

# Package ‘SpikeInSubset’

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**Title** Part of Affymetrix’s Spike-In Experiment Data

**Version** 1.2.12

**Author** Rafael Irizarry <rafa@jhu.edu> and Zhijin Wu

**Description**

Includes probe-level and expression data for the HGU133 and HGU95 spike-in experiments

**Maintainer** Rafael A. Irizarry <rafa@jhu.edu>

**License** LGPL

**Depends** R (>= 2.4.0), Biobase (>= 2.5.5), affy (>= 1.23.4)

**biocViews** ExperimentData

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hgu133a.spikein.xhyb    *Cross hybridizers*

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## Description

Probe Sets likely to crosshybridize to spiked-in probesets in the Affymetrix HGU133A spike in  
This object is list. Each component of the list contains probeset names of possible crosshybridizers.  
The sequences of each spiked-in clone were collected and blasted against all HG-U133A target  
sequences. Target sequences are the ~600bp regions from which probes were selected. Thresholds  
of 100, 150 and 200bp were used and define the three components of the list.

## Usage

```
data(hgu133a.spikein.xhyb)
```

## Format

A list

**Source**

Simon Cawley <simon\_cawley@affymetrix.com>

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SpikeIn

*Subset of Affymetrix SpikeIn Experiment Data*

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**Description**

Probe-level and pre-processed data for six arrays (two triplicates) from the HGU95 and HGU133 SpikeIn experiments.

**Usage**

```
data(spikein95)
data(rma95)
data(mas95)
```

```
data(spikein133)
data(rma133)
data(mas133)
```

**Format**

SpikeIn is [ProbeSet](#) containing the \$PM\$ and \$MM\$ intensities for a gene spiked in at different concentrations. Use pData to see the concentrations.

**Source**

spikein95 and spikein133 are instances of [ProbeSet](#) with the probe-level data for six arrays (two triplicates) from the HGU95 and HGU133 SpikeIn experiments respectively. rma95 and rma133 contain the data pre-processed with RMA. mas95 and mas133 contain the data preprocessed with mas5 (expression and present/absent calls). The calls are in objects called pacalls95 and pacalls133.

For more information see Irizarry, R.A., et al. NAR (2003) <http://www.biostat.jhsph.edu/~ririzarr/papers/index.html>

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