

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: 20260905T132943+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 90 mentions in open access literature.

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

, et al. (2026) A Community Standard Multispecies Cell Atlas of the Basal Ganglia. bioRxiv : the preprint server for biology.

Panji S, et al. (2026) Unleashing potential: assessing Africa's readiness for the data science revolution to impact health. Nature communications, 17(1).

Harrison BR, et al. (2026) Dogs and humans share biomarkers of mortality. The journals of gerontology. Series A, Biological sciences and medical sciences, 81(4).

Lacy-Roberts N, et al. (2026) Bridging the bioinformatics gap: tool selection for decentralized AMR genomic surveillance in Africa. Frontiers in public health, 14, 1756324.

Huang KK, et al. (2026) Mutational Signatures and Clonal Hematopoiesis in Intestinal Metaplasia across Countries with Varying Stomach Cancer Incidence. Cancer discovery, 16(3), 497.

Jaiswal A, et al. (2026) Spatial transcriptomics reveals altered communities and drivers of aberrant epithelia and pro-fibrotic fibroblasts in interstitial lung diseases. Cell genomics, 6(3), 101066.

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

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

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

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).

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).

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

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.

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

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).

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

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

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