

# Package ‘gcspikelite’

April 11, 2023

**Version** 1.36.0

**Date** 2010/10/16

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

**Author** Mark Robinson <mrobinson@wehi.edu.au>

**Maintainer** Mark Robinson <mrobinson@wehi.edu.au>

**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>

**git\_branch** RELEASE\_3\_16

**git\_last\_commit** aecba87

**git\_last\_commit\_date** 2022-11-01

**Date/Publication** 2023-04-11

## 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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