pybiopax

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CONTENTS

CHAPTER

ONE

PYBIOPAX API

pybiopax.api.**model_from_biocyc**(*identifier*)

Return a BioPAX model from a BioCyc entry.

BioCyc contains pathways for model eukaryotes and microbes.

Parameters
identifier (str) – The BioCyc identifier for a pathway (e.g., P105-PWY for TCA cycle IV (2-oxoglutarate decarboxylase))

Return type
BioPaxModel

Returns
A BioPAX model obtained from the BioCyc pathway.

pybiopax.api.**model_from_ecocyc**(*identifier*)

Return a BioPAX model from a EcoCyc entry.

EcoCyc contains pathways for Escherichia coli K-12 MG1655.

Parameters
identifier (str) – The EcoCyc identifier for a pathway (e.g., TCA for TCA cycle I (prokaryotic))

Return type
BioPaxModel

Returns
A BioPAX model obtained from the EcoCyc pathway.

pybiopax.api.**model_from_humancyc**(*identifier*)

Return a BioPAX model from a HumanCyc entry.

Parameters
identifier (str) – The HumanCyc identifier for a pathway (e.g., PWY66-398 for TCA cycle)

Return type
BioPaxModel

Returns
A BioPAX model obtained from the HumanCyc pathway.

pybiopax.api.**model_from_metacyc**(*identifier*)

Return a BioPAX model from a MetaCyc entry.

MetaCyc contains pathways for all organisms

Parameters
identifier (str) – The MetaCyc identifier for a pathway (e.g., TCA for TCA cycle I (prokaryotic))

Return type
BioPaxModel

Returns
A BioPAX model obtained from the MetaCyc pathway.

pybiopax.api.**model_from_netpath**(*identifier*)

Return a BioPAX model from a NetPath entry.

Parameters
identifier (str) – The NetPath identifier for a pathway (e.g., 22 for the leptin signaling pathway

Return type
BioPaxModel

Returns
A BioPAX model obtained from the NetPath resource.

pybiopax.api.**model_from_owl_file**(*fname*, *encoding=None*)

Return a BioPAX Model from an OWL string.

Parameters

- **fname** (Union[str, Path, PathLike]) – A path to an OWL file of BioPAX content.
- **encoding** (Optional[str]) – The encoding type to be passed to open().

Return type
BioPaxModel

Returns
A BioPAX Model deserialized from the OWL file.

pybiopax.api.**model_from_owl_gz**(*path*)

Return a BioPAX Model from an OWL file (gzipped).

Parameters
path (Union[str, Path, PathLike]) – A path to a gzipped OWL file of BioPAX content.

Return type
BioPaxModel

Returns
A BioPAX Model deserialized from the OWL file.

pybiopax.api.**model_from_owl_str**(*owl_str*)

Return a BioPAX Model from an OWL string.

Parameters
owl_str (str) – A OWL string of BioPAX content.

Returns
A BioPAX Model deserialized from the OWL string.

Return type
pybiopax.biopax.BioPaxModel

pybiopax.api.**model_from_owl_url**(*url*, *request_params=None*)

Return a BioPAX Model from an URL pointing to an OWL file.

Parameters

- **url** (str) – A OWL URL with BioPAX content.
- **request_params** (Optional[Mapping[str, Any]]) – Additional keyword arguments to pass to requests.get()

Return type
BioPaxModel

Returns
A BioPAX Model deserialized from the OWL file.

pybiopax.api.**model_from_pc_query**(*kind*, *source*, *target=None*, ***query_params*)

Return a BioPAX Model from a Pathway Commons query.

For more information on these queries, see http://www.pathwaycommons.org/pc2/#graph

Parameters

- **kind** (*str*) – The kind of graph query to perform. Currently 3 options are implemented, 'neighborhood', 'pathsbetween' and 'pathsfromto'.
- **source** (*list[str]*) – A single gene name or a list of gene names which are the source set for the graph query.
- **target** (*Optional[list[str]]*) – A single gene name or a list of gene names which are the target set for the graph query. Only needed for 'pathsfromto' queries.
- **limit** (*Optional[int]*) – This limits the length of the longest path considered in the graph query. Default: 1
- **organism** (*Optional[str]*) – The organism used for the query. Default: '9606' corresponding to human.
- **datasource** (*Optional[list[str]]*) – A list of database sources that the query results should include. Example: ['pid', 'panther']. By default, all databases are considered.

Returns
A BioPAX Model obtained from the results of the Pathway Commons query.

Return type
pybiopax.biopax.BioPaxModel

pybiopax.api.**model_from_reactome**(*identifier*)

Return a BioPAX model from a Reactome entry (pathway, event, etc.).

Parameters
identifier (str) – The Reactome identifier for a pathway (e.g., 177929 for Signaling by EGFR) or reaction (e.g., 177946 for Pro-EGF is cleaved to form mature EGF). For human pathways, the identifier for the BioPAX download is the same as the part that comes after R-HSA-. For non-human pathways, this is not so clear.

Return type
BioPaxModel

Returns
A BioPAX model obtained from the Reactome resource.

pybiopax.api.**model_to_owl_file**(*model*, *fname*)

Write an OWL string serialized from a BioPaxModel object into a file.

Parameters

- **model** (*BioPaxModel*) – The BioPaxModel to serialize into an OWL file.
- **fname** (Union[str, Path, PathLike]) – The path to the target OWL file.

pybiopax.api.**model_to_owl_str**(*model*)

Return an OWL string serialized from a BioPaxModel object.

Parameters

model (*BioPaxModel*) – The BioPaxModel to serialize into an OWL string.

Return type

str

Returns

The OWL string for the model.

CHAPTER

TWO

BIOPAX OBJECT MODEL

This module implements the BioPAX Level 3 object model as a set of classes with inheritance. At the top of the class hierarchy is the generic BioPaxObject.

class pybiopax.biopax.model.**BioPaxModel**(*objects*, *xml_base='http://www.biopax.org/release/biopax-level3.owl#'*)

Bases: `object`

BioPAX Model.

Parameters

- **objects** (*dict or list*) – A dict of BioPaxObject instances keyed by their URI string or a list of BioPaxObject instances, which will get converted into a dict keyed their URI strings
- **xml_base** (*str*) – The XML base namespace for the content being represented.

objects

A dict of BioPaxObject instances keyed by their URI string that are part of the model.

Type
dict

xml_base

The XML base namespace for the content being represented. If not provided, the default BioPAX Level 3 base namespace is used.

Type
Optional[str]

classmethod from_xml(*tree*)

Return a BioPAX Model from an OWL/XML element tree.

Parameters
tree – An element tree from which the model is extracted

Return type
BioPaxModel

Returns
A BioPAX Model deserialized from the OWL XML tree.

to_xml()

Return an OWL string from the content of the model.

Return type
str

pybiopax.biopax.model.**PYBIOPAX_TQDM_CONFIG = {'unit_scale': True}**

Default configuration for tqdm progress bars in pybiopax. To modify the tqdm configuration, modify this module-level variable. For example, to disable the progress bars, set the `disable` key to `True`.

2.1 Base classes

class pybiopax.biopax.base.**BioPaxObject**(*uid*, *comment=None*, ***kwargs*)

Bases: `object`

Generic BioPAX Object. It is the parent class of all more specific BioPAX classes.

class pybiopax.biopax.base.**Controller**(***kwargs*)

Bases: `object`

BioPAX Controller.

class pybiopax.biopax.base.**Entity**(*availability=None*, *data_source=None*, ***kwargs*)

Bases: *BioPaxObject*, *Observable*, *Named*

BioPAX Entity.

availability

Type
str

data_source

Type
List[*Provenance*]

property name

All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.base.**Gene**(*organism*, ***kwargs*)

Bases: *Entity*

BioPAX Gene

organism

Type
BioSource

property name

All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.base.**Named**(*display_name=None*, *standard_name=None*, *name=None*, ***kwargs*)

Bases: *XReferrable*

A mixin class to add names to a BioPaxObject.

display_name

Type
str

standard_name

Type
str

name

Type
str

property name
All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.base.**Observable**(*evidence=None*, ***kwargs*)

Bases: `object`

A mixin class to add evidence to a BioPaxObject.

evidence

Type
List[*Evidence*]

class pybiopax.biopax.base.**Pathway**(*pathway_component=None*, *pathway_order=None*, *organism=None*, ***kwargs*)

Bases: *Entity*, *Controller*

BioPAX Pathway.

property name
All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.base.**Unresolved**(*obj_id*)

Bases: `object`

A placeholder class used while deserializing BioPAX models.

class pybiopax.biopax.base.**XReferrable**(*xref=None*, ***kwargs*)

Bases: `object`

A mixin class to add xrefs to a BioPaxObject.

xref

Type
List[*Xref*]

2.2 Interactions

class pybiopax.biopax.interaction.**BiochemicalReaction**(*delta_s=None*, *delta_h=None*, *delta_g=None*, *k_e_q=None*, *e_c_number=None*, ***kwargs*)

Bases: *Conversion*

BioPAX BiochemicalReaction.

delta_s

Type
List[float]

delta_h

Type
List[float]

delta_g

Type
List[*DeltaG*]

k_e_q

Type
List[*KPrime*]

e_c_number

Type
List[str]

property name
All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.interaction.**Catalysis**(*catalysis_direction=None*, *cofactor=None*, ***kwargs*)

Bases: *Control*

BioPAX Catalysis.

catalysis_direction

Type
str

cofactor

Type
List[*PhysicalEntity*]

property name
All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.interaction.**ComplexAssembly**(*left=None*, *right=None*, *conversion_direction=None*, *participant_stoichiometry=None*, *spontaneous=None*, ***kwargs*)

Bases: *Conversion*

BioPAX ComplexAssembly.

property name
All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.interaction.**Control**(*control_type=None*, *controller=None*, *controlled=None*, ***kwargs*)

Bases: *Interaction*

BioPAX Control.

control_type

Type
str

controller

Type
List[*Process*]

controlled

Type
Process

property name
All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.interaction.**Conversion**(*left=None*, *right=None*, *conversion_direction=None*, *participant_stoichiometry=None*, *spontaneous=None*, ***kwargs*)

Bases: *Interaction*

BioPAX Conversion.

left

Type
List[*PhysicalEntity*]

right

Type
List[*PhysicalEntity*]

conversion_direction

Type
str

participant_stoichiometry

Type
List[*Stoichiometry*]

spontaneous

Type
bool

property name
All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.interaction.**Degradation**(*left=None*, *right=None*, *conversion_direction=None*, *participant_stoichiometry=None*, *spontaneous=None*, ***kwargs*)

Bases: *Conversion*

BioPAX Degradation.

property name
All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.interaction.**GeneticInteraction**(*participant=None*, *interaction_type=None*, ***kwargs*)

Bases: *Interaction*

BioPAX GeneticInteraction.

property name

All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.interaction.**Interaction**(*participant=None*, *interaction_type=None*, ***kwargs*)

Bases: *Process*

BioPAX Interaction.

participant

Type
List[*Entity*]

interaction_type

Type
List[str]

property name

All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.interaction.**Modulation**(*control_type=None*, *controller=None*, *controlled=None*, ***kwargs*)

Bases: *Control*

BioPAX Modulation.

property name

All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.interaction.**MolecularInteraction**(*participant=None*, *interaction_type=None*, ***kwargs*)

Bases: *Interaction*

BioPAX MolecularInteraction.

property name

All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.interaction.**Process**(***kwargs*)

Bases: *Entity*

BioPAX Process.

property name

All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.interaction.**TemplateReaction**(*template=None*, *product=None*, *template_direction=None*, ***kwargs*)

Bases: *Interaction*

BioPAX TemplateReaction.

template

Type
NucleicAcid

product

Type
List[*PhysicalEntity*]

template_direction

Type
str

property name
All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.interaction.**TemplateReactionRegulation**(*control_type=None*, *controller=None*, *controlled=None*, ***kwargs*)

Bases: *Control*

BioPAX TemplateReactionRegulation.

property name
All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.interaction.**Transport**(*left=None*, *right=None*, *conversion_direction=None*, *participant_stoichiometry=None*, *spontaneous=None*, ***kwargs*)

Bases: *Conversion*

BioPAX Transport.

property name
All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.interaction.**TransportWithBiochemicalReaction**(*delta_s=None*, *delta_h=None*, *delta_g=None*, *k_e_q=None*, *e_c_number=None*, ***kwargs*)

Bases: *BiochemicalReaction*

BioPAX TransportWithBiochemicalReaction.

property name
All names associated with the object including the standard and display name, if available.

2.3 Physical entities

class pybiopax.biopax.physical_entity.**Complex**(*component=None*, *component_stoichiometry=None*, ***kwargs*)

Bases: *PhysicalEntity*

BioPAX Complex.

component

Type
List[*PhysicalEntity*]

component_stoichiometry

Type
List[*Stoichiometry*]

property name

All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.physical_entity.**Dna**(*entity_reference=None*, ***kwargs*)

Bases: *SimplePhysicalEntity*

BioPAX Dna.

property name

All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.physical_entity.**DnaRegion**(*entity_reference=None*, ***kwargs*)

Bases: *SimplePhysicalEntity*

BioPAX DnaRegion

property name

All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.physical_entity.**PhysicalEntity**(*feature=None*, *not_feature=None*, *member_physical_entity=None*, *cellular_location=None*, ***kwargs*)

Bases: *Entity*, *Controller*

BioPAX PhysicalEntity.

feature

Type
List[*EntityFeature*]

not_feature

Type
List[*EntityFeature*]

member_physical_entity

Type
List[*PhysicalEntity*]

cellular_location

Type
CellularLocationVocabulary

property name
All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.physical_entity.**Protein**(*entity_reference=None*, ***kwargs*)
Bases: *SimplePhysicalEntity*

BioPAX Protein.

property name
All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.physical_entity.**Rna**(*entity_reference=None*, ***kwargs*)
Bases: *SimplePhysicalEntity*

BioPAX Rna.

property name
All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.physical_entity.**RnaRegion**(*entity_reference=None*, ***kwargs*)
Bases: *SimplePhysicalEntity*

BioPAX RnaRegion

property name
All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.physical_entity.**SimplePhysicalEntity**(*entity_reference=None*, ***kwargs*)
Bases: *PhysicalEntity*

BioPAX SimplePhysicalEntity.

entity_reference

Type
EntityReference

property name
All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.physical_entity.**SmallMolecule**(*entity_reference=None*, ***kwargs*)
Bases: *SimplePhysicalEntity*

BioPAX SmallMolecule.

property name
All names associated with the object including the standard and display name, if available.

2.4 Utility classes

class pybiopax.biopax.util.**BindingFeature**(*binds_to=None*, *intra_molecular=None*, ***kwargs*)

Bases: *EntityFeature*

BioPAX BindingFeature.

binds_to

Type
BindingFeature

intra_molecular

Type
bool

class pybiopax.biopax.util.**BioSource**(*cell_type=None*, *tissue=None*, *taxon_xref=None*, ***kwargs*)

Bases: *UtilityClass*, *Named*

BioPAX BioSource.

cell_type

Type
CellVocabulary

tissue

Type
TissueVocabulary

property name

All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.util.**BiochemicalPathwayStep**(*step_conversion=None*, *step_direction=None*, ***kwargs*)

Bases: *PathwayStep*

BioPAX BiochemicalPathwayStep.

step_conversion

Type
Conversion

step_direction

Type
str

class pybiopax.biopax.util.**CellVocabulary**(*term=None*, ***kwargs*)

Bases: *ControlledVocabulary*

BioPAX CellVocabulary.

class pybiopax.biopax.util.**CellularLocationVocabulary**(*term=None*, ***kwargs*)

Bases: *ControlledVocabulary*

BioPAX CellularLocationVocabulary.

class pybiopax.biopax.util.**ChemicalConstant**(*ionic_strength=None*, *ph=None*, *p_mg=None*, *tempterature=None*, ***kwargs*)

Bases: *UtilityClass*

BioPAX ChemicalConstant.

ionic_strength

Type
float

ph

Type
float

p_mg

Type
float

temperature

Type
float

class pybiopax.biopax.util.**ChemicalStructure**(*structure_format=None*, *structure_data=None*, ***kwargs*)

Bases: *UtilityClass*

BioPAX ChemicalStructure.

structure_format

Type
str

structure_data

Type
str

class pybiopax.biopax.util.**ControlledVocabulary**(*term=None*, ***kwargs*)

Bases: *UtilityClass*, *XReferrable*

BioPAX ControlledVocabulary.

term

Type
List[str]

class pybiopax.biopax.util.**DeltaG**(*delta_g_prime0=None*, ***kwargs*)

Bases: *ChemicalConstant*

BioPAX DeltaG.

delta_g_prime

Type
float

class pybiopax.biopax.util.**DnaReference**(*sub_region=None*, ***kwargs*)

Bases: *NucleicAcidReference*

BioPAX DnaReference.

property name

All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.util.**DnaRegionReference**(*absolute_region=None*, *region_type=None*, ***kwargs*)

Bases: *NucleicAcidRegionReference*

BioPAX DnaRegionReference.

property name

All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.util.**EntityFeature**(*owner_entity_reference=None*, *feature_location=None*, *member_feature=None*, *feature_location_type=None*, ***kwargs*)

Bases: *UtilityClass*, *Observable*

BioPAX UtilityClass.

owner_entity_reference

Type
EntityReference

feature_location

Type
SequenceLocation

member_feature

Type
List[*EntityFeature*]

feature_location_type

Type
SequenceRegionVocabulary

class pybiopax.biopax.util.**EntityReference**(*entity_feature=None*, *entity_reference_type=None*, *member_entity_reference=None*, *owner_entity_reference=None*, ***kwargs*)

Bases: *UtilityClass*, *Named*, *Observable*

BioPAX EntityReference.

entity_feature

Type
List[*EntityFeature*]

entity_reference_type

Type
List[*EntityReferenceTypeVocabulary*]

member_entity_reference

Type
List[*EntityReference*]

owner_entity_reference

Type
List[*EntityReference*]

property name

All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.util.**EntityReferenceTypeVocabulary**(*term=None*, ***kwargs*)

Bases: *ControlledVocabulary*

BioPAX EntityReferenceTypeVocabulary.

class pybiopax.biopax.util.**Evidence**(*confidence=None*, *evidence_code=None*, *experimental_form=None*, ***kwargs*)

Bases: *UtilityClass*, *XReferrable*

BioPAX Evidence.

confidence

Type
List[*Score*]

evidence_code

Type
List[*EvidenceCodeVocabulary*]

experimental_form

Type
List[*ExperimentalForm*]

class pybiopax.biopax.util.**EvidenceCodeVocabulary**(*term=None*, ***kwargs*)

Bases: *ControlledVocabulary*

BioPAX EvidenceCodeVocabulary.

class pybiopax.biopax.util.**ExperimentalForm**(*experimental_form_entity=None*, *experimental_form_description=None*, *experimental_feature=None*, ***kwargs*)

Bases: *UtilityClass*

BioPAX ExperimentalForm.

experimental_form_entity

Type
Entity

experimental_form_description

Type
List[*ExperimentalFormVocabulary*]

experimental_feature

Type
List[*EntityFeature*]

class pybiopax.biopax.util.**ExperimentalFormVocabulary**(*term=None*, ***kwargs*)

Bases: *ControlledVocabulary*

BioPAX ExperimentalFormVocabulary.

class pybiopax.biopax.util.**FragmentFeature**(*owner_entity_reference=None*, *feature_location=None*, *member_feature=None*, *feature_location_type=None*, ***kwargs*)

Bases: *EntityFeature*

BioPAX FragmentFeature.

class pybiopax.biopax.util.**InteractionVocabulary**(*term=None*, ***kwargs*)

Bases: *ControlledVocabulary*

BioPAX InteractionVocabulary.

class pybiopax.biopax.util.**KPrime**(*k_prime*, ***kwargs*)

Bases: *ChemicalConstant*

BioPAX KPrime.

k_prime

Type
float

class pybiopax.biopax.util.**ModificationFeature**(*modification_type=None*, ***kwargs*)

Bases: *EntityFeature*

BioPAX ModificationFeature.

modification_type

Type
SequenceModificationVocabulary

class pybiopax.biopax.util.**NucleicAcidReference**(*sub_region=None*, ***kwargs*)

Bases: *SequenceEntityReference*

BioPAX NucleicAcidReference

sub_region

Type
List[*NucleicAcidRegionReference*]

property name

All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.util.**NucleicAcidRegionReference**(*absolute_region=None*, *region_type=None*, ***kwargs*)

Bases: *NucleicAcidReference*

BioPAX NucleicAcidRegionReference

absolute_region

Type
SequenceLocation

region_type

Type
List[*SequenceRegionVocabulary*]

property name
All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.util.**PathwayStep**(*step_process=None*, *next_step=None*, ***kwargs*)

Bases: *UtilityClass*, *Observable*

BioPAX PathwayStep.

step_process

Type
List[*Process*]

next_step

Type
List[*Process*]

class pybiopax.biopax.util.**PhenotypeVocabulary**(*term=None*, ***kwargs*)

Bases: *ControlledVocabulary*

BioPAX PhenotypeVocabulary.

class pybiopax.biopax.util.**ProteinReference**(*organism=None*, *sequence=None*, ***kwargs*)

Bases: *SequenceEntityReference*

BioPAX ProteinReference.

property name
All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.util.**Provenance**(***kwargs*)

Bases: *UtilityClass*, *Named*

BioPAX Provenance.

property name
All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.util.**PublicationXref**(*title=None*, *url=None*, *source=None*, *author=None*, *year=None*, ***kwargs*)

Bases: *Xref*

BioPAX PublicationXref.

title

Type
str

url

Type
List[str]

source

Type
List[str]

author

Type
List[str]

year

Type
int

class pybiopax.biopax.util.**RelationshipTypeVocabulary**(*term=None*, ***kwargs*)

Bases: *ControlledVocabulary*

BioPAX RelationshipTypeVocabulary.

class pybiopax.biopax.util.**RelationshipXref**(*relationship_type=None*, ***kwargs*)

Bases: *Xref*

BioPAX RelationshipXref.

relationship_type

Type
RelationshipTypeVocabulary

class pybiopax.biopax.util.**RnaReference**(*sub_region=None*, ***kwargs*)

Bases: *NucleicAcidReference*

BioPAX RnaReference.

property name

All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.util.**RnaRegionReference**(*absolute_region=None*, *region_type=None*, ***kwargs*)

Bases: *NucleicAcidRegionReference*

BioPAX RnaRegionReference.

property name

All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.util.**Score**(*score_source=None*, *value=None*, ***kwargs*)

Bases: *UtilityClass*, *XReferrable*

BioPAX Score.

score_source

Type
Provenance

value

Type
str

class pybiopax.biopax.util.**SequenceEntityReference**(*organism=None*, *sequence=None*, ***kwargs*)

Bases: *EntityReference*

BioPAX SequenceEntityReference.

organism

Type
BioSource

sequence

Type
str

property name

All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.util.**SequenceInterval**(*sequence_interval_begin=None*, *sequence_interval_end=None*, ***kwargs*)

Bases: *SequenceLocation*

BioPAX SequenceInterval.

sequence_interval_begin

Type
SequenceSite

sequence_interval_end

Type
SequenceSite

class pybiopax.biopax.util.**SequenceLocation**(*region_type=None*, ***kwargs*)

Bases: *UtilityClass*

BioPAX SequenceLocation.

region_type

Type
List[*SequenceRegionVocabulary*]

class pybiopax.biopax.util.**SequenceModificationVocabulary**(*term=None*, ***kwargs*)

Bases: *ControlledVocabulary*

BioPAX SequenceModificationVocabulary.

class pybiopax.biopax.util.**SequenceRegionVocabulary**(*term=None*, ***kwargs*)

Bases: *ControlledVocabulary*

BioPAX SequenceRegionVocabulary.

class pybiopax.biopax.util.**SequenceSite**(*position_status=None*, *sequence_position=None*, ***kwargs*)

Bases: *SequenceLocation*

BioPAX SequenceSite.

position_status

Type
str

sequence_position

Type
int

class pybiopax.biopax.util.**SmallMoleculeReference**(*structure=None*, *chemical_formula=None*, *molecular_weight=None*, ***kwargs*)

Bases: *EntityReference*

BioPAX SmallMoleculeReference.

structure

Type
ChemicalStructure

chemical_formula

Type
str

molecular_weight

Type
float

property name

All names associated with the object including the standard and display name, if available.

class pybiopax.biopax.util.**Stoichiometry**(*stoichiometric_coefficient=None*, *physical_entity=None*, ***kwargs*)

Bases: *UtilityClass*

BioPAX Stoichiometry.

stoichiometric_coefficient

Type
float

physical_entity

Type
PhysicalEntity

class pybiopax.biopax.util.**TissueVocabulary**(*term=None*, ***kwargs*)

Bases: *ControlledVocabulary*

BioPAX TissueVocabulary.

class pybiopax.biopax.util.**UnificationXref**(*db=None*, *id=None*, *db_version=None*, *id_version=None*, ***kwargs*)

Bases: *Xref*

BioPAX UnificationXref.

class pybiopax.biopax.util.**UtilityClass**(*uid*, *comment=None*, ***kwargs*)

Bases: *BioPaxObject*

BioPAX UtilityClass.

class pybiopax.biopax.util.**Xref**(*db=None*, *id=None*, *db_version=None*, *id_version=None*, ***kwargs*)

Bases: *UtilityClass*

BioPAX Xref.

db

Type
str

id

Type
str

db_version

Type
str

id_version

Type
str

CHAPTER

THREE

PATHWAY COMMONS CLIENT

A client to the PathwayCommons REST API. For more details about the service, see the documentation at https://www.pathwaycommons.org/pc2/.

pybiopax.pc_client.**graph_query**(*kind*, *source*, *target=None*, ***query_params*)

Perform a graph query on PathwayCommons.

For more information on these queries, see http://www.pathwaycommons.org/pc2/#graph

Parameters

- **kind** (*str*) – The kind of graph query to perform. Currently 3 options are implemented, 'neighborhood', 'pathsbetween' and 'pathsfromto'.
- **source** (*list[str]*) – A single gene name or a list of gene names which are the source set for the graph query.
- **target** (*Optional[list[str]]*) – A single gene name or a list of gene names which are the target set for the graph query. Only needed for 'pathsfromto' queries.
- **limit** (*Optional[int]*) – This limits the length of the longest path considered in the graph query. Default: 1
- **organism** (*Optional[str]*) – The organism used for the query. Default: '9606' corresponding to human.
- **datasource** (*Optional[list[str]]*) – A list of database sources that the query results should include. Example: ['pid', 'panther']. By default, all databases are considered.

Returns

A BioPAX OWL string that can then be deserialized into a BioPaxModel.

Return type

str

CHAPTER

FOUR

PATH FINDING

This module implements finding paths in a BioPaxModel starting from a given object using a path constraint string.

exception pybiopax.paths.**BiopaxClassConstraintError**(*cls_str*)

Bases: KeyError

pybiopax.paths.**find_objects**(*start_obj*, *path_str*)

Return objects matching the given path specification.

Parameters

- **start_obj** (*BioPaxObject*) – The object to start the search from.
- **path_str** (str) – A path specification string which consists of one or more parts separated by /. Each part is the name of an object attribute, and can optionally contain a class name as well, separated by : to constrain the class of the target of the attribute to consider. Optionally, each attribute can also have a * suffix to make the search recursive.

Return type

List[*BioPaxObject*]

Returns

A list of BioPaxObjects satisfying the given path specification.

CHAPTER

FIVE

XML/OWL PROCESSING UTILITIES

pybiopax.xml_util.**camel_to_snake**(*txt*)

Return snake case from camel case

pybiopax.xml_util.**get_attr_tag**(*element*)

Return the tag of an element as an attribute name.

pybiopax.xml_util.**get_datatype**(*attrib*)

Return the RDF data type of an element attribute.

pybiopax.xml_util.**get_id_or_about**(*element*)

Return the ID or the about associated with an element

pybiopax.xml_util.**get_ns**(*element*)

Return the name space of a given element.

pybiopax.xml_util.**get_resource**(*attrib*)

Return the resource associated with an element attribute.

pybiopax.xml_util.**get_tag**(*element*)

Return the tag of an element.

pybiopax.xml_util.**has_ns**(*element*, *ns*)

Return True if the element is from a given name space.

pybiopax.xml_util.**is_datatype**(*attrib*, *prefix*, *datatype*)

Return True of the given attribute is of a given type.

pybiopax.xml_util.**is_url**(*txt*)

Return true if the given string is an URL.

pybiopax.xml_util.**nselem**(*ns*, *elem*)

Return a full namespaced string with curly brackets with a suffix.

pybiopax.xml_util.**nssuffix**(*ns*, *suffix*)

Return a full namespaced string with a suffix.

pybiopax.xml_util.**snake_to_camel**(*txt*)

Return camel case from snake case.

pybiopax.xml_util.**wrap_xml_elements**(*elements*, *xml_base*)

Return a valid BioPAX OWL wrapping XML-serialized BioPAX objects.

pybiopax.xml_util.**xml_to_file**(*xml*, *fname*)

Write an XML element tree to a given file.

pybiopax.xml_util.**xml_to_str**(*xml*)

Return the OWL string for an XML element tree.

- genindex
- modindex

PYTHON MODULE INDEX

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