

Resource Summary Report

Generated by [kravitz2](#) on Sep 2, 2026

CLEAR

RRID:SCR_021663

Type: Tool

Proper Citation

CLEAR (RRID:SCR_021663)

Resource Information

URL: <https://github.com/YangLab/CLEAR>

Proper Citation: CLEAR (RRID:SCR_021663)

Description: Software tool as computational pipeline for circular and linear RNA expression analysis from ribosomal-RNA depleted RNA-seq. CIRCexplorer3-CLEAR is CLEAR pipeline for direct comparison of circular and linear RNA expression.

Synonyms: CLEAR/circExplorer3, Circular and Linear RNA Expression Analysis from Ribosomal-RNA depleted (Ribo???) RNA-seq, CIRCexplorer3-CLEAR

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: [PMID:31904419](#), [DOI:10.1101/668657](#)

Funding: Howard Hughes Medical Institute International Program ;
National Natural Science Foundation of China ;
Strategic Priority Research Program of Chinese Academy of Sciences

Availability: Free, Available for download, Freely available

Resource Name: CLEAR

Resource ID: SCR_021663

License: GPLv3

Record Creation Time: 20220129T080356+0000

Record Last Update: 20260829T182716+0000

Ratings and Alerts

No rating or validation information has been found for CLEAR.

No alerts have been found for CLEAR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Lopez I, et al. (2025) Clinical entity augmented retrieval for clinical information extraction. NPJ digital medicine, 8(1), 45.

Utleay D, et al. (2025) Camelina circRNA landscape: Implications for gene regulation and fatty acid metabolism. The plant genome, 18(1), e20537.

McGrail C, et al. (2024) Genetic association and machine learning improves discovery and prediction of type 1 diabetes. medRxiv : the preprint server for health sciences.

Feng XY, et al. (2023) New insight into circRNAs: characterization, strategies, and biomedical applications. Experimental hematology & oncology, 12(1), 91.

Rebolledo C, et al. (2023) Computational approaches for circRNAs prediction and in silico characterization. Briefings in bioinformatics, 24(3).

Yuan GH, et al. (2023) RNAlight: a machine learning model to identify nucleotide features determining RNA subcellular localization. Briefings in bioinformatics, 24(1).

Manivannan N, et al. (2023) Mercury speciation in selenium enriched wheat plants hydroponically exposed to mercury pollution. Scientific reports, 13(1), 21132.

Han W, et al. (2022) Self-supervised contrastive learning for integrative single cell RNA-seq data analysis. Briefings in bioinformatics, 23(5).

Ma XK, et al. (2021) CIRCexplorer pipelines for circRNA annotation and quantification from non-polyadenylated RNA-seq datasets. Methods (San Diego, Calif.), 196, 3.

Pedraz-Valdunciel C, et al. (2021) Defining the landscape of circRNAs in non-small cell lung cancer and their potential as liquid biopsy biomarkers: a complete review including current methods. Extracellular vesicles and circulating nucleic acids, 2(2), 179.

Workman B, et al. (2021) Evaluation of a Program to Reduce Home Environment Risks for Children with Asthma Residing in Urban Areas. International journal of environmental research and public health, 19(1).

Santos-Rodriguez G, et al. (2021) Evolutionary dynamics of circular RNAs in primates. *eLife*, 10.

Walker LA, et al. (2020) CLEAR: coverage-based limiting-cell experiment analysis for RNA-seq. *Journal of translational medicine*, 18(1), 63.

Vlachos C, et al. (2019) Optimizing the Power to Identify the Genetic Basis of Complex Traits with Evolve and Resequencing Studies. *Molecular biology and evolution*, 36(12), 2890.

Ma XK, et al. (2019) CIRCexplorer3: A CLEAR Pipeline for Direct Comparison of Circular and Linear RNA Expression. *Genomics, proteomics & bioinformatics*, 17(5), 511.