# Choosing Discipline-Specific Research Data Repositories

## In what cases cannot research data be deposited in RSU Dataverse?

The RSU Research Data Management Procedure foresees the deposit of datasets created by RSU researchers in the institutional repository RSU Dataverse, except in cases where:

- the terms of the project funding institution determine that data be deposited in another discipline-specific research data repository;
- it is generally accepted in the respective discipline to store data sets in another repository;
- RSU Dataverse is unable to ensure effective cooperation with any specific data processing or analytics tools;
- the size of the dataset is too large to be stored in RSU Dataverse (the size of one dataset may not exceed 50 GB);
- the project or other cooperation agreement stipulates otherwise.

## What requirements must a repository meet?

In cases where data is not stored in RSU Dataverse, the requirements for research data repositories or data archives are as follows:

- ensures secure storage by performing regular data backups every 24 hours;
- offers open standards for data access and metadata standards;
- assigns a permanent unique identifier (e.g., DOI);
- is registered or certified (e.g., Re3Data, EOSC, CoreTrustSeal);
- grants licences (e.g., Creative Commons);
- clearly defines the access and duration of data and metadata storage;
- if applicable, provides options for storing sensitive information in restricted or closed access;
- provides automated versioning and description of changes in the event of revisions;
- data storage and processing take place in the EU or the European Economic Area (EEA). If processing takes place outside the EU/EEA, a data processing agreement must be concluded, which is coordinated with the Data Security and Management Unit and the Department of Information Technology.

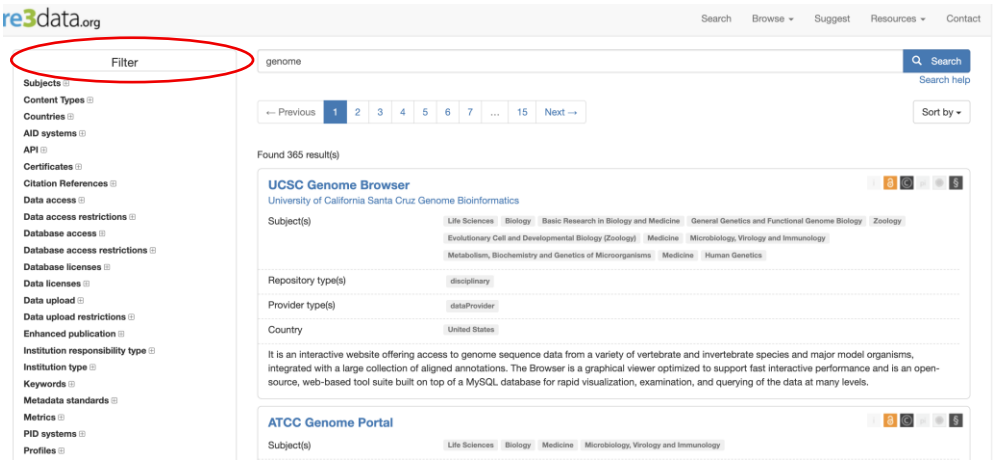
## Practical instructions for searching repositories

As mentioned above, one of the signs of a trusted repository is its registration on Open Science platforms such as Re3Data and EOSC. The presence of the repository on these platforms means that most of the basic requirements are met.

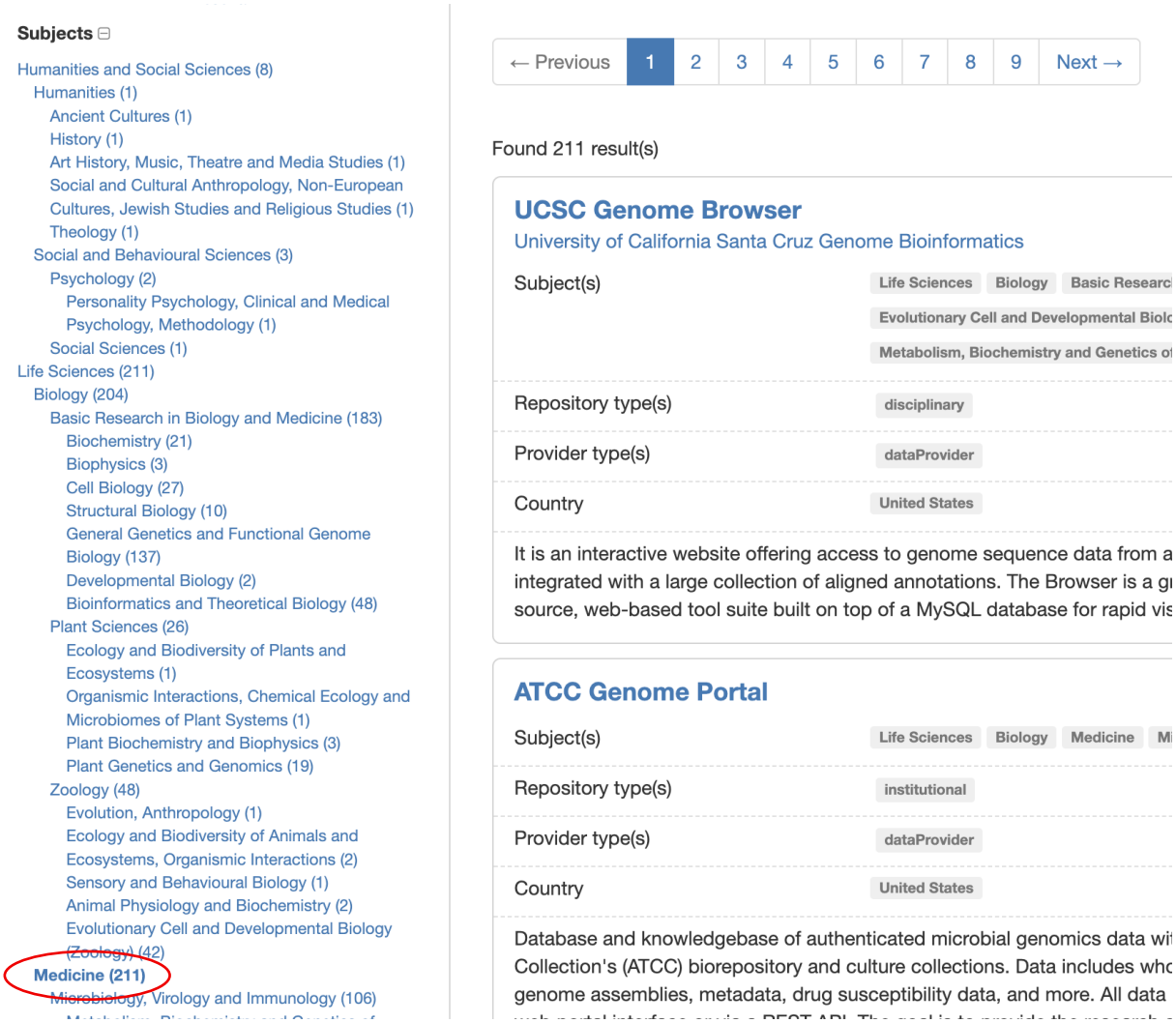
When looking for a discipline-specific repository, a good strategy is to use the Re3Data registry.

1. Visit the website https://www.re3data.org/.

2. Entering keywords for selecting repositories (e.g., genome), into the search engine will return 365 entries, which is a disproportionately large number for manual review. Therefore, it is recommended to use the filtering options available on the left side of the page.

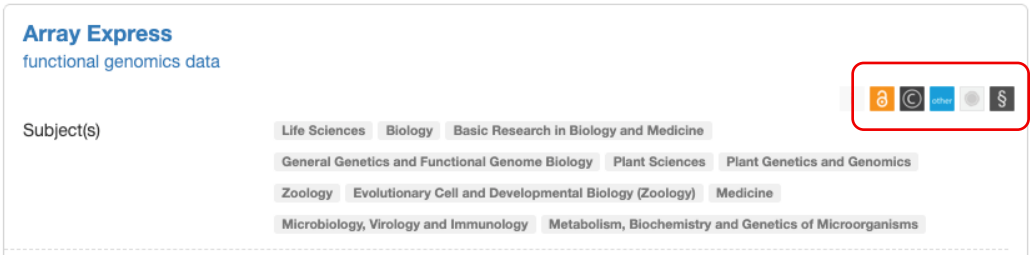



3. By selecting the first criterion (Subject), you can significantly reduce the number of results. Below is an example of selecting the medical subject.



4. By looking at the selection options more carefully and choosing specific medical topic subsections, the number of results narrows down.


5. The remaining selection options can be used as needed – depending on the publication or funder's requirements.
6. Next, you need to evaluate the selected repository, for which we will look at Array Express as an example.




It is necessary to pay attention to the indicated emblems in the upper right corner of the repository description – each icon represents a specific functionality or element of the repository.

- Offers a description of the services it provides.
- Offers open access to data.
- Provides licensing.
- Assigns a permanent unique identifier (e.g., DOI).
- The repository is certified or uses a generally accepted repository standard.
- The repository has its own policy document created and available.

If the particular emblem is coloured, the repository provides the given element. So we can conclude that Array Express provides open access, licensing, permanent unique identifier assignment, and a policy document is available.

Unfortunately, in very rare cases, repositories provide all 6 elements, but this does not necessarily mean that this is a reason not to use the repository. In order for a repository to meet the basic requirements set by RSU, it must necessarily provide the following elements:

- Offers open access to data.
- Provides licensing.
- Assigns a permanent unique identifier (e.g., DOI).

The repository you plan to use should have at least these 3 badges highlighted.

It should also be noted that sometimes the information in the register may not be updated, and some of the elements provided in the repository may not yet be appropriately indicated in the register.

In the case of sensitive data, it is also important to ensure that the data is stored and processed within the EU or the European Economic Area (EEA). If, however, the chosen repository stores the data outside the EU or EEA, it is necessary to contact the RSU data protection officer or data curators.

### Specific cases – large amounts of genetic data

In cases where, due to technical limitations (large amount of data or specific file format), it is not possible to deposit a dataset in RSU Dataverse, it is recommended to use Re3Data to search for another appropriate repository.

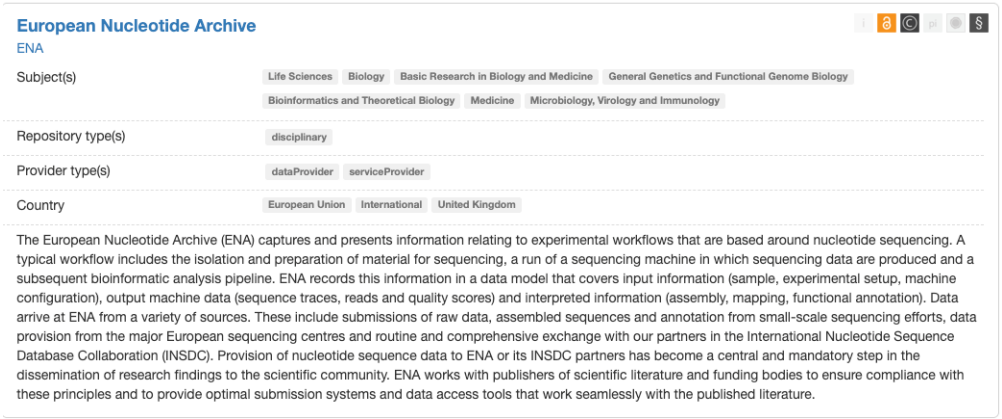
In such situations, it is advisable to be guided by the following parameters:

- the repository is included in Re3Data;
- it provides open access to data;
- it complies with GDPR requirements (if the dataset contains sensitive data).

### GDPR-compliant repositories

Below are listed the most popular open non-commercial repositories where this type of data can be deposited.

It should be noted that currently the registry does not mark all 3 basic functionality conditions for the repositories shown below, although in fact these repositories provide it for the majority of deposited datasets. For example, ENA and the assignment of independent identifiers to a dataset, DOIs are not assigned in this repository, but rather accession numbers. These numbers are not as functional as DOIs in finding datasets, therefore this functionality is not indicated as existing in the registry. Taking into account the fact that there are not many repositories in which the functional capabilities allow uploading large amounts of data and at the same time ensure GDPR requirements, not assigning DOIs does not limit the use of this repository.



## The European Genome-phenome Archive

EGA

| | |
|---|---|
| Subject(s) | Life Sciences · Biology · Basic Research in Biology and Medicine · Structural Biology · Medicine · Medicine · Human Genetics |
| Repository type(s) | disciplinary |
| Provider type(s) | dataProvider · serviceProvider |
| Country | European Union · Spain |

The European Genome-phenome Archive (EGA) is designed to be a repository for all types of sequence and genotype experiments, including case-control, population, and family studies. We will include SNP and CNV genotypes from array based methods and genotyping done with re-sequencing methods. The EGA will serve as a permanent archive that will archive several levels of data including the raw data (which could, for example, be re-analysed in the future by other algorithms) as well as the genotype calls provided by the submitters. We are developing data mining and access tools for the database. For controlled access data, the EGA will provide the necessary security required to control access, and maintain patient confidentiality, while providing access to those researchers and clinicians authorised to view the data. In all cases, data access decisions will be made by the appropriate data access-granting organisation (DAO) and not by the EGA. The DAO will normally be the same organisation that approved and monitored the initial study protocol or a designate of this approving organisation. The European Genome-phenome Archive (EGA) allows you to explore datasets from genomic studies, provided by a range of data providers. Access to datasets must be approved by the specified Data Access Committee (DAC).

## Array Express

functional genomics data

| | |
|---|---|
| Subject(s) | Life Sciences · Biology · Basic Research in Biology and Medicine · General Genetics and Functional Genome Biology · Plant Sciences · Plant Genetics and Genomics · Zoology · Evolutionary Cell and Developmental Biology (Zoology) · Medicine · Microbiology, Virology and Immunology · Metabolism, Biochemistry and Genetics of Microorganisms |
| Repository type(s) | disciplinary |
| Provider type(s) | dataProvider · serviceProvider |
| Country | United Kingdom · United States · European Union |

ArrayExpress is one of the major international repositories for high-throughput functional genomics data from both microarray and high-throughput sequencing studies, many of which are supported by peer-reviewed publications. Data sets are submitted directly to ArrayExpress and curated by a team of specialist biological curators. In the past (until 2018) datasets from the NCBI Gene Expression Omnibus database were imported on a weekly basis. Data is collected to MIAME and MINSEQE standards.

If the data is not sensitive, options for depositing data sets in the following repositories may be considered:

## GenBank

| | |
|---|---|
| Subject(s) | Life Sciences · Biology · Basic Research in Biology and Medicine · General Genetics and Functional Genome Biology · Bioinformatics and Theoretical Biology · Medicine · Microbiology, Virology and Immunology |
| Repository type(s) | disciplinary |
| Provider type(s) | dataProvider · serviceProvider |
| Country | United States · United Kingdom |

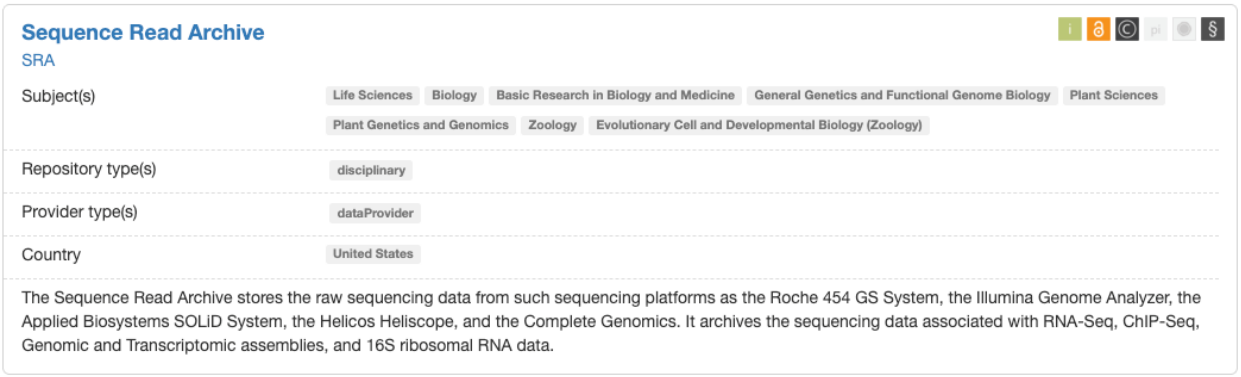
GenBank® is a comprehensive database that contains publicly available nucleotide sequences for almost 260 000 formally described species. These sequences are obtained primarily through submissions from individual laboratories and batch submissions from large-scale sequencing projects, including whole-genome shotgun (WGS) and environmental sampling projects. Most submissions are made using the web-based BankIt or standalone Sequin programs, and GenBank staff assigns accession numbers upon data receipt. Daily data exchange with the European Nucleotide Archive (ENA) and the DNA Data Bank of Japan (DDBJ) ensures worldwide coverage. GenBank is accessible through the NCBI Entrez retrieval system, which integrates data from the major DNA and protein sequence databases along with taxonomy, genome, mapping, protein structure and domain information, and the biomedical journal literature via PubMed. BLAST provides sequence similarity searches of GenBank and other sequence databases. Complete bimonthly releases and daily updates of the GenBank database are available by FTP.

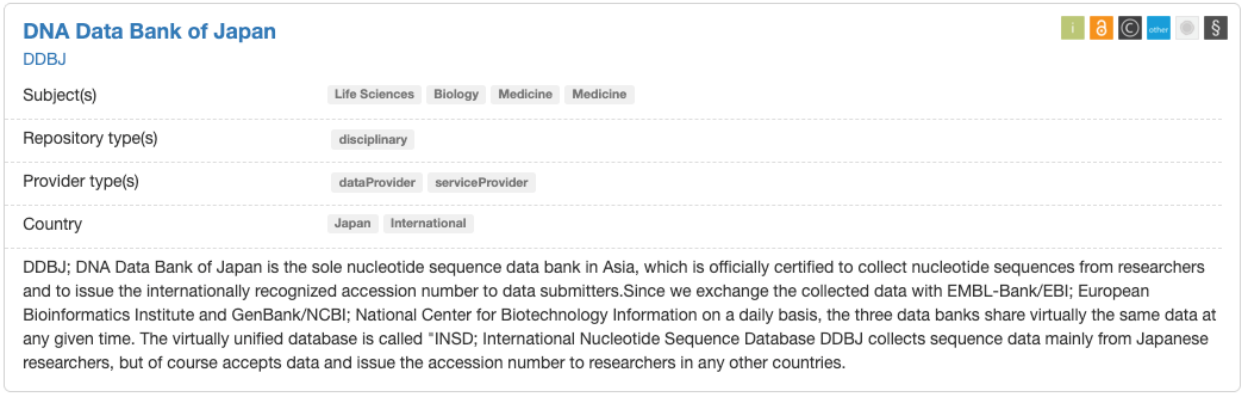
## Gene Expression Omnibus

GEO

| | |
|---|---|
| Subject(s) | Life Sciences · Biology · Basic Research in Biology and Medicine · General Genetics and Functional Genome Biology |
| Repository type(s) | disciplinary |
| Provider type(s) | serviceProvider |
| Country | United States |

Gene Expression Omnibus: a public functional genomics data repository supporting MIAME-compliant data submissions. Array- and sequence-based data are accepted. Tools are provided to help users query and download experiments and curated gene expression profiles.




This list is not complete, as, depending on the additional specifications of the particular repository (e.g., certain tumour types or specific diseases), there are also other repositories in Re3Data where it is possible to deposit large amounts of genetic data.

! In the case of large amounts of genetic data, it is recommended to select a deposit location in a timely manner (if possible - before data generation), because:

- discipline-specific repositories have specific data structure, format, and metadata requirements, so it would be easier to follow them from the first day of data acquisition;
- it is often necessary to include detailed information about the hardware used, its settings, and the software used in the metadata, even specifying its version, so it is more convenient to record this information during data acquisition rather than trying to obtain the information retrospectively;
- open access repositories are non-commercial, with limited human resources, where quality control of data sets can take several weeks, so the duration of the deposit process needs to be taken into account when planning the publication deadlines for project results.