

# Resource Summary Report

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## Scooby

RRID:SCR\_028110

Type: Tool

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### Proper Citation

Scooby (RRID:SCR\_028110)

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### Resource Information

**URL:** <https://github.com/gagneurlab/scooby/>

**Proper Citation:** Scooby (RRID:SCR\_028110)

**Description:** Software application to predict scRNA-seq coverage and scATAC-seq insertion profiles along the genome at single-cell resolution. It leverages the pre-trained multi-omics profile predictor Borzoi as a foundation model, equips it with a cell-specific decoder, and fine-tunes its sequence embeddings.

**Resource Type:** software application, source code, software resource

**Defining Citation:** [PMID:41125796](#)

**Keywords:** convolutional neural networks, predict RNA-seq coverage, scATAC-seq insertion profiles, Borzoi, cell-specific decoder,

**Funding:** European Research Council ;  
Gene Regulation Observatory at the Broad Institute of MIT & Harvard ;  
NHLBI 5P01HL131477;  
NHGRI UM1 HG011986;  
NHLBI DP2 HL151353;  
German Research Foundation

**Availability:** Free, Available for download, Freely available

**Resource Name:** Scooby

**Resource ID:** SCR\_028110

**License:** MIT license

**Record Creation Time:** 20260314T064515+0000

**Record Last Update:** 20260817T040740+0000

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## Ratings and Alerts

No rating or validation information has been found for Scooby.

No alerts have been found for Scooby.

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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.