
Bio2BEL HGNC Documentation

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

    build_entrez_id_to_hgnc_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_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_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.

property 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, use_tqdm: bool = False*) → 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, use_tqdm: bool = False*) → 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.

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