

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

CyVerse

RRID:SCR_014531

Type: Tool

Proper Citation

CyVerse (RRID:SCR_014531)

Resource Information

URL: <http://www.cyverse.org/>

Proper Citation: CyVerse (RRID:SCR_014531)

Description: A google drive interface for scientific big data. CyVerse cyberinfrastructure is applicable to all life sciences disciplines and works equally well on data from plants, animals, or microbes. It provides life scientists with computational infrastructure to handle large datasets and complex analyses. Its extensible platforms provide data storage, bioinformatics tools, image analyses, cloud services, and APIs.

Synonyms: iPlant

Resource Type: data or information resource, database

Defining Citation: [PMID:26752627](#), [PMID:22645531](#)

Keywords: cyberinfrastructure, cyber, infrastructure, life science, computational infrastructure, FASEB list

Funding: NSF Directorate for Biological Sciences

Resource Name: CyVerse

Resource ID: SCR_014531

Record Creation Time: 20220129T080320+0000

Record Last Update: 20260905T133210+0000

Ratings and Alerts

No rating or validation information has been found for CyVerse.

No alerts have been found for CyVerse.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 200 mentions in open access literature.

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

Meng TG, et al. (2026) Ultra-low-input rG4-seq reveals the RNA G-quadruplex regulome in gene expression and genome integrity. *Nucleic acids research*, 54(3).

Amaradasa BS, et al. (2026) Transcriptomic and Root Microbiome Responses of Lettuce to Beneficial Endophytic Bacteria in Hydroponic Systems. *International journal of molecular sciences*, 27(7).

He XZ, et al. (2026) *Ophiorrhiza xishuiensis* (Rubiaceae), a new species endemic to Guizhou, Sichuan, and Chongqing, China. *PhytoKeys*, 275, 163.

Qiu Y, et al. (2026) Intersite differences in gut microbiome are associated with habitat quality in a limestone forest-dwelling langur. *BMC microbiology*, 26(1).

Lin Z, et al. (2026) From environment to biomass: trait-mediated effects on submerged macrophyte biomass in a subtropical shallow restored lake. *BMC plant biology*, 26(1).

Liu Y, et al. (2025) SpatialSNV: A novel method for identifying and analyzing spatially resolved SNVs in tumor microenvironments. *GigaScience*, 14.

Li C, et al. (2025) Leaf carbon nitrogen and phosphorus concentrations in dominant trees across China's forests from 2005 to 2020. *Scientific data*, 12(1), 1438.

Li C, et al. (2025) Evaluation of acaricidal effect of terpinolene and ??-terpinene on *Hyalomma anatolicum* and in silico screening of herbs. *Journal of veterinary science*, 26(2), e19.

Yung ML, et al. (2025) A User-Friendly Machine Learning Pipeline for Automated Leaf Segmentation in *Atriplex lentiformis*. *Bioinformatics and biology insights*, 19, 11779322251344033.

Shih MM, et al. (2025) Targeted single cell expression profiling identifies integrators of sleep and metabolic state. *G3 (Bethesda, Md.)*, 15(7).

Langwig MV, et al. (2025) Endemism shapes viral ecology and evolution in globally distributed hydrothermal vent ecosystems. *Nature communications*, 16(1), 4076.

Zheng H, et al. (2025) Transcriptomic analysis reveals key genes and pathways involved in fruit abscission of *Epimedium pubescens*. *BMC plant biology*, 26(1), 36.

Ozair F, et al. (2025) Phenotypic plasticity in maize grain yield: Genetic and environmental insights of response to environmental gradients. *The plant genome*, 18(3), e70078.

Xu T, et al. (2025) Discovery and characterization of complete genomes of 38 head-tailed proviruses in four predominant phyla of archaea. *Microbiology spectrum*, 13(1), e0049224.

Engelhorn J, et al. (2025) Genetic variation at transcription factor binding sites largely explains phenotypic heritability in maize. *Nature genetics*, 57(9), 2313.

Ji J, et al. (2025) Evaluation of the impact of ecological factors on the habitat suitability and bioactive components accumulation of the medicinal holoparasitic plant *Cynomorium songaricum* using machine learning models. *Frontiers in plant science*, 16, 1586682.

Guo X, et al. (2025) Predicting habitat suitability for an endangered medicinal plant, *Saussurea medusa*: insights from ensemble species distribution models. *Frontiers in plant science*, 16, 1590206.

Wambulwa MC, et al. (2025) Incorporating Genetic Diversity to Optimize the Plant Conservation Network in the Third Pole. *Global change biology*, 31(3), e70122.

Prigge MJ, et al. (2025) Comparative mutant analyses reveal a novel mechanism of ARF regulation in land plants. *Nature plants*, 11(4), 821.

Rai S, et al. (2025) Transcript profiling of plastid ferrochelatase two mutants reveals that chloroplast singlet oxygen signals lead to global changes in RNA profiles and are mediated by Plant U-Box 4. *BMC plant biology*, 25(1), 747.