Resource Summary Report

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seqsero

RRID:SCR_024333
Type: Tool

Proper Citation

seqsero (RRID:SCR_024333)

Resource Information

URL: https://github.com/denglab/SeqSero

Proper Citation: seqsero (RRID:SCR_024333)

Description: Software pipeline for Salmonella serotype determination from raw sequencing reads or genome assemblies.

Resource Type: software toolkit, software resource

Defining Citation: PMID:25762776

Keywords: Salmonella serotype determination, raw sequencing reads, genome assemblies,

Funding:

Availability: Free, Available for download, Freely available,

Resource Name: seqsero

Resource ID: SCR_024333

Alternate IDs: OMICS_21700

Alternate URLs: https://sources.debian.org/src/seqsero/

License: GPL-2.0 license

Record Creation Time: 20230830T050217+0000

Record Last Update: 20250412T060651+0000

Ratings and Alerts

No rating or validation information has been found for seqsero.

No alerts have been found for seqsero.

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 FDI Lab - SciCrunch.org.

Benevides VP, et al. (2024) Genomic Features and Phylogenetic Analysis of Antimicrobial-Resistant Salmonella Mbandaka ST413 Strains. Microorganisms, 12(2).

Leão C, et al. (2024) Genetic Diversity of Salmonella enterica subsp. enterica Serovar Enteritidis from Human and Non-Human Sources in Portugal. Pathogens (Basel, Switzerland), 13(2).

Yang SM, et al. (2022) Genomic characteristics and comparative genomics of Salmonella enterica subsp. enterica serovar Schwarzengrund strain S16 isolated from chicken feces. Gut pathogens, 14(1), 1.

Pardo-Esté C, et al. (2021) Genetic Characterization of Salmonella Infantis with Multiple Drug Resistance Profiles Isolated from a Poultry-Farm in Chile. Microorganisms, 9(11).

Beauvais W, et al. (2021) The effectiveness of treating irrigation water using ultraviolet radiation or sulphuric acid fertilizer for reducing generic Escherichia coli on fresh produce-a controlled intervention trial. Journal of applied microbiology, 131(3), 1360.

Win AT, et al. (2021) Sequence Analyses and Phenotypic Characterization Revealed Multidrug Resistant Gene Insertions in the Genomic Region Encompassing Phase 2 Flagellin Encoding fljAB Genes in Monophasic Variant Salmonella enterica Serovar 4,5,12:i:- Isolates From Various Sources in Thailand. Frontiers in microbiology, 12, 720604.

Luo L, et al. (2021) Elucidation of global and national genomic epidemiology of Salmonella enterica serovar Enteritidis through multilevel genome typing. Microbial genomics, 7(7).

Banerji S, et al. (2020) Genome-based Salmonella serotyping as the new gold standard. Scientific reports, 10(1), 4333.

Longo A, et al. (2019) Characterizing Salmonella enterica Serovar Choleraesuis, var. Kunzendorf: A Comparative Case Study. Frontiers in veterinary science, 6, 316.

Silveira L, et al. (2019) Multidrug-Resistant Salmonella enterica Serovar Rissen Clusters Detected in Azores Archipelago, Portugal. International journal of genomics, 2019, 1860275.

Graham RMA, et al. (2018) Comparative genomics identifies distinct lineages of S. Enteritidis from Queensland, Australia. PloS one, 13(1), e0191042.

Ibrahim GM, et al. (2018) Salmonella Serotyping Using Whole Genome Sequencing. Frontiers in microbiology, 9, 2993.

Yachison CA, et al. (2017) The Validation and Implications of Using Whole Genome Sequencing as a Replacement for Traditional Serotyping for a National Salmonella Reference Laboratory. Frontiers in microbiology, 8, 1044.