

Single Cell Datasets

Load a single cell data from an online repository.

Outputs

- Data: A single cell dataset containing cells and their gene expression or gene markers.

Single Cell Datasets retrieves a selected data set from the data base server and sends the data to the output. Gene expression data sets include cells in rows and genes in columns. The data set file is downloaded to the local memory, and for subsequent requests instantly available even without the internet connection.

Single Cell Datasets

Info: 18 data sets, No data sets cached

Filter: mouse

Title	Size	Instances	Variables	Target	Tags
Cell Cycle in mESC (Fluidigm)	3.7 MB	182	38294	Categorical	mouse, expression, mesc, mus-musculus
Cell Cycle in mESC (Fluidigm, cell cycle genes)	133.3 KB	182	564	Categorical	mouse, expression, mesc, mus-musculus
Cell Cycle in mESC (QuartzSeq)	666.8 KB	35	36808	Categorical	mouse, expression, mesc, mus-musculus
Cell Cycle in mESC (QuartzSeq, cell cycle genes)	20.3 KB	35	562	Categorical	mouse, expression, mesc, mus-musculus
Cell Cycle in mESC (bulk RNA-seq)	287.0 KB	4	38294	Categorical	mouse, expression, mesc, mus-musculus, rna-seq
Cell Cycle in mESC (bulk RNA-seq, cell cycle genes)	7.0 KB	4	554	Categorical	mouse, expression, mesc, mus-musculus, rna-seq
Cell cycle in T-cells	4.3 MB	81	38293		mouse, expression, tcell, mus-musculus
Cell cycle in T-cells (cell cycle genes)	220.2 KB	81	553		mouse, expression, tcell, mus-musculus
Cell cycle in mouse liver	125.9 KB	5	20683		mouse, expression, liver, mus-musculus
Cell cycle in mouse liver (cell cycle genes)	3.5 KB	5	537		mouse, expression, liver, mus-musculus
Mouse retinal bipolar neurons	11.0 MB	12606	4982	Categorical	expression, mouse, mus-musculus, neuron, drop...
Mouse retinal bipolar neurons (unlabelled)	7.7 MB	6243	6861		expression, mouse, mus-musculus, neuron, drop...

Description: **Cell Cycle in mESC (bulk RNA-seq, cell cycle genes)** (2015), from [ArrayExpress](#)

Mouse embryonic stem cells (mESCs) were FACS sorted for cell cycle stages (G1, S and G2M). Approximately 150,000–300,000 cells from an asynchronous population and from each cell cycle fractions (G1, S and G2M) were used for bulk mRNA sequencing, with libraries being generated using the Illumina TruSeq Stranded RNA Sample preparation kit. All libraries were prepared and sequenced using the Wellcome Trust Sanger Institute sample preparation pipeline. Sequencing quality control and data quality checks were performed by the Sanger Sequencing facility. The reduced data set contains expression of 553 genes related to cell cycle based on Gene Ontology (GO) terms.

See Also: [PMBio / cyclone](#) (GitHub resource).

☒ Send Data Automatically

1. Information on the number of data sets available and the number of them downloaded to the local memory.
2. List of available data sets with information on the number of cells (instances) and genes (variables).
3. Textual description of the selected data set and its source.

4. If *Send Data Automatically* is ticked, selected data set automatically loaded and pushed to the output of the widget. Notice that some data sets are big and downloading them may take time. Alternatively, uncheck the *Send Data Automatically*, browse through the data set list and press *Send Data* upon finding a suitable one for analysis.