
Bio2BEL FamPlex Documentation

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Charles Tapley Hoyt

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Bio2BEL FamPlex.

This repository contains utilities for downloading, parsing, and serializing FamPlex to BEL.

Manager for Bio2BEL FamPlex.

```
class bio2bel_famplex.manager.Manager (*args, **kwargs)
```

Protein family and complex hierarchy.

```
count_entries ()
```

Count the number of entries in the database.

Return type `int`

```
count_relations ()
```

Count the number of relationships in the database.

Return type `int`

```
static is_populated ()
```

Return if the database is populated.

Return type `bool`

```
normalize_terms (graph, use_tqdm=False)
```

Normalize FamPlex nodes in the graph.

Return type `None`

```
summarize ()
```

Summarize the database.

Return type `Mapping[str, int]`

```
to_bel ()
```

Generate a BEL graph.

Return type `BELGraph`

BIO2BEL_FAMPLEX

Default connection at None

using Bio2BEL v0.2.1

```
bio2bel_famplex [OPTIONS] COMMAND [ARGS]...
```

Options

-c, --connection <connection>
Defaults to None

1.1 bel

Manage BEL.

```
bio2bel_famplex bel [OPTIONS] COMMAND [ARGS]...
```

1.1.1 upload

Upload BEL to network store.

```
bio2bel_famplex bel upload [OPTIONS]
```

Options

-c, --connection <connection>

1.1.2 write

Write as BEL Script.

```
bio2bel_famplex bel write [OPTIONS]
```

Options

-o, --output <output>

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