

# Package ‘serumStimulation’

October 9, 2025

**Version** 1.44.0

**Date** 2011-08-09

**Title** serumStimulation is a data package which is used by examples in package pcaGoPromoter

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**Description** Contains 13 micro array data results from a serum stimulation experiment

**biocViews** ExperimentData, MicroarrayData

**LazyLoad** yes

**License** GPL (>= 2)

**Depends** R (>= 2.10)

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

**git\_branch** RELEASE\_3\_21

**git\_last\_commit** df629e2

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.21

**Date/Publication** 2025-10-09

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| serumStimulation | <i>Data set from serum stimulation DNA micro array</i> |
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**Description**

The serumStimulation data set is from an DNA micro array analysis of 13 samples from a serum stimulation experiment. There is 5 controls, 5 serum stimulated with inhibitor and 3 serum stimulation without inhibitor.

The original .CEL files have been read with ReadAffy and normalized with rma.

The data is the output of `exprs( rma( ReadAffy() ) )`

**Usage**

```
serumStimulation
```

**Format**

See `exprs` for description of output.

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## \* **datasets**

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