

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

[groHMM](#)

RRID:SCR_024237

Type: Tool

Proper Citation

groHMM (RRID:SCR_024237)

Resource Information

URL: <https://bioconductor.org/packages/groHMM/>

Proper Citation: groHMM (RRID:SCR_024237)

Description: Software R package for analysis of GRO-seq data. Used for identifying unannotated and cell type-specific transcription units from global run-on sequencing data

Synonyms: grohmm

Resource Type: software resource, software toolkit

Defining Citation: [PMID:26173492](#)

Keywords: analysis of GRO-seq data, identifying unannotated and cell type-specific transcription units, global run-on sequencing data,

Availability: Free, Available for download, Freely available,

Resource Name: groHMM

Resource ID: SCR_024237

Alternate IDs: OMICS_07953

Alternate URLs: <https://sources.debian.org/src/r-bioc-grohmm/>

Record Creation Time: 20230830T050216+0000

Record Last Update: 20260801T190859+0000

Ratings and Alerts

No rating or validation information has been found for groHMM.

No alerts have been found for groHMM.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.