

# Package ‘DLBCL’

October 31, 2024

**Type** Package

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

**Version** 1.47.0

**Date** 2010-03-26

**Author** Marcus Dittrich and Daniela Beisser

**Maintainer** Marcus Dittrich <marcus.dittrich@biozentrum.uni-wuerzburg.de>

**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, graph

**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** devel

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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)**

Marcus Dittrich, Daniela Beisser

Maintainer: Marcus Dittrich <marcus.dittrich@biozentrum.uni-wuerzburg.de>

**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	<i>Additional data for the lymphoma microarray chip (exprLym)</i>
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**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	<i>Expression set diffuse large B-cell lymphomas</i>
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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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