

Pardis C Sabeti

List of Publications by Year in descending order

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Version: 2024-02-01

93
papers

27,772
citations

50276

46
h-index

49909

87
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117
all docs

117
docs citations

117
times ranked

50522
citing authors

#	ARTICLE	IF	CITATIONS
1	Detection of Neanderthal Adaptively Introgressed Genetic Variants That Modulate Reporter Gene Expression in Human Immune Cells. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	24
2	Serological Markers of SARS-CoV-2 Reinfection. <i>MBio</i> , 2022, 13, e0214121.	4.1	8
3	Containing the spread of mumps on college campuses. <i>Royal Society Open Science</i> , 2022, 9, 210948.	2.4	6
4	Multiplexed CRISPR-based microfluidic platform for clinical testing of respiratory viruses and identification of SARS-CoV-2 variants. <i>Nature Medicine</i> , 2022, 28, 1083-1094.	30.7	127
5	The case for altruism in institutional diagnostic testing. <i>Scientific Reports</i> , 2022, 12, 1857.	3.3	3
6	Transmission from vaccinated individuals in a large SARS-CoV-2 Delta variant outbreak. <i>Cell</i> , 2022, 185, 485-492.e10.	28.9	38
7	Unrecognized introductions of SARS-CoV-2 into the US state of Georgia shaped the early epidemic. <i>Virus Evolution</i> , 2022, 8, veac011.	4.9	2
8	Designing sensitive viral diagnostics with machine learning. <i>Nature Biotechnology</i> , 2022, 40, 1123-1131.	17.5	30
9	Synthetic DNA spike-ins (SDSIs) enable sample tracking and detection of inter-sample contamination in SARS-CoV-2 sequencing workflows. <i>Nature Microbiology</i> , 2022, 7, 108-119.	13.3	6
10	Multiplexed detection of bacterial nucleic acids using Cas13 in droplet microarrays. , 2022, 1, pgac021.		15
11	Analysis of 6.4 million SARS-CoV-2 genomes identifies mutations associated with fitness. <i>Science</i> , 2022, 376, 1327-1332.	12.6	172
12	Simplified Cas13-based assays for the fast identification of SARS-CoV-2 and its variants. <i>Nature Biomedical Engineering</i> , 2022, 6, 932-943.	22.5	76
13	Phylogenetic analysis of SARS-CoV-2 in Boston highlights the impact of superspreading events. <i>Science</i> , 2021, 371, .	12.6	226
14	Testing in a Pandemic – Improving Access, Coordination, and Prioritization. <i>New England Journal of Medicine</i> , 2021, 384, 197-199.	27.0	24
15	Fatal Case of Chronic Jamestown Canyon Virus Encephalitis Diagnosed by Metagenomic Sequencing in Patient Receiving Rituximab. <i>Emerging Infectious Diseases</i> , 2021, 27, 238-242.	4.3	17
16	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. <i>Nature</i> , 2021, 595, 107-113.	27.8	537
17	Detect and destroy: CRISPR-based technologies for the response against viruses. <i>Cell Host and Microbe</i> , 2021, 29, 689-703.	11.0	50
18	Development of a qualitative real-time RT-PCR assay for the detection of SARS-CoV-2: a guide and case study in setting up an emergency-use, laboratory-developed molecular microbiological assay. <i>Journal of Clinical Pathology</i> , 2021, 74, 496-503.	2.0	5

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19	Profiling SARS-CoV-2 HLA-I peptidome reveals T cell epitopes from out-of-frame ORFs. <i>Cell</i> , 2021, 184, 3962-3980.e17.	28.9	98
20	Direct characterization of cis-regulatory elements and functional dissection of complex genetic associations using HCR-FlowFISH. <i>Nature Genetics</i> , 2021, 53, 1166-1176.	21.4	36
21	The Origins and Future of Sentinel: An Early-Warning System for Pandemic Preemption and Response. <i>Viruses</i> , 2021, 13, 1605.	3.3	8
22	SARS-CoV-2 Reinfection in a Liver Transplant Recipient. <i>Annals of Internal Medicine</i> , 2021, 174, 1178-1180.	3.9	10
23	Genome-wide functional screen of 3' UTR variants uncovers causal variants for human disease and evolution. <i>Cell</i> , 2021, 184, 5247-5260.e19.	28.9	62
24	Directed evolution of a family of AAV capsid variants enabling potent muscle-directed gene delivery across species. <i>Cell</i> , 2021, 184, 4919-4938.e22.	28.9	193
25	Intrathecal inflammatory responses in the absence of SARS-CoV-2 nucleic acid in the CSF of COVID-19 hospitalized patients. <i>Journal of the Neurological Sciences</i> , 2021, 430, 120023.	0.6	27
26	Powassan Virus Neuropathology and Genomic Diversity in Patients With Fatal Encephalitis. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa392.	0.9	19
27	A MicroRNA Linking Human Positive Selection and Metabolic Disorders. <i>Cell</i> , 2020, 183, 684-701.e14.	28.9	46
28	Structural and Functional Analysis of the D614G SARS-CoV-2 Spike Protein Variant. <i>Cell</i> , 2020, 183, 739-751.e8.	28.9	924
29	Preventing Outbreaks through Interactive, Experiential Real-Life Simulations. <i>Cell</i> , 2020, 182, 1366-1371.	28.9	2
30	Streamlined inactivation, amplification, and Cas13-based detection of SARS-CoV-2. <i>Nature Communications</i> , 2020, 11, 5921.	12.8	299
31	Diagnostic Approach for Arboviral Infections in the United States. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	35
32	Deployable CRISPR-Cas13a diagnostic tools to detect and report Ebola and Lassa virus cases in real-time. <i>Nature Communications</i> , 2020, 11, 4131.	12.8	101
33	Single-Cell Profiling of Ebola Virus Disease In Vivo Reveals Viral and Host Dynamics. <i>Cell</i> , 2020, 183, 1383-1401.e19.	28.9	79
34	Lassa Virus Genetics. <i>Current Topics in Microbiology and Immunology</i> , 2020, , 1.	1.1	4
35	Massively multiplexed nucleic acid detection with Cas13. <i>Nature</i> , 2020, 582, 277-282.	27.8	492
36	Combining genomics and epidemiology to track mumps virus transmission in the United States. <i>PLoS Biology</i> , 2020, 18, e3000611.	5.6	37

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37	Reporter Assays for Ebola Virus Nucleoprotein Oligomerization, Virion-Like Particle Budding, and Minigenome Activity Reveal the Importance of Nucleoprotein Amino Acid Position 111. <i>Viruses</i> , 2020, 12, 105.	3.3	9
38	Identification of Common CD8 ⁺ T Cell Epitopes from Lassa Fever Survivors in Nigeria and Sierra Leone. <i>Journal of Virology</i> , 2020, 94, .	3.4	15
39	Jamestown Canyon virus in Massachusetts: clinical case series and vector screening. <i>Emerging Microbes and Infections</i> , 2020, 9, 903-912.	6.5	20
40	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
41	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
42	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
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45	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
46	Benchmarking Metagenomics Tools for Taxonomic Classification. <i>Cell</i> , 2019, 178, 779-794.	28.9	364
47	Identifying gene expression programs of cell-type identity and cellular activity with single-cell RNA-Seq. <i>ELife</i> , 2019, 8, .	6.0	252
48	Programmable Inhibition and Detection of RNA Viruses Using Cas13. <i>Molecular Cell</i> , 2019, 76, 826-837.e11.	9.7	286
49	Machine-learning Prognostic Models from the 2014-16 Ebola Outbreak: Data-harmonization Challenges, Validation Strategies, and mHealth Applications. <i>EClinicalMedicine</i> , 2019, 11, 54-64.	7.1	38
50	Development of a SNP barcode to genotype Babesia microti infections. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007194.	3.0	5
51	New filovirus disease classification and nomenclature. <i>Nature Reviews Microbiology</i> , 2019, 17, 261-263.	28.6	84
52	Capturing sequence diversity in metagenomes with comprehensive and scalable probe design. <i>Nature Biotechnology</i> , 2019, 37, 160-168.	17.5	96
53	Clinical and laboratory predictors of Lassa fever outcome in a dedicated treatment facility in Nigeria: a retrospective, observational cohort study. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 684-695.	9.1	100
54	Field validation of recombinant antigen immunoassays for diagnosis of Lassa fever. <i>Scientific Reports</i> , 2018, 8, 5939.	3.3	39

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55	Identifying the favored mutation in a positive selective sweep. <i>Nature Methods</i> , 2018, 15, 279-282.	19.0	56
56	Field-deployable viral diagnostics using CRISPR-Cas13. <i>Science</i> , 2018, 360, 444-448.	12.6	982
57	Comparative evidence for the independent evolution of hair and sweat gland traits in primates. <i>Journal of Human Evolution</i> , 2018, 125, 99-105.	2.6	36
58	Genomic Analysis of Lassa Virus during an Increase in Cases in Nigeria in 2018. <i>New England Journal of Medicine</i> , 2018, 379, 1745-1753.	27.0	135
59	Acute Lassa Virus Encephalitis with Lassa Virus in the Cerebrospinal Fluid but Absent in the Blood: A Case Report with a Positive Outcome. <i>Case Reports in Neurology</i> , 2018, 10, 150-158.	0.7	12
60	Predicting gene expression in massively parallel reporter assays: A comparative study. <i>Human Mutation</i> , 2017, 38, 1240-1250.	2.5	39
61	Nucleic acid detection with CRISPR-Cas13a/C2c2. <i>Science</i> , 2017, 356, 438-442.	12.6	2,275
62	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017, 546, 401-405.	27.8	298
63	Zika virus evolution and spread in the Americas. <i>Nature</i> , 2017, 546, 411-415.	27.8	323
64	Evidence of Ebola Virus Replication and High Concentration in Semen of a Patient During Recovery. <i>Clinical Infectious Diseases</i> , 2017, 65, 1400-1403.	5.8	26
65	An Outbreak of Ebola Virus Disease in the Lassa Fever Zone. <i>Journal of Infectious Diseases</i> , 2016, 214, S110-S121.	4.0	34
66	Roots, Not Parachutes: Research Collaborations Combat Outbreaks. <i>Cell</i> , 2016, 166, 5-8.	28.9	48
67	Ebola Virus Epidemiology and Evolution in Nigeria. <i>Journal of Infectious Diseases</i> , 2016, 214, S102-S109.	4.0	19
68	Most neutralizing human monoclonal antibodies target novel epitopes requiring both Lassa virus glycoprotein subunits. <i>Nature Communications</i> , 2016, 7, 11544.	12.8	148
69	Genomic Analysis of Viral Outbreaks. <i>Annual Review of Virology</i> , 2016, 3, 173-195.	6.7	61
70	In vivo Ebola virus infection leads to a strong innate response in circulating immune cells. <i>BMC Genomics</i> , 2016, 17, 707.	2.8	54
71	Ebola Virus Glycoprotein with Increased Infectivity Dominated the 2013-2016 Epidemic. <i>Cell</i> , 2016, 167, 1088-1098.e6.	28.9	173
72	Unbiased Deep Sequencing of RNA Viruses from Clinical Samples. <i>Journal of Visualized Experiments</i> , 2016, . .	0.3	26

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73	Direct Identification of Hundreds of Expression-Modulating Variants using a Multiplexed Reporter Assay. <i>Cell</i> , 2016, 165, 1519-1529.	28.9	378
74	GB Virus C Coinfections in West African Ebola Patients. <i>Journal of Virology</i> , 2015, 89, 2425-2429.	3.4	65
75	Evaluation of the Potential Impact of Ebola Virus Genomic Drift on the Efficacy of Sequence-Based Candidate Therapeutics. <i>MBio</i> , 2015, 6, .	4.1	62
76	COIL: a methodology for evaluating malarial complexity of infection using likelihood from single nucleotide polymorphism data. <i>Malaria Journal</i> , 2015, 14, 4.	2.3	71
77	Strand-specific RNA sequencing in <i>Plasmodium falciparum</i> malaria identifies developmentally regulated long non-coding RNA and circular RNA. <i>BMC Genomics</i> , 2015, 16, 454.	2.8	160
78	Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. <i>Cell</i> , 2015, 161, 1516-1526.	28.9	275
79	A genetic basis of variation in eccrine sweat gland and hair follicle density. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9932-9937.	7.1	57
80	Discovery of Novel Rhabdoviruses in the Blood of Healthy Individuals from West Africa. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003631.	3.0	56
81	Distinct lineages of Ebola virus in Guinea during the 2014 West African epidemic. <i>Nature</i> , 2015, 524, 102-104.	27.8	96
82	Development of a Single Nucleotide Polymorphism Barcode to Genotype <i>Plasmodium vivax</i> Infections. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003539.	3.0	90
83	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	27.8	13,998
84	Clinical Sequencing Uncovers Origins and Evolution of Lassa Virus. <i>Cell</i> , 2015, 162, 738-750.	28.9	230
85	Filovirus RefSeq Entries: Evaluation and Selection of Filovirus Type Variants, Type Sequences, and Names. <i>Viruses</i> , 2014, 6, 3663-3682.	3.3	49
86	Nomenclature- and Database-Compatible Names for the Two Ebola Virus Variants that Emerged in Guinea and the Democratic Republic of the Congo in 2014. <i>Viruses</i> , 2014, 6, 4760-4799.	3.3	83
87	Lassa Fever in Post-Conflict Sierra Leone. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2748.	3.0	172
88	Enhanced methods for unbiased deep sequencing of Lassa and Ebola RNA viruses from clinical and biological samples. <i>Genome Biology</i> , 2014, 15, 519.	8.8	129
89	Natural selection and infectious disease in human populations. <i>Nature Reviews Genetics</i> , 2014, 15, 379-393.	16.3	353
90	Cleaning up the record on the maximal information coefficient and equitability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3362-3.	7.1	27

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91	<i>Cosı2</i> : an efficient simulator of exact and approximate coalescent with selection. <i>Bioinformatics</i> , 2014, 30, 3427-3429.	4.1	40
92	Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. <i>Science</i> , 2014, 345, 1369-1372.	12.6	1,083
93	Identification and Functional Validation of the Novel Antimalarial Resistance Locus PF10_0355 in <i>Plasmodium falciparum</i> . <i>PLoS Genetics</i> , 2011, 7, e1001383.	3.5	85