

# Package ‘iptmnetr’

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**Type** Package

**Title** Interface to the 'iPTMnet' API

**Version** 0.1.8

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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

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**Repository** CRAN

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|                 |   |
|-----------------|---|
| get_api_version | <i>Get the version of iPTMnet API being used.</i> |
|-----------------|---|

---

## Description

Get the version of the api that is being used by the client for making the requests.

## Usage

```
get_api_version()
```

## Value

A string representing the version being used.

## Examples

```
version <- get_api_version()
```

---

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

---

**Description**

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

**Usage**

```
get_host_url()
```

**Value**

A string representing the URL.

**Examples**

```
url <- get_host_url()
```

---

|          |                         |
|----------|-------------------------|
| get_info | <i>Get information.</i> |
|----------|-------------------------|

---

**Description**

Get the information for given iPTMnet ID.

**Usage**

```
get_info(id)
```

**Arguments**

id                    A string representing iPTMnet ID

**Value**

A list containing the information for the iPTMnet ID.

**Examples**

```
info <- get_info("Q15796")
```

get\_ppi\_for\_proteofoms

*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_proteofoms(id)
```

**Arguments**

id                    A string representing iPTMnet ID.

**Value**

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

**Examples**

```
ppi_proteofoms <- get_ppi_for_proteofoms("Q15796")
```

---

get\_proteofoms

*Get proteoforms*

---

**Description**

Get proteoforms

**Usage**

```
get_proteofoms(id)
```

**Arguments**

id                    A string representing iPTMnet ID.

**Value**

A dataframe containing the proteoforms for the given iPTMnet ID.

**Examples**

```
proteofoms <- get_proteofoms("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

```
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 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 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**

```
substrates <- get_substrates("Q15796")
```

---

|              |                      |
|--------------|----------------------|
| get_variants | <i>Get variants.</i> |
|--------------|----------------------|

---

**Description**

Get variants for the given iPTMnet ID.

**Usage**

```
get_variants(id)
```

**Arguments**

id                    A string representing iPTMnet ID.

**Value**

A dataframe containing the variants for the given iPTMnet ID.

**Examples**

```
variants <- get_variants("Q15796")
```

---

|          |  |
|----------|--|
| PTMTypes | <i>PTMTypes Returns a list of strings that represents the PTM types to be used in <a href="#">search_ipmnet</a> function</i> |
|----------|--|

---

**Description**

PTMTypes Returns a list of strings that represents the PTM types to be used in [search\\_ipmnet](#) 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 <a href="#">search_ipTMnet</a> 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 <a href="#">TermType</a> 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 <a href="#">Role</a> function for getting a list of possible values. Example - <code>TermType()\$.UniProtID</code>    |
| ptm_vector      | A vector representing the PTM types to filter by. Use the <a href="#">PTMTypes</a> function for getting a list of possible values. Pass empty vector if you don't want filter by PTMTypes. Example - <code>c(PTMType()\$Acetylation,PTMType()\$Phosphorylation)</code> |
| organism_vector | A vector of integers representing the taxon codes for organisms to filter by.  |

**Value**

A dataframe with search results.

**Examples**

```
result <- search_iptmnet(search_term = "smad2",
                        term_type=TermType()$ALL,
                        Role()$EnzymeOrSubstrate,
                        ptm_vector=c(),
                        organism_vector=c())
```

---

|                 |   |
|-----------------|---|
| set_api_version | <i>Set the version of the API to use.</i> |
|-----------------|---|

---

**Description**

This function can be used to change the version of the api to use.

**Usage**

```
set_api_version(version)
```

**Arguments**

|         |  |
|---------|--|
| version | A string representing the new iTPMnet api version. |
|---------|--|

**Examples**

```
set_api_version("v1")
```

---

|              |   |
|--------------|---|
| 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 iPTMnet api server URL. |
|-----|---|

**Examples**

```
set_host_url("http://www.example.com")
```

---

|          |  |
|----------|--|
| TermType | <i>TermTypes Returns a list of strings that represent the term types to be used in <a href="#">search_ipmnet</a> function.</i> |
|----------|--|

---

**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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