

Resource Summary Report

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

Starcode

RRID:SCR_025483

Type: Tool

Proper Citation

Starcode (RRID:SCR_025483)

Resource Information

URL: <https://github.com/gui11aume/starcode>

Proper Citation: Starcode (RRID:SCR_025483)

Description: Software for DNA sequence clustering. General purpose DNA sequence clustering tool with strong focus on error correction.

Resource Type: source code, software resource

Defining Citation: [PMID:25638815](#)

Keywords: DNA sequence clustering, sequence clustering algorithm, error correction,

Funding: Government of Catalonia ;
Spanish Ministry of Economy and Competitiveness

Availability: Free, Available for download, Freely available,

Resource Name: Starcode

Resource ID: SCR_025483

License: GNU GPL v3

Record Creation Time: 20240716T053232+0000

Record Last Update: 20260810T040845+0000

Ratings and Alerts

No rating or validation information has been found for Starcode.

No alerts have been found for Starcode.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Ishiguro S, et al. (2026) A multi-kingdom genetic barcoding system for precise clone isolation. *Nature biotechnology*, 44(4), 616.

Li J, et al. (2026) AP-1 mediates cellular adaptation and memory formation. *Nature communications*, 17(1).

Rebecca VW, et al. (2026) Dasatinib resensitizes BRAF/MEK inhibitor efficacy in patient-derived xenografts from patients with progression on BRAF/MEK inhibitor treatment. *iScience*, 29(2), 114669.

Simmons SK, et al. (2026) Experimental and computational methods for allelic imbalance analysis from single-nucleus RNA-seq data. *Genome biology*, 27(1).

Miller D, et al. (2025) Pooled PPIseq: Screening the SARS-CoV-2 and human interface with a scalable multiplexed protein-protein interaction assay platform. *PloS one*, 20(1), e0299440.

Simmons SK, et al. (2024) Experimental and Computational Methods for Allelic Imbalance Analysis from Single-Nucleus RNA-seq Data. *bioRxiv : the preprint server for biology*.

Li J, et al. (2024) AP-1 Mediates Cellular Adaptation and Memory Formation During Therapy Resistance. *bioRxiv : the preprint server for biology*.

Martinez-Ara M, et al. (2024) Large-scale analysis of the integration of enhancer-enhancer signals by promoters. *eLife*, 12.

Jain N, et al. (2023) Retrospective identification of intrinsic factors that mark pluripotency potential in rare somatic cells. *bioRxiv : the preprint server for biology*.

Reffsin S, et al. (2023) Single cell susceptibility to SARS-CoV-2 infection is driven by variable cell states. *bioRxiv : the preprint server for biology*.

Jiang CL, et al. (2022) Cell type determination for cardiac differentiation occurs soon after seeding of human-induced pluripotent stem cells. *Genome biology*, 23(1), 90.