

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
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. | 27.8 | 13,998 |
| 2 | Nucleic acid detection with CRISPR-Cas13a/C2c2. <i>Science</i> , 2017, 356, 438-442. | 12.6 | 2,275 |
| 3 | Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. <i>Science</i> , 2014, 345, 1369-1372. | 12.6 | 1,083 |
| 4 | Field-deployable viral diagnostics using CRISPR-Cas13. <i>Science</i> , 2018, 360, 444-448. | 12.6 | 982 |
| 5 | Structural and Functional Analysis of the D614G SARS-CoV-2 Spike Protein Variant. <i>Cell</i> , 2020, 183, 739-751.e8. | 28.9 | 924 |
| 6 | COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. <i>Nature</i> , 2021, 595, 107-113. | 27.8 | 537 |
| 7 | Massively multiplexed nucleic acid detection with Cas13. <i>Nature</i> , 2020, 582, 277-282. | 27.8 | 492 |
| 8 | Direct Identification of Hundreds of Expression-Modulating Variants using a Multiplexed Reporter Assay. <i>Cell</i> , 2016, 165, 1519-1529. | 28.9 | 378 |
| 9 | Benchmarking Metagenomics Tools for Taxonomic Classification. <i>Cell</i> , 2019, 178, 779-794. | 28.9 | 364 |
| 10 | Natural selection and infectious disease in human populations. <i>Nature Reviews Genetics</i> , 2014, 15, 379-393. | 16.3 | 353 |
| 11 | Zika virus evolution and spread in the Americas. <i>Nature</i> , 2017, 546, 411-415. | 27.8 | 323 |
| 12 | Streamlined inactivation, amplification, and Cas13-based detection of SARS-CoV-2. <i>Nature Communications</i> , 2020, 11, 5921. | 12.8 | 299 |
| 13 | Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017, 546, 401-405. | 27.8 | 298 |
| 14 | Programmable Inhibition and Detection of RNA Viruses Using Cas13. <i>Molecular Cell</i> , 2019, 76, 826-837.e11. | 9.7 | 286 |
| 15 | Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. <i>Cell</i> , 2015, 161, 1516-1526. | 28.9 | 275 |
| 16 | Identifying gene expression programs of cell-type identity and cellular activity with single-cell RNA-Seq. <i>ELife</i> , 2019, 8, . | 6.0 | 252 |
| 17 | Clinical Sequencing Uncovers Origins and Evolution of Lassa Virus. <i>Cell</i> , 2015, 162, 738-750. | 28.9 | 230 |
| 18 | Phylogenetic analysis of SARS-CoV-2 in Boston highlights the impact of superspreading events. <i>Science</i> , 2021, 371, . | 12.6 | 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. | 28.9 | 193 |
| 20 | Ebola Virus Glycoprotein with Increased Infectivity Dominated the 2013–2016 Epidemic. <i>Cell</i> , 2016, 167, 1088-1098.e6. | 28.9 | 173 |
| 21 | Lassa Fever in Post-Conflict Sierra Leone. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2748. | 3.0 | 172 |
| 22 | Analysis of 6.4 million SARS-CoV-2 genomes identifies mutations associated with fitness. <i>Science</i> , 2022, 376, 1327-1332. | 12.6 | 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. | 2.8 | 160 |
| 24 | Most neutralizing human monoclonal antibodies target novel epitopes requiring both Lassa virus glycoprotein subunits. <i>Nature Communications</i> , 2016, 7, 11544. | 12.8 | 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. | 27.0 | 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. | 8.8 | 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. | 30.7 | 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. | 12.8 | 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. | 9.1 | 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. | 28.9 | 98 |
| 31 | Distinct lineages of Ebola virus in Guinea during the 2014 West African epidemic. <i>Nature</i> , 2015, 524, 102-104. | 27.8 | 96 |
| 32 | Capturing sequence diversity in metagenomes with comprehensive and scalable probe design. <i>Nature Biotechnology</i> , 2019, 37, 160-168. | 17.5 | 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. | 3.0 | 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. | 3.5 | 85 |
| 35 | New filovirus disease classification and nomenclature. <i>Nature Reviews Microbiology</i> , 2019, 17, 261-263. | 28.6 | 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. | 3.3 | 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. | 28.9 | 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. | 22.5 | 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. | 2.3 | 71 |
| 40 | GB Virus C Coinfections in West African Ebola Patients. <i>Journal of Virology</i> , 2015, 89, 2425-2429. | 3.4 | 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, . | 4.1 | 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. | 28.9 | 62 |
| 43 | Genomic Analysis of Viral Outbreaks. <i>Annual Review of Virology</i> , 2016, 3, 173-195. | 6.7 | 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. | 7.1 | 57 |
| 45 | 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 |
| 46 | Identifying the favored mutation in a positive selective sweep. <i>Nature Methods</i> , 2018, 15, 279-282. | 19.0 | 56 |
| 47 | In vivo Ebola virus infection leads to a strong innate response in circulating immune cells. <i>BMC Genomics</i> , 2016, 17, 707. | 2.8 | 54 |
| 48 | Detect and destroy: CRISPR-based technologies for the response against viruses. <i>Cell Host and Microbe</i> , 2021, 29, 689-703. | 11.0 | 50 |
| 49 | Filovirus RefSeq Entries: Evaluation and Selection of Filovirus Type Variants, Type Sequences, and Names. <i>Viruses</i> , 2014, 6, 3663-3682. | 3.3 | 49 |
| 50 | Roots, Not Parachutes: Research Collaborations Combat Outbreaks. <i>Cell</i> , 2016, 166, 5-8. | 28.9 | 48 |
| 51 | A MicroRNA Linking Human Positive Selection and Metabolic Disorders. <i>Cell</i> , 2020, 183, 684-701.e14. | 28.9 | 46 |
| 52 | <i>Cos2</i> : an efficient simulator of exact and approximate coalescent with selection. <i>Bioinformatics</i> , 2014, 30, 3427-3429. | 4.1 | 40 |
| 53 | Predicting gene expression in massively parallel reporter assays: A comparative study. <i>Human Mutation</i> , 2017, 38, 1240-1250. | 2.5 | 39 |
| 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 | Machine-learning Prognostic Models from the 2014â€“16 Ebola Outbreak: Data-harmonization Challenges, Validation Strategies, and mHealth Applications. <i>EClinicalMedicine</i> , 2019, 11, 54-64. | 7.1 | 38 |
| 56 | Transmission from vaccinated individuals in a large SARS-CoV-2 Delta variant outbreak. <i>Cell</i> , 2022, 185, 485-492.e10. | 28.9 | 38 |
| 57 | Combining genomics and epidemiology to track mumps virus transmission in the United States. <i>PLoS Biology</i> , 2020, 18, e3000611. | 5.6 | 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. | 2.6 | 36 |
| 59 | Direct characterization of cis-regulatory elements and functional dissection of complex genetic associations using HCRâ€“FlowFISH. <i>Nature Genetics</i> , 2021, 53, 1166-1176. | 21.4 | 36 |
| 60 | Diagnostic Approach for Arboviral Infections in the United States. <i>Journal of Clinical Microbiology</i> , 2020, 58, . | 3.9 | 35 |
| 61 | An Outbreak of Ebola Virus Disease in the Lassa Fever Zone. <i>Journal of Infectious Diseases</i> , 2016, 214, S110-S121. | 4.0 | 34 |
| 62 | Designing sensitive viral diagnostics with machine learning. <i>Nature Biotechnology</i> , 2022, 40, 1123-1131. | 17.5 | 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. | 7.1 | 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. | 0.6 | 27 |
| 65 | Unbiased Deep Sequencing of RNA Viruses from Clinical Samples. <i>Journal of Visualized Experiments</i> , 2016, , . | 0.3 | 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. | 5.8 | 26 |
| 67 | Testing in a Pandemic â€” Improving Access, Coordination, and Prioritization. <i>New England Journal of Medicine</i> , 2021, 384, 197-199. | 27.0 | 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, . | 8.9 | 24 |
| 69 | Jamestown Canyon virus in Massachusetts: clinical case series and vector screening. <i>Emerging Microbes and Infections</i> , 2020, 9, 903-912. | 6.5 | 20 |
| 70 | Ebola Virus Epidemiology and Evolution in Nigeria. <i>Journal of Infectious Diseases</i> , 2016, 214, S102-S109. | 4.0 | 19 |
| 71 | Powassan Virus Neuropathology and Genomic Diversity in Patients With Fatal Encephalitis. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa392. | 0.9 | 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. | 4.3 | 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, . | 3.4 | 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. | 0.7 | 12 |
| 76 | SARS-CoV-2 Reinfection in a Liver Transplant Recipient. <i>Annals of Internal Medicine</i> , 2021, 174, 1178-1180. | 3.9 | 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. | 3.3 | 9 |
| 78 | The Origins and Future of Sentinel: An Early-Warning System for Pandemic Preemption and Response. <i>Viruses</i> , 2021, 13, 1605. | 3.3 | 8 |
| 79 | Serological Markers of SARS-CoV-2 Reinfection. <i>MBio</i> , 2022, 13, e0214121. | 4.1 | 8 |
| 80 | Containing the spread of mumps on college campuses. <i>Royal Society Open Science</i> , 2022, 9, 210948. | 2.4 | 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. | 13.3 | 6 |
| 82 | Development of a SNP barcode to genotype Babesia microti infections. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007194. | 3.0 | 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. | 2.0 | 5 |
| 84 | Lassa Virus Genetics. <i>Current Topics in Microbiology and Immunology</i> , 2020, , 1. | 1.1 | 4 |
| 85 | The case for altruism in institutional diagnostic testing. <i>Scientific Reports</i> , 2022, 12, 1857. | 3.3 | 3 |
| 86 | Preventing Outbreaks through Interactive, Experiential Real-Life Simulations. <i>Cell</i> , 2020, 182, 1366-1371. | 28.9 | 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. | 4.9 | 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 |
| 90 | Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611. | | 0 |

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| 91 | 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 |