

# Suman R Das

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10704241/publications.pdf>

Version: 2024-02-01

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	Hemagglutinin Receptor Binding Avidity Drives Influenza A Virus Antigenic Drift. <i>Science</i> , 2009, 326, 734-736.	6.0	429
2	Defining B cell immunodominance to viruses. <i>Nature Immunology</i> , 2017, 18, 456-463.	7.0	218
3	The soft palate is an important site of adaptation for transmissible influenza viruses. <i>Nature</i> , 2015, 526, 122-125.	13.7	133
4	Fitness costs limit influenza A virus hemagglutinin glycosylation as an immune evasion strategy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E1417-22.	3.3	122
5	Defining Influenza A Virus Hemagglutinin Antigenic Drift by Sequential Monoclonal Antibody Selection. <i>Cell Host and Microbe</i> , 2013, 13, 314-323.	5.1	97
6	Deep Sequencing of Influenza A Virus from a Human Challenge Study Reveals a Selective Bottleneck and Only Limited Intra-host Genetic Diversification. <i>Journal of Virology</i> , 2016, 90, 11247-11258.	1.5	97
7	Glycosylation Focuses Sequence Variation in the Influenza A Virus H1 Hemagglutinin Globular Domain. <i>PLoS Pathogens</i> , 2010, 6, e1001211.	2.1	95
8	Differences in the Nasopharyngeal Microbiome During Acute Respiratory Tract Infection With Human Rhinovirus and Respiratory Syncytial Virus in Infancy. <i>Journal of Infectious Diseases</i> , 2016, 214, 1924-1928.	1.9	84
9	Contemporary Circulating Enterovirus D68 Strains Have Acquired the Capacity for Viral Entry and Replication in Human Neuronal Cells. <i>MBio</i> , 2018, 9, .	1.8	79
10	Respiratory Syncytial Virus whole-genome sequencing identifies convergent evolution of sequence duplication in the C-terminus of the G gene. <i>Scientific Reports</i> , 2016, 6, 26311.	1.6	77
11	Nasopharyngeal Lactobacillus is associated with a reduced risk of childhood wheezing illnesses following acute respiratory syncytial virus infection in infancy. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 142, 1447-1456.e9.	1.5	74
12	Comprehensive Genome Scale Phylogenetic Study Provides New Insights on the Global Expansion of Chikungunya Virus. <i>Journal of Virology</i> , 2016, 90, 10600-10611.	1.5	72
13	RNA Binding Targets Aminoacyl-tRNA Synthetases to Translating Ribosomes. <i>Journal of Biological Chemistry</i> , 2011, 286, 20688-20700.	1.6	71
14	Influenza A Virus Hemagglutinin Antibody Escape Promotes Neuraminidase Antigenic Variation and Drug Resistance. <i>PLoS ONE</i> , 2011, 6, e15190.	1.1	67
15	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. <i>MBio</i> , 2012, 3, .	1.8	63
16	Nasopharyngeal Microbiome in Respiratory Syncytial Virus Resembles Profile Associated with Increased Childhood Asthma Risk. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 193, 1180-1183.	2.5	63
17	Molecular Evolution and Intraclade Recombination of Enterovirus D68 during the 2014 Outbreak in the United States. <i>Journal of Virology</i> , 2016, 90, 1997-2007.	1.5	59
18	Dietary Arginine Regulates Severity of Experimental Colitis and Affects the Colonic Microbiome. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 66.	1.8	58

#	ARTICLE	IF	CITATIONS
19	SARS-CoV-2 infection and viral load are associated with the upper respiratory tract microbiome. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 1226-1233.e2.	1.5	58
20	Infant Viral Respiratory Infection Nasal Immune-Response Patterns and Their Association with Subsequent Childhood Recurrent Wheeze. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 198, 1064-1073.	2.5	56
21	Molecular epidemiology of human enterovirus 71 at the origin of an epidemic of fatal hand, foot and mouth disease cases in Cambodia. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-9.	3.0	54
22	Minimally Invasive Sampling Method Identifies Differences in Taxonomic Richness of Nasal Microbiomes in Young Infants Associated with Mode of Delivery. <i>Microbial Ecology</i> , 2016, 71, 233-242.	1.4	54
23	Poor Immunogenicity, Not Vaccine Strain Egg Adaptation, May Explain the Low H3N2 Influenza Vaccine Effectiveness in 2012-2013. <i>Clinical Infectious Diseases</i> , 2018, 67, 327-333.	2.9	53
24	Phylogenetics of Enterovirus A71-Associated Hand, Foot, and Mouth Disease in Viet Nam. <i>Journal of Virology</i> , 2015, 89, 8871-8879.	1.5	51
25	Objectives, design and enrollment results from the Infant Susceptibility to Pulmonary Infections and Asthma Following RSV Exposure Study (INSPIRE). <i>BMC Pulmonary Medicine</i> , 2015, 15, 45.	0.8	45
26	The effective rate of influenza reassortment is limited during human infection. <i>PLoS Pathogens</i> , 2017, 13, e1006203.	2.1	42
27	Interim analysis of an open-label randomized controlled trial evaluating nasal irrigations in non-hospitalized patients with coronavirus disease 2019. <i>International Forum of Allergy and Rhinology</i> , 2020, 10, 1325-1328.	1.5	32
28	Large-Scale Complete-Genome Sequencing and Phylogenetic Analysis of Eastern Equine Encephalitis Virus Reveals Source-Sink Transmission Dynamics in the United States. <i>Journal of Virology</i> , 2018, 92, .	1.5	31
29	Evolutionary Dynamics of Influenza A Viruses in US Exhibition Swine. <i>Journal of Infectious Diseases</i> , 2016, 213, 173-182.	1.9	28
30	Enterovirus D-68 Infection, Prophylaxis, and Vaccination in a Novel Permissive Animal Model, the Cotton Rat ( <i>Sigmodon hispidus</i> ). <i>PLoS ONE</i> , 2016, 11, e0166336.	1.1	28
31	Lack of selective resistance of influenza A virus in presence of host-targeted antiviral, UV-4B. <i>Scientific Reports</i> , 2019, 9, 7484.	1.6	27
32	Severe COVID-19 Is Associated With an Altered Upper Respiratory Tract Microbiome. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 781968.	1.8	27
33	Whole-genome sequencing and analyses identify high genetic heterogeneity, diversity and endemicity of rotavirus genotype P[6] strains circulating in Africa. <i>Infection, Genetics and Evolution</i> , 2018, 63, 79-88.	1.0	26
34	Differing epidemiological dynamics of Chikungunya virus in the Americas during the 2014-2015 epidemic. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006670.	1.3	23
35	The emergence and evolution of influenza A (H1N1) viruses in swine in Canada and the United States. <i>Journal of General Virology</i> , 2017, 98, 2663-2675.	1.3	23
36	Exclusive breast-feeding, the early-life microbiome and immune response, and common childhood respiratory illnesses. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 150, 612-621.	1.5	23

#	ARTICLE	IF	CITATIONS
37	Introduction, Evolution, and Dissemination of Influenza A Viruses in Exhibition Swine in the United States during 2009 to 2013. <i>Journal of Virology</i> , 2016, 90, 10963-10971.	1.5	22
38	Diversifying Selection Analysis Predicts Antigenic Evolution of 2009 Pandemic H1N1 Influenza A Virus in Humans. <i>Journal of Virology</i> , 2015, 89, 5427-5440.	1.5	21
39	Complex Epidemiological Dynamics of Eastern Equine Encephalitis Virus in Florida. <i>American Journal of Tropical Medicine and Hygiene</i> , 2019, 100, 1266-1274.	0.6	21
40	Metatranscriptomics to characterize respiratory virome, microbiome, and host response directly from clinical samples. <i>Cell Reports Methods</i> , 2021, 1, 100091.	1.4	19
41	Distinct mucosal microbial communities in infants with surgical necrotizing enterocolitis correlate with age and antibiotic exposure. <i>PLoS ONE</i> , 2018, 13, e0206366.	1.1	14
42	Nasopharyngeal Haemophilus and local immune response during infant respiratory syncytial virus infection. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 1097-1101.e6.	1.5	12
43	Upper respiratory tract bacterial-immune interactions during respiratory syncytial virus infection in infancy. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 149, 966-976.	1.5	11
44	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. <i>Emerging Microbes and Infections</i> , 2020, 9, 1638-1650.	3.0	10
45	The transmission dynamics and diversity of human metapneumovirus in Peru. <i>Influenza and Other Respiratory Viruses</i> , 2018, 12, 508-513.	1.5	6
46	Nearly Complete Genome Sequences of 17 Enterovirus D68 Strains from Kansas City, Missouri, 2018. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	6
47	Genomic analysis of serologically untypable human enteroviruses in Taiwan. <i>Journal of Biomedical Science</i> , 2019, 26, 49.	2.6	5
48	Evaluation of the upper airway microbiome and immune response with nasal epithelial lining fluid absorption and nasal washes. <i>Scientific Reports</i> , 2020, 10, 20618.	1.6	4
49	Cysteinyl-tRNA Deacylation Can Be Uncoupled from Protein Synthesis. <i>PLoS ONE</i> , 2012, 7, e33072.	1.1	3
50	Microbial community structure and composition is associated with host species and sex in Sigmodon cotton rats. <i>Animal Microbiome</i> , 2021, 3, 29.	1.5	3
51	First Complete Genome Sequences of Two Keystone Viruses from Florida. <i>Genome Announcements</i> , 2015, 3, .	0.8	2