

Ren Sun

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

3,983
citations

249298

26
h-index

156644

58
g-index

68
all docs

68
docs citations

68
times ranked

7780
citing authors

#	ARTICLE	IF	CITATIONS
1	Latency reversal plus natural killer cells diminish HIV reservoir in vivo. <i>Nature Communications</i> , 2022, 13, 121.	5.8	36
2	Unlocking capacities of genomics for the COVID-19 response and future pandemics. <i>Nature Methods</i> , 2022, 19, 374-380.	9.0	35
3	Ex vivo and in vivo chemoprotective activity and potential mechanism of Martynoside against 5-fluorouracil-induced bone marrow cytotoxicity. <i>Biomedicine and Pharmacotherapy</i> , 2021, 138, 111501.	2.5	7
4	Riok3 inhibits the antiviral immune response by facilitating TRIM40-mediated RIG-I and MDA5 degradation. <i>Cell Reports</i> , 2021, 35, 109272.	2.9	24
5	A CRISPR Activation Screen Identifies an Atypical Rho GTPase That Enhances Zika Viral Entry. <i>Viruses</i> , 2021, 13, 2113.	1.5	10
6	Maternal HBV Viremia and Association With Adverse Infant Outcomes in Women Living With HIV and HBV. <i>Pediatric Infectious Disease Journal</i> , 2021, 40, e56-e61.	1.1	5
7	On-demand nanozyme signal enhancement at the push of a button for the improved detection of SARS-CoV-2 nucleocapsid protein in serum. <i>Analyst, The</i> , 2021, 146, 7386-7393.	1.7	14
8	The epitope arrangement on flavivirus particles contributes to Mab C10's extraordinary neutralization breadth across Zika and dengue viruses. <i>Cell</i> , 2021, 184, 6052-6066.e18.	13.5	38
9	Discovery of SARS-CoV-2 antiviral drugs through large-scale compound repurposing. <i>Nature</i> , 2020, 586, 113-119.	13.7	672
10	Deletion of immune evasion genes provides an effective vaccine design for tumor-associated herpesviruses. <i>Npj Vaccines</i> , 2020, 5, 102.	2.9	8
11	mRNA display with library of even-distribution reveals cellular interactors of influenza virus NS1. <i>Nature Communications</i> , 2020, 11, 2449.	5.8	8
12	Benchmarking of computational error-correction methods for next-generation sequencing data. <i>Genome Biology</i> , 2020, 21, 71.	3.8	26
13	Zika Virus Mucosal Infection Provides Protective Immunity. <i>Journal of Virology</i> , 2020, 94, .	1.5	12
14	Predominance of positive epistasis among drug resistance-associated mutations in HIV-1 protease. <i>PLoS Genetics</i> , 2020, 16, e1009009.	1.5	25
15	Tracking HIV Rebound following Latency Reversal Using Barcoded HIV. <i>Cell Reports Medicine</i> , 2020, 1, 100162.	3.3	11
16	DNA-Packing Portal and Capsid-Associated Tegument Complexes in the Tumor Herpesvirus KSHV. <i>Cell</i> , 2019, 178, 1329-1343.e12.	13.5	45
17	Increased risk for T cell autoreactivity to γ -cell antigens in the mice expressing the <i>Avy</i> obesity-associated gene. <i>Scientific Reports</i> , 2019, 9, 4269.	1.6	1
18	Differential Metabolic Reprogramming by Zika Virus Promotes Cell Death in Human versus Mosquito Cells. <i>Cell Metabolism</i> , 2019, 29, 1206-1216.e4.	7.2	59

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19	The Ca ²⁺ sensor STIM1 regulates the type I interferon response by retaining the signaling adaptor STING at the endoplasmic reticulum. <i>Nature Immunology</i> , 2019, 20, 152-162.	7.0	228
20	Transmission of Zika Virus Through the Rectal Route Leads to Mucosal and Systemic Infection with Reduced Neuropathology in Mice. <i>FASEB Journal</i> , 2019, 33, 662.57.	0.2	0
21	High-Throughput Fitness Profiling of Zika Virus E Protein Reveals Different Roles for Glycosylation during Infection of Mammalian and Mosquito Cells. <i>IScience</i> , 2018, 1, 97-111.	1.9	29
22	Genome-wide identification of interferon-sensitive mutations enables influenza vaccine design. <i>Science</i> , 2018, 359, 290-296.	6.0	64
23	Emergence of Integrase Resistance Mutations During Initial Therapy Containing Dolutegravir. <i>Clinical Infectious Diseases</i> , 2018, 67, 791-794.	2.9	27
24	Proteomics of Bronchoalveolar Lavage Fluid Reveals a Lung Oxidative Stress Response in Murine Herpesvirus-68 Infection. <i>Viruses</i> , 2018, 10, 670.	1.5	3
25	Inhibition of murine herpesvirus-68 replication by IFN-gamma in macrophages is counteracted by the induction of SOCS1 expression. <i>PLoS Pathogens</i> , 2018, 14, e1007202.	2.1	12
26	Systematic identification of anti-interferon function on hepatitis C virus genome reveals p7 as an immune evasion protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 2018-2023.	3.3	29
27	Long Single-Molecule Reads Can Resolve the Complexity of the Influenza Virus Composed of Rare, Closely Related Mutant Variants. <i>Journal of Computational Biology</i> , 2017, 24, 558-570.	0.8	14
28	Virus-Like Vesicles of Kaposi's Sarcoma-Associated Herpesvirus Activate Lytic Replication by Triggering Differentiation Signaling. <i>Journal of Virology</i> , 2017, 91, .	1.5	17
29	25-Hydroxycholesterol Protects Host against Zika Virus Infection and Its Associated Microcephaly in a Mouse Model. <i>Immunity</i> , 2017, 46, 446-456.	6.6	276
30	Comparative analysis of protein evolution in the genome of pre-epidemic and epidemic Zika virus. <i>Infection, Genetics and Evolution</i> , 2017, 51, 74-85.	1.0	23
31	In situ structures of the genome and genome-delivery apparatus in a single-stranded RNA virus. <i>Nature</i> , 2017, 541, 112-116.	13.7	137
32	Self-Organized Cerebral Organoids with Human-Specific Features Predict Effective Drugs to Combat Zika Virus Infection. <i>Cell Reports</i> , 2017, 21, 517-532.	2.9	305
33	Quantifying perinatal transmission of Hepatitis B viral quasispecies by tag linkage deep sequencing. <i>Scientific Reports</i> , 2017, 7, 10168.	1.6	6
34	Effects of Mutations on Replicative Fitness and Major Histocompatibility Complex Class I Binding Affinity Are Among the Determinants Underlying Cytotoxic-T-Lymphocyte Escape of HIV-1 Gag Epitopes. <i>MBio</i> , 2017, 8, .	1.8	17
35	HIV-1 epitopes presented by MHC class I types associated with superior immune containment of viremia have highly constrained fitness landscapes. <i>PLoS Pathogens</i> , 2017, 13, e1006541.	2.1	12
36	Proteomic and phylogenetic coevolution analyses of pM79 and pM92 identify interactions with RNA polymerase II and delineate the murine cytomegalovirus late transcription complex. <i>Journal of General Virology</i> , 2017, 98, 242-250.	1.3	7

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37	High-throughput identification of protein mutant stability computed from a double mutant fitness landscape. <i>Protein Science</i> , 2016, 25, 530-539.	3.1	13
38	A Herpesvirus Protein Selectively Inhibits Cellular mRNA Nuclear Export. <i>Cell Host and Microbe</i> , 2016, 20, 642-653.	5.1	40
39	Annotating Protein Functional Residues by Coupling High-Throughput Fitness Profile and Homologous-Structure Analysis. <i>MBio</i> , 2016, 7, .	1.8	11
40	Coupling high-throughput genetics with phylogenetic information reveals an epistatic interaction on the influenza A virus M segment. <i>BMC Genomics</i> , 2016, 17, 46.	1.2	24
41	A benchmark study on error-correction by read-pairing and tag-clustering in amplicon-based deep sequencing. <i>BMC Genomics</i> , 2016, 17, 108.	1.2	27
42	Adaptation in protein fitness landscapes is facilitated by indirect paths. <i>ELife</i> , 2016, 5, .	2.8	184
43	M1 of Murine Gamma-Herpesvirus 68 Induces Endoplasmic Reticulum Chaperone Production. <i>Scientific Reports</i> , 2015, 5, 17228.	1.6	4
44	Rational Design and Adaptive Management of Combination Therapies for Hepatitis C Virus Infection. <i>PLoS Computational Biology</i> , 2015, 11, e1004040.	1.5	19
45	Functional Constraint Profiling of a Viral Protein Reveals Discordance of Evolutionary Conservation and Functionality. <i>PLoS Genetics</i> , 2015, 11, e1005310.	1.5	50
46	2SNV: Quasispecies reconstruction from PacBio reads. , 2015, , .		0
47	Limiting Cholesterol Biosynthetic Flux Spontaneously Engages Type I IFN Signaling. <i>Cell</i> , 2015, 163, 1716-1729.	13.5	322
48	CryoEM and mutagenesis reveal that the smallest capsid protein cements and stabilizes Kaposi's sarcoma-associated herpesvirus capsid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E649-56.	3.3	27
49	Evasion of Innate Cytosolic DNA Sensing by a Gammaherpesvirus Facilitates Establishment of Latent Infection. <i>Journal of Immunology</i> , 2015, 194, 1819-1831.	0.4	88
50	High-resolution genetic profile of viral genomes: why it matters. <i>Current Opinion in Virology</i> , 2015, 14, 62-70.	2.6	13
51	RIOK3 Is an Adaptor Protein Required for IRF3-Mediated Antiviral Type I Interferon Production. <i>Journal of Virology</i> , 2014, 88, 7987-7997.	1.5	46
52	Reconstruction of influenza a virus variants from PacBio reads. , 2014, , .		0
53	High-Throughput Identification of Loss-of-Function Mutations for Anti-Interferon Activity in the Influenza A Virus NS Segment. <i>Journal of Virology</i> , 2014, 88, 10157-10164.	1.5	33
54	VGA: A method for viral quasispecies assembly from ultra-deep sequencing data. , 2014, , .		3

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55	Accurate viral population assembly from ultra-deep sequencing data. <i>Bioinformatics</i> , 2014, 30, i329-i337.	1.8	48
56	A Quantitative High-Resolution Genetic Profile Rapidly Identifies Sequence Determinants of Hepatitis C Viral Fitness and Drug Sensitivity. <i>PLoS Pathogens</i> , 2014, 10, e1004064.	2.1	66
57	High-throughput profiling of point mutations across the HIV-1 genome. <i>Retrovirology</i> , 2014, 11, 124.	0.9	35
58	Kaposi's Sarcoma-Associated Herpesvirus ORF18 and ORF30 Are Essential for Late Gene Expression during Lytic Replication. <i>Journal of Virology</i> , 2014, 88, 11369-11382.	1.5	40
59	A Comprehensive Biophysical Description of Pairwise Epistasis throughout an Entire Protein Domain. <i>Current Biology</i> , 2014, 24, 2643-2651.	1.8	281
60	Organization of Capsid-Associated Tegument Components in Kaposi's Sarcoma-Associated Herpesvirus. <i>Journal of Virology</i> , 2014, 88, 12694-12702.	1.5	49
61	High-throughput profiling of influenza A virus hemagglutinin gene at single-nucleotide resolution. <i>Scientific Reports</i> , 2014, 4, 4942.	1.6	147
62	HIV-1 Quasispecies Delineation by Tag Linkage Deep Sequencing. <i>PLoS ONE</i> , 2014, 9, e97505.	1.1	25
63	Unraveling Gene Regulatory Networks Using an Integrated Microfluidic Platform. , 2007, , .		0
64	Bortezomib Is a Novel Inducer of Latent Epstein Barr Virus (EBV) in EBV+ Lymphoma Cell Lines.. <i>Blood</i> , 2006, 108, 2511-2511.	0.6	3
65	Auto-activation of the rta gene of human herpesvirus-8/Kaposi's sarcoma-associated herpesvirus. <i>Journal of General Virology</i> , 2000, 81, 3043-3048.	1.3	137