
Bio2BEL miRTarBase Documentation

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bio2bel_mirtarbase can be installed easily from [PyPI](#) with the following code in your favorite terminal:

```
$ python3 -m pip install bio2bel_mirtarbase
```

or from the latest code on [GitHub](#) with:

```
$ python3 -m pip install git+https://github.com/bio2bel/mirtarbase.git@master
```


MANAGER

Manager for Bio2BEL miRTarBase.

```
class bio2bel_mirtarbase.manager.Manager (*args, **kwargs)
    miRNA-target interactions.
```

```
    edge_model
        alias of bio2bel_mirtarbase.models.Interaction
```

```
    is_populated () → bool
        Check if the database is already populated.
```

```
    populate (source: Optional[str] = None, update: bool = False) → None
        Populate database with the data from miRTarBase.
```

Parameters

- **source** – path or link to data source needed for `get_data()`
- **update** – Should HGNC an miRBase be updated?

```
    count_targets () → int
        Count the number of targets in the database.
```

```
    count_mirnas () → int
        Count the number of miRNAs in the database.
```

```
    count_interactions () → int
        Count the number of interactions in the database.
```

```
    count_evidences () → int
        Count the number of evidences in the database.
```

```
    list_evidences () → List[bio2bel_mirtarbase.models.Evidence]
        List the evidences in the database.
```

```
    count_species () → int
        Count the number of species in the database.
```

```
    summarize () → Mapping[str, int]
        Return a summary dictionary over the content of the database.
```

```
    query_mirna_by_mirtarbase_identifier (mirtarbase_id: str) → Optional[bio2bel_mirtarbase.models.Mirna]
        Get an miRNA by the miRTarBase interaction identifier.
```

Parameters **mirtarbase_id** – An miRTarBase interaction identifier

```
    query_mirna_by_mirtarbase_name (name: str) → Optional[bio2bel_mirtarbase.models.Mirna]
        Get an miRNA by its miRTarBase name.
```

Parameters `name` – An miRTarBase name

query_mirna_by_hgnc_identifier (*hgnc_id: str*) → Optional[bio2bel_mirtarbase.models.Mirna] Op-
 Query for a miRNA by its HGNC identifier.

Parameters `hgnc_id` – HGNC gene identifier

query_mirna_by_hgnc_symbol (*hgnc_symbol: str*) → Optional[bio2bel_mirtarbase.models.Mirna] Op-
 Query for a miRNA by its HGNC gene symbol.

Parameters `hgnc_symbol` – HGNC gene symbol

query_target_by_entrez_id (*entrez_id: str*) → Optional[bio2bel_mirtarbase.models.Target]
 Query for one target.

Parameters `entrez_id` – Entrez gene identifier

query_target_by_hgnc_symbol (*hgnc_symbol: str*) → Optional[bio2bel_mirtarbase.models.Target] Op-
 Query for one target.

Parameters `hgnc_symbol` – HGNC gene symbol

query_target_by_hgnc_identifier (*hgnc_id: str*) → Optional[bio2bel_mirtarbase.models.Target] Op-
 Query for one target.

Parameters `hgnc_id` – HGNC gene identifier

enrich_rnas (*graph: pybel.struct.graph.BELGraph*)
 Add all of the miRNA inhibitors of the RNA nodes in the graph.

enrich_mirnas (*graph: pybel.struct.graph.BELGraph*)
 Add all target RNAs to the miRNA nodes in the graph.

get_mirna_interaction_evidences ()
 Get interaction evidences.

to_bel () → *pybel.struct.graph.BELGraph*
 Serialize miRNA-target interactions to BEL.

MODELS

SQLAlchemy models for Bio2BEL miRTarBase.

```
class bio2bel_mirtarbase.models.Species (**kwargs)
```

Represents a species.

A simple constructor that allows initialization from kwargs.

Sets attributes on the constructed instance using the names and values in `kwargs`.

Only keys that are present as attributes of the instance's class are allowed. These could be, for example, any mapped columns or relationships.

taxonomy_id

The NCBI taxonomy identifier

name

The scientific name for the species

to_json (*include_id: bool = True*) → Mapping

Serialize to JSON.

Parameters include_id – Include the database identifier?

```
class bio2bel_mirtarbase.models.Mirna (**kwargs)
```

Create mirna table that stores information about the miRNA.

A simple constructor that allows initialization from kwargs.

Sets attributes on the constructed instance using the names and values in `kwargs`.

Only keys that are present as attributes of the instance's class are allowed. These could be, for example, any mapped columns or relationships.

name

miRTarBase name

mirbase_id

miRBase identifier

entrez_id

Entrez Gene identifier

species_id

The host species

as_bel () → pybel.dsl.node_classes.MicroRna

Serialize to a PyBEL node data dictionary.

static filter_name_in (*names: Iterable[str]*)

Build a name filter.

class bio2bel_mirtarbase.models.Target (**kwargs)

Represents a target RNA.

A simple constructor that allows initialization from kwargs.

Sets attributes on the constructed instance using the names and values in kwargs.

Only keys that are present as attributes of the instance's class are allowed. These could be, for example, any mapped columns or relationships.

name

Target gene name

entrez_id

Entrez gene identifier

hgnc_symbol

HGNC gene symbol

hgnc_id

HGNC gene identifier

species_id

The host species

serialize_to_entrez_node() → pybel.dsl.node_classes.Rna

Serialize to PyBEL node data dictionary.

serialize_to_hgnc_node() → pybel.dsl.node_classes.Rna

Serialize to PyBEL node data dictionary.

to_json(include_id=True) → Mapping

Return this object as JSON.

class bio2bel_mirtarbase.models.Interaction (**kwargs)

Build Interaction table used to store miRNA and target relations.

A simple constructor that allows initialization from kwargs.

Sets attributes on the constructed instance using the names and values in kwargs.

Only keys that are present as attributes of the instance's class are allowed. These could be, for example, any mapped columns or relationships.

mirtarbase_id

miRTarBase interaction identifier which is unique for a pair of miRNA and RNA targets

mirna_id

The miRTarBase identifier of the interacting miRNA

target_id

The Entrez gene identifier of the interacting RNA

class bio2bel_mirtarbase.models.Evidence (**kwargs)

Build Evidence table used to store MTI's and their evidence.

A simple constructor that allows initialization from kwargs.

Sets attributes on the constructed instance using the names and values in kwargs.

Only keys that are present as attributes of the instance's class are allowed. These could be, for example, any mapped columns or relationships.

experiment

Experiments made to find miRNA - target interaction. E.g. 'Luciferase reporter assay//qRT-PCR//Western blot'

support

Type and strength of the miRNA - target interaction. E.g. 'Functional MTI (Weak)'

reference

Reference PubMed Identifier

interaction_id

The interaction for which this evidence was captured

add_to_graph (*graph*: *pybel.struct.graph.BELGraph*) → str

Add this edge to the BEL graph and return the ket for that edge.

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