

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

## groHMM

RRID:SCR\_024237

Type: Tool

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### Proper Citation

groHMM (RRID:SCR\_024237)

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### 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:** 20260905T133106+0000

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### Ratings and Alerts

No rating or validation information has been found for groHMM.

No alerts have been found for groHMM.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.