

# Package ‘frmaExampleData’

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**Title** Frma Example Data

**Version** 1.36.0

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**Author** Matthew N. McCall <mmccall@jhsp.h.edu>

**Description** Data files used by the examples in frma and frmaTools packages

**Maintainer** Matthew N. McCall <mmccall@jhsp.h.edu>

**Depends** R (>= 2.10.0)

**License** GPL (>= 2)

**biocViews** Homo\_sapiens\_Data, MicroarrayData

**git\_url** <https://git.bioconductor.org/packages/frmaExampleData>

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**Description**

An example AffyBatch for use with frmaTools.

**Usage**

```
data(AffyBatch133a)
```

**Examples**

```
data(AffyBatch133a)
```

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|                  |                                |
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| AffyBatch133atag | <i>HGU133atag Example Data</i> |
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**Description**

An example AffyBatch for use with frmaTools.

**Usage**

```
data(AffyBatch133atag)
```

**Examples**

```
data(AffyBatch133atag)
```

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|                   |                                 |
|-------------------|---------------------------------|
| AffyBatch133plus2 | <i>HGU133plus2 Example Data</i> |
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**Description**

An example AffyBatch for use with frmaTools.

**Usage**

```
data(AffyBatch133plus2)
```

**Examples**

```
data(AffyBatch133plus2)
```

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| AffyBatchExample | <i>AffyBatch Example Data</i> |
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**Description**

An example AffyBatch for use with frma.

**Usage**

```
data(AffyBatchExample)
```

**Examples**

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data(AffyBatchExample)
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