

Pardis C Sabeti

List of Publications by Year in descending order

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Version: 2024-02-01

93
papers

27,772
citations

50170

46
h-index

49773

87
g-index

117
all docs

117
docs citations

117
times ranked

50522
citing authors

#	ARTICLE	IF	CITATIONS
1	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
2	Nucleic acid detection with CRISPR-Cas13a/C2c2. <i>Science</i> , 2017, 356, 438-442.	6.0	2,275
3	Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. <i>Science</i> , 2014, 345, 1369-1372.	6.0	1,083
4	Field-deployable viral diagnostics using CRISPR-Cas13. <i>Science</i> , 2018, 360, 444-448.	6.0	982
5	Structural and Functional Analysis of the D614G SARS-CoV-2 Spike Protein Variant. <i>Cell</i> , 2020, 183, 739-751.e8.	13.5	924
6	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. <i>Nature</i> , 2021, 595, 107-113.	13.7	537
7	Massively multiplexed nucleic acid detection with Cas13. <i>Nature</i> , 2020, 582, 277-282.	13.7	492
8	Direct Identification of Hundreds of Expression-Modulating Variants using a Multiplexed Reporter Assay. <i>Cell</i> , 2016, 165, 1519-1529.	13.5	378
9	Benchmarking Metagenomics Tools for Taxonomic Classification. <i>Cell</i> , 2019, 178, 779-794.	13.5	364
10	Natural selection and infectious disease in human populations. <i>Nature Reviews Genetics</i> , 2014, 15, 379-393.	7.7	353
11	Zika virus evolution and spread in the Americas. <i>Nature</i> , 2017, 546, 411-415.	13.7	323
12	Streamlined inactivation, amplification, and Cas13-based detection of SARS-CoV-2. <i>Nature Communications</i> , 2020, 11, 5921.	5.8	299
13	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017, 546, 401-405.	13.7	298
14	Programmable Inhibition and Detection of RNA Viruses Using Cas13. <i>Molecular Cell</i> , 2019, 76, 826-837.e11.	4.5	286
15	Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. <i>Cell</i> , 2015, 161, 1516-1526.	13.5	275
16	Identifying gene expression programs of cell-type identity and cellular activity with single-cell RNA-Seq. <i>ELife</i> , 2019, 8, .	2.8	252
17	Clinical Sequencing Uncovers Origins and Evolution of Lassa Virus. <i>Cell</i> , 2015, 162, 738-750.	13.5	230
18	Phylogenetic analysis of SARS-CoV-2 in Boston highlights the impact of superspreading events. <i>Science</i> , 2021, 371, .	6.0	226

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19	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.	13.5	193
20	Ebola Virus Glycoprotein with Increased Infectivity Dominated the 2013–2016 Epidemic. <i>Cell</i> , 2016, 167, 1088-1098.e6.	13.5	173
21	Lassa Fever in Post-Conflict Sierra Leone. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2748.	1.3	172
22	Analysis of 6.4 million SARS-CoV-2 genomes identifies mutations associated with fitness. <i>Science</i> , 2022, 376, 1327-1332.	6.0	172
23	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.	1.2	160
24	Most neutralizing human monoclonal antibodies target novel epitopes requiring both Lassa virus glycoprotein subunits. <i>Nature Communications</i> , 2016, 7, 11544.	5.8	148
25	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.	13.9	135
26	Enhanced methods for unbiased deep sequencing of Lassa and Ebola RNA viruses from clinical and biological samples. <i>Genome Biology</i> , 2014, 15, 519.	3.8	129
27	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.	15.2	127
28	Deployable CRISPR-Cas13a diagnostic tools to detect and report Ebola and Lassa virus cases in real-time. <i>Nature Communications</i> , 2020, 11, 4131.	5.8	101
29	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.	4.6	100
30	Profiling SARS-CoV-2 HLA-I peptidome reveals T cell epitopes from out-of-frame ORFs. <i>Cell</i> , 2021, 184, 3962-3980.e17.	13.5	98
31	Distinct lineages of Ebola virus in Guinea during the 2014 West African epidemic. <i>Nature</i> , 2015, 524, 102-104.	13.7	96
32	Capturing sequence diversity in metagenomes with comprehensive and scalable probe design. <i>Nature Biotechnology</i> , 2019, 37, 160-168.	9.4	96
33	Development of a Single Nucleotide Polymorphism Barcode to Genotype <i>Plasmodium vivax</i> Infections. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003539.	1.3	90
34	Identification and Functional Validation of the Novel Antimalarial Resistance Locus PF10_0355 in <i>Plasmodium falciparum</i> . <i>PLoS Genetics</i> , 2011, 7, e1001383.	1.5	85
35	New filovirus disease classification and nomenclature. <i>Nature Reviews Microbiology</i> , 2019, 17, 261-263.	13.6	84
36	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.	1.5	83

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37	Single-Cell Profiling of Ebola Virus Disease In Vivo Reveals Viral and Host Dynamics. <i>Cell</i> , 2020, 183, 1383-1401.e19.	13.5	79
38	Simplified Cas13-based assays for the fast identification of SARS-CoV-2 and its variants. <i>Nature Biomedical Engineering</i> , 2022, 6, 932-943.	11.6	76
39	COIL: a methodology for evaluating malarial complexity of infection using likelihood from single nucleotide polymorphism data. <i>Malaria Journal</i> , 2015, 14, 4.	0.8	71
40	GB Virus C Coinfections in West African Ebola Patients. <i>Journal of Virology</i> , 2015, 89, 2425-2429.	1.5	65
41	Evaluation of the Potential Impact of Ebola Virus Genomic Drift on the Efficacy of Sequence-Based Candidate Therapeutics. <i>MBio</i> , 2015, 6, .	1.8	62
42	Genome-wide functional screen of 3' UTR variants uncovers causal variants for human disease and evolution. <i>Cell</i> , 2021, 184, 5247-5260.e19.	13.5	62
43	Genomic Analysis of Viral Outbreaks. <i>Annual Review of Virology</i> , 2016, 3, 173-195.	3.0	61
44	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.	3.3	57
45	Discovery of Novel Rhabdoviruses in the Blood of Healthy Individuals from West Africa. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003631.	1.3	56
46	Identifying the favored mutation in a positive selective sweep. <i>Nature Methods</i> , 2018, 15, 279-282.	9.0	56
47	In vivo Ebola virus infection leads to a strong innate response in circulating immune cells. <i>BMC Genomics</i> , 2016, 17, 707.	1.2	54
48	Detect and destroy: CRISPR-based technologies for the response against viruses. <i>Cell Host and Microbe</i> , 2021, 29, 689-703.	5.1	50
49	Filovirus RefSeq Entries: Evaluation and Selection of Filovirus Type Variants, Type Sequences, and Names. <i>Viruses</i> , 2014, 6, 3663-3682.	1.5	49
50	Roots, Not Parachutes: Research Collaborations Combat Outbreaks. <i>Cell</i> , 2016, 166, 5-8.	13.5	48
51	A MicroRNA Linking Human Positive Selection and Metabolic Disorders. <i>Cell</i> , 2020, 183, 684-701.e14.	13.5	46
52	<i>Cos2</i> : an efficient simulator of exact and approximate coalescent with selection. <i>Bioinformatics</i> , 2014, 30, 3427-3429.	1.8	40
53	Predicting gene expression in massively parallel reporter assays: A comparative study. <i>Human Mutation</i> , 2017, 38, 1240-1250.	1.1	39
54	Field validation of recombinant antigen immunoassays for diagnosis of Lassa fever. <i>Scientific Reports</i> , 2018, 8, 5939.	1.6	39

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55	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.	3.2	38
56	Transmission from vaccinated individuals in a large SARS-CoV-2 Delta variant outbreak. <i>Cell</i> , 2022, 185, 485-492.e10.	13.5	38
57	Combining genomics and epidemiology to track mumps virus transmission in the United States. <i>PLoS Biology</i> , 2020, 18, e3000611.	2.6	37
58	Comparative evidence for the independent evolution of hair and sweat gland traits in primates. <i>Journal of Human Evolution</i> , 2018, 125, 99-105.	1.3	36
59	Direct characterization of cis-regulatory elements and functional dissection of complex genetic associations using HCR–FlowFISH. <i>Nature Genetics</i> , 2021, 53, 1166-1176.	9.4	36
60	Diagnostic Approach for Arboviral Infections in the United States. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	35
61	An Outbreak of Ebola Virus Disease in the Lassa Fever Zone. <i>Journal of Infectious Diseases</i> , 2016, 214, S110-S121.	1.9	34
62	Designing sensitive viral diagnostics with machine learning. <i>Nature Biotechnology</i> , 2022, 40, 1123-1131.	9.4	30
63	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.	3.3	27
64	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.	0.3	27
65	Unbiased Deep Sequencing of RNA Viruses from Clinical Samples. <i>Journal of Visualized Experiments</i> , 2016, . .	0.2	26
66	Evidence of Ebola Virus Replication and High Concentration in Semen of a Patient During Recovery. <i>Clinical Infectious Diseases</i> , 2017, 65, 1400-1403.	2.9	26
67	Testing in a Pandemic – Improving Access, Coordination, and Prioritization. <i>New England Journal of Medicine</i> , 2021, 384, 197-199.	13.9	24
68	Detection of Neanderthal Adaptively Introgressed Genetic Variants That Modulate Reporter Gene Expression in Human Immune Cells. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	24
69	Jamestown Canyon virus in Massachusetts: clinical case series and vector screening. <i>Emerging Microbes and Infections</i> , 2020, 9, 903-912.	3.0	20
70	Ebola Virus Epidemiology and Evolution in Nigeria. <i>Journal of Infectious Diseases</i> , 2016, 214, S102-S109.	1.9	19
71	Powassan Virus Neuropathology and Genomic Diversity in Patients With Fatal Encephalitis. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa392.	0.4	19
72	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.	2.0	17

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73	Identification of Common CD8 ⁺ T Cell Epitopes from Lassa Fever Survivors in Nigeria and Sierra Leone. <i>Journal of Virology</i> , 2020, 94, .	1.5	15
74	Multiplexed detection of bacterial nucleic acids using Cas13 in droplet microarrays. , 2022, 1, pgac021.		15
75	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.	0.3	12
76	SARS-CoV-2 Reinfection in a Liver Transplant Recipient. <i>Annals of Internal Medicine</i> , 2021, 174, 1178-1180.	2.0	10
77	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.	1.5	9
78	The Origins and Future of Sentinel: An Early-Warning System for Pandemic Preemption and Response. <i>Viruses</i> , 2021, 13, 1605.	1.5	8
79	Serological Markers of SARS-CoV-2 Reinfection. <i>MBio</i> , 2022, 13, e0214121.	1.8	8
80	Containing the spread of mumps on college campuses. <i>Royal Society Open Science</i> , 2022, 9, 210948.	1.1	6
81	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.	5.9	6
82	Development of a SNP barcode to genotype Babesia microti infections. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007194.	1.3	5
83	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.	1.0	5
84	Lassa Virus Genetics. <i>Current Topics in Microbiology and Immunology</i> , 2020, , 1.	0.7	4
85	The case for altruism in institutional diagnostic testing. <i>Scientific Reports</i> , 2022, 12, 1857.	1.6	3
86	Preventing Outbreaks through Interactive, Experiential Real-Life Simulations. <i>Cell</i> , 2020, 182, 1366-1371.	13.5	2
87	Unrecognized introductions of SARS-CoV-2 into the US state of Georgia shaped the early epidemic. <i>Virus Evolution</i> , 2022, 8, veac011.	2.2	2
88	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
89	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
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93	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0