

Jishnu Das

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

3,521
citations

236925

25
h-index

206112

48
g-index

59
all docs

59
docs citations

59
times ranked

7342
citing authors

#	ARTICLE	IF	CITATIONS
1	Upper and lower respiratory tract correlates of protection against respiratory syncytial virus following vaccination of nonhuman primates. <i>Cell Host and Microbe</i> , 2022, 30, 41-52.e5.	11.0	44
2	Essential Regression: A generalizable framework for inferring causal latent factors from multi-omic datasets. <i>Patterns</i> , 2022, 3, 100473.	5.9	8
3	Fungal sensing enhances neutrophil metabolic fitness by regulating antifungal Glut1 activity. <i>Cell Host and Microbe</i> , 2022, 30, 530-544.e6.	11.0	21
4	Functional reprogramming of monocytes in patients with acute and convalescent severe COVID-19. <i>JCI Insight</i> , 2022, 7, .	5.0	19
5	A network-based approach to identify expression modules underlying rejection in pediatric liver transplantation. <i>Cell Reports Medicine</i> , 2022, 3, 100605.	6.5	5
6	Autoreactive CD8+ T cells are restrained by an exhaustion-like program that is maintained by LAG3. <i>Nature Immunology</i> , 2022, 23, 868-877.	14.5	32
7	Antibodies targeting conserved non-canonical antigens and endemic coronaviruses associate with favorable outcomes in severe COVID-19. <i>Cell Reports</i> , 2022, 39, 111020.	6.4	11
8	Mechanisms of Impaired Lung Development and Ciliation in Mannosidase-1-Alpha-2 (Man1a2) Mutants. <i>Frontiers in Physiology</i> , 2021, 12, 658518.	2.8	2
9	Delayed fractional dosing with RTS,S/AS01 improves humoral immunity to malaria via a balance of polyfunctional NANP6- and Pf16-specific antibodies. <i>Med</i> , 2021, 2, 1269-1286.e9.	4.4	17
10	People critically ill with COVID-19 exhibit peripheral immune profiles predictive of mortality and reflective of SARS-CoV-2 lung viral burden. <i>Cell Reports Medicine</i> , 2021, 2, 100476.	6.5	11
11	Extracellular Matrix Injury of Kidney Allografts in Antibody-Mediated Rejection: A Proteomics Study. <i>Journal of the American Society of Nephrology: JASN</i> , 2020, 31, 2705-2724.	6.1	29
12	Glucosylation by the Legionella Effector SetA Promotes the Nuclear Localization of the Transcription Factor TFEB. <i>IScience</i> , 2020, 23, 101300.	4.1	18
13	Mining for humoral correlates of HIV control and latent reservoir size. <i>PLoS Pathogens</i> , 2020, 16, e1008868.	4.7	19
14	Mapping functional humoral correlates of protection against malaria challenge following RTS,S/AS01 vaccination. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	100
15	Co-immunization of DNA and Protein in the Same Anatomical Sites Induces Superior Protective Immune Responses against SHIV Challenge. <i>Cell Reports</i> , 2020, 31, 107624.	6.4	43
16	Latency reversal agents modulate HIV antigen processing and presentation to CD8 T cells. <i>PLoS Pathogens</i> , 2020, 16, e1008442.	4.7	8
17	Epigenetic basis for monocyte dysfunction in patients with severe alcoholic hepatitis. <i>Journal of Hepatology</i> , 2020, 73, 303-314.	3.7	24
18	Antibody Fc Glycosylation Discriminates Between Latent and Active Tuberculosis. <i>Journal of Infectious Diseases</i> , 2020, 222, 2093-2102.	4.0	47

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19	Antibiotics-Driven Gut Microbiome Perturbation Alters Immunity to Vaccines in Humans. <i>Cell</i> , 2019, 178, 1313-1328.e13.	28.9	402
20	Extensive disruption of protein interactions by genetic variants across the allele frequency spectrum in human populations. <i>Nature Communications</i> , 2019, 10, 4141.	12.8	48
21	Fc Glycan-Mediated Regulation of Placental Antibody Transfer. <i>Cell</i> , 2019, 178, 202-215.e14.	28.9	157
22	Latent Model-Based Clustering for Biological Discovery. <i>IScience</i> , 2019, 14, 125-135.	4.1	5
23	Genetic Polymorphisms in the Open Reading Frame of the CCR5 gene From HIV-1 Seronegative and Seropositive Individuals From National Capital Regions of India. <i>Scientific Reports</i> , 2019, 9, 7594.	3.3	8
24	Initiation of Antiretroviral Therapy Before Pregnancy Reduces the Risk of Infection-related Hospitalization in Human Immunodeficiency Virus-exposed Uninfected Infants Born in a High-income Country. <i>Clinical Infectious Diseases</i> , 2019, 68, 1193-1203.	5.8	60
25	Reply to Slogrove et al. <i>Clinical Infectious Diseases</i> , 2019, 68, 2158-2158.	5.8	2
26	Impact of dietary fat and sucrose consumption on cardiac fibrosis in rhesus monkeys and mice. <i>FASEB Journal</i> , 2019, 33, lb467.	0.5	0
27	Effect of dietary fat and sucrose consumption on cardiac fibrosis in mice and rhesus monkeys. <i>JCI Insight</i> , 2019, 4, .	5.0	5
28	A multi-landing pad DNA integration platform for mammalian cell engineering. <i>Nucleic Acids Research</i> , 2018, 46, 4072-4086.	14.5	110
29	Temporal variation in HIV-specific IgG subclass antibodies during acute infection differentiates spontaneous controllers from chronic progressors. <i>Aids</i> , 2018, 32, 443-450.	2.2	35
30	Route of immunization defines multiple mechanisms of vaccine-mediated protection against SIV. <i>Nature Medicine</i> , 2018, 24, 1590-1598.	30.7	129
31	The transcription factors Runx3 and ThPOK cross-regulate acquisition of cytotoxic function by human Th1 lymphocytes. <i>ELife</i> , 2018, 7, .	6.0	57
32	Control of Heterologous Simian Immunodeficiency Virus SIV _{smE660} Infection by DNA and Protein Coimmunization Regimens Combined with Different Toll-Like-Receptor-4-Based Adjuvants in Macaques. <i>Journal of Virology</i> , 2018, 92, .	3.4	39
33	Analysis of Complement-Mediated Lysis of Simian Immunodeficiency Virus (SIV) and SIV-Infected Cells Reveals Sex Differences in Vaccine-Induced Immune Responses in Rhesus Macaques. <i>Journal of Virology</i> , 2018, 92, .	3.4	26
34	A Role for Fc Function in Therapeutic Monoclonal Antibody-Mediated Protection against Ebola Virus. <i>Cell Host and Microbe</i> , 2018, 24, 221-233.e5.	11.0	182
35	mutation3D: Cancer Gene Prediction Through Atomic Clustering of Coding Variants in the Structural Proteome. <i>Human Mutation</i> , 2016, 37, 447-456.	2.5	94
36	A Proteome-wide Fission Yeast Interactome Reveals Network Evolution Principles from Yeasts to Human. <i>Cell</i> , 2016, 164, 310-323.	28.9	106

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37	Studying Autism in Context. Cell Systems, 2015, 1, 312-313.	6.2	0
38	Phosphoproteomics Reveals Distinct Modes of Mec1/ATR Signaling during DNA Replication. Molecular Cell, 2015, 57, 1124-1132.	9.7	106
39	ENCAPP: elastic-net-based prognosis prediction and biomarker discovery for human cancers. BMC Genomics, 2015, 16, 263.	2.8	30
40	A Massively Parallel Pipeline to Clone DNA Variants and Examine Molecular Phenotypes of Human Disease Mutations. PLoS Genetics, 2014, 10, e1004819.	3.5	47
41	Predicting Cancer Prognosis Using Functional Genomics Data Sets. Cancer Informatics, 2014, 13s5, CIN.S14064.	1.9	9
42	Elucidating Common Structural Features of Human Pathogenic Variations Using Large-Scale Atomic-Resolution Protein Networks. Human Mutation, 2014, 35, 585-593.	2.5	18
43	Exploring mechanisms of human disease through structurally resolved protein interactome networks. Molecular BioSystems, 2014, 10, 9-17.	2.9	27
44	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	12.6	341
45	Dissecting Disease Inheritance Modes in a Three-Dimensional Protein Network Challenges the "Guilt-by-Association" Principle. American Journal of Human Genetics, 2013, 93, 78-89.	6.2	44
46	INstruct: a database of high-quality 3D structurally resolved protein interactome networks. Bioinformatics, 2013, 29, 1577-1579.	4.1	129
47	Cross-Species Protein Interactome Mapping Reveals Species-Specific Wiring of Stress Response Pathways. Science Signaling, 2013, 6, ra38.	3.6	47
48	Three-dimensional reconstruction of protein networks provides insight into human genetic disease. Nature Biotechnology, 2012, 30, 159-164.	17.5	378
49	Genome-scale analysis of interaction dynamics reveals organization of biological networks. Bioinformatics, 2012, 28, 1873-1878.	4.1	50
50	HINT: High-quality protein interactomes and their applications in understanding human disease. BMC Systems Biology, 2012, 6, 92.	3.0	366
51	Computational design of soluble variants of transmembrane proteins. , 2010, , .		0
52	Latent Model-Based Clustering for Biological Discovery. SSRN Electronic Journal, 0, , .	0.4	0