

Resource Summary Report

Generated by [NIF](#) on Aug 27, 2026

GUSHR

RRID:SCR_021166

Type: Tool

Proper Citation

GUSHR (RRID:SCR_021166)

Resource Information

URL: <https://github.com/Gaius-Augustus/GUSHR>

Proper Citation: GUSHR (RRID:SCR_021166)

Description: Software tool for assembly free construction of UTRs from short read RNA-Seq data on basis of coding sequence annotation.

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

Keywords: UTRs assembly free construction, short read RNA-Seq data, coding sequence annotation

Availability: Free, Available for download, Freely available

Resource Name: GUSHR

Resource ID: SCR_021166

License: GNU General Public License v3.0

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260821T194151+0000

Ratings and Alerts

No rating or validation information has been found for GUSHR .

No alerts have been found for GUSHR .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Cristofari R, et al. (2026) Lifestyle change accelerates epigenetic ageing in King penguins. Nature communications, 17(1).

Fujiwara K, et al. (2025) A Near Complete Genome Assembly of the Oshima Cherry *Cerasus speciosa*. Scientific data, 12(1), 162.

Yi L, et al. (2025) Chromosome-level genome assemblies of sunflower oilseed and confectionery cultivars. Scientific data, 12(1), 24.

Çiftçi O, et al. (2024) Long-Read-Based Hybrid Genome Assembly and Annotation of Snow Algal Strain CCCryo 101-99 (cf. *Sphaerocystis* sp., Chlamydomonadales). Genome biology and evolution, 16(7).

Legeai F, et al. (2024) Chromosome-Level Assembly and Annotation of the Pearly Heath *Coenonympha arcania* Butterfly Genome. Genome biology and evolution, 16(3).

Cicconardi F, et al. (2023) Evolutionary dynamics of genome size and content during the adaptive radiation of Heliconiini butterflies. Nature communications, 14(1), 5620.