
Bio2BEL HGNC Documentation

Release 0.2.4-dev

Charles Tapley Hoyt

May 01, 2019

CONTENTS:

1	Manager	1
2	Indices and tables	5
	Python Module Index	7

MANAGER

Bio2BEL HGNC Manager.

```
class bio2bel_hgnc.manager.Manager (*args, **kwargs)
    Human gene nomenclature and orthologies to mouse and rat.

    add_central_dogma (graph: pybel.struct.graph.BELGraph, node:
                       pybel.dsl.node_classes.BaseEntity) → Op-
                       tional[pybel.dsl.node_classes.CentralDogma]
        Add the central dogma of biology.

    add_namespace_to_graph (graph: pybel.struct.graph.BELGraph)
        Add this manager's namespace to the graph.

    build_entrez_id_symbol_mapping () → Mapping[str, str]
        Build a mapping from Entrez gene identifier to HGNC gene symbols.

    build_hgnc_id_symbol_mapping () → Mapping[str, str]
        Build a mapping from HGNC identifiers to HGNC gene symbols.

    build_hgnc_id_uniprot_ids_mapping ()
        Build a mapping from HGNC identifier to UniProt identifiers.

        Return type dict[str,set[str]]

    build_hgnc_symbol_entrez_id_mapping () → Mapping[str, str]
        Build a mapping from HGNC symbol to ENTREZ identifier.

    build_hgnc_symbol_id_mapping () → Mapping[str, str]
        Build a mapping from HGNC gene symbols to HGNC identifiers.

    build_hgnc_symbol_uniprot_ids_mapping ()
        Build a mapping from HGNC gene symbols to UniProt identifiers.

        Return type dict[str,set[str]]

    build_uniprot_id_hgnc_id_mapping () → Mapping[str, str]
        Build a mapping from UniProt identifiers to HGNC identifiers.

    build_uniprot_id_hgnc_symbol_mapping () → Mapping[str, str]
        Build a mapping from UniProt identifiers to HGNC gene symbols.

    count_families () → int
        Count the number of human gene families in the database.

    count_human_genes () → int
        Count the number of human genes in the database.

    count_mouse_genes () → int
        Count the number of mouse genes in the database.
```

count_proteins () → int
 Count the number of UniProt proteins in the database.

count_rat_genes () → int
 Count the number of rat genes in the database.

enrich_families_with_genes (*graph: pybel.struct.graph.BELGraph*)
 Enrich gene families in the BEL graph with their member genes.

enrich_genes_with_equivalences (*graph: pybel.struct.graph.BELGraph*) → None
 Enrich genes with their corresponding UniProt.

enrich_genes_with_families (*graph: pybel.struct.graph.BELGraph*) → None
 Enrich genes in the BEL graph with their families.

enrich_hgnc_with_entrez_equivalences (*graph: pybel.struct.graph.BELGraph*)
 Add equivalent Entrez nodes for all HGNC genes.

get_all_hgnc_symbols () → Set[str]
 Return the set of HGNC gene symbols in the database.

get_all_hgnc_symbols_family () → Set[str]
 Get all Gene symbols that appear in gene families.

get_enzyme_by_ec_number (*ec_number: str*) → Optional[pyhgnc.manager.models.HGNC]
 Get a enzyme by its associated EC number.

Parameters ec_number – EC number

get_family_by_id (*family_identifier: str*) → Optional[pyhgnc.manager.models.GeneFamily]
 Get a gene family by its hgnc.genefamily identifier, if it exists.

get_family_by_name (*family_name: str*) → Optional[pyhgnc.manager.models.GeneFamily]
 Get a gene family by its name, if it exists.

get_gene_by_ensembl_id (*ensembl_id: str*) → Optional[pyhgnc.manager.models.HGNC]
 Get a human gene by its ENSEMBL gene identifier.

Parameters ensembl_id – The ENSEMBL gene identifier

get_gene_by_entrez_id (*entrez_id: str*) → Optional[pyhgnc.manager.models.HGNC]
 Get a human gene by its Entrez gene identifier.

Parameters entrez_id – The Entrez gene identifier

get_gene_by_hgnc_id (*hgnc_id: str*) → Optional[pyhgnc.manager.models.HGNC]
 Get a human gene by HGNC identifier.

Parameters hgnc_id – The HGNC gene identifier

get_gene_by_hgnc_symbol (*hgnc_symbol: str*) → Optional[pyhgnc.manager.models.HGNC]
 Get a human gene by HGNC symbol.

Parameters hgnc_symbol – The HGNC gene symbol

get_gene_by_mgi_id (*mgi_id: str*) → Optional[pyhgnc.manager.models.HGNC]
 Get a human gene by an orthologous MGI identifier.

Parameters mgi_id – MGI identifier

get_gene_by_rgd_id (*rgd_id: str*) → Optional[pyhgnc.manager.models.HGNC]
 Get a human gene by an orthologous RGD identifier.

Parameters rgd_id – RGD identifier

get_gene_by_uniprot_id (*uniprot_id: str*) → Optional[pyhgnc.manager.models.HGNC]
 Get a human gene by its UniProt gene identifier.

Parameters *uniprot_id* – The UniProt gene identifier

get_hgnc_from_alias_symbol (*alias_symbol: str*) → Optional[pyhgnc.manager.models.HGNC]
 Get HGNC from alias symbol.

Parameters *alias_symbol* – alias symbol

get_node (*node: pybel.dsl.node_classes.BaseEntity*) → Optional[pyhgnc.manager.models.HGNC]
 Get a node from the database, whether it has a HGNC, RGD, MGI, or EG identifier.

Parameters *node* – The node to look for

Raises `KeyError`

get_pathway_size_distribution () → collections.Counter
 Get the pathway size distribution.

hgnc_symbol_entrez_id_mapping
 Get a mapping from Entrez gene identifiers to HGNC gene symbols.

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

iter_genes (*graph: pybel.struct.graph.BELGraph*) → Iterable[Tuple[pybel.dsl.node_classes.BaseEntity, pyhgnc.manager.models.HGNC]]
 Iterate over pairs of BEL nodes and HGNC genes.

list_families () → List[pyhgnc.manager.models.GeneFamily]
 List families in the database.

list_human_genes () → List[pyhgnc.manager.models.HGNC]
 List human genes in the database.

namespace_model
 alias of `pyhgnc.manager.models.HGNC`

normalize_genes (*graph: pybel.struct.graph.BELGraph*) → None
 Add identifiers to all HGNC genes.

populate (*silent=False, hgnc_file_path=None, use_hcop=False, hcop_file_path=None, low_memory=False*)
 Populate the database.

summarize () → Mapping[str, int]
 Summarize the database.

to_bel () → pybel.struct.graph.BELGraph
 Export gene family definitions as a BEL graph.

INDICES AND TABLES

- genindex
- modindex
- search

PYTHON MODULE INDEX

b

`bio2bel_hgnc.manager`, 1

A

add_central_dogma()
(bio2bel_hgnc.manager.Manager method),
 1

add_namespace_to_graph()
(bio2bel_hgnc.manager.Manager method),
 1

B

bio2bel_hgnc.manager (*module*), 1

build_entrez_id_symbol_mapping()
(bio2bel_hgnc.manager.Manager method),
 1

build_hgnc_id_symbol_mapping()
(bio2bel_hgnc.manager.Manager method),
 1

build_hgnc_id_uniprot_ids_mapping()
(bio2bel_hgnc.manager.Manager method), 1

build_hgnc_symbol_entrez_id_mapping()
(bio2bel_hgnc.manager.Manager method), 1

build_hgnc_symbol_id_mapping()
(bio2bel_hgnc.manager.Manager method),
 1

build_hgnc_symbol_uniprot_ids_mapping()
(bio2bel_hgnc.manager.Manager method), 1

build_uniprot_id_hgnc_id_mapping()
(bio2bel_hgnc.manager.Manager method), 1

build_uniprot_id_hgnc_symbol_mapping()
(bio2bel_hgnc.manager.Manager method), 1

C

count_families() (*bio2bel_hgnc.manager.Manager method*), 1

count_human_genes()
(bio2bel_hgnc.manager.Manager method),
 1

count_mouse_genes()
(bio2bel_hgnc.manager.Manager method),
 1

count_proteins() (*bio2bel_hgnc.manager.Manager method*), 1

count_rat_genes()
(bio2bel_hgnc.manager.Manager method),
 2

E

enrich_families_with_genes()
(bio2bel_hgnc.manager.Manager method),
 2

enrich_genes_with_equivalences()
(bio2bel_hgnc.manager.Manager method),
 2

enrich_genes_with_families()
(bio2bel_hgnc.manager.Manager method),
 2

enrich_hgnc_with_entrez_equivalences()
(bio2bel_hgnc.manager.Manager method), 2

G

get_all_hgnc_symbols()
(bio2bel_hgnc.manager.Manager method),
 2

get_all_hgnc_symbols_family()
(bio2bel_hgnc.manager.Manager method),
 2

get_enzyme_by_ec_number()
(bio2bel_hgnc.manager.Manager method),
 2

get_family_by_id()
(bio2bel_hgnc.manager.Manager method),
 2

get_family_by_name()
(bio2bel_hgnc.manager.Manager method),
 2

get_gene_by_ensembl_id()
(bio2bel_hgnc.manager.Manager method),
 2

get_gene_by_entrez_id()
(bio2bel_hgnc.manager.Manager method),
 2

get_gene_by_hgnc_id()
(bio2bel_hgnc.manager.Manager method),
 2

`get_gene_by_hgnc_symbol()`
 (*bio2bel_hgnc.manager.Manager* *method*),
 2

`get_gene_by_mgi_id()`
 (*bio2bel_hgnc.manager.Manager* *method*),
 2

`get_gene_by_rgd_id()`
 (*bio2bel_hgnc.manager.Manager* *method*),
 2

`get_gene_by_uniprot_id()`
 (*bio2bel_hgnc.manager.Manager* *method*),
 2

`get_hgnc_from_alias_symbol()`
 (*bio2bel_hgnc.manager.Manager* *method*),
 3

`get_node()` (*bio2bel_hgnc.manager.Manager*
 method), 3

`get_pathway_size_distribution()`
 (*bio2bel_hgnc.manager.Manager* *method*),
 3

H

`hgnc_symbol_entrez_id_mapping`
 (*bio2bel_hgnc.manager.Manager* *attribute*), 3

I

`is_populated()` (*bio2bel_hgnc.manager.Manager*
 method), 3

`iter_genes()` (*bio2bel_hgnc.manager.Manager*
 method), 3

L

`list_families()` (*bio2bel_hgnc.manager.Manager*
 method), 3

`list_human_genes()`
 (*bio2bel_hgnc.manager.Manager* *method*),
 3

M

`Manager` (*class in bio2bel_hgnc.manager*), 1

N

`namespace_model` (*bio2bel_hgnc.manager.Manager*
 attribute), 3

`normalize_genes()`
 (*bio2bel_hgnc.manager.Manager* *method*),
 3

P

`populate()` (*bio2bel_hgnc.manager.Manager*
 method), 3

S

`summarize()` (*bio2bel_hgnc.manager.Manager*
 method), 3

T

`to_bel()` (*bio2bel_hgnc.manager.Manager* *method*), 3