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

Nick Juty

BioModels.net

8th December 2011, SWAT4LS, London
General introduction of metadata

MIRIAM Registry of namespaces
  information captured
  supporting facilities
  export and access
  submissions

Identifiers.org resolving service
  levels of information
  information access
Cross-references allow the unambiguous identification of:

- physical entities (records in a database)
  - molecular entities
  - diseases
  - clinical trials
  - ...
- information artefacts
  - ontological terms
  - scientific publications
  - books
  - ...
  - ...
  - ...
Cross-references, and generally metadata, are essential for:

- understanding data
- reusing data
- comparing data
- integrating data
- converting data
- providing efficient search strategies

...
Set of technologies helping to link data of different natures and different locations in a meaningful way:

**Uniform Resource Identifiers** (URIs) to unambiguously identify pieces of data

**Controlled vocabularies** to characterise the relationships between data entity (SKOS, RDFs, ontologies)

Syntaxes to encode the **relationships** between data entity (RDF)

**Query** languages, to retrieve information encoded using semantic web technologies (SPARQL)
Towards globally unique identifiers

**Namespace**
- Identifies a data collection

**Entity identifier**
- Identifies a data entry within the data collection
Towards globally unique identifiers

**Namespace**
- Identifies a data collection
- Provided by the data collection, from a shared list of *namespaces*

**Entity identifier**
- Identifies a data entry within the data collection
- Provided by the data collection, unique within the data collection, format defined by the data collection
Human calmodulin: **P62158** in **UniProt**

http://identifiers.org/uniprot/P62158

Alcohol dehydrogenase: **1.1.1.1** in **EC code**

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

Activation of MAPKK activity: **GO:0000186** in **Gene Ontology**

http://identifiers.org/obo.go/GO:0000186
- **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)

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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

Browse
by data type name
by tags

Search
generic search

Web Services
services available
usage of the services
online demonstration

Exports
XML

http://www.ebi.ac.uk/miriam/
## List of data collections

<table>
<thead>
<tr>
<th>Name</th>
<th>Namespace</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>Protein Model Database</td>
<td>pmdb</td>
<td>The Protein Model DataBase (PMDB), is a database that collects manually built three dimensional protein models, obtained by different structure prediction techniques.</td>
</tr>
<tr>
<td>MIRIAM Registry collection</td>
<td>miriam.collection</td>
<td>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.</td>
</tr>
<tr>
<td>TEDDY</td>
<td>biomodels.teddy</td>
<td>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.</td>
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<tr>
<td>UniProt</td>
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<td>edam</td>
<td>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).</td>
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<tr>
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<td>obo.obi</td>
<td>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).</td>
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<td>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.</td>
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<td>FMA</td>
<td>obo.fma</td>
<td>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 phenotypic structure of the human body. Specifically, the FMA is a domain catalog that represents a hierarchy of hierarchical categories.</td>
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## Data collection: Enzyme Nomenclature

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<thead>
<tr>
<th>Name</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Identifier</td>
<td>MIR:00000004</td>
</tr>
<tr>
<td>Name</td>
<td>Enzyme Nomenclature</td>
</tr>
<tr>
<td>Synonyms</td>
<td>Enzyme Classification EC code</td>
</tr>
<tr>
<td></td>
<td>EC</td>
</tr>
</tbody>
</table>

### 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**: ^d+\-\-\-\-\-\d+\-\-\-\-\-\d+\-\-\-\d+\-\-\-\-\d+\-\-\-\-\-\(n)?\d+\$

### URIs

<table>
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<th>Namespace</th>
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</tr>
</thead>
<tbody>
<tr>
<td>Root URL</td>
<td><a href="http://identifiers.org/ec-code/">http://identifiers.org/ec-code/</a></td>
</tr>
<tr>
<td>Root URN</td>
<td><a href="">urn:miriam:ec-code:</a></td>
</tr>
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### Physical Locations

<table>
<thead>
<tr>
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<th>Access URL</th>
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</tr>
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<tbody>
<tr>
<td></td>
<td>Description: KEGG Ligand Database for Enzyme Nomenclature</td>
<td></td>
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<td>Institution: Kyoto University Bioinformatics Center, Japan</td>
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### References

- [http://www.chem.qmul.ac.uk/jubmb/enzyme/](http://www.chem.qmul.ac.uk/jubmb/enzyme/)
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**Information**

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**

`^d+\d+\d+\d+\d+\d+\d+\d+\d+\d+\d+\d+\d+\d+(n)?id+$`

**URLs**

- **Namespace**: ec-code
- **Root URL**: http://identifiers.org/ec-code/
- **Root URN**: urn:miriam:ec-code:

**Physical Locations**

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### Health history: MIR:********

#### Health history of: MIR:********

##### 2010

|   | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 |
|---|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|
| **January** | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| **February** | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| **March** | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| **April** | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| **May** | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| **June** | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| **July** | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| **August** | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| **September** | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| **October** | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| **November** | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| **December** | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
### Resource: MIR:00100050

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

<table>
<thead>
<tr>
<th>Health statistics</th>
</tr>
</thead>
<tbody>
<tr>
<td>Last known state</td>
</tr>
<tr>
<td>Last check</td>
</tr>
<tr>
<td>Uptime ratio</td>
</tr>
<tr>
<td>Downtime ratio</td>
</tr>
<tr>
<td>Unknown ratio</td>
</tr>
<tr>
<td>URL used</td>
</tr>
</tbody>
</table>

Health history

Full record of the health checks performed on this resource.

2011

|   1 |   2 |   3 |   4 |   5 |   6 |   7 |   8 |   9 |  10 |  11 |  12 |  13 |  14 |  15 |  16 |  17 |  18 |  19 |  20 |  21 |  22 |  23 |  24 |  25 |  26 |  27 |  28 |  29 |  30 |  31 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
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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...
Submit a new data collection

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<table>
<thead>
<tr>
<th>Resource</th>
<th>MIR:00100002</th>
<th>MIR:00100003</th>
<th>MIR:00100001</th>
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</thead>
<tbody>
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<td>Description</td>
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[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
Human calmodulin: **P62158** in **UniProt**

http://identifiers.org/uniprot/P62158

Alcohol dehydrogenase: **1.1.1.1** in **EC code**

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

Activation of MAPKK activity: **GO:0000186** in **Gene Ontology**

http://identifiers.org/obo.go/G0:0000186
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.

Links

- About
- Help
- Examples URIs
- MIRIAM Registry

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)
- Pascale Gaudet (Swiss Institute of Bioinformatics, Geneva, Switzerland - BioDBCore)
- Michael Hucka (California Institute of Technology, Pasadena, USA - SBML)
- 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
Basic access

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

3 physical locations (or resources) are available for accessing 1.1.1.1 (from Enzyme Nomenclature):

- **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%)*

- **KEGG Ligand Database for Enzyme Nomenclature**
  Kyoto University Bioinformatics Center
  *Japan*
  *(Uptime: 100%)*
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

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

- **HubMed**
  Alfred D. Eaton
  United Kingdom
  (Uptime: 97%)

- **SRS@EBI**
  European Bioinformatics Institute
  United Kingdom
  (Uptime: 100%)

- **CiteXplore**
  European Bioinformatics Institute
  United Kingdom
  (Uptime: 99%)

- **free digital archive of biomedical and life sciences journal literature**
  National Center for Biotechnology Information
  USA
  (Uptime: 100%)

Powered by [MIRIAM Registry](http://identifiers.org)
http://identifiers.org/pubmed/16333295?resource=MIR:00100032

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.

CiteXplore - citation details

Pubmed Id 16333295
Title Minimum information requested in the annotation of biochemical models (MIRIAM).
Authors Le Novère N, Finney A, Huick M, Bhalla US, Campagne F, Collado-Vides J, Crampin EJ, Hainstead M, Klipp E, Mendes P. See all...
Affiliation European Bioinformatics Institute, Hinxton, CB10 1SD, UK. lenov@ebi.ac.uk
Language English

Publication type Journal Article;
Full text article doi>
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.
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

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

**GO Browser**
The Jackson Laboratory
United States
(Uptime: 100%)

**QuickGO (Gene Ontology browser)**
European Bioinformatics Institute
United Kingdom
(Uptime: 100%)

**GO through BioPortal**
National Center for Biomedical Ontology, Stanford
United States
(Uptime: 97%)

**AmiGO**
The Gene Ontology Consortium
United States
(Uptime: 99%)

Powered by MIRIAM Registry

Information also available in: RDF
Resolving using a specific profile

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

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.

<table>
<thead>
<tr>
<th>Term Information</th>
<th>Ancestor Chart</th>
<th>Child Terms</th>
<th>Protein Annotation</th>
<th>Co-occurring Terms</th>
<th>Change Log</th>
</tr>
</thead>
<tbody>
<tr>
<td>ID</td>
<td>GO:0006915</td>
<td></td>
<td></td>
<td></td>
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</tr>
<tr>
<td>Name</td>
<td>apoptosis</td>
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<td></td>
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<tr>
<td>Ontology</td>
<td>Biological Process</td>
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<tr>
<td>Definition</td>
<td>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.</td>
<td></td>
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</tr>
<tr>
<td>Comment</td>
<td>GO:0008632</td>
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<td>GONUTS</td>
<td>GO:0006915 Wiki Page</td>
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<tr>
<td>Synonyms</td>
<td>Cross-references</td>
<td>Replaces</td>
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</tr>
</tbody>
</table>
Resolving using a specific profile

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

Generation of always up-to-date (hyper)links without requirement for any specific code
Resolving: using the most reliable resource

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

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.
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**
What to store in the database?

http://identifiers.org/ec-code/1.1.1.1
What to use in your import/export formats?

http://identifiers.org/ec-code/1.1.1.1
What to use in your user interfaces?

http://identifiers.org/ec-code/1.1.1.1
Where to get the data?

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

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Identifiers.org board of trustees

Michel Dumontier (WC3 HCLS, Bio2RDF)
Pascale Gaudet (BioDBCore)
Michael Hucka (SBML)
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Philippe Rocca-Serra (BioSharing)
Mark Wilkinson (SADI, LSRN)