

# Package ‘OmnipathR’

December 2, 2024

**Type** Package

**Title** OmniPath web service client and more

**Version** 3.15.0

**Description** A client for the OmniPath web service (<https://www.omnipathdb.org>) and many other resources. It also includes functions to transform and pretty print some of the downloaded data, functions to access a number of other resources such as BioPlex, ConsensusPathDB, EVEX, Gene Ontology, Guide to Pharmacology (IUPHAR/BPS), Harmonizome, HTRIdb, Human Phenotype Ontology, InWeb InBioMap, KEGG Pathway, Pathway Commons, Ramilowski et al. 2015, RegNetwork, ReMap, TF census, TRRUST and Vinayagam et al. 2011. Furthermore, OmnipathR features a close integration with the NicheNet method for ligand activity prediction from transcriptomics data, and its R implementation `nichenetr` (available only on github).

**License** MIT + file LICENSE

**URL** <https://r.omnipathdb.org/>

**BugReports** <https://github.com/saezlab/OmnipathR/issues>

**biocViews** GraphAndNetwork, Network, Pathways, Software, ThirdPartyClient, DataImport, DataRepresentation, GeneSignaling, GeneRegulation, SystemsBiology, Transcriptomics, SingleCell, Annotation, KEGG

**Encoding** UTF-8

**VignetteBuilder** knitr

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**Imports** checkmate, crayon, curl, digest, dplyr(>= 1.1.0), httr, igraph, jsonlite, later, logger, lubridate, magrittr, progress, purrr, rappdirs, readr(>= 2.0.0), readxl, rlang, rmarkdown, RSQLite, R.utils, rvest, stats, stringi, stringr, tibble, tidyr, tidyselect, tools, utils, vctrs, withr, XML, xml2, yaml, zip

**Suggests** BiocStyle, bookdown, ggplot2, ggraph, gprofiler2, knitr, mlrMBO, parallelMap, ParamHelpers, Rgraphviz, R.matlab, sigmajs, smooof, supraHex, testthat

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---

.omnipathr\_options\_defaults  
*Default values for the package options*

---

**Description**

These options describe the default settings for OmnipathR so you do not need to pass these parameters at each function call. Currently the only option useful for the public web service at [omnipathdb.org](http://omnipathdb.org) is “omnipathr.license“. If you are a for-profit user set it to “commercial“ to make sure all the data you download from OmniPath is legally allowed for commercial use. Otherwise just leave it as it is: “academic“. If you don’t use [omnipathdb.org](http://omnipathdb.org) but within your organization you deployed your own pypath server and want to share data with a limited availability to outside users, you may want to use a password. For this you can use the “omnipathr.password“ option. Also

if you want the R package to work from another pypath server instead of omnipathdb.org, you can change the option “omnipathr.url”.

### Usage

```
.omnipathr_options_defaults
```

### Format

An object of class `list` of length 25.

### Value

Nothing, this is not a function but a list.

---

all_uniprots	<i>A table with all UniProt records</i>
--------------	---

---

### Description

Retrieves a table from UniProt with all proteins for a certain organism.

### Usage

```
all_uniprots(fields = "accession", reviewed = TRUE, organism = 9606L)
```

### Arguments

fields	Character vector of fields as defined by UniProt. For possible values please refer to <a href="https://www.uniprot.org/help/return_fields">https://www.uniprot.org/help/return_fields</a>
reviewed	Retrieve only reviewed ('TRUE'), only unreviewed ('FALSE') or both ('NULL').
organism	Character or integer: name or identifier of the organism.

### Value

Data frame (tibble) with the requested UniProt entries and fields.

### Examples

```
human_swissprot_entries <- all_uniprots(fields = 'id')
human_swissprot_entries
# # A tibble: 20,396 x 1
#   `Entry name`
#   <chr>
# 1 OR4K3_HUMAN
# 2 O52A1_HUMAN
# 3 O2AG1_HUMAN
# 4 O10S1_HUMAN
# 5 O11G2_HUMAN
# # . with 20,386 more rows
```



---

all_uniprot_acs	<i>All UniProt ACs for one organism</i>
-----------------	---

---

**Description**

All UniProt ACs for one organism

**Usage**

```
all_uniprot_acs(organism = 9606, reviewed = TRUE)
```

**Arguments**

organism	Character or integer: name or identifier of the organism.
reviewed	Retrieve only reviewed ('TRUE'), only unreviewed ('FALSE') or both ('NULL').

**Value**

Character vector of UniProt accession numbers.

**Examples**

```
human_swissprot_acs <- all_uniprot_acs()
human_swissprot_acs[1:5]
# [1] "P51451" "A6H8Y1" "O60885" "Q9Y3X0" "P22223"
length(human_swissprot_acs)
# [1] 20376
mouse_swissprot_acs <- all_uniprot_acs("mouse")
```

---

ancestors	<i>All ancestors in the ontology tree</i>
-----------	---

---

**Description**

Starting from the selected nodes, recursively walks the ontology tree until it reaches the root. Collects all visited nodes, which are the ancestors (parents) of the starting nodes.

**Usage**

```
ancestors(
  terms,
  db_key = "go_basic",
  ids = TRUE,
  relations = c("is_a", "part_of", "occurs_in", "regulates", "positively_regulates",
    "negatively_regulates")
)
```

## Arguments

terms	Character vector of ontology term IDs or names. A mixture of IDs and names can be provided.
db_key	Character: key to identify the ontology database. For the available keys see <a href="#">omnipath_show_db</a> .
ids	Logical: whether to return IDs or term names.
relations	Character vector of ontology relation types. Only these relations will be used.

## Details

Note: this function relies on the database manager, the first call might take long because of the database load process. Subsequent calls within a short period should be faster. See [get\\_ontology\\_db](#).

## Value

Character vector of ontology IDs. If the input terms are all root nodes, NULL is returned. The starting nodes won't be included in the result unless some of them are ancestors of other starting nodes.

## Examples

```
ancestors('GO:0005035', ids = FALSE)
# [1] "molecular_function"
# [2] "transmembrane signaling receptor activity"
# [3] "signaling receptor activity"
# [4] "molecular transducer activity"
```

---

annotated_network	<i>Network interactions with annotations</i>
-------------------	--

---

## Description

Annotations are often useful in a network context, e.g. one might want to label the interacting partners by their pathway membership. This function takes a network data frame and joins an annotation data frame from both the left and the right side, so both the source and target molecular entities will be labeled by their annotations. If one entity has many annotations these will yield many rows, hence the interacting pairs won't be unique across the data frame any more. Also if one entity has really many annotations the resulting data frame might be huge, we recommend to be careful with that. Finally, if you want to do the same but with intercell annotations, there is the [import\\_intercell\\_network](#) function.

**Usage**

```
annotated_network(
  network = NULL,
  annot = NULL,
  network_args = list(),
  annot_args = list(),
  ...
)
```

**Arguments**

- network            Behaviour depends on type: if list, will be passed as arguments to [omnipath\\_interactions](#) to obtain a network data frame; if a data frame or tibble, it will be used as a network data frame; if a character vector, will be assumed to be a set of resource names and interactions will be queried from these resources.
- annot             Either the name of an annotation resource (for a list of available resources call [annotation\\_resources](#)), or an annotation data frame. If the data frame contains more than one resources, only the first one will be used.
- network\_args     List: if 'network' is a resource name, pass these additional arguments to [omnipath\\_interactions](#).
- annot\_args        List: if 'annot' is a resource name, pass these additional arguments to [annotations](#).
- ...                Column names selected from the annotation data frame (passed to `dplyr::select`, if empty all columns will be selected.)

**Value**

A data frame of interactions with annotations for both interacting entities.

**Examples**

```
signalink_with_pathways <-
  annotated_network("SignalLink3", "SignalLink_pathway")
```

---

annotations                            *Protein and gene annotations from OmniPath*

---

**Description**

Protein and gene annotations about function, localization, expression, structure and other properties, from the <https://omnipathdb.org/annotations> endpoint of the OmniPath web service. Note: there might be also a few miRNAs annotated; a vast majority of protein complex annotations are inferred from the annotations of the members: if all members carry the same annotation the complex inherits.

**Usage**

```
annotations(proteins = NULL, wide = FALSE, ...)
```

**Arguments**

proteins	Vector containing the genes or proteins for whom annotations will be retrieved (UniProt IDs or HGNC Gene Symbols or miRBase IDs). It is also possible to download annotations for protein complexes. To do so, write 'COMPLEX:' right before the genesymbols of the genes integrating the complex. Check the vignette for examples.
wide	Convert the annotation table to wide format, which corresponds more or less to the original resource. If the data comes from more than one resource a list of wide tables will be returned. See examples at <a href="#">pivot_annotations</a> .
...	Arguments passed on to <a href="#">omnipath_query</a>
organism	Character or integer: name or NCBI Taxonomy ID of the organism. OmniPath is built of human data, and the web service provides orthology translated interactions and enzyme-substrate relationships for mouse and rat. For other organisms and query types, orthology translation will be called automatically on the downloaded human data before returning the result.
resources	Character vector: name of one or more resources. Restrict the data to these resources. For a complete list of available resources, call the '<query_type>_resources' functions for the query type of interest.
genesymbols	Character or logical: TRUE or FALSE or "yes" or "no". Include the 'genesymbols' column in the results. OmniPath uses UniProt IDs as the primary identifiers, gene symbols are optional.
fields	Character vector: additional fields to include in the result. For a list of available fields, call 'query_info("interactions")'.
default_fields	Logical: if TRUE, the default fields will be included.
silent	Logical: if TRUE, no messages will be printed. By default a summary message is printed upon successful download.
logicals	Character vector: fields to be cast to logical.
format	Character: if "json", JSON will be retrieved and processed into a nested list; any other value will return data frame.
download_args	List: parameters to pass to the download function, which is 'readr::read_tsv' by default, and 'jsonlite::safe_load'.
add_counts	Logical: if TRUE, the number of references and number of resources for each record will be added to the result.
license	Character: license restrictions. By default, data from resources allowing "academic" use is returned by OmniPath. If you use the data for work in a company, you can provide "commercial" or "for-profit", which will restrict the data to those records which are supported by resources that allow for-profit use.
password	Character: password for the OmniPath web service. You can provide a special password here which enables the use of 'license = "ignore"' option, completely bypassing the license filter.
exclude	Character vector: resource or dataset names to be excluded. The data will be filtered after download to remove records of the excluded datasets and resources.

`strict_evidences` Logical: reconstruct the "sources" and "references" columns of interaction data frames based on the "evidences" column, strictly filtering them to the queried datasets and resources. Without this, the "sources" and "references" fields for each record might contain information for datasets and resources other than the queried ones, because the downloaded records are a result of a simple filtering of an already integrated data frame.

`genesymbol_resource` Character: "uniprot" (default) or "ensembl". The OmniPath web service uses the primary gene symbols as provided by UniProt. By passing "ensembl" here, the UniProt gene symbols will be replaced by the ones used in Ensembl. This translation results in a loss of a few records, and multiplication of another few records due to ambiguous translation.

`cache` Logical: use caching, load data from and save to the. The cache directory by default belongs to the user, located in the user's default cache directory, and named "OmnipathR". Find out about it by `getOption("omnipathr.cachedir")`. Can be changed by `omnipath_set_cachedir`.

### Details

Downloading the full annotations dataset is disabled by default because the size of this data is around 1GB. We recommend to retrieve the annotations for a set of proteins or only from a few resources, depending on your interest. You can always download the full database from [https://archive.omnipathdb.org/omnipath\\_webservice\\_annotations\\_\\_recent.tsv](https://archive.omnipathdb.org/omnipath_webservice_annotations__recent.tsv) using any standard R or readr method.

### Value

A data frame or list of data frames:

- If `wide=FALSE` (default), all the requested resources will be in a single long format data frame.
- If `wide=TRUE`: one or more data frames with columns specific to the requested resources. If more than one resources is requested a list of data frames is returned.

### See Also

- [annotation\\_resources](#)
- [pivot\\_annotations](#)
- [query\\_info](#)
- [omnipath\\_query](#)
- [annotated\\_network](#)

### Examples

```

annotations <- annotations(
  proteins = c("TP53", "LMNA"),
  resources = c("HPA_subcellular")
)

```

---

annotation\_categories *Annotation categories and resources*

---

### Description

A full list of annotation resources, keys and values.

### Usage

```
annotation_categories()
```

### Value

A data frame with resource names, annotation key labels and for each key all possible values.

### Examples

```
annot_cat <- annotation_categories()
annot_cat
# # A tibble: 46,307 x 3
#   source          label      value
#   <chr>          <chr>    <chr>
# 1 connectomeDB2020 role      ligand
# 2 connectomeDB2020 role      receptor
# 3 connectomeDB2020 location ECM
# 4 connectomeDB2020 location plasma membrane
# 5 connectomeDB2020 location secreted
# 6 KEGG-PC        pathway Alanine, aspartate and glutamate metabolism
# 7 KEGG-PC        pathway Amino sugar and nucleotide sugar metabolism
# 8 KEGG-PC        pathway Aminoacyl-tRNA biosynthesis
# 9 KEGG-PC        pathway Arachidonic acid metabolism
# 10 KEGG-PC       pathway Arginine and proline metabolism
```

---

annotation\_resources *Retrieves a list of available resources in the annotations database of OmniPath*

---

### Description

Get the names of the resources from <https://omnipathdb.org/annotations>.

### Usage

```
annotation_resources(dataset = NULL, ...)
```

**Arguments**

dataset	ignored for this query type
...	optional additional arguments

**Value**

character vector with the names of the annotation resources

**See Also**

- [resources](#)
- [annotations](#)

**Examples**

```
annotation_resources()
```

---

biomart_query	<i>Query the Ensembl BioMart web service</i>
---------------	--

---

**Description**

Query the Ensembl BioMart web service

**Usage**

```
biomart_query(
  attrs = NULL,
  filters = NULL,
  transcript = FALSE,
  peptide = FALSE,
  gene = FALSE,
  dataset = "hsapiens_gene_ensembl"
)
```

**Arguments**

attrs	Character vector: one or more Ensembl attribute names.
filters	Character vector: one or more Ensembl filter names.
transcript	Logical: include Ensembl transcript IDs in the result.
peptide	Logical: include Ensembl peptide IDs in the result.
gene	Logical: include Ensembl gene IDs in the result.
dataset	Character: An Ensembl dataset name.

**Value**

Data frame with the query result

**Examples**

```
cel_genes <- biomart_query(
  attrs = c("external_gene_name", "start_position", "end_position"),
  gene = TRUE,
  dataset = "celegans_gene_ensembl"
)
cel_genes
# # A tibble: 46,934 × 4
#   ensembl_gene_id external_gene_name start_position end_position
#   <chr>           <chr>           <dbl>         <dbl>
# 1 WBGene000000001 aap-1           5107843       5110183
# 2 WBGene000000002 aat-1           9599178       9601695
# 3 WBGene000000003 aat-2           9244402       9246360
# 4 WBGene000000004 aat-3           2552260       2557736
# 5 WBGene000000005 aat-4           6272529       6275721
# # . with 46,924 more rows
```

---

bioplex1

*Downloads the BioPlex version 1.0 interaction dataset*

---

**Description**

This dataset contains ~24,000 interactions detected in HEK293T cells using 2,594 baits. More details at <https://bioplex.hms.harvard.edu/interactions.php>.

**Usage**

```
bioplex1()
```

**Value**

Data frame (tibble) with interactions.

**See Also**

- [bioplex2](#)
- [bioplex3](#)
- [bioplex\\_hct116\\_1](#)
- [bioplex\\_all](#)



**Examples**

```
bioplex_interactions <- bioplex1()
nrow(bioplex_interactions)
# [1] 23744
colnames(bioplex_interactions)
# [1] "GeneA"      "GeneB"      "UniprotA"   "UniprotB"
# [5] "SymbolA"    "SymbolB"    "p_wrong"    "p_no_interaction"
# [9] "p_interaction"
```

---

**bioplex2***Downloads the BioPlex version 2.0 interaction dataset*

---

**Description**

This dataset contains ~56,000 interactions detected in HEK293T cells using 5,891 baits. More details at <https://bioplex.hms.harvard.edu/interactions.php>

**Usage**

```
bioplex2()
```

**Value**

Data frame (tibble) with interactions.

**See Also**

- [bioplex1](#)
- [bioplex3](#)
- [bioplex\\_hct116\\_1](#)
- [bioplex\\_all](#)

**Examples**

```
bioplex_interactions <- bioplex2()
nrow(bioplex_interactions)
# [1] 56553
colnames(bioplex_interactions)
# [1] "GeneA"      "GeneB"      "UniprotA"   "UniprotB"
# [5] "SymbolA"    "SymbolB"    "p_wrong"    "p_no_interaction"
# [9] "p_interaction"
```

---

 bioplex3

*Downloads the BioPlex version 3.0 interaction dataset*


---

### Description

This dataset contains ~120,000 interactions detected in HEK293T cells using 10,128 baits. More details at <https://bioplex.hms.harvard.edu/interactions.php>.

### Usage

```
bioplex3()
```

### Value

Data frame (tibble) with interactions.

### See Also

- [bioplex1](#)
- [bioplex2](#)
- [bioplex\\_hct116\\_1](#)
- [bioplex\\_all](#)

### Examples

```
bioplex_interactions <- bioplex3()
nrow(bioplex_interactions)
# [1] 118162
colnames(bioplex_interactions)
# [1] "GeneA"      "GeneB"      "UniprotA"   "UniprotB"
# [5] "SymbolA"    "SymbolB"    "p_wrong"    "p_no_interaction"
# [9] "p_interaction"
```

---

 bioplex\_all

*Downloads all BioPlex interaction datasets*


---

### Description

BioPlex provides four interaction datasets: version 1.0, 2.0, 3.0 and HCT116 version 1.0. This function downloads all of them, merges them to one data frame, removes the duplicates (based on unique pairs of UniProt IDs) and separates the isoform numbers from the UniProt IDs. More details at <https://bioplex.hms.harvard.edu/interactions.php>.

**Usage**

```
bioplex_all(unique = TRUE)
```

**Arguments**

**unique** Logical. Collapse the duplicate interactions into single rows or keep them as they are. In case of merging duplicate records the maximum p value will be chosen for each record.

**Value**

Data frame (tibble) with interactions.

**See Also**

- [bioplex1](#)
- [bioplex2](#)
- [bioplex3](#)
- [bioplex\\_hct116\\_1](#)

**Examples**

```
bioplex_interactions <- bioplex_all()
bioplex_interactions
# # A tibble: 195,538 x 11
#   UniprotA IsoformA UniprotB IsoformB GeneA GeneB SymbolA SymbolB
#   <chr>      <int> <chr>      <int> <dbl> <dbl> <chr>    <chr>
# 1 A0AV02      2 Q5K4L6      NA 84561 11000 SLC12A8 SLC27A3
# 2 A0AV02      2 Q8N5V2      NA 84561 25791 SLC12A8 NGEF
# 3 A0AV02      2 Q9H6S3      NA 84561 64787 SLC12A8 EPS8L2
# 4 A0AV96      2 O00425      2 54502 10643 RBM47   IGF2BP3
# 5 A0AV96      2 O00443      NA 54502 5286 RBM47   PIK3C2A
# 6 A0AV96      2 O43426      NA 54502 8867 RBM47   SYNJ1
# 7 A0AV96      2 O75127      NA 54502 26024 RBM47   PTC1D1
# 8 A0AV96      2 O95208      2 54502 22905 RBM47   EPN2
# 9 A0AV96      2 O95900      NA 54502 26995 RBM47   TRUB2
# 10 A0AV96     2 P07910      2 54502 3183 RBM47   HNRNPC
# # . with 195,528 more rows, and 3 more variables: p_wrong <dbl>,
# #   p_no_interaction <dbl>, p_interaction <dbl>
```

---

bioplex\_hct116\_1

*Downloads the BioPlex HCT116 version 1.0 interaction dataset*

---

**Description**

This dataset contains ~71,000 interactions detected in HCT116 cells using 5,522 baits. More details at <https://bioplex.hms.harvard.edu/interactions.php>.

**Usage**

```
bioplex_hct116_1()
```

**Value**

Data frame (tibble) with interactions.

**See Also**

- [bioplex1](#)
- [bioplex2](#)
- [bioplex3](#)
- [bioplex\\_all](#)

**Examples**

```
bioplex_interactions <- bioplex_hct116_1()
nrow(bioplex_interactions)
# [1] 70966
colnames(bioplex_interactions)
# [1] "GeneA"      "GeneB"      "UniprotA"   "UniprotB"
# [5] "SymbolA"    "SymbolB"    "p_wrong"    "p_no_interaction"
# [9] "p_interaction"
```

---

bma\_motif\_es

*BMA motifs from a sequence of edges*

---

**Description**

These motifs can be added to a BMA canvas.

**Usage**

```
bma_motif_es(edge_seq, G, granularity = 2)
```

**Arguments**

edge_seq	An igraph edge sequence.
G	An igraph graph object.
granularity	Numeric: granularity value.

**Value**

Character: BMA motifs as a single string.

### Examples

```
interactions <- omnipath(resources = "ARN")
graph <- interaction_graph(interactions)
motifs <- bma_motif_es(igraph::E(graph)[1], graph)
```

---

bma_motif_vs	<i>Prints a BMA motif to the screen from a sequence of nodes, which can be copy/pasted into the BMA canvas</i>
--------------	--

---

### Description

Intended to parallel print\_path\_vs

### Usage

```
bma_motif_vs(node_seq, G)
```

### Arguments

node_seq	An igraph node sequence.
G	An igraph graph object.

### Value

Character: BMA motifs as a single string.

### Examples

```
interactions <- omnipath(resources = "ARN")
graph <- interaction_graph(interactions)
bma_string <- bma_motif_vs(
  igraph::all_shortest_paths(
    graph,
    from = 'ULK1',
    to = 'ATG13'
  )$res,
  graph
)
```

---

`chalmers_gem`*Genome scale metabolic model by Wang et al. 2021*

---

### Description

Process the GEMs from Wang et al., 2021 (<https://github.com/SysBioChalmers>) into convenient tables.

### Usage

```
chalmers_gem(organism = "Human", orphans = TRUE)
```

### Arguments

<code>organism</code>	Character or integer: an organism (taxon) identifier. Supported taxons are 9606 (Homo sapiens), 10090 (Mus musculus), 10116 (Rattus norvegicus), 7955 (Danio rerio), 7227 (Drosophila melanogaster) and 6239 (Caenorhabditis elegans).
<code>orphans</code>	Logical: include orphan reactions (reactions without known enzyme).

### Value

List containing the following elements:

- `reactions`: tibble of reaction data;
- `metabolites`: tibble of metabolite data;
- `reaction_ids`: translation table of reaction identifiers;
- `metabolite_ids`: translation table of metabolite identifiers;
- `S`: Stoichiometric matrix (sparse).

### References

Wang H, Robinson JL, Kocabas P, Gustafsson J, Anton M, Cholley PE, Huang S, Gobom J, Svensson T, Uhlen M, Zetterberg H, Nielsen J. Genome-scale metabolic network reconstruction of model animals as a platform for translational research. Proc Natl Acad Sci U S A. 2021 Jul 27;118(30):e2102344118. doi: [doi:10.1073/pnas.2102344118](https://doi.org/10.1073/pnas.2102344118).

### See Also

- [chalmers\\_gem\\_network](#)
- [chalmers\\_gem\\_metabolites](#)
- [chalmers\\_gem\\_reactions](#)
- [chalmers\\_gem\\_raw](#)
- [chalmers\\_gem\\_id\\_mapping\\_table](#)
- [cosmos\\_pkn](#)

**Examples**

```
gem <- chalmers_gem()
```

---

```
chalmers_gem_id_mapping_table
```

*Metabolite ID translation tables from Chalmers Sysbio*

---

**Description**

Metabolite ID translation tables from Chalmers Sysbio

**Usage**

```
chalmers_gem_id_mapping_table(to, from = "metabolicatlas", organism = "Human")
```

**Arguments**

to	Character: type of ID to translate to, either label used internally in this package, or a column name from "metabolites.tsv" distributed by Chalmers Sysbio. NSE is supported.
from	Character: type of ID to translate from, same format as "to".
organism	Character or integer: name or identifier of the organism. Supported taxons are 9606 (Homo sapiens), 10090 (Mus musculus), 10116 (Rattus norvegicu), 7955 (Danio rerio), 7227 (Drosophila melanogaster) and 6239 (Caenorhabditis elegans).

**Value**

Tibble with two columns, "From" and "To", with the corresponding ID types.

**Examples**

```
chalmers_gem_id_mapping_table('metabolicatlas', 'hmdb')
```

---

chalmers\_gem\_id\_type *Metabolite identifier type label used in Chalmers Sysbio GEM*

---

### Description

Metabolite identifier type label used in Chalmers Sysbio GEM

### Usage

```
chalmers_gem_id_type(label)
```

### Arguments

label                    Character: an ID type label, as shown in the table at [translate\\_ids](#)

### Value

Character: the Chalmers GEM specific ID type label, or the input unchanged if it could not be translated (still might be a valid identifier name). These labels should be column names from the "metabolites.tsv" distributed with the GEMs.

### See Also

- [hmdb\\_id\\_type](#)
- [uniprot\\_id\\_type](#)
- [ensembl\\_id\\_type](#)
- [uploadlists\\_id\\_type](#)

### Examples

```
chalmers_gem_id_type("metabolicatlas")  
# [1] "metsNoComp"
```

---

chalmers\_gem\_metabolites  
*Metabolites from the Chalmers SysBio GEM (Wang et al., 2021)*

---

### Description

Metabolites from the Chalmers SysBio GEM (Wang et al., 2021)

### Usage

```
chalmers_gem_metabolites(organism = "Human")
```



## Arguments

organism      Character or integer: an organism (taxon) identifier. Supported taxons are 9606 (Homo sapiens), 10090 (Mus musculus), 10116 (Rattus norvegicus), 7955 (Danio rerio), 7227 (Drosophila melanogaster) and 6239 (Caenorhabditis elegans).

## Value

Data frame of metabolite identifiers.

## References

Wang H, Robinson JL, Kocabas P, Gustafsson J, Anton M, Cholley PE, Huang S, Gobom J, Svensson T, Uhlen M, Zetterberg H, Nielsen J. Genome-scale metabolic network reconstruction of model animals as a platform for translational research. Proc Natl Acad Sci U S A. 2021 Jul 27;118(30):e2102344118. doi: [doi:10.1073/pnas.2102344118](https://doi.org/10.1073/pnas.2102344118).

## See Also

- [chalmers\\_gem\\_network](#)
- [chalmers\\_gem\\_reactions](#)
- [chalmers\\_gem](#)
- [chalmers\\_gem\\_raw](#)
- [chalmers\\_gem\\_id\\_mapping\\_table](#)
- [cosmos\\_pkn](#)

## Examples

```
chalmers_gem_metabolites()
```

---

chalmers\_gem\_network    *Chalmers SysBio GEM in the form of gene-metabolite interactions*

---

## Description

Processing GEMs from Wang et al., 2021 (<https://github.com/SysBioChalmers>) to generate PKN for COSMOS

## Usage

```
chalmers_gem_network(  
  organism_or_gem = "Human",  
  metab_max_degree = 400L,  
  protein_ids = c("uniprot", "genesymbol"),  
  metabolite_ids = c("hmdb", "kegg")  
)
```

## Arguments

organism_or_gem	Character or integer or list or data frame: either an organism (taxon) identifier or a list containing the “reactions“ data frame as it is provided by <code>chalmers_gem</code> , or the reactions data frame itself. Supported taxons are 9606 (Homo sapiens), 10090 (Mus musculus), 10116 (Rattus norvegicus), 7955 (Danio rerio), 7227 (Drosophila melanogaster) and 6239 (Caenorhabditis elegans).
metab_max_degree	Degree cutoff used to prune metabolites with high degree assuming they are cofactors (400 by default).
protein_ids	Character: translate the protein identifiers to these ID types. Each ID type results two extra columns in the output, for the "a" and "b" sides of the interaction, respectively. The default ID type for proteins is Esembl Gene ID, and by default UniProt IDs and Gene Symbols are included.
metabolite_ids	Character: translate the protein identifiers to these ID types. Each ID type results two extra columns in the output, for the "a" and "b" sides of the interaction, respectively. The default ID type for metabolites is Metabolic Atlas ID, and HMDB IDs and KEGG IDs are included.

## Value

Data frame (tibble) of gene-metabolite interactions.

## References

Wang H, Robinson JL, Kocabas P, Gustafsson J, Anton M, Cholley PE, Huang S, Gobom J, Svensson T, Uhlen M, Zetterberg H, Nielsen J. Genome-scale metabolic network reconstruction of model animals as a platform for translational research. Proc Natl Acad Sci U S A. 2021 Jul 27;118(30):e2102344118. doi: [doi:10.1073/pnas.2102344118](https://doi.org/10.1073/pnas.2102344118).

## See Also

- [chalmers\\_gem](#)
- [chalmers\\_gem\\_metabolites](#)
- [chalmers\\_gem\\_reactions](#)
- [chalmers\\_gem\\_raw](#)
- [chalmers\\_gem\\_id\\_mapping\\_table](#)
- [cosmos\\_pkn](#)

## Examples

```
gem <- chalmers_gem_network()
```

---

chalmers_gem_raw	<i>GEM matlab file from Chalmers Sysbio (Wang et al., 2021)</i>
------------------	---

---

### Description

Downloads and imports the matlab file containing the genome scale metabolic models created by Chalmers SysBio.

### Usage

```
chalmers_gem_raw(organism = "Human")
```

### Arguments

organism	Character or integer: name or identifier of the organism. Supported taxons are 9606 (Homo sapiens), 10090 (Mus musculus), 10116 (Rattus norvegicu), 7955 (Danio rerio), 7227 (Drosophila melanogaster) and 6239 (Caenorhabditis elegans).
----------	---

### Details

The Matlab object is parsed into a nested list containing a number of vectors and two sparse matrices. The top level contains a single element under the name "ihuman" for human; under this key there is an array of 31 elements. These elements are labeled by the row names of the array.

### Value

Matlab object containing the GEM.

### References

Wang H, Robinson JL, Kocabas P, Gustafsson J, Anton M, Cholley PE, Huang S, Gobom J, Svensson T, Uhlen M, Zetterberg H, Nielsen J. Genome-scale metabolic network reconstruction of model animals as a platform for translational research. Proc Natl Acad Sci U S A. 2021 Jul 27;118(30):e2102344118. doi: [doi:10.1073/pnas.2102344118](https://doi.org/10.1073/pnas.2102344118).

### See Also

- [chalmers\\_gem\\_network](#)
- [chalmers\\_gem\\_reactions](#)
- [chalmers\\_gem](#)
- [chalmers\\_gem\\_reactions](#)
- [chalmers\\_gem\\_id\\_mapping\\_table](#)
- [cosmos\\_pkn](#)

## Examples

```
chalmers_gem_raw()
```

---

```
chalmers_gem_reactions
```

*Reactions from the Chalmers SysBio GEM (Wang et al., 2021)*

---

## Description

Reactions from the Chalmers SysBio GEM (Wang et al., 2021)

## Usage

```
chalmers_gem_reactions(organism = "Human")
```

## Arguments

**organism** Character or integer: an organism (taxon) identifier. Supported taxons are 9606 (Homo sapiens), 10090 (Mus musculus), 10116 (Rattus norvegicus), 7955 (Danio rerio), 7227 (Drosophila melanogaster) and 6239 (Caenorhabditis elegans).

## Value

Data frame of reaction identifiers.

## References

Wang H, Robinson JL, Kocabas P, Gustafsson J, Anton M, Cholley PE, Huang S, Gobom J, Svensson T, Uhlen M, Zetterberg H, Nielsen J. Genome-scale metabolic network reconstruction of model animals as a platform for translational research. Proc Natl Acad Sci U S A. 2021 Jul 27;118(30):e2102344118. doi: [doi:10.1073/pnas.2102344118](https://doi.org/10.1073/pnas.2102344118).

## See Also

- [chalmers\\_gem\\_network](#)
- [chalmers\\_gem\\_metabolites](#)
- [chalmers\\_gem](#)
- [chalmers\\_gem\\_raw](#)
- [chalmers\\_gem\\_id\\_mapping\\_table](#)
- [cosmos\\_pkn](#)

## Examples

```
chalmers_gem_reactions()
```

---

common_name	<i>Common (English) names of organisms</i>
-------------	--

---

**Description**

Common (English) names of organisms

**Usage**

```
common_name(name)
```

**Arguments**

name            Vector with any kind of organism name or identifier, can be also mixed type.

**Value**

Character vector with common (English) taxon names, NA if a name in the input could not be found.

**See Also**

- [ncbi\\_taxid](#)
- [latin\\_name](#)
- [ensembl\\_name](#)

**Examples**

```
common_name(c(10090, "cjacchus", "Vicugna pacos"))  
# [1] "Mouse" "White-tufted-ear marmoset" "Alpaca"
```

---

complexes	<i>Protein complexes from OmniPath</i>
-----------	--

---

**Description**

A comprehensive dataset of protein complexes from the <https://omnipathdb.org/complexes> endpoint of the OmniPath web service.

**Usage**

```
complexes(...)
```

## Arguments

...

Arguments passed on to [omnipath\\_query](#)

**organism** Character or integer: name or NCBI Taxonomy ID of the organism. OmniPath is built of human data, and the web service provides orthology translated interactions and enzyme-substrate relationships for mouse and rat. For other organisms and query types, orthology translation will be called automatically on the downloaded human data before returning the result.

**resources** Character vector: name of one or more resources. Restrict the data to these resources. For a complete list of available resources, call the '`<query_type>_resources`' functions for the query type of interest.

**genesymbols** Character or logical: TRUE or FALSE or "yes" or "no". Include the 'genesymbols' column in the results. OmniPath uses UniProt IDs as the primary identifiers, gene symbols are optional.

**fields** Character vector: additional fields to include in the result. For a list of available fields, call '`query_info("interactions")`'.

**default\_fields** Logical: if TRUE, the default fields will be included.

**silent** Logical: if TRUE, no messages will be printed. By default a summary message is printed upon successful download.

**logicals** Character vector: fields to be cast to logical.

**format** Character: if "json", JSON will be retrieved and processed into a nested list; any other value will return data frame.

**download\_args** List: parameters to pass to the download function, which is '`readr::read_tsv`' by default, and '`jsonlite::safe_load`'.

**add\_counts** Logical: if TRUE, the number of references and number of resources for each record will be added to the result.

**license** Character: license restrictions. By default, data from resources allowing "academic" use is returned by OmniPath. If you use the data for work in a company, you can provide "commercial" or "for-profit", which will restrict the data to those records which are supported by resources that allow for-profit use.

**password** Character: password for the OmniPath web service. You can provide a special password here which enables the use of '`license = "ignore"`' option, completely bypassing the license filter.

**exclude** Character vector: resource or dataset names to be excluded. The data will be filtered after download to remove records of the excluded datasets and resources.

**strict\_evidences** Logical: reconstruct the "sources" and "references" columns of interaction data frames based on the "evidences" column, strictly filtering them to the queried datasets and resources. Without this, the "sources" and "references" fields for each record might contain information for datasets and resources other than the queried ones, because the downloaded records are a result of a simple filtering of an already integrated data frame.

**genesymbol\_resource** Character: "uniprot" (default) or "ensembl". The OmniPath web service uses the primary gene symbols as provided by UniProt. By passing "ensembl" here, the UniProt gene symbols will be replaced by

the ones used in Ensembl. This translation results in a loss of a few records, and multiplication of another few records due to ambiguous translation.

cache Logical: use caching, load data from and save to the. The cache directory by default belongs to the user, located in the user's default cache directory, and named "OmnipathR". Find out about it by `getOption("omnipathr.cachedir")`. Can be changed by `omnipath_set_cachedir`.

### Value

A data frame of protein complexes.

### See Also

- [complex\\_resources](#)
- [query\\_info](#)
- [omnipath\\_query](#)

### Examples

```
cplx <- complexes(resources = c("CORUM", "hu.MAP"))
```

---

complex_genes	<i>Get all the molecular complexes for a given gene(s)</i>
---------------	--

---

### Description

This function returns all the molecular complexes where an input set of genes participate. User can choose to retrieve every complex where any of the input genes participate or just retrieve these complexes where all the genes in input set participate together.

### Usage

```
complex_genes(complexes = complexes(), genes, all_genes = FALSE)
```

### Arguments

complexes	Data frame of protein complexes (obtained using <a href="#">complexes</a> ).
genes	Character: search complexes where these genes present.
all_genes	Logical: select only complexes where all of the genes present together. By default complexes where any of the genes can be found are returned.

### Value

Data frame of complexes

**See Also**

[complexes](#)

**Examples**

```
complexes <- complexes(resources = c("CORUM", "hu.MAP"))
query_genes <- c("LMNA", "BANF1")
complexes_with_query_genes <- complex_genes(complexes, query_genes)
```

---

complex_resources	<i>Retrieve a list of complex resources available in Omnipath</i>
-------------------	---

---

**Description**

Get the names of the resources from <https://omnipathdb.org/complexes>

**Usage**

```
complex_resources(dataset = NULL)
```

**Arguments**

dataset            ignored for this query type

**Value**

character vector with the names of the databases

**See Also**

- [resources](#)
- [complexes](#)

**Examples**

```
complex_resources()
```



---

 consensuspathdb\_download

*Retrieves the ConsensusPathDB network*


---

## Description

Compiles a table of binary interactions from ConsensusPathDB (<http://cpdb.molgen.mpg.de/>) and translates the UniProtKB ACs to Gene Symbols.

## Usage

```
consensuspathdb_download(complex_max_size = 4, min_score = 0.9)
```

## Arguments

complex\_max\_size

Numeric: do not expand complexes with a higher number of elements than this. ConsensusPathDB does not contain conventional interactions but lists of participants, which might be members of complexes. Some records include dozens of participants and expanding them to binary interactions result thousands, sometimes hundreds of thousands of interactions from one single record. At the end, this process consumes >10GB of memory and results rather unusable data, hence it is recommended to limit the complex sizes at some low number.

min\_score

Numeric: each record in ConsensusPathDB comes with a confidence score, expressing the amount of evidences. The default value, a minimum score of 0.9 retains approx. the top 30 percent of the interactions.

## Value

Data frame (tibble) with interactions.

## Examples

```
## Not run:
cpdb_data <- consensuspathdb_download(
  complex_max_size = 1,
  min_score = .99
)
nrow(cpdb_data)
# [1] 252302
colnames(cpdb_data)
# [1] "databases" "references" "uniprot_a" "confidence" "record_id"
# [6] "uniprot_b" "in_complex" "genesymbol_a" "genesymbol_b"
cpdb_data
# # A tibble: 252,302 x 9
#   databases references uniprot_a confidence record_id uniprot_b in_com
#   <chr>      <chr>      <chr>      <dbl>     <int> <chr>    <lgl>
# 1 Reactome  NA          SUMF2_HU.    1         1 SUMF1_HU. TRUE
# 2 Reactome  NA          SUMF1_HU.    1         1 SUMF2_HU. TRUE
```

```
# 3 DIP,Reac. 22210847,. STIM1_HU. 0.998 2 TRPC1_HU. TRUE
# 4 DIP,Reac. 22210847,. TRPC1_HU. 0.998 2 STIM1_HU. TRUE
# # . with 252,292 more rows, and 2 more variables: genesymbol_a <chr>,
# # genesymbol_b <chr>

## End(Not run)
```

---

consensuspathdb\_raw\_table

*Downloads interaction data from ConsensusPathDB*

---

### Description

Downloads interaction data from ConsensusPathDB

### Usage

```
consensuspathdb_raw_table()
```

### Value

Data frame (tibble) with interactions.

### Examples

```
cpdb_raw <- consensuspathdb_raw_table()
```

---

cookie

*Acquire a cookie if necessary*

---

### Description

Acquire a cookie if necessary

### Usage

```
cookie(
  url,
  init_url = NULL,
  post = NULL,
  payload = NULL,
  init_post = NULL,
  init_payload = NULL,
  curl_verbose = FALSE
)
```

**Arguments**

<code>url</code>	Character. URL to download to get the cookie.
<code>init_url</code>	Character. An initial URL to download to get the cookie, before downloading “url” with the cookie.
<code>post</code>	List: HTTP POST parameters.
<code>payload</code>	Data to send as payload.
<code>init_post</code>	List: HTTP POST parameters for “init_url”.
<code>init_payload</code>	Data to send as payload with “init_url”.
<code>curl_verbos</code>	Logical. Perform CURL requests in verbose mode for debugging purposes.

**Value**

A list with cache file path, cookies and response headers.

---

<code>cosmos_pkn</code>	<i>Prior knowledge network (PKN) for COSMOS</i>
-------------------------	---

---

**Description**

The prior knowledge network (PKN) used by COSMOS is a network of heterogenous causal interactions: it contains protein-protein, reactant-enzyme and enzyme-product interactions. It is a combination of multiple resources:

- Genome-scale metabolic model (GEM) from Chalmers Sysbio (Wang et al., 2021.)
- Network of chemical-protein interactions from STITCH (<https://stitch.embl.de/>)
- Protein-protein interactions from Omnipath (Türei et al., 2021)

This function downloads, processes and combines the resources above. With all downloads and processing the build might take 30-40 minutes. Data is cached at various levels of processing, shortening processing times. With all data downloaded and HMDB ID translation data preprocessed, the build takes 3-4 minutes; the complete PKN is also saved in the cache, if this is available, loading it takes only a few seconds.

**Usage**

```
cosmos_pkn(
  organism = "human",
  protein_ids = c("uniprot", "genesymbol"),
  metabolite_ids = c("hmdb", "kegg"),
  chalmers_gem_metab_max_degree = 400L,
  stitch_score = 700L,
  ...
)
```

**Arguments**

organism	Character or integer: name or NCBI Taxonomy ID of an organism. Supported organisms vary by resource: the Chalmers GEM is available only for human, mouse, rat, fish, fly and worm. OmniPath can be translated by orthology, but for non-vertebrate or less researched taxa very few orthologues are available. STITCH is available for a large number of organisms, please refer to their web page: <a href="https://stitch.embl.de/">https://stitch.embl.de/</a> .
protein_ids	Character: translate the protein identifiers to these ID types. Each ID type results two extra columns in the output, for the "source" and "target" sides of the interaction, respectively. The default ID type for proteins depends on the resource, hence the "source" and "target" columns are heterogenous. By default UniProt IDs and Gene Symbols are included. The Gene Symbols used in the COSMOS PKN are provided by Ensembl, and do not completely agree with the ones provided by UniProt and used in OmniPath data by default.
metabolite_ids	Character: translate the metabolite identifiers to these ID types. Each ID type results two extra columns in the output, for the "source" and "target" sides of the interaction, respectively. The default ID type for metabolites depends on the resource, hence the "source" and "target" columns are heterogenous. By default HMDB IDs and KEGG IDs are included.
chalmers_gem_metab_max_degree	Numeric: remove metabolites from the Chalmers GEM network with degrees larger than this. Useful to remove cofactors and over-promiscuous metabolites.
stitch_score	Include interactions from STITCH with combined confidence score larger than this.
...	Further parameters to <a href="#">omnipath_interactions</a> .

**Value**

A data frame of binary causal interactions with effect signs, resource specific attributes and translated to the desired identifiers. The "record\_id" column identifies the original records within each resource. If one "record\_id" yields multiple records in the final data frame, it is the result of one-to-many ID translation or other processing steps. Before use, it is recommended to select one pair of ID type columns (by combining the preferred ones) and perform "distinct" by the identifier columns and sign.

**References**

Wang H, Robinson JL, Kocabas P, Gustafsson J, Anton M, Cholley PE, et al. Genome-scale metabolic network reconstruction of model animals as a platform for translational research. *Proceedings of the National Academy of Sciences*. 2021 Jul 27;118(30):e2102344118.

Türei D, Valdeolivas A, Gul L, Palacio-Escat N, Klein M, Ivanova O, et al. Integrated intra- and intercellular signaling knowledge for multicellular omics analysis. *Molecular Systems Biology*. 2021 Mar;17(3):e9923.

**See Also**

- [chalmers\\_gem\\_network](#)

- [stitch\\_network](#)
- [omnipath\\_for\\_cosmos](#)
- [omnipath-interactions](#)

## Examples

```
## Not run:
  human_cosmos <- cosmos_pkn(organism = "human")

## End(Not run)
```

---

```
curated_ligand_receptor_interactions
  Curated ligand-receptor interactions
```

---

## Description

The OmniPath *intercell* database annotates individual proteins and complexes, and we combine these annotations with network interactions on the client side, using [import\\_intercell\\_network](#). The architecture of this database is complex, aiming to cover a broad range of knowledge on various levels of details and confidence. We can use the [intercell\\_consensus\\_filter](#) and [filter\\_intercell\\_network](#) functions for automated, data driven quality filtering, in order to enrich the cell-cell communication network in higher confidence interactions. However, for many users, a simple combination of the most established, expert curated ligand-receptor resources, provided by this function, fits better their purpose.

## Usage

```
curated_ligand_receptor_interactions(
  curated_resources = c("Guide2Pharma", "HPRM", "ICELLNET", "Kirouac2010", "CellTalkDB",
    "CellChatDB", "connectomeDB2020"),
  cellphonedb = TRUE,
  cellinker = TRUE,
  talklr = TRUE,
  signalink = TRUE,
  ...
)
```

## Arguments

`curated_resources`

Character vector of the resource names which are considered to be expert curated. You can include any post-translational network resource here, but if you include non ligand-receptor or non curated resources, the result will not fulfill the original intention of this function.

cellphonedb	Logical: include the curated interactions from <i>CellPhoneDB</i> (not the whole <i>CellPhoneDB</i> but a subset of it).
cellinker	Logical: include the curated interactions from <i>Cellinker</i> (not the whole <i>Cellinker</i> but a subset of it).
talklr	Logical: include the curated interactions from <i>talklr</i> (not the whole <i>talklr</i> but a subset of it).
signalink	Logical: include the ligand-receptor interactions from <i>SignalLink</i> . These are all expert curated.
...	Passed to <a href="#">import_post_translational_interactions</a> : further parameters for the interaction data. Should not contain 'resources' argument as that would interfere with the downstream calls.

### Details

Some resources are a mixture of curated and bulk imported interactions, and sometimes it's not trivial to separate these, we take care of these here. This function does not use the *intercell* database of OmniPath, but retrieves and filters a handful of network resources. The returned data frame has the layout of *interactions* (network) data frames, and the *source* and *target* partners implicitly correspond to *ligand* and *receptor*. The data frame shows all resources and references for all interactions, but each interaction is supported by at least one ligand-receptor resource which is supposed to be based on expert curation in a ligand-receptor context.

### Value

A data frame similar to *interactions* (network) data frames, the *source* and *target* partners being ligand and receptor, respectively.

### See Also

- [import\\_intercell\\_network](#)
- [filter\\_intercell\\_network](#)
- [annotated\\_network](#)
- [import\\_post\\_translational\\_interactions](#)
- [import\\_ligrecextra\\_interactions](#)
- [curated\\_ligrec\\_stats](#)

### Examples

```
lr <- curated_ligand_receptor_interactions()
lr
```

---

curated\_ligrec\_stats *Statistics about literature curated ligand-receptor interactions*

---

## Description

Statistics about literature curated ligand-receptor interactions

## Usage

```
curated_ligrec_stats(...)
```

## Arguments

... Passed to [curated\\_ligand\\_receptor\\_interactions](#), determines the set of all curated L-R interactions which will be compared against each of the individual resources.

## Details

The data frame contains the total number of interactions, the number of interactions which overlap with the set of curated interactions (*curated\_overlap*), the number of interactions with literature references from the given resource (*literature*) and the number of interactions which are curated by the given resource (*curated\_self*). This latter we defined according to our best knowledge, in many cases it's not possible to distinguish curated interactions). All these numbers are also presented as a percent of the total. Importantly, here we consider interactions curated only if they've been curated in a cell-cell communication context.

## Value

A data frame with estimated counts of curated ligand-receptor interactions for each L-R resource.

## See Also

[curated\\_ligand\\_receptor\\_interactions](#)

## Examples

```
clr <- curated_ligrec_stats()
clr
```

---

database_summary	<i>Summary of the annotations and intercell database contents</i>
------------------	---

---

### Description

The ‘annotations\_summary’ and ‘intercell\_summary’ query types return detailed information on the contents of these databases. It includes all the available resources, fields and values in the database.

### Usage

```
database_summary(query_type, return_df = FALSE)
```

### Arguments

query_type	Character: either "annotations" or "intercell".
return_df	Logical: return a data frame instead of list.

### Value

Summary of the database contents: the available resources, fields, and their possible values. As a nested list if format is "json", otherwise a data frame.

### Examples

```
annotations_summary <- database_summary('annotations')
```

---

datasets_one_column	<i>Create a column with dataset names listed</i>
---------------------	--

---

### Description

From logical columns for each dataset, here we create a column that is a list of character vectors, containing dataset labels.

### Usage

```
datasets_one_column(data, remove_logicals = TRUE)
```

### Arguments

data	Interactions data frame with dataset columns (i.e. queried with the option ‘fields = "datasets"’).
remove_logicals	Logical: remove the per dataset logical columns.



**Value**

The input data frame with the new column "datasets" added.

---

descendants	<i>All descendants in the ontology tree</i>
-------------	---

---

**Description**

Starting from the selected nodes, recursively walks the ontology tree until it reaches the leaf nodes. Collects all visited nodes, which are the descendants (children) of the starting nodes.

**Usage**

```
descendants(
  terms,
  db_key = "go_basic",
  ids = TRUE,
  relations = c("is_a", "part_of", "occurs_in", "regulates", "positively_regulates",
               "negatively_regulates")
)
```

**Arguments**

terms	Character vector of ontology term IDs or names. A mixture of IDs and names can be provided.
db_key	Character: key to identify the ontology database. For the available keys see <a href="#">omnipath_show_db</a> .
ids	Logical: whether to return IDs or term names.
relations	Character vector of ontology relation types. Only these relations will be used.

**Details**

Note: this function relies on the database manager, the first call might take long because of the database load process. Subsequent calls within a short period should be faster. See [get\\_ontology\\_db](#).

**Value**

Character vector of ontology IDs. If the input terms are all leaves NULL is returned. The starting nodes won't be included in the result unless some of them are descendants of other starting nodes.

**Examples**

```
descendants('GO:0005035', ids = FALSE)
# [1] "tumor necrosis factor-activated receptor activity"
# [2] "TRAIL receptor activity"
# [3] "TNFSF11 receptor activity"
```

---

ensembl_dataset	<i>Ensembl dataset name from organism</i>
-----------------	---

---

**Description**

Ensembl dataset name from organism

**Usage**

```
ensembl_dataset(organism)
```

**Arguments**

organism	Character or integer: an organism (taxon) name or identifier. If an Ensembl dataset name is provided
----------	--

**Value**

Character: name of an ensembl dataset.

**Examples**

```
ensembl_dataset(10090)
# [1] "mmusculus_gene_ensembl"
```

---

ensembl_id_mapping_table	<i>Identifier translation table from Ensembl</i>
--------------------------	--

---

**Description**

Identifier translation table from Ensembl

**Usage**

```
ensembl_id_mapping_table(to, from = "uniprot", organism = 9606)
```

**Arguments**

to	Character or symbol: target ID type. See Details for possible values.
from	Character or symbol: source ID type. See Details for possible values.
organism	Character or integer: NCBI Taxonomy ID or name of the organism (by default 9606 for human).

**Details**

The arguments to and from can be provided either as character or as symbol (NSE). Their possible values are either Ensembl attribute names or synonyms listed at [translate\\_ids](#).

**Value**

A data frame (tibble) with columns 'From' and 'To'.

**See Also**

- [translate\\_ids](#)
- [uniprot\\_full\\_id\\_mapping\\_table](#)
- [uniprot\\_id\\_mapping\\_table](#)
- [hmdb\\_id\\_mapping\\_table](#)
- [chalmers\\_gem\\_id\\_mapping\\_table](#)

**Examples**

```
ensp_up <- ensembl_id_mapping_table("ensp")
ensp_up
# # A tibble: 119,129 × 2
#   From   To
#   <chr> <chr>
# 1 P03886 ENSP00000354687
# 2 P03891 ENSP00000355046
# 3 P00395 ENSP00000354499
# 4 P00403 ENSP00000354876
# 5 P03928 ENSP00000355265
# # . with 119,124 more rows
```

---

ensembl_id_type	<i>Ensembl identifier type label</i>
-----------------	--------------------------------------

---

**Description**

Ensembl identifier type label

**Usage**

```
ensembl_id_type(label)
```

**Arguments**

label                    Character: an ID type label, as shown in the table at [translate\\_ids](#)

**Value**

Character: the Ensembl specific ID type label, or the input unchanged if it could not be translated (still might be a valid identifier name). These labels should be valid Ensembl attribute names, directly usable in Ensembl queries.

**See Also**

- [uniprot\\_id\\_type](#)
- [uploadlists\\_id\\_type](#)
- [chalmers\\_gem\\_id\\_type](#)
- [hmdb\\_id\\_type](#)

**Examples**

```
ensembl_id_type("uniprot")  
# [1] "uniprotswissprot"
```

---

ensembl_name	<i>Ensembl identifiers of organisms</i>
--------------	---

---

**Description**

Ensembl identifiers of organisms

**Usage**

```
ensembl_name(name)
```

**Arguments**

name            Vector with any kind of organism name or identifier, can be also mixed type.

**Value**

Character vector with Ensembl taxon names, NA if a name in the input could not be found.

**See Also**

- [ncbi\\_taxid](#)
- [common\\_name](#)
- [latin\\_name](#)

**Examples**

```
ensembl_name(c(9606, "cat", "dog"))
# [1] "hsapiens" "fcatus" "clfamilialis"
ensembl_name(c("human", "kitten", "cow"))
# [1] "hsapiens" NA "btaurus"
```

---

ensembl\_organisms      *Organism names and identifiers from Ensembl*

---

**Description**

A table with various taxon names and identifiers: English common names, latin (scientific) names, Ensembl organism IDs and NCBI taxonomy IDs.

**Usage**

```
ensembl_organisms()
```

**Value**

A data frame with the above mentioned columns.

**Examples**

```
ens_org <- ensembl_organisms()
ens_org
```

---

ensembl\_organisms\_raw      *Table of Ensembl organisms*

---

**Description**

A table with various taxon IDs and metadata about related Ensembl database contents, as shown at <https://www.ensembl.org/info/about/species.html>. The "Taxon ID" column contains the NCBI Taxonomy identifiers.

**Usage**

```
ensembl_organisms_raw()
```

**Value**

The table described above as a data frame.

**Examples**

```
ens_org <- ensembl_organisms_raw()
ens_org
```

---

ensembl_orthology	<i>Orthologous gene pairs from Ensembl</i>
-------------------	--

---

**Description**

Orthologous gene pairs from Ensembl

**Usage**

```
ensembl_orthology(
  organism_a = 9606,
  organism_b = 10090,
  attrs_a = NULL,
  attrs_b = NULL,
  colrename = TRUE
)
```

**Arguments**

organism_a	Character or integer: organism name or identifier for the left side organism. We query the Ensembl dataset of this organism and add the orthologues of the other organism to it. Ideally this is the organism you translate from.
organism_b	Character or integer: organism name or identifier for the right side organism. We add orthology information of this organism to the gene records of the left side organism.
attrs_a	Further attributes about organism_a genes. Will be simply added to the attributes list.
attrs_b	Further attributes about organism_b genes (orthologues). The available attributes are: "associated_gene_name", "chromosome", "chrom_start", "chrom_end", "wga_coverage", "goc_score", "perc_id_r1", "perc_id", "subtype". Attributes included by default: "ensembl_gene", "ensembl_peptide", "canonical_transcript_protein", "orthology_confidence" and "orthology_type".
colrename	Logical: replace prefixes from organism_b attribute column names, so the returned table always have the same column names, no matter the organism. E.g. for mouse these columns all have the prefix "mmusculus_homolog_", which this option changes to "b_".

**Details**

Only the records with orthology information are returned. The order of columns is the following: defaults of organism\_a, extra attributes of organism\_b, defaults of organism\_b, extra attributes of organism\_b.

**Value**

A data frame of orthologous gene pairs with gene, transcript and peptide identifiers and confidence values.

**Examples**

```
## Not run:
sffish <- ensembl_orthology(
  organism_b = 'Siamese fighting fish',
  attrs_a = 'external_gene_name',
  attrs_b = 'associated_gene_name'
)
sffish
# # A tibble: 175,608 × 10
#   ensembl_gene_id ensembl_transcript_id ensembl_peptide. external_gene_n.
#   <chr>          <chr>                <chr>          <chr>
# 1 ENSG00000277196 ENST00000621424      ENSP00000481127 NA
# 2 ENSG00000277196 ENST00000615165      ENSP00000482462 NA
# 3 ENSG00000278817 ENST00000613204      ENSP00000482514 NA
# 4 ENSG00000274847 ENST00000400754      ENSP00000478910 MAFIP
# 5 ENSG00000273748 ENST00000612919      ENSP00000479921 NA
# # . with 175,603 more rows, and 6 more variables:
# #   b_ensembl_peptide <chr>, b_ensembl_gene <chr>,
# #   b_orthology_type <chr>, b_orthology_confidence <dbl>,
# #   b_canonical_transcript_protein <chr>, b_associated_gene_name <chr>
#
## End(Not run)
```

---

ensure\_igraph

*Converts a network to igraph object unless it is already one*

---

**Description**

Converts a network to igraph object unless it is already one

**Usage**

```
ensure_igraph(network)
```

**Arguments**

network Either an OmniPath interaction data frame, or an igraph graph object.

**Value**

An igraph graph object.

---

enzsub_graph	<i>Enzyme-substrate graph</i>
--------------	-------------------------------

---

**Description**

Transforms the a data frame with enzyme-substrate relationships (obtained by [enzyme\\_substrate](#)) to an igraph graph object.

**Usage**

```
enzsub_graph(enzsub)
```

**Arguments**

enzsub            Data frame created by [enzyme\\_substrate](#)

**Value**

An igraph directed graph object.

**See Also**

- [enzyme\\_substrate](#)
- [giant\\_component](#)
- [find\\_all\\_paths](#)

**Examples**

```
enzsub <- enzyme_substrate(resources = c('PhosphoSite', 'SIGNOR'))  
enzsub_g <- enzsub_graph(enzsub = enzsub)
```

---

enzsub_resources	<i>Retrieves a list of enzyme-substrate resources available in OmniPath</i>
------------------	---

---

**Description**

Get the names of the enzyme-substrate relationship resources available in <https://omnipathdb.org/enzsub>

**Usage**

```
enzsub_resources(dataset = NULL)
```



**Arguments**

dataset ignored for this query type

**Value**

character vector with the names of the enzyme-substrate resources

**See Also**

- [resources](#)
- [enzyme\\_substrate](#)

**Examples**

```
enzsub_resources()
```

---

enzyme\_substrate      *Enzyme-substrate (PTM) relationships from OmniPath*

---

**Description**

Imports the enzyme-substrate (more exactly, enzyme-PTM) relationship database from <https://omnipathdb.org/enzsub>. These are mostly kinase-substrate relationships, with some acetylation and other types of PTMs.

**Usage**

```
enzyme_substrate(...)
```

**Arguments**

... Arguments passed on to [omnipath\\_query](#)

organism Character or integer: name or NCBI Taxonomy ID of the organism. OmniPath is built of human data, and the web service provides orthology translated interactions and enzyme-substrate relationships for mouse and rat. For other organisms and query types, orthology translation will be called automatically on the downloaded human data before returning the result.

resources Character vector: name of one or more resources. Restrict the data to these resources. For a complete list of available resources, call the '[<query\\_type>\\_resources](#)' functions for the query type of interest.

genesymbols Character or logical: TRUE or FALSE or "yes" or "no". Include the 'genesymbols' column in the results. OmniPath uses UniProt IDs as the primary identifiers, gene symbols are optional.

fields Character vector: additional fields to include in the result. For a list of available fields, call '[query\\_info\("interactions"\)](#)'.

`default_fields` Logical: if TRUE, the default fields will be included.

`silent` Logical: if TRUE, no messages will be printed. By default a summary message is printed upon successful download.

`logicals` Character vector: fields to be cast to logical.

`format` Character: if "json", JSON will be retrieved and processed into a nested list; any other value will return data frame.

`download_args` List: parameters to pass to the download function, which is 'readr::read\_tsv' by default, and 'jsonlite::safe\_load'.

`add_counts` Logical: if TRUE, the number of references and number of resources for each record will be added to the result.

`license` Character: license restrictions. By default, data from resources allowing "academic" use is returned by OmniPath. If you use the data for work in a company, you can provide "commercial" or "for-profit", which will restrict the data to those records which are supported by resources that allow for-profit use.

`password` Character: password for the OmniPath web service. You can provide a special password here which enables the use of 'license = "ignore"' option, completely bypassing the license filter.

`exclude` Character vector: resource or dataset names to be excluded. The data will be filtered after download to remove records of the excluded datasets and resources.

`strict_evidences` Logical: reconstruct the "sources" and "references" columns of interaction data frames based on the "evidences" column, strictly filtering them to the queried datasets and resources. Without this, the "sources" and "references" fields for each record might contain information for datasets and resources other than the queried ones, because the downloaded records are a result of a simple filtering of an already integrated data frame.

`genesymbol_resource` Character: "uniprot" (default) or "ensembl". The OmniPath web service uses the primary gene symbols as provided by UniProt. By passing "ensembl" here, the UniProt gene symbols will be replaced by the ones used in Ensembl. This translation results in a loss of a few records, and multiplication of another few records due to ambiguous translation.

`cache` Logical: use caching, load data from and save to the. The cache directory by default belongs to the user, located in the user's default cache directory, and named "OmnipathR". Find out about it by `getOption("omnipathr.cachedir")`. Can be changed by `omnipath_set_cachedir`.

## Value

A data frame of enzymes and their PTM substrates.

## See Also

- [enzsub\\_resources](#)
- [omnipath\\_interactions](#)
- [enzsub\\_graph](#)

- `print_interactions`
- `query_info`
- `omnipath_query`

## Examples

```
enzsub <- enzyme_substrate(  
  resources = c("PhosphoSite", "SIGNOR"),  
  organism = 9606  
)
```

---

evex\_download

*Interactions from the EVEX database*

---

## Description

Downloads interactions from EVEX, a versatile text mining resource (<http://evexdb.org>). Translates the Entrez Gene IDs to Gene Symbols and combines the interactions and references into a single data frame.

## Usage

```
evex_download(  
  min_confidence = NULL,  
  remove_negatives = TRUE,  
  top_confidence = NULL  
)
```

## Arguments

`min_confidence` Numeric: a threshold for confidence scores. EVEX confidence scores span roughly from -3 to 3. By providing a numeric value in this range the lower confidence interactions can be removed. If NULL no filtering performed.

`remove_negatives` Logical: remove the records with the "negation" attribute set.

`top_confidence` Confidence cutoff as quantile (a number between 0 and 1). If NULL no filtering performed.

## Value

Data frame (tibble) with interactions.

**Examples**

```

evex_interactions <- evex_download()
evex_interactions
# # A tibble: 368,297 x 13
#   general_event_id source_entrezge. target_entrezge. confidence negation
#   <dbl> <chr> <chr> <dbl> <dbl>
# 1      98 8651      6774      -1.45      0
# 2     100 8431      6774      -1.45      0
# 3     205 6261      6263       0.370      0
# 4     435 1044      1045      -1.09      0
# . with 368,287 more rows, and 8 more variables: speculation <dbl>,
#   coarse_type <chr>, coarse_polarity <chr>, refined_type <chr>,
#   refined_polarity <chr>, source_genesymbol <chr>,
#   target_genesymbol <chr>, references <chr>

```

---

evidences

*Show evidences for an interaction*


---

**Description**

Show evidences for an interaction

**Usage**

```

evidences(
  partner_a,
  partner_b,
  interactions = NULL,
  directed = FALSE,
  open = TRUE,
  browser = NULL,
  max_pages = 25L
)

```

**Arguments**

partner_a	Identifier or name of one interacting partner. The order of the partners matter only if 'directed' is 'TRUE'. For both partners, vectors of more than one identifiers can be passed.
partner_b	Identifier or name of the other interacting partner.
interactions	An interaction data frame. If not provided, all interactions will be loaded within this function, but that takes noticeable time. If a 'list' is provided, it will be used as parameters for <a href="#">omnipath_interactions</a> . This way you can define the organism, datasets or the interaction type.
directed	Logical: does the direction matter? If 'TRUE', only a → b interactions will be shown.
open	Logical: open online articles in a web browser.

browser	Character: override the web browser executable used to open online articles.
max_pages	Numeric: largest number of pages to open. This is to prevent opening hundreds or thousands of pages at once.

### Details

If the number of references is larger than ‘max\_pages’, the most recent ones will be opened. URLs are passed to the browser in order of decreasing publication date, though browsers do not seem to respect the order at all. In addition Firefox, if it’s not open already, tends to randomly open empty tab for the first or last URL, have no idea what to do about it.

### Value

Nothing.

### Examples

```
## Not run:
evidences('CALM1', 'TRPC1', list(datasets = 'omnipath'))

## End(Not run)
```

---

extra_attrs	<i>Extra attribute names in an interaction data frame</i>
-------------	---

---

### Description

Interaction data frames might have an ‘extra\_attrs’ column if this field has been requested in the query by passing the ‘fields = ‘extra\_attrs’ argument. This column contains resource specific attributes for the interactions. The names of the attributes consist of the name of the resource and the name of the attribute, separated by an underscore. This function returns the names of the extra attributes available in the provided data frame.

### Usage

```
extra_attrs(data)
```

### Arguments

data	An interaction data frame, as provided by any of the <a href="#">omnipath-interactions</a> functions.
------	---

### Value

Character: the names of the extra attributes in the data frame.

**See Also**

- [extra\\_attrs\\_to\\_cols](#)
- [has\\_extra\\_attrs](#)
- [with\\_extra\\_attrs](#)
- [filter\\_extra\\_attrs](#)
- [extra\\_attr\\_values](#)

**Examples**

```
i <- omnipath(fields = "extra_attrs")
extra_attrs(i)
```

---

extra\_attrs\_to\_cols    *New columns from extra attributes*

---

**Description**

New columns from extra attributes

**Usage**

```
extra_attrs_to_cols(data, ..., flatten = FALSE, keep_empty = TRUE)
```

**Arguments**

data	An interaction data frame.
...	The names of the extra attributes; NSE is supported. Custom column names can be provided as argument names.
flatten	Logical: unnest the list column even if some records have multiple values for the attributes; these will yield multiple records in the resulted data frame.
keep_empty	Logical: if 'flatten' is 'TRUE', shall we keep the records which do not have the attribute?

**Value**

Data frame with the new column created; the new column is list type if one interaction might have multiple values of the attribute, or character type if

**See Also**

- [extra\\_attrs](#)
- [has\\_extra\\_attrs](#)
- [with\\_extra\\_attrs](#)
- [filter\\_extra\\_attrs](#)
- [extra\\_attr\\_values](#)

## Examples

```
i <- omnipath(fields = "extra_attrs")
extra_attrs_to_cols(i, Cellinker_type, Macrophage_type)
extra_attrs_to_cols(
  i,
  Cellinker_type,
  Macrophage_type,
  flatten = TRUE,
  keep_empty = FALSE
)
```

---

extra_attr_values	<i>Possible values of an extra attribute</i>
-------------------	--

---

## Description

Extracts all unique values of an extra attribute occurring in this data frame.

## Usage

```
extra_attr_values(data, key)
```

## Arguments

data	An interaction data frame with <i>extra_attrs</i> column.
key	The name of an extra attribute.

## Details

Note, at the end we unlist the result, which means it works well for attributes which are atomic vectors but gives not so useful result if the attribute values are more complex objects. As the time of writing this, no such complex extra attribute exist in OmniPath.

## Value

A vector, most likely character, with the unique values of the extra attribute occurring in the data frame.

## See Also

- [extra\\_attrs\\_to\\_cols](#)
- [has\\_extra\\_attrs](#)
- [with\\_extra\\_attrs](#)
- [filter\\_extra\\_attrs](#)
- [extra\\_attrs](#)

**Examples**

```
op <- omnipath(fields = "extra_attrs")
extra_attr_values(op, SIGNOR_mechanism)
```

---

filter\_by\_resource      *Filters OmniPath data by resources*

---

**Description**

Keeps only those records which are supported by any of the resources of interest.

**Usage**

```
filter_by_resource(data, resources = NULL)
```

**Arguments**

data	A data frame downloaded from the OmniPath web service (interactions, enzyme-substrate or complexes).
resources	Character vector with resource names to keep.

**Value**

The data frame filtered.

**Examples**

```
interactions <- omnipath()
signor <- filter_by_resource(interactions, resources = "SIGNOR")
```

---

filter\_evidences      *Filter evidences by dataset, resource and license*

---

**Description**

Filter evidences by dataset, resource and license

**Usage**

```
filter_evidences(data, ..., datasets = NULL, resources = NULL, exclude = NULL)
```



**Arguments**

data	An interaction data frame with some columns containing evidences as nested lists.
...	The evidences columns to filter: tidyselect syntax is supported. By default the columns "evidences", "positive", "negative", "directed" and "undirected" are filtered, if present.
datasets	A character vector of dataset names.
resources	A character vector of resource names.
exclude	Character vector of resource names to be excluded.

**Value**

The input data frame with the evidences in the selected columns filtered.

**See Also**

- [only\\_from](#)
- [unnest\\_evidences](#)
- [from\\_evidences](#)

---

filter\_extra\_attrs      *Filter interactions by extra attribute values*

---

**Description**

Filter interactions by extra attribute values

**Usage**

```
filter_extra_attrs(data, ..., na_ok = TRUE)
```

**Arguments**

data	An interaction data frame with <i>extra_attrs</i> column.
...	Extra attribute names and values. The contents of the extra attribute <i>name</i> for each record will be checked against the values provided. The check by default is a set intersection: if any element is common between the user provided values and the values of the extra attribute for the record, the record will be matched. Alternatively, any value can be a custom function which accepts the value of the extra attribute and returns a single logical value. Finally, if the extra attribute name starts with a dot, the result of the check will be negated.
na_ok	Logical: keep the records which do not have the extra attribute. Typically these are the records which are not from the resource providing the extra attribute.

**Value**

The input data frame with records removed according to the filtering criteria.

**See Also**

- [extra\\_attrs](#)
- [has\\_extra\\_attrs](#)
- [extra\\_attrs\\_to\\_cols](#)
- [with\\_extra\\_attrs](#)
- [extra\\_attr\\_values](#)

**Examples**

```
cl <- post_translational(  
  resources = "Cellinker",  
  fields = "extra_attrs"  
)  
# Only cell adhesion interactions from Cellinker  
filter_extra_attrs(cl, Cellinker_type = "Cell adhesion")  
  
op <- omnipath(fields = "extra_attrs")  
# Any mechanism except phosphorylation  
filter_extra_attrs(op, .SIGNOR_mechanism = "phosphorylation")
```

---

filter\_intercell      *Filter intercell annotations*

---

**Description**

Filters a data frame retrieved by [intercell](#).

**Usage**

```
filter_intercell(  
  data,  
  categories = NULL,  
  resources = NULL,  
  parent = NULL,  
  scope = NULL,  
  aspect = NULL,  
  source = NULL,  
  transmitter = NULL,  
  receiver = NULL,  
  secreted = NULL,  
  plasma_membrane_peripheral = NULL,  
  plasma_membrane_transmembrane = NULL,
```

```

    proteins = NULL,
    causality = NULL,
    topology = NULL,
    ...
)

```

### Arguments

data	An intercell annotation data frame as provided by <a href="#">intercell</a> .
categories	Character: allow only these values in the category column.
resources	Character: allow records only from these resources.
parent	Character: filter for records with these parent categories.
scope	Character: filter for records with these annotation scopes. Possible values are generic and specific.
aspect	Character: filter for records with these annotation aspects. Possible values are functional and locational.
source	Character: filter for records with these annotation sources. Possible values are composite and resource_specific.
transmitter	Logical: if TRUE only transmitters, if FALSE only non-transmitters will be selected, if NULL it has no effect.
receiver	Logical: works the same way as transmitters.
secreted	Logical: works the same way as transmitters.
plasma_membrane_peripheral	Logical: works the same way as transmitters.
plasma_membrane_transmembrane	Logical: works the same way as transmitters.
proteins	Character: filter for annotations of these proteins. Gene symbols or UniProt IDs can be used.
causality	Character: filter for records with these causal roles. Possible values are transmitter and receiver. The filter applied simultaneously to the transmitter and receiver arguments, it's just a different notation for the same thing.
topology	Character: filter for records with these localization topologies. Possible values are secreted, plasma_membrane_peripheral and plasma_membrane_transmembrane; the shorter notations sec, pmp and pmtm can be used. Has the same effect as the logical type arguments, just uses a different notation.
...	Ignored.

### Value

The intercell annotation data frame filtered according to the specified conditions.

**See Also**

- [intercell](#)
- [intercell\\_categories](#)
- [intercell\\_generic\\_categories](#)
- [intercell\\_summary](#)
- [intercell\\_network](#)

**Examples**

```
ic <- intercell()
ic <- filter_intercell(
  ic,
  transmitter = TRUE,
  secreted = TRUE,
  scope = "specific"
)
```

---

filter\_intercell\_network

*Quality filter an intercell network*

---

**Description**

The intercell database of OmniPath covers a very broad range of possible ways of cell to cell communication, and the pieces of information, such as localization, topology, function and interaction, are combined from many, often independent sources. This unavoidably result some weird and unexpected combinations which are false positives in the context of intercellular communication. [intercell\\_network](#) provides a shortcut (high\_confidence) to do basic quality filtering. For custom filtering or experimentation with the parameters we offer this function.

**Usage**

```
filter_intercell_network(
  network,
  transmitter_topology = c("secreted", "plasma_membrane_transmembrane",
    "plasma_membrane_peripheral"),
  receiver_topology = "plasma_membrane_transmembrane",
  min_curation_effort = 2,
  min_resources = 1,
  min_references = 0,
  min_provenances = 1,
  consensus_percentile = 50,
  loc_consensus_percentile = 30,
  ligand_receptor = FALSE,
  simplify = FALSE,
```

```

    unique_pairs = FALSE,
    omnipath = TRUE,
    ligreextra = TRUE,
    kinaseextra = FALSE,
    pathwayextra = FALSE,
    ...
)

```

## Arguments

network	An intercell network data frame, as provided by <a href="#">intercell_network</a> , without simplify.
transmitter_topology	Character vector: topologies allowed for the entities in transmitter role. Abbreviations allowed: "sec", "pmtm" and "pmp".
receiver_topology	Same as transmitter_topology for the entities in the receiver role.
min_curation_effort	Numeric: a minimum value of curation effort (resource-reference pairs) for network interactions. Use zero to disable filtering.
min_resources	Numeric: minimum number of resources for interactions. The value 1 means no filtering.
min_references	Numeric: minimum number of references for interactions. Use zero to disable filtering.
min_provenances	Numeric: minimum number of provenances (either resources or references) for interactions. Use zero or one to disable filtering.
consensus_percentile	Numeric: percentile threshold for the consensus score of generic categories in intercell annotations. The consensus score is the number of resources supporting the classification of an entity into a category based on combined information of many resources. Here you can apply a cut-off, keeping only the annotations supported by a higher number of resources than a certain percentile of each category. If NULL no filtering will be performed. The value is either in the 0-1 range, or will be divided by 100 if greater than 1. The percentiles will be calculated against the generic composite categories and then will be applied to their resource specific annotations and specific child categories.
loc_consensus_percentile	Numeric: similar to consensus_percentile for major localizations. For example, with a value of 50, the secreted, plasma membrane transmembrane or peripheral attributes will be TRUE only where at least 50 percent of the resources support these.
ligand_receptor	Logical. If TRUE, only <i>ligand</i> and <i>receptor</i> annotations will be used instead of the more generic <i>transmitter</i> and <i>receiver</i> categories.
simplify	Logical: keep only the most often used columns. This function combines a network data frame with two copies of the intercell annotation data frames, all

of them already having quite some columns. With this option we keep only the names of the interacting pair, their intercellular communication roles, and the minimal information of the origin of both the interaction and the annotations.

unique_pairs	Logical: instead of having separate rows for each pair of annotations, drop the annotations and reduce the data frame to unique interacting pairs. See <a href="#">unique_intercell_network</a> for details.
omnipath	Logical: shortcut to include the <i>omnipath</i> dataset in the interactions query.
ligreextra	Logical: shortcut to include the <i>ligreextra</i> dataset in the interactions query.
kinaseextra	Logical: shortcut to include the <i>kinaseextra</i> dataset in the interactions query.
pathwayextra	Logical: shortcut to include the <i>pathwayextra</i> dataset in the interactions query.
...	If <code>simplify</code> or <code>unique_pairs</code> is TRUE, additional column names can be passed here to <code>dplyr::select</code> on the final data frame. Otherwise ignored.

### Value

An intercell network data frame filtered.

### See Also

- [intercell\\_network](#)
- [unique\\_intercell\\_network](#)
- [simplify\\_intercell\\_network](#)
- [intercell](#)
- [intercell\\_categories](#)
- [intercell\\_generic\\_categories](#)
- [intercell\\_summary](#)

### Examples

```
icn <- intercell_network()
icn_f <- filter_intercell_network(
  icn,
  consensus_percentile = 75,
  min_provenances = 3,
  simplify = TRUE
)
```

---

find_all_paths	<i>All paths between two groups of vertices</i>
----------------	---

---

### Description

Finds all paths up to length 'maxlen' between specified groups of vertices. This function is needed only because igraph's 'all\_shortest\_paths' finds only the shortest, not any path up to a defined length.

### Usage

```
find_all_paths(  
  graph,  
  start,  
  end,  
  attr = NULL,  
  mode = 'OUT',  
  maxlen = 2,  
  progress = TRUE  
)
```

### Arguments

graph	An igraph graph object.
start	Integer or character vector with the indices or names of one or more start vertices.
end	Integer or character vector with the indices or names of one or more end vertices.
attr	Character: name of the vertex attribute to identify the vertices by. Necessary if 'start' and 'end' are not igraph vertex ids but for example vertex names or labels.
mode	Character: IN, OUT or ALL. Default is OUT.
maxlen	Integer: maximum length of paths in steps, i.e. if maxlen = 3, then the longest path may consist of 3 edges and 4 nodes.
progress	Logical: show a progress bar.

### Value

List of vertex paths, each path is a character or integer vector.

### See Also

- [interaction\\_graph](#)
- [enzsub\\_graph](#)
- [giant\\_component](#)

## Examples

```
interactions <- import_omnipath_interactions()
graph <- interaction_graph(interactions)
paths <- find_all_paths(
  graph = graph,
  start = c('EGFR', 'STAT3'),
  end = c('AKT1', 'ULK1'),
  attr = 'name'
)
```

---

from\_evidences

*Recreate interaction records from evidences columns*

---

## Description

Recreate interaction records from evidences columns

## Usage

```
from_evidences(data, .keep = FALSE)
```

## Arguments

data	An interaction data frame from the OmniPath web service with evidences column.
.keep	Logical: keep the original "evidences" column when unnesting to separate columns by direction.

## Details

The OmniPath interaction data frames specify interactions primarily by three columns: "is\_directed", "is\_stimulation" and "is\_inhibition". Besides these, there are the "sources" and "references" columns that are always included in data frames created by OmnipathR and list the resources and literature references for each interaction, respectively. The optional "evidences" column is required to find out which of the resources and references support the direction or effect sign of the interaction. To properly recover information for arbitrary subsets of resources or datasets, the evidences can be filtered first, and then the standard data frame columns can be reconstructed from the selected evidences. This function is able to do the latter. It expects either an "evidences" column or evidences in their wide format 4 columns layout. It overwrites the standard columns of interaction records based on data extracted from the evidences, including the "curation\_effort" and "consensus..." columns.

**Note:** The "curation\_effort" might be calculated slightly differently from the version included in the OmniPath web service. Here we count the resources and the also add the number of references for each resource. E.g. a resource without any literatur reference counts as 1, while a resource with 3 references adds 4 to the value of the curation effort.



**Note:** If the "evidences" column has been already unnested to multiple columns ("positive", "negative", etc.) by [unnest\\_evidences](#), then these will be used; otherwise, the column will be unnested within this function.

**Note:** This function (or rather its wrapper, [only\\_from](#)) is automatically applied if the 'strict\_evidences' argument is passed to any function querying interactions (see [omnipath-interactions](#)).

### Value

A copy of the input data frame with all the standard columns describing the direction, effect, resources and references of the interactions recreated based on the contents of the nested list evidences column(s).

### See Also

- [filter\\_evidences](#)
- [unnest\\_evidences](#)
- [only\\_from](#)

### Examples

```
## Not run:
ci <- collectri(evidences = TRUE)
ci <- unnest_evidences(ci)
ci <- filter_evidences(datasets = 'collectri')
ci <- from_evidences(ci)
# the three lines above are equivalent to only_from(ci)
# and all the four lines above is equivalent to:
# collectri(strict_evidences = TRUE)

## End(Not run)
```

---

get\_db

*Access a built in database*

---

### Description

Databases are resources which might be costly to load but can be used many times by functions which usually automatically load and retrieve them from the database manager. Each database has a lifetime and will be unloaded automatically upon expiry.

### Usage

```
get_db(key, param = NULL, reload = FALSE, ...)
```

**Arguments**

key	Character: the key of the database to load. For a list of available keys see <a href="#">omnipath_show_db</a> .
param	List: override the defaults or pass further parameters to the database loader function. See the loader functions and their default parameters in <a href="#">omnipath_show_db</a> . If the database is already loaded with different parameters it will be reloaded with the new parameters only if the reload option is TRUE.
reload	Reload the database if param passed here is different from the parameters used the last time the database was loaded. If different functions with different parameters access the database repeatedly and request reload the frequent reloads might cost substantial time and resource use.
...	Arguments for the loader function of the database. These override the default arguments.

**Value**

An object with the database contents. The exact format depends on the database, most often it is a data frame or a list.

**See Also**

[omnipath\\_show\\_db](#).

**Examples**

```
organisms <- get_db('organisms')
```

---

get\_ontology\_db      *Access an ontology database*

---

**Description**

Retrieves an ontology database with relations in the desired data structure. The database is automatically loaded and the requested data structure is constructed if necessary. The databases stay loaded up to a certain time period (see the option `omnipathr.db_lifetime`). Hence the first one of repeated calls to this function might take long and the subsequent ones should be really quick.

**Usage**

```
get_ontology_db(key, rel_fmt = "tbl", child_parents = TRUE)
```

**Arguments**

key	Character: key of the ontology database. For the available keys see <a href="#">omnipath_show_db</a> .
rel_fmt	Character: the data structure of the ontology relations. Possible values are 1) "tbl" a data frame, 2) "lst" a list or 3) "gra" a graph.
child_parents	Logical: whether the ontology relations should point from child to parents (TRUE) or from parent to children (FALSE).

**Value**

A list with the following elements: 1) "names" a table with term IDs and names; 2) "namespaces" a table to connect term IDs and namespaces they belong to; 3) "relations" a table with relations between terms and their parent terms; 4) "subsets" a table with terms and the subsets they are part of; 5) "obsolete" character vector with all the terms labeled as obsolete.

**See Also**

- [omnipath\\_show\\_db](#)
- [get\\_db](#)

**Examples**

```
go <- get_ontology_db('go_basic', child_parents = FALSE)
```

---

giant_component	<i>Giant component of a graph</i>
-----------------	-----------------------------------

---

**Description**

For an igraph graph object returns its giant component.

**Usage**

```
giant_component(graph)
```

**Arguments**

graph	An igraph graph object.
-------	-------------------------

**Value**

An igraph graph object containing only the giant component.

**Examples**

```
interactions <- import_post_translational_interactions()
graph <- interaction_graph(interactions)
graph_gc <- giant_component(graph)
```

---

go\_annot\_download      *Gene annotations from Gene Ontology*

---

### Description

Gene Ontology is an ontology of gene subcellular localizations, molecular functions and involvement in biological processes. Gene products across many organisms are annotated with the ontology terms. This function downloads the gene-ontology term associations for certain model organisms or all organisms. For a description of the columns see <http://geneontology.org/docs/go-annotation-file-gaf-format-2.2/>.

### Usage

```
go_annot_download(organism = "human", aspects = c("C", "F", "P"), slim = NULL)
```

### Arguments

organism	Character: either "chicken", "cow", "dog", "human", "pig" or "uniprot_all".
aspects	Character vector with some of the following elements: "C" (cellular component), "F" (molecular function) and "P" (biological process). Gene Ontology is three separate ontologies called as three aspects. By this parameter you can control which aspects to include in the output.
slim	Character: if not NULL, the name of a GOsubset (slim). instead of the full GO annotation, the slim annotation will be returned. See details at <a href="#">go_annot_slim</a> . If TRUE, the "generic" slim will be used.

### Value

A tibble (data frame) of annotations as it is provided by the database

### Examples

```
goa_data <- go_annot_download()
goa_data
# # A tibble: 606,840 x 17
#   db      db_object_id db_object_symbol qualifier go_id  db_ref
#   <fct>   <chr>         <chr>           <fct>   <chr> <chr>
# 1 UniProt. A0A024RBG1  NUDT4B          NA       GO:000. GO_REF:00.
# 2 UniProt. A0A024RBG1  NUDT4B          NA       GO:000. GO_REF:00.
# 3 UniProt. A0A024RBG1  NUDT4B          NA       GO:004. GO_REF:00.
# 4 UniProt. A0A024RBG1  NUDT4B          NA       GO:005. GO_REF:00.
# 5 UniProt. A0A024RBG1  NUDT4B          NA       GO:005. GO_REF:00.
# # . with 606,830 more rows, and 11 more variables:
# #   evidence_code <fct>, with_or_from <chr>, aspect <fct>,
# #   db_object_name <chr>, db_object_synonym <chr>,
# #   db_object_type <fct>, taxon <fct>, date <date>,
# #   assigned_by <fct>, annotation_extension <chr>,
# #   gene_product_from_id <chr>
```

---

`go_annot_slim`*GO slim gene annotations*

---

## Description

GO slims are subsets of the full GO which "give a broad overview of the ontology content without the detail of the specific fine grained terms". In order to annotate genes with GO slim terms, we take the annotations and search all ancestors of the terms up to the root of the ontology tree. From the ancestors we select the terms which are part of the slim subset.

## Usage

```
go_annot_slim(  
  organism = "human",  
  slim = "generic",  
  aspects = c("C", "F", "P"),  
  cache = TRUE  
)
```

## Arguments

<code>organism</code>	Character: either "chicken", "cow", "dog", "human", "pig" or "uniprot_all".
<code>slim</code>	Character: the GO subset (GO slim) name. Available GO slims are: "agr" (Alliance for Genomics Resources), "generic", "aspergillus", "candida", "drosophila", "chembl", "metagenomic", "mouse", "plant", "pir" (Protein Information Resource), "pombe" and "yeast".
<code>aspects</code>	Character vector with some of the following elements: "C" (cellular component), "F" (molecular function) and "P" (biological process). Gene Ontology is three separate ontologies called as three aspects. By this parameter you can control which aspects to include in the output.
<code>cache</code>	Logical: Load the result from cache if available.

## Details

Building the GO slim is resource intensive in its current implementation. For human annotation and generic GO slim it might take around 20 minutes. The result is saved into the cache so next time loading the data from there is really quick. If the cache option is FALSE the data will be built fresh (the annotation and ontology files still might come from cache), and the newly build GO slim will overwrite the cache instance.

## Value

A tibble (data frame) of genes annotated with ontology terms in in the GO slim (subset).

**See Also**

- [go\\_annot\\_download](#)
- [go\\_ontology\\_download](#)
- [get\\_db](#)

**Examples**

```
## Not run:
goslim <- go_annot_slim(organism = 'human', slim = 'generic')
goslim
# # A tibble: 276,371 x 8
#   db      db_object_id db_object_symbol go_id aspect db_object_name
#   <fct> <chr>          <chr>          <chr> <fct> <chr>
# 1 UniPr. A0A024RBG1  NUDT4B          GO:0. F    Diphosphoinosito.
# 2 UniPr. A0A024RBG1  NUDT4B          GO:0. F    Diphosphoinosito.
# 3 UniPr. A0A024RBG1  NUDT4B          GO:0. C    Diphosphoinosito.
# 4 UniPr. A0A024RBG1  NUDT4B          GO:0. C    Diphosphoinosito.
# 5 UniPr. A0A024RBG1  NUDT4B          GO:0. C    Diphosphoinosito.
# # . with 276,366 more rows, and 2 more variables:
# #   db_object_synonym <chr>, db_object_type <fct>

## End(Not run)
```

---

go\_ontology\_download *The Gene Ontology tree*

---

**Description**

The Gene Ontology tree

**Usage**

```
go_ontology_download(
  basic = TRUE,
  tables = TRUE,
  subset = NULL,
  relations = c("is_a", "part_of", "occurs_in", "regulates", "positively_regulates",
    "negatively_regulates")
)
```

**Arguments**

**basic** Logical: use the basic or the full version of GO. As written on the GO home page: "the basic version of the GO is filtered such that the graph is guaranteed to be acyclic and annotations can be propagated up the graph. The relations included are is a, part of, regulates, negatively regulates and positively regulates. This version excludes relationships that cross the 3 GO hierarchies. This version should be used with most GO-based annotation tools."

tables	In the result return data frames or nested lists. These later can be converted to each other if necessary. However converting from table to list is faster.
subset	Character: the GO subset (GO slim) name. GO slims are subsets of the full GO which "give a broad overview of the ontology content without the detail of the specific fine grained terms". This option, if not NULL, overrides the basic parameter. Available GO slims are: "agr" (Alliance for Genomics Resources), "generic", "aspergillus", "candida", "drosophila", "chembl", "metagenomic", "mouse", "plant", "pir" (Protein Information Resource), "pombe" and "yeast".
relations	Character vector: the relations to include in the processed data.

### Value

A list with the following elements: 1) "names" a list with terms as names and names as values; 2) "namespaces" a list with terms as names and namespaces as values; 3) "relations" a list with relations between terms: terms are keys, values are lists with relations as names and character vectors of related terms as values; 4) "subsets" a list with terms as keys and character vectors of subset names as values (or NULL if the term does not belong to any subset); 5) "obsolete" character vector with all the terms labeled as obsolete. If the tables parameter is TRUE, "names", "namespaces", "relations" and "subsets" will be data frames (tibbles).

### Examples

```
# retrieve the generic GO slim, a small subset of the full ontology
go <- go_ontology_download(subset = 'generic')
```

---

graph_interaction	<i>Interaction data frame from igraph graph object</i>
-------------------	--

---

### Description

Convert an igraph graph object to interaction data frame. This is the reverse of the operation done by the [interaction\\_graph](#) function. Networks can be easily converted to igraph objects, then you can make use of all igraph methods, and at the end, get back the interactions in a data frame, along with all new edge and node attributes.

### Usage

```
graph_interaction(graph, implode = FALSE)
```

### Arguments

graph	An igraph graph object created formerly from an OmniPath interactions data frame.
implode	Logical: restore the original state of the list type columns by imploding them to character vectors, subitems separated by semicolons.

**Value**

An interaction data frame.

**See Also**

[interaction\\_graph](#)

---

guide2pharma\_download *Downloads interactions from the Guide to Pharmacology database*

---

**Description**

Downloads ligand-receptor interactions from the Guide to Pharmacology (IUPHAR/BPS) database (<https://www.guidetopharmacology.org/>).

**Usage**

```
guide2pharma_download()
```

**Value**

A tibble (data frame) of interactions as it is provided by the database

**Examples**

```
g2p_data <- guide2pharma_download()
g2p_data
# # A tibble: 21,586 x 38
#   target target_id target_gene_sym. target_uniprot target_ensembl_
#   <chr>      <dbl> <chr>                <chr>         <chr>
# 1 12S-L.      1387 ALOX12             P18054        ENSG00000108839
# 2 15-LO.      1388 ALOX15             P16050        ENSG00000161905
# 3 15-LO.      1388 ALOX15             P16050        ENSG00000161905
# 4 15-LO.      1388 ALOX15             P16050        ENSG00000161905
# # . with 21,576 more rows, and 33 more variables: target_ligand <chr>,
# #   target_ligand_id <chr>, target_ligand_gene_symbol <chr>,
# # ... (truncated)
```



---

harmonizome\_download *Downloads a Harmonizome network dataset*

---

### Description

Downloads a single network dataset from Harmonizome <https://maayanlab.cloud/Harmonizome>.

### Usage

```
harmonizome_download(dataset)
```

### Arguments

dataset            The dataset part of the URL. Please refer to the download section of the Harmonizome webpage.

### Value

Data frame (tibble) with interactions.

### Examples

```
harmonizome_data <- harmonizome_download('phosphositeplus')
harmonizome_data
# # A tibble: 6,013 x 7
#   source source_desc source_id target target_desc target_id weight
#   <chr>   <chr>         <dbl> <chr> <chr>         <dbl> <dbl>
# 1 TP53    na              7157 STK17A na           9263    1
# 2 TP53    na              7157 TP53RK na          112858  1
# 3 TP53    na              7157 SMG1  na           23049  1
# 4 UPF1    na              5976 SMG1  na           23049  1
# # . with 6,003 more rows
```

---

has\_extra\_attrs            *Tells if an interaction data frame has an extra\_attrs column*

---

### Description

Tells if an interaction data frame has an extra\_attrs column

### Usage

```
has_extra_attrs(data)
```

### Arguments

data                An interaction data frame.

**Value**

Logical: TRUE if the data frame has the "extra\_attrs" column.

**See Also**

- [extra\\_attrs](#)
- [extra\\_attrs\\_to\\_cols](#)
- [with\\_extra\\_attrs](#)
- [filter\\_extra\\_attrs](#)
- [extra\\_attr\\_values](#)

**Examples**

```
i <- omnipath(fields = "extra_attrs")
has_extra_attrs(i)
```

---

hmdb\_id\_mapping\_table *Identifier translation table from HMDB*

---

**Description**

Identifier translation table from HMDB

**Usage**

```
hmdb_id_mapping_table(to, from, entity_type = "metabolite")
```

**Arguments**

to	Character or symbol: target ID type. See Details for possible values.
from	Character or symbol: source ID type. See Details for possible values.
entity_type	Character: "gene" and "smol" are short symbols for proteins, genes and small molecules respectively. Several other synonyms are also accepted.

**Details**

The arguments to and from can be provided either as character or as symbol (NSE). Their possible values are either HMDB XML tag names or synonyms listed at [id\\_types](#).

**Value**

A data frame (tibble) with columns 'From' and 'To'.

**See Also**

- [translate\\_ids](#)
- [id\\_types](#)
- [hmdb\\_table](#)
- [uniprot\\_full\\_id\\_mapping\\_table](#)
- [uniprot\\_id\\_mapping\\_table](#)
- [ensembl\\_id\\_mapping\\_table](#)
- [chalmers\\_gem\\_id\\_mapping\\_table](#)

**Examples**

```
hmdb_kegg <- hmdb_id_mapping_table("kegg", "hmdb")
hmdb_kegg
```

---

hmdb_id_type	<i>HMDB identifier type label</i>
--------------	-----------------------------------

---

**Description**

HMDB identifier type label

**Usage**

```
hmdb_id_type(label)
```

**Arguments**

label                    Character: an ID type label, as shown in the table at [translate\\_ids](#)

**Value**

Character: the HMDB specific ID type label, or the input unchanged if it could not be translated (still might be a valid identifier name). These labels should be valid HMDB field names, as used in HMDB XML files.

**See Also**

- [chalmers\\_gem\\_id\\_type](#)
- [uniprot\\_id\\_type](#)
- [ensembl\\_id\\_type](#)
- [uploadlists\\_id\\_type](#)

**Examples**

```
hmdb_id_type("hmdb")
# [1] "accession"
```

hmdb\_metabolite\_fields

*Field names for the HMDB metabolite dataset*

---

**Description**

Field names for the HMDB metabolite dataset

**Usage**

```
hmdb_metabolite_fields()
```

**Value**

Character vector of field names.

**See Also**

- [hmdb\\_table](#)
- [hmdb\\_protein\\_fields](#)

**Examples**

```
hmdb_metabolite_fields()
```

---

hmdb\_protein\_fields

*Field names for the HMDB proteins dataset*

---

**Description**

Field names for the HMDB proteins dataset

**Usage**

```
hmdb_protein_fields()
```

**Value**

Character vector of field names.

**See Also**

- [hmdb\\_table](#)
- [hmdb\\_metabolite\\_fields](#)

## Examples

```
hmdb_protein_fields()
```

---

hmdb_table	<i>Download a HMDB XML file and process it into a table</i>
------------	---

---

## Description

Download a HMDB XML file and process it into a table

## Usage

```
hmdb_table(dataset = "metabolites", fields = NULL)
```

## Arguments

dataset	Character: name of an HMDB XML dataset, such as "metabolites", "proteins", "urine", "serum", "csf", "saliva", "feces", "sweat".
fields	Character: fields to extract from the XML. This is a very minimal parser that is able to extract the text content of simple fields and multiple value fields which contain a list of leaves within one container tag under the record tag. A full list of fields available in HMDB is available by the <a href="#">hmdb_protein_fields</a> and <a href="#">hmdb_metabolite_fields</a> functions. By default, all fields available in the dataset are extracted.

## Value

A data frame (tibble) with each column corresponding to a field.

## See Also

- [hmdb\\_protein\\_fields](#)
- [hmdb\\_metabolite\\_fields](#)

## Examples

```
hmdb_table()
```

---

homologene\_download     *Orthology table for a pair of organisms*

---

### Description

Orthologous pairs of genes for a pair of organisms from NCBI HomoloGene, using one identifier type.

### Usage

```
homologene_download(  
  target = 10090L,  
  source = 9606L,  
  id_type = "genesymbol",  
  hgroup_size = FALSE  
)
```

### Arguments

target	Character or integer: name or ID of the target organism.
source	Character or integer: name or ID of the source organism.
id_type	Symbol or character: identifier type, possible values are "genesymbol", "entrez", "refseq" or "gi".
hgroup_size	Logical: include a column with the size of the homology groups. This column distinguishes one-to-one and one-to-many or many-to-many mappings.

### Details

The operation of this function is symmetric, *\*source\** and *\*target\** are interchangeable but determine the column layout of the output. The column "hgroup" is a numeric identifier of the homology groups. Most of the groups consist of one pair of orthologous genes (one-to-one mapping), and a few of them multiple ones (one-to-many or many-to-many mappings).

### Value

A data frame with orthologous identifiers between the two organisms.

### See Also

- [homologene\\_raw](#)
- [homologene\\_uniprot\\_orthology](#)

## Examples

```
chimp_human <- homologene_download(chimpanzee, human, refseqp)
chimp_human
# # A tibble: 17,737 × 3
#   hgroup refseqp_source refseqp_target
#   <int> <chr>           <chr>
# 1     3 NP_000007.1      NP_001104286.1
# 2     5 NP_000009.1      XP_003315394.1
# 3     6 NP_000010.1      XP_508738.2
# 4     7 NP_001096.1      XP_001145316.1
# 5     9 NP_000014.1      XP_523792.2
# # . with 17,732 more rows
```

---

homologene\_organisms *Organisms in NCBI HomoloGene*

---

## Description

Organisms in NCBI HomoloGene

## Usage

```
homologene_organisms(name_type = "ncbi")
```

## Arguments

name\_type      Character: type of the returned name or identifier. Many synonyms are accepted, the shortest ones: "latin", "ncbi", "common", "ensembl". Case insensitive.

## Details

Not all NCBI Taxonomy IDs can be translated to common or latin names. It means some organisms will be missing if translated to those name types. In the future we will address this issue, until then if you want to see all organisms use NCBI Taxonomy IDs.

## Value

A character vector of organism names.

---

homologene\_raw      *Orthology data from NCBI HomoloGene*

---

## Description

Retrieves NCBI HomoloGene data without any processing. Processed tables are more useful for most purposes, see below other functions that provide those. Genes of various organisms are grouped into homology groups ("hgroup" column). Organisms are identified by NCBI Taxonomy IDs, genes are identified by four different identifier types.

## Usage

```
homologene_raw()
```

## Value

A data frame as provided by NCBI HomoloGene.

## See Also

- [homologene\\_download](#)

## Examples

```
hg <- homologene_raw()
hg
# # A tibble: 275,237 × 6
#   hgroup ncbi_taxid entrez genesymbol gi refseqp
#   <int>   <int> <chr> <chr> <chr> <chr>
# 1     3     9606 34 ACADM 4557231 NP_000007.1
# 2     3     9598 469356 ACADM 160961497 NP_001104286.1
# 3     3     9544 705168 ACADM 109008502 XP_001101274.1
# 4     3     9615 490207 ACADM 545503811 XP_005622188.1
# 5     3     9913 505968 ACADM 115497690 NP_001068703.1
# # . with 275,232 more rows

# which organisms are available?
common_name(unique(hg$ncbi_taxid))
# [1] "Human" "Chimpanzee" "Macaque" "Dog" "Cow" "Mouse" "Rat" "Zebrafish"
# [9] "D. melanogaster" "Caenorhabditis elegans (PRJNA13758)"
# [11] "Tropical clawed frog" "Chicken"
# ...and 9 more organisms with missing English names.
```



---

homologene\_uniprot\_orthology  
*Orthology table with UniProt IDs*

---

## Description

Orthologous pairs of UniProt IDs for a pair of organisms, based on NCBI HomoloGene data.

## Usage

```
homologene_uniprot_orthology(target = 10090L, source = 9606L, by = entrez, ...)
```

## Arguments

target	Character or integer: name or ID of the target organism.
source	Character or integer: name or ID of the source organism.
by	Symbol or character: the identifier type in NCBI HomoloGene to use. Possible values are "refseq", "entrez", "genesymbol", "gi".
...	Further arguments passed to <a href="#">translate_ids</a> .

## Value

A data frame with orthologous pairs of UniProt IDs.

## Examples

```
homologene_uniprot_orthology(by = genesymbol)
# # A tibble: 14,235 × 2
#   source target
#   <chr> <chr>
# 1 P11310 P45952
# 2 P49748 P50544
# 3 P24752 Q8QZT1
# 4 Q04771 P37172
# 5 Q16586 P82350
# # . with 14,230 more rows
```

---

hpo\_download                      *Downloads protein annotations from Human Phenotype Ontology*

---

### Description

Human Phenotype Ontology (HPO) provides a standardized vocabulary of phenotypic abnormalities encountered in human disease. Each term in the HPO describes a phenotypic abnormality. HPO currently contains over 13,000 terms and over 156,000 annotations to hereditary diseases. See more at <https://hpo.jax.org/app/>.

### Usage

```
hpo_download()
```

### Value

A tibble (data frame) of annotations as it is provided by the database

### Examples

```
hpo_data <- hpo_download()
hpo_data
# # A tibble: 231,738 x 9
#   entrez_gene_id entrez_gene_symb. hpo_term_id hpo_term_name
#   <dbl> <chr> <chr> <chr>
# 1     8192 CLPP      HP:0000013 Hypoplasia of the ute.
# 2     8192 CLPP      HP:0004322 Short stature
# 3     8192 CLPP      HP:0000786 Primary amenorrhea
# 4     8192 CLPP      HP:0000007 Autosomal recessive i.
# 5     8192 CLPP      HP:0000815 Hypergonadotropic hyp.
# # . with 231,733 more rows, and 5 more variables:
# #   frequency_raw <chr>, frequency_hpo <chr>, info_gd_source <chr>,
# #   gd_source <chr>, disease_id <chr>
```

---

htridb\_download                      *Downloads TF-target interactions from HTRIdb*

---

### Description

HTRIdb (<https://www.lbbc.ibb.unesp.br/htri/>) is a database of literature curated human TF-target interactions. As the database is recently offline, the data is distributed by the OmniPath rescued data repository (<https://rescued.omnipathdb.org/>).

### Usage

```
htridb_download()
```

**Value**

Data frame (tibble) with interactions.

**Examples**

```

htridb_data <- htridb_download()
htridb_data
# # A tibble: 18,630 x 7
#   OID GENEID_TF SYMBOL_TF GENEID_TG SYMBOL_TG TECHNIQUE
#   <dbl> <dbl> <chr> <dbl> <chr> <chr>
# 1 32399 142 PARP1 675 BRCA2 Electrophoretic Mobi.
# 2 32399 142 PARP1 675 BRCA2 Chromatin Immunoprec.
# 3 28907 196 AHR 1543 CYP1A1 Chromatin Immunoprec.
# 4 29466 196 AHR 1543 CYP1A1 Electrophoretic Mobi.
# 5 28911 196 AHR 1543 CYP1A1 Chromatin Immunoprec.
# # . with 18,620 more rows, and 1 more variable: PUBMED_ID <chr>

```

---

id\_translation\_resources

*List available ID translation resources*

---

**Description**

List available ID translation resources

**Usage**

```
id_translation_resources()
```

**Value**

A character vector with the names of the available ID translation resources.

**Examples**

```
id_translation_resources()
```

---

`id_types`*ID types and synonyms in identifier translation*

---

**Description**

ID types and synonyms in identifier translation

**Usage**

```
id_types()
```

**Value**

Data frame with 4 columns: the ID type labels in the resource, their synonyms in OmniPath (this package), the name of the ID translation resource, and the entity type.

**See Also**

- [translate\\_ids](#)
- [translate\\_ids\\_multi](#)
- [ensembl\\_id\\_mapping\\_table](#)
- [uniprot\\_id\\_mapping\\_table](#)
- [hmdb\\_id\\_mapping\\_table](#)
- [chalmers\\_gem\\_id\\_mapping\\_table](#)
- [uniprot\\_full\\_id\\_mapping\\_table](#)
- [ensembl\\_id\\_type](#)
- [uniprot\\_id\\_type](#)
- [hmdb\\_id\\_type](#)
- [chalmers\\_gem\\_id\\_type](#)

**Examples**

```
id_types()
```

---

inbiomap_download	<i>Downloads and preprocesses network data from InWeb InBioMap</i>
-------------------	--

---

## Description

Downloads the data by [inbiomap\\_raw](#), extracts the UniProt IDs, Gene Symbols and scores and removes the irrelevant columns.

## Usage

```
inbiomap_download(...)
```

## Arguments

... Passed to [inbiomap\\_raw](#).

## Value

A data frame (tibble) of interactions.

## See Also

[inbiomap\\_raw](#)

## Examples

```
## Not run:
inbiomap_interactions <- inbiomap_download()
inbiomap_interactions

## End(Not run)
# # A tibble: 625,641 x 7
#   uniprot_a uniprot_b genesymbol_a genesymbol_b inferred score1 score2
#   <chr>     <chr>     <chr>         <chr>         <lg1>  <dbl> <dbl>
# 1 A0A5B9    P01892    TRBC2         HLA-A         FALSE  0.417 0.458
# 2 A0AUZ9    Q96CV9    KANSL1L      OPTN          FALSE  0.155 0.0761
# 3 A0AV02    P24941    SLC12A8      CDK2          TRUE   0.156 0.0783
# 4 A0AV02    Q00526    SLC12A8      CDK3          TRUE   0.157 0.0821
# 5 A0AV96    P0CG48    RBM47        UBC           FALSE  0.144 0.0494
# # . with 625,631 more rows
```

---

inbiomap_raw	<i>Downloads network data from InWeb InBioMap</i>
--------------	---

---

**Description**

Downloads the data from <https://inbio-discover.com/map.html#downloads> in tar.gz format, extracts the PSI MITAB table and returns it as a data frame.

**Usage**

```
inbiomap_raw(curl_verbose = FALSE)
```

**Arguments**

curl\_verbose Logical. Perform CURL requests in verbose mode for debugging purposes.

**Value**

A data frame (tibble) with the extracted interaction table.

**See Also**

[inbiomap\\_download](#)

**Examples**

```
## Not run:  
inbiomap_psimitab <- inbiomap_raw()  
  
## End(Not run)
```

---

interaction_datasets	<i>Datasets in the OmniPath Interactions database</i>
----------------------	---

---

**Description**

Datasets in the OmniPath Interactions database

**Usage**

```
interaction_datasets()
```

**Value**

Character: labels of interaction datasets.

**Examples**

```
interaction_datasets()
```

---

interaction_graph	<i>Build Omnipath interaction graph</i>
-------------------	---

---

**Description**

Transforms the interactions data frame to an igraph graph object.

**Usage**

```
interaction_graph(interactions = interactions)
```

**Arguments**

interactions    data.frame created by

- [enzyme\\_substrate](#)
- [omnipath-interactions](#)

**Value**

An igraph graph object.

**See Also**

- [graph\\_interaction](#)
- [import\\_omnipath\\_interactions](#)
- [import\\_pathwayextra\\_interactions](#)
- [import\\_kinaseextra\\_interactions](#)
- [import\\_ligrecextra\\_interactions](#)
- [import\\_dorothea\\_interactions](#)
- [import\\_mirnatarget\\_interactions](#)
- [import\\_all\\_interactions](#)
- [giant\\_component](#)
- [find\\_all\\_paths](#)

**Examples**

```
interactions <- import_omnipath_interactions(resources = c('Signalink3'))  
g <- interaction_graph(interactions)
```

---

interaction\_resources *Interaction resources available in Omnipath*

---

**Description**

Names of the resources available in <https://omnipathdb.org/interactions>.

**Usage**

```
interaction_resources(dataset = NULL)
```

**Arguments**

dataset a dataset within the interactions query type. Currently available datasets are 'omnipath', 'kinaseextra', 'pathwayextra', 'ligreextra', 'collectri', 'dorothea', 'tf\_target', 'tf\_mirna', 'mirnatarget', 'lncrna\_mrna' and 'small\_molecule\_protein'.

**Value**

Character: names of the interaction resources.

**See Also**

- [resources](#)
- [omnipath](#)
- [pathwayextra](#)
- [kinaseextra](#)
- [ligreextra](#)
- [post\\_translational](#)
- [dorothea](#)
- [collectri](#)
- [tf\\_target](#)
- [transcriptional](#)
- [mirna\\_target](#)
- [tf\\_mirna](#)
- [small\\_molecule](#)
- [all\\_interactions](#)

**Examples**

```
interaction_resources()
```



---

interaction_types	<i>Interaction types in the OmniPath Interactions database</i>
-------------------	--

---

**Description**

Interaction types in the OmniPath Interactions database

**Usage**

```
interaction_types()
```

**Value**

Character: labels of interaction types.

**Examples**

```
interaction_types()
```

---

intercell	<i>Cell-cell communication roles from OmniPath</i>
-----------	--

---

**Description**

Roles of proteins in intercellular communication from the <https://omnipathdb.org/intercell> endpoint of the OmniPath web service. It provides information on the roles in inter-cellular signaling. E.g. if a protein is a ligand, a receptor, an extracellular matrix (ECM) component, etc.

**Usage**

```
intercell(  
  categories = NULL,  
  parent = NULL,  
  scope = NULL,  
  aspect = NULL,  
  source = NULL,  
  transmitter = NULL,  
  receiver = NULL,  
  secreted = NULL,  
  plasma_membrane_peripheral = NULL,  
  plasma_membrane_transmembrane = NULL,  
  proteins = NULL,  
  topology = NULL,  
  causality = NULL,  
  consensus_percentile = NULL,
```

```

    loc_consensus_percentile = NULL,
    ...
)

```

### Arguments

categories	vector containing the categories to be retrieved. All the genes belonging to those categories will be returned. For further information about the categories see <a href="#">get_intercell_categories</a> .
parent	vector containing the parent classes to be retrieved. All the genes belonging to those classes will be returned. For further information about the main classes see <a href="#">get_intercell_categories</a> .
scope	either 'specific' or 'generic'
aspect	either 'locational' or 'functional'
source	either 'resource_specific' or 'composite'
transmitter	logical, include only transmitters i.e. proteins delivering signal from a cell to its environment.
receiver	logical, include only receivers i.e. proteins delivering signal to the cell from its environment.
secreted	logical, include only secreted proteins
plasma_membrane_peripheral	logical, include only plasma membrane peripheral membrane proteins.
plasma_membrane_transmembrane	logical, include only plasma membrane transmembrane proteins.
proteins	limit the query to certain proteins
topology	topology categories: one or more of 'secreted' (sec), 'plasma_membrane_peripheral' (pmp), 'plasma_membrane_transmembrane' (pmtm) (both short or long notation can be used).
causality	'transmitter' (trans), 'receiver' (rec) or 'both' (both short or long notation can be used).
consensus_percentile	Numeric: a percentile cut off for the consensus score of generic categories. The consensus score is the number of resources supporting the classification of an entity into a category based on combined information of many resources. Here you can apply a cut-off, keeping only the annotations supported by a higher number of resources than a certain percentile of each category. If NULL no filtering will be performed. The value is either in the 0-1 range, or will be divided by 100 if greater than 1. The percentiles will be calculated against the generic composite categories and then will be applied to their resource specific annotations and specific child categories.
loc_consensus_percentile	Numeric: similar to consensus_percentile for major localizations. For example, with a value of 50, the secreted, plasma membrane transmembrane or peripheral attributes will be true only where at least 50 percent of the resources support these.

...

Arguments passed on to `omnipath_query`

`organism` Character or integer: name or NCBI Taxonomy ID of the organism.

OmniPath is built of human data, and the web service provides orthology translated interactions and enzyme-substrate relationships for mouse and rat. For other organisms and query types, orthology translation will be called automatically on the downloaded human data before returning the result.

`resources` Character vector: name of one or more resources. Restrict the data to these resources. For a complete list of available resources, call the `<query_type>_resources` functions for the query type of interest.

`fields` Character vector: additional fields to include in the result. For a list of available fields, call `query_info("interactions")`.

`default_fields` Logical: if TRUE, the default fields will be included.

`silent` Logical: if TRUE, no messages will be printed. By default a summary message is printed upon successful download.

`logicals` Character vector: fields to be cast to logical.

`format` Character: if "json", JSON will be retrieved and processed into a nested list; any other value will return data frame.

`download_args` List: parameters to pass to the download function, which is `readr::read_tsv` by default, and `jsonlite::safe_load`.

`license` Character: license restrictions. By default, data from resources allowing "academic" use is returned by OmniPath. If you use the data for work in a company, you can provide "commercial" or "for-profit", which will restrict the data to those records which are supported by resources that allow for-profit use.

`password` Character: password for the OmniPath web service. You can provide a special password here which enables the use of `license = "ignore"` option, completely bypassing the license filter.

`exclude` Character vector: resource or dataset names to be excluded. The data will be filtered after download to remove records of the excluded datasets and resources.

`json_param` List: parameters to pass to the `jsonlite::fromJSON` when processing JSON columns embedded in the downloaded data. Such columns are "extra\_attrs" and "evidences". These are optional columns which provide a lot of extra details about interactions.

`strict_evidences` Logical: reconstruct the "sources" and "references" columns of interaction data frames based on the "evidences" column, strictly filtering them to the queried datasets and resources. Without this, the "sources" and "references" fields for each record might contain information for datasets and resources other than the queried ones, because the downloaded records are a result of a simple filtering of an already integrated data frame.

`genesymbol_resource` Character: "uniprot" (default) or "ensembl". The OmniPath web service uses the primary gene symbols as provided by UniProt. By passing "ensembl" here, the UniProt gene symbols will be replaced by the ones used in Ensembl. This translation results in a loss of a few records, and multiplication of another few records due to ambiguous translation.

cache Logical: use caching, load data from and save to the. The cache directory by default belongs to the user, located in the user's default cache directory, and named "OmnipathR". Find out about it by `getOption("omnipathr.cachedir")`. Can be changed by `omnipath_set_cachedir`.

**Value**

A data frame of intercellular communication roles.

**See Also**

- [intercell\\_network](#)
- [intercell\\_consensus\\_filter](#)
- [filter\\_intercell](#)
- [intercell\\_categories](#)
- [intercell\\_generic\\_categories](#)
- [intercell\\_resources](#)
- [intercell\\_summary](#)
- [intercell\\_network](#)

**Examples**

```
ecm_proteins <- intercell(categories = "ecm")
```

---

`intercell_categories` *Categories in the intercell database of OmniPath*

---

**Description**

Retrieves a list of categories from <https://omnipathdb.org/intercell>.

**Usage**

```
intercell_categories()
```

**Value**

character vector with the different intercell categories

**See Also**

- [intercell](#)
- [intercell\\_generic\\_categories](#)
- [intercell\\_summary](#)

## Examples

```
intercell_categories()
```

---

```
intercell_consensus_filter
```

*Quality filter for intercell annotations*

---

## Description

Quality filter for intercell annotations

## Usage

```
intercell_consensus_filter(  
  data,  
  percentile = NULL,  
  loc_percentile = NULL,  
  topology = NULL  
)
```

## Arguments

data	A data frame with intercell annotations, as provided by <a href="#">intercell</a> .
percentile	Numeric: a percentile cut off for the consensus score of composite categories. The consensus score is the number of resources supporting the classification of an entity into a category based on combined information of many resources. Here you can apply a cut-off, keeping only the annotations supported by a higher number of resources than a certain percentile of each category. If NULL no filtering will be performed. The value is either in the 0-1 range, or will be divided by 100 if greater than 1. The percentiles will be calculated against the generic composite categories and then will be applied to their resource specific annotations and specific child categories.
loc_percentile	Numeric: similar to percentile for major localizations. For example, with a value of 50, the secreted, plasma membrane transmembrane or peripheral attributes will be TRUE only where at least 50 percent of the resources support these.
topology	Character vector: list of allowed topologies, possible values are <code>"secreted"</code> , <code>"plasma_membrane_peripheral"</code> and <code>"plasma_membrane_transmembrane"</code> .

## Value

The data frame in data filtered by the consensus scores.

**See Also**

- [resources](#)
- [intercell](#)
- [filter\\_intercell](#)
- [intercell\\_categories](#)
- [intercell\\_generic\\_categories](#)
- [intercell\\_resources](#)
- [intercell\\_summary](#)
- [intercell\\_network](#)

**Examples**

```
ligand_receptor <- intercell(parent = c("ligand", "receptor"))
nrow(ligand_receptor)
# [1] 50174
lr_q50 <- intercell_consensus_filter(ligand_receptor, 50)
nrow(lr_q50)
# [1] 42863
```

---

`intercell_generic_categories`

*Retrieves a list of the generic categories in the intercell database of OmniPath*

---

**Description**

Retrieves a list of the generic categories from <https://omnipathdb.org/intercell>.

**Usage**

```
intercell_generic_categories()
```

**Value**

character vector with the different intercell main classes

**See Also**

- [intercell](#)
- [intercell\\_categories](#)
- [intercell\\_summary](#)

**Examples**

```
intercell_generic_categories()
```

---

intercell_network	<i>Intercellular communication network</i>
-------------------	--

---

## Description

Imports an intercellular network by combining intercellular annotations and protein interactions. First imports a network of protein-protein interactions. Then, it retrieves annotations about the proteins intercellular communication roles, once for the transmitter (delivering information from the expressing cell) and second, the receiver (receiving signal and relaying it towards the expressing cell) side. These 3 queries can be customized by providing parameters in lists which will be passed to the respective methods ([omnipath\\_interactions](#) for the network and [intercell](#) for the annotations). Finally the 3 data frames combined in a way that the source proteins in each interaction annotated by the transmitter, and the target proteins by the receiver categories. If undirected interactions present (these are disabled by default) they will be duplicated, i.e. both partners can be both receiver and transmitter.

## Usage

```
intercell_network(  
  interactions_param = list(),  
  transmitter_param = list(),  
  receiver_param = list(),  
  resources = NULL,  
  entity_types = NULL,  
  ligand_receptor = FALSE,  
  high_confidence = FALSE,  
  simplify = FALSE,  
  unique_pairs = FALSE,  
  consensus_percentile = NULL,  
  loc_consensus_percentile = NULL,  
  omnipath = TRUE,  
  ligreextra = TRUE,  
  kinaseextra = !high_confidence,  
  pathwayextra = !high_confidence,  
  ...  
)
```

## Arguments

**interactions\_param** a list with arguments for an interactions query; [omnipath-interactions](#).

**transmitter\_param** a list with arguments for [intercell](#), to define the transmitter side of intercellular connections

**receiver\_param** a list with arguments for [intercell](#), to define the receiver side of intercellular connections

resources	A character vector of resources to be applied to both the interactions and the annotations. For example, resources = 'CellChatDB' will download the transmitters and receivers defined by CellChatDB, connected by connections from CellChatDB.
entity_types	Character, possible values are "protein", "complex" or both.
ligand_receptor	Logical. If TRUE, only <i>ligand</i> and <i>receptor</i> annotations will be used instead of the more generic <i>transmitter</i> and <i>receiver</i> categories.
high_confidence	Logical: shortcut to do some filtering in order to include only higher confidence interactions. The intercell database of OmniPath covers a very broad range of possible ways of cell to cell communication, and the pieces of information, such as localization, topology, function and interaction, are combined from many, often independent sources. This unavoidably result some weird and unexpected combinations which are false positives in the context of intercellular communication. This option sets some minimum criteria to remove most (but definitely not all!) of the wrong connections. These criteria are the followings: 1) the receiver must be plasma membrane transmembrane; 2) the curation effort for interactions must be larger than one; 3) the consensus score for annotations must be larger than the 50 percentile within the generic category (you can override this by consensus_percentile). 4) the transmitter must be secreted or exposed on the plasma membrane. 5) The major localizations have to be supported by at least 30 percent of the relevant resources ( you can override this by loc_consensus_percentile). 6) The datasets with lower level of curation ( <i>kinaseextra</i> and <i>pathwayextra</i> ) will be disabled. These criteria are of medium stringency, you can always tune them to be more relaxed or stringent by filtering manually, using <a href="#">filter_intercell_network</a> .
simplify	Logical: keep only the most often used columns. This function combines a network data frame with two copies of the intercell annotation data frames, all of them already having quite some columns. With this option we keep only the names of the interacting pair, their intercellular communication roles, and the minimal information of the origin of both the interaction and the annotations.
unique_pairs	Logical: instead of having separate rows for each pair of annotations, drop the annotations and reduce the data frame to unique interacting pairs. See <a href="#">unique_intercell_network</a> for details.
consensus_percentile	Numeric: a percentile cut off for the consensus score of generic categories in intercell annotations. The consensus score is the number of resources supporting the classification of an entity into a category based on combined information of many resources. Here you can apply a cut-off, keeping only the annotations supported by a higher number of resources than a certain percentile of each category. If NULL no filtering will be performed. The value is either in the 0-1 range, or will be divided by 100 if greater than 1. The percentiles will be calculated against the generic composite categories and then will be applied to their resource specific annotations and specific child categories.
loc_consensus_percentile	Numeric: similar to consensus_percentile for major localizations. For example, with a value of 50, the secreted, plasma membrane transmembrane or



	peripheral attributes will be TRUE only where at least 50 percent of the resources support these.
omnipath	Logical: shortcut to include the <i>omnipath</i> dataset in the interactions query.
ligreextra	Logical: shortcut to include the <i>ligreextra</i> dataset in the interactions query.
kinaseextra	Logical: shortcut to include the <i>kinaseextra</i> dataset in the interactions query.
pathwayextra	Logical: shortcut to include the <i>pathwayextra</i> dataset in the interactions query.
...	If <code>simplify</code> or <code>unique_pairs</code> is TRUE, additional column names can be passed here to <code>dplyr::select</code> on the final data frame. Otherwise ignored.

### Details

By default this function creates almost the largest possible network of intercellular interactions. However, this might contain a large number of false positives. Please refer to the documentation of the arguments, especially `high_confidence`, and the `filter_intercell_network` function. Note: if you restrict the query to certain intercell annotation resources or small categories, it's not recommended to use the `consensus_percentile` or `high_confidence` options, instead filter the network with `filter_intercell_network` for more consistent results.

### Value

A dataframe containing information about protein-protein interactions and the inter-cellular roles of the proteins involved in those interactions.

### See Also

- [intercell](#)
- [intercell\\_summary](#)
- [intercell\\_categories](#)
- [intercell\\_generic\\_categories](#)
- [intercell](#)
- [omnipath](#)
- [pathwayextra](#)
- [kinaseextra](#)
- [ligreextra](#)
- [unique\\_intercell\\_network](#)
- [simplify\\_intercell\\_network](#)
- [filter\\_intercell\\_network](#)

### Examples

```
intercell_network <- intercell_network(
  interactions_param = list(datasets = 'ligreextra'),
  receiver_param = list(categories = c('receptor', 'transporter')),
  transmitter_param = list(categories = c('ligand', 'secreted_enzyme'))
)
```

---

intercell_resources	<i>Retrieves a list of intercellular communication resources available in OmniPath</i>
---------------------	--

---

### Description

Retrieves a list of the databases from <https://omnipathdb.org/intercell>.

### Usage

```
intercell_resources(dataset = NULL)
```

### Arguments

dataset            ignored at this query type

### Value

character vector with the names of the databases

### See Also

- [resources](#)
- [intercell](#)
- [filter\\_intercell](#)
- [intercell\\_categories](#)
- [intercell\\_generic\\_categories](#)
- [intercell\\_summary](#)
- [intercell\\_network](#)

### Examples

```
intercell_resources()
```

---

intercell\_summary      *Full list of intercell categories and resources*

---

**Description**

Full list of intercell categories and resources

**Usage**

```
intercell_summary()
```

**Value**

A data frame of categories and resources.

**Examples**

```
ic_cat <- intercell_categories()
ic_cat
# # A tibble: 1,125 x 3
#   category          parent          database
#   <chr>             <chr>             <chr>
# 1 transmembrane    transmembrane     UniProt_location
# 2 transmembrane    transmembrane     UniProt_topology
# 3 transmembrane    transmembrane     UniProt_keyword
# 4 transmembrane    transmembrane_predicted Phobius
# 5 transmembrane_phobius transmembrane_predicted Almen2009
# # . with 1,120 more rows
```

---

is\_ontology\_id      *Looks like an ontology ID*

---

**Description**

Tells if the input has the typical format of ontology IDs, i.e. a code of capital letters, a colon, followed by a numeric code.

**Usage**

```
is_ontology_id(terms)
```

**Arguments**

terms      Character vector with strings to check.

**Value**

A logical vector with the same length as the input.

**Examples**

```
is_ontology_id(c('GO:000001', 'reproduction'))
# [1] TRUE FALSE
```

---

is_swissprot	<i>Check for SwissProt IDs</i>
--------------	--------------------------------

---

**Description**

Check for SwissProt IDs

**Usage**

```
is_swissprot(uniprot, organism = 9606)
```

**Arguments**

uniprot	Character vector of UniProt IDs.
organism	Character or integer: name or identifier of the organism.

**Value**

Logical vector TRUE for SwissProt IDs and FALSE for any other element.

**Examples**

```
is_swissprot(c("Q05BL1", "A0A654IBU3", "P00533"))
# [1] FALSE FALSE TRUE
```

---

is_trembl	<i>Check for TrEMBL IDs</i>
-----------	-----------------------------

---

**Description**

Check for TrEMBL IDs

**Usage**

```
is_trembl(uniprots, organism = 9606)
```

**Arguments**

uniprots	Character vector of UniProt IDs.
organism	Character or integer: name or identifier of the organism.

**Value**

Logical vector TRUE for TrEMBL IDs and FALSE for any other element.

**Examples**

```
is_trembl(c("Q05BL1", "A0A654IBU3", "P00533"))  
# [1] TRUE TRUE FALSE
```

---

is_uniprot	<i>Looks like a UniProt ID?</i>
------------	---------------------------------

---

**Description**

This function checks only the format of the IDs, no guarantee that these IDs exist in UniProt.

**Usage**

```
is_uniprot(identifiers)
```

**Arguments**

identifiers	Character: one or more identifiers (typically a single string, a vector or a data frame column).
-------------	--

**Value**

Logical: true if all elements in the input (except NAs) looks like valid UniProt IDs. If the input is not a character vector, 'FALSE' is returned.

**Examples**

```
is_uniprot(all_uniprot_acs())
# [1] TRUE
is_uniprot("P00533")
# [1] TRUE
is_uniprot("pizza")
# [1] FALSE
```

---

kegg\_info

*Information about a KEGG Pathway*

---

**Description**

Information about a KEGG Pathway

**Usage**

```
kegg_info(pathway_id)
```

**Arguments**

pathway\_id      Character: a KEGG Pathway identifier, e.g. "hsa04710". For a complete list of IDs see [kegg\\_pathway\\_list](#).

**Value**

List with the pathway information.

**See Also**

- [kegg\\_pathway\\_list](#)
- [kegg\\_picture](#)
- [kegg\\_open](#)

**Examples**

```
kegg_info('map00563')
```

---

kegg_open	<i>Open a KEGG Pathway diagram in the browser</i>
-----------	---

---

### Description

Open a KEGG Pathway diagram in the browser

### Usage

```
kegg_open(pathway_id)
```

### Arguments

pathway\_id      Character: a KEGG Pathway identifier, e.g. "hsa04710". For a complete list of IDs see [kegg\\_pathway\\_list](#).

### Details

To open URLs in the web browser the "browser" option must to be set to a a valid executable. You can check the value of this option by `getOption("browser")`. If your browser is firefox and the executable is located in the system path, you can set the option to point to it: `options(browser = "firefox")`. To make it a permanent setting, you can also include this in your `.Rprofile` file.

### Value

Returns NULL.

### See Also

- [kegg\\_pathway\\_list](#)
- [kegg\\_picture](#)
- [kegg\\_info](#)

### Examples

```
if(any(getOption('browser') != '')) kegg_open('hsa04710')
```

---

kegg\_pathways\_download

*Download the KEGG Pathways database*


---

## Description

Downloads all pathway diagrams in the KEGG Pathways database in KGML format and processes the XML to extract the interactions.

## Usage

```
kegg_pathways_download(max_expansion = NULL, simplify = FALSE)
```

## Arguments

**max\_expansion** Numeric: the maximum number of relations derived from a single relation record. As one entry might represent more than one molecular entities, one relation might yield a large number of relations in the processing. This happens in a combinatorial way, e.g. if the two entries represent 3 and 4 entities, that results 12 relations. If NULL, all relations will be expanded.

**simplify** Logical: remove KEGG's internal identifiers and the pathway annotations, keep only unique interactions with direction and effect sign.

## Value

A data frame (tibble) of interactions.

## See Also

- [kegg\\_pathway\\_list](#)
- [kegg\\_process](#)
- [kegg\\_pathway\\_download](#)

## Examples

```
## Not run:
kegg_pw <- kegg_pathways_download(simplify = TRUE)
kegg_pw
# # A tibble: 6,765 x 6
#   uniprot_source uniprot_target type effect genesymbol_source
#   <chr>          <chr>          <chr> <chr> <chr>
# 1 Q03113        Q15283          PPre1 activ. GNA12
# 2 Q9Y4G8        P62070          PPre1 activ. RAPGEF2
# 3 Q13972        P62070          PPre1 activ. RASGRF1
# 4 O95267        P62070          PPre1 activ. RASGRP1
# 5 P62834        P15056          PPre1 activ. RAP1A
# # . with 6,760 more rows, and 1 more variable: genesymbol_target <chr>
```



```
## End(Not run)
```

---

```
kegg_pathway_annotations  
  Protein pathway annotations
```

---

## Description

Downloads all KEGG pathways and creates a table of protein-pathway annotations.

## Usage

```
kegg_pathway_annotations(pathways = NULL)
```

## Arguments

pathways            A table of KEGG pathways as produced by [kegg\\_pathways\\_download](#).

## Value

A data frame (tibble) with UniProt IDs and pathway names.

## See Also

[kegg\\_pathways\\_download](#)

## Examples

```
## Not run:  
kegg_pw_annot <- kegg_pathway_annotations()  
kegg_pw_annot  
# # A tibble: 7,341 x 4  
#   uniprot genesymbol pathway          pathway_id  
#   <chr>   <chr>      <chr>          <chr>  
# 1 Q03113  GNA12      MAPK signaling pathway hsa04010  
# 2 Q9Y4G8  RAPGEF2    MAPK signaling pathway hsa04010  
# 3 Q13972  RASGRF1    MAPK signaling pathway hsa04010  
# 4 O95267  RASGRP1    MAPK signaling pathway hsa04010  
# 5 P62834  RAP1A      MAPK signaling pathway hsa04010  
# # . with 7,336 more rows  
  
## End(Not run)
```

---

kegg\_pathway\_download *Download one KEGG pathway*

---

### Description

Downloads one pathway diagram from the KEGG Pathways database in KGML format and processes the XML to extract the interactions.

### Usage

```
kegg_pathway_download(  
  pathway_id,  
  process = TRUE,  
  max_expansion = NULL,  
  simplify = FALSE  
)
```

### Arguments

pathway_id	Character: a KEGG pathway identifier, for example "hsa04350".
process	Logical: process the data or return it in raw format. processing means joining the entries and relations into a single data frame and adding UniProt IDs.
max_expansion	Numeric: the maximum number of relations derived from a single relation record. As one entry might represent more than one molecular entities, one relation might yield a large number of relations in the processing. This happens in a combinatorial way, e.g. if the two entries represent 3 and 4 entities, that results 12 relations. If NULL, all relations will be expanded.
simplify	Logical: remove KEGG's internal identifiers and the pathway annotations, keep only unique interactions with direction and effect sign.

### Value

A data frame (tibble) of interactions if process is TRUE, otherwise a list with two data frames: "entries" is a raw table of the entries while "relations" is a table of relations extracted from the KGML file.

### See Also

- [kegg\\_process](#)
- [kegg\\_pathways\\_download](#)
- [kegg\\_pathway\\_list](#)

**Examples**

```

tgf_pathway <- kegg_pathway_download('hsa04350')
tgf_pathway
# # A tibble: 50 x 12
#   source target type effect arrow relation_id kegg_id_source
#   <chr> <chr> <chr> <chr> <chr> <chr> <chr>
# 1 51 49 PPre1 activ. --> hsa04350:1 hsa:7040 hsa:.
# 2 57 55 PPre1 activ. --> hsa04350:2 hsa:151449 hs.
# 3 34 32 PPre1 activ. --> hsa04350:3 hsa:3624 hsa:.
# 4 20 17 PPre1 activ. --> hsa04350:4 hsa:4838
# 5 60 46 PPre1 activ. --> hsa04350:5 hsa:4086 hsa:.
# # . with 45 more rows, and 5 more variables: genesymbol_source <chr>,
# # uniprot_source <chr>, kegg_id_target <chr>,
# # genesymbol_target <chr>, uniprot_target <chr>

```

---

kegg\_pathway\_list      *List of KEGG pathways*

---

**Description**

Retrieves a list of available KEGG pathways.

**Usage**

```
kegg_pathway_list()
```

**Value**

Data frame of pathway names and identifiers.

**See Also**

- [kegg\\_process](#)
- [kegg\\_pathway\\_download](#)
- [kegg\\_pathways\\_download](#)
- [kegg\\_open](#)
- [kegg\\_picture](#)
- [kegg\\_info](#)

**Examples**

```

kegg_pws <- kegg_pathway_list()
kegg_pws
# # A tibble: 521 x 2
#   id      name
#   <chr> <chr>

```

```
# 1 map01100 Metabolic pathways
# 2 map01110 Biosynthesis of secondary metabolites
# 3 map01120 Microbial metabolism in diverse environments
# 4 map01200 Carbon metabolism
# 5 map01210 2-Oxocarboxylic acid metabolism
# 6 map01212 Fatty acid metabolism
# 7 map01230 Biosynthesis of amino acids
# # . with 514 more rows
```

---

kegg\_picture

*Download a pathway diagram as a picture*

---

### Description

Downloads a KEGG Pathway diagram as a PNG image.

### Usage

```
kegg_picture(pathway_id, path = NULL)
```

### Arguments

pathway_id	Character: a KEGG Pathway identifier, e.g. "hsa04710". For a complete list of IDs see <a href="#">kegg_pathway_list</a> .
path	Character: save the image to this path. If NULL, the image will be saved in the current directory under the name <pathway_id>.png.

### Value

Invisibly returns the path to the downloaded file.

### See Also

[kegg\\_pathway\\_list](#)

- [kegg\\_pathway\\_list](#)
- [kegg\\_open](#)
- [kegg\\_info](#)

### Examples

```
kegg_picture('hsa04710')
kegg_picture('hsa04710', path = 'foo/bar')
kegg_picture('hsa04710', path = 'foo/bar/circadian.png')
```

---

kegg\_process                      *Interactions from KGML*

---

### Description

Processes KEGG Pathways data extracted from a KGML file. Joins the entries and relations into a single data frame and translates the Gene Symbols to UniProt IDs.

### Usage

```
kegg_process(entries, relations, max_expansion = NULL, simplify = FALSE)
```

### Arguments

entries	A data frames with entries extracted from a KGML file by <a href="#">kegg_pathway_download</a> .
relations	A data frames with relations extracted from a KGML file by <a href="#">kegg_pathway_download</a> .
max_expansion	Numeric: the maximum number of relations derived from a single relation record. As one entry might represent more than one molecular entities, one relation might yield a large number of relations in the processing. This happens in a combinatorial way, e.g. if the two entries represent 3 and 4 entities, that results 12 relations. If NULL, all relations will be expanded.
simplify	Logical: remove KEGG's internal identifiers and the pathway annotations, keep only unique interactions with direction and effect sign.

### Value

A data frame (tibble) of interactions. In rare cases when a pathway doesn't contain any relation, returns NULL.

### See Also

- [kegg\\_pathway\\_download](#)
- [kegg\\_pathways\\_download](#)
- [kegg\\_pathway\\_list](#)

### Examples

```
hsa04350 <- kegg_pathway_download('hsa04350', process = FALSE)
tgf_pathway <- kegg_process(hsa04350$entries, hsa04350$relations)
tgf_pathway
# # A tibble: 50 x 12
#   source target type effect arrow relation_id kegg_id_source
#   <chr> <chr> <chr> <chr> <chr> <chr> <chr>
# 1 51     49   PPrel activ. --> hsa04350:1 hsa:7040 hsa:.
# 2 57     55   PPrel activ. --> hsa04350:2 hsa:151449 hs.
# 3 34     32   PPrel activ. --> hsa04350:3 hsa:3624 hsa:.
# 4 20     17   PPrel activ. --> hsa04350:4 hsa:4838
```

```
# 5 60      46      PPre1 activ. --> hsa04350:5 hsa:4086 hsa:.  
# # . with 45 more rows, and 5 more variables: genesymbol_source <chr>,  
# # uniprot_source <chr>, kegg_id_target <chr>,  
# # genesymbol_target <chr>, uniprot_target <chr>
```

---

latin_name	<i>Latin (scientific) names of organisms</i>
------------	--

---

## Description

Latin (scientific) names of organisms

## Usage

```
latin_name(name)
```

## Arguments

name            Vector with any kind of organism name or identifier, can be also mixed type.

## Value

Character vector with latin (scientific) names, NA if a name in the input could not be found.

## See Also

- [ncbi\\_taxid](#)
- [common\\_name](#)
- [ensembl\\_name](#)

## Examples

```
latin_name(c(9606, "cat", "dog"))  
# [1] "Homo sapiens" "Felis catus" "Canis lupus familiaris"  
latin_name(c(9606, "cat", "doggy"))  
# [1] "Homo sapiens" "Felis catus" NA
```

---

load_db	<i>Load a built in database</i>
---------	---------------------------------

---

### Description

Load a built in database

### Usage

```
load_db(key, param = list())
```

### Arguments

key	Character: the key of the database to load. For a list of available keys see <a href="#">omnipath_show_db</a> .
param	List: override the defaults or pass further parameters to the database loader function. See the loader functions and their default parameters in <a href="#">omnipath_show_db</a> .

### Details

This function loads a database which is stored within the package namespace until its expiry. The loaded database is accessible by [get\\_db](#) and the loading process is typically initiated by [get\\_db](#), not by the users directly.

### Value

Returns NULL.

### See Also

[omnipath\\_show\\_db](#), [get\\_db](#)

### Examples

```
load_db('go_slim')
omnipath_show_db()
```

---

ncbi_taxid	<i>NCBI Taxonomy IDs of organisms</i>
------------	---------------------------------------

---

**Description**

NCBI Taxonomy IDs of organisms

**Usage**

```
ncbi_taxid(name)
```

**Arguments**

name                    Vector with any kind of organism name or identifier, can be also mixed type.

**Value**

Integer vector with NCBI Taxonomy IDs, NA if a name in the input could not be found.

**See Also**

- [latin\\_name](#)
- [common\\_name](#)
- [ensembl\\_name](#)

**Examples**

```
ncbi_taxid(c("Homo sapiens", "cat", "dog"))
# [1] 9606 9685 9615
ncbi_taxid(c(9606, "cat", "doggy"))
# [1] 9606 9685 NA
```

---

nichenet_build_model	<i>Construct a NicheNet ligand-target model</i>
----------------------	---

---

**Description**

Construct a NicheNet ligand-target model

**Usage**

```
nichenet_build_model(optimization_results, networks, use_weights = TRUE)
```



**Arguments**

optimization_results	The outcome of NicheNet parameter optimization as produced by <a href="#">nichenet_optimization</a> .
networks	A list with NicheNet format signaling, ligand-receptor and gene regulatory networks as produced by <a href="#">nichenet_networks</a> .
use_weights	Logical: whether to use the optimized weights.

**Value**

A named list with two elements: 'weighted\_networks' and 'optimized\_parameters'.

**Examples**

```
## Not run:
expression <- nichenet_expression_data()
networks <- nichenet_networks()
optimization_results <- nichenet_optimization(networks, expression)
nichenet_model <- nichenet_build_model(optimization_results, networks)

## End(Not run)
```

---

nichenet\_expression\_data

*Expression data from ligand-receptor perturbation experiments used by NicheNet*

---

**Description**

NicheNet uses expression data from a collection of published ligand or receptor KO or perturbation experiments to build its model. This function retrieves the original expression data, deposited in Zenodo (<https://zenodo.org/record/3260758>).

**Usage**

```
nichenet_expression_data()
```

**Value**

Nested list, each element contains a data frame of processed expression data and key variables about the experiment.

**Examples**

```
exp_data <- nichenet_expression_data()
head(names(exp_data))
# [1] "bmp4_tgfb"      "tgfb_bmp4"      "nodal_Nodal"    "spectrum_IL4"
# [5] "spectrum_Tnf"  "spectrum_Ifng"
purrr::map_chr(head(exp_data), 'from')
#      bmp4_tgfb      tgfb_bmp4      nodal_Nodal      spectrum_IL4      spectrum_Tnf
#      "BMP4"        "TGFB1"        "NODAL"          "IL4"             "TNF"
# spectrum_Ifng
#      "IFNG"
```

---

nichenet\_gr\_network     *Builds a NicheNet gene regulatory network*

---

**Description**

Builds gene regulatory network prior knowledge for NicheNet using multiple resources.

**Usage**

```
nichenet_gr_network(
  omnipath = list(),
  harmonizome = list(),
  regnetwork = list(),
  htridb = list(),
  remap = list(),
  evex = list(),
  pathwaycommons = list(),
  trrust = list(),
  only_omnipath = FALSE
)
```

**Arguments**

omnipath	List with paramaters to be passed to <a href="#">nichenet_gr_network_omnipath</a> .
harmonizome	List with paramaters to be passed to <a href="#">nichenet_gr_network_harmonizome</a> .
regnetwork	List with paramaters to be passed to <a href="#">nichenet_gr_network_regnetwork</a> .
htridb	List with paramaters to be passed to <a href="#">nichenet_gr_network_htridb</a> .
remap	List with paramaters to be passed to <a href="#">nichenet_gr_network_remap</a> .
evex	List with paramaters to be passed to <a href="#">nichenet_gr_network_evex</a> .
pathwaycommons	List with paramaters to be passed to <a href="#">nichenet_gr_network_pathwaycommons</a> .
trrust	List with paramaters to be passed to <a href="#">nichenet_gr_network_trrust</a> .
only_omnipath	Logical: a shortcut to use only OmniPath as network resource.

**Value**

A network data frame (tibble) with gene regulatory interactions suitable for use with NicheNet.

**See Also**

- [nichenet\\_gr\\_network\\_evex](#)
- [nichenet\\_gr\\_network\\_harmonizome](#)
- [nichenet\\_gr\\_network\\_htridb](#)
- [nichenet\\_gr\\_network\\_omnipath](#)
- [nichenet\\_gr\\_network\\_pathwaycommons](#)
- [nichenet\\_gr\\_network\\_regnetwork](#)
- [nichenet\\_gr\\_network\\_remap](#)
- [nichenet\\_gr\\_network\\_trrust](#)

**Examples**

```
# load everything with the default parameters:
gr_network <- nichenet_gr_network()

# less targets from ReMap, not using RegNetwork:
gr_network <- nichenet_gr_network(
  # I needed to disable ReMap here due to some issues
  # of one of the Bioconductor build servers
  # remap = list(top_targets = 200),
  remap = NULL,
  regnetwork = NULL,
)

# use only OmniPath:
gr_network_omnipath <- nichenet_gr_network(only_omnipath = TRUE)
```

---

nichenet\_gr\_network\_evex

*NicheNet gene regulatory network from EVEX*

---

**Description**

Builds a gene regulatory network using data from the EVEX database and converts it to a format suitable for NicheNet.

**Usage**

```
nichenet_gr_network_evex(
  top_confidence = 0.75,
  indirect = FALSE,
  regulation_of_expression = FALSE
)
```

**Arguments**

top\_confidence Double, between 0 and 1. Threshold based on the quantile of the confidence score.

indirect Logical: whether to include indirect interactions.

regulation\_of\_expression Logical: whether to include also the "regulation of expression" type interactions.

**Value**

Data frame of interactions in NicheNet format.

Data frame with gene regulatory interactions in NicheNet format.

**See Also**

- [nichenet\\_gr\\_network](#)
- [evex\\_download](#)

**Examples**

```
# use only the 10% with the highest confidence:
evex_gr_network <- nichenet_gr_network_evex(top_confidence = .9)
```

---

```
nichenet_gr_network_harmonizome
NicheNet gene regulatory network from Harmonizome
```

---

**Description**

Builds gene regulatory network prior knowledge for NicheNet using Harmonizome

**Usage**

```
nichenet_gr_network_harmonizome(
  datasets = c("cheappi", "encodetfppi", "jasparpwm", "transfac", "transfacpwm",
    "motifmap", "geotf", "geokinase", "geogene"),
  ...
)
```

**Arguments**

datasets The datasets to use. For possible values please refer to default value and the Harmonizome webpage.

... Ignored.

**Value**

Data frame with gene regulatory interactions in NicheNet format.

**See Also**

- [nichenet\\_gr\\_network](#)
- [harmonizome\\_download](#)

**Examples**

```
# use only JASPAR and TRANSFAC:
hz_gr_network <- nichenet_gr_network_harmonizome(
  datasets = c('jasparpwm', 'transfac', 'transfacpwm')
)
```

---

nichenet\_gr\_network\_htridb

*NicheNet gene regulatory network from HTRIdb*

---

**Description**

Builds a gene regulatory network using data from the HTRIdb database and converts it to a format suitable for NicheNet.

**Usage**

```
nichenet_gr_network_htridb()
```

**Value**

Data frame with gene regulatory interactions in NicheNet format.

**See Also**

[htridb\\_download](#), [nichenet\\_gr\\_network](#)

**Examples**

```
htri_gr_network <- nichenet_gr_network_htridb()
```

---

`nichenet_gr_network_omnipath`*Builds gene regulatory network for NicheNet using OmniPath*

---

### Description

Retrieves network prior knowledge from OmniPath and provides it in a format suitable for NicheNet. This method never downloads the ‘ligreextra’ dataset because the ligand-receptor interactions are supposed to come from [nichenet\\_lr\\_network\\_omnipath](#).

### Usage

```
nichenet_gr_network_omnipath(min_curation_effort = 0, ...)
```

### Arguments

<code>min_curation_effort</code>	Lower threshold for curation effort
<code>...</code>	Passed to <a href="#">import_transcriptional_interactions</a>

### Value

A network data frame (tibble) with gene regulatory interactions suitable for use with NicheNet.

### See Also

- [nichenet\\_gr\\_network\\_evex](#)
- [nichenet\\_gr\\_network\\_harmonizome](#)
- [nichenet\\_gr\\_network\\_htridb](#)
- [nichenet\\_gr\\_network\\_omnipath](#)
- [nichenet\\_gr\\_network\\_pathwaycommons](#)
- [nichenet\\_gr\\_network\\_regnetwork](#)
- [nichenet\\_gr\\_network\\_remap](#)
- [nichenet\\_gr\\_network\\_trust](#)

### Examples

```
# use interactions up to confidence level "C" from DoRothEA:  
op_gr_network <- nichenet_gr_network_omnipath(  
  dorothea_levels = c('A', 'B', 'C')  
)
```

---

`nichenet_gr_network_pathwaycommons`*NicheNet gene regulatory network from PathwayCommons*

---

**Description**

Builds gene regulation prior knowledge for NicheNet using PathwayCommons.

**Usage**

```
nichenet_gr_network_pathwaycommons(  
  interaction_types = "controls-expression-of",  
  ...  
)
```

**Arguments**

`interaction_types`

Character vector with PathwayCommons interaction types. Please refer to the default value and the PathwayCommons webpage.

`...` Ignored.

**Value**

Data frame with gene regulatory interactions in NicheNet format.

**See Also**

- [nichenet\\_gr\\_network](#)
- [pathwaycommons\\_download](#)

**Examples**

```
pc_gr_network <- nichenet_gr_network_pathwaycommons()
```

---

`nichenet_gr_network_regnetwork`*NicheNet gene regulatory network from RegNetwork*

---

**Description**

Builds a gene regulatory network using data from the RegNetwork database and converts it to a format suitable for NicheNet.

**Usage**

```
nichenet_gr_network_regnetwork()
```

**Value**

Data frame with gene regulatory interactions in NicheNet format.

**See Also**

- [regnetwork\\_download](#)
- [nichenet\\_gr\\_network](#)

**Examples**

```
regn_gr_network <- nichenet_gr_network_regnetwork()
```

---

nichenet\_gr\_network\_remap

*NicheNet gene regulatory network from ReMap*

---

**Description**

Builds a gene regulatory network using data from the ReMap database and converts it to a format suitable for NicheNet.

**Usage**

```
nichenet_gr_network_remap(  
  score = 100,  
  top_targets = 500,  
  only_known_tfs = TRUE  
)
```

**Arguments**

score	Numeric: a minimum score between 0 and 1000, records with lower scores will be excluded. If NULL no filtering performed.
top_targets	Numeric: the number of top scoring targets for each TF. Essentially the maximum number of targets per TF. If NULL the number of targets is not restricted.
only_known_tfs	Logical: whether to exclude TFs which are not in TF census.

**Value**

Data frame with gene regulatory interactions in NicheNet format.



**See Also**

- [remap\\_filtered](#)
- [nichenet\\_gr\\_network](#)

**Examples**

```
# use only max. top 100 targets for each TF:  
remap_gr_network <- nichenet_gr_network_remap(top_targets = 100)
```

---

nichenet\_gr\_network\_trrust

*NicheNet gene regulatory network from TRRUST*

---

**Description**

Builds a gene regulatory network using data from the TRRUST database and converts it to a format suitable for NicheNet.

**Usage**

```
nichenet_gr_network_trrust()
```

**Value**

Data frame with gene regulatory interactions in NicheNet format.

**See Also**

- [trrust\\_download](#)
- [nichenet\\_gr\\_network](#)

**Examples**

```
trrust_gr_network <- nichenet_gr_network_trrust()
```

---

nichenet\_ligand\_activities

*Calls the NicheNet ligand activity analysis*


---

## Description

Calls the NicheNet ligand activity analysis

## Usage

```
nichenet_ligand_activities(
  ligand_target_matrix,
  lr_network,
  expressed_genes_transmitter,
  expressed_genes_receiver,
  genes_of_interest,
  background_genes = NULL,
  n_top_ligands = 42,
  n_top_targets = 250
)
```

## Arguments

ligand\_target\_matrix

A matrix with rows and columns corresponding to ligands and targets, respectively. Produced by [nichenet\\_ligand\\_target\\_matrix](#) or `nichenetr::construct_ligand_target_matrix`.

lr\_network

A data frame with ligand-receptor interactions, as produced by [nichenet\\_lr\\_network](#).

expressed\_genes\_transmitter

Character vector with the gene symbols of the genes expressed in the cells transmitting the signal.

expressed\_genes\_receiver

Character vector with the gene symbols of the genes expressed in the cells receiving the signal.

genes\_of\_interest

Character vector with the gene symbols of the genes of interest. These are the genes in the receiver cell population that are potentially affected by ligands expressed by interacting cells (e.g. genes differentially expressed upon cell-cell interaction).

background\_genes

Character vector with the gene symbols of the genes to be used as background.

n\_top\_ligands

How many of the top ligands to include in the ligand-target table.

n\_top\_targets

For each ligand, how many of the top targets to include in the ligand-target table.

**Value**

A named list with 'ligand\_activities' (a tibble giving several ligand activity scores; following columns in the tibble: \$test\_ligand, \$aucroc, \$aupr and \$pearson) and 'ligand\_target\_links' (a tibble with columns ligand, target and weight (i.e. regulatory potential score)).

**Examples**

```
## Not run:
networks <- nichenet_networks()
expression <- nichenet_expression_data()
optimization_results <- nichenet_optimization(networks, expression)
nichenet_model <- nichenet_build_model(optimization_results, networks)
lt_matrix <- nichenet_ligand_target_matrix(
  nichenet_model$weighted_networks,
  networks$lr_network,
  nichenet_model$optimized_parameters
)
ligand_activities <- nichenet_ligand_activities(
  ligand_target_matrix = lt_matrix,
  lr_network = networks$lr_network,
  # the rest of the parameters should come
  # from your transcriptomics data:
  expressed_genes_transmitter = expressed_genes_transmitter,
  expressed_genes_receiver = expressed_genes_receiver,
  genes_of_interest = genes_of_interest
)

## End(Not run)
```

---

nichenet\_ligand\_target\_links

*Compiles a table with weighted ligand-target links*

---

**Description**

A wrapper around `nichenetr::get_weighted_ligand_target_links` to compile a data frame with weighted links from the top ligands to their top targets.

**Usage**

```
nichenet_ligand_target_links(
  ligand_activities,
  ligand_target_matrix,
  genes_of_interest,
  n_top_ligands = 42,
  n_top_targets = 250
)
```

**Arguments**

- `ligand_activities` Ligand activity table as produced by `nichenetr::predict_ligand_activities`.
- `ligand_target_matrix` Ligand-target matrix as produced by `nichenetr::construct_ligand_target_matrix` or the wrapper around it in the current package: `nichenet_ligand_target_matrix`.
- `genes_of_interest` Character vector with the gene symbols of the genes of interest. These are the genes in the receiver cell population that are potentially affected by ligands expressed by interacting cells (e.g. genes differentially expressed upon cell-cell interaction).
- `n_top_ligands` How many of the top ligands to include in the ligand-target table.
- `n_top_targets` For each ligand, how many of the top targets to include in the ligand-target table.

**Value**

A tibble with columns `ligand`, `target` and `weight` (i.e. regulatory potential score).

**Examples**

```
## Not run:
networks <- nichenet_networks()
expression <- nichenet_expression_data()
optimization_results <- nichenet_optimization(networks, expression)
nichenet_model <- nichenet_build_model(optimization_results, networks)
lt_matrix <- nichenet_ligand_target_matrix(
  nichenet_model$weighted_networks,
  networks$lr_network,
  nichenet_model$optimized_parameters
)
ligand_activities <- nichenet_ligand_activities(
  ligand_target_matrix = lt_matrix,
  lr_network = networks$lr_network,
  # the rest of the parameters should come
  # from your transcriptomics data:
  expressed_genes_transmitter = expressed_genes_transmitter,
  expressed_genes_receiver = expressed_genes_receiver,
  genes_of_interest = genes_of_interest
)
lt_links <- nichenet_ligand_target_links(
  ligand_activities = ligand_activities,
  ligand_target_matrix = lt_matrix,
  genes_of_interest = genes_of_interest,
  n_top_ligands = 20,
  n_top_targets = 100
)

## End(Not run)
```

---

```
nichenet_ligand_target_matrix
```

*Creates a NicheNet ligand-target matrix*

---

## Description

Creates a NicheNet ligand-target matrix

## Usage

```
nichenet_ligand_target_matrix(  
  weighted_networks,  
  lr_network,  
  optimized_parameters,  
  use_weights = TRUE,  
  construct_ligand_target_matrix_param = list()  
)
```

## Arguments

`weighted_networks` Weighted networks as provided by [nichenet\\_build\\_model](#).

`lr_network` A data frame with ligand-receptor interactions, as produced by [nichenet\\_lr\\_network](#).

`optimized_parameters` The outcome of NicheNet parameter optimization as produced by [nichenet\\_build\\_model](#).

`use_weights` Logical: whether the network sources are weighted. In this function it only affects the output file name.

`construct_ligand_target_matrix_param` Override parameters for `nichenetr::construct_ligand_target_matrix`.

## Value

A matrix containing ligand-target probability scores.

## Examples

```
## Not run:  
networks <- nichenet_networks()  
expression <- nichenet_expression_data()  
optimization_results <- nichenet_optimization(networks, expression)  
nichenet_model <- nichenet_build_model(optimization_results, networks)  
lt_matrix <- nichenet_ligand_target_matrix(  
  nichenet_model$weighted_networks,  
  networks$lr_network,  
  nichenet_model$optimized_parameters  
)
```

```
## End(Not run)
```

---

nichenet\_lr\_network *Builds a NicheNet ligand-receptor network*

---

## Description

Builds ligand-receptor network prior knowledge for NicheNet using multiple resources.

## Usage

```
nichenet_lr_network(  
  omnipath = list(),  
  guide2pharma = list(),  
  ramilowski = list(),  
  only_omnipath = FALSE,  
  quality_filter_param = list()  
)
```

## Arguments

**omnipath** List with paramaters to be passed to [nichenet\\_lr\\_network\\_omnipath](#).  
**guide2pharma** List with paramaters to be passed to [nichenet\\_lr\\_network\\_guide2pharma](#).  
**ramilowski** List with paramaters to be passed to [nichenet\\_lr\\_network\\_ramilowski](#).  
**only\_omnipath** Logical: a shortcut to use only OmniPath as network resource.  
**quality\_filter\_param** Arguments for [filter\\_intercell\\_network](#) (quality filtering of the OmniPath ligand-receptor network). It is recommended to check these parameters and apply some quality filtering. The defaults already ensure certain filtering, but you might want more relaxed or stringent options.

## Value

A network data frame (tibble) with ligand-receptor interactions suitable for use with NicheNet.

## See Also

- [nichenet\\_lr\\_network\\_omnipath](#)
- [nichenet\\_lr\\_network\\_guide2pharma](#)
- [nichenet\\_lr\\_network\\_ramilowski](#)
- [filter\\_intercell\\_network](#)

**Examples**

```
# load everything with the default parameters:
lr_network <- nichenet_lr_network()

# don't use Ramilowski:
lr_network <- nichenet_lr_network(ramilowski = NULL)

# use only OmniPath:
lr_network_omnipath <- nichenet_lr_network(only_omnipath = TRUE)
```

---

nichenet\_lr\_network\_guide2pharma

*Ligand-receptor network from Guide to Pharmacology*

---

**Description**

Downloads ligand-receptor interactions from the Guide to Pharmacology database and converts it to a format suitable for NicheNet.

**Usage**

```
nichenet_lr_network_guide2pharma()
```

**Value**

Data frame with ligand-receptor interactions in NicheNet format.

**See Also**

[nichenet\\_lr\\_network](#), [guide2pharma\\_download](#)

**Examples**

```
g2p_lr_network <- nichenet_lr_network_guide2pharma()
```

---

`nichenet_lr_network_omnipath`*Builds ligand-receptor network for NicheNet using OmniPath*

---

## Description

Retrieves network prior knowledge from OmniPath and provides it in a format suitable for NicheNet. This method never downloads the ‘ligreextra’ dataset because the ligand-receptor interactions are supposed to come from [nichenet\\_lr\\_network\\_omnipath](#).

## Usage

```
nichenet_lr_network_omnipath(quality_filter_param = list(), ...)
```

## Arguments

`quality_filter_param`

List with arguments for [filter\\_intercell\\_network](#). It is recommended to check these parameters and apply some quality filtering. The defaults already ensure certain filtering, but you might want more relaxed or stringent options.

`...`

Passed to [import\\_intercell\\_network](#)

## Value

A network data frame (tibble) with ligand-receptor interactions suitable for use with NicheNet.

## See Also

- [nichenet\\_lr\\_network](#)
- [import\\_intercell\\_network](#)

## Examples

```
# use only ligand-receptor interactions (not for example ECM-adhesion):
op_lr_network <- nichenet_lr_network_omnipath(ligand_receptor = TRUE)

# use only CellPhoneDB and Guide to Pharmacology:
op_lr_network <- nichenet_lr_network_omnipath(
  resources = c('CellPhoneDB', 'Guide2Pharma')
)

# only interactions where the receiver is a transporter:
op_lr_network <- nichenet_lr_network_omnipath(
  receiver_param = list(parent = 'transporter')
)
```



---

`nichenet_lr_network_ramilowski`*Ligand-receptor network from Ramilowski 2015*

---

## Description

Downloads ligand-receptor interactions from Supplementary Table 2 of the paper 'A draft network of ligand-receptor-mediated multicellular signalling in human' (Ramilowski et al. 2015, <https://www.nature.com/articles/ncomms8866>). It converts the downloaded table to a format suitable for NicheNet.

## Usage

```
nichenet_lr_network_ramilowski(  
  evidences = c("literature supported", "putative")  
)
```

## Arguments

`evidences`      Character: evidence types, "literature supported", "putative" or both.

## Value

Data frame with ligand-receptor interactions in NicheNet format.

## See Also

- [nichenet\\_lr\\_network](#)
- [ramilowski\\_download](#)

## Examples

```
# use only the literature supported data:  
rami_lr_network <- nichenet_lr_network_ramilowski(  
  evidences = 'literature supported'  
)
```

---

nichenet\_main

*Executes the full NicheNet pipeline*


---

### Description

Builds all prior knowledge data required by NicheNet. For this it calls a multitude of methods to download and combine data from various databases according to the settings. The content of the prior knowledge data is highly customizable, see the documentation of the related functions. After the prior knowledge is ready, it performs parameter optimization to build a NicheNet model. This results a weighted ligand- target matrix. Then, considering the expressed genes from user provided data, a gene set of interest and background genes, it executes the NicheNet ligand activity analysis.

### Usage

```
nichenet_main(
  only_omnipath = FALSE,
  expressed_genes_transmitter = NULL,
  expressed_genes_receiver = NULL,
  genes_of_interest = NULL,
  background_genes = NULL,
  use_weights = TRUE,
  n_top_ligands = 42,
  n_top_targets = 250,
  signaling_network = list(),
  lr_network = list(),
  gr_network = list(),
  small = FALSE,
  tiny = FALSE,
  make_multi_objective_function_param = list(),
  objective_function_param = list(),
  mlrmo_optimization_param = list(),
  construct_ligand_target_matrix_param = list(),
  results_dir = NULL,
  quality_filter_param = list()
)
```

### Arguments

- only\_omnipath** Logical: use only OmniPath for network knowledge. This is a simple switch for convenience, further options are available by the other arguments. By default we use all available resources. The networks can be customized on a resource by resource basis, as well as providing custom parameters for individual resources, using the parameters ‘signaling\_network’, ‘lr\_network’ and ‘gr\_network’.
- expressed\_genes\_transmitter** Character vector with the gene symbols of the genes expressed in the cells transmitting the signal.

expressed_genes_receiver	Character vector with the gene symbols of the genes expressed in the cells receiving the signal.
genes_of_interest	Character vector with the gene symbols of the genes of interest. These are the genes in the receiver cell population that are potentially affected by ligands expressed by interacting cells (e.g. genes differentially expressed upon cell-cell interaction).
background_genes	Character vector with the gene symbols of the genes to be used as background.
use_weights	Logical: calculate and use optimized weights for resources (i.e. one resource seems to be better than another, hence the former is considered with a higher weight).
n_top_ligands	How many of the top ligands to include in the ligand-target table.
n_top_targets	How many of the top targets (for each of the top ligands) to consider in the ligand-target table.
signaling_network	A list of parameters for building the signaling network, passed to <a href="#">nichenet_signaling_network</a> .
lr_network	A list of parameters for building the ligand-receptor network, passed to <a href="#">nichenet_lr_network</a> .
gr_network	A list of parameters for building the gene regulatory network, passed to <a href="#">nichenet_gr_network</a> .
small	Logical: build a small network for testing purposes, using only OmniPath data. It is also a high quality network, it is reasonable to try the analysis with this small network.
tiny	Logical: build an even smaller network for testing purposes. As this involves random subsetting, it's not recommended to use this network for analysis.
make_multi_objective_function_param	Override parameters for <code>smoof::makeMultiObjectiveFunction</code> .
objective_function_param	Override additional arguments passed to the objective function.
mlrmo_optimization_param	Override arguments for <code>nichenetr::mlrmo_optimization</code> .
construct_ligand_target_matrix_param	Override parameters for <code>nichenetr::construct_ligand_target_matrix</code> .
results_dir	Character: path to the directory to save intermediate and final outputs from NicheNet methods.
quality_filter_param	Arguments for <a href="#">filter_intercell_network</a> (quality filtering of the OmniPath ligand-receptor network). It is recommended to check these parameters and apply some quality filtering. The defaults already ensure certain filtering, but you might want more relaxed or stringent options.

## Details

About *small* and *tiny* networks: Building a NicheNet model is computationally demanding, taking several hours to run. As this is related to the enormous size of the networks, to speed up testing we

can use smaller networks, around 1,000 times smaller, with few thousands of interactions instead of few millions. Random subsetting of the whole network would result disjunct fragments, instead we load only a few resources. To run the whole pipeline with tiny networks use [nichenet\\_test](#).

### Value

A named list with the intermediate and final outputs of the pipeline: 'networks', 'expression', 'optimized\_parameters', 'weighted\_networks' and 'ligand\_target\_matrix'.

### See Also

- [nichenet\\_networks](#)
- [nichenet\\_signaling\\_network](#)
- [nichenet\\_lr\\_network](#)
- [nichenet\\_gr\\_network](#)
- [nichenet\\_test](#)
- [nichenet\\_workarounds](#)
- [nichenet\\_results\\_dir](#)

### Examples

```
## Not run:
nichenet_results <- nichenet_main(
  # altering some network resource parameters, the rest
  # of the resources will be loaded according to the defaults
  signaling_network = list(
    cpdb = NULL, # this resource will be excluded
    inbiomap = NULL,
    evex = list(min_confidence = 1.0) # override some parameters
  ),
  gr_network = list(only_omnipath = TRUE),
  n_top_ligands = 20,
  # override the default number of CPU cores to use
  mlrmo_optimization_param = list(ncores = 4)
)

## End(Not run)
```

---

nichenet\_networks

*Builds NicheNet network prior knowledge*

---

### Description

Builds network knowledge required by NicheNet. For this it calls a multitude of methods to download and combine data from various databases according to the settings. The content of the prior knowledge data is highly customizable, see the documentation of the related functions.

**Usage**

```
nichenet_networks(
  signaling_network = list(),
  lr_network = list(),
  gr_network = list(),
  only_omnipath = FALSE,
  small = FALSE,
  tiny = FALSE,
  quality_filter_param = list()
)
```

**Arguments**

signaling_network	A list of parameters for building the signaling network, passed to <a href="#">nichenet_signaling_network</a>
lr_network	A list of parameters for building the ligand-receptor network, passed to <a href="#">nichenet_lr_network</a>
gr_network	A list of parameters for building the gene regulatory network, passed to <a href="#">nichenet_gr_network</a>
only_omnipath	Logical: a shortcut to use only OmniPath as network resource.
small	Logical: build a small network for testing purposes, using only OmniPath data. It is also a high quality network, it is reasonable to try the analysis with this small network.
tiny	Logical: build an even smaller network for testing purposes. As this involves random subsetting, it's not recommended to use this network for analysis.
quality_filter_param	Arguments for <a href="#">filter_intercell_network</a> (quality filtering of the OmniPath ligand-receptor network). It is recommended to check these parameters and apply some quality filtering. The defaults already ensure certain filtering, but you might want more relaxed or stringent options.

**Value**

A named list with three network data frames (tibbles): the signaling, the ligand-receptor (lr) and the gene regulatory (gr) networks.

**See Also**

- [nichenet\\_signaling\\_network](#)
- [nichenet\\_lr\\_network](#)
- [nichenet\\_gr\\_network](#)

**Examples**

```
## Not run:
networks <- nichenet_networks()
dplyr::sample_n(networks$gr_network, 10)
# # A tibble: 10 x 4
#   from to source database
```

```

# <chr> <chr> <chr> <chr>
# 1 MAX ALG3 harmonizome_ENCODE harmonizome
# 2 MAX IMPDH1 harmonizome_ENCODE harmonizome
# 3 SMAD5 LCP1 Remap_5 Remap
# 4 HNF4A TNFRSF19 harmonizome_CHEA harmonizome
# 5 SMC3 FAP harmonizome_ENCODE harmonizome
# 6 E2F6 HIST1H1B harmonizome_ENCODE harmonizome
# 7 TFAP2C MAT2B harmonizome_ENCODE harmonizome
# 8 USF1 TBX4 harmonizome_TRANSFAC harmonizome
# 9 MIR133B FETUB harmonizome_TRANSFAC harmonizome
# 10 SP4 HNRNP2 harmonizome_ENCODE harmonizome

## End(Not run)

# use only OmniPath:
omnipath_networks <- nichenet_networks(only_omnipath = TRUE)

```

---

nichenet\_optimization *Optimizes NicheNet model parameters*

---

## Description

Optimize NicheNet method parameters, i.e. PageRank parameters and source weights, based on a collection of experiments where the effect of a ligand on gene expression was measured.

## Usage

```

nichenet_optimization(
  networks,
  expression,
  make_multi_objective_function_param = list(),
  objective_function_param = list(),
  mlrmo_optimization_param = list()
)

```

## Arguments

networks	A list with NicheNet format signaling, ligand-receptor and gene regulatory networks as produced by <a href="#">nichenet_networks</a> .
expression	A list with expression data from ligand perturbation experiments, as produced by <a href="#">nichenet_expression_data</a> .
make_multi_objective_function_param	Override parameters for <code>snoof::makeMultiObjectiveFunction</code> .
objective_function_param	Override additional arguments passed to the objective function.
mlrmo_optimization_param	Override arguments for <code>nichenetr::mlrmo_optimization</code> .

**Value**

A result object from the function `m1rMBO::mbo`. Among other things, this contains the optimal parameter settings, the output corresponding to every input etc.

**Examples**

```
## Not run:
networks <- nichenet_networks()
expression <- nichenet_expression_data()
optimization_results <- nichenet_optimization(networks, expression)

## End(Not run)
```

---

`nichenet_remove_orphan_ligands`*Removes experiments with orphan ligands*

---

**Description**

Removes from the expression data the perturbation experiments involving ligands without connections.

**Usage**

```
nichenet_remove_orphan_ligands(expression, lr_network)
```

**Arguments**

<code>expression</code>	Expression data as returned by <a href="#">nichenet_expression_data</a> .
<code>lr_network</code>	A NicheNet format ligand-receptor network data frame as produced by <a href="#">nichenet_lr_network</a> .

**Value**

The same list as ‘`expression`’ with certain elements removed.

**Examples**

```
lr_network <- nichenet_lr_network()
expression <- nichenet_expression_data()
expression <- nichenet_remove_orphan_ligands(expression, lr_network)
```

---

nichenet\_results\_dir *Path to the current NicheNet results directory*

---

**Description**

Path to the directory to save intermediate and final outputs from NicheNet methods.

**Usage**

```
nichenet_results_dir()
```

**Value**

Character: path to the NicheNet results directory.

**Examples**

```
nichenet_results_dir()
# [1] "nichenet_results"
```

---

nichenet\_signaling\_network  
*Builds a NicheNet signaling network*

---

**Description**

Builds signaling network prior knowledge for NicheNet using multiple resources.

**Usage**

```
nichenet_signaling_network(  
  omnipath = list(),  
  pathwaycommons = list(),  
  harmonizome = list(),  
  vinayagam = list(),  
  cpdb = list(),  
  evex = list(),  
  inbiomap = list(),  
  only_omnipath = FALSE  
)
```



**Arguments**

omnipath	List with paramaters to be passed to <a href="#">nichenet_signaling_network_omnipath</a> .
pathwaycommons	List with paramaters to be passed to <a href="#">nichenet_signaling_network_pathwaycommons</a> .
harmonizome	List with paramaters to be passed to <a href="#">nichenet_signaling_network_harmonizome</a> .
vinayagam	List with paramaters to be passed to <a href="#">nichenet_signaling_network_vinayagam</a> .
cpdb	List with paramaters to be passed to <a href="#">nichenet_signaling_network_cpdb</a> .
evex	List with paramaters to be passed to <a href="#">nichenet_signaling_network_evex</a> .
inbiomap	List with paramaters to be passed to <a href="#">nichenet_signaling_network_inbiomap</a> .
only_omnipath	Logical: a shortcut to use only OmniPath as network resource.

**Value**

A network data frame (tibble) with signaling interactions suitable for use with NicheNet.

**See Also**

- [nichenet\\_signaling\\_network\\_omnipath](#)
- [nichenet\\_signaling\\_network\\_pathwaycommons](#)
- [nichenet\\_signaling\\_network\\_harmonizome](#)
- [nichenet\\_signaling\\_network\\_vinayagam](#)
- [nichenet\\_signaling\\_network\\_cpdb](#)
- [nichenet\\_signaling\\_network\\_evex](#)
- [nichenet\\_signaling\\_network\\_inbiomap](#)

**Examples**

```
# load everything with the default parameters:
# we don't load inBio Map due to the - hopefully
# temporary - issues of their server
sig_network <- nichenet_signaling_network(inbiomap = NULL, cpdb = NULL)

# override parameters for some resources:
sig_network <- nichenet_signaling_network(
  omnipath = list(resources = c('SIGNOR', 'Signalink3', 'SPIKE')),
  pathwaycommons = NULL,
  harmonizome = list(datasets = c('phosphositeplus', 'depod')),
  # we can not include this in everyday tests as it takes too long:
  # cpdb = list(complex_max_size = 1, min_score = .98),
  cpdb = NULL,
  evex = list(min_confidence = 1.5),
  inbiomap = NULL
)

# use only OmniPath:
sig_network_omnipath <- nichenet_signaling_network(only_omnipath = TRUE)
```

nichenet\_signaling\_network\_cpdb

*Builds signaling network for NicheNet using ConsensusPathDB*

---

### Description

Builds signaling network prior knowledge using ConsensusPathDB (CPDB) data. Note, the interactions from CPDB are not directed and many of them comes from complex expansion. Find out more at <http://cpdb.molgen.mpg.de/>.

### Usage

```
nichenet_signaling_network_cpdb(...)
```

### Arguments

... Passed to [consensuspathdb\\_download](#).

### Value

A network data frame (tibble) with signaling interactions suitable for use with NicheNet.

### See Also

- [nichenet\\_signaling\\_network](#)
- [consensuspathdb\\_download](#)

### Examples

```
# use some parameters stricter than default:
cpdb_signaling_network <- nichenet_signaling_network_cpdb(
  complex_max_size = 2,
  min_score = .99
)
```

---

nichenet\_signaling\_network\_evex

*NicheNet signaling network from EVEX*

---

### Description

Builds signaling network prior knowledge for NicheNet from the EVEX database.

### Usage

```
nichenet_signaling_network_evex(top_confidence = 0.75, indirect = FALSE, ...)
```

**Arguments**

top\_confidence Double, between 0 and 1. Threshold based on the quantile of the confidence score.

indirect Logical: whether to include indirect interactions.

... Ignored.

**Value**

A network data frame (tibble) with signaling interactions suitable for use with NicheNet.

**See Also**

- [evex\\_download](#)
- [nichenet\\_signaling\\_network](#)

**Examples**

```
ev_signaling_network <- nichenet_signaling_network_evex(  
  top_confidence = .9  
)
```

---

nichenet\_signaling\_network\_harmonizome  
*NicheNet signaling network from Harmonizome*

---

**Description**

Builds signaling network prior knowledge for NicheNet using Harmonizome

**Usage**

```
nichenet_signaling_network_harmonizome(  
  datasets = c("phosphositeplus", "kea", "depod"),  
  ...  
)
```

**Arguments**

datasets The datasets to use. For possible values please refer to default value and the Harmonizome webpage.

... Ignored.

**Value**

A network data frame (tibble) with signaling interactions suitable for use with NicheNet.

**Examples**

```
# use only KEA and PhosphoSite:
hz_signaling_network <- nichenet_signaling_network_harmonizome(
  datasets = c('kea', 'phosphositeplus')
)
```

---

nichenet\_signaling\_network\_inbiomap

*NicheNet signaling network from InWeb InBioMap*

---

**Description**

Builds signaling network prior knowledge for NicheNet from the InWeb InBioMap database.

**Usage**

```
nichenet_signaling_network_inbiomap(...)
```

**Arguments**

... Ignored.

**Value**

A network data frame (tibble) with signaling interactions suitable for use with NicheNet.

**See Also**

[nichenet\\_signaling\\_network](#), [inbiomap\\_download](#)

**Examples**

```
## Not run:
ib_signaling_network <- nichenet_signaling_network_inbiomap()

## End(Not run)
```

---

`nichenet_signaling_network_omnipath`*Builds signaling network for NicheNet using OmniPath*

---

### Description

Retrieves network prior knowledge from OmniPath and provides it in a format suitable for NicheNet. This method never downloads the 'ligreextra' dataset because the ligand-receptor interactions are supposed to come from [nichenet\\_lr\\_network\\_omnipath](#).

### Usage

```
nichenet_signaling_network_omnipath(min_curation_effort = 0, ...)
```

### Arguments

`min_curation_effort`

Lower threshold for curation effort

`...`

Passed to [import\\_post\\_translational\\_interactions](#)

### Value

A network data frame (tibble) with signaling interactions suitable for use with NicheNet.

### See Also

- [nichenet\\_signaling\\_network](#)

### Examples

```
# use interactions with at least 2 evidences (reference or database)
op_signaling_network <- nichenet_signaling_network_omnipath(
  min_curation_effort = 2
)
```

---

`nichenet_signaling_network_pathwaycommons`*NicheNet signaling network from PathwayCommons*

---

### Description

Builds signaling network prior knowledge for NicheNet using PathwayCommons.

**Usage**

```
nichenet_signaling_network_pathwaycommons(
  interaction_types = c("catalysis-precedes", "controls-phosphorylation-of",
    "controls-state-change-of", "controls-transport-of", "in-complex-with",
    "interacts-with"),
  ...
)
```

**Arguments**

```
interaction_types      Character vector with PathwayCommons interaction types. Please refer to the
                        default value and the PathwayCommons webpage.
...                    Ignored.
```

**Value**

A network data frame (tibble) with signaling interactions suitable for use with NicheNet.

**Examples**

```
# use only the "controls-transport-of" interactions:
pc_signaling_network <- nichenet_signaling_network_pathwaycommons(
  interaction_types = 'controls-transport-of'
)
```

---

```
nichenet_signaling_network_vinayagam
```

*NicheNet signaling network from Vinayagam*

---

**Description**

Builds signaling network prior knowledge for NicheNet using Vinayagam 2011 Supplementary Table S6. Find out more at <https://doi.org/10.1126/scisignal.2001699>.

**Usage**

```
nichenet_signaling_network_vinayagam(...)
```

**Arguments**

```
...                    Ignored.
```

**Value**

A network data frame (tibble) with signaling interactions suitable for use with NicheNet.

## Examples

```
vi_signaling_network <- nichenet_signaling_network_vinayagam()
```

---

nichenet\_test

*Run the NicheNet pipeline with a little dummy network*

---

## Description

Loads a tiny network and runs the NicheNet pipeline with low number of iterations in the optimization process. This way the pipeline runs in a reasonable time in order to test the code. Due to the random subsampling disconnected networks might be produced sometimes. If you see an error like "Error in if (sd(prediction\_vector) == 0) ... missing value where TRUE/FALSE needed", the random subsampled input is not appropriate. In this case just interrupt and call again. This test ensures the computational integrity of the pipeline. If it fails during the optimization process, try to start it over several times, even restarting R. The unpredictability is related to mlrMBO and nichenetr not being prepared to handle certain conditions, and it's also difficult to find out which conditions lead to which errors. At least 3 different errors appear time to time, depending on the input. It also seems like restarting R sometimes helps, suggesting that the entire system might be somehow stateful. You can ignore the Parallelization was not stopped warnings on repeated runs.

## Usage

```
nichenet_test(...)
```

## Arguments

... Passed to [nichenet\\_main](#).

## Value

A named list with the intermediate and final outputs of the pipeline: 'networks', 'expression', 'optimized\_parameters', 'weighted\_networks' and 'ligand\_target\_matrix'.

## Examples

```
## Not run:  
nnt <- nichenet_test()  
  
## End(Not run)
```

---

nichenet\_workarounds    *Workarounds using NicheNet without attaching the package*

---

### Description

NicheNet requires the availability of some lazy loaded external data which are not available if the package is not loaded and attached. Also, the `BBmisc::convertToShortString` used for error reporting in `m1rMBO::evalTargetFun.OptState` is patched here to print longer error messages. Maybe it's a better solution to attach `nichenetr` before running the NicheNet pipeline. Alternatively you can try to call this function in the beginning. Why we don't call this automatically is just because we don't want to load datasets from another package without the user knowing about it.

### Usage

```
nichenet_workarounds()
```

### Value

Returns NULL.

### Examples

```
## Not run:  
nichenet_workarounds()  
  
## End(Not run)
```

---

obo\_parser                    *Generic OBO parser*

---

### Description

Reads the contents of an OBO file and processes it into data frames or a list based data structure.

### Usage

```
obo_parser(  
  path,  
  relations = c("is_a", "part_of", "occurs_in", "regulates", "positively_regulates",  
               "negatively_regulates"),  
  shorten_namespace = TRUE,  
  tables = TRUE  
)
```



**Arguments**

path	Path to the OBO file.
relations	Character vector: process only these relations.
shorten_namespace	Logical: shorten the namespace to a single letter code (as usual for Gene Ontology, e.g. cellular_component = "C").
tables	Logical: return data frames (tibbles) instead of nested lists.

**Value**

A list with the following elements: 1) "names" a list with terms as names and names as values; 2) "namespaces" a list with terms as names and namespaces as values; 3) "relations" a list with relations between terms: terms are keys, values are lists with relations as names and character vectors of related terms as values; 4) "subsets" a list with terms as keys and character vectors of subset names as values (or NULL if the term does not belong to any subset); 5) "obsolete" character vector with all the terms labeled as obsolete. If the tables parameter is TRUE, "names", "namespaces", "relations" and "subsets" will be data frames (tibbles).

**See Also**

- [relations\\_list\\_to\\_table](#)
- [relations\\_table\\_to\\_list](#)
- [swap\\_relations](#)

**Examples**

```
goslim_url <-
  "http://current.geneontology.org/ontology/subsets/goslim_generic.obo"
path <- tempfile()
httr::GET(goslim_url, httr::write_disk(path, overwrite = TRUE))
obo <- obo_parser(path, tables = FALSE)
unlink(path)
names(obo)
# [1] "names"      "namespaces" "relations"   "subsets"    "obsolete"
head(obo$relations, n = 2)
# $`GO:0000001`
# $`GO:0000001`$is_a
# [1] "GO:0048308" "GO:0048311"
#
# $`GO:0000002`
# $`GO:0000002`$is_a
# [1] "GO:0007005"
```

---

oma_code	<i>Orthologous Matrix (OMA) codes of organisms</i>
----------	--

---

**Description**

Note: OMA species codes are whenever possible identical to UniProt codes.

**Usage**

```
oma_code(name)
```

**Arguments**

name                    Vector with any kind of organism name or identifier, can be also mixed type.

**Value**

A character vector with the Orthologous Matrix (OMA) codes of the organisms.

**See Also**

- [ncbi\\_taxid](#)
- [latin\\_name](#)
- [ensembl\\_name](#)
- [common\\_name](#)

**Examples**

```
oma_code(c(10090, "cjacchus", "Vicugna pacos"))  
# [1] "MOUSE" "CALJA" "VICPA"
```

---

oma_organisms	<i>Organism identifiers from the Orthologous Matrix</i>
---------------	---

---

**Description**

Organism identifiers from the Orthologous Matrix

**Usage**

```
oma_organisms()
```

**Value**

A data frame with organism identifiers.

**See Also**[ensembl\\_organisms](#)**Examples**

```
oma_organisms()
```

---

`oma_pairwise`*Orthologous gene pairs between two organisms*

---

**Description**

From the web API of Orthologous Matrix (OMA). Items which could not be translated to 'id\_type' (but present in the data with their internal OMA IDs) are removed.

**Usage**

```
oma_pairwise(  
  organism_a = "human",  
  organism_b = "mouse",  
  id_type = "uniprot",  
  mappings = c("1:1", "1:m", "n:1", "n:m"),  
  only_ids = TRUE  
)
```

**Arguments**

<code>organism_a</code>	Name or identifier of an organism.
<code>organism_b</code>	Name or identifier of another organism.
<code>id_type</code>	The gene or protein identifier to use in the table. For a list of supported ID types see 'omnipathr.env\$id_types\$oma'. In addition, "genesymbol" is supported, in this case <a href="#">oma_pairwise_genesymbols</a> will be called automatically.
<code>mappings</code>	Character vector: control ambiguous mappings: <ul style="list-style-type: none"> <li>• 1:1 - unambiguous</li> <li>• 1:m - one-to-many</li> <li>• n:1 - many-to-one</li> <li>• n:m - many-to-many</li> </ul>
<code>only_ids</code>	Logical: include only the two identifier columns, not the mapping type and the orthology group columns.

**Value**

A data frame with orthologous gene pairs.

**Examples**

```
oma_pairwise("human", "mouse", "uniprot")
# # A tibble: 21,753 × 4
#   id_organism_a id_organism_b mapping oma_group
#   <chr>         <chr>         <chr>     <dbl>
# 1 Q15326        Q8R5C8         1:1       1129380
# 2 Q9Y2E4        B2RQ71         1:1       681224
# 3 Q92615        Q6A0A2         1:1       1135087
# 4 Q9BZE4        Q99ME9         1:1       1176239
# 5 Q9BXS1        Q8BFZ6         1:m          NA
# # ... with 21,743 more rows
```

---

```
oma_pairwise_genesymbols
```

*Orthologous pairs of gene symbols between two organisms*

---

**Description**

The Orthologous Matrix (OMA), a resource of orthologous relationships between genes, doesn't provide gene symbols, the identifier preferred in many bioinformatics pipelines. Hence this function wraps `oma_pairwise` by translating the identifiers used in OMA to gene symbols. Items that can not be translated to 'id\_type' (but present in the data with their internal OMA IDs) will be removed. Then, in this function we translate the identifiers to gene symbols.

**Usage**

```
oma_pairwise_genesymbols(
  organism_a = "human",
  organism_b = "mouse",
  oma_id_type = "uniprot_entry",
  mappings = c("1:1", "1:m", "n:1", "n:m"),
  only_ids = TRUE
)
```

**Arguments**

<code>organism_a</code>	Name or identifier of an organism.
<code>organism_b</code>	Name or identifier of another organism.
<code>oma_id_type</code>	Character: the gene or protein identifier to be queried from OMA. These IDs will be translated to 'id_type'.
<code>mappings</code>	Character vector: control ambiguous mappings: <ul style="list-style-type: none"> <li>• 1:1 - unambiguous</li> <li>• 1:m - one-to-many</li> <li>• n:1 - many-to-one</li> <li>• n:m - many-to-many</li> </ul>
<code>only_ids</code>	Logical: include only the two identifier columns, not the mapping type and the orthology group columns.

**Value**

A data frame with orthologous gene pairs.

**Examples**

```
oma_pairwise_genesymbols("human", "mouse")
```

---

```
oma_pairwise_translated
```

*Orthologous pairs between two organisms for ID types not supported by OMA*

---

**Description**

The Orthologous Matrix (OMA), a resource of orthologous relationships between genes, doesn't provide gene symbols, the identifier preferred in many bioinformatics pipelines. Hence this function wraps [oma\\_pairwise](#) by translating the identifiers used in OMA to gene symbols. Items that can not be translated to 'id\_type' (but present in the data with their internal OMA IDs) will be removed. Then, in this function we translate the identifiers to the desired ID type.

**Usage**

```
oma_pairwise_translated(
  organism_a = "human",
  organism_b = "mouse",
  id_type = "uniprot",
  oma_id_type = "uniprot_entry",
  mappings = c("1:1", "1:m", "n:1", "n:m"),
  only_ids = TRUE
)
```

**Arguments**

organism_a	Name or identifier of an organism.
organism_b	Name or identifier of another organism.
id_type	The gene or protein identifier to use in the table. For a list of supported ID types see 'omnipathr.env\$id_types\$oma'. These are the identifiers that will be translated to gene symbols.
oma_id_type	Character: the gene or protein identifier to be queried from OMA. These IDs will be translated to 'id_type'.
mappings	Character vector: control ambiguous mappings: <ul style="list-style-type: none"> <li>• 1:1 - unambiguous</li> <li>• 1:m - one-to-many</li> <li>• n:1 - many-to-one</li> </ul>

only\_ids 

- n:m - many-to-many

 Logical: include only the two identifier columns, not the mapping type and the orthology group columns.

**Value**

A data frame with orthologous gene pairs.

**Examples**

```
oma_pairwise_translated("human", "mouse")
```

---

omnipath-interactions *Molecular interactions from OmniPath*

---

**Description**

The functions listed here all download pairwise, causal molecular interactions from the <https://omnipathdb.org/interactions> endpoint of the OmniPath web service. They are different only in the type of interactions and the kind of resources and data they have been compiled from. A complete list of these functions is available below, these cover the interaction datasets and types currently available in OmniPath:

Interactions from the <https://omnipathdb.org/interactions> endpoint of the OmniPath web service. By default, it downloads only the "omnipath" dataset, which corresponds to the curated causal interactions described in Turei et al. 2016.

Imports interactions from the 'omnipath' dataset of OmniPath, a dataset that inherits most of its design and contents from the original OmniPath core from the 2016 publication. This dataset consists of about 40k interactions.

Imports the dataset from: <https://omnipathdb.org/interactions?datasets=pathwayextra>, which contains activity flow interactions without literature reference. The activity flow interactions supported by literature references are part of the 'omnipath' dataset.

Imports the dataset from: <https://omnipathdb.org/interactions?datasets=kinaseextra>, which contains enzyme-substrate interactions without literature reference. The enzyme-substrate interactions supported by literature references are part of the 'omnipath' dataset.

Imports the dataset from: <https://omnipathdb.org/interactions?datasets=ligreextra>, which contains ligand-receptor interactions without literature reference. The ligand-receptor interactions supported by literature references are part of the 'omnipath' dataset.

Imports interactions from all post-translational datasets of OmniPath. The datasets are "omnipath", "kinaseextra", "pathwayextra" and "ligreextra".

Imports the dataset from: <https://omnipathdb.org/interactions?datasets=dorothea> which contains transcription factor (TF)-target interactions from DoRothEA <https://github.com/saezlab/DoRothEA> DoRothEA is a comprehensive resource of transcriptional regulation, consisting of 16 original resources, in silico TFBS prediction, gene expression signatures and ChIP-Seq binding site analysis.

Imports the dataset from: [https://omnipathdb.org/interactions?datasets=tf\\_target](https://omnipathdb.org/interactions?datasets=tf_target), which contains transcription factor-target protein coding gene interactions. Note: this is not the only TF-target dataset in OmniPath, 'dorothea' is the other one and the 'tf\_mirna' dataset provides TF-miRNA gene interactions.

Imports the dataset from: [https://omnipathdb.org/interactions?datasets=tf\\_target,dorothea](https://omnipathdb.org/interactions?datasets=tf_target,dorothea), which contains transcription factor-target protein coding gene interactions.

CollectRI is a comprehensive resource of transcriptional regulation, published in 2023, consisting of 14 resources and original literature curation.

Imports the dataset from: <https://omnipathdb.org/interactions?datasets=mirnatarget>, which contains miRNA-mRNA interactions.

Imports the dataset from: [https://omnipathdb.org/interactions?datasets=tf\\_mirna](https://omnipathdb.org/interactions?datasets=tf_mirna), which contains transcription factor-miRNA gene interactions

Imports the dataset from: [https://omnipathdb.org/interactions?datasets=lncrna\\_mrna](https://omnipathdb.org/interactions?datasets=lncrna_mrna), which contains lncRNA-mRNA interactions

Imports the dataset from: [https://omnipathdb.org/interactions?datasets=small\\_molecule](https://omnipathdb.org/interactions?datasets=small_molecule), which contains small molecule-protein interactions. Small molecules can be metabolites, intrinsic ligands or drug compounds.

## Usage

```
omnipath_interactions(...)  
  
omnipath(...)  
  
pathwayextra(...)  
  
kinaseextra(...)  
  
ligreextra(...)  
  
post_translational(...)  
  
dorothea(dorothea_levels = c("A", "B"), ...)  
  
tf_target(...)  
  
transcriptional(dorothea_levels = c("A", "B"), ...)  
  
collectri(...)  
  
mirna_target(...)  
  
tf_mirna(...)  
  
lncrna_mrna(...)  
  
small_molecule(...)
```

```

all_interactions(
  dorothea_levels = c("A", "B"),
  types = NULL,
  fields = NULL,
  exclude = NULL,
  ...
)

```

## Arguments

- ... Arguments passed on to `omnipath_query`, `omnipath_query`, `omnipath_query`, `omnipath_query`, `omnipath_query`, `omnipath_query`, `omnipath_query`, `omnipath_query`, `omnipath_query`, `omnipath_query`, `omnipath_query`, `omnipath_query`, `omnipath_query`, `omnipath_query`.
- `organism` Character or integer: name or NCBI Taxonomy ID of the organism. OmniPath is built of human data, and the web service provides orthology translated interactions and enzyme-substrate relationships for mouse and rat. For other organisms and query types, orthology translation will be called automatically on the downloaded human data before returning the result.
- `resources` Character vector: name of one or more resources. Restrict the data to these resources. For a complete list of available resources, call the `<query_type>_resources` functions for the query type of interest.
- `datasets` Character vector: name of one or more datasets. In the interactions query type a number of datasets are available. The default is called "omnipath", and corresponds to the curated causal signaling network published in the 2016 OmniPath paper.
- `genesymbols` Character or logical: TRUE or FALSE or "yes" or "no". Include the `'genesymbols'` column in the results. OmniPath uses UniProt IDs as the primary identifiers, gene symbols are optional.
- `default_fields` Logical: if TRUE, the default fields will be included.
- `silent` Logical: if TRUE, no messages will be printed. By default a summary message is printed upon successful download.
- `logicals` Character vector: fields to be cast to logical.
- `format` Character: if "json", JSON will be retrieved and processed into a nested list; any other value will return data frame.
- `download_args` List: parameters to pass to the download function, which is `'readr::read_tsv'` by default, and `'jsonlite::safe_load'`.
- `references_by_resource` Logical: if TRUE, in the `'references'` column the PubMed IDs will be prefixed with the names of the resources they are coming from. If FALSE, the `'references'` column will be a list of unique PubMed IDs.
- `add_counts` Logical: if TRUE, the number of references and number of resources for each record will be added to the result.
- `license` Character: license restrictions. By default, data from resources allowing "academic" use is returned by OmniPath. If you use the data for work



in a company, you can provide "commercial" or "for-profit", which will restrict the data to those records which are supported by resources that allow for-profit use.

`password` Character: password for the OmniPath web service. You can provide a special password here which enables the use of 'license = "ignore"' option, completely bypassing the license filter.

`json_param` List: parameters to pass to the 'jsonlite::fromJSON' when processing JSON columns embedded in the downloaded data. Such columns are "extra\_attrs" and "evidences". These are optional columns which provide a lot of extra details about interactions.

`strict_evidences` Logical: reconstruct the "sources" and "references" columns of interaction data frames based on the "evidences" column, strictly filtering them to the queried datasets and resources. Without this, the "sources" and "references" fields for each record might contain information for datasets and resources other than the queried ones, because the downloaded records are a result of a simple filtering of an already integrated data frame.

`genesymbol_resource` Character: "uniprot" (default) or "ensembl". The OmniPath web service uses the primary gene symbols as provided by UniProt. By passing "ensembl" here, the UniProt gene symbols will be replaced by the ones used in Ensembl. This translation results in a loss of a few records, and multiplication of another few records due to ambiguous translation.

`cache` Logical: use caching, load data from and save to the. The cache directory by default belongs to the user, located in the user's default cache directory, and named "OmnipathR". Find out about it by `getOption("omnipathR.cachedir")`. Can be changed by [omnipath\\_set\\_cachedir](#).

`dorothea_levels`

The confidence levels of the dorothea interactions (TF-target) which range from A to D. Set to A and B by default.

`types`

Character: interaction types, such as "transcriptional", "post\_transcriptional", "post\_translational", etc.

`fields`

Character: additional fields (columns) to be included in the result. For a list of available fields, see [query\\_info](#).

`exclude`

Character: names of datasets or resource to be excluded from the result. By default, the records supported by only these resources or datasets will be removed from the output. If `strict_evidences = TRUE`, the resource, reference and causality information in the data frame will be reconstructed to remove all information coming from the excluded resources.

## Details

### Post-translational (protein-protein, PPI) interactions

- `omnipath`: the OmniPath data as defined in the 2016 paper, an arbitrary optimum between coverage and quality. This dataset contains almost entirely causal (stimulatory or inhibitory; i.e. activity flow, according to the SBGN standard), physical interactions between pairs of proteins, curated by experts from the literature.
- `pathwayextra`: activity flow interactions without literature references.

- *kinaseextra*: enzyme-substrate interactions without literature references.
- *ligreextra*: ligand-receptor interactions without literature references.
- *post\_translational*: all post-translational (protein-protein, PPI) interactions; this is the combination of the *omnipath*, *pathwayextra*, *kinaseextra* and *ligreextra* datasets.

#### **TF-target (gene regulatory, GRN) interactions**

- *collectri*: transcription factor (TF)-target interactions from CollecTRI.
- *dorothea*: transcription factor (TF)-target interactions from DoRothEA
- *tf\_target*: transcription factor (TF)-target interactions from other resources
- *transcriptional*: all transcription factor (TF)-target interactions; this is the combination of the *collectri*, *dorothea* and *tf\_target* datasets.

#### **Post-transcriptional (miRNA-target) and other RNA related interactions**

In these datasets we intend to collect the literature curated resources, hence we don't include some of the most well known large databases if those are based on predictions or high-throughput assays.

- *mirna\_target*: miRNA-mRNA interactions
- *tf\_mirna*: TF-miRNA interactions
- *lncrna\_mrna*: lncRNA-mRNA interactions

#### **Other interaction access functions**

- *small\_molecule*: interactions between small molecules and proteins. Currently this is a small, experimental dataset that includes drug-target, ligand-receptor, enzyme-metabolite and other interactions. In the future this will be largely expanded and divided into multiple datasets.
- *all\_interactions*: all the interaction datasets combined.

#### **Value**

A dataframe of molecular interactions.

A dataframe of literature curated, post-translational signaling interactions.

A dataframe containing activity flow interactions between proteins without literature reference

A dataframe containing enzyme-substrate interactions without literature reference

A dataframe containing ligand-receptor interactions including the ones without literature references

A dataframe containing post-translational interactions

A data frame of TF-target interactions from DoRothEA.

A dataframe containing TF-target interactions

A dataframe containing TF-target interactions.

A dataframe of TF-target interactions.

A dataframe containing miRNA-mRNA interactions

A dataframe containing TF-miRNA interactions

A dataframe containing lncRNA-mRNA interactions

A dataframe of small molecule-protein interactions

A dataframe containing all the datasets in the interactions query

**See Also**

- [interaction\\_resources](#)
- [interaction\\_graph](#)
- [print\\_interactions](#)
- [annotated\\_network](#)
  
- [omnipath\\_interactions](#)
- [post\\_translational](#)
- [interaction\\_resources](#)
- [all\\_interactions](#)
- [interaction\\_graph](#)
- [print\\_interactions](#)

**Examples**

```
op <- omnipath(resources = c("CA1", "SIGNOR", "Signalink3"))
op

interactions = omnipath_interactions(
  resources = "Signalink3",
  organism = 9606
)

pathways <- omnipath()
pathways

interactions <-
  pathwayextra(
    resources = c("BioGRID", "IntAct"),
    organism = 9606
  )

kinase_substrate <-
  kinaseextra(
    resources = c('PhosphoPoint', 'PhosphoSite'),
    organism = 9606
  )

ligand_receptor <- ligreextra(
  resources = c('HPRD', 'Guide2Pharma'),
  organism = 9606
)

interactions <- post_translational(resources = "BioGRID")

dorothea_grn <- dorothea(
  resources = c('DoRothEA', 'ARACNe-GTex_DoRothEA'),
  organism = 9606,
  dorothea_levels = c('A', 'B', 'C')
```

```

)
dorothea_grn

interactions <- tf_target(resources = c("DoRothEA", "SIGNOR"))

grn <- transcriptional(resources = c("PAZAR", "ORegAnno", "DoRothEA"))
grn

collectri_grn <- collectri()
collectri_grn

interactions <- mirna_target( resources = c("miRTarBase", "miRecords"))

interactions <- tf_mirna(resources = "TransmiR")

interactions <- lncrna_mrna(resources = c("ncRDeathDB"))

# What are the targets of aspirin?
interactions <- small_molecule(sources = "ASPIRIN")
# The prostaglandin synthases:
interactions

interactions <- all_interactions(
  resources = c("HPRD", "BioGRID"),
  organism = 9606
)

```

## Description

OmnipathR is an R package built to provide easy access to the data stored in the OmniPath web service:

<https://omnipathdb.org/>

And a number of other resources, such as BioPlex, ConsensusPathDB, EVEX, Guide to Pharmacology (IUPHAR/BPS), Harmonizome, HTRIdb, InWeb InBioMap, KEGG Pathway, Pathway Commons, Ramilowski et al. 2015, RegNetwork, ReMap, TF census, TRRUST and Vinayagam et al. 2011.

The OmniPath web service implements a very simple REST style API. This package make requests by the HTTP protocol to retrieve the data. Hence, fast Internet access is required for a proper use of OmnipathR.

The package also provides some utility functions to filter, analyse and visualize the data. Furthermore, OmnipathR features a close integration with the NicheNet method for ligand activity prediction from transcriptomics data, and its R implementation nichenetr (available in CRAN).

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**See Also**

Useful links:

- <https://r.omnipathdb.org/>
- Report bugs at <https://github.com/saezlab/OmnipathR/issues>

**Examples**

```
## Not run:
# Download post-translational modifications:
enzsub <- enzyme_substrate(resources = c("PhosphoSite", "SIGNOR"))

# Download protein-protein interactions
interactions <- omnipath(resources = "SignalLink3")

# Convert to igraph objects:
enzsub_g <- enzsub_graph(enzsub = enzsub)
OPI_g <- interaction_graph(interactions = interactions)

# Print some interactions:
print_interactions(head(enzsub))

# interactions with references:
print_interactions(tail(enzsub), writeRefs = TRUE)

# find interactions between kinase and substrate:
print_interactions(dplyr::filter(ptms, enzyme_genesymbol=="MAP2K1",
  substrate_genesymbol=="MAPK3"))

# find shortest paths on the directed network between proteins
print_path_es(shortest_paths(OPI_g, from = "TYRO3", to = "STAT3",
  output = 'epath')$epath[[1]], OPI_g)

# find all shortest paths between proteins
print_path_vs(
  all_shortest_paths(
    enzsub_g,
    from = "SRC",
    to = "STAT1"
  )$res,
  enzsub_g
)

## End(Not run)
```

omnipath\_cache\_autoclean

*Keeps only the latest versions of complete downloads*

---

### **Description**

Removes the old versions, the failed downloads and the files in the cache directory which are missing from the database. For more flexible operations use [omnipath\\_cache\\_remove](#) and [omnipath\\_cache\\_clean](#).

### **Usage**

```
omnipath_cache_autoclean()
```

### **Value**

Invisibl returns the cache database (list of cache records).

### **Examples**

```
## Not run:  
omnipath_cache_autoclean()  
  
## End(Not run)
```

---

omnipath\_cache\_clean *Removes the items from the cache directory which are unknown by the cache database*

---

### **Description**

Removes the items from the cache directory which are unknown by the cache database

### **Usage**

```
omnipath_cache_clean()
```

### **Value**

Returns 'NULL'.

### **Examples**

```
omnipath_cache_clean()
```

---

`omnipath_cache_clean_db`*Removes the cache database entries without existing files*

---

**Description**

Removes the cache database entries without existing files

**Usage**

```
omnipath_cache_clean_db(...)
```

**Arguments**

... Ignored.

**Value**

Returns 'NULL'.

**Examples**

```
omnipath_cache_clean_db()
```

---

`omnipath_cache_download_ready`*Sets the download status to ready for a cache item*

---

**Description**

Sets the download status to ready for a cache item

**Usage**

```
omnipath_cache_download_ready(version, key = NULL)
```

**Arguments**

`version` Version of the cache item. If does not exist a new version item will be created  
`key` Key of the cache item

**Value**

Character: invisibly returns the version number of the cache version item.

**Examples**

```

bioc_url <- 'https://bioconductor.org/'
# request a new version item (or retrieve the latest)
new_version <- omnipath_cache_latest_or_new(url = bioc_url)
# check if the version item is not a finished download
new_version$status
# [1] "unknown"
# download the file
httr::GET(bioc_url, httr::write_disk(new_version$path, overwrite = TRUE))
# report to the cache database that the download is ready
omnipath_cache_download_ready(new_version)
# now the status is ready:
version <- omnipath_cache_latest_or_new(url = bioc_url)
version$status
# "ready"
version$dl_finished
# [1] "2021-03-09 16:48:38 CET"
omnipath_cache_remove(url = bioc_url) # cleaning up

```

---

omnipath\_cache\_filter\_versions

*Filters the versions from one cache record*

---

**Description**

Filters the versions based on multiple conditions: their age and status

**Usage**

```

omnipath_cache_filter_versions(
  record,
  latest = FALSE,
  max_age = NULL,
  min_age = NULL,
  status = CACHE_STATUS$READY
)

```

**Arguments**

record	A cache record
latest	Return the most recent version
max_age	The maximum age in days (e.g. 5: 5 days old or more recent)
min_age	The minimum age in days (e.g. 5: 5 days old or older)
status	Character vector with status codes. By default only the versions with ‘ready’ (completed download) status are selected



**Value**

Character vector with version IDs, NA if no version satisfies the conditions.

**Examples**

```
# creating an example cache record
bioc_url <- 'https://bioconductor.org/'
version <- omnipath_cache_latest_or_new(url = bioc_url)
httr::GET(bioc_url, httr::write_disk(version$path, overwrite = TRUE))
omnipath_cache_download_ready(version)
record <- dplyr::first(omnipath_cache_search('biocond'))

# only the versions with status "ready"
version_numbers <- omnipath_cache_filter_versions(record, status = 'ready')
omnipath_cache_remove(url = bioc_url) # cleaning up
```

---

omnipath\_cache\_get      *Retrieves one item from the cache directory*

---

**Description**

Retrieves one item from the cache directory

**Usage**

```
omnipath_cache_get(
  key = NULL,
  url = NULL,
  post = NULL,
  payload = NULL,
  create = TRUE,
  ...
)
```

**Arguments**

key	The key of the cache record
url	URL pointing to the resource
post	HTTP POST parameters as a list
payload	HTTP data payload
create	Create a new entry if doesn't exist yet
...	Passed to omnipath_cache_record (internal function)

**Value**

Cache record: an existing record if the entry already exists, otherwise a newly created and inserted record

## Examples

```
# create an example cache record
bioc_url <- 'https://bioconductor.org/'
version <- omnipath_cache_latest_or_new(url = bioc_url)
omnipath_cache_remove(url = bioc_url) # cleaning up

# retrieve the cache record
record <- omnipath_cache_get(url = bioc_url)
record$key
# [1] "41346a00fb20d2a9df03aa70cf4d50bf88ab154a"
record$url
# [1] "https://bioconductor.org/"
```

---

omnipath_cache_key	<i>Generates a hash which identifies an element in the cache database</i>
--------------------	---

---

## Description

Generates a hash which identifies an element in the cache database

## Usage

```
omnipath_cache_key(url, post = NULL, payload = NULL)
```

## Arguments

url	Character vector with URLs
post	List with the HTTP POST parameters or a list of lists if the url vector is longer than 1. NULL for queries without POST parameters.
payload	HTTP data payload. List with multiple items if the url vector is longer than 1. NULL for queries without data.

## Value

Character vector of cache record keys.

## Examples

```
bioc_url <- 'https://bioconductor.org/'
omnipath_cache_key(bioc_url)
# [1] "41346a00fb20d2a9df03aa70cf4d50bf88ab154a"
```

---

 omnipath\_cache\_latest\_or\_new

*The latest or a new version of a cache record*


---

## Description

Looks up a record in the cache and returns its latest valid version. If the record doesn't exist or no valid version available, creates a new one.

## Usage

```
omnipath_cache_latest_or_new(
  key = NULL,
  url = NULL,
  post = NULL,
  payload = NULL,
  create = TRUE,
  ...
)
```

## Arguments

key	The key of the cache record
url	URL pointing to the resource
post	HTTP POST parameters as a list
payload	HTTP data payload
create	Logical: whether to create and return a new version. If FALSE only the latest existing valid version is returned, if available.
...	Passed to <a href="#">omnipath_cache_get</a>

## Value

A cache version item.

## Examples

```
## Not run:
# retrieve the latest version of the first cache record
# found by the search keyword "bioplex"
latest_bioplex <-
  omnipath_cache_latest_or_new(
    names(omnipath_cache_search('bioplex'))[1]
  )

latest_bioplex$dl_finished
# [1] "2021-03-09 14:28:50 CET"
latest_bioplex$path
```

```
# [1] "/home/denes/.cache/OmnipathR/378e0def2ac97985f629-1.rds"

## End(Not run)

# create an example cache record
bioc_url <- 'https://bioconductor.org/'
version <- omnipath_cache_latest_or_new(url = bioc_url)
omnipath_cache_remove(url = bioc_url) # cleaning up
```

---

```
omnipath_cache_latest_version
```

*Finds the most recent version in a cache record*

---

### Description

Finds the most recent version in a cache record

### Usage

```
omnipath_cache_latest_version(record)
```

### Arguments

record            A cache record

### Value

Character: the version ID with the most recent download finished time

---

```
omnipath_cache_load    Loads an R object from the cache
```

---

### Description

Loads the object from RDS format.

### Usage

```
omnipath_cache_load(
  key = NULL,
  version = NULL,
  url = NULL,
  post = NULL,
  payload = NULL
)
```

**Arguments**

key	Key of the cache item
version	Version of the cache item. If does not exist or NULL, the latest version will be retrieved
url	URL of the downloaded resource
post	HTTP POST parameters as a list
payload	HTTP data payload

**Value**

Object loaded from the cache RDS file.

**See Also**

[omnipath\\_cache\\_save](#)

**Examples**

```
url <- paste0(
  'https://omnipathdb.org/intercell?resources=Adhesome,Almen2009,',
  'Baccin2019,CSPA,CellChatDB&license=academic'
)
result <- read.delim(url, sep = '\t')
omnipath_cache_save(result, url = url)
# works only if you have already this item in the cache
intercell_data <- omnipath_cache_load(url = url)
class(intercell_data)
# [1] "data.frame"
nrow(intercell_data)
# [1] 16622
attr(intercell_data, 'origin')
# [1] "cache"

# basic example of saving and loading to and from the cache:
bioc_url <- 'https://bioconductor.org/'
bioc_html <- readChar(url(bioc_url), nchars = 99999)
omnipath_cache_save(bioc_html, url = bioc_url)
bioc_html <- omnipath_cache_load(url = bioc_url)
```

---

omnipath\_cache\_move\_in

*Moves an existing file into the cache*

---

**Description**

Either the key or the URL (with POST and payload) must be provided.

**Usage**

```
omnipath_cache_move_in(  
  path,  
  key = NULL,  
  version = NULL,  
  url = NULL,  
  post = NULL,  
  payload = NULL,  
  keep_original = FALSE  
)
```

**Arguments**

path	Path to the source file
key	Key of the cache item
version	Version of the cache item. If does not exist a new version item will be created
url	URL of the downloaded resource
post	HTTP POST parameters as a list
payload	HTTP data payload
keep_original	Whether to keep or remove the original file

**Value**

Character: invisibly returns the version number of the cache version item.

**See Also**

[omnipath\\_cache\\_save](#)

**Examples**

```
path <- tempfile()  
saveRDS(rnorm(100), file = path)  
omnipath_cache_move_in(path, url = 'the_download_address')  
  
# basic example of moving a file to the cache:  
  
bioc_url <- 'https://bioconductor.org/'  
html_file <- tempfile(fileext = '.html')  
httr::GET(bioc_url, httr::write_disk(html_file, overwrite = TRUE))  
omnipath_cache_move_in(path = html_file, url = bioc_url)  
omnipath_cache_remove(url = bioc_url) # cleaning up
```

---

omnipath\_cache\_remove *Removes contents from the cache directory*

---

### Description

According to the parameters, it can remove contents older than a certain age, or contents having a more recent version, one specific item, or wipe the entire cache.

### Usage

```
omnipath_cache_remove(key = NULL, url = NULL, post = NULL,  
    payload = NULL, max_age = NULL, min_age = NULL, status = NULL,  
    only_latest = FALSE, wipe = FALSE, autoclean = TRUE)
```

### Arguments

key	The key of the cache record
url	URL pointing to the resource
post	HTTP POST parameters as a list
payload	HTTP data payload
max_age	Age of cache items in days. Remove everything that is older than this age
min_age	Age of cache items in days. Remove everything more recent than this age
status	Remove items having any of the states listed here
only_latest	Keep only the latest version
wipe	Logical: if TRUE, removes all files from the cache and the cache database. Same as calling <a href="#">omnipath_cache_wipe</a> .
autoclean	Remove the entries about failed downloads, the files in the cache directory which are missing from the cache database, and the entries without existing files in the cache directory

### Value

Invisibly returns the cache database (list of cache records).

### See Also

- [omnipath\\_cache\\_wipe](#)
- [omnipath\\_cache\\_clean](#)
- [omnipath\\_cache\\_autoclean](#)

## Examples

```
## Not run:
# remove all cache data from the BioPlex database
cache_records <- omnipath_cache_search(
  'bioplex',
  ignore.case = TRUE
)
omnipath_cache_remove(names(cache_records))

# remove a record by its URL
regnetwork_url <- 'http://www.regnetworkweb.org/download/human.zip'
omnipath_cache_remove(url = regnetwork_url)

# remove all records older than 30 days
omnipath_cache_remove(max_age = 30)

# for each record, remove all versions except the latest
omnipath_cache_remove(only_latest = TRUE)

## End(Not run)

bioc_url <- 'https://bioconductor.org/'
version <- omnipath_cache_latest_or_new(url = bioc_url)
httr::GET(bioc_url, httr::write_disk(version$path, overwrite = TRUE))
omnipath_cache_download_ready(version)
key <- omnipath_cache_key(bioc_url)
omnipath_cache_remove(key = key)
```

---

omnipath\_cache\_save *Saves an R object to the cache*

---

## Description

Exports the object in RDS format, creates new cache record if necessary.

## Usage

```
omnipath_cache_save(
  data,
  key = NULL,
  version = NULL,
  url = NULL,
  post = NULL,
  payload = NULL
)
```



**Arguments**

data	An object
key	Key of the cache item
version	Version of the cache item. If does not exist a new version item will be created
url	URL of the downloaded resource
post	HTTP POST parameters as a list
payload	HTTP data payload

**Value**

Returns invisibly the data itself.

Invisibly returns the 'data'.

**See Also**

[omnipath\\_cache\\_move\\_in](#)

**Examples**

```
mydata <- data.frame(a = c(1, 2, 3), b = c('a', 'b', 'c'))
omnipath_cache_save(mydata, url = 'some_dummy_address')
from_cache <- omnipath_cache_load(url = 'some_dummy_address')
from_cache
#   a b
# 1 1 a
# 2 2 b
# 3 3 c
attr(from_cache, 'origin')
# [1] "cache"

# basic example of saving and loading to and from the cache:
bioc_url <- 'https://bioconductor.org/'
bioc_html <- readChar(url(bioc_url), nchars = 99999)
omnipath_cache_save(bioc_html, url = bioc_url)
bioc_html <- omnipath_cache_load(url = bioc_url)
```

---

omnipath\_cache\_search *Searches for cache items*

---

**Description**

Searches the cache records by matching the URL against a string or regexp.

**Usage**

```
omnipath_cache_search(pattern, ...)
```

**Arguments**

pattern           String or regular expression.  
...                Passed to grep

**Value**

List of cache records matching the pattern.

**Examples**

```
# find all cache records from the BioPlex database
bioplex_cache_records <- omnipath_cache_search(
  'bioplex',
  ignore.case = TRUE
)
```

---

omnipath\_cache\_set\_ext

*Sets the file extension for a cache record*

---

**Description**

Sets the file extension for a cache record

**Usage**

```
omnipath_cache_set_ext(key, ext)
```

**Arguments**

key                Character: key for a cache item, alternatively a version entry.  
ext                Character: the file extension, e.g. "zip".

**Value**

Returns 'NULL'.

**Examples**

```
bioc_url <- 'https://bioconductor.org/'
version <- omnipath_cache_latest_or_new(url = bioc_url)
version$path
# [1] "/home/denes/.cache/OmnipathR/41346a00fb20d2a9df03-1"
httr::GET(bioc_url, httr::write_disk(version$path, overwrite = TRUE))
key <- omnipath_cache_key(url = bioc_url)
omnipath_cache_set_ext(key = key, ext = 'html')
version <- omnipath_cache_latest_or_new(url = bioc_url)
```

```
version$path
# [1] "/home/denes/.cache/OmnipathR/41346a00fb20d2a9df03-1.html"
record <- omnipath_cache_get(url = bioc_url)
record$ext
# [1] "html"
omnipath_cache_remove(url = bioc_url) # cleaning up
```

---

omnipath\_cache\_update\_status

*Updates the status of an existing cache record*

---

## Description

Updates the status of an existing cache record

## Usage

```
omnipath_cache_update_status(key, version, status,
                             dl_finished = NULL)
```

## Arguments

key	Key of the cache item
version	Version of the cache item. If does not exist a new version item will be created
status	The updated status value
dl_finished	Timestamp for the time when download was finished, if 'NULL' the value remains unchanged

## Value

Character: invisibly returns the version number of the cache version item.

## Examples

```
bioc_url <- 'https://bioconductor.org/'
latest_version <- omnipath_cache_latest_or_new(url = bioc_url)
key <- omnipath_cache_key(bioc_url)
omnipath_cache_update_status(
  key = key,
  version = latest_version$number,
  status = 'ready',
  dl_finished = Sys.time()
)
omnipath_cache_remove(url = bioc_url) # cleaning up
```

omnipath\_cache\_wipe *Permanently removes all the cache contents*

---

**Description**

After this operation the cache directory will be completely empty, except an empty cache database file.

**Usage**

```
omnipath_cache_wipe(...)
```

**Arguments**

... Ignored.

**Value**

Returns 'NULL'.

**See Also**

[omnipath\\_cache\\_remove](#)

**Examples**

```
## Not run:
omnipath_cache_wipe()
# the cache is completely empty:
print(omnipathr.env$cache)
# list()
list.files(omnipath_get_cachedir())
# [1] "cache.json"

## End(Not run)
```

---

omnipath\_config\_path *Current config file path of OmnipathR*

---

**Description**

Current config file path of OmnipathR  
Current config file path for a certain package

**Usage**

```
omnipath_config_path(user = FALSE)

config_path(user = FALSE, pkg = "OmnipathR")
```

**Arguments**

user	Logical: prioritize the user level config even if a config in the current working directory is available.
pkg	Character: name of the package.

**Value**

Character: path to the config file.

**Examples**

```
omnipath_config_path()
```

---

omnipath\_for\_cosmos    *OmniPath PPI for the COSMOS PKN*

---

**Description**

OmniPath PPI for the COSMOS PKN

**Usage**

```
omnipath_for_cosmos(
  organism = 9606L,
  resources = NULL,
  datasets = NULL,
  interaction_types = NULL,
  id_types = c("uniprot", "genesymbol"),
  ...
)
```

**Arguments**

organism	Character or integer: name or NCBI Taxonomy ID of the organism.
resources	Character: names of one or more resources. Correct spelling is important.
datasets	Character: one or more network datasets in OmniPath.
interaction_types	Character: one or more interaction type

`id_types` Character: translate the protein identifiers to these ID types. Each ID type results two extra columns in the output, for the "source" and "target" sides of the interaction, respectively. The default ID type for proteins is Ensembl Gene ID, and by default UniProt IDs and Gene Symbols are included. The UniProt IDs returned by the web service are left intact, while the Gene Symbols are queried from Ensembl. These Gene Symbols are different from the ones returned from the web service, and match the Ensembl Gene Symbols used by other components of the COSMOS PKN.

... Further parameters to [omnipath\\_interactions](#).

**Value**

Data frame with the columns source, target and sign.

**See Also**

- [cosmos\\_pkn](#)
- [omnipath-interactions](#)

**Examples**

```
op_cosmos <- omnipath_for_cosmos()
op_cosmos
```

---

`omnipath_load_config` *Load the package configuration from a config file*

---

**Description**

Load the package configuration from a config file

Load the configuration of a certain package

**Usage**

```
omnipath_load_config(path = NULL, title = "default", user = FALSE, ...)

load_config(
  path = NULL,
  title = "default",
  user = FALSE,
  pkg = "OmnipathR",
  ...
)
```

**Arguments**

path	Path to the config file.
title	Load the config under this title. One config file might contain multiple configurations, each identified by a title. If the title is not available the first section of the config file will be used.
user	Force to use the user level config even if a config file exists in the current directory. By default, the local config files have priority over the user level config.
...	Passed to <code>yaml::yaml.load_file</code> .
pkg	Character: name of the package

**Value**

Invisibly returns the config as a list.

**Examples**

```
## Not run:
# load the config from a custom config file:
omnipath_load_config(path = 'my_custom_omnipath_config.yml')

## End(Not run)
```

---

omnipath\_log

*Browse the current OmnipathR log file*


---

**Description**

Browse the current OmnipathR log file

Browse the latest log from a package

**Usage**

```
omnipath_log()

read_log(pkg = "OmnipathR")
```

**Arguments**

pkg	Character: name of a package.
-----	-------------------------------

**Value**

Returns 'NULL'.

**See Also**

[omnipath\\_logfile](#)

**Examples**

```
## Not run:
omnipath_log()
# then you can browse the log file, and exit with `q`

## End(Not run)
```

---

omnipath_logfile	<i>Path to the current OmnipathR log file</i>
------------------	---

---

**Description**

Path to the current OmnipathR log file  
Path to the current logfile of a package

**Usage**

```
omnipath_logfile()
logfile(pkg = "OmnipathR")
```

**Arguments**

pkg                    Character: name of a package.

**Value**

Character: path to the current logfile, or NULL if no logfile is available.

**See Also**

[omnipath\\_log](#)

**Examples**

```
omnipath_logfile()
# [1] "/home/denes/omnipathr/omnipathr-log/omnipathr-20210309-1642.log"
```



---

`omnipath_msg`*Dispatch a message to the OmnipathR logger*

---

**Description**

Any package or script can easily send log messages and establish a logging facility with the fantastic ‘logger’ package. This function serves the only purpose if you want to inject messages into the logger of OmnipathR. Otherwise we recommend to use the ‘logger’ package directly.

**Usage**

```
omnipath_msg(level, ...)
```

**Arguments**

<code>level</code>	Character, numeric or class loglevel. A log level, if character one of the followings: "fatal", "error", "warn", "success", "info", "trace".
<code>...</code>	Arguments for string formatting, passed <code>sprintf</code> or <code>str_glue</code> .

**Value**

Returns ‘NULL’.

**Examples**

```
omnipath_msg(  
  level = 'success',  
  'Talking to you in the name of OmnipathR, my favourite number is %d',  
  round(runif(1, 1, 10))  
)
```

---

`omnipath_query`*Download data from the OmniPath web service*

---

**Description**

This is the most generic method for accessing data from the OmniPath web service. All other functions retrieving data from OmniPath call this function with various parameters. In general, every query can retrieve data in tabular or JSON format, the tabular (data frame) being the default.

**Usage**

```

omnipath_query(
  query_type,
  organism = 9606L,
  resources = NULL,
  datasets = NULL,
  types = NULL,
  genesymbols = "yes",
  fields = NULL,
  default_fields = TRUE,
  silent = FALSE,
  logicals = NULL,
  download_args = list(),
  format = "data.frame",
  references_by_resource = TRUE,
  add_counts = TRUE,
  license = NULL,
  password = NULL,
  exclude = NULL,
  json_param = list(),
  strict_evidences = FALSE,
  genesymbol_resource = "UniProt",
  cache = NULL,
  ...
)

```

**Arguments**

query_type	Character: "interactions", "enzsub", "complexes", "annotations", or "intercell".
organism	Character or integer: name or NCBI Taxonomy ID of the organism. OmniPath is built of human data, and the web service provides orthology translated interactions and enzyme-substrate relationships for mouse and rat. For other organisms and query types, orthology translation will be called automatically on the downloaded human data before returning the result.
resources	Character vector: name of one or more resources. Restrict the data to these resources. For a complete list of available resources, call the ' <code>&lt;query_type&gt;_resources</code> ' functions for the query type of interest.
datasets	Character vector: name of one or more datasets. In the interactions query type a number of datasets are available. The default is called "omnipath", and corresponds to the curated causal signaling network published in the 2016 OmniPath paper.
types	Character vector: one or more interaction types, such as "transcriptional" or "post_translational". For a full list of interaction types see ' <code>query_info("interaction")\$types</code> '.
genesymbols	Character or logical: TRUE or FALSE or "yes" or "no". Include the ' <code>genesymbols</code> ' column in the results. OmniPath uses UniProt IDs as the primary identifiers, gene symbols are optional.

fields	Character vector: additional fields to include in the result. For a list of available fields, call <code>'query_info("interactions")'</code> .
default_fields	Logical: if TRUE, the default fields will be included.
silent	Logical: if TRUE, no messages will be printed. By default a summary message is printed upon successful download.
logicals	Character vector: fields to be cast to logical.
download_args	List: parameters to pass to the download function, which is <code>'readr::read_tsv'</code> by default, and <code>'jsonlite::safe_load'</code> .
format	Character: if "json", JSON will be retrieved and processed into a nested list; any other value will return data frame.
references_by_resource	Logical: if TRUE, in the 'references' column the PubMed IDs will be prefixed with the names of the resources they are coming from. If FALSE, the 'references' column will be a list of unique PubMed IDs.
add_counts	Logical: if TRUE, the number of references and number of resources for each record will be added to the result.
license	Character: license restrictions. By default, data from resources allowing "academic" use is returned by OmniPath. If you use the data for work in a company, you can provide "commercial" or "for-profit", which will restrict the data to those records which are supported by resources that allow for-profit use.
password	Character: password for the OmniPath web service. You can provide a special password here which enables the use of <code>'license = "ignore"'</code> option, completely bypassing the license filter.
exclude	Character vector: resource or dataset names to be excluded. The data will be filtered after download to remove records of the excluded datasets and resources.
json_param	List: parameters to pass to the <code>'jsonlite::fromJSON'</code> when processing JSON columns embedded in the downloaded data. Such columns are "extra_attrs" and "evidences". These are optional columns which provide a lot of extra details about interactions.
strict_evidences	Logical: reconstruct the "sources" and "references" columns of interaction data frames based on the "evidences" column, strictly filtering them to the queried datasets and resources. Without this, the "sources" and "references" fields for each record might contain information for datasets and resources other than the queried ones, because the downloaded records are a result of a simple filtering of an already integrated data frame.
genesymbol_resource	Character: "uniprot" (default) or "ensembl". The OmniPath web service uses the primary gene symbols as provided by UniProt. By passing "ensembl" here, the UniProt gene symbols will be replaced by the ones used in Ensembl. This translation results in a loss of a few records, and multiplication of another few records due to ambiguous translation.
cache	Logical: use caching, load data from and save to the. The cache directory by default belongs to the user, located in the user's default cache directory, and named "OmniPathR". Find out about it by <code>getOption("omnipathR.cachedir")</code> . Can be changed by <a href="#">omnipath_set_cachedir</a> .

... Additional parameters for the OmniPath web service. These parameters will be processed, validated and included in the query string. Many parameters are already explicitly set by the arguments above. A number of query type specific parameters are also available, learn more about these by the [query\\_info](#) function. For functions more specific than [omnipath\\_query](#), arguments for all downstream functions are also passed here.

### Value

Data frame (tibble) or list: the data returned by the OmniPath web service (or loaded from cache), after processing. Nested list if the "format" parameter is "json", otherwise a tibble.

### Examples

```
interaction_data <- omnipath_query("interaction", datasets = "omnipath")
interaction_data
```

---

`omnipath_save_config` *Save the current package configuration*

---

### Description

Save the current package configuration  
 Save the configuration of a certain package

### Usage

```
omnipath_save_config(path = NULL, title = "default", local = FALSE)

save_config(path = NULL, title = "default", local = FALSE, pkg = "OmniPathR")
```

### Arguments

<code>path</code>	Path to the config file. Directories and the file will be created if don't exist.
<code>title</code>	Save the config under this title. One config file might contain multiple configurations, each identified by a title.
<code>local</code>	Save into a config file in the current directory instead of a user level config file. When loading, the config in the current directory has priority over the user level config.
<code>pkg</code>	Character: name of the package

### Value

Returns 'NULL'.

## Examples

```
## Not run:  
# after this, all downloads will default to commercial licenses  
# i.e. the resources that allow only academic use will be excluded:  
options(omnipathr.license = 'commercial')  
omnipath_save_config()  
  
## End(Not run)
```

---

omnipath\_set\_cachedir *Change the cache directory*

---

## Description

Change the cache directory

## Usage

```
omnipath_set_cachedir(path = NULL)
```

## Arguments

path	Character: path to the new cache directory. If don't exist, the directories will be created. If the path is an existing cache directory, the package's cache database for the current session will be loaded from the database in the directory. If NULL, the cache directory will be set to its default path.
------	--

## Value

Returns NULL.

## Examples

```
tmp_cache <- tempdir()  
omnipath_set_cachedir(tmp_cache)  
# restore the default cache directory:  
omnipath_set_cachedir()
```

omnipath\_set\_console\_loglevel

*Sets the log level for the console*

---

### Description

Use this method to change during a session which messages you want to be printed on the console. Before loading the package, you can set it also by the config file, with the `omnipathr.console_loglevel` key.

### Usage

```
omnipath_set_console_loglevel(level)
```

### Arguments

`level`                   Character or class 'loglevel'. The desired log level.

### Value

Returns 'NULL'.

### See Also

[omnipath\\_set\\_logfile\\_loglevel](#)

### Examples

```
omnipath_set_console_loglevel('warn')  
# or:  
omnipath_set_console_loglevel(logger::WARN)
```

---

omnipath\_set\_logfile\_loglevel

*Sets the log level for the logfile*

---

### Description

Use this method to change during a session which messages you want to be written into the logfile. Before loading the package, you can set it also by the config file, with the `"omnipathr.loglevel"` key.

### Usage

```
omnipath_set_logfile_loglevel(level)
```

**Arguments**

level                    Character or class 'loglevel'. The desired log level.

**Value**

Returns 'NULL'.

**See Also**

[omnipath\\_set\\_console\\_loglevel](#)

**Examples**

```
omnipath_set_logfile_loglevel('info')
# or:
omnipath_set_logfile_loglevel(logger::INFO)
```

---

`omnipath_set_loglevel` *Sets the log level for the package logger*

---

**Description**

Sets the log level for the package logger

Sets the log level for any package

**Usage**

```
omnipath_set_loglevel(level, target = "logfile")

set_loglevel(level, target = "logfile", pkg = "OmnipathR")
```

**Arguments**

level                    Character or class 'loglevel'. The desired log level.

target                   Character, either 'logfile' or 'console'

pkg                      Character: name of the package.

**Value**

Returns 'NULL'.

**Examples**

```
omnipath_set_loglevel(logger::FATAL, target = 'console')
```

---

omnipath\_show\_db      *Built in database definitions*

---

### Description

Databases are resources which might be costly to load but can be used many times by functions which usually automatically load and retrieve them from the database manager. Each database has a lifetime and will be unloaded automatically upon expiry.

### Usage

```
omnipath_show_db()
```

### Value

A data frame with the built in database definitions.

### Examples

```
database_definitions <- omnipath_show_db()
database_definitions
# # A tibble: 14 x 10
#   name      last_used      lifetime package loader loader_p.
#   <chr>    <dtm>          <dbl> <chr>   <chr>   <list>
# 1 Gene Onto. 2021-04-04 20:19:15    300 Omnipat. go_ontol. <named l.
# 2 Gene Onto. NA                300 Omnipat. go_ontol. <named l.
# 3 Gene Onto. NA                300 Omnipat. go_ontol. <named l.
# 4 Gene Onto. NA                300 Omnipat. go_ontol. <named l.
# 5 Gene Onto. NA                300 Omnipat. go_ontol. <named l.
# ... (truncated)
# # . with 4 more variables: latest_param <list>, loaded <lgl>, db <list>,
# #   key <chr>
```

---

omnipath\_unlock\_cache\_db  
*Removes the lock file from the cache directory*

---

### Description

A lock file in the cache directory avoids simultaneous write and read. It's supposed to be removed after each read and write operation. This might not happen if the process crashes during such an operation. In this case you can manually call this function.

### Usage

```
omnipath_unlock_cache_db()
```



**Value**

Logical: returns TRUE if the cache was locked and now is unlocked; FALSE if it was not locked.

**Examples**

```
omnipath_unlock_cache_db()
```

---

only_from	<i>Recreate interaction data frame based on certain datasets and resources</i>
-----------	--

---

**Description**

Recreate interaction data frame based on certain datasets and resources

**Usage**

```
only_from(
  data,
  datasets = NULL,
  resources = NULL,
  exclude = NULL,
  .keep = FALSE
)
```

**Arguments**

data	An interaction data frame from the OmniPath web service with evidences column.
datasets	Character: a vector of dataset labels. Only evidences from these datasets will be used.
resources	Character: a vector of resource labels. Only evidences from these resources will be used.
exclude	Character vector of resource names to be excluded.
.keep	Logical: keep the "evidences" column.

**Details**

The OmniPath interactions database fully integrates all attributes from all resources for each interaction. This comes with the advantage that interaction data frames are ready for use in most of the applications; however, it makes it impossible to know which of the resources and references support the direction or effect sign of the interaction. This information can be recovered from the "evidences" column. The "evidences" column preserves all the details about interaction provenances. In cases when you want to use a faithful copy of a certain resource or dataset, this function

will help you do so. Still, in most of the applications the best is to use the interaction data as it is returned by the web service.

**Note:** This function is automatically applied if the ‘strict\_evidences’ argument is passed to any function querying interactions (e.g. [omnipath-interactions](#)).

### Value

A copy of the interaction data frame restricted to the given datasets and resources.

### See Also

- [omnipath-interactions](#)
- [filter\\_evidences](#)
- [unnest\\_evidences](#)
- [from\\_evidences](#)

### Examples

```
## Not run:
ci <- collectri(evidences = TRUE)
ci <- only_from(ci, datasets = 'collectri')

## End(Not run)
```

---

ontology\_ensure\_id      *Only ontology IDs*

---

### Description

Converts a mixture of ontology IDs and names to only IDs. If an element of the input is missing from the chosen ontology it will be dropped. This can happen if the ontology is a subset (slim) version, but also if the input is not a valid ID or name.

### Usage

```
ontology_ensure_id(terms, db_key = "go_basic")
```

### Arguments

terms                    Character: ontology IDs or term names.

db\_key                    Character: key to identify the ontology database. For the available keys see [omnipath\\_show\\_db](#).

### Value

Character vector of ontology IDs.

**Examples**

```
ontology_ensure_id(c('mitochondrion inheritance', 'GO:0001754'))
# [1] "GO:0000001" "GO:0001754"
```

---

ontology\_ensure\_name    *Only ontology term names*

---

**Description**

Converts a mixture of ontology IDs and names to only names. If an element of the input is missing from the chosen ontology it will be dropped. This can happen if the ontology is a subset (slim) version, but also if the input is not a valid ID or name.

**Usage**

```
ontology_ensure_name(terms, db_key = "go_basic")
```

**Arguments**

terms                    Character: ontology IDs or term names.

db\_key                    Character: key to identify the ontology database. For the available keys see [omnipath\\_show\\_db](#).

**Value**

Character vector of ontology term names.

**Examples**

```
ontology_ensure_name(c('reproduction', 'GO:0001754', 'foo bar'))
# [1] "eye photoreceptor cell differentiation" "reproduction"
```

---

ontology\_name\_id        *Translate between ontology IDs and names*

---

**Description**

Makes sure that the output contains only valid IDs or term names. The input can be a mixture of IDs and names. The order of the input won't be preserved in the output.

**Usage**

```
ontology_name_id(terms, ids = TRUE, db_key = "go_basic")
```

**Arguments**

terms	Character: ontology IDs or term names.
ids	Logical: the output should contain IDs or term names.
db_key	Character: key to identify the ontology database. For the available keys see <a href="#">omnipath_show_db</a> .

**Value**

Character vector of ontology IDs or term names.

**Examples**

```
ontology_name_id(c('mitochondrion inheritance', 'reproduction'))
# [1] "GO:0000001" "GO:0000003"
ontology_name_id(c('GO:0000001', 'reproduction'), ids = FALSE)
# [1] "mitochondrion inheritance" "reproduction"
```

---

organism\_for

*Make sure the resource supports the organism and it has the ID*

---

**Description**

Make sure the resource supports the organism and it has the ID

**Usage**

```
organism_for(organism, resource, error = TRUE)
```

**Arguments**

organism	Character or integer: name or NCBI Taxonomy ID of the organism.
resource	Character: name of the resource.
error	Logical: raise an error if the organism is not supported in the resource. Otherwise it only emits a warning.

**Value**

Character: the ID of the organism as it is used by the resource. NA if the organism can not be translated to the required identifier type.

**Examples**

```

organism_for(10116, 'chalmers-gem')
# [1] "Rat"
organism_for(6239, 'chalmers-gem')
# [1] "Worm"
organism_for('foobar', 'chalmers-gem')
# Error in organism_for("foobar", "chalmers-gem") :
# Organism `foobar` (common_name: `NA`; common_name: `NA`)
# is not supported by resource `chalmers-gem`. Supported organisms:
# Human, Mouse, Rat, Zebrafish, Drosophila melanogaster (Fruit fly),
# Caenorhabditis elegans (PRJNA13758).

```

---

orthology\_translate\_column

*Translate a column of identifiers by orthologous gene pairs*

---

**Description**

Translate a column of identifiers by orthologous gene pairs

**Usage**

```

orthology_translate_column(
  data,
  column,
  id_type = NULL,
  target_organism = "mouse",
  source_organism = "human",
  resource = "oma",
  replace = FALSE,
  one_to_many = NULL,
  keep_untranslated = FALSE,
  translate_complexes = FALSE,
  uniprot_by_id_type = "entrez"
)

```

**Arguments**

data	A data frame with the column to be translated.
column	Name of a character column with identifiers of the source organism of type 'id_type'.
id_type	Type of identifiers in 'column'. Available ID types include "uniprot", "entrez", "ensg", "refseq" and "swissprot" for OMA, and "uniprot", "entrez", "genesymbol", "refseq" and "gi" for NCBI HomoloGene. If you want to translate an ID type not directly available in your preferred resource, use first <a href="#">translate_ids</a> to translate to an ID type directly available in the orthology resource. If not provided, it is assumed the column name is the ID type.

target_organism	Name or NCBI Taxonomy ID of the target organism.
source_organism	Name or NCBI Taxonomy ID of the source organism.
resource	Character: source of the orthology mapping. Currently Orthologous Matrix (OMA) and NCBI HomoloGene are available, refer to them by "oma" and "homologene", respectively.
replace	Logical or character: replace the column with the translated identifiers, or create a new column. If it is character, it will be used as the name of the new column.
one_to_many	Integer: maximum number of orthologous pairs for one gene of the source organism. Genes mapping to higher number of orthologues will be dropped.
keep_untranslated	Logical: keep records without orthologous pairs. If 'replace' is TRUE, this option is ignored, and untranslated records will be dropped. Genes with more than 'one_to_many' orthologues will always be dropped.
translate_complexes	Logical: translate the complexes by translating their components.
uniprot_by_id_type	Character: translate NCBI HomoloGene to UniProt by this ID type. One of "genesymbol", "entrez", "refseq" or "gi".

**Value**

The data frame with identifiers translated to other organism.

---

pathwaycommons\_download

*Interactions from PathwayCommons*

---

**Description**

PathwayCommons (<http://www.pathwaycommons.org/>) provides molecular interactions from a number of databases, in either BioPAX or SIF (simple interaction format). This function retrieves all interactions in SIF format. The data is limited to the interacting pair and the type of the interaction.

**Usage**

```
pathwaycommons_download()
```

**Value**

A data frame (tibble) with interactions.

**Examples**

```
pc_interactions <- pathwaycommons_download()
pc_interactions
# # A tibble: 1,884,849 x 3
#   from type to
#   <chr> <chr> <chr>
# 1 A1BG controls-expression-of A2M
# 2 A1BG interacts-with ABCC6
# 3 A1BG interacts-with ACE2
# 4 A1BG interacts-with ADAM10
# 5 A1BG interacts-with ADAM17
# # . with 1,884,839 more rows
```

---

`pivot_annotatations`      *Converts annotation tables to a wide format*

---

**Description**

Use this method to reconstitute the annotation tables into the format of the original resources. With the ‘wide=TRUE’ option [annotatations](#) applies this function to the downloaded data.

**Usage**

```
pivot_annotatations(annotatations)
```

**Arguments**

`annotatations`      A data frame of annotations downloaded from the OmniPath web service by [annotatations](#).

**Value**

A wide format data frame (tibble) if the provided data contains annotations from one resource, otherwise a list of wide format tibbles.

**See Also**

[annotatations](#)

**Examples**

```
# single resource: the result is a data frame
disgenet <- annotatations(resources = "DisGeNet")
disgenet <- pivot_annotatations(disgenet)
disgenet
# # A tibble: 126,588 x 11
#   uniprot genesymbol entity_type disease type score dsi dpi
#   <chr> <chr> <chr> <chr> <chr> <dbl> <dbl> <dbl>
```

```

# 1 P04217 A1BG      protein    Schizophren. dise. 0.3 0.7 0.538
# 2 P04217 A1BG      protein    Hepatomegaly phen. 0.3 0.7 0.538
# 3 P01023 A2M       protein    Fibrosis, L. dise. 0.3 0.529 0.769
# 4 P01023 A2M       protein    Acute kidne. dise. 0.3 0.529 0.769
# 5 P01023 A2M       protein    Mental Depr. dise. 0.3 0.529 0.769
# # . with 126,583 more rows, and 3 more variables: nof_pmids <dbl>,
# #   nof_snps <dbl>, source <chr>

# multiple resources: the result is a list
annot_long <- annotations(
  resources = c("DisGeNet", "Signalink_function", "DGIdb", "kinase.com")
)
annot_wide <- pivot_annotations(annot_long)
names(annot_wide)
# [1] "DGIdb"           "DisGeNet"         "kinase.com"
# [4] "Signalink_function"
annot_wide$kinase.com
# # A tibble: 825 x 6
#   uniprot genesymbol entity_type group family subfamily
#   <chr>   <chr>       <chr>      <chr> <chr> <chr>
# 1 P31749 AKT1        protein    AGC   Akt   NA
# 2 P31751 AKT2        protein    AGC   Akt   NA
# 3 Q9Y243 AKT3        protein    AGC   Akt   NA
# 4 014578 CIT         protein    AGC   DMPK  CRIK
# 5 Q09013 DMPK        protein    AGC   DMPK  GEK
# # . with 815 more rows

```

---

```
preppi_download
```

```
Interactions from PrePPI
```

---

## Description

Retrieves predicted protein-protein interactions from the PrePPI database (<http://honig.c2b2.columbia.edu/preppi>). The interactions in this table are supposed to be correct with a > 0.5 probability.

## Usage

```
preppi_download(...)
```

## Arguments

... Minimum values for the scores. The available scores are: str, protpep, str\_max, red, ort, phy, coexp, go, total, exp and final. Furthermore, an operator can be passed, either .op = '&' or .op = '|', which is then used for combined filtering by multiple scores.



## Details

PrePPI is a combination of many prediction methods, each resulting a score. For an explanation of the scores see <https://honiglab.c2b2.columbia.edu/hfpd/help/Manual.html>. The minimum, median and maximum values of the scores:

Score	Minimum	Median	Maximum
str	0	5.5	6,495
protpep	0	3.53	38,138
str_max	0	17.9	38,138
red	0	1.25	24.4
ort	0	0	5,000
phy	0	2.42	2.42
coexp	0	2.77	45.3
go	0	5.86	181
total	0	1,292	106,197,000,000
exp	1	958	4,626
final	600	1,778	4.91e14

## Value

A data frame (tibble) of interactions with scores, databases and literature references.

## See Also

[preppi\\_filter](#)

## Examples

```
preppi <- preppi_download()
preppi
# # A tibble: 1,545,710 x 15
#   prot1 prot2 str_score protpep_score str_max_score red_score ort_score
#   <chr> <chr>   <dbl>         <dbl>         <dbl>   <dbl>   <dbl>
# 1 Q131. P146.   18.6           6.45           18.6     4.25    0.615
# 2 P064. Q96N.    1.83           14.3           14.3     4.25     0
# 3 Q7Z6. Q8NC.    4.57            0              4.57     0        0
# 4 P370. P154.   485.            0              485.     1.77    0.615
# 5 O004. Q9NR.   34.0            0              34.0     0.512    0
# # . with 1,545,700 more rows, and 8 more variables: phy_score <dbl>,
# #   coexp_score <dbl>, go_score <dbl>, total_score <dbl>, dbs <chr>,
# #   pubs <chr>, exp_score <dbl>, final_score <dbl>
```

---

preppi_filter	<i>Filter PrePPI interactions by scores</i>
---------------	---

---

## Description

Filter PrePPI interactions by scores

## Usage

```
preppi_filter(data, ..., .op = "&")
```

## Arguments

data	A data frame of PrePPI interactions as provided by <a href="#">preppi_download</a> .
...	Minimum values for the scores. The available scores are: str, protpep, str_max, red, ort, phy, coexp, go, total, exp and final. See more about the scores at <a href="#">preppi_download</a> .
.op	The operator to combine the scores with: either '&' or ' '. With the former, only records where all scores are above the threshold will be kept; with the latter, records where at least one score is above its threshold will be kept.

## Value

The input data frame (tibble) filtered by the score thresholds.

## See Also

[preppi\\_download](#)

## Examples

```
preppi <- preppi_download()
preppi_filtered <- preppi_filter(preppi, red = 10, str = 4.5, ort = 1)
nrow(preppi_filtered)
# [1] 8443
```

---

print\_bma\_motif\_es      *Prints BMA motifs to the screen from a sequence of edges*

---

## Description

The motifs can be copy-pasted into a BMA canvas.

## Usage

```
print_bma_motif_es(edge_seq, G, granularity = 2)
```

## Arguments

edge_seq	An igraph edge sequence.
G	An igraph graph object.
granularity	Numeric: granularity value.

## Value

Returns 'NULL'.

## Examples

```
interactions <- omnipath(resources = "ARN")
graph <- interaction_graph(interactions)
print_bma_motif_es(igraph::E(graph)[1], graph)
# {"Model": {
#   "Name": "Omnipath motif",
#   "Variables": [{
#     "Name": "ULK1",
#     "Id": 1,
#     "RangeFrom": 0,
#     "RangeTo": 2,
#     "Formula": ""
#   }],
#   {
#     "Name": "ATG13",
#     ...
#   }],
# ... (truncated)
# }}
```

---

print\_bma\_motif\_vs      *Prints BMA motifs to the screen from a sequence of nodes*

---

**Description**

The motifs can be copy-pasted into a BMA canvas.

**Usage**

```
print_bma_motif_vs(node_seq, G)
```

**Arguments**

node\_seq      An igraph node sequence.  
G              An igraph graph object.

**Value**

Returns 'NULL'.

**Examples**

```
interactions <- omnipath(resources = "ARN")  
graph <- interaction_graph(interactions)  
print_bma_motif_vs(  
  igraph::all_shortest_paths(  
    graph,  
    from = 'ULK1',  
    to = 'ATG13'  
  )$res,  
  graph  
)
```

---

print\_interactions      *Print OmniPath interactions*

---

**Description**

Prints the interactions or enzyme-substrate relationships in a nice format.

**Usage**

```
print_interactions(interactions, refs = FALSE)
```

**Arguments**

interactions    Data frame with the interactions generated by any of the functions in [omnipath-interactions](#).  
 refs            Logical: include PubMed IDs where available.

**Value**

Returns 'NULL'.

**Examples**

```
enzsub <- enzyme_substrate()
print_interactions(head(enzsub))
print_interactions(tail(enzsub), refs = TRUE)
print_interactions(
  dplyr::filter(
    enzsub,
    enzyme_genesymbol == 'MAP2K1',
    substrate_genesymbol == 'MAPK3'
  )
)

signor <- omnipath(resources = "SIGNOR")
print_interactions(head(signor))
#           source interaction           target n_resources
# 6 MAPK14 (Q16539) ==(+)==> MAPKAPK2 (P49137)      23
# 4 TRPM7 (Q96QT4) ==(+)==> ANXA1 (P04083)      10
# 1 PRKG1 (Q13976) ==(-)==> TRPC3 (Q13507)       8
# 2 PTPN1 (P18031) ==(-)==> TRPV6 (Q9H1D0)       6
# 5 PRKACA (P17612) ==(-)==> MCOLN1 (Q9GZU1)      6
# 3 RACK1 (P63244) ==(-)==> TRPM6 (Q9BX84)       2
```

---

print\_path\_es                    *Prints network paths in an edge sequence*

---

**Description**

Pretty prints the interactions in a path.

**Usage**

```
print_path_es(edges, G)
```

**Arguments**

edges            An igraph edge sequence object.  
 G                igraph object (from ptms or any interaction dataset)

**Value**

Returns 'NULL'.

**See Also**

- [print\\_path\\_vs](#)

**Examples**

```
interactions <- omnipath(resources = "Signalink3")
OPI_g <- interaction_graph(interactions = interactions)
print_path_es(
  suppressWarnings(igraph::shortest_paths(
    OPI_g,
    from = 'TYR03',
    to = 'STAT3',
    output = 'epath'
  ))$path[[1]],
  OPI_g
)
```

---

print\_path\_vs

*Print networks paths given by node sequence*

---

**Description**

Prints the interactions in the path in a nice format.

**Usage**

```
print_path_vs(nodes, G)
```

**Arguments**

nodes            An igraph node sequence object.  
G                An igraph graph object (from ptms or interactions)

**Value**

Returns 'NULL'.

**See Also**

[print\\_path\\_es](#)

**Examples**

```

interactions <- omnipath(resources = "SignalLink3")
OPI_g <- interaction_graph(interactions = interactions)
print_path_vs(
  igraph::all_shortest_paths(
    OPI_g,
    from = 'TYR03',
    to = 'STAT3'
  )$vpath,
  OPI_g
)
enzsub <- enzyme_substrate(resources=c("PhosphoSite", "SIGNOR"))
enzsub_g <- enzsub_graph(enzsub)
print_path_vs(
  igraph::all_shortest_paths(
    enzsub_g,
    from = 'SRC',
    to = 'STAT1'
  )$res,
  enzsub_g
)

```

pubmed\_open

*Open one or more PubMed articles***Description**

Open one or more PubMed articles

**Usage**

```
pubmed_open(pmids, browser = NULL, sep = ";", max_pages = 25L)
```

**Arguments**

pmids	Character or numeric vector of one or more PubMed IDs.
browser	Character: name of the web browser executable. If 'NULL', the default web browser will be used.
sep	Character: split the PubMed IDs by this separator.
max_pages	Numeric: largest number of pages to open. This is to prevent opening hundreds or thousands of pages at once.

**Value**

Returns 'NULL'.

### Examples

```
interactions <- omnipath()
pubmed_open(interactions$references[1])
```

---

query_info	<i>OmniPath query parameters</i>
------------	----------------------------------

---

### Description

All parameter names and their possible values for a query type. Note: parameters with ‘NULL’ values have too many possible values to list them.

### Usage

```
query_info(query_type)
```

### Arguments

query\_type      Character: interactions, annotations, complexes, enz\_sub or intercell.

### Value

A named list with the parameter names and their possible values.

### Examples

```
ia_param <- query_info('interactions')
ia_param$datasets[1:5]
# [1] "dorothea"      "kinaseextra" "ligreextra" "lncrna_mrna" "mirnatarget"
```

---

ramilowski_download	<i>Downloads ligand-receptor interactions from Ramilowski et al. 2015</i>
---------------------	---

---

### Description

Curated ligand-receptor pairs from Supplementary Table 2 of the article "A draft network of ligand-receptor mediated multicellular signaling in human" (<https://www.nature.com/articles/ncomms8866>).

### Usage

```
ramilowski_download()
```

### Value

A data frame (tibble) with interactions.



## Examples

```
rami_interactions <- ramiowski_download()
rami_interactions
# # A tibble: 2,557 x 16
#   Pair.Name Ligand.Approved. Ligand.Name Receptor.Approv.
#   <chr>      <chr>                <chr>          <chr>
# 1 A2M_LRP1  A2M                    alpha-2-ma.  LRP1
# 2 AANAT_MT. AANAT                  aralkylami. MTNR1A
# 3 AANAT_MT. AANAT                  aralkylami. MTNR1B
# 4 ACE_AGTR2 ACE                    angiotensi. AGTR2
# 5 ACE_BDKR. ACE                    angiotensi. BDKRB2
# # . with 2,547 more rows, and 12 more variables: Receptor.Name <chr>,
# #   DLRP <chr>, HPMR <chr>, IUPHAR <chr>, HPRD <chr>,
# #   STRING.binding <chr>, STRING.experiment <chr>, HPMR.Ligand <chr>,
# #   HPMR.Receptor <chr>, PMID.Manual <chr>, Pair.Source <chr>,
# #   Pair.Evidence <chr>
```

---

ramp\_id\_mapping\_table *Pairwise ID translation table from RaMP database*

---

## Description

Pairwise ID translation table from RaMP database

## Usage

```
ramp_id_mapping_table(from, to, version = "2.5.4")
```

## Arguments

from	Character or Symbol. Name of an identifier type.
to	Character or Symbol. Name of an identifier type.
version	Character. The version of RaMP to download.

## Value

Dataframe of pairs of identifiers.

## See Also

- [ramp\\_sqlite](#)
- [ramp\\_tables](#)
- [ramp\\_table](#)
- [translate\\_ids](#)
- [id\\_types](#)

- [hmdb\\_table](#)
- [uniprot\\_full\\_id\\_mapping\\_table](#)
- [uniprot\\_id\\_mapping\\_table](#)
- [ensembl\\_id\\_mapping\\_table](#)
- [chalmers\\_gem\\_id\\_mapping\\_table](#)

### Examples

```
ramp_id_mapping_table('hmdb', 'kegg')
```

---

ramp_id_type	<i>RaMP identifier type label</i>
--------------	-----------------------------------

---

### Description

RaMP identifier type label

### Usage

```
ramp_id_type(label)
```

### Arguments

label            Character: an ID type label, as shown in the table returned by [id\\_types](#)

### Value

Character: the RaMP specific ID type label, or the input unchanged if it could not be translated (still might be a valid identifier name). These labels should be valid value names, as used in RaMP SQL database.

### See Also

- [chalmers\\_gem\\_id\\_type](#)
- [uniprot\\_id\\_type](#)
- [ensembl\\_id\\_type](#)
- [uploadlists\\_id\\_type](#)

### Examples

```
ramp_id_type("rhea")
# [1] "rhea-comp"
```

---

ramp_sqlite	<i>Download and open RaMP database SQLite</i>
-------------	---

---

**Description**

Download and open RaMP database SQLite

**Usage**

```
ramp_sqlite(version = "2.5.4")
```

**Arguments**

version            Character. The version of RaMP to download.

**Value**

SQLite connection.

**See Also**

- [ramp\\_tables](#)

**Examples**

```
sqlite_con <- ramp_sqlite()
```

---

ramp_table	<i>Return table from RaMP database</i>
------------	--

---

**Description**

Return table from RaMP database

**Usage**

```
ramp_table(name, version = "2.5.4")
```

**Arguments**

name            Character. The name of the RaMP table to fetch.

version        Character. The version of RaMP to download.

**Value**

Character vector of table names in the RaMP SQLite database.

**See Also**

- [ramp\\_sqlite](#)
- [ramp\\_tables](#)

**Examples**

```
ramp_table('source')
```

---

ramp_tables	<i>List tables in RaMP database</i>
-------------	-------------------------------------

---

**Description**

List tables in RaMP database

**Usage**

```
ramp_tables(version = "2.5.4")
```

**Arguments**

version            Character. The version of RaMP to download.

**Value**

Character vector of table names in the RaMP SQLite database.

**See Also**

- [ramp\\_sqlite](#)

**Examples**

```
ramp_tables()
```

---

regnetwork\_directions *Transcription factor effects from RegNetwork*

---

**Description**

Transcription factor effects from RegNetwork

**Usage**

```
regnetwork_directions(organism = "human")
```

**Arguments**

organism            Character: either human or mouse.

**Value**

A data frame (tibble) of TF-target interactions with effect signs.

**Examples**

```
regn_dir <- regnetwork_directions()
regn_dir
# # A tibble: 3,954 x 5
#   source_genesymb. source_entrez target_genesymb. target_entrez
#   <chr>           <chr>           <chr>           <chr>
# 1 AHR              196             CDKN1B          1027
# 2 APLNR            187             PIK3C3          5289
# 3 APLNR            187             PIK3R4          30849
# 4 AR               367             KLK3            354
# 5 ARNT             405             ALDOA           226
# # . with 3,944 more rows, and 1 more variable: effect <dbl>
```

---

regnetwork\_download *Interactions from RegNetwork*

---

**Description**

Downloads transcriptional and post-transcriptional regulatory interactions from the RegNetwork database (<http://www.regnetworkweb.org/>). The information about effect signs (stimulation or inhibition), provided by [regnetwork\\_directions](#) are included in the result.

**Usage**

```
regnetwork_download(organism = "human")
```

**Arguments**

organism            Character: either human or mouse.

**Value**

Data frame with interactions.

**Examples**

```
regnetwork_interactions <- regnetwork_download()
regnetwork_interactions
## # A tibble: 372,778 x 7
##   source_genesymb. source_entrez target_genesymb. target_entrez
##   <chr>            <chr>          <chr>          <chr>
## 1 USF1             7391           S100A6         6277
## 2 USF1             7391           DUSP1          1843
## 3 USF1             7391           C4A            720
## 4 USF1             7391           ABCA1           19
## 5 TP53            7157           TP73           7161
## # . with 372,768 more rows, and 3 more variables: effect <dbl>,
## #   source_type <chr>, target_type <chr>
```

---

relations\_list\_to\_table

*Table from a nested list of ontology relations*

---

**Description**

Converting the nested list to a table is a more costly operation, it takes a few seconds. Best to do it only once, or pass `tables = TRUE` to `obo_parser`, and convert the data frame to list, if you also need it in list format.

**Usage**

```
relations_list_to_table(relations, direction = NULL)
```

**Arguments**

`relations`            A nested list of ontology relations (the "relations" element of the list returned by `obo_parser` in case its argument 'tables' is FALSE).

`direction`            Override the direction (i.e. child -> parents or parent -> children). The nested lists produced by functions in the current package add an attribute "direction" thus no need to pass this value. If the attribute and the argument are both missing, the column will be named simply "side2" and it won't be clear whether the relations point from "term" to "side2" or the other way around. The direction should be a character vector of length 2 with the values "parents" and "children".

**Value**

The relations converted to a data frame (tibble).

**See Also**

- [swap\\_relations](#)
- [relations\\_table\\_to\\_list](#)
- [obo\\_parser](#)

**Examples**

```
goslim_url <-  
  "http://current.geneontology.org/ontology/subsets/goslim_generic.obo"  
path <- tempfile()  
httr::GET(goslim_url, httr::write_disk(path, overwrite = TRUE))  
obo <- obo_parser(path, tables = FALSE)  
unlink(path)  
rel_tbl <- relations_list_to_table(obo$relations)
```

---

relations\_table\_to\_graph

*Graph from a table of ontology relations*

---

**Description**

Graph from a table of ontology relations

**Usage**

```
relations_table_to_graph(relations)
```

**Arguments**

**relations** A data frame of ontology relations (the "relations" element of the list returned by [obo\\_parser](#) in case its argument 'tables' is TRUE).

**Details**

By default the relations point from child to parents, the edges in the graph will be of the same direction. Use [swap\\_relations](#) on the data frame to reverse the direction.

**Value**

The relations converted to an igraph graph object.

## Examples

```
## Not run:
go <- get_db('go_basic')
go_graph <- relations_table_to_graph(go$relations)

## End(Not run)
```

---

relations\_table\_to\_list

*Nested list from a table of ontology relations*

---

## Description

Nested list from a table of ontology relations

## Usage

```
relations_table_to_list(relations)
```

## Arguments

**relations**      A data frame of ontology relations (the "relations" element of the list returned by [obo\\_parser](#) in case its argument 'tables' is TRUE).

## Value

The relations converted to a nested list.

## See Also

- [relations\\_list\\_to\\_table](#)
- [swap\\_relations](#)
- [obo\\_parser](#)

## Examples

```
goslim_url <-
  "http://current.geneontology.org/ontology/subsets/goslim_generic.obo"
path <- tempfile()
httr::GET(goslim_url, httr::write_disk(path, overwrite = TRUE))
obo <- obo_parser(path, tables = TRUE)
unlink(path)
rel_list <- relations_table_to_list(obo$relations)
```



---

`remap_dorothea_download`*Downloads TF-target interactions from ReMap*

---

## Description

ReMap (<http://remap.univ-amu.fr/>) is a database of ChIP-Seq experiments. It provides raw and merged peaks and CRMs (cis regulatory motifs) with their associations to regulators (TFs). TF-target relationships can be derived as it is written in Garcia-Alonso et al. 2019: "For ChIP-seq, we downloaded the binding peaks from ReMap and scored the interactions between each TF and each gene according to the distance between the TFBSs and the genes' transcription start sites. We evaluated different filtering strategies that consisted of selecting only the top-scoring 100, 200, 500, and 1000 target genes for each TF." (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6673718/#s1title>). This function returns the top TF-target relationships as used in DoRothEA: [https://github.com/saezlab/dorothea/blob/master/inst/scripts/02\\_chip\\_seq.R](https://github.com/saezlab/dorothea/blob/master/inst/scripts/02_chip_seq.R)).

## Usage

```
remap_dorothea_download()
```

## Value

Data frame with TF-target relationships.

## See Also

[remap\\_tf\\_target\\_download](#)

## Examples

```
remap_interactions <- remap_dorothea_download()
remap_interactions
# # A tibble: 136,988 x 2
#   tf      target
#   <chr> <chr>
# 1 ADNP  ABCC1
# 2 ADNP  ABCC6
# 3 ADNP  ABHD5
# 4 ADNP  ABT1
# 5 ADNP  AC002066.1
# # . with 136,978 more rows
```

---

remap_filtered	<i>Downloads TF-target interactions from ReMap</i>
----------------	--

---

### Description

Downloads the ReMap TF-target interactions as processed by Garcia-Alonso et al. (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6673718/#s1title>) and filters them based on a score threshold, the top targets and whether the TF is included in the TF census (Vaquerizas et al. 2009). The code for filtering is adapted from DoRothEA, written by Christian Holland.

### Usage

```
remap_filtered(score = 100, top_targets = 500, only_known_tfs = TRUE)
```

### Arguments

score	Numeric: a minimum score between 0 and 1000, records with lower scores will be excluded. If NULL no filtering performed.
top_targets	Numeric: the number of top scoring targets for each TF. Essentially the maximum number of targets per TF. If NULL the number of targets is not restricted.
only_known_tfs	Logical: whether to exclude TFs which are not in TF census.

### Value

Data frame with TF-target relationships.

### See Also

- [remap\\_tf\\_target\\_download](#)
- [remap\\_filtered](#)
- [tfcensus\\_download](#)

### Examples

```
## Not run:
remap_interactions <- remap_filtered()
nrow(remap_interactions)
# [1] 145680

remap_interactions <- remap_filtered(top_targets = 100)
remap_interactions
# # A tibble: 30,330 x 2
#   source_genesymbol target_genesymbol
#   <chr>             <chr>
# 1 ADNP              ABCC1
# 2 ADNP              ABT1
# 3 ADNP              AC006076.1
```

```
# 4 ADNP          AC007792.1
# 5 ADNP          AC011288.2
# # . with 30,320 more rows

## End(Not run)
```

---

```
remap_tf_target_download
```

*Downloads TF-target interactions from ReMap*

---

## Description

ReMap (<http://remap.univ-amu.fr/>) is a database of ChIP-Seq experiments. It provides raw and merged peaks and CRMs (cis regulatory motifs) with their associations to regulators (TFs). TF-target relationships can be derived as it is written in Garcia-Alonso et al. 2019: "For ChIP-seq, we downloaded the binding peaks from ReMap and scored the interactions between each TF and each gene according to the distance between the TFBSs and the genes' transcription start sites. We evaluated different filtering strategies that consisted of selecting only the top-scoring 100, 200, 500, and 1000 target genes for each TF." (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6673718/#s1title>). This function retrieves the full processed TF-target list from the data deposited in <https://zenodo.org/record/3713238>.

## Usage

```
remap_tf_target_download()
```

## Value

Data frame with TF-target relationships.

## See Also

- [remap\\_dorothea\\_download](#)
- [remap\\_filtered](#)

## Examples

```
## Not run:
remap_interactions <- remap_tf_target_download()
remap_interactions
# # A tibble: 9,546,470 x 4
#   source_genesymbol target_genesymbol target_ensembl   score
#   <chr>              <chr>              <chr>          <dbl>
# 1 ADNP                PTPRS                ENSG00000105426.16 1000
# 2 AFF4                PRKCH                ENSG00000027075.14 1000
# 3 AHR                 CTNND2               ENSG00000169862.18 1000
# 4 AR                  PDE4D                ENSG00000113448.18 1000
```

```
# 5 ARID1A          PLEC          ENSG00000178209.14 1000
# # . with 9,546,460 more rows

## End(Not run)
```

---

reset_config	<i>Restore the built-in default values of all config parameters of a package</i>
--------------	--

---

### Description

Restore the built-in default values of all config parameters of a package  
 Restore the built-in default values of all config parameters of OmnipathR

### Usage

```
reset_config(save = NULL, reset_all = FALSE, pkg = "OmnipathR")

omnipath_reset_config(...)
```

### Arguments

save	If a path, the restored config will be also saved to this file. If TRUE, the config will be saved to the current default config path (see <a href="#">omnipath_config_path</a> ).
reset_all	Reset to their defaults also the options already set in the R options.
pkg	Character: name of a package
...	Ignored.

### Value

The config as a list.

### See Also

[omnipath\\_load\\_config](#), [omnipath\\_save\\_config](#)

### Examples

```
## Not run:
# restore the defaults and write them to the default config file:
omnipath_reset_config()
omnipath_save_config()

## End(Not run)
```

---

resources	<i>Retrieve the available resources for a given query type</i>
-----------	--

---

**Description**

Collects the names of the resources available in OmniPath for a certain query type and optionally for a dataset within that.

**Usage**

```
resources(query_type, datasets = NULL, generic_categories = NULL)
```

**Arguments**

query_type	one of the query types ‘interactions’, ‘enz_sub’, ‘complexes’, ‘annotations’ or ‘intercell’
datasets	currently within the ‘interactions’ query type only, multiple datasets are available: ‘omnipath’, ‘kinaseextra’, ‘pathwayextra’, ‘ligreextra’, ‘dorothea’, ‘tf_target’, ‘tf_mirna’, ‘mirnatarget’ and ‘lncrna_mrna’.
generic_categories	for the ‘intercell’ query type, restrict the search for some generic categories e.g. ‘ligand’ or ‘receptor’.

**Value**

a character vector with resource names

**Examples**

```
resources(query_type = "interactions")
```

---

resources_colname	<i>Name of the column with the resources</i>
-------------------	--

---

**Description**

Unfortunately the column title is different across the various query types in the OmniPath web service, so we need to guess.

**Usage**

```
resources_colname(data)
```

**Arguments**

data	A data frame downloaded by any import_... function in the current package.
------	--

**Value**

Character: the name of the column, if any of the column names matches.

**Examples**

```
co <- complexes()
resources_colname(co)
# [1] "sources"
```

---

resources_in	<i>Collect resource names from a data frame</i>
--------------	---

---

**Description**

Collect resource names from a data frame

**Usage**

```
resources_in(data)
```

**Arguments**

data            A data frame from an OmniPath query.

**Value**

Character: resource names occurring in the data frame.

**Examples**

```
pathways <- omnipath_interactions()
resources_in(pathways)
```

---

resource_info	<i>OmniPath resource information</i>
---------------	--------------------------------------

---

**Description**

The ‘resources’ query type provides resource metadata in JSON format. Here we retrieve this JSON and return it as a nested list structure.

**Usage**

```
resource_info()
```

**Value**

A nested list structure with resource metadata.

**Examples**

```
resource_info()
```

---

show\_network

*Visualize node neighborhood with SigmaJS*

---

**Description**

This function takes an OmniPath interaction data frame as input and returns a sigmaJS object for the subgraph formed by the neighbors of a node of interest.

**Usage**

```
show_network(interactions, node = NULL)
```

**Arguments**

`interactions` An OmniPath interaction data frame.  
`node` The node of interest.

**Value**

A sigmaJS object, check <http://sigmajs.john-coene.com/index.html> for further details and customization options.

**Examples**

```
## Not run:  
# get interactions from omnipath  
interactions <- omnipath()  
# create and plot the network containing ATM neighbors  
viz_sigmajs_neighborhood(interactions_df = interactions, int_node = "ATM")  
  
## End(Not run)
```

---

signed\_ptms                      *Causal effect enzyme-PTM interactions*

---

### Description

Enzyme-substrate data does not contain sign (activation/inhibition), we generate this information based on the interaction network.

### Usage

```
signed_ptms(
  enzsub = enzyme_substrate(),
  interactions = omnipath_interactions()
)
```

### Arguments

enzsub                      Enzyme-substrate data frame generated by [enzyme\\_substrate](#)  
interactions                interaction data frame generated by an OmniPath interactions query: [omnipath-interactions](#)

### Value

Data frame of enzyme-substrate relationships with is\_inhibition and is\_stimulation columns.

### See Also

- [enzyme\\_substrate](#)
- [omnipath-interactions](#)

### Examples

```
enzsub <- enzyme_substrate(resources = c("PhosphoSite", "SIGNOR"))
interactions <- omnipath_interactions()
enzsub <- signed_ptms(enzsub, interactions)
```

---

simplify\_intercell\_network  
                                    *Simplify an intercell network*

---

### Description

The intercellular communication network data frames, created by [intercell\\_network](#), are combinations of a network data frame with two copies of the intercell annotation data frames, all of them already having quite some columns. Here we keep only the names of the interacting pair, their intercellular communication roles, and the minimal information of the origin of both the interaction and the annotations. Optionally further columns can be selected.



**Usage**

```
simplify_intercell_network(network, ...)
```

**Arguments**

network            An intercell network data frame, as provided by [intercell\\_network](#).  
...                Optional, further columns to select.

**Value**

An intercell network data frame with some columns removed.

**See Also**

- [intercell\\_network](#)
- [filter\\_intercell\\_network](#)
- [unique\\_intercell\\_network](#)
- [intercell](#)
- [intercell\\_categories](#)
- [intercell\\_generic\\_categories](#)
- [intercell\\_summary](#)

**Examples**

```
icn <- intercell_network()  
icn_s <- simplify_intercell_network(icn)
```

---

static\_table

*Retrieve a static table from OmniPath*

---

**Description**

A few resources and datasets are available also as plain TSV files and can be accessed without TLS. The purpose of these tables is to make the most often used OmniPath data available on computers with configuration issues. These tables are not the recommended way to access OmniPath data, and a warning is issued each time they are accessed.

**Usage**

```
static_table(  
  query,  
  resource,  
  organism = 9606L,  
  strict_evidences = TRUE,  
  wide = TRUE,  
  dorothea_levels = c("A", "B", "C")  
)
```

**Arguments**

query	Character: a query type such as "annotations" or "interactions".
resource	Character: name of the resource or dataset, such as "CollecTRI" or "PROGENy".
organism	Integer: NCBI Taxonomy of the organism: 9606 for human, 10090 for mouse and 10116 for rat.
strict_evidences	Logical: restrict the evidences to the queried datasets and resources. If set to FALSE, the directions and effect signs and references might be based on other datasets and resources.
wide	Convert the annotation table to wide format, which corresponds more or less to the original resource. If the data comes from more than one resource a list of wide tables will be returned. See examples at <a href="#">pivot_annotations</a> .
dorothea_levels	Vector detailing the confidence levels of the interactions to be downloaded. In dorothea, every TF-target interaction has a confidence score ranging from A to E, being A the most reliable interactions. By default here we take A, B and C level interactions (c("A", "B", "C")). It is to note that E interactions are not available in OmnipathR.

**Value**

A data frame (tibble) with the requested resource.

**See Also**

[static\\_tables](#)

**Examples**

```
static_table("annotations", "PROGENy")
```

---

static\_tables

*List the static tables available from OmniPath*

---

**Description**

A few resources and datasets are available also as plain TSV files and can be accessed without TLS. The purpose of these tables is to make the most often used OmniPath data available on computers with configuration issues. These tables are not the recommended way to access OmniPath data, and a warning is issued each time they are accessed.

**Usage**

```
static_tables()
```

**Value**

A data frame listing the available tables.

**See Also**

[static\\_table](#)

**Examples**

```
static_tables()
```

---

stitch_actions	<i>Retrieve the STITCH actions dataset</i>
----------------	--

---

**Description**

Retrieve the STITCH actions dataset

**Usage**

```
stitch_actions(organism = "human", prefixes = FALSE)
```

**Arguments**

organism	Character or integer: name or NCBI Taxonomy ID of an organism. STITCH supports many organisms, please refer to their web site at <a href="https://stitch.embl.de/">https://stitch.embl.de/</a> .
prefixes	Logical: include the prefixes in front of identifiers.

**Value**

Data frame of STITCH actions.

**See Also**

- [stitch\\_actions](#)
- [stitch\\_links](#)
- [stitch\\_network](#)

**Examples**

```
sta <- stitch_actions(organism = 'mouse')
```

---

stitch_links	<i>Retrieve the STITCH links dataset</i>
--------------	--

---

**Description**

Retrieve the STITCH links dataset

**Usage**

```
stitch_links(organism = "human", prefixes = FALSE)
```

**Arguments**

organism	Character or integer: name or NCBI Taxonomy ID of an organism. STITCH supports many organisms, please refer to their web site at <a href="https://stitch.embl.de/">https://stitch.embl.de/</a> .
prefixes	Logical: include the prefixes in front of identifiers.

**Value**

Data frame: organism specific STITCH links dataset.

**See Also**

- [stitch\\_actions](#)
- [stitch\\_links](#)
- [stitch\\_network](#)

**Examples**

```
stl <- stitch_links()
```

---

stitch_network	<i>Chemical-protein interactions from STITCH</i>
----------------	--

---

**Description**

Chemical-protein interactions from STITCH

## Usage

```
stitch_network(  
  organism = "human",  
  min_score = 700L,  
  protein_ids = c("uniprot", "genesymbol"),  
  metabolite_ids = c("hmdb", "kegg"),  
  cosmos = FALSE  
)
```

## Arguments

organism	Character or integer: name or NCBI Taxonomy ID of an organism. STITCH supports many organisms, please refer to their web site at <a href="https://stitch.embl.de/">https://stitch.embl.de/</a> .
min_score	Confidence cutoff used for STITCH connections (700 by default).
protein_ids	Character: translate the protein identifiers to these ID types. Each ID type results two extra columns in the output, for the "a" and "b" sides of the interaction, respectively. The default ID type for proteins is Esembl Protein ID, and by default UniProt IDs and Gene Symbols are included.
metabolite_ids	Character: translate the protein identifiers to these ID types. Each ID type results two extra columns in the output, for the "a" and "b" sides of the interaction, respectively. The default ID type for metabolites is PubChem CID, and HMDB IDs and KEGG IDs are included.
cosmos	Logical: use COSMOS format?

## Value

A data frame of STITCH chemical-protein and protein-chemical interactions with their effect signs, and optionally with identifiers translated.

## See Also

- [stitch\\_actions](#)
- [stitch\\_links](#)
- [stitch\\_remove\\_prefixes](#)

## Examples

```
stn <- stitch_network(protein_ids = 'genesymbol', metabolite_ids = 'hmdb')
```

---

`stitch_remove_prefixes`*Remove the prefixes from STITCH identifiers*

---

### Description

STITCH adds the NCBI Taxonomy ID as a prefix to Ensembl protein identifiers, e.g. "9606.ENSP00000170630", and "CID" followed by "s" or "m" (stereospecific or merged, respectively) in front of PubChem Compound Identifiers. It also pads the CID with zeros. This function removes these prefixes, leaving only the identifiers.

### Usage

```
stitch_remove_prefixes(d, ..., remove = TRUE)
```

### Arguments

<code>d</code>	Data frame, typically the output of <a href="#">stitch_links</a> or <a href="#">stitch_actions</a> .
<code>...</code>	Names of columns to remove prefixes from. NSE is supported.
<code>remove</code>	Logical: remove the prefixes? If FALSE, this function does nothing.

### Value

Data frame with prefixes removed in the specified columns.

### See Also

- [stitch\\_actions](#)
- [stitch\\_links](#)
- [stitch\\_network](#)

### Examples

```
stitch_remove_prefixes(  
  data.frame(a = c('9606.ENSP00000170630', 'CIDs00012345')),  
  a  
)
```

---

subnetwork	<i>Extract a custom subnetwork from a large network</i>
------------	---

---

### Description

Extract a custom subnetwork from a large network

### Usage

```
subnetwork(  
  network,  
  nodes = NULL,  
  order = 1L,  
  mode = "all",  
  mindist = 0L,  
  return_df = TRUE  
)
```

### Arguments

network	Either an OmniPath interaction data frame, or an igraph graph object.
nodes	Character or integer vector: names, identifiers or indices of the nodes to build the subnetwork around.
order	Integer: order of neighbourhood around nodes; i.e., number of steps starting from the provided nodes.
mode	Character: "all", "out" or "in". Follow directed edges from the provided nodes in any, outbound or inbound direction, respectively.
mindist	Integer: The minimum distance to include the vertex in the result.
return_df	Logical: return an interaction data frame instead of an igraph object.

### Value

A network data frame or an igraph object, depending on the “return\_df” parameter.

### See Also

- [interaction\\_graph](#)
- [graph\\_interaction](#)
- [show\\_network](#)

---

swap_relations	<i>Reverse the direction of ontology relations</i>
----------------	--

---

### Description

Reverse the direction of ontology relations

### Usage

```
swap_relations(relations)
```

### Arguments

**relations**      The ‘relations’ component of the data returned by [obo\\_parser](#) or any ‘...ontology\_download’ function such as [go\\_ontology\\_download](#). Depending on the `tables` argument of those functions the ‘relations’ can be a data frame or a nested list.

### Value

Same type as the input, but the relations swapped: if in the input these pointed from each child to the parents, in the output they point from each parent to their children, and vice versa.

### See Also

- [relations\\_list\\_to\\_table](#)
- [relations\\_table\\_to\\_list](#)
- [obo\\_parser](#)

### Examples

```
goslim_url <-  
  "http://current.geneontology.org/ontology/subsets/goslim_generic.obo"  
path <- tempfile()  
httr::GET(goslim_url, httr::write_disk(path, overwrite = TRUE))  
obo <- obo_parser(path)  
unlink(path)  
rel_swapped <- swap_relations(obo$relations)
```



---

swissprots_only	<i>Retain only SwissProt IDs</i>
-----------------	----------------------------------

---

**Description**

Retain only SwissProt IDs

**Usage**

```
swissprots_only(uniprots, organism = 9606)
```

**Arguments**

uniprots	Character vector of UniProt IDs.
organism	Character or integer: name or identifier of the organism.

**Value**

Character vector with only SwissProt IDs.

**Examples**

```
swissprots_only(c("Q05BL1", "A0A654IBU3", "P00533"))  
# [1] "P00533"
```

---

tfcensus_download	<i>Downloads the list of transcription factors from TF census</i>
-------------------	---

---

**Description**

Vaquerizas et al. published in 2009 a list of transcription factors. This function retrieves Supplementary Table 2 from the article (<http://www.nature.com/nrg/journal/v10/n4/index.html>).

**Usage**

```
tfcensus_download()
```

**Value**

A data frame (tibble) listing transcription factors.

**Examples**

```
tfcensus <- tfcensus_download()
tfcensus
# # A tibble: 1,987 x 7
#   Class `Ensembl ID` `IPI ID` `Interpro DBD` `Interpro DNA-b.
#   <chr> <chr> <chr> <chr> <chr>
# 1 a ENSG000000000. IPI0021. NA IPR001289
# 2 a ENSG000000000. IPI0004. IPR000047;IPR. NA
# 3 a ENSG000000000. IPI0001. IPR001356;IPR. NA
# 4 a ENSG000000000. IPI0029. IPR000910;IPR. NA
# 5 a ENSG000000000. IPI0001. IPR007087;IPR. IPR006794
# # . with 1,977 more rows, and 2 more variables: `HGNC symbol` <chr>,
# # `Tissue-specificity` <chr>
```

---

 translate\_ids

*Translate gene, protein and small molecule identifiers*


---

**Description**

Translates a vector of identifiers, resulting a new vector, or a column of identifiers in a data frame by creating another column with the target identifiers.

**Usage**

```
translate_ids(
  d,
  ...,
  uploadlists = FALSE,
  ensembl = FALSE,
  hmdb = FALSE,
  ramp = FALSE,
  chalmers = FALSE,
  entity_type = NULL,
  keep_untranslated = TRUE,
  return_df = FALSE,
  organism = 9606,
  reviewed = TRUE,
  complexes = NULL,
  complexes_one_to_many = NULL
)
```

**Arguments**

d Character vector or data frame.

...	At least two arguments, with or without names. The first of these arguments describes the source identifier, the rest of them describe the target identifier(s). The values of all these arguments must be valid identifier types as shown in Details. The names of the arguments are column names. In case of the first (source) ID the column must exist. For the rest of the IDs new columns will be created with the desired names. For ID types provided as arguments without names, the name of the ID type will be used for column name.
uploadlists	Force using the uploadlists service from UniProt. By default the plain query interface is used (implemented in <a href="#">uniprot_full_id_mapping_table</a> in this package). If any of the provided ID types is only available in the uploadlists service, it will be automatically selected. The plain query interface is preferred because in the long term, with caching, it requires less download and data storage.
ensembl	Logical: use data from Ensembl BioMart instead of UniProt.
hmdb	Logical: use HMDB ID translation data.
ramp	Logical: use RaMP ID translation data.
chalmers	Logical: use ID translation data from Chalmers Sysbio GEM.
entity_type	Character: "gene" and "smol" are short symbols for proteins, genes and small molecules respectively. Several other synonyms are also accepted.
keep_untranslated	In case the output is a data frame, keep the records where the source identifier could not be translated. At these records the target identifier will be NA.
return_df	Return a data frame even if the input is a vector.
organism	Character or integer, name or NCBI Taxonomy ID of the organism (by default 9606 for human). Matters only if uploadlists is FALSE.
reviewed	Translate only reviewed (TRUE), only unreviewed (FALSE) or both (NULL) UniProt records. Matters only if uploadlists is FALSE.
complexes	Logical: translate complexes by their members. Only complexes where all members can be translated will be included in the result. If NULL, the option <code>omnipathr.complex_translation</code> will be used.
complexes_one_to_many	Logical: allow combinatorial expansion or use only the first target identifier for each member of each complex. If NULL, the option <code>omnipathr.complex_translation_one_to_many</code> will be used.

## Details

This function, depending on the `uploadlists` parameter, uses either the `uploadlists` service of UniProt or plain UniProt queries to obtain identifier translation tables. The possible values for `from` and `to` are the identifier type abbreviations used in the UniProt API, please refer to the table here: [https://www.uniprot.org/help/api\\_idmapping](https://www.uniprot.org/help/api_idmapping). In addition, simple synonyms are available which realize a uniform API for the `uploadlists` and UniProt query based backends. These are the followings:

OmnipathR	Uploadlists	UniProt query	Ensembl BioMart
-----------	-------------	---------------	-----------------

uniprot	ACC	id	uniprotswissprot
uniprot_entry	ID	entry name	
trembl	<i>reviewed = FALSE</i>	<i>reviewed = FALSE</i>	uniprotsptrmbl
genesymbol	GENENAME	genes(PREFERRED)	external_gene_name
genesymbol_syn		genes(ALTERNATIVE)	external_synonym
hgnc	HGNC_ID	database(HGNC)	hgnc_symbol
entrez	P_ENTREZGENEID	database(GeneID)	
ensembl	ENSEMBL_ID		ensembl_gene_id
ensg	ENSEMBL_ID		ensembl_gene_id
enst	ENSEMBL_TRS_ID	database(Ensembl)	ensembl_transcript_id
ensp	ENSEMBL_PRO_ID		ensembl_peptide_id
ensg	ENSEMBLGENOME_ID		
ensgt	ENSEMBLGENOME_TRS_ID		
ensgp	ENSEMBLGENOME_PRO_ID		
protein_name		protein names	
pir	PIR	database(PIR)	
ccds		database(CCDS)	
refseqp	P_REFSEQ_AC	database(refseq)	
ipro			interpro
ipro_desc			interpro_description
ipro_sdesc			interpro_short_description
wikigene			wikigene_name
rnacentral			rnacentral
gene_desc			description
wormbase		database(WormBase)	
flybase		database(FlyBase)	
xenbase		database(Xenbase)	
zfin		database(ZFIN)	
pbd	PBD_ID	database(PDB)	pbd

For a complete list of ID types and their synonyms, including metabolite and chemical ID types which are not shown here, see [id\\_types](#).

The mapping between identifiers can be ambiguous. In this case one row in the original data frame yields multiple rows or elements in the returned data frame or vector(s).

### Value

- Data frame: if the input is a data frame or the input is a vector and `return_df` is TRUE.
- Vector: if the input is a vector, there is only one target ID type and `return_df` is FALSE.
- List of vectors: if the input is a vector, there are more than one target ID types and `return_df` is FALSE. The names of the list will be ID types (as they were column names, see the description of the `...` argument), and the list will also include the source IDs.

### See Also

- [translate\\_ids\\_multi](#)

- uniprot\_id\_mapping\_table
- uniprot\_full\_id\_mapping\_table
- ensembl\_id\_mapping\_table
- hmdb\_id\_mapping\_table
- id\_types
- ensembl\_id\_type
- uniprot\_id\_type
- uploadlists\_id\_type
- hmdb\_id\_type
- chalmers\_gem\_id\_type

### Examples

```
d <- data.frame(uniprot_id = c('P00533', 'Q9ULV1', 'P43897', 'Q9Y2P5'))
d <- translate_ids(d, uniprot_id = uniprot, genesymbol)
d
#   uniprot_id genesymbol
# 1   P00533      EGFR
# 2   Q9ULV1      FZD4
# 3   P43897      TSFM
# 4   Q9Y2P5   SLC27A5
```

---

translate_ids_multi	<i>Translate gene, protein and small molecule identifiers from multiple columns</i>
---------------------	---

---

### Description

Especially when translating network interactions, where two ID columns exist (source and target), it is convenient to call the same ID translation on multiple columns. The `translate_ids` function is already able to translate to multiple ID types in one call, but is able to work only from one source column. Here too, multiple target IDs are supported. The source columns can be listed explicitly, or they might share a common stem, in this case the first element of `...` will be used as stem, and the column names will be created by adding the suffixes. The suffixes are also used to name the target columns. If no suffixes are provided, the name of the source columns will be added to the name of the target columns. ID types can be defined the same way as for `translate_ids`. The only limitation is that, if the source columns are provided as stem+suffixes, they must be the same ID type.

**Usage**

```

translate_ids_multi(
  d,
  ...,
  suffixes = NULL,
  suffix_sep = "_",
  uploadlists = FALSE,
  ensembl = FALSE,
  hmdb = FALSE,
  chalmers = FALSE,
  entity_type = NULL,
  keep_untranslated = TRUE,
  organism = 9606,
  reviewed = TRUE
)

```

**Arguments**

d	A data frame.
...	At least two arguments, with or without names. These arguments describe identifier columns, either the ones we translate from (source), or the ones we translate to (target). Columns existing in the data frame will be used as source columns. All the rest will be considered target columns. Alternatively, the source columns can be defined as a stem and a vector of suffixes, plus a separator between the stem and suffix. In this case, the source columns will be the ones that exist in the data frame with the suffixes added. The values of all these arguments must be valid identifier types as shown at <a href="#">translate_ids</a> . If ID type is provided only for the first source column, the rest of the source columns will be assumed to have the same ID type. For the target identifiers new columns will be created with the desired names, with the suffixes added. If no suffixes provided, the names of the source columns will be used instead.
suffixes	Column name suffixes in case the names should be composed of stem and suffix.
suffix_sep	Character: separator between the stem and suffixes.
uploadlists	Force using the 'uploadlists' service from UniProt. By default the plain query interface is used (implemented in <a href="#">uniprot_full_id_mapping_table</a> in this package). If any of the provided ID types is only available in the uploadlists service, it will be automatically selected. The plain query interface is preferred because in the long term, with caching, it requires less download and data storage.
ensembl	Logical: use data from Ensembl BioMart instead of UniProt.
hmdb	Logical: use HMDB ID translation data.
chalmers	Logical: use ID translation data from Chalmers Sysbio GEM.
entity_type	Character: "gene" and "smol" are short symbols for proteins, genes and small molecules respectively. Several other synonyms are also accepted.

keep_untranslated	In case the output is a data frame, keep the records where the source identifier could not be translated. At these records the target identifier will be NA.
organism	Character or integer, name or NCBI Taxonomy ID of the organism (by default 9606 for human). Matters only if <code>uploadlists</code> is FALSE.
reviewed	Translate only reviewed (TRUE), only unreviewed (FALSE) or both (NULL) UniProt records. Matters only if <code>uploadlists</code> is FALSE.

**Value**

A data frame with all source columns translated to all target identifiers. The number of new columns is the product of source and target columns. The target columns are distinguished by the suffixes added to their names.

**See Also**

[translate\\_ids](#)

**Examples**

```
ia <- omnipath()
translate_ids_multi(ia, source = uniprot, target, ensp, ensembl = TRUE)
```

---

trembls_only	<i>Retain only TrEMBL IDs</i>
--------------	-------------------------------

---

**Description**

Retain only TrEMBL IDs

**Usage**

```
trembls_only(uniprots, organism = 9606)
```

**Arguments**

uniprots	Character vector of UniProt IDs.
organism	Character or integer: name or identifier of the organism.

**Value**

Character vector with only TrEMBL IDs.

**Examples**

```
trembls_only(c("Q05BL1", "A0A654IBU3", "P00533"))
# [1] "Q05BL1" "A0A654IBU3"
```

---

trrust_download	<i>Downloads TF-target interactions from TRRUST</i>
-----------------	---

---

**Description**

TRRUST v2 (<https://www.grnpedia.org/trrust/>) is a database of literature mined TF-target interactions for human and mouse.

**Usage**

```
trrust_download(organism = "human")
```

**Arguments**

organism            Character: either "human" or "mouse".

**Value**

A data frame of TF-target interactions.

**Examples**

```
trrust_interactions <- trrust_download()
trrust_interactions
# # A tibble: 11,698 x 4
#   source_genesymbol target_genesymbol effect reference
#   <chr>             <chr>             <dbl> <chr>
# 1 AATF              BAX                 -1 22909821
# 2 AATF              CDKN1A              0 17157788
# 3 AATF              KLK3                0 23146908
# 4 AATF              MYC                 1 20549547
# 5 AATF              TP53                0 17157788
# 6 ABL1              BAX                 1 11753601
# 7 ABL1              BCL2               -1 11753601
# # . with 11,688 more rows
```

---

uniprot\_full\_id\_mapping\_table

*Creates an ID translation table from UniProt data*

---

**Description**

Creates an ID translation table from UniProt data



**Usage**

```
uniprot_full_id_mapping_table(  
  to,  
  from = "accession",  
  reviewed = TRUE,  
  organism = 9606  
)
```

**Arguments**

to	Character or symbol: target ID type. See Details for possible values.
from	Character or symbol: source ID type. See Details for possible values.
reviewed	Translate only reviewed (TRUE), only unreviewed (FALSE) or both (NULL) UniProt records.
organism	Integer, NCBI Taxonomy ID of the organism (by default 9606 for human).

**Details**

For both source and target ID type, this function accepts column codes used by UniProt and some simple shortcuts defined here. For the UniProt codes please refer to <https://www.uniprot.org/help/uniprotkb>. The shortcuts are `entrez`, `genesymbol`, `genesymbol_syn` (synonym gene symbols), `hgnc`, `embl`, `ref-seqp` (RefSeq protein), `enst` (Ensembl transcript), `uniprot_entry` (UniProtKB AC, e.g. EGFR\_HUMAN), `protein_name` (full name of the protein), `uniprot` (UniProtKB ID, e.g. P00533). For a complete table please refer to [translate\\_ids](#).

**Value**

A data frame (tibble) with columns 'From' and 'To', UniProt IDs and the corresponding foreign IDs, respectively.

**See Also**

- [translate\\_ids](#)
- [ensembl\\_id\\_mapping\\_table](#)
- [uniprot\\_id\\_mapping\\_table](#)

**Examples**

```
uniprot_entrez <- uniprot_full_id_mapping_table(to = 'entrez')  
uniprot_entrez  
# # A tibble: 20,723 x 2  
#   From To  
#   <chr> <chr>  
# 1 Q96R72 NA  
# 2 Q9UKL2 23538  
# 3 Q9H205 144125  
# 4 Q8NGN2 219873  
# 5 Q8NGC1 390439
```

```
# # . with 20,713 more rows
```

---

```
uniprot_genesymbol_cleanup
```

```
TrEMBL to SwissProt by gene names
```

---

## Description

TrEMBL to SwissProt by gene names

## Usage

```
uniprot_genesymbol_cleanup(uniprots, organism = 9606, only_trembls = TRUE)
```

## Arguments

uniprots	Character vector possibly containing TrEMBL IDs.
organism	Character or integer: organism name or identifier.
only_trembls	Attempt to convert only known TrEMBL IDs of the organism. This is the recommended practice.

## Details

Sometimes one gene or protein is represented by multiple identifiers in UniProt. These are typically slightly different isoforms, some of them having TrEMBL IDs, some of the SwissProt. For the purposes of most systems biology application, the most important is to identify the protein or gene in a way that we can recognize it in other datasets. Unfortunately UniProt or Ensembl do not seem to offer solution for this issue. Hence, if we find that a TrEMBL ID has a gene name which is also associated with a SwissProt ID, we replace this TrEMBL ID by that SwissProt. There might be a minor difference in their sequence, but most of the omics analyses do not even consider isoforms. And it is quite possible that later UniProt will convert the TrEMBL record to an isoform within the SwissProt record. Typically this translation is not so important (but still beneficial) for human, but for other organisms it is critical especially when translating from foreign identifiers.

This function accepts a mixed input of UniProt IDs and provides a distinct translation table that you can use to translate your data.

## Value

Data frame with two columns: "input" and "output". The first one contains all identifiers from the input vector 'uniprots'. The second one has the corresponding identifiers which are either SwissProt IDs with gene names identical to the TrEMBL IDs in the input, or if no such records are available, the output has the input items unchanged.

**Examples**

```
## Not run:
uniprot_genesymbol_cleanup('Q6PB82', organism = 10090)
# # A tibble: 1 × 2
#   input output
#   <chr> <chr>
# 1 Q6PB82 070405

## End(Not run)
```

---

uniprot\_idmapping\_id\_types

*ID types available in the UniProt ID Mapping service*

---

**Description**

ID types available in the UniProt ID Mapping service

**Usage**

```
uniprot_idmapping_id_types()
```

**Value**

A data frame listing the ID types.

**Examples**

```
uniprot_idmapping_id_types()
```

---

uniprot\_id\_mapping\_table

*ID translation data from UniProt ID Mapping*

---

**Description**

Retrieves an identifier translation table from the UniProt ID Mapping service ([https://www.uniprot.org/help/id\\_mapping](https://www.uniprot.org/help/id_mapping)).

**Usage**

```
uniprot_id_mapping_table(identifiers, from, to, chunk_size = NULL)
```

**Arguments**

identifiers	Character vector of identifiers
from	Character or symbol: type of the identifiers provided. See Details for possible values.
to	Character or symbol: identifier type to be retrieved from UniProt. See Details for possible values.
chunk_size	Integer: query the identifiers in chunks of this size. If you are experiencing download failures, try lower values.

**Details**

This function uses the uploadlists service of UniProt to obtain identifier translation tables. The possible values for 'from' and 'to' are the identifier type abbreviations used in the UniProt API, please refer to the table here: [uniprot\\_idmapping\\_id\\_types](#) or the table of synonyms supported by the current package: [translate\\_ids](#). Note: if the number of identifiers is larger than the chunk size the log message about the cache origin is not guaranteed to be correct (most of the times it is still correct).

**Value**

A data frame (tibble) with columns 'From' and 'To', the identifiers provided and the corresponding target IDs, respectively.

**See Also**

[translate\\_ids](#)

**Examples**

```
uniprot_genesymbol <- uniprot_id_mapping_table(
  c('P00533', 'P23771'), uniprot, genesymbol
)
uniprot_genesymbol
# # A tibble: 2 x 2
#   From To
#   <chr> <chr>
# 1 P00533 EGFR
# 2 P23771 GATA3
```

---

uniprot\_id\_type

*UniProt identifier type label*

---

**Description**

UniProt identifier type label

**Usage**

```
uniprot_id_type(label)
```

**Arguments**

label                    Character: an ID type label, as shown in the table at [translate\\_ids](#)

**Value**

Character: the UniProt specific ID type label, or the input unchanged if it could not be translated (still might be a valid identifier name). This is the label that one can use in UniProt REST queries.

**See Also**

- [ensembl\\_id\\_type](#)
- [uploadlists\\_id\\_type](#)

**Examples**

```
ensembl_id_type("entrez")  
# [1] "database(GeneID)"
```

---

```
unique_intercell_network
```

*Unique intercellular interactions*

---

**Description**

In the intercellular network data frames produced by [intercell\\_network](#), by default each pair of annotations for an interaction is represented in a separate row. This function drops the annotations and keeps only the distinct interacting pairs.

**Usage**

```
unique_intercell_network(network, ...)
```

**Arguments**

network                  An intercellular network data frame as produced by [intercell\\_network](#).  
...                      Additional columns to keep. Note: if these have multiple values for an interacting pair, only the first row will be preserved.

**Value**

A data frame with interacting pairs and interaction attributes.

**See Also**

- [intercell\\_network](#)
- [simplify\\_intercell\\_network](#)
- [filter\\_intercell\\_network](#)
- [intercell](#)
- [intercell\\_categories](#)
- [intercell\\_generic\\_categories](#)
- [intercell\\_summary](#)

**Examples**

```
icn <- intercell_network()
icn_unique <- unique_intercell_network(icn)
```

---

unnest_evidences	<i>Separate evidences by direction and effect sign</i>
------------------	--

---

**Description**

Separate evidences by direction and effect sign

**Usage**

```
unnest_evidences(data, longer = FALSE, .keep = FALSE)
```

**Arguments**

<code>data</code>	An interaction data frame with "evidences" column.
<code>longer</code>	Logical: If TRUE, the "evidences" column is split into rows.
<code>.keep</code>	Logical: keep the "evidences" column. When unnesting to longer data frame, the "evidences" column will contain the unnested evidences, while the original column will be retained under the "all_evidences" name (if <code>' .keep = TRUE'</code> ).

**Value**

The data frame with new columns or new rows by direction and sign.

**See Also**

- [only\\_from](#)
- [filter\\_evidences](#)
- [from\\_evidences](#)

### Examples

```
## Not run:
op <- omnipath_interactions(fields = "evidences")
op <- unnest_evidences(op)
colnames(op)

## End(Not run)
```

---

uploadlists_id_type	<i>UniProt Uploadlists identifier type label</i>
---------------------	--

---

### Description

UniProt Uploadlists identifier type label

### Usage

```
uploadlists_id_type(label, side = "from")
```

### Arguments

label	Character: an ID type label, as shown in the table at <a href="#">translate_ids</a>
side	Character: either "from" or "to": direction of the mapping.

### Value

Character: the UniProt Uploadlists specific ID type label, or the input unchanged if it could not be translated (still might be a valid identifier name). This is the label that one can use in UniProt Uploadlists (ID Mapping) queries.

### See Also

- [ensembl\\_id\\_type](#)
- [uniprot\\_id\\_type](#)
- [hmdb\\_id\\_type](#)
- [chalmers\\_gem\\_id\\_type](#)

### Examples

```
ensembl_id_type("entrez")
# [1] "GeneID"
```

---

vinayagam\_download      *Protein-protein interactions from Vinayagam 2011*

---

### Description

Retrieves the Supplementary Table S6 from Vinayagam et al. 2011. Find out more at <https://doi.org/10.1126/scisignal.2001699>.

### Usage

```
vinayagam_download()
```

### Value

A data frame (tibble) with interactions.

### Examples

```
vinayagam_interactions <- vinayagam_download()
vinayagam_interactions
# # A tibble: 34,814 x 5
#   `Input-node Gen.` `Input-node Gen.` `Output-node Ge.` `Output-node Ge.`
#   <chr>              <dbl> <chr>              <dbl>
# 1 C1orf103           55791 MNAT1             4331
# 2 MAST2             23139 DYNLL1             8655
# 3 RAB22A           57403 APPL2             55198
# 4 TRAP1            10131 EXT2             2132
# 5 STAT2            6773  COPS4             51138
# # . with 34,804 more rows, and 1 more variable:
# #   `Edge direction score` <dbl>
```

---

walk\_ontology\_tree      *All nodes of a subtree starting from the selected nodes*

---

### Description

Starting from the selected nodes, recursively walks the ontology tree until it reaches either the root or leaf nodes. Collects all visited nodes.



**Usage**

```
walk_ontology_tree(
  terms,
  ancestors = TRUE,
  db_key = "go_basic",
  ids = TRUE,
  method = "gra",
  relations = c("is_a", "part_of", "occurs_in", "regulates", "positively_regulates",
               "negatively_regulates")
)
```

**Arguments**

terms	Character vector of ontology term IDs or names. A mixture of IDs and names can be provided.
ancestors	Logical: if FALSE the ontology tree is traversed towards the leaf nodes; if TRUE, the tree is traversed until the root. The former returns the ancestors (parents), the latter the descendants (children).
db_key	Character: key to identify the ontology database. For the available keys see <a href="#">omnipath_show_db</a> .
ids	Logical: whether to return IDs or term names.
method	Character: either "gra" or "lst". The implementation to use for traversing the ontology tree. The graph based implementation is faster than the list based, the latter will be removed in the future.
relations	Character vector of ontology relation types. Only these relations will be used.

**Details**

Note: this function relies on the database manager, the first call might take long because of the database load process. Subsequent calls within a short period should be faster. See [get\\_ontology\\_db](#).

**Value**

Character vector of ontology IDs. If the input terms are all leaves or roots NULL is returned. The starting nodes won't be included in the result unless they fall onto the traversal path from other nodes.

**See Also**

- [omnipath\\_show\\_db](#)
- [get\\_ontology\\_db](#)

**Examples**

```
walk_ontology_tree(c('GO:0006241', 'GO:0044211'))
# [1] "GO:0006139" "GO:0006220" "GO:0006221" "GO:0006241" "GO:0006725"
# [6] "GO:0006753" "GO:0006793" "GO:0006796" "GO:0006807" "GO:0008150"
```

```
# ... (truncated)
walk_ontology_tree(c('GO:0006241', 'GO:0044211'), ancestors = FALSE)
# [1] "GO:0044210" "GO:0044211"
walk_ontology_tree(
  c('GO:0006241', 'GO:0044211'),
  ancestors = FALSE,
  ids = FALSE
)
# [1] "'de novo' CTP biosynthetic process" "CTP salvage"
```

---

with_extra_attrs	<i>Interaction records having certain extra attributes</i>
------------------	--

---

## Description

Interaction records having certain extra attributes

## Usage

```
with_extra_attrs(data, ...)
```

## Arguments

data	An interaction data frame.
...	The name(s) of the extra attributes; NSE is supported.

## Value

The data frame filtered to the records having the extra attribute.

## See Also

- [extra\\_attrs](#)
- [has\\_extra\\_attrs](#)
- [extra\\_attrs\\_to\\_cols](#)
- [filter\\_extra\\_attrs](#)
- [extra\\_attr\\_values](#)

## Examples

```
i <- omnipath(fields = "extra_attrs")
with_extra_attrs(i, Macrophage_type)
```

---

with_references	<i>Interactions having references</i>
-----------------	---------------------------------------

---

**Description**

Interactions having references

**Usage**

```
with_references(data, resources = NULL)
```

**Arguments**

data	An interaction data frame.
resources	Character: consider only these resources. If 'NULL', records with any reference will be accepted.

**Value**

A subset of the input interaction data frame.

**Examples**

```
cc <- import_post_translational_interactions(resources = 'CellChatDB')
with_references(cc, 'CellChatDB')
```

---

zenodo_download	<i>Retrieves data from Zenodo</i>
-----------------	-----------------------------------

---

**Description**

Zenodo is a repository of large scientific datasets. Many projects and publications make their datasets available at Zenodo. This function downloads an archive from Zenodo and extracts the requested file.

**Usage**

```
zenodo_download(
  path,
  reader = NULL,
  reader_param = list(),
  url_key = NULL,
  zenodo_record = NULL,
  zenodo_fname = NULL,
  url_param = list(),
```

```

    url_key_param = list(),
    ...
)

```

### Arguments

path	Character: path to the file within the archive.
reader	Optional, a function to read the connection.
reader_param	List: arguments for the reader function.
url_key	Character: name of the option containing the URL
zenodo_record	The Zenodo record ID, either integer or character.
zenodo_fname	The file name within the record.
url_param	List: variables to insert into the URL string (which is returned from the options).
url_key_param	List: variables to insert into the 'url_key'.
...	Passed to archive_extractor

### Value

A connection

### Examples

```

# an example from the OmnipathR::remap_tf_target_download function:
remap_dorothea <- zenodo_download(
  zenodo_record = 3713238,
  zenodo_fname = 'tf_target_sources.zip',
  path = (
    'tf_target_sources/chip_seq/remap/gene_tf_pairs_genesymbol.txt'
  ),
  reader = read_tsv,
  reader_param = list(
    col_names = c(
      'source_genesymbol',
      'target_genesymbol',
      'target_ensembl',
      'score'
    ),
    col_types = cols(),
    progress = FALSE
  ),
  resource = 'ReMap'
)

```

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