

# lumiMouseIDMapping

February 3, 2010

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lumiMouseIDMapping\_dbconn

*Collect information about the package annotation DB*

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## Description

Some convenience functions for getting a connection object to (or collecting information about) the package annotation DB.

## Usage

```
lumiMouseIDMapping_dbconn ()
lumiMouseIDMapping_dbfile ()
lumiMouseIDMapping_dbInfo ()
```

## Details

lumiMouseIDMapping\_dbconn returns a connection object to the package annotation DB.  
**IMPORTANT: Don't call `dbDisconnect` on the connection object returned by lumiMouseIDMapping\_dbconn or you will break all the `AnnDbObj` objects defined in this package!**

lumiMouseIDMapping\_dbfile returns the path (character string) to the package annotation DB (this is an SQLite file).

lumiMouseIDMapping\_dbInfo prints other information about the package annotation DB.

## Value

lumiMouseIDMapping\_dbconn: a DBIConnection object representing an open connection to the package annotation DB.

lumiMouseIDMapping\_dbfile: a character string with the path to the package annotation DB.

lumiMouseIDMapping\_dbInfo: none (invisible NULL).

## See Also

[dbConnect](#)

## Examples

```
## Show the database information (meta data)
lumiMouseIDMapping_dbInfo()

## List the tables included in the database
conn <- lumiMouseIDMapping_dbconn()
dbListTables(conn)
```

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lumiMouseIDMapping\_nuID

*Mapping nuIDs of Illumina Mouse chips to the most recent Mus musculus RefSeq release*

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## Description

We mapped nuIDs of Illumina Mouse chips by BLASTing each probe sequence (converted from nuID) against the the most recent Mus musculus RefSeq release. The mapping also includes the mapping quality information.

## Usage

```
lumiMouseIDMapping_nuID()
```

## Details

The nuID mapping information is kept in the nuID\\_MappingInfo table in the ID Mapping library. The nuID mapping table includes following fields (columns):

1. nuID: nuID for the probe sequence
2. Refseq: The refseq IDs with perfect matching with probe sequence. If there are more than one refseq IDs, they are separated by ",".
3. EntrezID: The Entrez gene IDs correspond to the refseq IDs. If there are more than one Entrez gene IDs, they are separated by ",".
4. QualityScore: The mapping quality from probe sequence to RefSeq, see reference 2 for more details.
5. Refseq\\_old: the refseq ID provided by Illumina company when they designed the chip (included in the chip manifest file).

For the version after 1.4.0, the mapping information was got from the Computational Biology Group at University of Cambridge, see reference link for more details.

## Value

lumiMouseIDMapping\_nuID returns a nuID mapping summary of Illumina Mouse chips.

## References

1. Du, P., Kibbe, W.A. and Lin, S.M., "nuID: A universal naming schema of oligonucleotides for Illumina, Affymetrix, and other microarrays", *Biology Direct* 2007, 2:16 (31May2007). 2. <http://www.compbio.group.cam.ac.uk/Resources/Annotation/index.html>

**Examples**

```
## List the fields in the nuID_MappingInfo table
conn <- lumiMouseIDMapping_dbconn()
dbListFields(conn, 'nuID_MappingInfo')

## Summary of nuID mapping
lumiMouseIDMapping_nuID()
```

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*lumiMouseIDMapping* *Illumina ID Mapping information of all Mouse expression chips*

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**Description**

Welcome to the lumiMouseIDMapping ID mapping Package. The purpose of this package is to provide ID mappings between different types of Illumina identifiers of Mouse Expression chips and nuIDs, and also mappings from nuIDs to the the most recent *Mus musculus* RefSeq release. The library includes the data tables corresponding to all released Illumian Mouse Expression chips before the package releasing date. Each table includes columns "Search\\_key" ("Search\\_Key"), "Target" ("ILMN\\_Gene"), "Accession", "Symbol", "ProbeId" ("Probe\\_Id") and "nuID". It also includes a nuID\\_MappingInfo table, which keeps the mapping information of nuID to RefSeq ID and its related mapping quality information. For the version after 1.4.0, the mapping information was got from the Computational Biology Group at University of Cambridge, see reference link for more details. Another table, metadata, keeps other information, like RefSeq version, species. The package is supposed to be used together with the Bioconductor lumi package.

You can learn what objects this package supports with the following command:

```
ls("package:lumiMouseIDMapping")
```

Each of these objects has their own manual page detailing where relevant data was obtained along with some examples of how to use it.

**References**

1. <http://www.compbio.group.cam.ac.uk/Resources/Annotation/index.html>

**Examples**

```
ls("package:lumiMouseIDMapping")
```

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