

Package ‘iptmnetr’

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Type Package

Title Interface to the 'iPTMnet' API

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Description

Provides an R interface to the 'iPTMnet' database REST API, which can be used to retrieve Post Translational Modification (PTM) data in systems biology context. This package handles all the aspects of communicating with the API, which involve sending the request, checking the error codes and parsing the response in a format that is ready to integrate into existing workflows.

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URL <https://research.bioinformatics.udel.edu/iptmnet/>,
<https://github.com/udel-cbcb/iptmnetr>

Encoding UTF-8

LazyData true

Suggests testthat

Imports httr, jsonlite

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get_host_url	<i>Get the url of iPTMnet API server.</i>
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Description

Get the URL that is being used by the client for making the requests.

Usage

```
get_host_url()
```

Value

A string representing the URL.

Examples

```
## Not run: url <- get_host_url()
```

get_info	<i>Get information.</i>
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Description

Get the information for given iPTMnet ID.

Usage

```
get_info(id)
```

Arguments

id	A string representing iPTMnet ID
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Value

A list containing the information for the iPTMnet ID.

Examples

```
## Not run: info <- get_info("Q15796")
```

get_ppi_for_proteoforms *Get Protein-Protein interactions along with corresponding proteoforms.*

Description

Get Protein-Protein interactions along with corresponding proteoforms for the given iPTMnet ID.

Usage

```
get_ppi_for_proteoforms(id)
```

Arguments

id A string representing iPTMnet ID.

Value

A dataframe containing the PTm dependent PPI for the given iPTMnet ID.

Examples

```
## Not run: ppi_proteoforms <- get_ppi_for_proteoforms("Q15796")
```

get_proteoforms *Get proteoforms*

Description

Get proteoforms

Usage

```
get_proteoforms(id)
```

Arguments

id A string representing iPTMnet ID.

Value

A dataframe containing the proteoforms for the given iPTMnet ID.

Examples

```
## Not run: proteoforms <- get_proteoforms("Q15796")
```

get_ptm_dependent_ppi *Get Post translational modification(PTM) dependent Protein-Protein interactions.*

Description

Get Post translational modification(PTM) dependent Protein-Protein interactions for the given iPTMnet ID.

Usage

```
get_ptm_dependent_ppi(id)
```

Arguments

id A string representing iPTMnet ID.

Value

A dataframe containing the PTM dependent PPI for the given iPTMnet ID.

Examples

```
## Not run: ptm_dependent_ppi <- get_ptm_dependent_ppi("Q15796")
```

get_ptm_enzymes_from_file
Get PTM Enzymes using a file

Description

This function is similar to [get_ptm_enzymes_from_list](#) except that it loads the kinases from TSV file.

Usage

```
get_ptm_enzymes_from_file(file_name)
```

Arguments

file_name A string representing file name of the file containing the list of kinases. The file should be a Tab separated file with three columns "substrate_ac", "site_residue" and "position" without headers. Example : Q13619 S 10 Q8TDM6 S 1021 Q6ZRV2 S 1025 Q15121 S 104 O15164 S 1042 Q8NDI1 S 1058 P00533 S 1064 Q16555 S 107 Q8NFC6 S 1077

Value

A Dataframe representing the enzymes

Examples

```
## Not run: enzymes = get_ptm_enzymes_from_file("kinases.txt")
```

```
get_ptm_enzymes_from_list
```

Get PTM Enzymes from list

Description

Retrieve PTM enzymes from the given list of kinases. The kinase object should have three fields - "substrate_ac", "site_residue", "site_position". All with the type String

Usage

```
get_ptm_enzymes_from_list(items)
```

Arguments

items A list of kinases.

Value

A Dataframe representing the enzymes

Examples

```
## Not run:
kinases = list(
  list(
    substrate_ac="Q15796",
    site_residue="K",
    site_position="19"
  ),
  list(
    substrate_ac="Q15796",
    site_residue="T",
```

```

        site_position="8"
    ),
    list(
        substrate_ac="P04637",
        site_residue="K",
        site_position="120"
    )
)
enzymes = get_ptm_enzymes_from_list(kinases)

## End(Not run)

```

get_ptm_ppi_from_file *Get post translational modification (PTM) dependent protein-protein interaction for kinases from file*

Description

This function is similar to [get_ptm_ppi_from_list](#) except that it loads the kinases from TSV file

Usage

```
get_ptm_ppi_from_file(file_name)
```

Arguments

file_name	A string representing file name of the file containing the list of kinases. The file should be a Tab seperated file with three columns "substrate_ac", "site_residue" and "position" without headers. Example : Q13619 S 10 Q8TDM6 S 1021 Q6ZRV2 S 1025 Q15121 S 104 O15164 S 1042 Q8NDI1 S 1058 P00533 S 1064 Q16555 S 107 Q8NFC6 S 1077
-----------	---

Value

A dataframe containing the PTM dependent PPI interaction information.

Examples

```
## Not run: ptm_dep_ppi = get_ptm_ppi_from_file(kinases.txt)
```

get_ptm_ppi_from_list *Get post translational modification (PTM) dependent protein-protein interaction for the given list of kinases.*

Description

Retrieve a list of post translational modification (PTM) dependent protein-protein interaction for the given list of kinases. The kinase object should have three fields - "substrate_ac", "site_residue", "site_position". All with the type String

Usage

```
get_ptm_ppi_from_list(items)
```

Arguments

items A list of kinases.

Value

A dataframe containing the PTM dependent PPI interaction information.

Examples

```
## Not run:
kinases = list(
  list(
    substrate_ac="Q15796",
    site_residue="K",
    site_position="19"
  ),
  list(
    substrate_ac="Q15796",
    site_residue="T",
    site_position="8"
  ),
  list(
    substrate_ac="P04637",
    site_residue="K",
    site_position="120"
  )
)
ptm_dep_ppi = get_ptm_ppi_from_list(kinases)

## End(Not run)
```

get_substrates *Get substrates.*

Description

Retrieves the substrates for the given iPTMnet ID.

Usage

```
get_substrates(id)
```

Arguments

id A string representing iPTMnet ID.

Value

A dataframe containing the substrates for the given iPTMnet ID.

Examples

```
## Not run: substrates <- get_substrates("Q15796")
```

PTMTypes *PTMTypes Returns a list of strings that represents the PTM types to be used in [search_iptmnet](#) function*

Description

PTMTypes Returns a list of strings that represents the PTM types to be used in [search_iptmnet](#) function

Usage

```
PTMTypes()
```

Value

A list of strings representing PTM types

Examples

```
PTMTypes()$Acetylation
PTMTypes()$CGlycosylation
PTMTypes()$Myristoylation
PTMTypes()$Ubiquitination
PTMTypes()$NGlycosylation
PTMTypes()$SGlycosylation
PTMTypes()$Phosphorylation
PTMTypes()$SNitrosylation
PTMTypes()$OGlycosylation
PTMTypes()$Methylation
PTMTypes()$Sumoylation
```

Role	<i>Role Returns a list of strings that represent the role to be used in search_ipTMnet function</i>
------	---

Description

Role Returns a list of strings that represent the role to be used in [search_ipTMnet](#) function

Usage

```
Role()
```

Value

A list of strings representing the role

Examples

```
Role()$EnzymeOrSubstrate
Role()$Enzyme
Role()$Substrate
Role()$EnzymeAndSubstrate
```

search_ipTMnet	<i>Search iPTMNet</i>
----------------	-----------------------

Description

Searches the iPTMNet database with the given search parameters

Usage

```
search_ipTMnet(search_term, term_type, role, ptm_vector = c(),
  organism_vector = c())
```

Arguments

search_term	A string representing the search Term
term_type	A string specifying type of search term. Supported values are "All", "UniProtID", "Protein/Gene Name", "PMID". Use the TermType function for getting a list of possible values.
role	A string representing the roles to filter by. Supported Values are "Enzyme or Substrate", "Enzyme", "Substrate", "Enzyme and Substrate". Use the Role function for getting a list of possible values. Example - TermType()\$.UniProtID
ptm_vector	A vector representing the PTM types to filter by. Use the PTMTypes function for getting a list of possible values. Pass empty vector if you don't want filter by PTMTypes. Example - c(PTMType()\$Acetylation,PTMType()\$Phosphorylation)
organism_vector	A vector of integers representing the taxon codes for organisms to filter by.

Value

A dataframe with search results.

Examples

```
## Not run:
result <- search_iptmnet(search_term = "smad2",
                        term_type=TermType()$ALL,
                        Role()$EnzymeOrSubstrate,
                        ptm_vector=c(),
                        organism_vector=c())

## End(Not run)
```

set_host_url	<i>Set the url of iPTMnet API server.</i>
--------------	---

Description

This function can be used to change the URL to use your own self hosted instance of iPTMnet API server.

Usage

```
set_host_url(url)
```

Arguments

url	A string representing the new iTPMnet api server URL.
-----	---

Examples

```
## Not run: set_host_url("http://www.example.com")
```

TermType	<i>TermTypes Returns a list of strings that represent the term types to be used in search_ipmnet function.</i>
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Description

TermTypes Returns a list of strings that represent the term types to be used in [search_ipmnet](#) function.

Usage

```
TermType()
```

Value

A list of strings that represent the term types.

Examples

```
TermType()$ALL  
TermType()$UniprotID
```

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