

# Package ‘FlowSorted.DLPFC.450k’

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**Version** 1.24.0

**Title** Illumina HumanMethylation data on sorted frontal cortex cell populations

**Description** Raw data objects for the Illumina 450k DNA methylation microarrays.

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**License** Artistic-2.0

**Depends** R (>= 2.13.0), minfi (>= 1.21.2)

**LazyData** yes

**biocViews** ExperimentData, Homo\_sapiens\_Data, Tissue, MicroarrayData, TissueMicroarrayData, MethylationArrayData

**git\_url** <https://git.bioconductor.org/packages/FlowSorted.DLPFC.450k>

**git\_branch** RELEASE\_3\_11

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**Date/Publication** 2020-10-12

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

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## Description

This RChannelSet contains 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.

**Usage**

```
data(FlowSorted.DLPFC.450k)
```

**Format**

An object of class `RGChannelSet`.

**Details**

The `FlowSorted.DLPFC.450k` objects 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.

**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**

```
data(FlowSorted.DLPFC.450k)
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