Resource Summary Report

Generated by NIF on May 23, 2025

Broad Terra cloud commons for pathogen surveillance

RRID:SCR_018278
Type: Tool

Proper Citation

Broad Terra cloud commons for pathogen surveillance (RRID:SCR_018278)

Resource Information

URL: https://app.terra.bio/#workspaces/pathogen-genomic-surveillance/COVID-19

Proper Citation: Broad Terra cloud commons for pathogen surveillance (RRID:SCR_018278)

Description: Broad Terra cloud workspace for best practices with COVID-19 genomics data. Raw COVID-19 sequencing data from NCBI Sequence Read Archive. Workflows for genome assembly, quality control, metagenomic classification, and aggregate statistics.

Synonyms: Terra

Resource Type: data or information resource, portal

Keywords: COVID-19, COVID-19 data, analysis, collaborate, genomic data, sequencing data, NCBI SRA, genome assembly workflow, quality control, metagenomic classification

Related Condition: COVID-19

Funding:

Availability: Free, Freely available

Resource Name: Broad Terra cloud commons for pathogen surveillance

Resource ID: SCR_018278

Record Creation Time: 20220129T080339+0000

Record Last Update: 20250523T055314+0000

Ratings and Alerts

No rating or validation information has been found for Broad Terra cloud commons for pathogen surveillance.

No alerts have been found for Broad Terra cloud commons for pathogen surveillance.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 37 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Ramirez-Carvajal L, et al. (2018) Genetic stability of foot-and-mouth disease virus during long-term infections in natural hosts. PloS one, 13(2), e0190977.

Amuzu HE, et al. (2018) Wolbachia enhances insect-specific flavivirus infection in Aedes aegypti mosquitoes. Ecology and evolution, 8(11), 5441.

Delgado-Suárez EJ, et al. (2018) Whole genome sequencing reveals widespread distribution of typhoidal toxin genes and VirB/D4 plasmids in bovine-associated nontyphoidal Salmonella. Scientific reports, 8(1), 9864.

Landman S, et al. (2018) DNA Methyltransferase Inhibition Promotes Th1 Polarization in Human CD4+CD25high FOXP3+ Regulatory T Cells but Does Not Affect Their Suppressive Capacity. Journal of immunology research, 2018, 4973964.

Menachery VD, et al. (2018) MERS-CoV and H5N1 influenza virus antagonize antigen presentation by altering the epigenetic landscape. Proceedings of the National Academy of Sciences of the United States of America, 115(5), E1012.

Balmus G, et al. (2018) Targeting of NAT10 enhances healthspan in a mouse model of human accelerated aging syndrome. Nature communications, 9(1), 1700.

Lee H, et al. (2018) Minimum InDel pattern analysis of the Zika virus. BMC genomics, 19(1), 535.

Menicucci AR, et al. (2017) Transcriptome Analysis of Circulating Immune Cell Subsets Highlight the Role of Monocytes in Zaire Ebola Virus Makona Pathogenesis. Frontiers in immunology, 8, 1372.

Hueffer K, et al. (2017) Rabies virus modifies host behaviour through a snake-toxin like region of its glycoprotein that inhibits neurotransmitter receptors in the CNS. Scientific reports, 7(1), 12818.

Cherry JL, et al. (2017) A practical exact maximum compatibility algorithm for reconstruction of recent evolutionary history. BMC bioinformatics, 18(1), 127.

Menicucci AR, et al. (2017) Transcriptomic analysis reveals a previously unknown role for CD8+ T-cells in rVSV-EBOV mediated protection. Scientific reports, 7(1), 919.

Tripathi S, et al. (2017) A novel Zika virus mouse model reveals strain specific differences in virus pathogenesis and host inflammatory immune responses. PLoS pathogens, 13(3), e1006258.

Versteeg K, et al. (2017) Infection with the Makona variant results in a delayed and distinct host immune response compared to previous Ebola virus variants. Scientific reports, 7(1), 9730.

Kim JI, et al. (2016) Genome-Wide Analysis of Human Metapneumovirus Evolution. PloS one, 11(4), e0152962.

Weir W, et al. (2016) Population genomics reveals the origin and asexual evolution of human infective trypanosomes. eLife, 5, e11473.

Zhang Y, et al. (2016) Genetic changes found in a distinct clade of Enterovirus D68 associated with paralysis during the 2014 outbreak. Virus evolution, 2(1), vew015.

Bachert BA, et al. (2016) Unique Footprint in the scl1.3 Locus Affects Adhesion and Biofilm Formation of the Invasive M3-Type Group A Streptococcus. Frontiers in cellular and infection microbiology, 6, 90.

Pappalardo M, et al. (2016) Conserved differences in protein sequence determine the human pathogenicity of Ebolaviruses. Scientific reports, 6, 23743.

Dhanoa A, et al. (2016) Impact of dengue virus (DENV) co-infection on clinical manifestations, disease severity and laboratory parameters. BMC infectious diseases, 16(1), 406.

Yeung YA, et al. (2016) Germline-encoded neutralization of a Staphylococcus aureus virulence factor by the human antibody repertoire. Nature communications, 7, 13376.