

# Package ‘dominatRData’

August 4, 2026

**Type** Package

**Title** Datasets for R Package dominatR

**Version** 1.0.0

**Description** dominatRData is a data package useful for showcasing dominatR examples. dominatR is an R package for quantifying and visualizing feature dominance in datasets. dominatR makes use of entropy-based triangular projections and compositional comparison metrics.

**License** MIT + file LICENSE

**Encoding** UTF-8

**biocViews** ExperimentData, ChIPSeqData, Tissue, PackageTypeData

**LazyData** false

**URL** <https://github.com/VanBortleLab/dominatRData>

**BugReports** <https://github.com/VanBortleLab/dominatRData/issues>

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.2

**Depends** R (>= 4.5.0)

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**git\_url** <https://git.bioconductor.org/packages/dominatRData>

**git\_branch** RELEASE\_3\_23

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**git\_last\_commit\_date** 2026-04-28

**Repository** Bioconductor 3.23

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|--------------------|----------------------------------------------------|
| atac_tissue_counts | <i>ATAC-Seq rawcounts for POL3 Genes Dataframe</i> |
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Description

A list of tissues and the corresponding counts for RNA POL3 genes for each of them.

Usage

```
data('atac_tissue_counts')
```

Format

A dataframe with 9817 rows and 26 variables:

- core\_type** Category for genes based on their expression across tissues
- Chr** Chromosome where the RNA of interest is located
- Start** Gene start coordinate
- End** Gene end coordinate
- Gene** Gene name
- Index** Unique RNA Sequence identifier - Can be retrieved from RNA Central
- Type** Type of RNA POL3 Transcript
- Tissue** Remaining columns contain the name of different assessed tissues

Source

Created by The VanBortle lab at UIUC to serve as an example

References

Simon Lizarazo et al., 2025 bioRxiv Preprint

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|                   |                                                |
|-------------------|------------------------------------------------|
| atac_tissue_score | <i>ATAC-Seq Score for POL3 Genes Dataframe</i> |
|-------------------|------------------------------------------------|

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## Description

A list of tissues and the corresponding counts for RNA POL3 genes for each of them. Values represent a binary call on significance for accessibility. If the value is 1 the gene is accessible in the respective tissue.

## Usage

```
data('atac_tissue_score')
```

## Format

A dataframe with 9817 rows and 23 variables:

**core\_type** Category for genes based on their expression across tissues

**Chr** Chromosome where the RNA of interest is located

**Start** Gene start coordinate

**End** Gene end coordinate

**Gene** Gene name

**Index** Unique RNA Sequence identifier - Can be retrieved from RNA Central

**Type** Type of RNA POL3 Transcript

**Tissue** Remaining columns contain the name of different assessed tissues

## Source

Created by The VanBortle lab at UIUC to serve as an example

## References

Simon Lizarazo et al., 2025 bioRxiv Preprint

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|---------------|--------------------------------------------|
| rnapol_counts | <i>RNA Polymerase raw counts dataframe</i> |
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**Description**

A subset of data obtained from CHIP-Seq Data for RNA Polymerase I, II and III

**Usage**

```
data('rnapol_counts')
```

**Format**

A dataframe with 1061 rows and 7 variables:

- Chr** Chromosome where the gene is located
- Start** Gene start coordinate
- Stop** Gene stop coordinate
- RNA\_Type** Type of transcript
- pol1** Raw counts for RNA Polymerase I Chip-Seq
- pol2** Raw counts for RNA Polymerase II Chip-Seq
- pol3** Raw counts for RNA Polymerase III Chip-Seq

**Source**

Created by The VanBortle lab at UIUC to serve as an example

**References**

Rajendra K C et al., 2024 Molecular Cell

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|              |                                       |
|--------------|---------------------------------------|
| rnapol_score | <i>RNA Polymerase score dataframe</i> |
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**Description**

A subset of data obtained from CHIP-Seq Data for RNA Polymerase I, II and III. Values are represented as the -log10(p-value)

**Usage**

```
data('rnapol_score')
```

### **Format**

A dataframe with 1061 rows and 7 variables:

**Chr** Chromosome where the gene is located

**Start** Gene start coordinate

**Stop** Gene stop coordinate

**RNA\_Type** Type of transcript

**pol1** Score for RNA Polymerase I Chip-Seq

**pol2** Score for RNA Polymerase II Chip-Seq

**pol3** Score for RNA Polymerase III Chip-Seq

### **Source**

Created by The VanBortle lab at UIUC to serve as an example

### **References**

Rajendra K C et al., 2024 Molecular Cell

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