

# 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, cytofان, 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	<i>Reference Annotation</i>
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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:

- Source the name of the source (fcs) file
- Cell the cell type for the corresponding row in [refPhenoMat](#) or [refFuncMat](#)

### Source

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

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refFuncMat	<i>Reference Matrix (Functional)</i>
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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)*

---

**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)*

---

### 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:

- Source the name of the source (fcs) file
- Treatment the treatment for the corresponding row in [refPhenoMat](#) or [refFuncMat](#)
- Cell the cell type for the corresponding row in [refPhenoMat](#) or [refFuncMat](#)

### Source

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

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

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**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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