

# Package ‘DLBCL’

April 11, 2019

**Type** Package

**Title** Diffuse large B-cell lymphoma expression data

**Version** 1.22.0

**Date** 2010-03-26

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**Description** This package provides additional expression data on diffuse large B-cell lymphomas for the BioNet package.

**License** GPL (>=2)

**Depends** R(>= 2.11.0), Biobase

**LazyLoad** yes

**URL** <http://bionet.bioapps.biozentrum.uni-wuerzburg.de/>

**biocViews** ExperimentData, CancerData, MicroarrayData, ChipOnChipData

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

**git\_branch** RELEASE\_3\_8

**git\_last\_commit** 1deae00

**git\_last\_commit\_date** 2018-10-30

**Date/Publication** 2019-04-11

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DLBCL-package

*Routines for the functional analysis of biological networks*

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**Description**

This package provides an expression set on diffuse large B-cell lymphoma and an protein-protein interaction network obtained from HPRD release 6. It accompanies the BioNet packages as example data. For further information on the data and the BioNet package, see references below.

**Details**

Package: DLBCL  
Type: Package  
Version: 1.2  
Date: 2010-03-26  
License: GPL (>=2)  
LazyLoad: yes

**Author(s)**

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**References**

M. T. Dittrich, G. W. Klau, A. Rosenwald, T. Dandekar and T. Mueller (2008) Identifying functional modules in protein-protein interaction networks: an integrated exact approach. (*ISMB2008*) *Bioinformatics* 24: 13. i223-i231 Jul.

D. Beisser, G. W. Klau, T. Dandekar, T. Mueller and M. Dittrich (2009) BioNet: an R-package for the Functional Analysis of Biological Networks. *Bioinformatics*.

A. A. Alizadeh, M. B. Eisen, R. E. Davis et al. (2000) Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. *Nature* 403: 503-11.

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dataLym*Additional data for the lymphoma microarray chip (exprLym)*

---

**Description**

The dataset contains additional data for the exprLym dataset. It includes p-values for the gene expression, p-values for the survival data, an example score etc.

**Usage**

```
data(dataLym)
```

## References

A. Rosenwald et al. (2002). The use of molecular profiling to predict survival after chemotherapy for diffuse large-B-cell lymphoma. *N Engl J Med*, 346(25), 1937-1947.

## Examples

```
data(dataLym)
str(dataLym)
```

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exprLym

*Expression set diffuse large B-cell lymphomas*

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## Description

The dataset contains an expression set on diffuse large B-cell lymphoma. It accompanies the BioNet packages as example data. For further information on the data and the BioNet package see:

M. T. Dittrich, G. W. Klau, A. Rosenwald, T. Dandekar and T. Mueller (2008) Identifying functional modules in protein-protein interaction networks: an integrated exact approach. (*ISMB2008*) *Bioinformatics* 24: 13. i223-i231 Jul.

D. Beisser, G. W. Klau, T. Dandekar, T. Mueller and M. Dittrich (2009) BioNet: an R-package for the Functional Analysis of Biological Networks. *Bioinformatics*.

A. A. Alizadeh, M. B. Eisen, R. E. Davis et al. (2000) Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. *Nature* 403: 503-11.

## Usage

```
data(exprLym)
```

## Examples

```
data(exprLym)
exprs(exprLym)[1:10,]
```

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interactome

*Human protein-protein interaction network*

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## Description

The dataset contains the human proteome, extracted from the Human Protein Reference Database (HPRD) from 2006 that is used in the ABC GCB diffuse large B-cell lymphoma analysis. The format of the dataset is a graph object.

## Usage

```
data(interactome)
```

**References**

M. T. Dittrich, G. W. Klau, A. Rosenwald, T. Dandekar, T. Mueller (2008) Identifying functional modules in protein-protein interaction networks: an integrated exact approach. (*ISMB2008*) *Bioinformatics*, 24: 13. i223-i231 Jul.

**Examples**

```
data(interactome)
interactome
```

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