# Package 'bodenmiller'

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**Type** Package

**Title** Profiling of Peripheral Blood Mononuclear Cells using CyTOF

**Version** 0.1.1

**Depends** R (>= 3.1.0)

**Suggests** ggplot2, cytofan, dplyr, reshape2, RColorBrewer, knitr, rmarkdown

**Description**
This data package contains a subset of the Bodenmiller et al, Nat Biotech 2012 dataset for testing single cell, high dimensional analysis and visualization methods.

**License** CC0

**Encoding** UTF-8

**LazyData** TRUE

**LazyDataCompression** xz

**URL** https://github.com/yannabraham/bodenmiller

**BugReports** https://github.com/yannabraham/bodenmiller/issues

**VignetteBuilder** knitr

**RoxygenNote** 7.1.1

**NeedsCompilation** no

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**Repository** CRAN

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`refAnnots` *Reference Annotation*

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## Description

A `data.frame` containing the source file and cell type for every cell in `refPhenoMat` and `refFuncMat`. See Bodenmiller et al 2012 for details.

## Usage

```
refAnnots
```

## Format

a data.frame with 15792 rows and 2 variables:

- Sourcethe name of the source (fcs) file
- Cellsthe cell type for the corresponding row in `refPhenoMat` or `refFuncMat`

## Source

`https://reports.cytobank.org/105/v2/`

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`refFuncMat` *Reference Matrix (Functional)*

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## Description

a `matrix` containing the signal intensity for functional markers measured using CyTOF on different cell types. See Bodenmiller et al 2012 for details.

## Usage

```
refFuncMat
```

### Format

a matrix with 15792 rows and 14 variables:

- pStat1
- pSlp76
- pBtk
- pPlcg2
- pErk
- pLat
- pS6
- pNFkB
- pp38
- pStat5
- pAkt
- pSHP2
- pZap70
- pStat3

### Source

https://reports.cytobank.org/105/v2/

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## refPhenoMat *Reference Matrix (Phenotypic)*

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### Description

a `matrix` containing the signal intensity for phenotypic markers measured using CyTOF on different cell types. See Bodenmiller et al 2012 for details.

### Usage

```
refPhenoMat
```

### Format

a matrix with 15792 rows and 9 variables:

- CD20
- IgM
- CD4
- CD33

- HLA-DR
- CD14
- CD7
- CD3
- CD123

## Source

https://reports.cytobank.org/105/v2/

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`untreatedAnnots` *Untreated Samples with 4 Different Treatments (Annotation)*

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## Description

A `data.frame` containing the source file, cell type and stimulation for every cell in `refPhenoMat` and `refFuncMat`. Stimulations include BCR/FcR-XL, PMA/Ionomycin and vanadate.See Bodenmiller et al 2012 for details.

## Usage

```
untreatedAnnots
```

## Format

a data.frame with 15792 rows and 2 variables:

- Sourcethe name of the source (fcs) file
- Treatmentthe treatment for the corresponding row in `refPhenoMat` or `refFuncMat`
- Cellsthe cell type for the corresponding row in `refPhenoMat` or `refFuncMat`

## Source

https://reports.cytobank.org/105/v2/

`untreatedFuncMat` *Untreated Samples with 4 Different Treatments (Functional)*

## Description

a `matrix` containing the signal intensity for functional markers measured using CyTOF on different cell types, after stimulation with BCR/FcR-XL, PMA/Ionomycin and vanadate. See Bodenmiller et al 2012 for details.

## Usage

```
untreatedFuncMat
```

## Format

a matrix with 15792 rows and 14 variables:

- pStat1
- pSlp76
- pBtk
- pPlcg2
- pErk
- pLat
- pS6
- pNFkB
- pp38
- pStat5
- pAkt
- pSHP2
- pZap70
- pStat3

## Source

https://reports.cytobank.org/105/v2/

`untreatedPhenoMat` *Untreated Samples with 4 Different Treatments (Phenotypic)*

## Description

a `matrix` containing the signal intensity for phenotypic markers measured using CyTOF on different cell types, after stimulation with BCR/FcR-XL, PMA/Ionomycin and vanadate. See Bodenmiller et al 2012 for details.

## Usage

```
untreatedPhenoMat
```

## Format

a matrix with 15792 rows and 9 variables:

- CD20
- IgM
- CD4
- CD33
- HLA-DR
- CD14
- CD7
- CD3
- CD123

## Source

https://reports.cytobank.org/105/v2/

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