

Package ‘bugsigdbr’

July 7, 2025

Version 1.15.3

Title R-side access to published microbial signatures from BugSigDB

Description The bugsigdbr package implements convenient access to bugsigdb.org from within R/Bioconductor. The goal of the package is to facilitate import of BugSigDB data into R/Bioconductor, provide utilities for extracting microbe signatures, and enable

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`browseTaxon`*Displaying BugSigDB taxon pages in a web browser*

Description

Functionality for programmatically displaying BugSigDB taxon pages.

Arguments

sig character. Microbe signature containing taxonomic clades in MetaPhlAn format.

tax.id.type Character. Taxonomic ID type of the returned microbe sets. Either "metaphlan" (default) or "taxname".

getOntology	<i>Obtain the EFO and UBERON ontology</i>
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Usage

```
getSignatures(

```


Release v1.1.0:

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