

# Package ‘serumStimulation’

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**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>

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## R topics documented:

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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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