Resource Summary Report

Generated by <u>NIF</u> on May 4, 2025

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

Funding:

Availability: Available for download

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: 20250420T014134+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 <u>NIF</u>.

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.

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.

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.

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-Córdoba 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.