

# Package ‘EZsinglecell2’

January 7, 2022

**Title** Wrap up for routine single cell analysis

**Version** 0.0.0.9000

**Description** Wrap up for routine single cell analysis (one paragraph).

**Imports** EnsDb.Hsapiens.v86,Seurat,Signac,dplyr,ggplot2

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**Encoding** UTF-8

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ATAC_Wrapper	<i>Wrap Seurat ATAC clustering</i>
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## Description

This function allows you to perform standard sc-ATAC clustering

## Usage

```
ATAC_Wrapper(MTX, res = 0.3)
```

## Arguments

MTX	sparse Matrix of class "dgCMatrix", each row is a peak, each column is a cell,
res	clustering resolution, default=0.5

**Value**

this returns seurat object with ATAC clustering

**Examples**

```
bmmc.filtered.atac<-SeuratLSIClustering(PeakVSCell.filtered.Mtx) #each row is a peak, each column is a cell
```

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GEM_Wrapper	<i>Wrap Seurat RNA clustering</i>
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**Description**

This function allows you to perform standard sc-RNA clustering

**Usage**

```
GEM_Wrapper(mtx = bmmc.data$`Gene Expression`, exp = "DN1_BMMC1", res = 0.5)
```

**Arguments**

mtx	sparse Matrix of class "dgCMatrx", each row is a gene, each column is a cell,
exp	The name of this sample/experiment
res	clustering resolution, default=0.5

**Value**

this returns seurat object with RNA clustering

**Examples**

```
bmmc.data=Read10X(data.dir = "XX/CellRanger/Donor01_BMMC_1/outs/filtered_feature_bc_matrix")
docluster_GEM(mtx=bmmc.data$`Gene Expression`, exp="DN1_BMMC1")
```

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Multi_Wrapper	<i>Wrap Seurat Multiomics clustering</i>
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**Description**

This function allows you to perform standard sc-multiome clustering

**Usage**

```
Multi_Wrapper(
  path = "/lab/solexa_weissman/cweng/Projects/MitoTracing_Velocity/SecondaryAnalysis"
)
```

**Arguments**

path	this should be the path to the cell-ranger results XX/outs
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**Value**

this returns seurat object with both RNA and ATAC

**Examples**

```
MultiWrapper(path="XX/CellRanger/Donor01_BMMC_1/outs/")
```

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Tomerge_v2	<i>Tomerge_v2</i>
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**Description**

This function is to quickly merge two dataframe by rownames, but can choose to leave A or B all information

**Usage**

```
Tomerge_v2(A, B, leavex = T, leavey = F)
```

**Arguments**

A	dataframe A
B	dataframe B

**Value**

return a data frame with merged information

**Examples**

```
Tomerge_v2(A,B)
```

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