

# Package ‘DLBCL’

January 22, 2026

**Type** Package

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

**Version** 1.51.0

**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, 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

**git\_last\_commit** f638520

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.23

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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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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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