

# stjudem

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stjude

*Microarray Data from St.Jude Children Research Hospital (USA)*

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## Description

Example for list-structure used by many functions in MACAT. It's based on the gene expression data published by Yeoh et al. in 2002.[Yeoh et al. Classification, subtype discovery, and prediction of outcome in pediatric acute lymphoblastic leukemia by gene expression profiling. Cancer Cell. March 2002. 1: 133-143. The data has been preprocessed using 'vsn' on probe level and the probes have been summed up using 'median polish'.

## Usage

```
data(stjude)
```

## Format

List of class 'MACATData' with 6 components:

**geneName:** Identifiers of genes/probe sets in expression data

**geneLocation:** Location of genes on their chromosome as distance from 5'end in base pairs Negative numbers denote genes on the antisense strand.

**chromosome:** Chromosome of the respective gene. Components 'geneName', 'geneLocation', and 'chromosome' are in the same order.

**expr:** expression matrix with rows = genes and columns = samples/patients

**labels:** (disease) subtype of each sample, has length = number of columns of expression matrix

**chip:** Identifier for Microarray used for the experiments (here for the Affymetrix HG-U95av2 Oligonucleotide GeneChip)

## Source

Yeoh et al. Classification, subtype discovery, and prediction of outcome in pediatric acute lymphoblastic leukemia by gene expression profiling. Cancer Cell. March 2002. 1: 133-143.

## Examples

```
data(stjude)
summary(stjude)
```

# Index

\*Topic **datasets**

stjude, 1

stjude, 1