

# Package ‘gcspikelite’

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**Title** Spike-in data for GC/MS data and methods within flagme

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**Depends** R (>= 2.5.0)

**Description** Spike-in data for GC/MS data and methods within flagme

**License** LGPL

**biocViews** MassSpectrometryData

**git\_url** <https://git.bioconductor.org/packages/gcspikelite>

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## R topics documented:

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targets	<i>Targets file for gcspikelite data.</i>
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### Description

List of filenames and experimental group

### Usage

```
data(targets)
```

**Format**

Data frame with columns:

Filename a character vector

Group a character vector

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\* **datasets**  
    targets, 1

targets, 1