

# Package ‘GSE103322’

May 28, 2026

**Title** GEO accession data GSE103322 as a SingleCellExperiment

**Description** Single cell RNA-Seq data for 5902 cells from 18 patients with oral cavity head and neck squamous cell carcinoma available as GEO accession [GSE103322] (<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE103322>). GSE103322 data have been parsed into a SingleCellExperiment object available in ExperimentHub.

**Version** 1.19.0

**biocViews** ExperimentData, Genome, DNASEqData, RNASeqData, ExperimentData, ExpressionData, RNASeqData, Homo\_sapiens\_Data, CancerData, SingleCellData, GEO, ExperimentHub

**Depends** Biobase, GEOquery

**Suggests** ExperimentHub (>= 0.99.6), knitr, BiocStyle, rmarkdown, SummarizedExperiment, SingleCellExperiment

**License** Artistic-2.0

**VignetteBuilder** knitr

**NeedsCompilation** no

**git\_url** <https://git.bioconductor.org/packages/GSE103322>

**git\_branch** devel

**git\_last\_commit** bc1f79b

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

**Repository** Bioconductor 3.24

**Date/Publication** 2026-05-28

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GSE103322-package      *GEO accession GSE103322 available as an SingleCellExperiment object.*

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### Description

Single cell RNA-Seq data for 5902 cells from 18 patients with oral cavity head and neck squamous cell carcinoma available as GEO accession [GSE103322] (<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE103322>)  
GSE103322 data have been parsed into a SingleCellExperiment object available in ExperimentHub.

### Details

See the vignette for examples of using these data.

```
browseVignettes("GSE103322")
```

Details of how these data were created are in the scripts/ directory of the source package.

### Examples

```
library(ExperimentHub)
hub <- ExperimentHub()
x <- query(hub, "GSE103322")
x
## Not run:
## download resource
sce = x[[1]]

## End(Not run)
```

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\* **utilities**

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