Hemagglutinin Antigenic Drift by Sequential Monoclonal Antibody Selection. Cell Host and Microbe, 2013, 13, 314-323.	5.1	97
45	Antibody Pressure by a Human Monoclonal Antibody Targeting the 2009 Pandemic H1N1 Virus Hemagglutinin Drives the Emergence of a Virus with Increased Virulence in Mice. MBio, 2012, 3, .	1.8	63
46	Cysteinyl-tRNA Deacylation Can Be Uncoupled from Protein Synthesis. PLoS ONE, 2012, 7, e33072.	1.1	3
47	RNA Binding Targets Aminoacyl-tRNA Synthetases to Translating Ribosomes. Journal of Biological Chemistry, 2011, 286, 20688-20700.	1.6	71
48	Fitness costs limit influenza A virus hemagglutinin glycosylation as an immune evasion strategy. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E1417-22.	3.3	122
49	Influenza A Virus Hemagglutinin Antibody Escape Promotes Neuraminidase Antigenic Variation and Drug Resistance. PLoS ONE, 2011, 6, e15190.	1.1	67
50	Glycosylation Focuses Sequence Variation in the Influenza A Virus H1 Hemagglutinin Globular Domain. PLoS Pathogens, 2010, 6, e1001211.	2.1	95
51	Hemagglutinin Receptor Binding Avidity Drives Influenza A Virus Antigenic Drift. Science, 2009, 326, 734-736.	6.0	429