

# Package ‘metabolomicsWorkbenchR’

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**Type** Package

**Title** Metabolomics Workbench in R

**Version** 1.17.0

**Description** This package provides functions for interfacing with the Metabolomics Workbench RESTful API. Study, compound, protein and gene information can be searched for using the API. Methods to obtain study data in common Bioconductor formats such as SummarizedExperiment and MultiAssayExperiment are also included.

**License** GPL-3

**Encoding** UTF-8

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'helper\_fns.R' 'metabolomicsWorkbenchR.R'

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check_pattern	<i>Check input against acceptable input pattern</i>
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### Description

Checks an input\_value against a regex pattern to determine if the input\_value is valid. This method is used internally and not for intended for general use.

### Usage

```
check_pattern(I, input_value, match)
```

```
## S4 method for signature 'mw_input_item'
check_pattern(I, input_value, match)
```

### Arguments

I	An mw_input_item.
input_value	The value for the input item (character).
match	The type of match. One of "exact" or "partial".

### Value

TRUE if input matches the pattern, or throws an error.

### Examples

```
check_pattern(input_item$study_id, 'ST000001', 'exact')
```

---

check_puts	<i>Check inputs/outputs match</i>
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**Description**

Checks that the provided inputs and output are compatible. This method is used internally and not for intended for general use.

**Usage**

```
check_puts(input_item, output_item)

## S4 method for signature 'mw_input_item'
check_puts(input_item, output_item)
```

**Arguments**

input\_item     An mw\_input\_item.  
output\_item    An mw\_output\_item.

**Value**

TRUE if the items are compatible or throws an error if not.

**Examples**

```
check_puts(input_item$study_id,output_item$summary)
```

---

context	<i>Contexts</i>
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**Description**

A predefined list of mw\_context objects. The context have been created to mirror the metabolomics workbench API documentation contexts as closely as possible.

**Usage**

```
context
```

**Format**

An object of class list of length 7.

**Examples**

```
# list available contexts
names(context)

# get the context 'study'
context$study
```

---

context_inputs	<i>Valid inputs</i>
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**Description**

Get a list of valid input\_items for a context.

**Usage**

```
context_inputs(context)
```

**Arguments**

context            The name of a valid context (character)

**Value**

A list of input item names for a context

**Examples**

```
# list of input items for the "study" context
context_inputs("study")
```

---

context_outputs	<i>Valid outputs</i>
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---

**Description**

Get a list of valid output\_items for a context.

**Usage**

```
context_outputs(context)
```

**Arguments**

context            The name of a valid context (character)

**Value**

A list of output item names for a context

**Examples**

```
# list of output items for the "study" context
context_outputs("study")
```

---

do\_query

*Query the Metabolomics Workbench database*


---

**Description**

Sends a query to the metabolomics database and returns the result. Note that while objects derived from mw\_base can be used the recommended approach is to use character inputs.

**Usage**

```
do_query(context, input_item, input_value, output_item)

## S4 method for signature 'character,character,character,character'
do_query(context, input_item, input_value, output_item)

## S4 method for signature 'mw_moverz_context,list,character,mw_output_item'
do_query(context, input_item, input_value, output_item)

## S4 method for signature 'mw_moverz_context,list,character,character'
do_query(context, input_item, input_value, output_item)

## S4 method for signature 'mw_moverz_context,list,character,missing'
do_query(context, input_item, input_value, output_item)

## S4 method for signature 'mw_moverz_context,character,character,missing'
do_query(context, input_item, input_value, output_item)

## S4 method for signature 'character,character,character,missing'
do_query(context, input_item, input_value, output_item)

## S4 method for signature 'mw_exactmass_context,list,character,mw_output_item'
do_query(context, input_item, input_value, output_item)

## S4 method for signature 'mw_exactmass_context,list,character,character'
do_query(context, input_item, input_value, output_item)

## S4 method for signature 'mw_exactmass_context,list,character,missing'
do_query(context, input_item, input_value, output_item)
```

```

## S4 method for signature 'mw_exactmass_context,character,character,missing'
do_query(context, input_item, input_value, output_item)

## S4 method for signature 'character,character,character,missing'
do_query(context, input_item, input_value, output_item)

## S4 method for signature 'mw_context,mw_input_item,character,mw_output_item'
do_query(context, input_item, input_value, output_item)

## S4 method for signature 'mw_context,mw_input_item,character,mw_SE_item'
do_query(context, input_item, input_value, output_item)

## S4 method for signature
## 'mw_context,mw_input_item,character,mw_untarg_SE_item'
do_query(context, input_item, input_value, output_item)

## S4 method for signature 'mw_context,mw_input_item,character,mw_DE_item'
do_query(context, input_item, input_value, output_item)

## S4 method for signature
## 'mw_context,mw_input_item,character,mw_untarg_DE_item'
do_query(context, input_item, input_value, output_item)

## S4 method for signature 'mw_context,mw_input_item,character,mw_MAE_item'
do_query(context, input_item, input_value, output_item)

```

### Arguments

context	A valid context name (character)
input_item	A valid input_item name (character)
input_value	The value for the input item (character).
output_item	A valid output_item (character).

### Value

A data.frame, or other output appropriate to the output\_item.

### Examples

```

# Get a summary of all studies with "diabetes" in the title

df = do_query(
  context = 'study',
  input_item = 'study_title',
  input_value = 'diabetes',
  output_item = 'summary'
)

```

---

input_example	<i>Valid input_value for input_item</i>
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---

**Description**

Displays a valid input\_value for an input\_item and returns an example that matches the required input pattern.

**Usage**

```
input_example(input_item)
```

**Arguments**

input\_item      The name of a valid input\_item (character)

**Value**

An example input value matching the pattern required for the chosen input item.

**Examples**

```
# example input_value for input item "study_id"
input_example('study_id')
```

---

input_item	<i>Input items</i>
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---

**Description**

A predefined list of mw\_input\_item objects. The items have been created to mirror the Metabolomics Workbench API documentation input items as closely as possible.

**Usage**

```
input_item
```

**Format**

An object of class list of length 41.

**Examples**

```
# list available input_items
names(input_item)

# get the input item 'study_id'
input_item$study_id
```

---

`is_valid`*Check validity of context and inputs/outputs*

---

### Description

Compares the input and output items to the expected values for a context and returns TRUE if the inputs/puts are valid for the provided context or an error if not. This method is used internally and not for intended for general use.

### Usage

```
is_valid(context, input_item, input_value, output_item)

## S4 method for signature 'mw_context,character,character,character'
is_valid(context, input_item, input_value, output_item)

## S4 method for signature 'mw_moverz_context,character,character,missing'
is_valid(context, input_item, input_value)

## S4 method for signature 'mw_exactmass_context,character,character,missing'
is_valid(context, input_item, input_value)
```

### Arguments

<code>context</code>	An <code>mw_context</code> object.
<code>input_item</code>	An <code>mw_input_item</code> object, or the name of one.
<code>input_value</code>	The value for the input item (character).
<code>output_item</code>	An <code>mw_output_item</code> , or the name of one.

### Value

TRUE or an error.

### Examples

```
is_valid(context$study,
  input_item$study_id$name,
  'ST000001',
  output_item$summary$name
)
```



---

metabolomicsWorkbenchR

*metabolomicsWorkbenchR*

---

## Description

This package provides an interface to the Metabolomics Workbench API. It can be used to query the Metabolomics Workbench for study, compound, protein, gene information and more. All endpoints of the API are available via a simple `do_query` method. A number of convenience functions are included to import study data as `SummarizedExperiment` objects to facilitate use within R and the Bioconductor community.

## Author(s)

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## See Also

- [do\\_query](#) for a simple example.
- `browseVignettes("metabolomicsWorkbenchR")` for more info.
- Visit [https://www.metabolomicsworkbench.org/tools/mw\\_rest.php](https://www.metabolomicsworkbench.org/tools/mw_rest.php) for details of the API.

---

output\_item

*Output items*

---

## Description

A predefined list of `mw_output_item` objects. The items have been created to mirror the Metabolomics Workbench API documentation output items as closely as possible.

## Usage

```
output_item
```

## Format

An object of class `list` of length 31.

**Examples**

```
# list available output_items
names(output_item)

# get the output item 'summary'
output_item$summary
```

---

\$,mw\_base-method      *Get slot value from mw\_base objects*

---

**Description**

Gets the value of a slot from mw\_base objects, provided they are not listed as 'private'.

**Usage**

```
## S4 method for signature 'mw_base'
x$name
```

**Arguments**

x	An object derived from mw_base.
name	The name of the slot to access.

**Value**

The assigned to the slot.

**Examples**

```
# an object derived from mw_base object
C = context$study
# access the name slot
C$name
```

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