Resource Summary Report

Generated by ASWG on Aug 3, 2026

Analysis, Visualization, and Informatics Lab-space (AnVIL)

RRID:SCR_017469
Type: Tool

Proper Citation

Analysis, Visualization, and Informatics Lab-space (AnVIL) (RRID:SCR_017469)

Resource Information

URL: https://anvilproject.org/

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Description: Portal to facilitate integration and computing on and across large datasets generated by NHGRI programs, as well as initiatives funded by National Institutes of Health or by other agencies that support human genomics research. Resource for genomic scientific community, that leverages cloud based infrastructure for democratizing genomic data access, sharing and computing across large genomic, and genomic related data sets. Component of federated data ecosystem, and is expected to collaborate and integrate with other genomic data resources through adoption of FAIR (Findable, Accessible, Interoperable, Reusable) principles, as their specifications emerge from scientific community. Will provide collaborative environment, where datasets and analysis workflows can be shared within consortium and be prepared for public release to broad scientific community through AnVIL user interfaces.

Abbreviations: AnVIL

Synonyms: Visualization, and Informatics Lab-space, AnVIL, Analysis Visualization and Informatics Lab-space, Analysis

Resource Type: project portal, data or information resource, data repository, service resource, portal, storage service resource

Keywords: Dataset, NHGRI, program, NIH, initiative, funded, human, genomic, data, access, sharing, FAIR, analysis, workflow

Funding: NIH

Availability: Restricted

Resource Name: Analysis, Visualization, and Informatics Lab-space (AnVIL)

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Alternate URLs: https://www.genome.gov/Funded-Programs-Projects/Computational-Genomics-and-Data-Science-Program/Genomic-Analysis-Visualization-Informatics-Lab-space-AnVIL

Record Creation Time: 20220129T080335+0000

Record Last Update: 20260803T040750+0000

Ratings and Alerts

No rating or validation information has been found for Analysis, Visualization, and Informatics Lab-space (AnVIL).

No alerts have been found for Analysis, Visualization, and Informatics Lab-space (AnVIL).

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

Dardas Z, et al. (2025) Bi-allelic UGGT1 variants cause a congenital disorder of glycosylation. American journal of human genetics, 112(5), 1139.

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

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.

Wang Z, et al. (2024) NCI Cancer Research Data Commons: Resources to Share Key Cancer Data. Cancer research, 84(9), 1388.

Hou K, et al. (2024) Admix-kit: an integrated toolkit and pipeline for genetic analyses of admixed populations. Bioinformatics (Oxford, England), 40(4).

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).

Guitart X, et al. (2024) Independent expansion, selection and hypervariability of the TBC1D3 gene family in humans. bioRxiv : the preprint server for biology.

Pitsava G, et al. (2024) Genome sequencing reveals the impact of non-canonical exon inclusions in rare genetic disease. medRxiv : the preprint server for health sciences.

Nagasaki M, et al. (2023) Design and implementation of a hybrid cloud system for large-scale human genomic research. Human genome variation, 10(1), 6.

Seddighi S, et al. (2023) Mis-spliced transcripts generate de novo proteins in TDP-43-related ALS/FTD. bioRxiv : the preprint server for biology.

Hou K, et al. (2023) Admix-kit: An Integrated Toolkit and Pipeline for Genetic Analyses of Admixed Populations. bioRxiv : the preprint server for biology.

Liao WW, et al. (2023) A draft human pangenome reference. Nature, 617(7960), 312.

, et al. (2023) Shared and distinct ultra-rare genetic risk for diverse epilepsies: A whole-exome sequencing study of 54,423 individuals across multiple genetic ancestries. medRxiv : the preprint server for health sciences.

Guarracino A, et al. (2023) Recombination between heterologous human acrocentric chromosomes. Nature, 617(7960), 335.

Hamanaka K, et al. (2023) Genome-wide identification of tandem repeats associated with splicing variation across 49 tissues in humans. Genome research, 33(3), 435.

Schatz MC, et al. (2022) Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space. Cell genomics, 2(1).

, et al. (2022) The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2022 update. Nucleic acids research, 50(W1), W345.

Yuen D, et al. (2021) The Dockstore: enhancing a community platform for sharing reproducible and accessible computational protocols. Nucleic acids research, 49(W1), W624.

Wohler E, et al. (2021) PhenoDB, GeneMatcher and VariantMatcher, tools for analysis and sharing of sequence data. Orphanet journal of rare diseases, 16(1), 365.