# BioSharing.org

**Mapping the landscape of Standards, Databases and Data policies in the life, biomedical and environmental sciences**

Peter McQuilton

BioSharing Content Lead

@biosharing

# Outline

- What is BioSharing?
- Ensuring FAIR-ness for standards, databases and policies
- How do we describe and link records?
- Exploring the landscape of standards, databases and data policies in the life sciences

biosharing.org
standards, databases, policies

Standards | Databases | Policies | Collections | Add/Claim Content | Stats | My Profile

**A curated, informative and educational resource on inter-related data standards, databases, and policies in the life, environmental and biomedical sciences**

**Find**

**Recommendations**

Standards and/or databases recommended by journal or funder data policies.

**Discover**

**Collections**

Standards and/or databases grouped by domain, species or organization.

**Learn**

**Educational**

About standards, their use in databases and policies, and how we can help you.

Search BioSharing | Search

☑ Standards ☑ Databases ☑ Policies ☑ Collections/Recommendations

**Advanced Search**

Fine grained control over your search.

**Search Wizard**

ask biosharing

Let us guide you to your results.

**666 Standards**

| | |
|---|---|
| Terminology Artifact | 346 |
| Model/Format | 210 |
| Reporting Guideline | 110 |

View all

**811 Databases**

| | |
|---|---|
| Protein | 163 |
| Genome | 126 |
| DNA | 84 |

View all

**81 Policies**

| | |
|---|---|
| Funder | 19 |
| Journal | 56 |
| Society | 2 |

View all

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standards, databases, policies

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About standards, their use in databases and policies, and how we can help you.

A web-based, curated and searchable portal that monitors the development and **evolution** of standards, their **use** in databases and the adoption of both in data policies, to **inform** and **educate** the user community.

**666 Standards**

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Standards are digital objects too and we make them FAIR

**666 Standards**

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| | |
|---|---|
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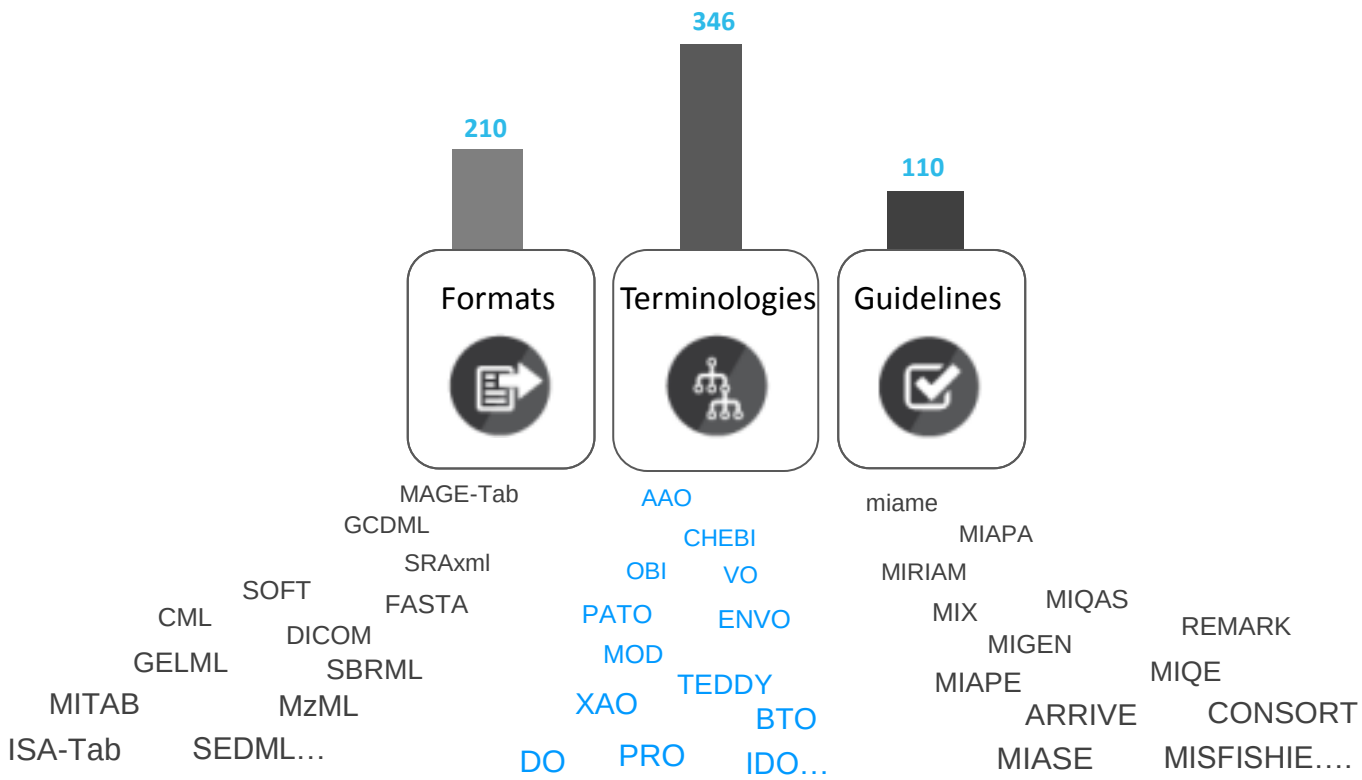
| Society | 2 |

View all

# There are over 650 standards in the life sciences

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# Enablers: to better describe, share and query data

***Models/Formats = Conceptual model, conceptual schema, exchange formats***

- Allow data to flow from one system to another
- e.g. FASTA


***Guidelines = Minimum information reporting requirements, checklists***

- Report the same core, essential information
- e.g. ARRIVE guidelines

***Terminologies = Controlled vocabularies, taxonomies, thesauri, ontologies*** etc.

- Use the same word and refer to the same 'thing'
- e.g. Gene Ontology

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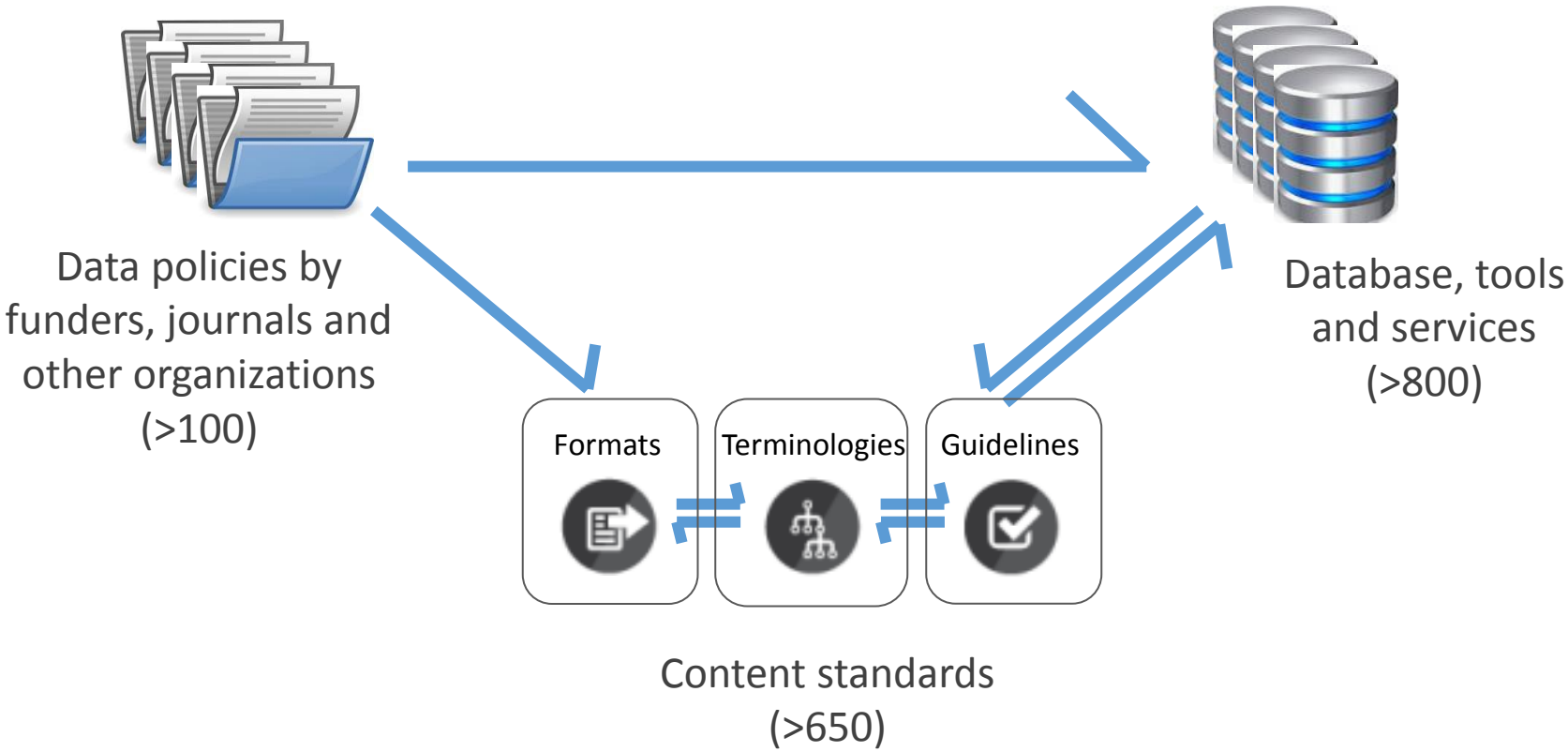
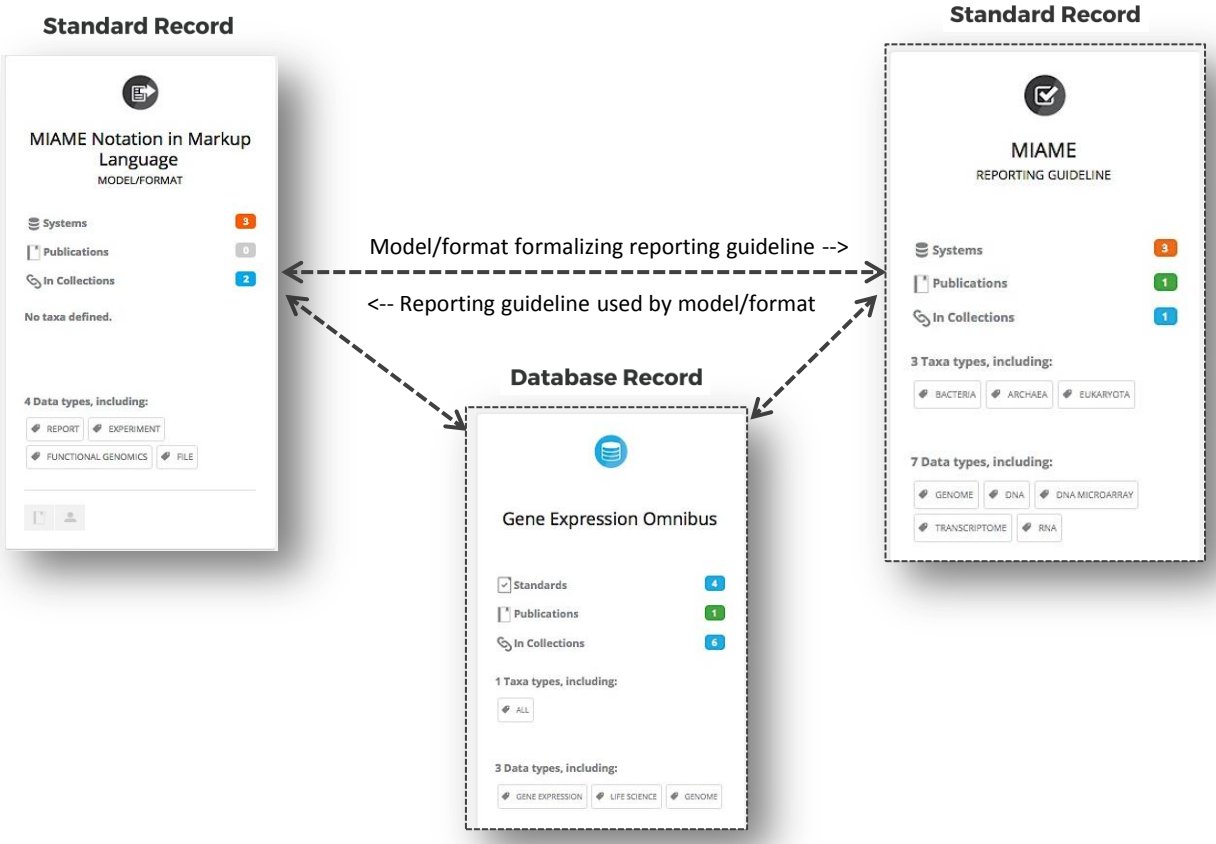
Information Resources

# Complex and evolving landscape



# Cross-linking standards to standards and databases

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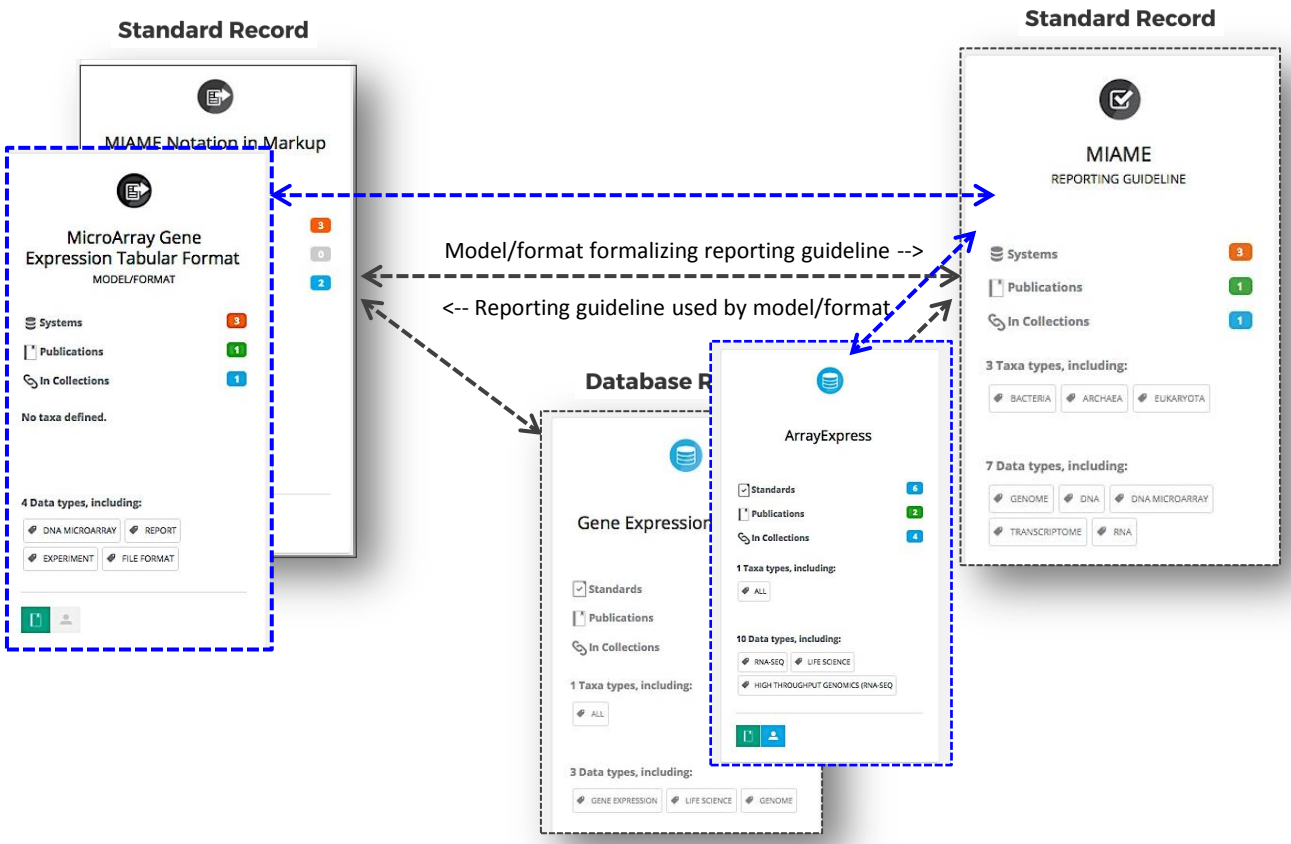


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Information Resources

# Helping users make the right decision

My funder's data policy recommends the use of **established standards**, but which ones are widely **endorsed** and applicable to my toxicological and clinical data?

What are the **mature standards** and **standards-compliant databases** we should recommend to our authors?

RESEARCHERS

FUNDERS & JOURNAL EDITORS


CURATORS & DEVELOPERS

LIBRARIANS & DATA MANAGERS

Am I using the **most up-to-date version** of this terminology to annotate cell-based assays?

I understand this format has been **deprecated**; what has it been **replaced** by and is it appropriate for this data?

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Information Resources

# How do we describe and link records

Using standards as an example

# Criteria for evaluating standards

Perspective

## A sea of standards for omics data: sink or swim?

Jessica D Tenenbaum,[1] Susanna-Assunta Sansone,[2] Melissa Haendel[3]

Tenenbaum JD, *et al*. *J Am Med Inform Assoc* 2013;**0**:1–4. doi:10.1136/amiajnl-2013-002066

- The standard itself
  - specification documentation
  - ease of implementation (eg, level of documentation, requirement for programmer support)
  - human and machine readability
  - formal structure
  - expressivity—the breadth of information that can be represented
  - ease of use, for example, minimal required fields, text-based interface familiarity to biologists.
- Adoption and user community
  - broad adoption and implementation, outside the initial group
  - support supplied by the user community
  - use by community databases
  - software development that supports the standard (eg, for curating, submitting to databases)
  - responsiveness to community requests
  - availability of examples of use
  - requirements of relevant authoritative bodies, for example, funders (NIH, National Science Foundation, Centers for Medicare & Medicaid Services), publishers, etc.
- Additional factors
  - integration/compatibility with other standards
  - extensibility and flexibility to cover new domains
  - conversion and mapping, when applicable
  - cost (eg, open vs licensing fee).

# System Biology Markup Language

Abbreviation:SBML

MODEL/FORMAT

RECOMMENDED

## General Information

The Systems Biology Markup Language (SBML) is a machine-readable exchange format for computational models of biological processes. Its strength is in representating phenomena at the scale of biochemical reactions, but it is not limited to that. By supporting SBML as an input and output format, different software tools can operate on the same representation of a model, removing chances for errors in translation and assuring a common starting point for analyses and simulations.

**Homepage** http://sbml.org

**Developed in** Worldwide

**Created in** 1999

### Taxonomic range

All

### Scope and data types

Computational Model
Network Interaction Model
Molecular Entity
Pathway Model
Enzymatic Reaction
Cellular Organisms

Record added: May 14, 2015, 11:14 a.m. Record updated: Feb. 24, 2016, 3:26 p.m. by The BioSharing Team .

## Recommended by

Computational Modeling

EMBO Press

## Support

| | |
|---|---|
| help | http://sbml.org/Documents/FAQ |
| mailing list | sbml-discuss@googlegroups.com |
| online documentation | http://sbml.org/Documents/Specifications |
| rss | http://sbml.org/index.php?title=News&act ... |
| twitter | @sbmlnews |

Training

### Additional Information

| | |
|---|---|
| Contact | SBML Forum |

## Tools

No tools defined

## Conditions of Use

### License

## Related Standards

### Reporting Guidelines

Minimal Information Required In the Annotation of Models

### Terminology Artifacts

Systems Biology Ontology

### Models and Formats

Systems Biology Graphical Notation
Simulation Experiment Description Markup Language
CellML

## Implementing Databases (13)

MetaCrop 2.0: managing and exploring information about crop plant metabolism
Biochemical pathways and enzymes in crop plants

IPAVS
Integrated Pathway Analysis and Visualization System

The Comprehensive Enzyme Information System
BRENDA is the main collection of enzyme functional data available to the scientific community.

A repository of mathematical models of biological and biomedical systems
BioModels is a repository of computational models of biological processes. It allows users to search and retrieve mathematical models published in the literature. Many models are manually curated (to ensure reproducibility) and extensively cross-linked to publicly available reference information.

Scroll for more...

# Linking standards and databases to training material

elixir Training Portal

elixir Data for Life excelerate

Events Materials Packages Workflows Content Providers Nodes About Search

/ Content providers / European Bioinformatics ... / **MetaboLights: Quick tour**

**MetaboLights: Quick tour**

Content Provider

EMBL-EBI

**European Bioinformatics Institute (EBI)**

EMBL-EBI provides freely available data from life science experiments, performs basic research in computational biology and offers an extensive user training programme,... read more

**Home page:**

http://www.ebi.ac.uk

ELIXIR Node

Material Packages Activity log

## MetaboLights: Quick tour

This quick tour provides a brief introduction to the EBI's metabolomics resource: MetaboLights.

### Details

| Field | Value |
|---|---|
| Source URL | http://www.ebi.ac.uk/training/online/course/metabolights-quick-tour-0 |
| Last updated | June 4, 2015, 15:16 |
| Created | April 1, 2015, 14:16 |

### Tags

Chemical biology Systems

### Related events

*This training material has no additional events*

### Additional resources

**MetaboLights record on Biosharing.org**

This record summarises the details of the MetaboLights database, including... Open

MetaboLights

Abbreviation: MTBLS

General Information

MetaboLights is a database for Metabolomics experiments and derived information. The database is cross-species, cross-technique and covers metabolite structures and their reference spectra as well as their biological roles, locations and concentrations, and experimental data from metabolic experiments. We offer user-submission tools and have strong reporting capabilities. We will utilise and further develop de-facto standard formats where various components are encapsulated, such as the encoded spectral and chromatographic data, and associated information about the chemical structure, as well as metadata describing assays and the study as a whole. We are dedicated to collaborate closely with major parties in world-wide metabolomics communities, such as the Metabolomics Society and the associated Metabolomics Standards Initiative (MSI).

Last updated: Oct. 30, 2015, 3:51 p.m.

Homepage http://www.ebi.ac.uk/metabolights/
Developed in United Kingdom , European Union
Created in 2012

Taxonomic range

ALL

Database scope and data types

METABOLITE METABOLOMICS LIPIDOMICS MASS SPECTROMETRY NUCLEAR MAGNETIC RESONANCE SPECTROSCOPY FLUXOMICS PUBLICATIONS LIFE SCIENCE

Support

online documentation http://www.ebi.ac.uk/metabolights/help

training http://tess-elixir.csc.fi/dataset/europe ...

Additional Information

Contact Reza Salek ORCID

MIRIAM Registry None

Tools

ISACreator http://www.isa-tools.org/

In Collections

Journal: Scientific Data Recommended Repositories

Project: Metabolomics Standards and Databases

Related Standards

Reporting Guidelines

Core Information for Metabolomics Reporting

Terminology Artifacts

Nuclear Magnetic Resonance Controlled Vocabulary
Ontology for Biomedical Investigations
Nuclear Magnetic Resonance Controlled Vocabulary
Mass Spectrometry
Chemical Entities of Biological Interest

Models and Formats

Investigation Study Assay Tabular
Nuclear Magnetic Resonance Markup Language

Related Databases

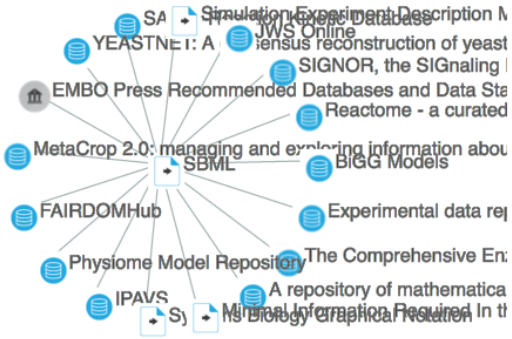
No related databases defined

Implementing Policies

Scientific Data's Recommended Data Repositories

No License Specified.

## Connectivity




## Schemas

**Name:** SBML
**Version:** l2v4
Download Show

**Name:** SBML
**Version:** l2v3
Download Show

**Name:** SBML
**Version:** l2v2
Download Show

## Implementing Policies

EMBO Press Recommended Databases and Data Standards

## Credit

### Record Maintainer

This record is maintained by skeating ORCID

### Development Group

SBML Community

### Funders

California Institute of Technology
EMBL-EBI
NIGMS NIH HHS

### Grant Number(s)

R01 GM070923 (NIGMS NIH HHS)

### Collaborators

COMBINE

## Publications

The systems biology markup language (SBML): a medium for representation and exchange of biochemical network models.

Hucka M,Finney A,Sauro HM,Bolouri H,Doyle JC,Kitano H,Arkin AP,Bornstein BJ,Bray D,Cornish-Bowden A,Cuellar AA,Dronov S,Gilles ED,Ginkel M,Gor V,Goryanin II,Hedley

# Using indicators to describe the ‘status’ of a resource

R Ready for use, implementation, or recommendation

Dev In development

U Status uncertain

D Deprecated as subsumed or superseded

Manually curated, approved by the community

D

~~LINCS 1: Cell Lines~~

~~LINCS Pilot Phase 1 Metadata Standards: Cell Lines~~

REPORTING GUIDELINE

DEPRECATED

Implementing databases 1

Publications 0

In Collections 1

Recommended 0

1 Taxa types, including:

Homo Sapiens

3 Data types, including:

Cell-Based Assays | Gene Expression | Life Science

NIH LINCS PROGRAM

R

LINCS 2: Cell lines

LINCS Production Phase 2 Extended Metadata Standard: Cell lines

REPORTING GUIDELINE

Implementing databases 1

Publications 1

In Collections 1

Recommended 0

1 Taxa types, including:

Homo Sapiens

6 Data types, including:

Cell-Based Assays | Cell Lines | Enzyme Assays | Gene Expression

D

~~LINCS 1: Cell Lines~~

~~LINCS Pilot Phase 1 Metadata Standards: Cell Lines~~

REPORTING GUIDELINE

DEPRECATED

Implementing databases 1

Publications 0

In Collections 1

Recommended

1 Taxa types, including:

Homo Sapiens

3 Data types, including:

Cell-Based Assays

Life Science

R

LINCS 2: Cell lines

LINCS Production Phase 2 Extended Metadata Standard: Cell lines

REPORTING GUIDELINE

Implementing databases 1

Publications 1

In Collections 1

0

l Lines

Expression

D LINCS Pilot Phase 1 Metadata Standards: Cell Lines

Abbreviation:LINCS 1: Cell Lines

REPORTING GUIDELINE

General Information

This record was deprecated on Aug. 10, 2016 for the following reason(s): This standard was a pilot study for the LINC2 Cell line standard (https://biosharing.org/bsg-s000651) and as such has been superseded by this standard.

The LINCS Pilot Phase 1 metadata standards annotate reagents outside the context of the experiments in which they were used. The underlying theme among all cell types is their association with a tissue or organ from which the cells were derived.

This record is replaced by:
LINCS Production Phase 2 Extended Metadata Standard: Cell lines

Homepage http://www.lincsproject.org/data/data-standards/

Developed in United States of America

Created in 2012

Taxonomic range

Homo Sapiens

Dev

## LCI facility data repository

DATABASE

| | |
|---|---|
| Standards | 0 |
| Publications | 0 |
| In Collections | 1 |
| Recommended | 0 |

No taxa defined.

3 Data types, including:

- Biological Imaging
- High-Content Screening

EURO-BIOIMAGING

https://biosharing.org/collection/EuroBioImaging

U

## CPO

### Cell Phenotype Ontology

TERMINOLOGY ARTIFACT

| | |
|---|---|
| Implementing databases | 0 |
| Publications | 1 |
| In Collections | 1 |
| Recommended | 0 |

1 Taxa types, including:

- All

2 Data types, including:

- Cell
- Phenotype

biosharing.org
Information Resources

# BioSharing allows you to

- Track the provenance and evolution of a standard or database
- See which standards a database uses
- Explore the resources appropriate to your domain, species, technique etc.
- Map the resources available from a particular funder, country or with a particular access license
- See which standards and databases a publisher, funder or institution/organisation recommends

biosharing.org
standards, databases, policies

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## THE BASICS OF STANDARDS

### 1. Generic information

#### 1.1 What is a standard?

In essence, a standard is an agreed way of doing something. A standard provides the requirements, specifications, guidelines or characteristics that can be used for the description, interoperability, citation, sharing, publication, or preservation of all kinds of digital objects such as data, code, algorithms, workflows, software, or papers.

#### 1.2 How many types are there and what are they for?

#### 1.3 Who should care about them, and why?

#### 1.4 What are the FAIR principles and why are standards key?

### 2. Focussing on data/metadata standards

#### 2.1 What are they and how many types are there?

#### 2.2 What are they used for and by whom?

Broadly, these standards allow data and its associated contextual/experimental metadata to be harmonized, with respect to structure, format and annotation. This opens their content to transparent interpretation, reuse, integrative analysis and comparison. Data and metadata standards are essential for the implementation of the FAIR principles.
Data and metadata standards are used and implemented by many stakeholders, communities, data services and resources in the public, private and governmental sectors for the collection, reporting, storage, publishing and dissemination of research information, and to make it more accessible to benefit the wider scientific community. Better standards = Better data and metadata = Better science!

#### 2.3 What is a *de jure* and a *de facto* standard?

#### 2.4 Who are the community involved and how are they organized?

### 3. Developing, contributing and using a data/metadata standards

#### 3.1 What is the typical standard life cycle?

#### 3.2 Create a new standard or join an existing effort?

## HOW BIOSHARING HELPS YOU

### 5. Linking standards, databases and data policies, and to other resources

#### 5.1 Why it is important to link these types of resource?

By interlinking standards, databases and policies, BioSharing guides users to discover existing databases and standards, to identify those standards that are implemented by databases, and to find the policies that refer to them. The latter two points also provide evidence of use and are important indicators when users select a standards or a database.

The relationships between standards, databases and policies are not a static but evolve over time (new links are added, others removed). BioSharing fulfills the essential job of mapping this dynamic landscape and in doing so helps a variety of users in their tasks. Examples include:

- *Researchers* - to find journals that meet their funder requirements, journal standards, the specific needs for a data management plan, and to enable their data to be shared as widely as possible (as per funding and publication requirements).
- *Publishers* - to link from journals to repositories that meet the requirements as set down by their data policies and to meet any necessary content standards.
- *Funders* - to understand which journals and repositories meet their policies; and knowledge of the current landscape of community defined-standards and databases to refine their recommendations.
- *Developers* and curators of repositories and standards - to ensure their products are discoverable and well described so they can be:
  - evaluated and recommended by journals and funders in their policies;
  - used by researchers to meet their funder policies and the policies of the journals they wish to publish in; or reused and/or extended by other developers and curators, according to the products' licence, to meet their specific needs.
- *Librarians* to support scholars to:
  - utilize data standards; and conform to journal, institutional, and funder policies;
  - develop and maintain institutional data and publication repositories.

#### 5.2 Why and how do we link to other terminology portals?

#### 5.3 What about tools and training materials for standards and databases?

#### 5.4 Which are the communities we work with and for?

### 6. Looking for guidance on standards, databases and policies

#### 6.1 Are you a Researcher creating a Data Management Plan?

#### 6.2 Are you a curator or data manager?

#### 6.3 Are you a standard or database developer?

## HOW TO USE THE BIOSHARING PORTAL

### 7. Search functionalities to help find what you need

7.1 When should I use the search box and how can I see all content?

7.2 When should I use the wizard?

Our step-by-step wizard guides users through the process of searching the three registries of standards, databases, and data policies, refining the search via data type, scope and species. Users should employ the wizard when they are unsure as to what to look for, or if they simply want to browse the data in a more stepwise manner.

7.3 How can I search for a standard, database and policy in a particular area/domain/species, or from a particular funder, country or organisation?

7.4 When should I use the advanced search?

7.5 Which view should I use to browse BioSharing's standard, database and policy content?

### 8. Indicators and descriptors to help you selecting resources

8.1 What information do we house for each standard?

8.2 What information do we provide for each database?

8.3 What information do we have on data policies?

8.4 Are there indicators of the maturity status of standards and databases available?

8.5 Which databases or standards are recommended by journals, funders and other data policies?

8.6 Which databases implement which standards?

8.7 What is a Collection?

8.8 What is a Recommendation?

# Using BioSharing to explore the landscape

# Finding and Accessing the data

View as Table | View as Grid

Sort by: Best Match

Recommended Records: Recommended

Associated Publication?: No Publication | Has Publication

Claimed?: No Maintainer | Has Maintainer

Record Status: Uncertain | Deprecated | In developmen | Ready

**Domains**

- Life Science 515
- Protein 163
- Genome 126
- Biomedical Science 123

Show More

**Taxonomies**

- All 284
- Homo Sapiens 259
- Mus Musculus 109
- Bacteria 43

Show More

**Countries**

- United States Of America 321
- United Kingdom 96
- France 62
- European Union 53

Show More

**Foundry Membership**

- OBO Foundry Member 0
- MIBBI Foundry Member 0

Search BioSharing | Search

Standards | Databases | Policies | Collections/Recommendations

**Advanced Search**

Fine grained control over your search.

**Search Wizard**

ask biosharing

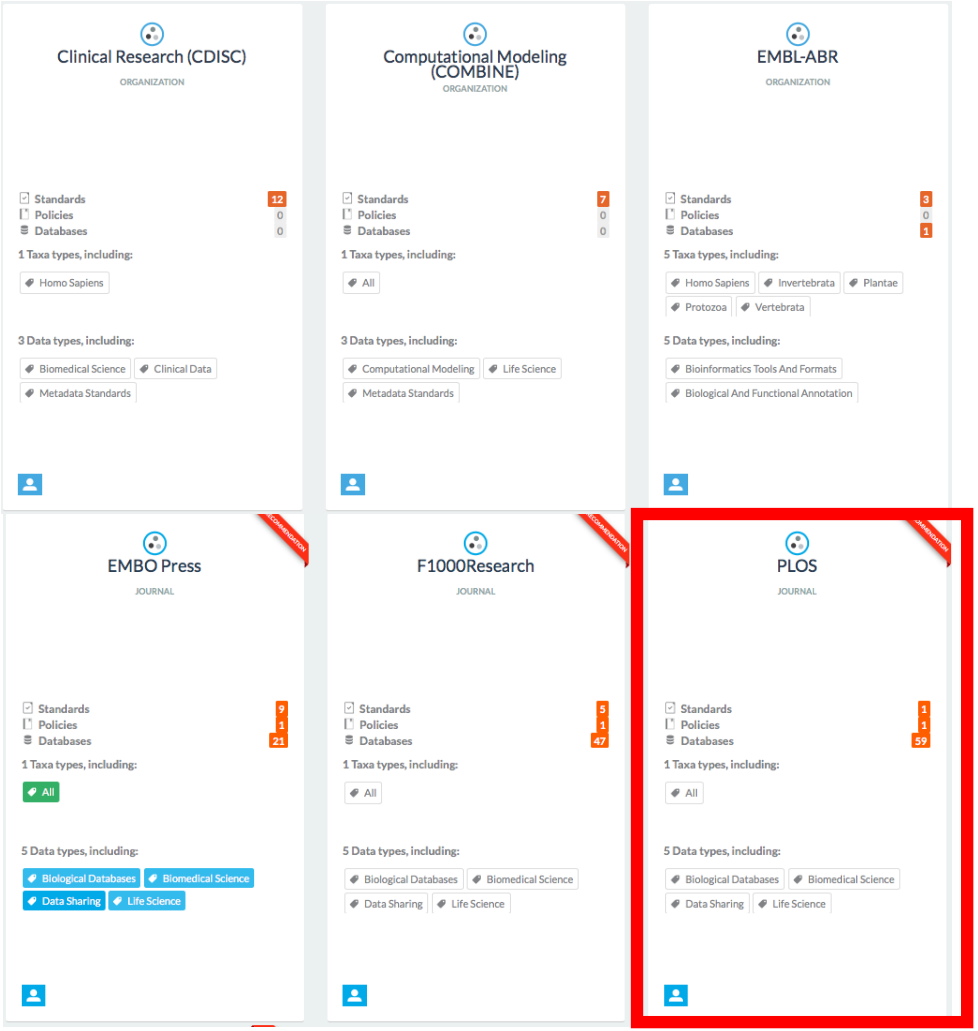
Let us guide you to your results.

| Registry | Name | Abbreviation | Type | Domain | Taxonomy | Related Database | Related Standard | Related Policy | In Collection/Recommendation | Status |
|---|---|---|---|---|---|---|---|---|---|---|
| | ~~Amphibian gross Anatomy Ontology~~ | ~~AAO~~ | Standard | Anatomy | Amphibia | None | None | None | OBO Foundry | D |
| | ~~Amphibian Taxonomy Ontology~~ | ~~ATO~~ | Standard | Taxonomic Information | Amphibia | None | None | None | OBO Foundry | D |
| | Anatomical Entity Ontology | AEO | Standard | Anatomy | Invertebrata, Vertebrata | None | CARO EHDAA2 | None | OBO Foundry | R |
| | Animals in Research: Reporting In Vivo Experiments | ARRIVE | Standard | Animal Research, In-vivo Study, Living Animal | Animalia, Metazoa | None | None | BioMed Central - Minimum Standards of Reporting Checklist F1000 Research Recommended Repositories | F1000Research, BioMed Central | R |
| | ~~Bilateria anatomy~~ | ~~BILA~~ | Standard | Anatomy | Bilateria | 4DXpress | None | None | OBO Foundry | D |
| | Biological Imaging methods | FBbi | Standard | Drosophila, Experiment, Images, Imaging, Life Science | All | FlyBase The Cell: An Image Library | None | None | OBO Foundry | R |

# Grouping the data

**Collections** group together one or more types of resource by domain, project or organization.

**Recommendations** are a core-set of resources that are selected and recommended by a funder or journal data policy.



PLOS has identified a set of established repositories and data standards, which are recognized and trusted within their respective communities, for their journals PLOS Biology, PLOS Medicine, PLOS ONE, PLOS Genetics, PLOS Computational Biology, PLOS Pathogens, and PLOS Neglected Tropical Diseases. PLOS requires that authors comply with field-specific standards for preparation and recording of data and select repositories appropriate to their field, for example deposition of microarray data in ArrayExpress or GEO; deposition of gene sequences in GenBank, EMBL or DDBJ; and deposition of ecological data in Dryad. Authors are encouraged to select repositories that meet accepted criteria as trustworthy digital repositories.

This record is maintained by: eganley , PLOSData

This recommendation is taken from the following policy:

PLOS Recommended Data Repositories.

Record updated: Aug. 18, 2016, 11:28 a.m. by The BioSharing Team.

Homepage | Reference

## Taxonomic range

All

## Scope and data types

Biological Databases | Biomedical Science | Data Sharing | Life Science | Metadata Standards

View as Graph on Preview Server (BETA)

View as Grid | View as Table

Sort by

Best Match

Recommended Records

Recommended

Associated Publication?

No Publication | Has Publication

Claimed?

No Maintainer | Has Maintainer

Record Status

Uncertain | Deprecated | In developme | Ready

Standard Type

Showing records 1 - 50 of 62.

« 1 2 »

R

RECOMMENDED

ArrayExpress

DATABASE

Standards 6

Publications 2

In Collections 1

Recommended 6

1 Taxa types, including:

R

RECOMMENDED

BioGRID

Biological General Repository for Interaction Datasets

DATABASE

BioGRID

Standards 3

Publications 1

In Collections 3

Recommended 2

3 Taxa types, including:

R

RECOMMENDED

BMRB

Biological Magnetic Resonance Databank

DATABASE

Standards 3

Publications 2

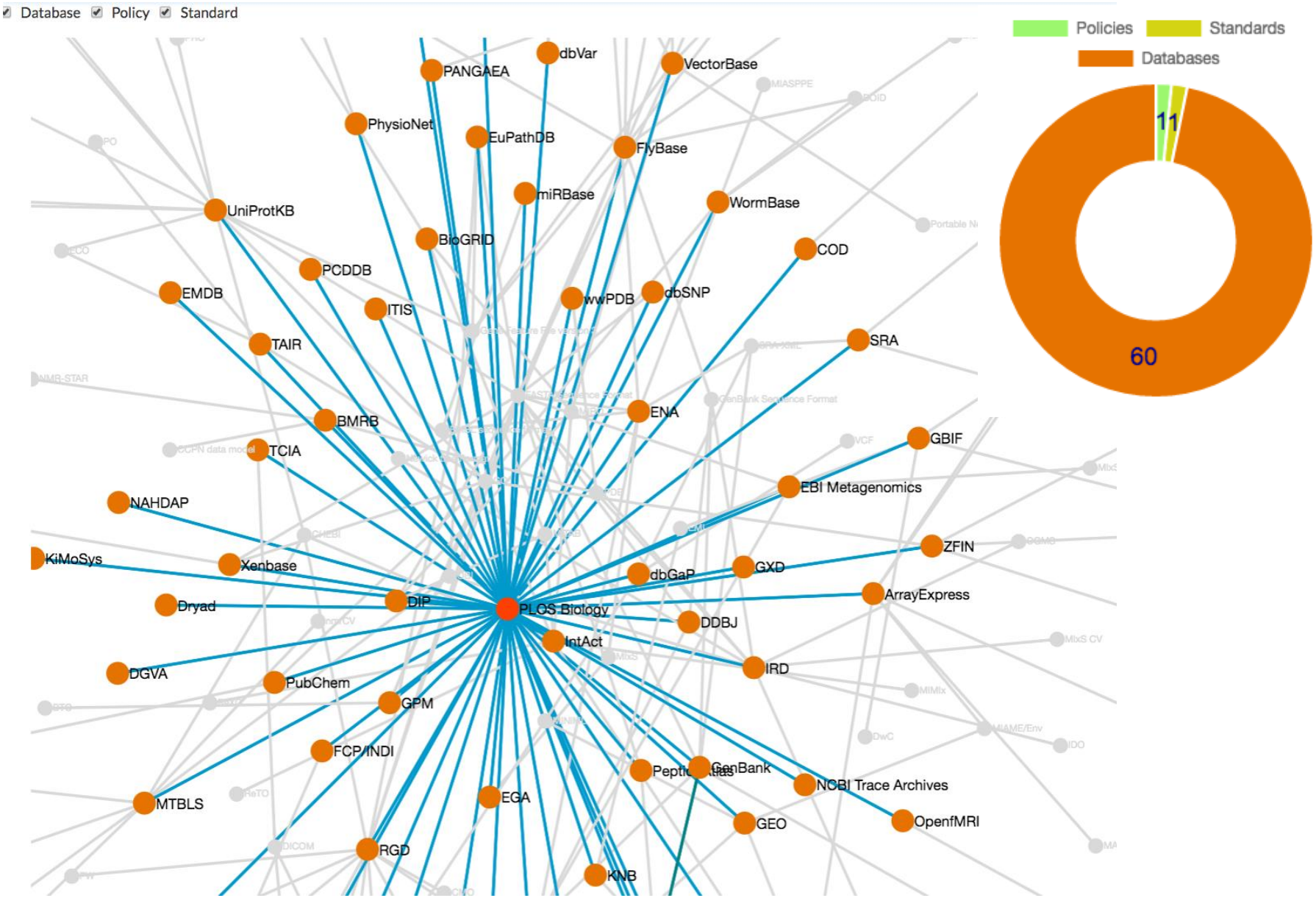
In Collections 1

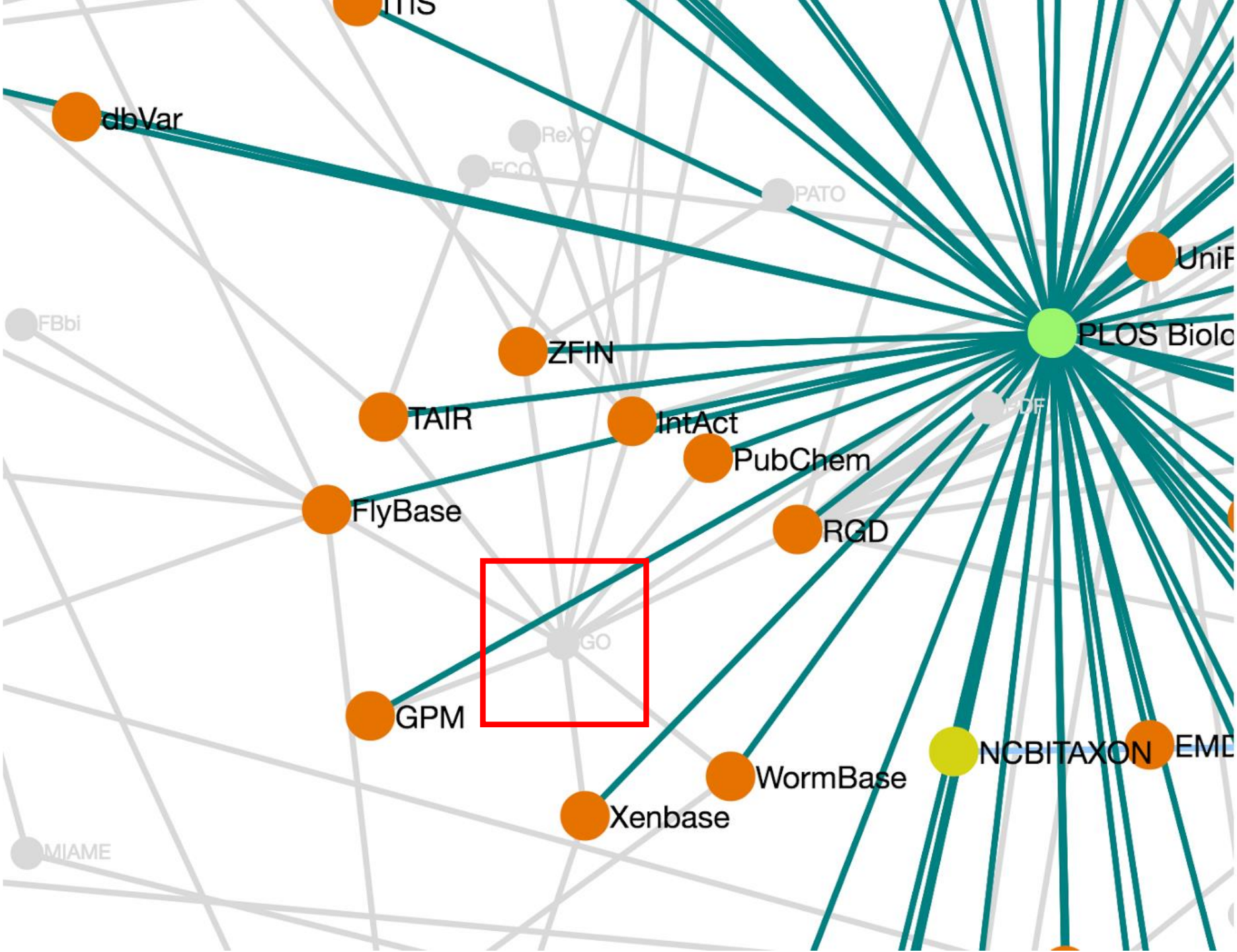
Recommended 2

1 Taxa types, including:

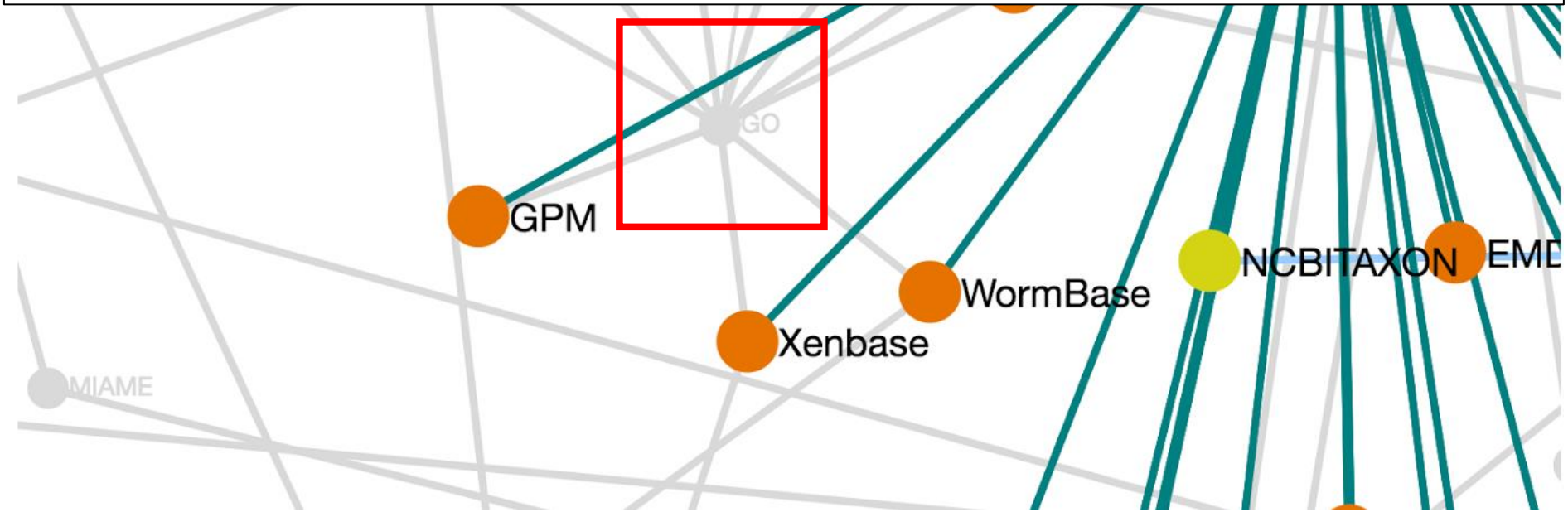
PLOS

View as Graph on Preview Server (BETA)

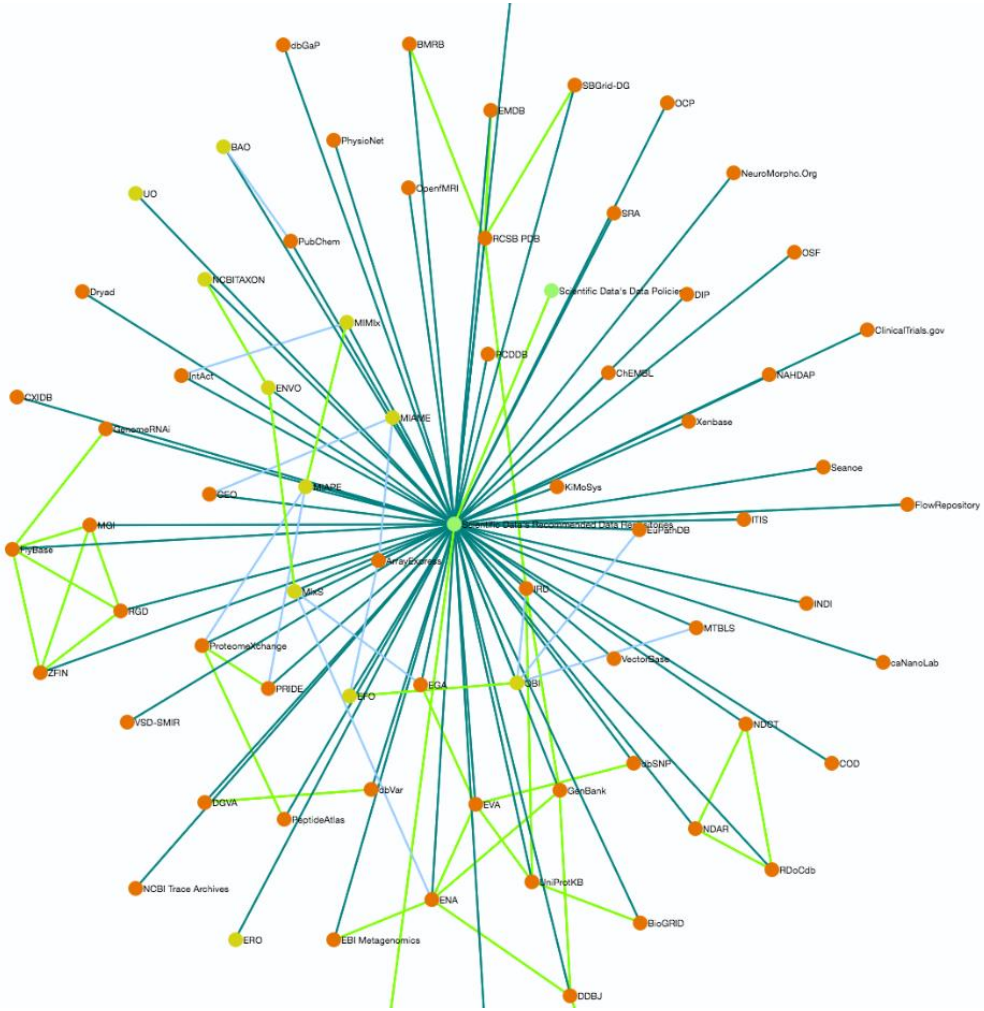


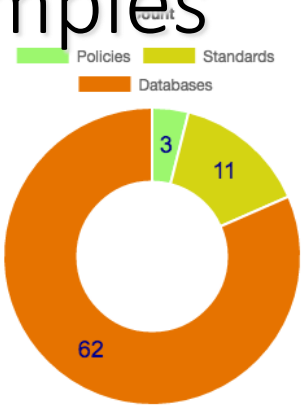

dbVar
ReXO
ECO
PATO
FBbi
ZFIN
TAIR
IntAct
PubChem
FlyBase
RGD
GO
GPM
WormBase
Xenbase
NCBITAXON
MIAME

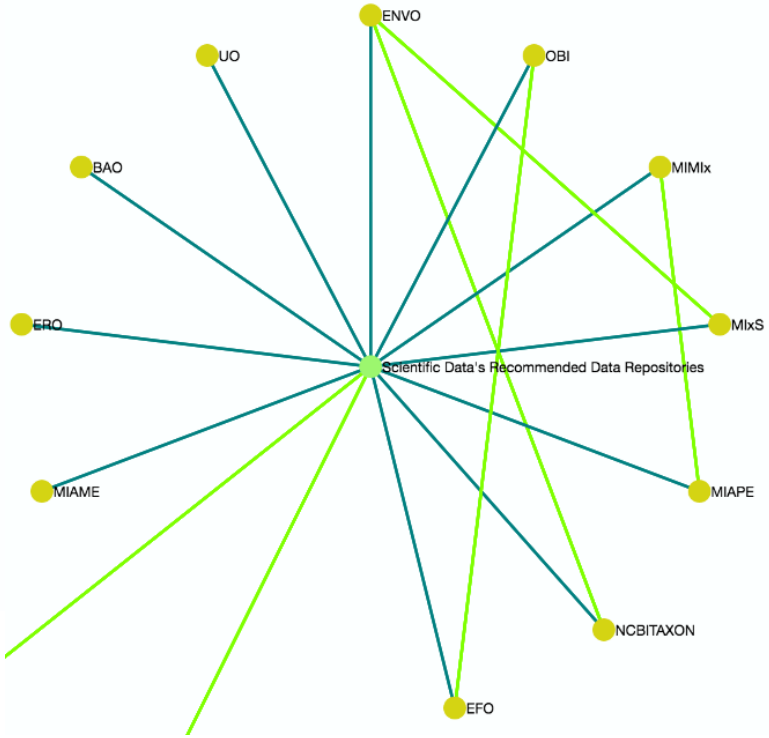

*"BioSharing and its interactive browser will allow us to discover which databases and standards are not currently included in our author guidelines, enabling us to regularly monitor and refine our policies as appropriate, in support of our mission to help our authors enhance the reproducibility of their work."* – Holly Murray, F1000Research



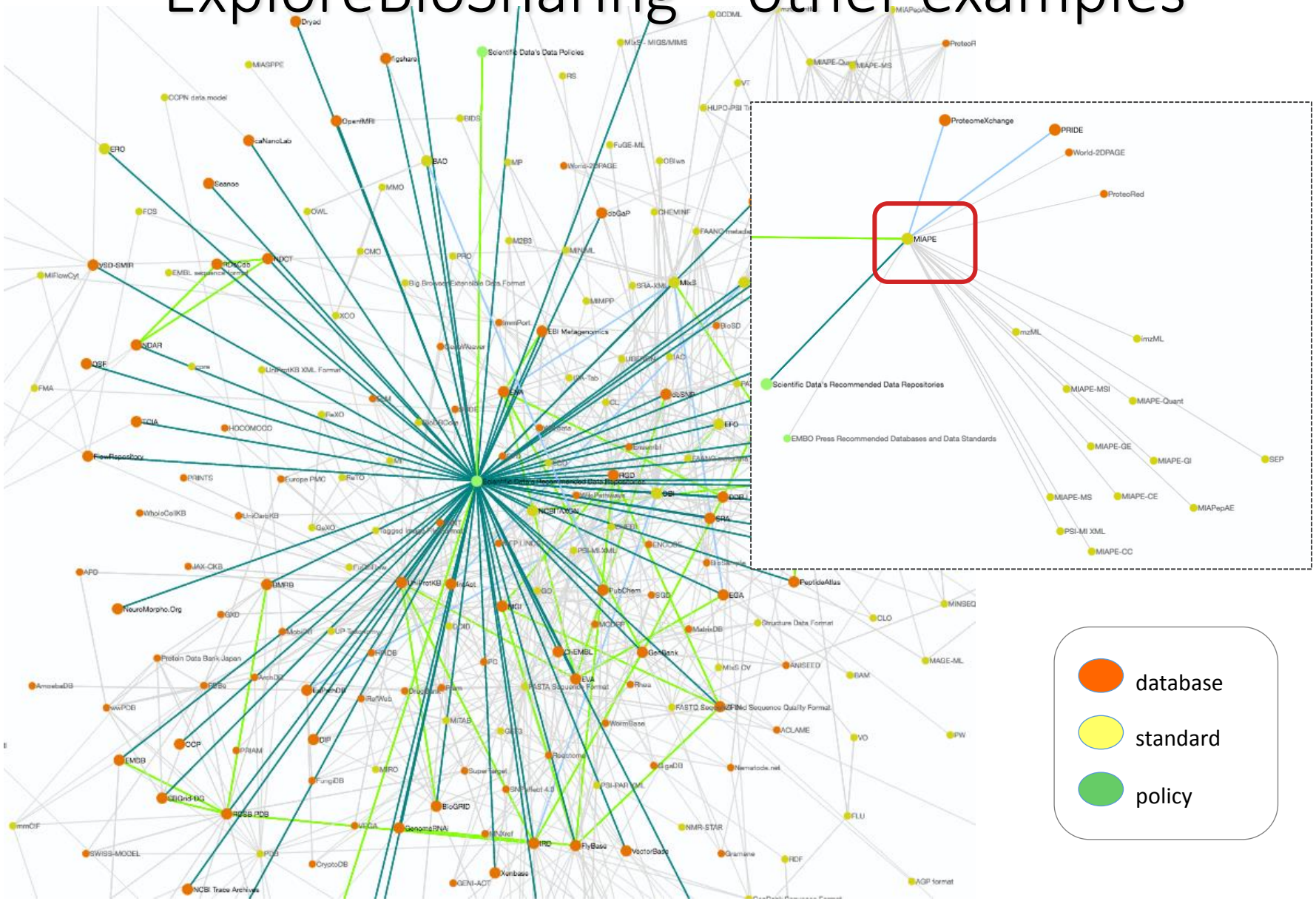
# ExploreBioSharing – other examples



# ExploreBioSharing – other examples



# What we do

**Inform** – what's out there, which databases use which standards. *Map the landscape.*

**Educate** – what databases are recommended by your funder, or journal of choice, which standards should you be using, which standards and databases should you recommend? *Explore the landscape.*

# Adopters/users of BioSharing

## Infrastructure:





## Standard developing communities:





## Journal Publishers:







## Projects/programmes:





## Institutional RDM services:




biosharing.org
Information Resources

# Ongoing engagements

- Database metadata - NBDC Integbio Database Catalog
- Funders - NIH BBSRC bioscience for the future wellcome trust
- Journal Publishers - OXFORD UNIVERSITY PRESS
- Societies – ISB International Society for Biocuration
- Infrastructure – Jisc
- FAIRDOM Collection FAIRDOM

Come and talk to us!

# Advisory Board

- **Susanna-Assunta Sansone** (University of Oxford, NPG Scientific Data), *Operational Team Lead and Co-Chair of the RDA/Force11 WG*
- **Emma Ganley** (PLOS) Co-chair
- **Varsha Khodiyar** (NPG) Co-chair
- **Michael Ball** (BBSRC)
- **Theo Bloom** (BMJ)
- **Jennifer Boyd** (OUP)
- **Scott Edmunds** (GigaScience, BGI)
- **Jeff Grethe** (USCD; NIF, NIDDK Information Network and NIH BD2K bioCADDIE )
- **Melissa Haendel** (OHSU, USA; Force11; Monarch Initiative)
- **Simon Hodson** (CODATA), *Co-Chair of the RDA/Force11 WG*
- **Rafael Jimenez** (ELIXIR)
- **Amye Kenall** (BMC)
- **Rebecca Lawrence** (F1000), *Co-Chair of the RDA/Force11 WG*
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- **Jennifer Lin** (CrossRef)
- **David Kernohan** (JISC)
- **Gabriella Rustici** (ELIXIR UK Node Industry Training Sector Lead, University of Cambridge, UK)
- **Helena Cousijn** (Elsevier)
- **Jonathan Tedds** (Ubiquity Press Open Health Data journal; University of Leicester, UK)
- **Jessica Tenenbaum** (Duke University, USA; Chair Elect for the American Medical Informatics Association's Genomics WG)
- **Todd Vision** (UNC Chapel Hill & NESCent, USA; Dryad)
- **Michael Witt** (re3data; Purdue University Libraries)

# Operational Team

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Senior Research Lecturer

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Research Lecturer

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Research Software Engineer

Allyson Lister
Knowledge Engineer

Peter McQuilton
Knowledge Engineer

David Johnson
Research Software Engineer

Massimiliano Izzo
Research Software Engineer

Eamonn Maguire
Contractor

Delphine Dauga
Contract Biocurator

Melanie Adekale
Contract Biocurator

## Team is funded by

# Thank – you!

- Add/link your standard to BioSharing
- Add/link your database
- Use us to inform your data policy (and add/link your policy)
- Make a collection or recommendation for your group/society

https://biosharing.org

**@biosharing**

**peter.mcquilton@oerc.ox.ac.uk**
**@drosophilic**