
Bio2BEL FlyBase Documentation

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A Bio2BEL package for FlyBase.

Manager for FlyBase.

```
class bio2bel_flybase.manager.Manager (*args, **kwargs)
    Drosophila gene nomenclature and orthologies.

    count_fly_genes ()
        Count the fly genes in the database.

        Return type int

    is_populated ()
        Check if the database is populated.

        Return type bool

    namespace_model
        alias of bio2bel_flybase.models.FlyGene

    populate (gene_mapping_url=None)
        Populate the database.

    summarize ()
        Summarize the database.

        Return type Mapping[str, int]
```

FlyBase database models.

```
class bio2bel_flybase.models.FlyGene (**kwargs)
    Gene table.

    serialize_to_protein_node ()
        Serialize to PyBEL node data dictionary.

        Return type Gene
```


BIO2BEL_FLYBASE

Default connection at `sqlite:///home/docs/.bio2bel/bio2bel.db`

using Bio2BEL v0.2.1

```
bio2bel_flybase [OPTIONS] COMMAND [ARGS]...
```

Options

-c, --connection <connection>
Defaults to `sqlite:///home/docs/.bio2bel/bio2bel.db`

1.1 belns

Manage BEL namespace.

```
bio2bel_flybase belns [OPTIONS] COMMAND [ARGS]...
```

1.1.1 drop

Clear names/identifiers to terminology store.

```
bio2bel_flybase belns drop [OPTIONS]
```

1.1.2 upload

Upload names/identifiers to terminology store.

```
bio2bel_flybase belns upload [OPTIONS]
```

Options

-u, --update

1.1.3 write

Write a BEL namespace names/identifiers to terminology store.

```
bio2bel_flybase belns write [OPTIONS]
```

Options

-f, --file <file>

-n, --use-names

1.2 cache

Manage cached data.

```
bio2bel_flybase cache [OPTIONS] COMMAND [ARGS]...
```

1.2.1 clear

Clear all files from the cache.

```
bio2bel_flybase cache clear [OPTIONS]
```

1.2.2 locate

Print the location of the data directory.

```
bio2bel_flybase cache locate [OPTIONS]
```

1.2.3 ls

List files in the cache.

```
bio2bel_flybase cache ls [OPTIONS]
```

1.3 drop

Drop the database.

```
bio2bel_flybase drop [OPTIONS]
```

Options

--yes

Confirm the action without prompting.

1.4 populate

Populate the database.

```
bio2bel_flybase populate [OPTIONS]
```

Options

--reset

Nuke database first

--force

Force overwrite if already populated

1.5 summarize

Summarize the contents of the database.

```
bio2bel_flybase summarize [OPTIONS]
```


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