

# Package ‘gcspikelite’

January 16, 2025

**Version** 1.44.0

**Date** 2010/10/16

**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>

**git\_branch** RELEASE\_3\_20

**git\_last\_commit** d4c95a8

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.20

**Date/Publication** 2025-01-16

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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

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