

# Package ‘serumStimulation’

October 17, 2024

**Version** 1.40.0

**Date** 2011-08-09

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

**Author** Morten Hansen <mhansen@sund.ku.dk>

**Maintainer** Morten Hansen, <mhansen@sund.ku.dk>

**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\_19

**git\_last\_commit** 118dd67

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.19

**Date/Publication** 2024-10-17

## Contents

serumStimulation . . . . .	2
<b>Index</b>	<b>3</b>

---

serumStimulation	<i>Data set from serum stimulation DNA micro array</i>
------------------	--

---

**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.

# Index

\* **datasets**

serumStimulation, [2](#)

serumStimulation, [2](#)