

# Package ‘QUBICdata’

October 8, 2016

**Type** Package

**Title** Data employed in the vignette of the QUBIC package

**Description** The data employed in the vignette of the QUBIC package. These data belong to the Many Microbe Microarrays Database.

**VignetteBuilder** knitr

**biocViews** Escherichia\_coli\_Data, OrganismData, ExperimentData

**Version** 1.0.2

**License** Unlimited | file LICENSE

**Depends** R (>= 3.1)

**Suggests** knitr, rmarkdown

**URL** <http://github.com/zy26/QUBICdata>

**BugReports** <http://github.com/zy26/QUBICdata/issues>

**NeedsCompilation** no

**Author** Yu Zhang [aut, cre],  
Qin Ma [aut]

**Maintainer** Yu Zhang <zy26@jlu.edu.cn>

## R topics documented:

ecoli . . . . .	2
<b>Index</b>	<b>3</b>

---

ecoli

*E.coli*

---

**Description**

Gene expression data matrix for experiments with E.coli from Many Microbe Microarrays Database (M3D).

**Usage**

```
data("ecoli")
```

**Format**

Data frame with information about the expression levels of 4297 genes over 466 conditions.

**Source**

<http://m3d.mssm.edu/>

**References**

Faith, JJ et al. (2008) Many Microbe Microarrays Database: uniformly normalized Affymetrix compendia with structured experimental metadata. *Nucleic Acids Res.* 36 D866-70

**Examples**

```
data(ecoli)
## maybe str(ecoli) ; plot(ecoli) ...
```

# Index

\*Topic **datasets**

ecoli, [2](#)

ecoli, [2](#)