

Resource Summary Report

Generated by [RRID](#) on Aug 12, 2026

[create_cisTarget_databases](#)

RRID:SCR_027473

Type: Tool

Proper Citation

create_cisTarget_databases (RRID:SCR_027473)

Resource Information

URL: https://github.com/aertslab/create_cisTarget_databases

Proper Citation: create_cisTarget_databases (RRID:SCR_027473)

Description: Code to create cisTarget databases.

Resource Type: source code, software resource

Keywords: create cisTarget databases, cisTarget, create databases,

Availability: Free, Available for download, Freely available

Resource Name: create_cisTarget_databases

Resource ID: SCR_027473

Record Creation Time: 20250927T062016+0000

Record Last Update: 20260810T040926+0000

Ratings and Alerts

No rating or validation information has been found for create_cisTarget_databases.

No alerts have been found for create_cisTarget_databases.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Xu X, et al. (2026) A single-cell transcriptomic atlas identifies key progenitor populations driving postnatal horn bud development in goats (*Capra hircus*). *Communications biology*, 9(1).

Islamuddin M, et al. (2026) The Reconstitution of the Macrophage Niche Reveals Dynamic Transcriptional and Renal Macrophage-Epithelial Communication Networks. *Cells*, 15(12).

Mota-Gómez I, et al. (2026) Chromatin spatial analysis by METALoci unveils sex-determining 3D regulatory hubs. *Nature structural & molecular biology*, 33(4), 577.

Kempynck N, et al. (2026) CREsted: modeling genomic and synthetic cell-type-specific enhancers across tissues and species. *Nature methods*, 23(5), 946.

Zhang M, et al. (2026) A pipeline for single-cell chromatin accessibility data analysis. *Blood science (Baltimore, Md.)*, 8(1), e00259.

Sarropoulos I, et al. (2026) The evolution of gene regulation in mammalian cerebellum development. *Science (New York, N.Y.)*, 391(6784), eadw9154.

Wang H, et al. (2025) The Neuropeptide Neuroparsin-A Regulates the Establishment of Dominance Hierarchy in Bumblebees. *International journal of molecular sciences*, 27(1).

Li Y, et al. (2025) Protocol for reconstructing spatially aware receptor-TF-target signaling cascades using spatial transcriptomics. *STAR protocols*, 6(4), 104237.

Mu X, et al. (2025) Single-nucleus and spatial transcriptomics identify brain landscape of gene regulatory networks associated with behavioral maturation in honeybees. *Nature communications*, 16(1), 3343.

Cao S, et al. (2024) Comprehensive integration of single-cell transcriptomic data illuminates the regulatory network architecture of plant cell fate specification. *Plant diversity*, 46(3), 372.

Bravo González-Blas C, et al. (2023) SCENIC+: single-cell multiomic inference of enhancers and gene regulatory networks. *Nature methods*, 20(9), 1355.

Cao S, et al. (2023) scPlant: A versatile framework for single-cell transcriptomic data analysis in plants. *Plant communications*, 4(5), 100631.

Liu C, et al. (2022) Spatiotemporal mapping of gene expression landscapes and developmental trajectories during zebrafish embryogenesis. *Developmental cell*, 57(10), 1284.

Qu J, et al. (2022) A reference single-cell regulomic and transcriptomic map of cynomolgus monkeys. *Nature communications*, 13(1), 4069.