

# SpikeInSubset

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SpikeIn	<i>Subset of Affymetrix SpikeIn Experiment Data</i>
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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 pre-processed 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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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**

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