

# Package ‘FlowSorted.DLPFC.450k’

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**Version** 1.4.0

**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

**LazyData** yes

**biocViews** Homo\_sapiens\_Data, MicroarrayData

**NeedsCompilation** no

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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 RGset 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 type. 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 RGset.

**Details**

The FlowSorted.DLPFC.450k objects is based an samples assayed as part of Guintivano et al (2013).

**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 Mar;8(3):290-302. <http://www.landesbioscience.com/journals/epi/abstract.php?id=23924>

**Examples**

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