# Package 'DDMarkerData'

August 1, 2016

**Type** Package

**Title** A Homo Sapiens Annotation Database for Diagnose and Detect Markers in Extracellular Circulating

**Version** 1.0

**Date** 2015-05-27

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**Description** A database is called HSAD, IFF, it entails the symbols among the genes, the proteins, the micro RNAs, the isoforms and their sequences by a deductive system.

**License** GPL (>= 2)

**LazyData** TRUE

## R topics documented:

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DDMarkerData-package     *A Homo Sapiens Annotation Database for Diagnose and Detect Markers in Extracellular Circulating*

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### Description

A database is called HSAD, IFF, it entails the symbols among the genes, the proteins, the micro RNAs, the isoforms and their sequences by a deductive system.

The main dataset of the package is data(EC0), and the more details you can find in EC ( EC0 ), it is the superset of the dataset EC from DDMarker ( ECV1 ), helpping DDMarker to diagnose and detect the sequence among the micro RNAs, the genes, the proteins, and the isoforms.

The hyperlink dataset of the package is data(MMC0), Minimal Metabolize Circulation, and the more details you can find in MMC0, it comes from the package DDMarkerMMC

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**Details**

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

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**References**

citation("DDMarkerData");
[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**

EC0 MMC0 EC1

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| EC0 | *A Homo Sapiens Annotation Database for Diagnose and Detect Markers in Extracellular Circulating* |

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## Description

A database is called HSAD, IFF, it entails the symbols among the genes, the proteins, the micro RNAs, the isoforms and their sequences by a deductive system.

## Usage

```
data(EC)
```

## Format

The format is: Large list [10 elements, 60.5 Mb] ... - attr(*, "dimnames")=List of 10 ..$Mi : "character" ... ..$G : "numeric" ... ..$P : "numeric" ... ..$HSAD : "list" ... ..$V : "numeric" ... ..$BG : "list" ... ..$BP : "list" ... ..$UG : "list" ... ..$UP : "list" ... ..$MS : "list" ...

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[5] http://bioinfosrv1.bmb.uga.edu/DMarker/
[6] Francesco Russo, et al. (2012) *miRandola: Extracellular Circulating MicroRNAs Database* PLoS ONE 2012, 7(10): e47786, 2012
[7] Francesco Russo, et al. (2014) *A knowledge base for the discovery of function, diagnostic*

*potential and drug effects on cellular and extracellular miRNAs* BMC Genomics 2014, 15(Suppl 3):S4, 2014

## See Also

[DDMarkerData-package](DDMarkerData-package)

## Examples

```
data(EC0);
```

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EC1                          *A Homo Sapiens Annotation Database Version One for Diagnose and Detect Markers in Extracellular Circulating*

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## Description

A database is called HSAD V1, IFF, it entails the symbols among the genes, the proteins, the micro RNAs, and the isoforms by a deductive system.

## Usage

```
data(DDMarkerEC)
```

## Format

The format is: Large list [5 elements, 18.1 Mb] ... - attr(*, "dimnames")=List of 5 ..$Mi : "character" ... ..$G : "numeric" ... ..$P : "numeric" ... ..$HSAD : "list" ... ..$V : "numeric" ...

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## See Also

DDMarkerData-package

## Examples

```
data(EC1);
```

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| MMC0 | *Minimal Metabolize Circulation for Diagnose and Detect Markers in Extracellular Circulating* |
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## Description

DMarkerData for DMarker

## Usage

```
data(MMC)
```

## Format

The format is: Large list [5 elements, 7.8 Mb] ... - attr(*, "dimnames")=List of 5 ..$TCGA : "character" ... ..$gene : "numeric" ... ..$DDMarkerUN : "character" ... ..$DDMarkerKEGG : "list" ... ..$V : "numeric" ...

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

## See Also

DDMarkerData-package

## Examples

```
data(MMC0);
```

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