Resource Summary Report

Generated by <u>dkNET</u> on May 16, 2025

<u>Terra</u>

RRID:SCR_021648 Type: Tool

Proper Citation

Terra (RRID:SCR_021648)

Resource Information

URL: https://terra.bio

Proper Citation: Terra (RRID:SCR_021648)

Description: Open ecosystem of data repositories hosted by various partner organizations, who work together to ensure that their data can be federated across participating platforms. Open source platform for biomedical researchers to access data, run analysis tools, and collaborate. Terra powers important scientific projects including AnVIL, BioData Catalyst, Human Cell Atlas, BICCN, and many others. Easily access both open and access-controlled datasets hosted in cloud repositories. Explore, analyze, and visualize data using Jupyter Notebooks, RStudio, RShinyApps, and Galaxy.

Synonyms: Terra Cloud Native Platform, BCDC cloud computing environment

Resource Type: data or information resource, portal

Keywords: Biomedical researcher platform, access data, run analysis tools, collaborate, access controlled datasets, cloud repositories

Funding:

Availability: Free, Freely available

Resource Name: Terra

Resource ID: SCR_021648

License URLs: https://terra.bio/about/terms-of-service/

Record Creation Time: 20220129T080356+0000

Record Last Update: 20250516T054240+0000

Ratings and Alerts

No rating or validation information has been found for Terra.

No alerts have been found for Terra.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 75 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Ng JK, et al. (2024) HAT: de novo variant calling for highly accurate short-read and long-read sequencing data. Bioinformatics (Oxford, England), 40(1).

Kabir F, et al. (2024) Mpox Viral Lineage Analysis and Technique Development Using Nextgeneration Sequencing Approach. The Journal of infectious diseases, 229(Supplement_2), S163.

Marin WM, et al. (2024) High-throughput complement component 4 genomic sequence analysis with C4Investigator. HLA, 103(1), e15273.

Heimlich JB, et al. (2024) Multiomic profiling of human clonal hematopoiesis reveals genotype and cell-specific inflammatory pathway activation. Blood advances, 8(14), 3665.

lyer S, et al. (2024) The BRAIN Initiative data-sharing ecosystem: Characteristics, challenges, benefits, and opportunities. eLife, 13.

Kuderna LFK, et al. (2024) Identification of constrained sequence elements across 239 primate genomes. Nature, 625(7996), 735.

Genner R, et al. (2024) Assessing methylation detection for primary human tissue using Nanopore sequencing. bioRxiv : the preprint server for biology.

Shannon ML, et al. (2024) Clonal hematopoiesis and inflammation in the vasculature: CHIVE, a prospective, longitudinal clonal hematopoiesis cohort and biorepository. Blood advances, 8(13), 3453.

Normandin E, et al. (2023) High-depth sequencing characterization of viral dynamics across tissues in fatal COVID-19 reveals compartmentalized infection. Nature communications, 14(1), 574.

Geiger-Schuller K, et al. (2023) Systematically characterizing the roles of E3-ligase family members in inflammatory responses with massively parallel Perturb-seq. bioRxiv : the preprint server for biology.

Gorzalski AJ, et al. (2023) Rapid Lineage Assignment of Severe Acute Respiratory Syndrome Coronavirus 2 Cases through Automated Library Preparation, Sequencing, and Bioinformatic Analysis. The Journal of molecular diagnostics : JMD, 25(4), 191.

Zhao B, et al. (2023) Contribution and therapeutic implications of retroelement insertions in ataxia telangiectasia. American journal of human genetics, 110(11), 1976.

Lemire G, et al. (2023) Exome copy number variant detection, analysis and classification in a large cohort of families with undiagnosed rare genetic disease. medRxiv : the preprint server for health sciences.

Ferguson D, et al. (2023) Serratia marcescens Outbreak at a Correctional Facility: Environmental Sampling, Laboratory Analyses and Genomic Characterization to Assess Sources and Persistence. International journal of environmental research and public health, 20(17).

Ambrosio FJ, et al. (2023) TheiaEuk: a species-agnostic bioinformatics workflow for fungal genomic characterization. Frontiers in public health, 11, 1198213.

Ramaiah A, et al. (2023) Genomic surveillance identifies SARS-CoV-2 transmission patterns in local university populations, Wisconsin, USA, 2020-2022. Microbial genomics, 9(3).

Cauwenberghs N, et al. (2023) Clinical and Echocardiographic Diversity Associated With Physical Fitness in the Project Baseline Health Study: Implications for Heart Failure Staging. Journal of cardiac failure, 29(11), 1477.

Oliva M, et al. (2023) DNA methylation QTL mapping across diverse human tissues provides molecular links between genetic variation and complex traits. Nature genetics, 55(1), 112.

Yang S, et al. (2023) Transient SARS-CoV-2 RNA-Dependent RNA Polymerase Mutations after Remdesivir Treatment for Chronic COVID-19 in Two Transplant Recipients: Case Report and Intra-Host Viral Genomic Investigation. Microorganisms, 11(8).

Pasquesi GIM, et al. (2023) Regulation of human interferon signaling by transposon exonization. bioRxiv : the preprint server for biology.