
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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