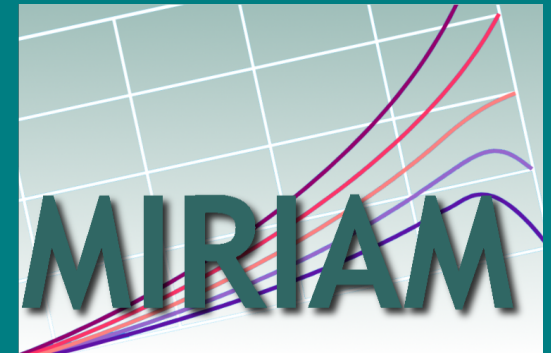


Identifiers.org and MIRIAM Registry: perennial identifiers for cross-referencing

Nick Juty

BioModels.net



Intro

URIs (Uniform Resource Identifiers)...

MIRIAM Registry (namespaces)

usage

Identifiers.org resolving service

levels of identification

customisation

usage



Intro

URIs (Uniform Resource Identifiers)...

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Identifiers.org resolving service

levels of identification

customisation

usage

CONTRIBUTE

USE





Computational Biology

need to specify **model components**

understanding data

reusing data

comparing data

integrating data

converting data

linking data

with **annotations** - identifiers/xref

- need for xrefs true of any kind of data



9606

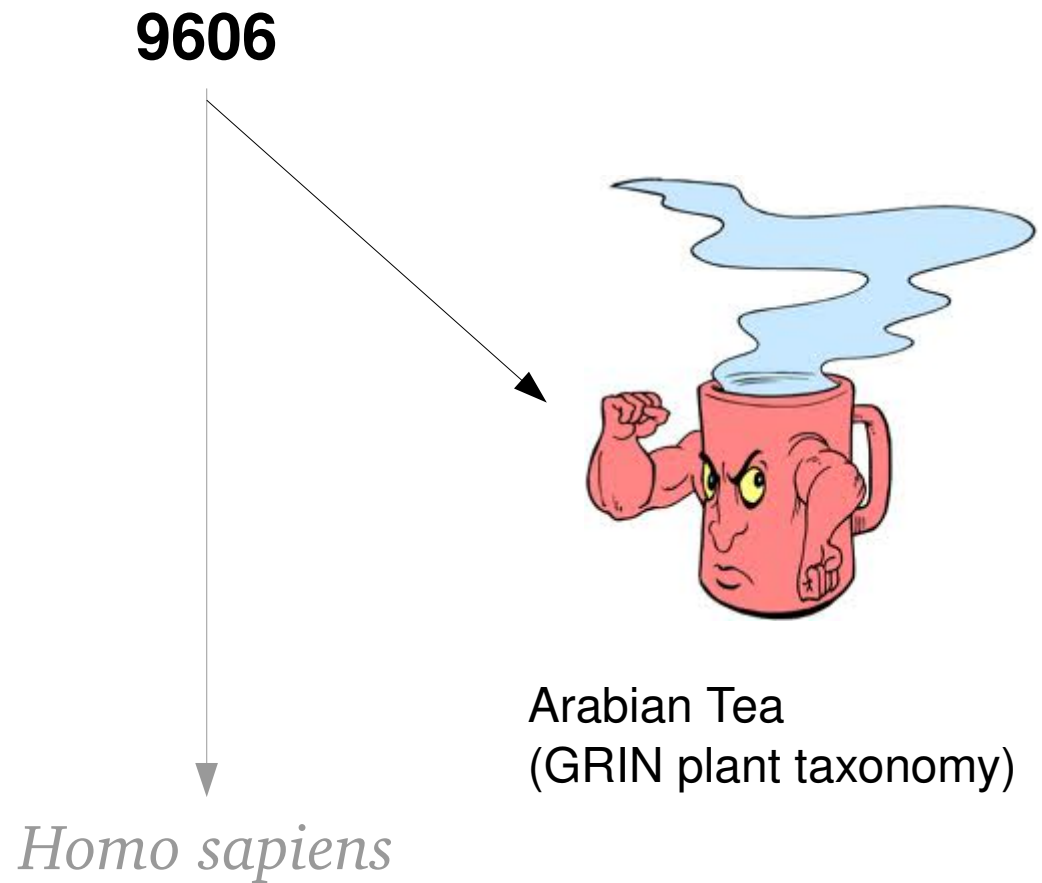


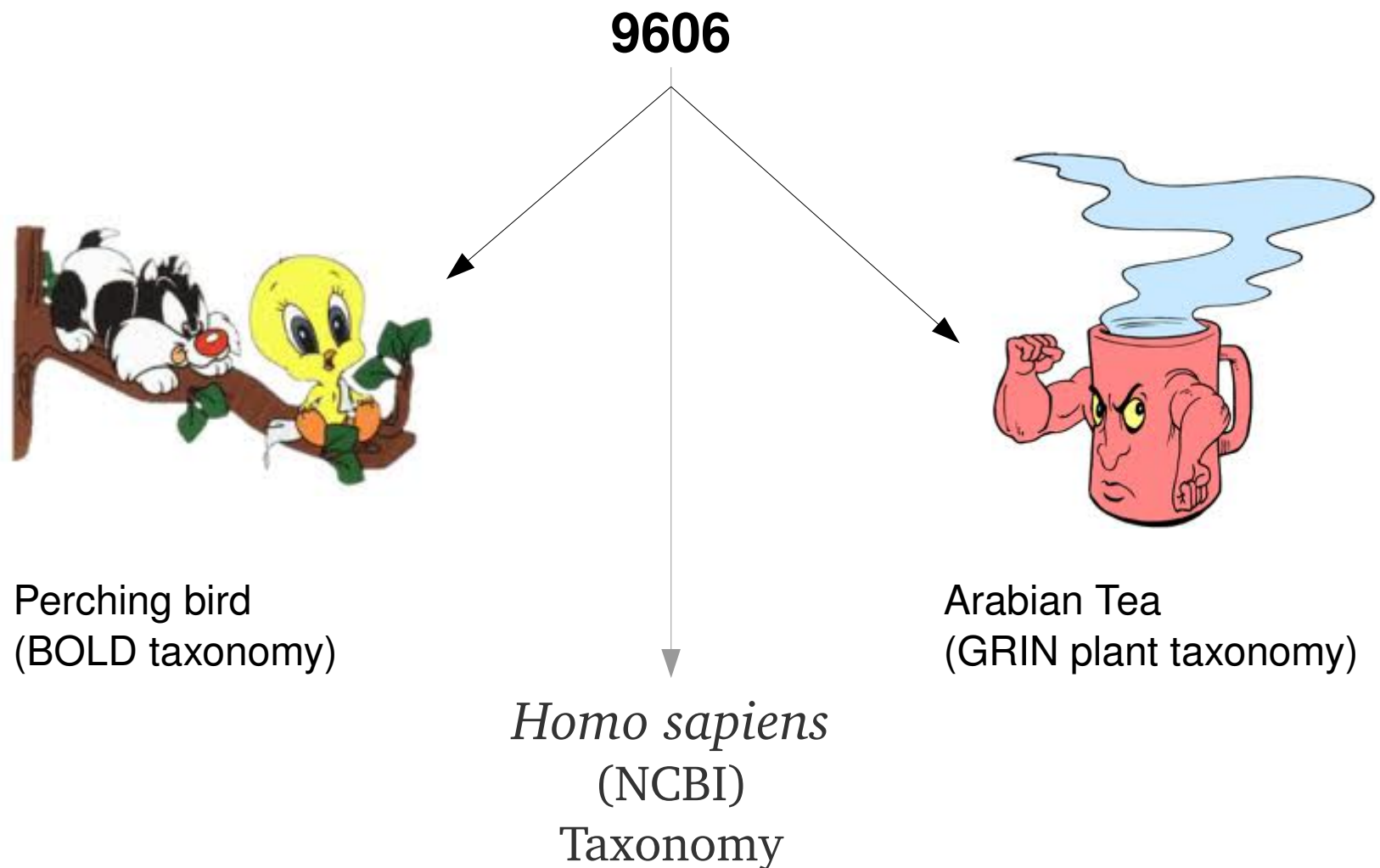
9606



Homo sapiens







Building Cross-references/identifiers

namespace – shared list (Registry)

data-set identifier – provided by collection

URI identifiers

URN	location independent	(not directly resolvable)
-----	----------------------	---------------------------



Building Cross-references/identifiers

namespace – shared list (Registry)

data-set identifier – provided by collection

URI identifiers

URN urn:miriam:**ABC**:**12345**



Building Cross-references/identifiers

namespace – shared list (Registry)

data-set identifier – provided by collection

URI identifiers

URN urn:miriam:**ABC**:**12345**

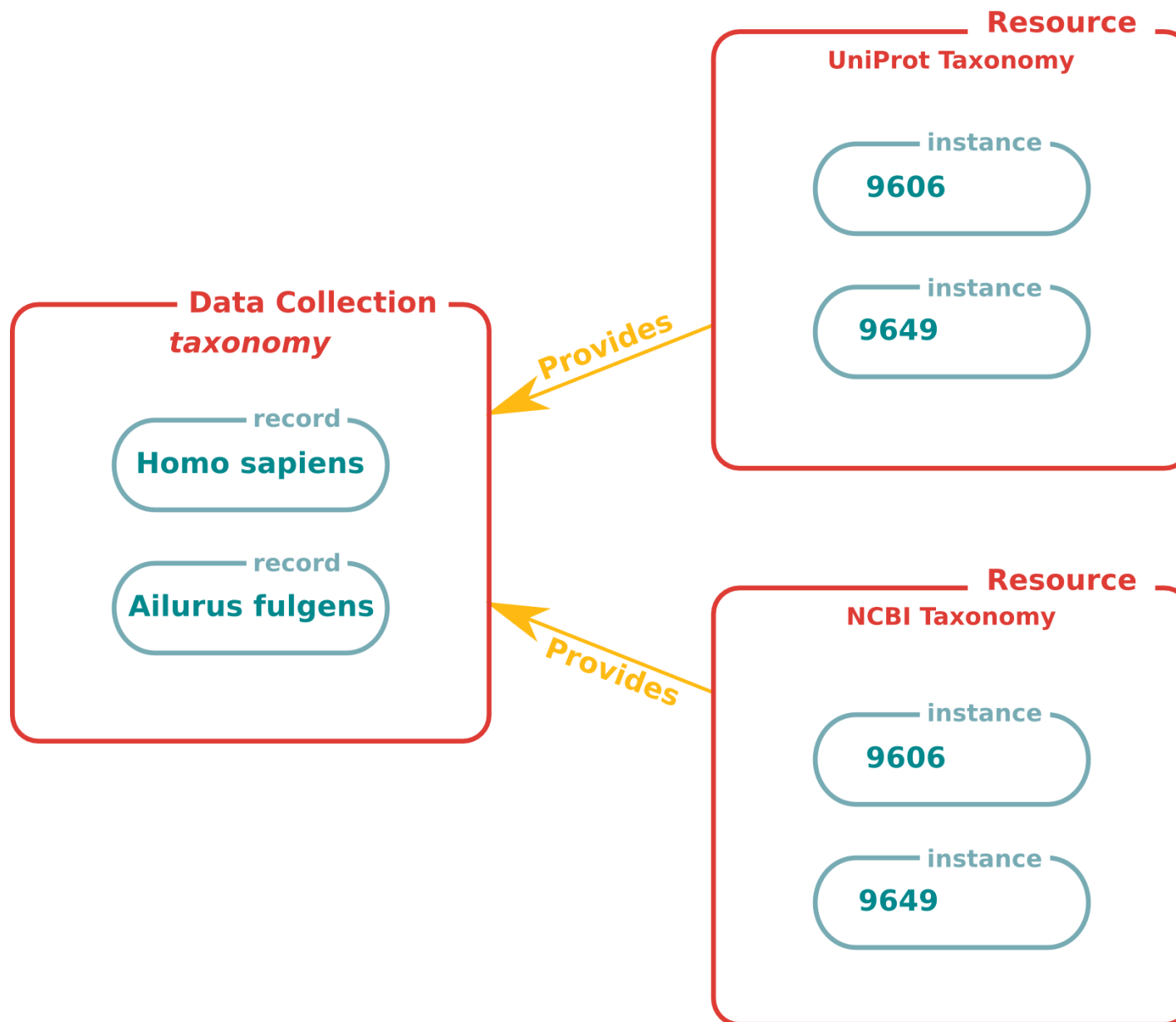
Identifiers.org: <http://identifiers.org/ABC/12345>


avoid URL fragility



convenience of resolvability


Created as a layer above the Registry







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 - [Guidelines](#) 
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 - [Documentation](#)
 - [Who's using MIRIAM?](#)
 - [Identification systems](#)
 - [News](#) 
 - [BioModels.net](#)
 - [Qualifiers](#)


- [MIRIAM on](#)

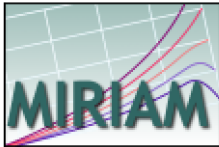
EBI > [Groups](#) > [Computational Neurobiology](#) > [Research](#) > [MIRIAM Registry](#)

MIRIAM Registry

MIRIAM Registry are a set of online services created in support of [MIRIAM](#), a set of guidelines for the annotation and curation of computational models.

The core of *MIRIAM Registry* is a catalogue of data types (namespaces corresponding to controlled vocabularies or databases), their URLs and the corresponding physical URLs or resources. Access to this data is made available via exports (XML) and Web Services (SOAP).


MIRIAM Registry is developed and maintained under the [BioModels.net](#)  initiative, and are free for use by all.



Quick links

<h4>Browse</h4> <ul style="list-style-type: none">by data type nameby tags	<h4>Web Services</h4> <ul style="list-style-type: none">services availableusage of the servicesonline demonstration
<h4>Search</h4> <ul style="list-style-type: none">generic search	<h4>Exports</h4> <ul style="list-style-type: none">XML

<http://www.ebi.ac.uk/miriam/>



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Name	Namespace	Definition
Protein Model Database	pmdb	The Protein Model DataBase (PMDb), is a database that collects manually built three dimensional protein models, obtained by different structure prediction techniques.
MIRIAM Registry collection	miriam.collection	MIRIAM Registry is an online resource created to catalogue collections (Gene Ontology, Taxonomy or PubMed are some examples), their URIs and the corresponding resources (physical locations), whether these are controlled vocabularies or databases.
TEDDY	biomodels.teddy	The Terminology for Description of Dynamics (TEDDY) is an ontology for dynamical behaviours, observable dynamical phenomena, and control elements of bio-models and biological systems in Systems Biology and Synthetic Biology.
UniProt	uniprot	UniProt (Universal Protein Resource) is the world's most comprehensive catalog of information on proteins. It is a central repository of protein sequence and function created by joining the information contained in Swiss-Prot, TrEMBL, and PIR.
PubChem-substance	pubchem.substance	PubChem provides information on the biological activities of small molecules. It is a component of NIH's Molecular Libraries Roadmap Initiative. PubChem Substance archives chemical substance records.
EDAM Ontology	edam	EDAM is an ontology of general bioinformatics concepts, including topics, data types, formats, identifiers and operations. EDAM provides a controlled vocabulary for the description, in semantic terms, of things such as: web services (e.g. WSDL files), applications, tool collections and packages, work-benches and workflow software, databases and ontologies, XSD data schema and data objects, data syntax and file formats, web portals and pages, resource catalogues and documents (such as scientific publications).
Ontology for Biomedical Investigations	obo.obo	The Ontology for Biomedical Investigations (OBI) project is developing an integrated ontology for the description of biological and clinical investigations. The ontology will represent the design of an investigation, the protocols and instrumentation used, the material used, the data generated and the type analysis performed on it. Currently OBI is being built under the Basic Formal Ontology (BFO).
MACiE	macie	MACiE (Mechanism, Annotation and Classification in Enzymes) is a database of enzyme reaction mechanisms. Each entry in MACiE consists of an overall reaction describing the chemical compounds involved, as well as the species name in which the reaction occurs. The individual reaction stages for each overall reaction are listed with mechanisms, alternative mechanisms, and amino acids involved.
FMA	obo.fma	The Foundational Model of Anatomy Ontology (FMA) is a biomedical informatics ontology. It is concerned with the representation of classes or types and relationships necessary for the symbolic representation of the anatomical structure of the human body. Specifically, the FMA is a domain ontology that represents a coherent



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TEDDY	biomodels.teddy	The Terminology for Description of Dynamics (TEDDY) is an ontology for dynamical behaviours, observable dynamical phenomena, and control elements of bio-models and biological systems in Systems Biology and Synthetic Biology.
UniProt	uniprot	UniProt (Universal Protein Resource) is the world's most comprehensive catalog of information on proteins. It is a central repository of protein sequence and function created by joining the information contained in Swiss-Prot, TrEMBL, and PIR.
PubChem-substance	pubchem.substance	PubChem provides information on the biological activities of small molecules. It is a component of NIH's Molecular Libraries Roadmap Initiative. PubChem Substance archives chemical substance records.
EDAM Ontology	edam	EDAM is an ontology of general bioinformatics concepts, including topics, data types, formats, identifiers and operations. EDAM provides a controlled vocabulary for the description, in semantic terms, of things such as: web services (e.g. WSDL files), applications, tool collections and packages, work-benches and workflow software, databases and ontologies, XSD data schema and data objects, data syntax and file formats, web portals and pages, resource catalogues and documents (such as scientific publications).
Ontology for Biomedical Investigations	obo.obo	The Ontology for Biomedical Investigations (OBI) project is developing an integrated ontology for the description of biological and clinical investigations. The ontology will represent the design of an investigation, the protocols and instrumentation used, the material used, the data generated and the type analysis performed on it. Currently OBI is being built under the Basic Formal Ontology (BFO).
MACiE	macie	MACiE (Mechanism, Annotation and Classification in Enzymes) is a database of enzyme reaction mechanisms. Each entry in MACiE consists of an overall reaction describing the chemical compounds involved, as well as the species name in which the reaction occurs. The individual reaction stages for each overall reaction are listed with mechanisms, alternative mechanisms, and amino acids involved.
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Overview

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Overview

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Resources



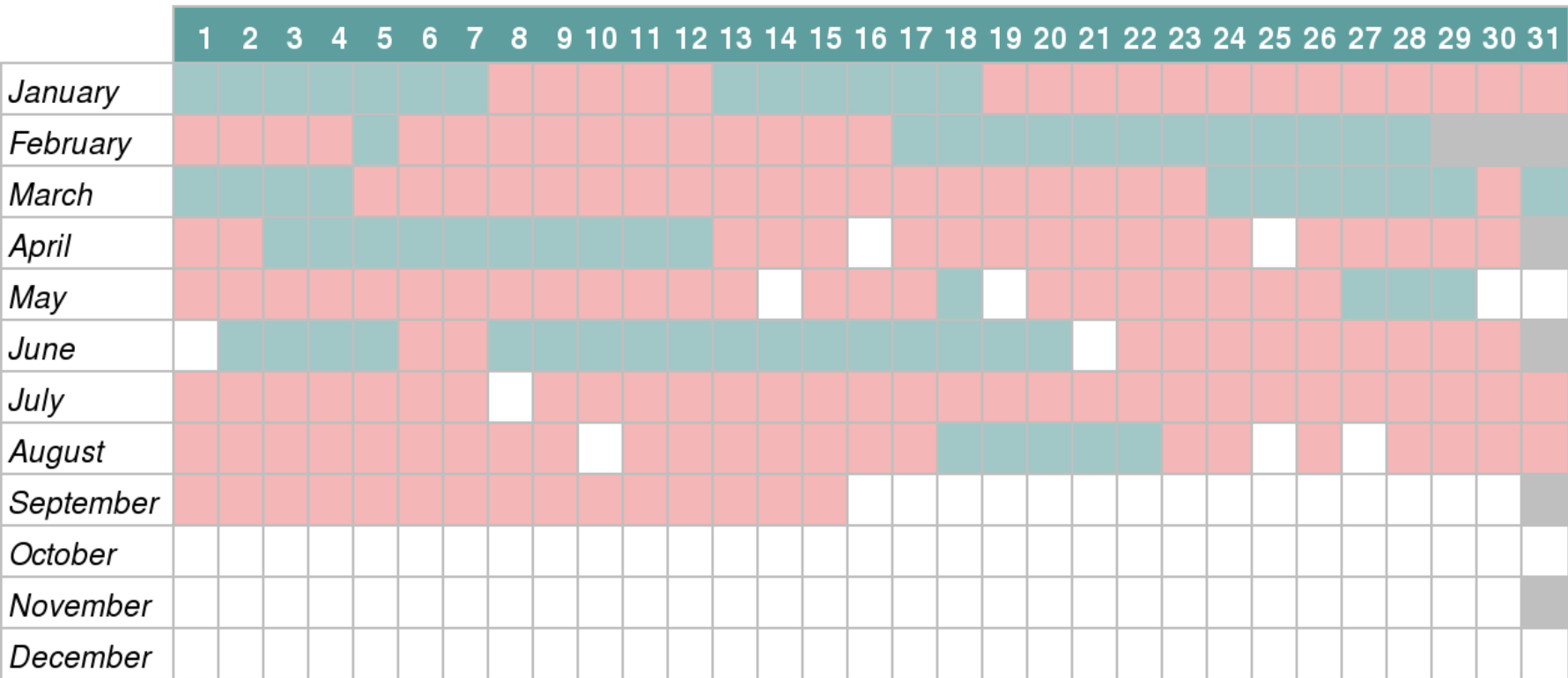
Physical Locations		
<u>Resource</u> MIR:00100308	Access URL	http://www.enzyme-database.org/query.php?ec=\$id [Example: 1.1.1.1 
	Website	http://www.enzyme-database.org/
	Description	ExploreEnz at Trinity College
	Institution	Trinity College, Dublin, Ireland
<u>Resource</u> MIR:00100002	Access URL	http://www.genome.jp/dbget-bin/www_bget?ec:\$id [Example: 1.1.1.1 
	Website	http://www.genome.jp/dbget-bin/www_bfind?enzyme
	Description	KEGG Ligand Database for Enzyme Nomenclature
	Institution	Kyoto University Bioinformatics Center, Japan
<u>Resource</u> MIR:00100001	Access URL	http://www.ebi.ac.uk/intenz/query?cmd=SearchEC&ec=\$id [Example: 1.1.1.1 
	Website	http://www.ebi.ac.uk/intenz/
	Description	IntEnZ (Integrated relational Enzyme database)
	Institution	European Bioinformatics Institute, United Kingdom
<u>Resource</u> MIR:00100003	Access URL	http://enzyme.expasy.org/EC/\$id [Example: 1.1.1.1 
	Website	http://enzyme.expasy.org/
	Description	Enzyme nomenclature database, ExPASy (Expert Protein Analysis System)
	Institution	Swiss Institute of Bioinformatics, Switzerland



Health history: MIR: [REDACTED]

Health history of: MIR: [REDACTED]

2010




2009



Resource: MIR:00100050

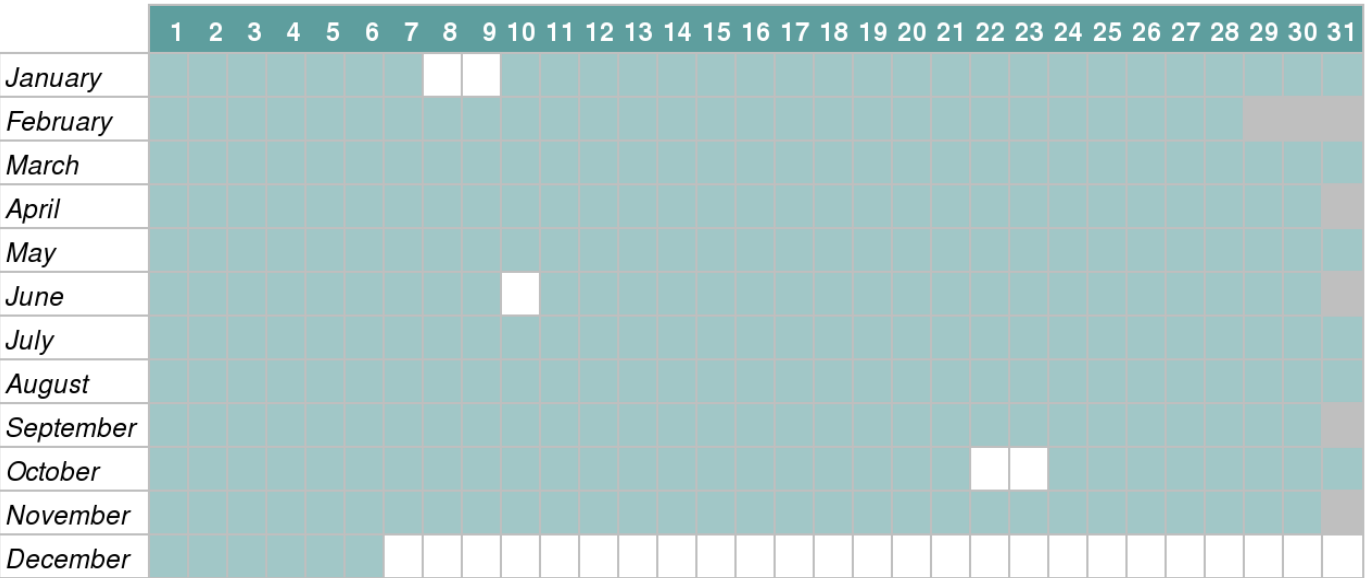
General information about the resource: *The FlyBase Database* (associated with the data collection: [FlyBase](#)).

Health statistics	
Last known state	up
Last check	2011-12-06 06:33:22
Uptime ratio	100% (1012 checks)
Downtime ratio	0% (0 checks)
Unknown ratio	0% (0 checks)
URL used	http://www.flybase.org/reports/FBgn0011293.html 

Health history

Full record of the health checks performed on this resource.

2011



Submit a new data collection

Please fill this form in order to submit a new data type to MIRIAM Registry. Alternatively, you can [contact us](#) with your query.

You **do not** need to fill all the fields, you can just enter the information you have.

The new data type will not be directly publicly available after you pressed the **Submit** button. A curator will first check if it complies with the terms and conditions of MIRIAM Registry and, if necessary, correct and complete it before publishing it.

Help

You can display all help bubbles by clicking on: [Displays all the help messages](#), or hide them: [Hides all the help messages](#).

Moreover, you can display the individual help by clicking on the button:  located in the title of each section.

Information about the new data type

First you need to enter the name of the data type you want to add to the database. After you can add as much synonyms as you want.

Name and synonyms

Primary name:

[\[Add a synonym\]](#)

Here is some information about the data type: definition and regular expression (*i.e.* pattern for identifiers of elements, following the PERL style).

Definition and pattern

Definition:

Enter definition here...

Identifier pattern:

Enter Identifier pattern here...



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Here is some information about the data type: definition and regular expression (*i.e.* pattern for identifiers of elements, following the PERL style).

Definition and pattern 

Definition:

Enter definition here...

Identifier pattern:

Enter Identifier pattern here...



Overview

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Overview of the data collection

Name	
Identifier	MIR:00000004
Name	Enzyme Nomenclature
Synonyms	Enzyme Classification
	EC code
	EC
Information	
Definition	The Enzyme Classification contains the recommendations of the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology on the nomenclature and classification of enzyme-catalysed reactions.
Identifier pattern	
Namespace	
Root URL	
Root URN	



Suggest modifications to this data collection

Physical Locations		
Resource MIR:00100002	Access URL	http://www.genome.jp/dbget-bin/www_bget?ec:\$id [Example: 1.1.1.1]
	Website	http://www.genome.jp/dbget-bin/www_bfind?enzyme
	Description	KEGG Ligand Database for Enzyme Nomenclature
	Institution	Kyoto University Bioinformatics Center, Japan
Resource MIR:00100003	Access URL	http://enzyme.expasy.org/EC/\$id [Example: 1.1.1.1]
	Website	http://enzyme.expasy.org/
	Description	Enzyme nomenclature database, ExPASy (Expert Protein Analysis System)
	Institution	Swiss Institute of Bioinformatics, Switzerland
Resource MIR:00100001	Access URL	http://www.ebi.ac.uk/intenz/query?cmd=SearchEC&ec=\$id [Example: 1.1.1.1]
	Website	http://www.ebi.ac.uk/intenz/
	Description	IntEnZ (Integrated relational Enzyme database)
	Institution	European Bioinformatics Institute, United Kingdom
References		
http://www.chem.qmul.ac.uk/iubmb/enzyme/		
+ http://srs.ebi.ac.uk/srsbin/cgi-bin/wgetz?-view+MedlineFull+[medline-PMID:10812475]		

[Go back to the list of data collections](#)

[Suggest modifications to this data collection](#)


list of **data collections**

web services and **XML export** available

community driven (everybody can submit new data collections or suggest modification of existing records)

curated resource

systems in place to **monitor** registered web resources

unrestricted scope (currently mainly focused on Life Sciences, but the scope is potentially unlimited)

free to use



Welcome to Identifiers.org!

Identifiers.org is a system providing resolvable persistent URIs used to identify data for the scientific community, with a current focus on the Life Sciences domain. The provision of a resolvable identifiers (URLs) fits well with the [Semantic Web](#) vision, and the [Linked Data](#) initiative.

For further information, please refer to the following publication: [Identifiers.org and MIRIAM Registry: community resources to provide persistent identification](#).

Links

- [About](#)
- [News](#)
- [Help](#)
- [Examples URIs](#)
- [MIRIAM Registry](#)

http://identifiers.org/

Board of trustees

Identifiers.org is a community project which activities are overseen by the following board of trustees:

- [Michel Dumontier](#) (Carleton University, Ottawa, Canada - [Bio2RDF](#), [W3C HCLS](#))
- [Michael Galperin](#) (NCBI, USA - [NAR Database issue](#))
- [Pascale Gaudet](#) (Swiss Institute of Bioinformatics, Geneva, Switzerland - [BioDBCore](#))
- [Lee Harland](#) (Connected Discovery, UK - [Open PHACTS](#))
- [Michael Hucka](#) (California Institute of Technology, Pasadena, USA - [SBML](#))
- [Toshiaki Katayama](#) (University of Tokyo, Japan - [BioRuby](#), [KEGG](#))
- [Nicolas Le Novère](#) (EMBL-EBI, Hinxton, UK - [BioModels Database](#))
- [Philippe Rocca-Serra](#) (Oxford University, Oxford, UK - [BioSharing](#))
- [Mark Wilkinson](#) (St. Paul's Hospital/UBC Vancouver, Canada - [LSRN](#), [SADI](#))

Contact

If you have any queries or experience any issues with this service, please contact: **biomodels-net-support [AT] lists.sf.net**



Data Collection:

<http://identifiers.org/ec-code/>

Record (location independent):

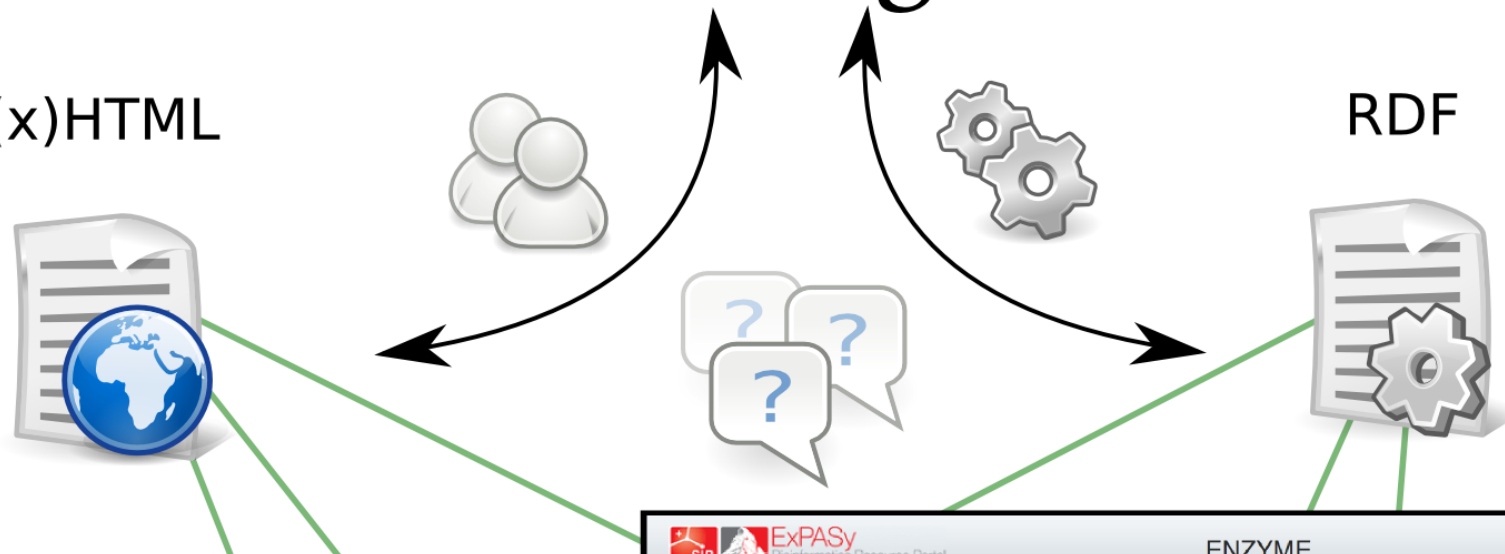
<http://identifiers.org/ec-code/1.1.1.1>



http://identifiers.org/ec-code/1.1.1.1

(x)HTML




RDF



KEGG

ENZYME: 1.1.1.1

Entry	EC 1.1.1.1	Enzyme
Name	alcohol dehydrogenase; aldehyde reductase; ADH; alcohol dehydrogenase (NAD); aliphatic alcohol dehydrogenase; ethanol dehydrogenase; NAD-dependent alcohol dehydrogenase; NAD-specific aromatic alcohol dehydrogenase; NADH-alcohol dehydrogenase; NADH-aldehyde dehydrogenase; primary alcohol dehydrogenase; yeast alcohol dehydrogenase	
Class	Oxidoreductases; Acting on the CH-OH group of donors With NAD+ or NADP+ as acceptor BRITE hierarchy	
Sysname	alcohol:NAD+ oxidoreductase	
Reaction(IUBMB)	(1) a primary alcohol + NAD+ = an aldehyde + NADH + H+ (2) a secondary alcohol + NAD+ = a ketone + NADH + H+	
Reaction(KEGG)	R07326 > R00623 R00624 > R06927 R08281 R08301	

ENZYME



Home | [Contact](#)

ENZYME entry: EC 1.1.1.1

Accepted Name
Alcohol dehydrogenase.
Alternative Name(s)
Aldehyde reductase.
Reaction catalysed
An alcohol + NAD(+) <=> an aldehyde or ketone + NADH

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Site Index  

EBI > Databases > Enzymes > IntEnz

[EC 1 - Oxidoreductases](#)

[EC 1.1 - Acting on the CH-OH Group of Donors](#)

[EC 1.1.1 - With NAD+ or NADP+ as acceptor](#)

[EC 1.1.1.1 - Alcohol dehydrogenase](#)

[IntEnz home](#)

[Advanced search](#)

[Browse EC](#)

[Data submission](#)

[Downloads](#)

[Documentation](#)

IntEnz Enzyme Nomenclature

EC 1.1.1.1



<http://identifiers.org/ec-code/1.1.1.1>

4 physical locations (or resources) are available for accessing *1.1.1.1* (from [Enzyme Nomenclature](#)):

**KEGG Ligand Database for Enzyme
Nomenclature**

Kyoto University Bioinformatics Center

Japan

(Uptime: 100%)

ExploreEnz at Trinity College

Trinity College, Dublin

Ireland

(Uptime: 100%)

**IntEnZ (Integrated relational Enzyme
database)**

European Bioinformatics Institute

United Kingdom

(Uptime: 100%)

**Enzyme nomenclature database, ExPASy
(Expert Protein Analysis System)**

Swiss Institute of Bioinformatics

Switzerland

(Uptime: 99%)



Custom queries + format:

Response format:

<http://identifiers.org/ec-code/1.1.1.1?format=rdfxml>

Specified resource:

<http://identifiers.org/ec-code/1.1.1.1?resource=MIR:00100001>

profiles (predefined resolution locations):

<http://identifiers.org/ec-code/1.1.1.1?profile=demo>



<http://identifiers.org/pubmed/16333295>

<http://identifiers.org/pubmed/16333295>

4 physical locations (or resources) are available for accessing 16333295 (from [PubMed](#)):

HubMed
Alfred D. Eaton
United Kingdom

(Uptime: 96%)

SRS@EBI
European Bioinformatics Institute
United Kingdom

(Uptime: 100%)

NCBI PubMed
National Center for Biotechnology
Information

USA

(Uptime: 100%)

CiteXplore
European Bioinformatics Institute
United Kingdom

(Uptime: 99%)



<http://identifiers.org/pubmed/16333295?resource=MIR:00100032>

<http://identifiers.org/pubmed/16333295>

[Close](#) ✕

Access to 16333295 (from [PubMed](#)) using the resource [MIR:00100032](#).

Entity available from 4 providers, for more information please refer to: <http://identifiers.org/pubmed/16333295>.

Powered by: [Identifiers.org](#) & [MIRIAM Registry](#)



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- E.P.O.
- Citeseer
- Whatizit
- iHOP

CiteXplore - citation details

Sort by: ☐ Publication Date ☐ Most cited ☒ Most relevant ☐ Synonyms

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Bookmark:

Pubmed Id 16333295

Title Minimum information requested in the annotation of biochemical models (MIRIAM).

Authors Le Novère N, Finney A, Hucka M, Bhalla US, Campagne F, Collado-Vides J, Crampin EJ, Halstead M, Klipp E, Mendes P [See all...](#)

Affiliation European Bioinformatics Institute, Hinxton, CB10 1SD, UK. lenov@ebi.ac.uk

Language English

Journal Nat. Biotechnol. (ISSN:1087-0156) (ESSN: 1546-1696)
[\[2005 Dec; Volume: 23 \(Issue: 12\)\]](#) Page info: 1509-15

Publication type Journal Article;

Full text article [doi>](#)

XML [XML](#)

Abstract Most of the published quantitative models in biology are lost for the community because they are either not made available or they are insufficiently characterized to allow them to be reused. The lack of a standard description format, lack of stringent reviewing and authors' carelessness are the main causes for incomplete model descriptions. With today's increased interest in detailed biochemical models, it is necessary to define a minimum quality standard for the encoding of those models. We propose a set of rules for curating quantitative models of biological systems. These rules define procedures for encoding and annotating models represented in machine-readable form. We believe their application will enable users to (i) have confidence that curated models are an accurate reflection of their associated reference descriptions, (ii) search collections of curated models with precision, (iii) quickly identify the biological phenomena that a given curated model or model constituent represents and (iv) facilitate model reuse and composition into large subcellular models.

Cited by

[Dry work in a wet world: computation in systems biology.](#)

Kahlem P, Birney E. *Mol. Syst. Biol.* (2006)

[Show Context](#)

[Cited: 102 Times](#) | [Web of Science? Times Cited:146](#)

[4 cite\(s\)](#)





Profiles:

list of data collections

subset of the Registry's content

each data collection in a profile can have settings (such as **one** preferred resource)

can be defined at the level of an institution, project, individual, ...

can be public (shareable) or private (protected by a key)

centrally managed in the Registry (*user interface in progress*)

have a unique shortname (used for identification purposes in URLs)

provide access to a custom XML export

Provide access to custom web services (*in progress*)



<http://identifiers.org/obo.go/GO:0006915>

<http://identifiers.org/obo.go/GO:0006915>

4 physical locations (or resources) are available for accessing *GO:0006915* (from [Gene Ontology](#)):

GO Browser
The Jackson Laboratory

USA

(Uptime: 100%)

QuickGO (Gene Ontology browser)
European Bioinformatics Institute

United Kingdom

(Uptime: 100%)

GO through BioPortal
National Center for Biomedical Ontology,
Stanford

USA

(Uptime: 97%)

AmiGO
The Gene Ontology Consortium

USA

(Uptime: 99%)

<http://identifiers.org/obo.go/GO:0006915?profile=demo>

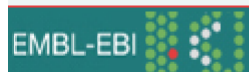
<http://identifiers.org/obo.go/GO:0006915>

[Close](#) 

Access to GO:0006915 (from [Gene Ontology](#)) using the preferred resource of the profile demo.

Entity available from 4 providers, for more information please refer to: <http://identifiers.org/obo.go/GO:0006915>.

Powered by: [Identifiers.org](#) & [MIRIAM Registry](#)



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EBI > Databases > QuickGO

GO:0006915 apoptosis



Click for example search

Search!



Web Services Dataset Term Basket: 0

Term Information

Ancestor Chart

Child Terms

Protein Annotation

Co-occurring Terms

Change Log

ID  GO:0006915

Name apoptosis

Ontology Biological Process

Definition A form of programmed cell death that begins when a cell receives internal or external signals that trigger the activity of proteolytic caspases, proceeds through a series of characteristic stages typically including rounding-up of the cell, retraction of pseudopodes, reduction of cellular volume (pyknosis), chromatin condensation, nuclear fragmentation (karyorrhexis), and plasma membrane blebbing (but maintenance of its integrity until the final stages of the process), and ends with the death of the cell.

Comment

Secondary IDs GO:0008632

GO:0006915 Wiki Page

GONUTS [GO:0006915 Wiki Page](#)

Synonyms

Cross-references

Replaces

<http://identifiers.org/obo.go/GO:0006915?profile=demo>

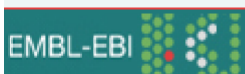
<http://identifiers.org/obo.go/GO:0006915>

[Close](#) 

Access to GO:0006915 (from [Gene Ontology](#)) using the preferred resource of the profile demo

Entity available from 4 providers, for more information please refer to: <http://identifiers.org/obo.go/GO:0006915>.

Powered by: [Identifiers.org](#) & [MIRIAM Registry](#)



Databases Tools Research

EBI > Databases > QuickGO

GO:0006915 apoptosis



Click for example search

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Protein Annotation

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Change Log

ID

 GO:0006915

Name

apoptosis

Ontology

Biological Process

Definition

A form of programmed cell death that begins when a cell receives internal or external signals that trigger the activity of proteolytic caspases, proceeds through a series of characteristic stages typically including rounding-up of the cell, retraction of pseudopodes, reduction of cellular volume (pyknosis), chromatin condensation, nuclear fragmentation (karyorrhexis), and plasma membrane blebbing (but maintenance of its integrity until the final stages of the process), and ends with the death of the cell.

Comment

Secondary

GO:0008632

IDs

GONUTS

[GO:0006915 Wiki Page](#)

Synonyms

Cross-references

Replaces

Generation of
always up-to-date
(hyper)links
without
requirement for
any specific code

http://identifiers.org/ec-code/1.1.1.1?profile=most_reliable

<http://identifiers.org/ec-code/1.1.1.1>

[Close](#) ✕

Access to 1.1.1.1 (from [Enzyme Nomenclature](#)) using the preferred resource of the profile most reliable.
Entity available from 3 providers, for more information please refer to: <http://identifiers.org/ec-code/1.1.1.1>.

Powered by: [Identifiers.org](http://identifiers.org) & [MIRIAM Registry](http://miriam.org)

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- Advanced search
- Browse EC
- Data submission
- Downloads
- Documentation
- Contact IntEnz

EBI > Databases > Enzymes > IntEnz

[EC 1 - Oxidoreductases](#)

[EC 1.1 - Acting on the CH-OH Group of Donors](#)

[EC 1.1.1 - With NAD⁺ or NADP⁺ as acceptor](#)

EC 1.1.1.1 - Alcohol dehydrogenase

IntEnz view

[ENZYME view](#)



[XML](#)

IntEnz Enzyme Nomenclature

EC 1.1.1.1

Names

Accepted name: alcohol dehydrogenase

Other names: ADH
NAD-dependent alcohol dehydrogenase
NAD-specific aromatic alcohol dehydrogenase
NADH-alcohol dehydrogenase
NADH-aldehyde dehydrogenase
alcohol dehydrogenase (NAD)
aldehyde reductase
aliphatic alcohol dehydrogenase
ethanol dehydrogenase



provides **uniform identifiers** for Life Sciences

unambiguous

perennial

directly resolvable

standard compliant (**URIs**)

location independent

identifiers available at **multiple levels** (data collection, resource, and data record)

customisable behaviours (formats available, preferred resource, ...)

responses encoded in **HTML** and **RDF** (either requested explicitly in the URLs or via *content negotiation*)

built on the **MIRIAM Registry**



<http://identifiers.org/ec-code/1.1.1.1>



<http://identifiers.org/ec-code/1.1.1.1>



<http://identifiers.org/ec-code/1.1.1.1>



<http://identifiers.org/ec-code/1.1.1.1>



Camille Laibe

Identifiers.org board of trustees:

Michel Dumontier (WC3 HCLS, Bio2RDF)

Pascale Gaudet (BioDBCore)

Michael Hucka (SBML)

Nicolas Le Novère

Philippe Rocca-Serra (BioSharing)

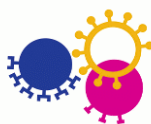
Mark Wilkinson (SADI, LSRN)

Lee Harland (Open PHACTS)

Toshiaki Katayama (BioRuby, KEGG)

Michael Galperin (NAR Database issue)

Biomodels-net-support
@lists.sf.net



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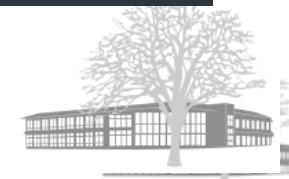
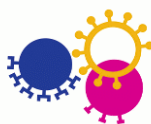
Lee Harland (Open PHACTS)

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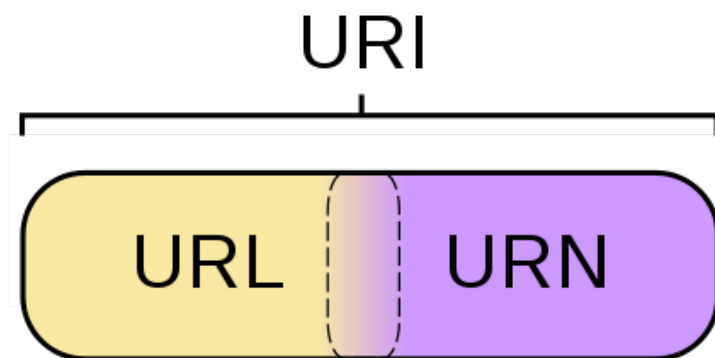
Michael Galperin (NAR Database issue)

**The Systems Biology
community for its
continued support
and feedback**

Biomodels-net-support
@lists.sf.net



A **Uniform Resource Identifier** (URI) is a string of characters used to **identify** a resource.



Uniform Resource Name (URN)

identifies a resource but does not imply its availability

Uniform Resource Locator (URL)

specifies where a resource is available on the Internet



<http://www.ebi.ac.uk/>

http://en.wikipedia.org/wiki/Uniform_Resource_Identifier

<https://www.ebi.ac.uk/chemblpdb/>

<ftp://public.ftp-servers.example.com/mydirectory/myfile.txt>

<ftp://ftp.uniprot.org/pub/databases/uniprot/uniref/>

<urn:ietf:rfc:2648>

<file:///home/username/presentation.pdf>

...





Namespace

Identifies a data collection

Entity identifier

Identifies a data entry within the data collection

Human calmodulin: P62158 in UniProt

➡ urn:miriam:uniprot:P62158

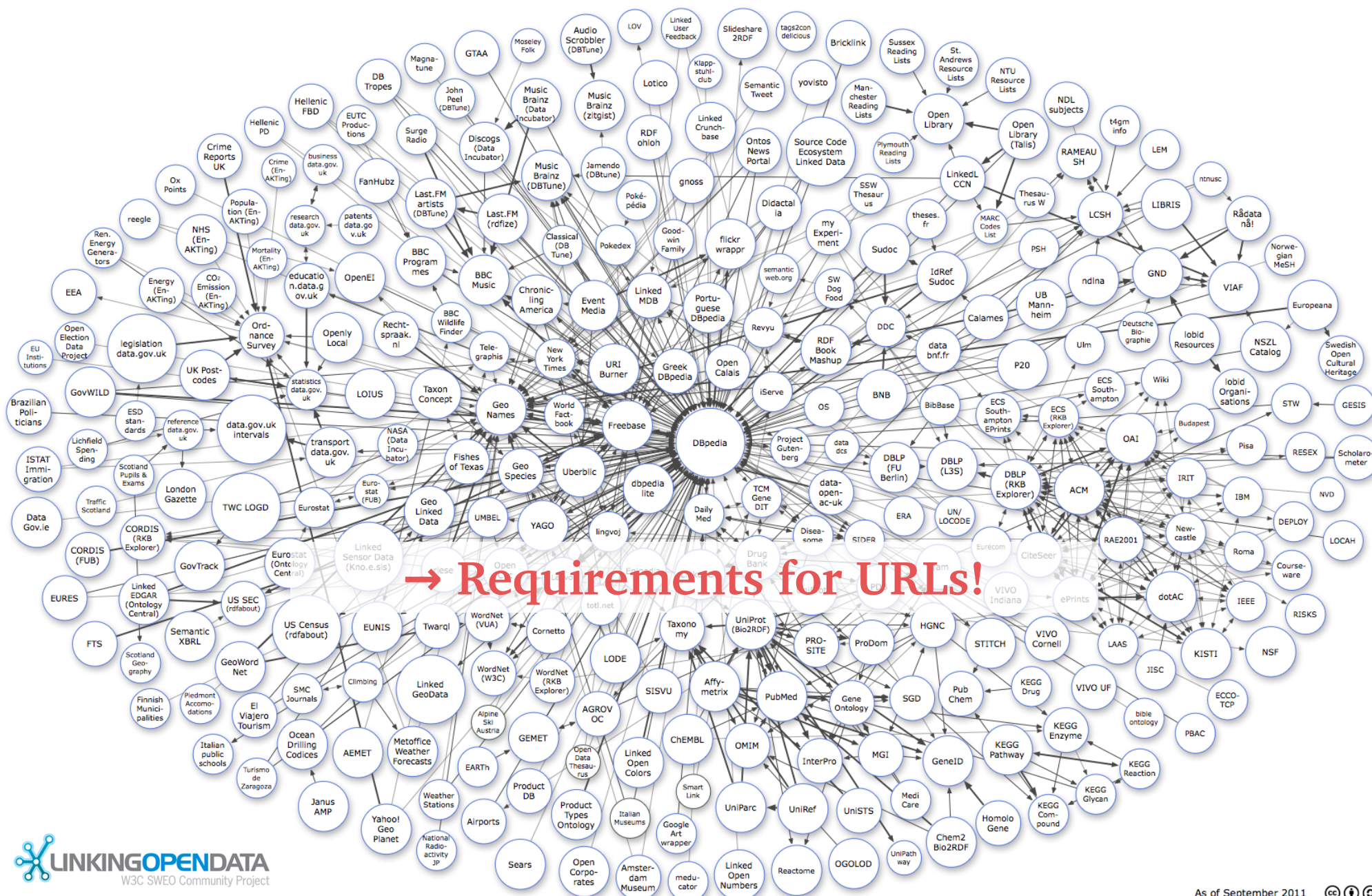
Alcohol dehydrogenase: 1.1.1.1 in EC code

➡ urn:miriam:ec-code:1.1.1.1

Activation of MAPKK activity: GO:0000186 in Gene Ontology

➡ urn:miriam:obo.go:GO%3A0000186





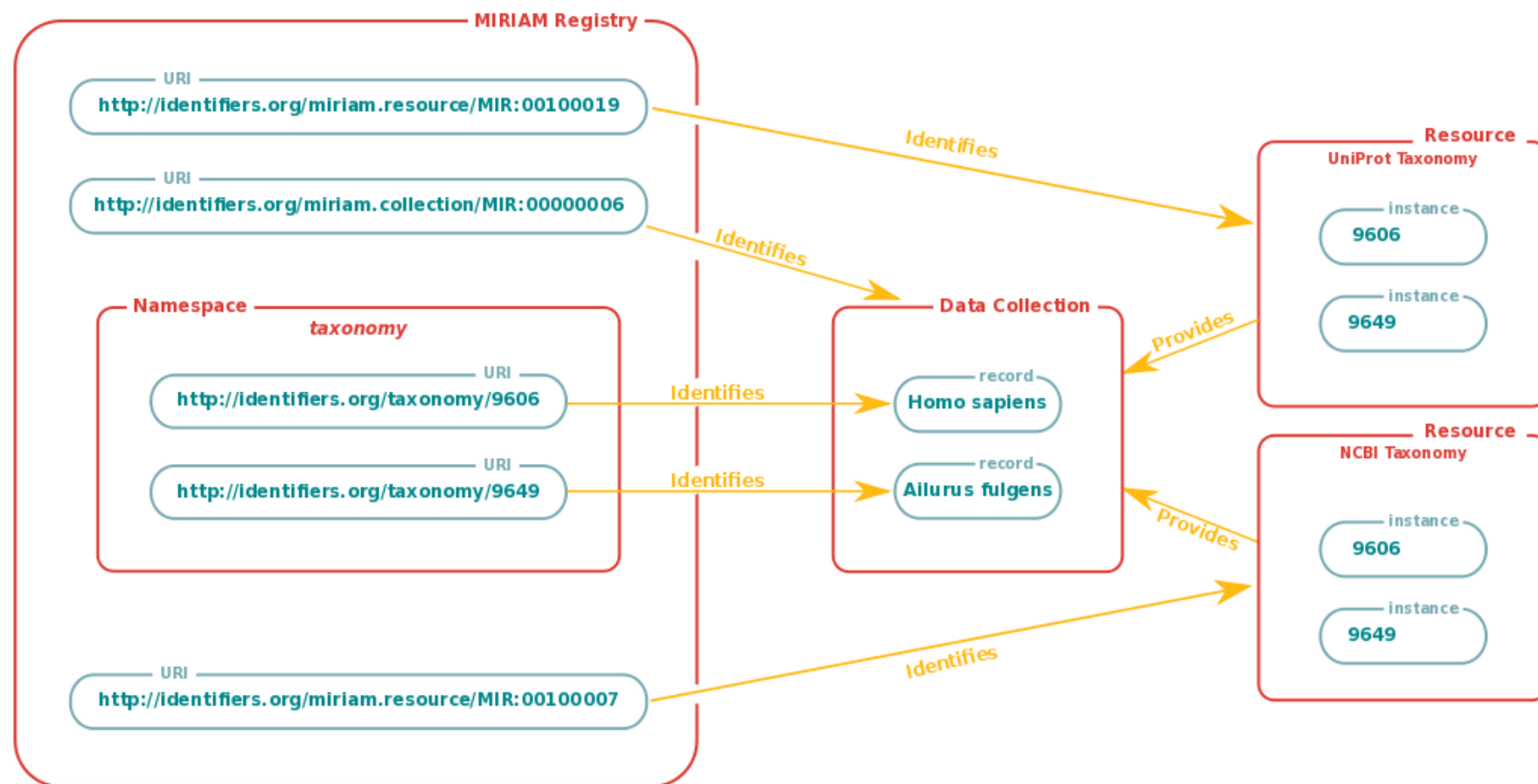


The Semantic Web provides a common framework that allows data to be shared and reused across application, enterprise, and community boundaries.

Goal: allows **machines** to understand the **semantics**, or meaning, of information on the **World Wide Web**.

Collaborative effort led by **W3C** with participation from a large number of researchers and industrial partners.





MIRIAM Database

collection catalogue

XML exports available

MIRIAM Web Services

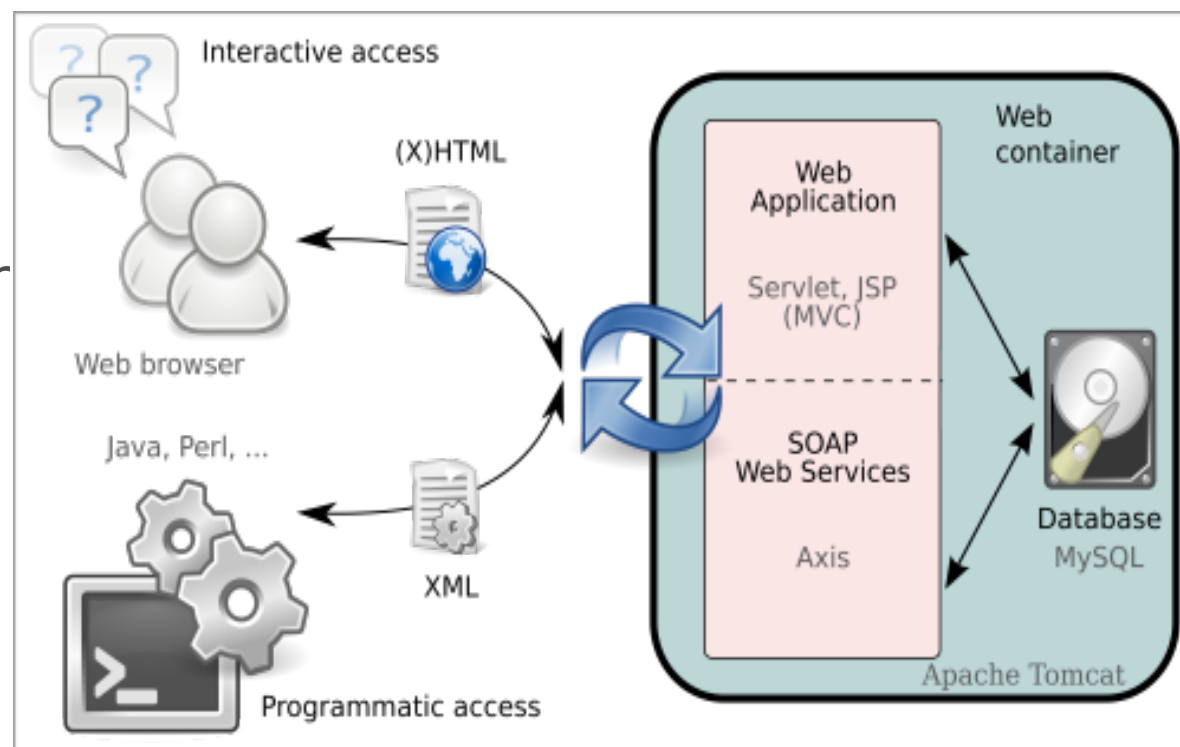
programming interface for
querying database

MIRIAM Library

ready to use Java code to
query and access

MIRIAM Web Site

web page for browsing and querying
allows new submission (curated)



Laibe and Le Novère.

**MIRIAM Resources: tools to generate
and resolve robust cross-references
in Systems Biology.**

BMC Systems Biology, 2007

