Package 'lipidmapsR'

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Type Package

Title Lipid Maps Rest Service

Version 1.0.4

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Depends R (>= 4.2.0)

Imports httr (>= 1.3.1), RJSONIO (>= 1.3-0)

Description Lipid Maps Rest service. Researchers can access the Lipid Maps Rest
service programmatically and conveniently integrate it into the current workflow
or packages.

License GPL-3

Encoding UTF-8

RoxygenNote 7.2.0

NeedsCompilation no

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R topics documented:

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compound_search   *A function for compound search*

Description

A function for compound search

Usage

```
compound_search(
  input_item = "lm_id",
  input_value,
  output_item,
  output_format = ""
)
```

Arguments

input_item	choose input item from the following options: "lm_id", "formula","inchi_key","pubchem_cid","hmdb_id"
input_value	input the value you want to search
output_item	select your output from following options:"all","classification","lm_id","name","sys_name","synonyms",
output_format	select your output format from following options: "json (default)","text"

Value

The search results

Author(s)

Mingzhuo Tian <tianmingzhuo@outlook.com> License: GPL (>= 3)

Examples

```
# Fetch compound name from LM_ID
compound_search("lm_id", "LMFA01010001", "name")

# Fetch all compound fields from LM_ID
compound_search("lm_id", "LMFA01010001", "all")

# Fetch all compound fields as text from LM_ID
compound_search("lm_id", "LMFA01010001", "all", "txt")

# Fetch compound smiles from PubChem CID
compound_search("pubchem_cid", "985", "smiles")

# Fetch compound sytematic name from inchi key
compound_search("inchi_key", "IPCSVZSSVZVIGE-UHFFFAOYSA-N", "sys_name")
```

```
# Fetch compound physicochemical properties from inchi key
compound_search("inchi_key", "IPCSVZSSVZVIGE-UHFFFAOYSA-N", "physchem")

# Fetch all compound fields from formula (multiple records)
compound_search("formula", "C20H34O", "all")

# Fetch compound classification hierarchy from PubChem CID
compound_search("pubchem_cid", "985", "classification")

# Fetch all compound fields from bulk abbreviation
compound_search("abbrev", "PA(38:0)", "all")

# Fetch all compound fields from chain abbreviation
compound_search("abbrev_chains", "PC(16:0_18:0)", "all")
```

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gene_search   *A function for Gene search*

Description

A function for Gene search

Usage

```
gene_search(
  input_item = "lmp_id",
  input_value,
  output_item,
  output_format = ""
)
```

Arguments

input_item	choose input item from the following options: "lm_id", "formula","inchi_key","pubchem_cid","hmdb_id"
input_value	input the value you want to search
output_item	select your output from following options:"all","classification","lm_id","name","sys_name","synonyms",
output_format	select your output format from following options: "json (default)","text"

Value

The search results

Author(s)

Mingzhuo Tian <tianmingzhuo@outlook.com> License: GPL (>= 3)

Examples

```
# Fetch all gene fields from gene symbol
gene_search("gene_symbol", "acaca", "all")

# Fetch gene name from Entrez gene id
gene_search("gene_id", "31", "gene_name")
```

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protein_search   *A function for Protein search*

Description

A function for Protein search

Usage

```
protein_search(input_item, input_value, output_item, output_format = "")
```

Arguments

input_item	choose input item from the following options: "lm_id", "formula","inchi_key","pubchem_cid","hmdb_id"
input_value	input the value you want to search
output_item	select your output from following options:"all","classification","lm_id","name","sys_name","synonyms",
output_format	select your output format from following options: "json (default)","text"

Value

The search results

Author(s)

Mingzhuo Tian <tianmingzhuo@outlook.com> License: GPL (>= 3)

Examples

```
# Fetch all protein fields from UniProt id
protein_search("uniprot_id", "Q13085", "all")
# Fetch all protein fields from Entrez gene id
protein_search("gene_id", "19", "all")
# Fetch mRNA id from protein Refseq id
protein_search("refseq_id", "NP_005493", "mrna_id")
```

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