

Resource Summary Report

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Terra

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

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: 20260806T054728+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 83 mentions in open access literature.

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

Resong PJ, et al. (2025) Genetic Confirmation of Clonal Spread of *Candida auris* from Southern to Northern Nevada. *Journal of fungi* (Basel, Switzerland), 11(6).

Zhang Y, et al. (2025) Benchmarking of duplex sequencing approaches to reveal somatic mutation landscapes. *bioRxiv : the preprint server for biology*.

Braun DA, et al. (2025) A neoantigen vaccine generates antitumour immunity in renal cell carcinoma. *Nature*, 639(8054), 474.

Speir ML, et al. (2025) Making genomic data FAIR through effective Data Portals. *Scientific data*, 12(1), 1872.

Thurimella K, et al. (2025) Protein language models uncover carbohydrate-active enzyme function in metagenomics. *BMC bioinformatics*, 26(1), 285.

Sun W, et al. (2025) TMEM175, SCARB2 and CTSB associations with Parkinson's disease risk across populations. *NPJ Parkinson's disease*, 11(1), 348.

Foster-Nyarko E, et al. (2025) Genomic diversity and antimicrobial resistance of *Vibrio cholerae* isolates from Africa: a PulseNet Africa initiative using nanopore sequencing to enhance genomic surveillance. *Microbial genomics*, 11(12).

Waks AG, et al. (2025) Efficacy, safety, and predictive biomarkers of neoadjuvant nab-paclitaxel and pembrolizumab in hormone receptor-positive breast cancer: A randomized pilot trial. *Nature communications*, 16(1), 10705.

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

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).

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.

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*.

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

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.

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.

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*.

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*.

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.