DATABASE
The Journal of Biological Databases and Curation

Database, 2016, 1–8
doi: 10.1093/database/baw075
Original article

Original article

BioSharing: curated and crowd-sourced metadata standards, databases and data policies in the life sciences

Peter McQuilton[1,*] Alejandra Gonzalez-Beltran[1] Philippe Rocca-Serra[1] Milo Thurston[1] Allyson Lister[1] Eamonn Maguire[2] and Susanna-Assunta Sansone[1]

[1]Oxford e-Research Centre, University of Oxford, 7 Keble Road, Oxford OX1 3QG, UK and [2]CERN European Laboratory for Particle Physics, Route de Meyrin, Geneva 23, 1211, CH, Switzerland

*Corresponding Author: Email: peter.mcquilton@oerc.ox.ac.uk

Citation details: McQuilton,P., Gonzalez-Beltran,A., Rocca-Serra,P. *et al.* BioSharing: curated and crowd-sourced metadata standards, databases and data policies in the life sciences. *Database* (2016) Vol. 2016: article ID baw075; doi:10.1093/database/baw075

Received 7 November 2015; Revised 24 March 2016; Accepted 22 April 2016

Abstract

BioSharing (http://www.biosharing.org) is a manually curated, searchable portal of three linked registries. These resources cover standards (terminologies, formats and models, and reporting guidelines), databases, and data policies in the life sciences, broadly encompassing the biological, environmental and biomedical sciences. Launched in 2011 and built by the same core team as the successful MIBBI portal, BioSharing harnesses community curation to collate and cross-reference resources across the life sciences from around the world. BioSharing makes these resources findable and accessible (the core of the FAIR principle). Every record is designed to be interlinked, providing a detailed description not only on the resource itself, but also on its relations with other life science infrastructures. Serving a variety of stakeholders, BioSharing cultivates a growing community, to which it offers diverse benefits. It is a resource for funding bodies and journal publishers to navigate the metadata landscape of the biological sciences; an educational resource for librarians and information advisors; a publicising platform for standard and database developers/curators; and a research tool for bench and computer scientists to plan their work. BioSharing is working with an increasing number of journals and other registries, for example linking standards and databases to training material and tools. Driven by an international Advisory Board, the BioSharing user-base has grown by over 40% (by unique IP address), in the last year thanks to successful engagement with researchers, publishers, librarians, developers and other stakeholders via several routes, including a joint RDA/Force11 working group and a collaboration with the International Society for Biocuration. In this article, we describe BioSharing, with a particular focus on community-led curation.

Database URL: https://www.biosharing.org

Rationale and Background

The growing movement for reproducible research and interoperability, along with an overall increase in data generation, has led to a proliferation of community-developed metadata standards, bringing with it many sociological and technological challenges (1, 2). As the costs of data production fall, the number of databases hosting that data has increased, leading to confusion over which database to use to store and search for the latest and most comprehensive data. Concurrently, there has been an increase in data standards as different community groups and databases develop different data formats, schema and reporting guidelines. This proliferation in content standards and databases creates a barrier for researchers and database maintainers, creating confusion over which standard they should use to format their data, or which database to submit their data to. There have been a number of projects that have helped bring order to this evolving field, such as the Nucleic Acid Research Database issue, this journal, and projects such as the JISC journal policy project (https://www.jisc.ac.uk/rd/projects/journal-research-data-policy-registry-pilot), which maps journal data policies with data standards and repositories. However, none of these projects connect all three aspects surrounding data deposition (i.e. the standards one should use, which particular database to deposit data, or which standards and repositories are recommended by a particular funder or journal), or answer questions such as 'Is a particular standard mature enough to be used, which version should be used, and is it actively maintained?' or 'Which databases implement the most widespread and endorsed standards?'. Both standard and database maintainers can struggle in gaining visibility for their resource, to help encourage their adoption and endorsement. Conversely, librarians, data specialists, funding agencies and journal publishers often lack the resources to make an informed judgement on which database or standard to recommend to their user group. BioSharing, composed of three registries covering content standards, databases and data policies in the life sciences, aims to map the landscape of community-developed standards and databases, linking between and from them to data policies from funding agencies and journal publishers. In doing so, BioSharing aims to promote harmonisation and consistency, to reduce the reinvention and needless proliferation of standards and databases. BioSharing is a pivotal resource for the implementation of the ELIXIR-supported FAIR principles, defining the characteristics that contemporary data resources, tools and infrastructures should exhibit—to be **F**indable, **A**ccessible, **I**nteroperable and **R**eusable by third-parties (3).

BioSharing is a curated, searchable portal of linked information on content standards, databases, and (progressively) journal and funder policies in the life sciences, broadly encompassing the biological, environmental and biomedical sciences. Launched in 2011, BioSharing is an extension and natural evolution of the MIBBI portal (4) (MIBBI, Minimum Information for Biological and Biomedical Investigations; BioSharing is founded by the same core team), and is maintained as a community resource closely embedded in and co-sponsored by several infrastructure programs, including the NIH Big Data to Knowledge Initiative's BioCADDIE (https://biocaddie.org) and CEDAR (http://med.stanford.edu/cedar.html) projects. BioSharing is also being enhanced as part of the Elixir UK node's contribution to the ELIXIR EXCELERATE program (http://www.elixir-europe.org/excelerate/interoperability). BioSharing ensures that data standards, biological databases and data policies are registered, informative and discoverable. As a one-stop shop for standards, databases and data policies in the life sciences, BioSharing not only links these resources, but also details the relationships between them, providing context and metrics, as standards evolve and are implemented in databases, and both standards and databases are recommended by journal or funding body data policies. BioSharing also provides a historical perspective on these standards and databases, detailing when different versions of a standard are created or deprecated, and when updates to a database or policy appear, so enabling users to assess the maturity and evolution of each resource.

Although all records in BioSharing are manually curated, many have been added and edited by the community themselves, rather than BioSharing curators. Users are able to claim the record(s) for the resource(s) they maintain. This allows them to not only gain personal recognition for their work, but also ensures that the data on their resource is accurate and completely up-to-date. This community curation aspect of BioSharing, along with the linking and embedding of each record into the landscape of standards and databases, helps make BioSharing an accurate and comprehensive representation of metadata standards, databases and policies in the life sciences.

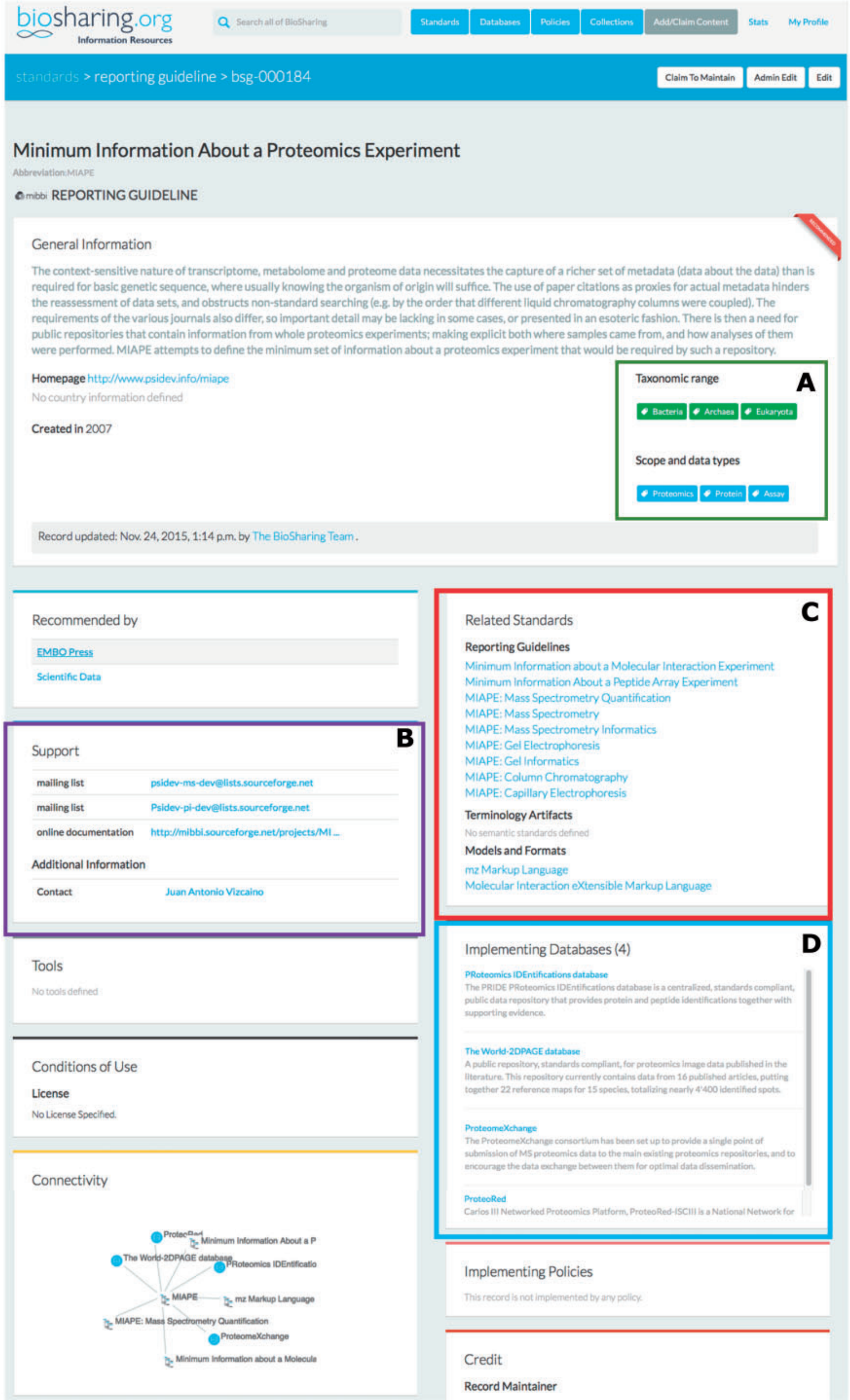
The Three Registries

BioSharing has grown year-on-year to contain over 1300 records, split between the three registries (Standards, Databases and Policies). The Standards registry is split further into three types of data standard according to the focus: Reporting Guideline (content), Model/Format (syntax) and Terminology artifact (semantics). The Reporting Guideline subtype details the information elements that need to be expressed in order to create a common core set of descriptors for different datasets. Examples include the ARRIVE (5) (Animal Research: Reporting in-vivo experiments) guidelines, which consist of a 20-item checklist and recommendations for authors for reporting study design, experimental procedures and experimental animals. The Model/Format subtype covers data models and exchange formats that are used in data sharing. An example is the ISA-Tab format (6), which is an extensible, hierarchical structure that describes the experimental metadata with elements such as the sample characteristics, technology and measurement types used and sample-to-data relationships. Where possible, the xsd schema files for these standards are available from BioSharing, so saving time for those users who wish to see the schema directly. The third standard subtype, Terminology artifacts, are semantic representations of a topic or field used to catalogue and organise data into structural hierarchies (ontologies) with coded relationships between them (e.g. the Disease Ontology (7), that categorises human diseases, such that Parkinson's Disease is a Neurodegenerative disease). This allows the organisation and retrieval of data in a structured manner and these standards are integral to data management and searching. This subtype is curated in collaboration with BioPortal (8) and the OBO Foundry (9).

Community standards arise and iterate as the data and requirements change. BioSharing reflects this evolution by tracking the versioning, extension, and deprecation of standards. The Proteomics Standards Initiative (10), defining community standards for data representation in proteomics, provide a good example to illustrate this. The original standard for proteomic experiments, MIAPE—Minimum Information About a Proteomics Experiment (11), is a Reporting Guideline first developed in 2007 to guide the capture of metadata pertaining to proteomic experiments. Over time this standard has diversified to include eight other standards, covering mass spectrometry experiments, informatics, quantification, gel electrophoresis, column chromatography and more. These extensions are standards in their own right, but are related to each other and the original MIAPE standard. We capture all this information using our Related Standards interface (see Figure 1). We also capture when these standards are implemented in a database (e.g. the PRIDE database at the EBI, see figure), so allowing users to see the level of adoption of a standard. These standards also evolve over time. We capture when a standard is replaced by a new version, or split into more than one standard. We also record when a standard is deprecated. We retain the record, but add a note explaining the deprecation and, where applicable, direct users to a new standard that is related to or that supersedes the deprecated standard.

The BioSharing Database registry contains around 700 entries, curated from the published literature and direct user input. Through collaboration with Oxford University Press, we semi-automatically curate database information from the yearly Nucleic Acids Research Database issue (from 2010 onwards). The database registry follows the BioDBcore guidelines (12), which we co-developed with the International Society for Biocuration (www.biocuration.org). The BioDBcore guidelines are a community-defined, uniform, generic description of the core attributes of a biological database. BioSharing encourages and drives database developers/biocurators to follow these guidelines when submitting or editing their records. We will use the Metabolights (13) record as an example to illustrate the registry (see Figure 2). At the top of the record, as with all records in BioSharing, there is a URL linking to the homepage of the resource, and a short free text description. Below this, there is country and taxonomy information, curated using a controlled set of tags based on the list of country names provided by the United Nations and the NCBI Taxonomy (14). The data type and scope of the resource is summarised using a community-generated set of tags (see the community curation section below for more information). Below the top section of the record, there are a number of sections relating to the support information about the resource (e.g. tutorials, help mail, FAQs), contact details, publications, and the tools and web services available from the database. The Credit section of the record details the group or organisation behind the resource, and grant or funding information. This section also contains a link to the maintainer of the record (where available). This maintainer is someone associated with the resource itself, and is able to edit and update the record directly (more information about becoming a maintainer and community curation can be found in the 'Community curation' section below). By collating this information into one resource, and augmenting it with links to our standard and policy registries, the BioSharing database registry is the most comprehensive catalogue of biological databases available today.

Our growing Policy registry will progressively collate data preservation, management and sharing policies from international funding agencies, regulators and journals.



Minimum Information About a Proteomics Experiment

Abbreviation:MIAPE

mibbi REPORTING GUIDELINE

General Information

The context-sensitive nature of transcriptome, metabolome and proteome data necessitates the capture of a richer set of metadata (data about the data) than is required for basic genetic sequence, where usually knowing the organism of origin will suffice. The use of paper citations as proxies for actual metadata hinders the reassessment of data sets, and obstructs non-standard searching (e.g. by the order that different liquid chromatography columns were coupled). The requirements of the various journals also differ, so important detail may be lacking in some cases, or presented in an esoteric fashion. There is then a need for public repositories that contain information from whole proteomics experiments; making explicit both where samples came from, and how analyses of them were performed. MIAPE attempts to define the minimum set of information about a proteomics experiment that would be required by such a repository.

Homepage http://www.psidev.info/miape

No country information defined

Created in 2007

Taxonomic range

Bacteria Archaea Eukaryota

Scope and data types

Proteomics Protein Assay

Record updated: Nov. 24, 2015, 1:14 p.m. by The BioSharing Team .

Recommended by

EMBO Press

Scientific Data

Support

mailing list	psidev-ms-dev@lists.sourceforge.net
mailing list	Psidev-pi-dev@lists.sourceforge.net
online documentation	http://mibbi.sourceforge.net/projects/MI ...

Additional Information

Contact	Juan Antonio Vizcaino

Tools

No tools defined

Conditions of Use

License

No License Specified.

Connectivity

Related Standards

Reporting Guidelines

Minimum Information about a Molecular Interaction Experiment
Minimum Information About a Peptide Array Experiment
MIAPE: Mass Spectrometry Quantification
MIAPE: Mass Spectrometry
MIAPE: Mass Spectrometry Informatics
MIAPE: Gel Electrophoresis
MIAPE: Gel Informatics
MIAPE: Column Chromatography
MIAPE: Capillary Electrophoresis

Terminology Artifacts

No semantic standards defined

Models and Formats

mz Markup Language
Molecular Interaction eXtensible Markup Language

Implementing Databases (4)

PRoteomics IDEntifications database
The PRIDE PRoteomics IDEntifications database is a centralized, standards compliant, public data repository that provides protein and peptide identifications together with supporting evidence.

The World-2DPAGE database
A public repository, standards compliant, for proteomics image data published in the literature. This repository currently contains data from 16 published articles, putting together 22 reference maps for 15 species, totalizing nearly 4'400 identified spots.

ProteomeXchange
The ProteomeXchange consortium has been set up to provide a single point of submission of MS proteomics data to the main existing proteomics repositories, and to encourage the data exchange between them for optimal data dissemination.

ProteoRed
Carlos III Networked Proteomics Platform, ProteoRed-ISCIII is a National Network for

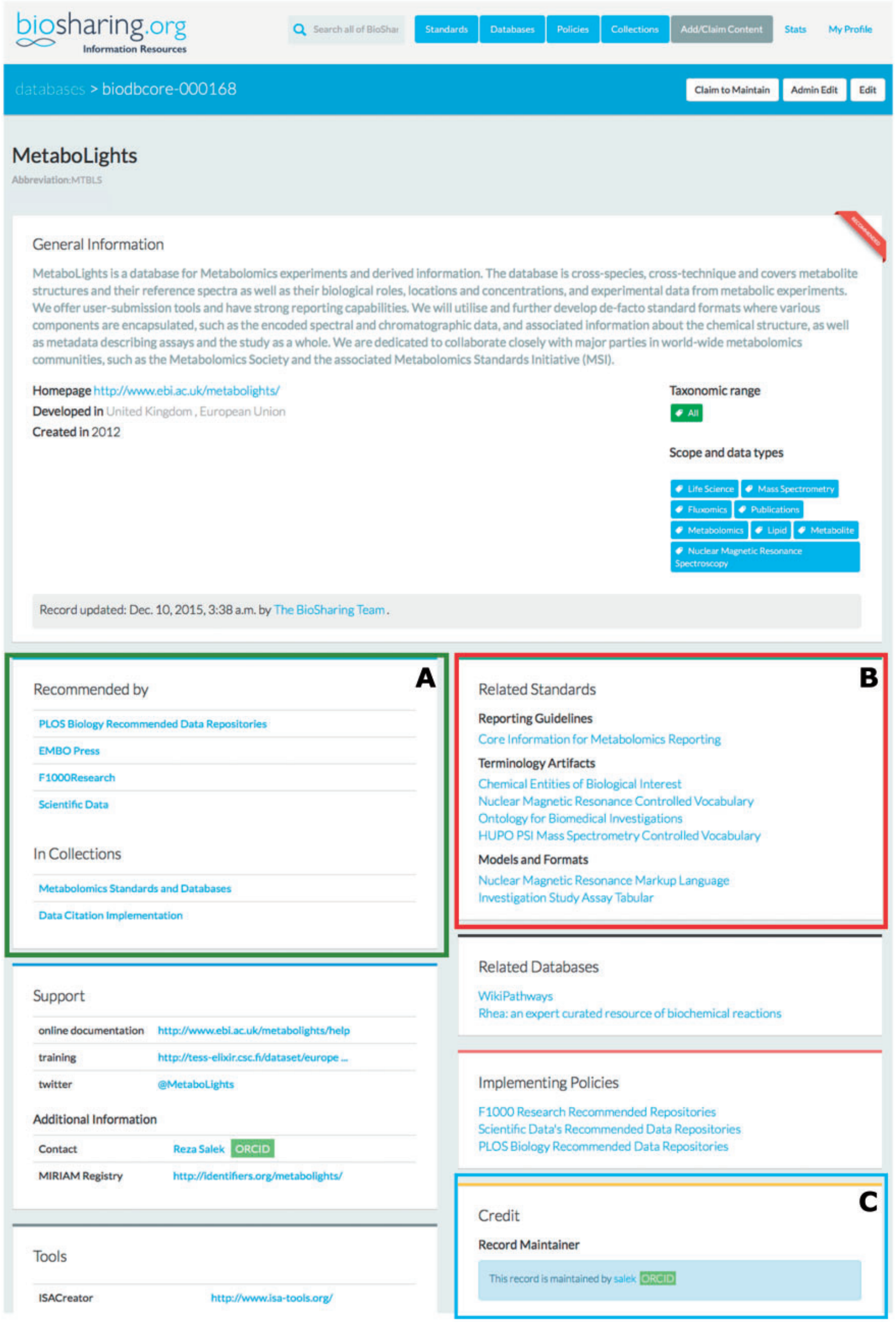
Implementing Policies

This record is not implemented by any policy.

Credit

Record Maintainer

Figure 1 The BioSharing MIAPE Standard Record (top section). In the General Information section, the Taxonomic Range and Scope and data types tags are highlighted in a green box **(A)**. Clicking on a tag from within these two fields initiates a search for all the records annotated with that tag. The Support section **(B**—highlighted in purple) contains information on help documentation, mailing lists and contact details. The Related Standards section **(C**—highlighted in red) contains links to other metadata standards, such as the extensions to the initial MIAPE standard. Beneath this section, the implementing databases section **(D**—highlighted in blue) provides links to those resources that have implemented the MIAPE standard (e.g. The PRIDE database).



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).

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

Taxonomic range

All

Scope and data types

Life Science · Mass Spectrometry · Fluxomics · Publications · Metabolomics · Lipid · Metabolite · Nuclear Magnetic Resonance Spectroscopy

Record updated: Dec. 10, 2015, 3:38 a.m. by The BioSharing Team .

Recommended by

- PLOS Biology Recommended Data Repositories
- EMBO Press
- F1000Research
- Scientific Data

In Collections

- Metabolomics Standards and Databases
- Data Citation Implementation

Support

online documentation	http://www.ebi.ac.uk/metabolights/help
training	http://tess-elixir.csc.fi/dataset/europe ...
twitter	@MetaboLights

Additional Information

Contact	Reza Salek ORCID
MIRIAM Registry	http://identifiers.org/metabolights/

Tools

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

Related Standards

Reporting Guidelines

Core Information for Metabolomics Reporting

Terminology Artifacts

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

Models and Formats

Nuclear Magnetic Resonance Markup Language
Investigation Study Assay Tabular

Related Databases

WikiPathways
Rhea: an expert curated resource of biochemical reactions

Implementing Policies

F1000 Research Recommended Repositories
Scientific Data's Recommended Data Repositories
PLOS Biology Recommended Data Repositories

Credit

Record Maintainer

This record is maintained by salek ORCID

Figure 2 The top section of the BioSharing Metabolights Database Record. Every record on BioSharing starts with a general information section, containing a description of the resource, and details of the domains and species that the resource covers. Further, more specific details are found in the boxes beneath this section. If a resource is selected in a Collection or Recommendation, this information is provided in the 'In Collections' section (**A**—highlighted in green). The standards implemented in the Metabolights database are found in the Related Standards section (**B**—highlighted in red), split into the three standard subtypes. The Metabolights database record is maintained by the resource themselves. This information is found in the Credit section (**C**—highlighted in blue). Clicking on the maintainer link takes you to the profile for the maintainer, with information linked from their ORCID account, if connected. This section also contains information on the group that has developed the resource and funding information. The Metabolights database is mentioned in four collections (as of November 2015). Clicking on any of the links in this section takes the user directly to the collection.

The registry currently records over 20 data policies and links these to both standards and databases. We expect this area of BioSharing to grow substantially in the future, in collaboration with JISC (the UK higher, further education and skills sectors' not-for-profit organisation for digital services and solutions) and as part of an RDA/Force11 joint working group (see the 'Community Curation' section below for more information).

Collections and Recommendations

Our 'Collection' feature allows organisations and selected users to collate records across the registries, appropriate to their field or focus. This 'grouping' feature generates a view of the standards, databases and policies that are particular to an organisation, project or area of interest. Some of our Collections are 'Recommendations'. These are core groupings of databases and/or standards for a particular domain, as recommended by a community group, funder, journal publisher or indeed the BioSharing team. An example of this is the Nature Publishing Group Scientific Data repositories and standards Recommendation which collates 58 databases and 5 data standards that are considered mature and stable enough to be recommended by the journal (https://biosharing.org/recommendation/ScientificData). Records mentioned in a Recommendation are flagged with a red 'Recommended' ribbon. We have Recommendations from a number of other journal publishers, such as BioMed Central and PLOS as well as Collections from projects such as NIH BD2K bioCADDIE and eTRIKS (https://www.etriks.org). Creating these Collections/Recommendations not only helps publishers, funding agencies, librarians and researchers filter through the sea of standards and databases in the life sciences, but also places the selected records in context within the BioSharing ecosystem, where we display information on which standards are implemented in each database, along with other relationships and links between the resources.

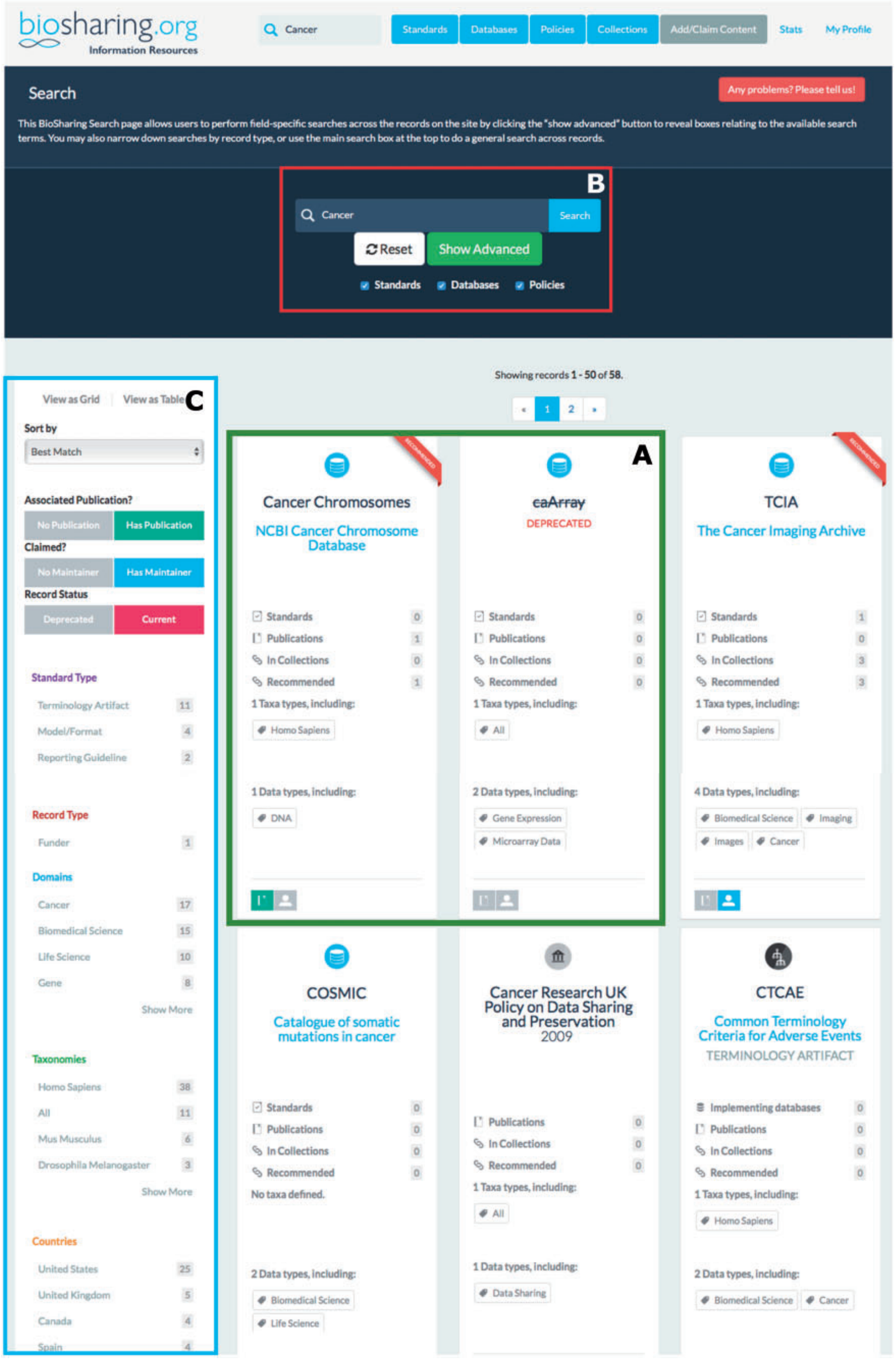
Browsing and Searching BioSharing

The whole of BioSharing, the three registries and the Collections/Recommendations, can be searched from the homepage using our main search box, or the smaller search box located in the top right hand side of every page. Clicking on our Advanced Search reveals 12 field-specific searches, such as resources with particular funders or licences, or for a specific species, country or domain. Clicking on the askBioSharing logo, to the right of the search box on the homepage, provides access both to the Recommendations and the BioSharing wizard. This wizard guides users through the data in a step-by-step manner (selecting the registry, domain and species) providing users with a short list of results tailored to their requirements. In addition to the search options, the homepage provides links to each registry and some brief statistics, alongside links to help and technical documentation, an orientation tour of BioSharing, and our community, collaborators and advisory board.

Search hits can be viewed in a table or as 'cards' that display some minimal information. An example search is shown in Figure 3. The retrieved list can be ordered and filtered using the filter matrix on the left-hand side of the page. Example filters include displaying only those records that have a publication associated with them, or that are open access, or that cover a particular domain or species. Access to browse each registry or the Collections is provided by buttons at the top of every page on BioSharing.

Community Curation

As a community effort, BioSharing offers the ability for users to add, edit and claim records and Collections. While the BioSharing team curates and integrates the descriptions of standards, databases and policies, we know that the creators and maintainers of these resources know their data best. If you are a database curator or developer, a standard maintainer, or policy advisor, you can help BioSharing by claiming and maintaining the record for your resource. If a resource is missing you can submit a new record in the appropriate registry. Why should you claim a record? First and foremost, to make your resource more discoverable to others. Second, to get credit, both for you and your group/organisation. Claiming a record is a one-off event, after which the BioSharing team will continue to link your resource(s) to others, making them even more visible. Once users have signed-up for an account, they can add or edit the record(s) for their resource via our online data entry forms. These forms, tailored to each registry type or subtype, are a mixture of optional and mandatory fields. To help users complete the forms, there is a short explanation above each field or section, detailing the type of data therein. Some fields are free text (e.g. the description field, common to all records), while others have a few restrictions (e.g. the homepage URL field must contain a valid URL). A third type of field contains a restricted list of options, accessible via a drop-down menu (e.g. the support section, containing options such as online documentation, tutorial, or contact email). Finally, a number of fields contain a semi-structured list of controlled vocabulary terms. For example, the Taxonomy and Scope and Data Types fields (present on Standard and Database records) capture the species covered using the NCBI taxonomy ontology, and the nature of the resource using controlled tags from



This BioSharing Search page allows users to perform field-specific searches across the records on the site by clicking the "show advanced" button to reveal boxes relating to the available search terms. You may also narrow down searches by record type, or use the main search box at the top to do a general search across records.

Showing records 1 - 50 of 58.

Standard Type

Terminology Artifact	11
Model/Format	4
Reporting Guideline	2

Record Type

Funder	1

Domains

Cancer	17
Biomedical Science	15
Life Science	10
Gene	8

Taxonomies

Homo Sapiens	38
All	11
Mus Musculus	6
Drosophila Melanogaster	3

Countries

United States	25
United Kingdom	5
Canada	4
Spain	4

Cancer Chromosomes
NCBI Cancer Chromosome Database

Standards	0
Publications	1
In Collections	0
Recommended	1

1 Taxa types, including: Homo Sapiens

1 Data types, including: DNA

~~caArray~~
DEPRECATED

Standards	0
Publications	0
In Collections	0
Recommended	0

1 Taxa types, including: All

2 Data types, including: Gene Expression, Microarray Data

TCIA
The Cancer Imaging Archive

Standards	1
Publications	0
In Collections	3
Recommended	3

1 Taxa types, including: Homo Sapiens

4 Data types, including: Biomedical Science, Imaging, Images, Cancer

COSMIC
Catalogue of somatic mutations in cancer

Standards	0
Publications	0
In Collections	0
Recommended	0

No taxa defined.

2 Data types, including: Biomedical Science, Life Science

Cancer Research UK Policy on Data Sharing and Preservation 2009

Publications	0
In Collections	0
Recommended	0

1 Taxa types, including: All

1 Data types, including: Data Sharing

CTCAE
Common Terminology Criteria for Adverse Events
TERMINOLOGY ARTIFACT

Implementing databases	0
Publications	0
In Collections	0
Recommended	0

1 Taxa types, including: Homo Sapiens

2 Data types, including: Biomedical Science, Cancer

Figure 3 Searching BioSharing. Every search in BioSharing returns a hit list displayed as either a table or grid. In this example search, for the text 'cancer', 56 records have been retrieved from across the three registries and collections. Each record 'card' provides a snapshot of information. Note that the first search hit is recommended, and the second search hit, caArray, is a deprecated database (**A**—both highlighted in green). This search can be defined further by clicking on the advanced search option in the top search section (**B**—highlighted in red), which leads to a field-specific search. The search can be refined using the filter matrix, found down the left-hand side of the search results (**C**—highlighted in blue). This filter allows the selection of records based on a range of information. For example, whether they have a publication associated with them, if they pertain to a particular species or domain, or are associated with a particular country or funding agency.

four categories—Process, Material, DataType and Property. These tags are taken from community ontologies, such as those of the OBO Foundry, and are currently organised in a semi-structured list.

If you are a database developer or curator, you can add a section to your database website where you describe your database, following the BioDBcore guidelines, detailing (among other information) what type of data is in the database, whether it is open access, and what tools and documentation are available. We are exploring methods to automatically ingest this information into BioSharing, so making it easier for maintainers to update the metadata surrounding their resource.

BioSharing is driven by the community it serves. An international Advisory Board, with members drawn from the worlds of research, publishing, content standards, funding agencies and data resources, provides guidance and advice on our direction, user interface and curation. We also receive feedback from record maintainers and users, along with community interest. BioSharing has many users, from different backgrounds and with different needs, from the standard developer to the journal editor. Coordinating, accommodating and serving these diverse requirements is an ongoing challenge. To help address this, BioSharing, with Advisory Board members and interested members of the community, has created a joint RDA/ FORCE11 BioSharing Working Group which aims to define the principles behind the links between the content standards, databases and policies in BioSharing. To further understand our user requirements, BioSharing has recently surveyed over 500 users from around the world as part of our work with the ELIXIR EXCELERATE program, to better assess their needs for and requirements from, a standards registry in the life sciences. Feedback from this survey, and through the BioSharing website, will help define our future priorites. Through this community engagement, we hope to continue to develop BioSharing as an information resource for the life sciences, building not only on the three registries but also on the links between them, in a progressive and comprehensive manner.

Acknowledgements

We are grateful to the University of Oxford e-Research Centre, IMI eTRIKS and the BBSRC COPO project, ELIXIR UK node and the NIH BD2K bioCADDIE and CEDAR projects for co-funding this work.

Conflict of interest. None declared.

References

1. Bourne,P.E., Lorsch,J.R. and Green,E.D. (2015) Perspective: Sustaining the big-data ecosystem. *Nature*, 527, S16–S17.
2. Tenenbaum,J.D., Sansone,S.-A. and Haendel,M. (2014) A sea of standards for omics data: sink or swim? *J. Am. Med. Inform. Assoc.*, 21, 200–203.
3. Wilkinson,M.D., Dumontier,M., Aalbersberg,I.J., *et al.* (2016) The FAIR Guiding Principles for scientific data management and stewardship. *Scientific Data*, 3, 160018.
4. Taylor,C.F., Field,D., Sansone,S.-A., *et al.* (2008) Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. *Nat. Biotechnol.*, 26, 889–896.
5. Kilkenny,C., Browne,W.J., Cuthill,I.C., *et al.* (2010) Improving bioscience research reporting: the ARRIVE guidelines for reporting animal research. *PLoS Biol.*, 8, e1000412. oi:10.1371/ journal.pbio.1000412.
6. Rocca-Serra,P., Brandizi,M., Maguire,E., *et al.* (2010) ISA software suite: supporting standards-compliant experimental annotation and enabling curation at the community level. *Bioinformatics*, 26, 2354–2356.
7. Schriml,L.M., Arze,C., Nadendla,S., *et al.* (2012) Disease Ontology: a backbone for disease semantic integration. *Nucleic Acids Res.*, 40, D940–D946.
8. Whetzel,P.L., Noy,N.F., Shah,N.H.,. *et al.* (2011) BioPortal: enhanced functionality via new Web services from the National Center for Biomedical Ontology to access and use ontologies in software applications. *Nucleic Acids Res.*, 39, W541–W545.
9. Smith,B., Ashburner,M., Rosse,C., *et al.* The OBI Consortium. (2007) The OBO Foundry: coordinated evolution of ontologies to support biomedical data integration. *Nat. Biotechnol.*, 25, 1251–1255.
10. Orchard,S., Hermajakob,H. and Apweiler,R. (2003) The proteomics standards initiative. *Proteomics*, 3, 1374–1376.
11. Taylor,C.F., Paton,N.W., Lilley,K.S., *et al.* (2007) The minimum information about a proteomics experiment (MIAPE). *Nat. Biotechnol.*, 25, 887–893.
12. Gaudet,P., Bairoch,A., Field,D., *et al.* (2011) Towards BioDBcore: a community-defined information specification for biological databases. *Database*, baq027.
13. Steinbeck, C., Conesa, P., Haug, K.,. *et al.* (2012) Metabolights: towards a new COSMOS of metabolomics data management. *Metabolomics*, 8, 757–760.
14. Sayers, E.W., Barrett, T., Benson, D.A., *et al.* (2009) Database resources of the National Center for Biotechnology Information. *Nucleic Acids Res.*, 37, D5–D25.