

Resource Summary Report

Generated by [NIF](#) on Aug 31, 2026

SURPI

RRID:SCR_003071

Type: Tool

Proper Citation

SURPI (RRID:SCR_003071)

Resource Information

URL: <http://chiulab.ucsf.edu/surpi/>

Proper Citation: SURPI (RRID:SCR_003071)

Description: Software providing a computational pipeline for pathogen identification from complex metagenomic next-generation sequencing (NGS) data generated from clinical samples.

Abbreviations: SURPI

Synonyms: Sequence-based Ultra-Rapid Pathogen Identification

Resource Type: software resource

Defining Citation: [PMID:24899342](#)

Keywords: pipeline, cloud based pipeline, pathogen identification

Resource Name: SURPI

Resource ID: SCR_003071

Alternate IDs: OMICS_04623

Alternate URLs: <https://github.com/chiulab/surpi>

License: BSD license

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260829T182121+0000

Ratings and Alerts

No rating or validation information has been found for SURPI.

No alerts have been found for SURPI.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Orf GS, et al. (2024) Next-generation sequencing survey of acute febrile illness in Senegal (2020-2022). *Frontiers in microbiology*, 15, 1362714.

Liang L, et al. (2024) An open-source MRI compatible frame for multimodal presurgical mapping in macaque and capuchin monkeys. *Journal of neuroscience methods*, 407, 110133.

Orf GS, et al. (2023) Purifying selection decreases the potential for Bangui orthobunyavirus outbreaks in humans. *Virus evolution*, 9(1), vead018.

Ciuoderis KA, et al. (2022) Oropouche virus as an emerging cause of acute febrile illness in Colombia. *Emerging microbes & infections*, 11(1), 2645.

Carroll T, et al. (2022) The B.1.427/1.429 (epsilon) SARS-CoV-2 variants are more virulent than ancestral B.1 (614G) in Syrian hamsters. *PLoS pathogens*, 18(2), e1009914.

Berg MG, et al. (2021) A high prevalence of potential HIV elite controllers identified over 30 years in Democratic Republic of Congo. *EBioMedicine*, 65, 103258.

Wang L, et al. (2021) Isolation and characterization of novel reassortant mammalian orthoreovirus from pigs in the United States. *Emerging microbes & infections*, 10(1), 1137.

Carroll T, et al. (2021) The B.1.427/1.429 (epsilon) SARS-CoV-2 variants are more virulent than ancestral B.1 (614G) in Syrian hamsters. *bioRxiv : the preprint server for biology*.

Cuevas-C??rdoba B, et al. (2021) A bioinformatics pipeline for Mycobacterium tuberculosis sequencing that cleans contaminant reads from sputum samples. *PloS one*, 16(10), e0258774.

Hebbandi Nanjundappa R, et al. (2017) A Gut Microbial Mimic that Hijacks Diabetogenic Autoreactivity to Suppress Colitis. *Cell*, 171(3), 655.

Flygare S, et al. (2016) Taxonomer: an interactive metagenomics analysis portal for universal pathogen detection and host mRNA expression profiling. *Genome biology*, 17(1), 111.

Greninger AL, et al. (2015) Rapid metagenomic identification of viral pathogens in clinical samples by real-time nanopore sequencing analysis. *Genome medicine*, 7, 99.

Forster M, et al. (2015) Vy-PER: eliminating false positive detection of virus integration events in next generation sequencing data. *Scientific reports*, 5, 11534.