

# Package ‘taxnames’

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**Version** 0.1.0

**Encoding** UTF-8

**Title** Formatting Taxonomic Names in Markdown

**Depends** R (>= 4.3.0)

**Imports** taxlist (>= 0.3.0)

**Suggests** testthat (>= 3.0.0)

**Description** A collection of functions used to format taxonomic names in Markdown documents. Those functions work with data structured according to Alvarez and Luebert (2018) <[doi:10.3897/bdj.6.e23635](https://doi.org/10.3897/bdj.6.e23635)>.

**License** GPL-3

**URL** <https://github.com/kamapu/taxnames>

**BugReports** <https://github.com/kamapu/taxnames/issues>

**RoxygenNote** 7.3.1

**NeedsCompilation** no

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## Contents

get_tax . . . . .	2
tn_an . . . . .	3
tn_aun . . . . .	4
tn_pan . . . . .	5

<b>Index</b>	<b>6</b>
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get\_tax

*Get or set a global taxonomy*


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### Description

For convenience and to simplify the call of name formats, the containing object (a `taxlist::taxlist` object) will be handled internally by all functions.

A standard taxonomic list is already set in this package and can be retrieved or replaced.

The function `set_style()` sets the style for the formatted names (default "markdown") and the standard collapse connectors.

### Usage

```
set_tax(tax)

## S3 method for class 'taxlist'
set_tax(tax)

get_tax()

set_style(style, collapse, secundum)

get_style()
```

### Arguments

tax	A <code>taxlist::taxlist</code> object set as standard taxonomy.
style	A character value setting the format style. It is passed to the homonymous parameter in <code>taxlist::print_name()</code> .
collapse	A character vector (length 1 or 2) setting the collapse connectors for multiple names. It is passed to the homonymous parameter in <code>taxlist::print_name()</code> .
secundum	A character value indicating the name of the column in slot <b>taxonViews</b> of the internal object, which will be used to indicate the respective taxon view.

### Value

`get_tax()` returns an object of class `taxlist::taxlist`, while `get_style()` returns a list with options set for the session.

### Examples

```
## Get the current taxonomy
get_tax()

## Get further settings
get_style()
```

## Description

Inserting formatted taxonomic names in documents require specific functions for every format, which are provided here.

These functions print only accepted names for the selected taxon concepts.

Suffixes in the function names are explained as follows:

- **fn**: Full name without author name.
- **fna**: Full name with author name.
- **fnas**: Full name with author name and taxon view (secundum).
- **an**: Abbreviated name without author name.
- **ana**: Abbreviated name with author name.

## Usage

```
tn_fn(x, ...)
```

```
tn_fna(x, ...)
```

```
tn_fnas(x, ...)
```

```
tn_an(x, ...)
```

```
tn_ana(x, ...)
```

## Arguments

x	A vector containing selected identifiers for taxon concepts ( <b>TaxonConceptID</b> ) included in the internal taxonomic object (see <a href="#">set_tax()</a> ).
...	Further arguments passed to <code>taxlist::print_name()</code> .

## Value

All these functions return a character value.

## Examples

```
## Compare all these outputs
tn_fn(13)
tn_fna(13)
tn_fnas(13)
tn_an(13)
tn_ana(13)
```

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tn\_aun

*Standard formats for taxonomic names*

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## Description

These functions work similarly to `tn_an()` and its alies but the names are accessed by their **TaxonUsageID** and work also for synonyms.

Suffixes in the function names are explained as follows:

- **fun**: Full usage name without author name.
- **funa**: Full usage name with author name.
- **aun**: Abbreviated usage name without author name.
- **auna**: Abbreviated usage name with author name.

## Usage

```
tn_fun(x, ...)
```

```
tn_funa(x, ...)
```

```
tn_aun(x, ...)
```

```
tn_auna(x, ...)
```

## Arguments

`x` A vector containing selected identifiers for taxon names (**TaxonUsageID**) included in the internal taxonomic object (see `set_tax()`).

`...` Further arguments passed to `taxlist::print_name()`.

## Value

All these functions return a character value.

## Examples

```
## Compare all these outputs
tn_fun(52613)
tn_funa(52613)
tn_aun(52613)
tn_auna(52613)
```

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tn_pan	<i>Print formatted names for parents</i>
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### Description

Displaying names of parent taxa.

Suffixes in the function names are explained as follows:

- **pfn**: Parent's full name without author name.
- **pfna**: Parent's full name with author name.
- **pfnas**: Parent's full name with author name and taxon view (secundum).
- **pan**: Parent's abbreviated name without author name.
- **pana**: Parent's abbreviated name with author name.

### Usage

```
tn_pfn(x, level, ...)
```

```
tn_pfna(x, level, ...)
```

```
tn_pfnas(x, level, ...)
```

```
tn_pan(x, level, ...)
```

```
tn_pana(x, level, ...)
```

### Arguments

- |       |   |
|-------|---|
| x     | A vector containing selected identifiers for taxon concepts ( <b>TaxonConceptID</b> ) included in the internal taxonomic object (see <a href="#">set_tax()</a> ). |
| level | A character value indicating the taxon rank set for parent taxa. I is passed to <a href="#">taxlist::parents()</a> .  |
| ...   | Further arguments passed to <a href="#">taxlist::print_name()</a> .   |

### Value

All these functions return a character value.

### Examples

```
## Compare all these outputs
tn_pfn(13, "family")
tn_pfna(13, "family")
tn_pfnas(13, "family")
tn_pan(13, "family")
tn_pana(13, "family")
```

# Index

`get_style (get_tax)`, 2  
`get_tax`, 2

`set_style (get_tax)`, 2  
`set_tax (get_tax)`, 2  
`set_tax()`, 3–5  
`set_tax`, taxlist-method (`get_tax`), 2  
`set_tax.taxlist (get_tax)`, 2

`taxlist::parents()`, 5  
`taxlist::print_name()`, 2–5  
`taxlist::taxlist`, 2  
`tn_an`, 3  
`tn_an()`, 4  
`tn_ana (tn_an)`, 3  
`tn_aun`, 4  
`tn_auna (tn_aun)`, 4  
`tn_fn (tn_an)`, 3  
`tn_fna (tn_an)`, 3  
`tn_fnas (tn_an)`, 3  
`tn_fun (tn_aun)`, 4  
`tn_funa (tn_aun)`, 4  
`tn_pan`, 5  
`tn_pana (tn_pan)`, 5  
`tn_pfn (tn_pan)`, 5  
`tn_pfna (tn_pan)`, 5  
`tn_pfnas (tn_pan)`, 5