

Package: FlowSorted.DLPFC.450k (via r-universe)

October 10, 2026

Version 1.49.2

Title Illumina HumanMethylation Data on Sorted Frontal Cortex Cell Populations

Description Provides a function to download (and cache locally via BiocFileCache) a data object for the Illumina 450k DNA methylation microarrays. The underlying data is hosted on Zenodo.

License Artistic-2.0

Depends R (>= 4.0.0), minfi (>= 1.21.2)

Imports BiocFileCache, tools

biocViews ExperimentData, Homo_sapiens_Data, Tissue, MicroarrayData, TissueMicroarrayData, MethylationArrayData

Config/pak/sysreqs make libbz2-dev libicu-dev liblzma-dev libpng-dev libxml2-dev libssl-dev libx11-dev xz-utils zlib1g-dev

Repository <https://bioc.r-universe.dev>

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RemoteUrl <https://github.com/bioc/FlowSorted.DLPFC.450k>

RemoteRef HEAD

RemoteSha 5ce8b4ed6f5357b860bcffb984bce1e7eb3b6865

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FlowSorted.DLPFC.450k *Illumina Human Methylation data from 450k on sorted frontal cortex cell populations*

Description

This function downloads (once; cached locally afterwards via [BiocFileCache](#)) and returns an `RGChannelSet` containing Illumina 450k DNA methylation measurements on 58 flow-sorted dorsolateral prefrontal cortex samples from non-psychiatric controls from Guintivano et al. 2013. These samples were separated into neuronal (NeuN+) and non-neuronal (NeuN-) cell types. These data can be used by the [minfi](#) package to estimate cellular composition from bulk frontal cortex samples. This data may also be useful to individuals as example Illumina 450k data for trying preprocessing methods across a variety of Bioconductor packages.

As of package version 1.49.2, this data is no longer bundled directly with the package; it is hosted on Zenodo ([doi:10.5281/zenodo.21998569](https://doi.org/10.5281/zenodo.21998569)) and downloaded on first use.

Usage

```
FlowSorted.DLPFC.450k
```

Details

The `FlowSorted.DLPFC.450k` object is based on samples assayed as part of Guintivano et al (2013). Please cite this paper, if the data is used. If you're using this data together with the [minfi](#) package, please see the package vignette for details on how to cite that package.

Value

An object of class `RGChannelSet`.

References

Guintivano J., Aryee M.J., Kaminsky Z.A. *A cell epigenotype specific model for the correction of brain cellular heterogeneity bias and its application to age, brain region and major depression*. Epigenetics (2013), 8(3):290-302. [doi:10.4161/epi.23924](https://doi.org/10.4161/epi.23924).

Examples

```
library(FlowSorted.DLPFC.450k)
rgset <- FlowSorted.DLPFC.450k
```

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* **datasets**

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