

# Package ‘DMarkerData’

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**Version** 1.0

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**Author** Yu Shang, Qiong Yu, Wei Du, Ying Xu

**Maintainer**

Yu Shang <yushang@uga.edu>, Qiong Yu <yuqiong@uga.edu>, Wei Du <weidu@uga.edu>

**Correspond** Ying Xu <xyn@bmb.uga.edu>

**Title** DMarkerData

**Description** DMarkerData is a package for sequences predict in DMarker package.

**Type** Package

**License** GPL (>= 2)

**LinkingTo** Rcpp

**LazyLoad** yes

**LazyData** true

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## Description

DMarkerData is a package for sequences predict in DMarker package.

The main dataset of the package is data(proseq), and the more details you can find in [proseq](#)

**Details**

Package: proseq  
Type: Package  
Version: 1.0  
Date: 2015-05-27  
License: GPL (>= 2)  
LazyLoad: yes  
LazyData: true

**Author(s)**

Yu Shang (JLU & UGA) <yushang@uga.edu>  
Qiong Yu (JLU & UGA) <yuqiong@uga.edu>  
Wei Du (JLU & UGA) <weidu@uga.edu>  
Ying Xu (JLU & UGA) <xyn@bmb.uga.edu>

Maintainer: Yu Shang (JLU & UGA) <yushang@uga.edu>

**References**

- [1] Yan Wang, et al. (2009) *DMarker: A Bio-Marker Inference System for Human Diseases based on Microarray Gene Expression Data* 2009
- [2] Juan Cui, et al. (2008) *Computational prediction of human proteins that can be secreted into the bloodstream* BIOINFORMATICS, Vol.24 no. 20 2008 pages 2370-2375
- [3] Jiaxin Wang, et al. (2013) *Computational Prediction of Human Salivary Proteins from Blood Circulation and Application to Diagnostic Biomarker Identification* PLoS ONE, DOI: 10.1371/journal.pone.0080211, 2013
- [4] S Hong, et al. (2011) *A Computational Method for Prediction of Excretory Proteins and Application to Identification of cancer markers in urine and application to gastric cancer* PLoS ONE,6(2):e16875, 2011
- [5] <http://bioinfosrv1.bmb.uga.edu/DMarker/>

**See Also**

[proseq](#)

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proseq

*DMarkerData for DMarker*

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**Description**

DMarkerData for DMarker

**Usage**

```
data(proseq)
```

**Format**

The format is: num [1:19905] ... - attr(\*, "dimnames")=List of 3 ..\$ : Class 'SeqFastadna' atomic  
... ..\$ : "name" ... ..\$ : "Annot" ... ..\$ : "class" ...

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Yu Shang (JLU & UGA) <yushang@uga.edu>

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Ying Xu (JLU & UGA) <xyn@bmb.uga.edu>

Maintainer: Yu Shang (JLU & UGA) <yushang@uga.edu>

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[1] Yan Wang, et al. (2009) *DMarker: A Bio-Marker Inference System for Human Diseases based on Microarray Gene Expression Data* 2009

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[5] <http://bioinfosrv1.bmb.uga.edu/DMarker/>

**See Also**

[DMarkerData-package](#)

**Examples**

```
data(proseq);
```

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