MetaBiobank - directory of biobanks and biorepositories

Wstęp / Introduction

MetaBiobank jest katalogiem informacji opisujących kolekcje próbek biologicznych zgromadzone w biobankach. MetaBiobank jest usługą dla Ciebie, jeśli:

- szukasz materiału biologicznego pobranego od odpowiednich dawców, w celu przeprowadzenia nań własnych badań
- chcesz opublikować informacje opisujące zgromadzone w Twoim biobanku próbki, aby udostępnić je (odpłatnie bądź nieodpłatnie) zainteresowanym naukowcom.

Nasz usługa publikuje metadane odnośnie kolekcji biobanków, które pomogą Ci zdecydować, czy określone próbki są dla Ciebie interesujące. Naszym celem jest dostarczenie naukowcom prostego sposobu wyszukiwania właściwych próbek materiału biologicznego. Jednocześnie chcemy w ten sposób stworzyć dodatkowy kanał rozpowszechniania informacji dla administratorów biobanków i biorepozytoriów.

Usługa jest dostępna publicznie dla wszystkich, w trybie wyszukiwania zbiorów, w dwóch wersjach językowych. Jeśli chcesz opublikować informacje o swoim biobanku, prosimy o założenie konta PL-Grid w celu uzyskania autoryzowanego dostępu. Sposób otrzymania konta PL-Grid znajdziesz w pod ręczniku użytkownika. Interfejs usługi jest intuicyjny i nie powinien sprawiać kłopotów w trakcie korzystania z serwisu - poniżej zamieszczamy dodatkowo krótką instrukcję w języku angielskim.

MetaBiobank is a catalogue of information describing biological sample collections stored in various biobanks. MetaBiobank is for you if:

- you are looking for specific biological samples to perform research on;
- you wish to share the contents of your biological sample repository with other scientists.

Our service provides sample collection metadata which can help you decide whether certain samples are of interest to you. Our aim is to provide a simple way to search for interesting biological samples (for researchers) while also providing an additional channel to spread information about biobank resources (for biorepository administrators).

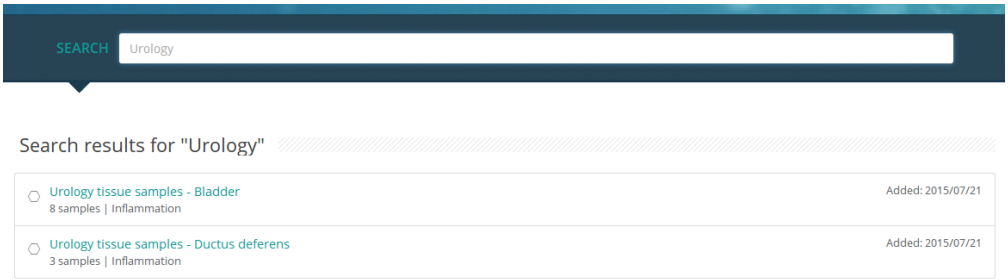
The service is publicly available to any person looking for sample collections, both in Polish and in English. People, who would like to publish information from their own biobank are requested to create a PL-Grid user account. PL-Grid User Manual describes the procedure of applying for such an account (it is free of charge).

Catalogue search and browsing

In order to search our biorepository catalogue, please navigate to the MetaBiobank front page, at:

https://biobank.plgrid.pl/

and type in the phrase you are looking for. You can search by disease, organs/anatomical part, sample material type or any other collection metadata element.



Clicking any of the resulting sample collections will redirect you to a sample collection view, such as the one below:

Mouse strain 129S2/SvPasCrl (129S2/SvPasCrl)

Collection fact sheet

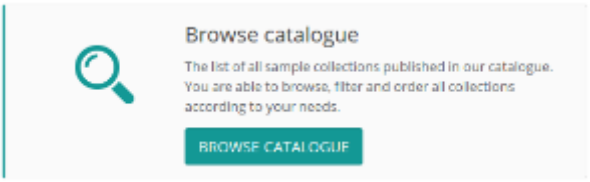
Biobank name	Biobank Graz
Sample count	6
Donors age range	9 - 27 weeks
Sex	Male, Female

Filter:

Name	Anatomical part	Storage temperature	Material type
blocks from liver tissue	liver	Room temperature	Tissue, paraffin preserved
brown adipose tissue, subcutaneous abdominal fat tissue, visceral fat tissue, colon, heart, brain, liver, spleen, kidney, femur, hamstring muscle	various	Liquid nitrogen	Tissue, cryo preserved
fekal pellets		Liquid nitrogen	Faeces
serum		-85°C to -60°C	Serum
slides from liver tissue	liver	Room temperature	Tissue, paraffin preserved
urine		-85°C to -60°C	Urine

Showing 1 to 6 of 6 entries

Here, you can obtain the details regarding the sample collection itself, as well as the specifics of samples available in the biobank (note, however, that some collections may come without a detailed list of samples). Clicking the "Biobank name" link will display more information about where the collection is located and how you can contact the responsible person. In this way you can initiate direct collaboration with the biobank's curators in order to obtain access to interesting samples.
An alternative way to browse collections is to directly view the catalogue by clicking an appropriate link on the front page:



This will take you to the summary table listing all published sample collections:

Filter: years

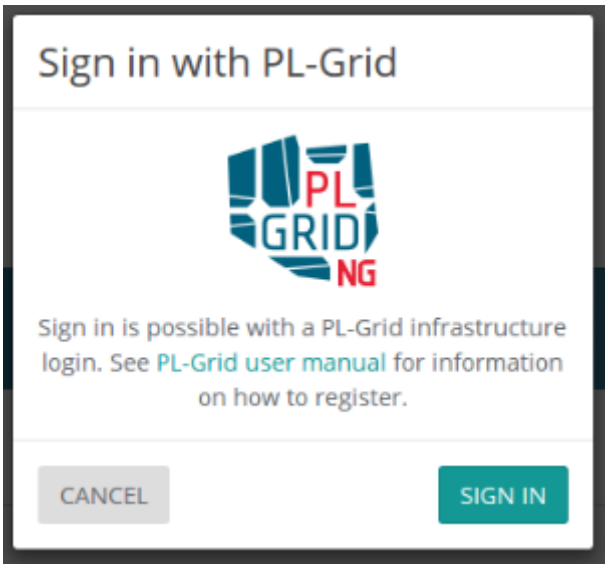
Biobank	Short name	Full name	Description	Donors age range	Samples	
NIGMS	NDPT107	SUBARACHNOID HEMORRHAGE, CAUCASIAN PANEL	This panel contains 5 micrograms of DNA from 92 unique and unrelated Caucasian individuals from North America with Subarachnoid Hemorrhage. Of these, 28 are males and 64 are females, with age at collection ranging from 25-61 years. Clinical data collected on these subjects, including a medical history, consisted of the NINDS Repository CVD Clinical Data Elements. A more detailed description is also available.	41 - 75 years	92	✓
MedUni Wien Biobank	APSOEM	APSOEM - Vienna Marathon Study - APSOEM	APSOEM (Austrian prospective cohort study in cognitive function of elderly marathon-runners) is a cohort study which has been designed to evaluate the effects of intensive endurance exercise training on cognition. For this, elderly marathon runners and bicyclists as well as a control cohort are examined.	59 - 77 years	6	✓
MedUni Wien Biobank	ORF	Mental stress and oxidative cell damage - ORF Symphony Orchestra study	48 Members of the Radio symphony orchestra have been included. Biochemical and psychological measures have been taken during the rehearsal and during the presumably most stressful concert of the year.	22 - 59 years	4	✓
NB	neue kolekzione	Nowa kolekcja do biobanku dodana		8 - 12 years	0	✓
NIGMS	APC	ADENOMATOUS POLYPOSIS OF THE COLON; APC		10 - 55 years	44	✓

Showing 1 to 5 of 5 entries (filtered from 9 total entries)

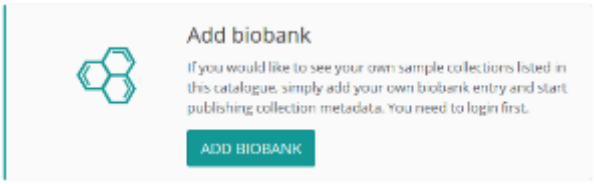
Each row represents a single biological sample collection. Here, you are able to filter results by selected keywords and sort by any of the columns. Clicking the biobank name will take you to the biobank fact sheet while clicking the collection name will display a detailed collection metadata view.

Submitting information about a biobank

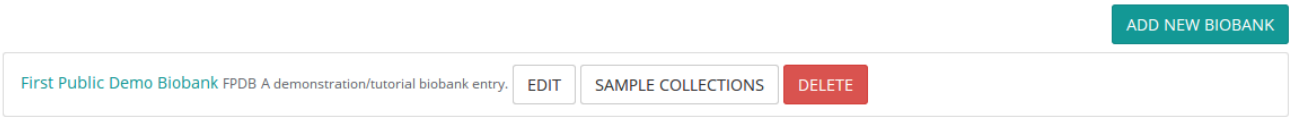
In order to publish information about your biobank and the samples it comprises, you need to obtain a user account. The MetaBiobank service is published in the PL-Grid Infrastructure and requires its users to have an active PL-Grid account. In order to obtain one, please use the PL-Grid Portal r egistration procedure (more information about this procedure is provided in the PL-Grid User Manual).
After successfully registering with PL-Grid, please go back to the MetaBiobank site and click the "LOGIN WITH PL-GRID" button in the top right-hand corner. This will display a login popup:



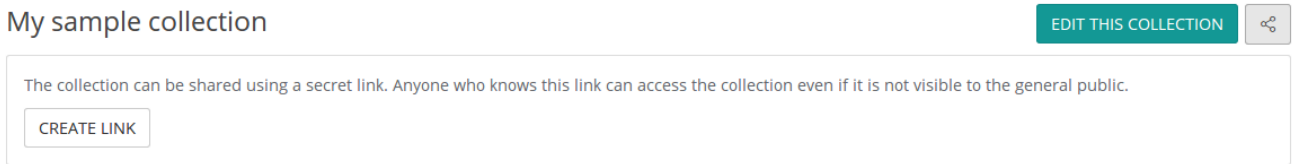
Please click the "SIGN IN" link - you will be redirected to PL-Grid OpenId identity provider server, where you should enter your PL-Grid login (it usually starts with the "plg" prefix) and password, in exactly the same way you log into the PL-Grid Portal. If you are logging into MetaBiobank for the first time, you may be presented with a request to activate access to MetaBiobank. Don't worry - this activation is automatic and you only have to approve it in order to proceed. Your consent will be remembered and you will not be forced to go through the same procedure during subsequent logins.
After signing in to MetaBiobank please use the second action button on the front page in order to add an entry about your organization (the one that manages your biobank or biorepository).



Please provide as much information as you can. Remember: the more details you give, the greater the chances that some external scientist will find what s/he needs in your biobank. Make sure to include contact details - the contact person may not necessarily be yourself, but it should be someone who can be contacted by persons wishing to obtain biosamples from your repository.
Note that your full organizational profile will not be visible to MetaBiobank users unless you check the "Public" flag - use this feature to hide incomplete (or outdated) information from other users. After submitting the form you will be able to review it in your dashboard:



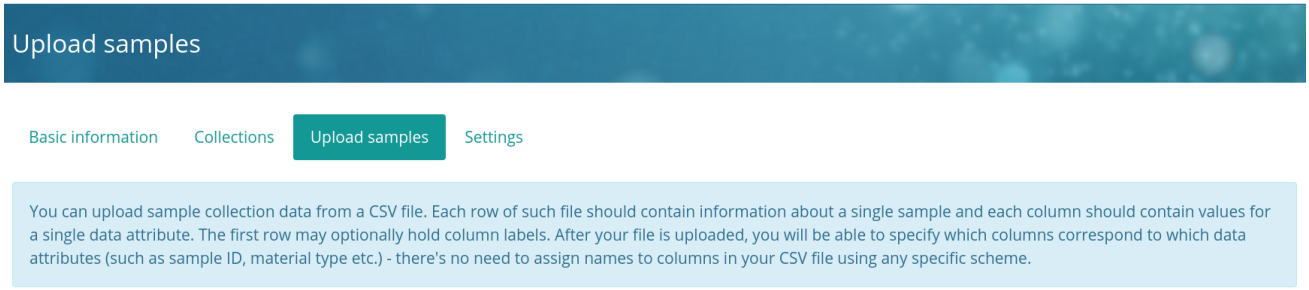
The dashboard is also accessible, after signing in, by clicking your name in the top right-hand corner of the screen. This section of the service enables you to adjust biobank data, remove entries completely from the system and manage biobank sample collections.
You can add new sample collections in pretty much the same way as adding biobank details. It is important to provide (among others) lists of applicable diseases, donor sex and study type information, as these might be crucial for the researchers looking for interesting samples. Take note of helpful hints provided by most of the form fields. Again, only a sample collection that has its 'Public' flag set to true will be publicly visible.
You are able to remove any information from inside MetaBiobank at any time, either by flagging selected data items as nonpublic, or by completely deleting any information you previously provided.
In case you would like to make one of your nonpublic collections available to a specific person, you are able to generate a unique access key for it. In this collection fact sheet view, please use the "chain link" icon to the right:



The "Create link" button will let you generate a unique URL link. Copy that link and send to the colleague you'd like to share the collection with. This person will be able to browse this collection. When you no longer wish to share that collection using the generated unique link, simply use the "Delete link" button to remove this possibility. The URL you shared will no longer work.

Importing sample collections

The MetaBiobank service offers the ability to import external sample collections from files. If you have a CSV file with information concerning individual samples (one sample per row), you can use the automated import facility to import it into one of your existing biobanks. This is done by clicking the **Upload samples** tab in the biobank management panel.



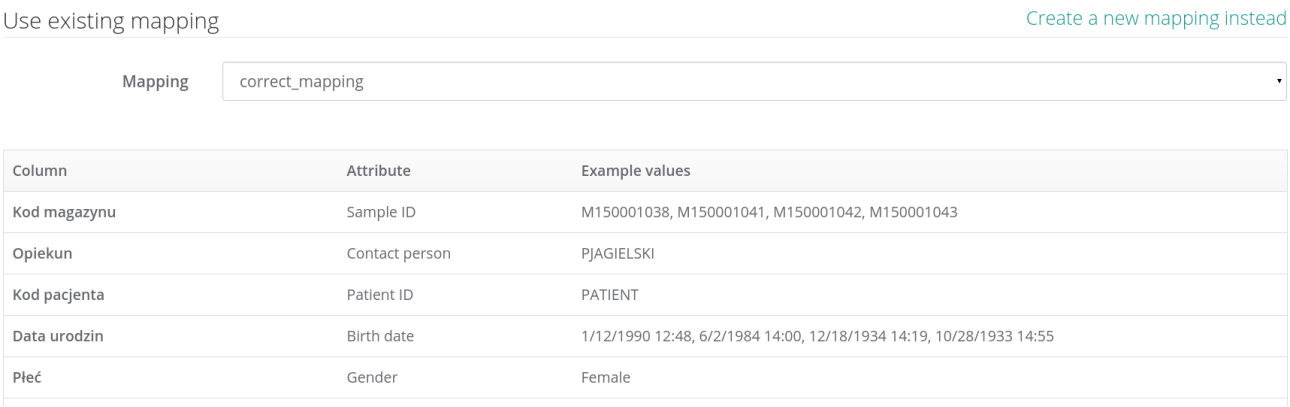
The service will present you with a page where you need to specify the name of the collection your samples will be uploaded to (a new collection will be created automatically if the selected collection doesn't yet exist) and choose a file stored on your hard drive to read samples from.

Below we present a sample (simplified) data import file:

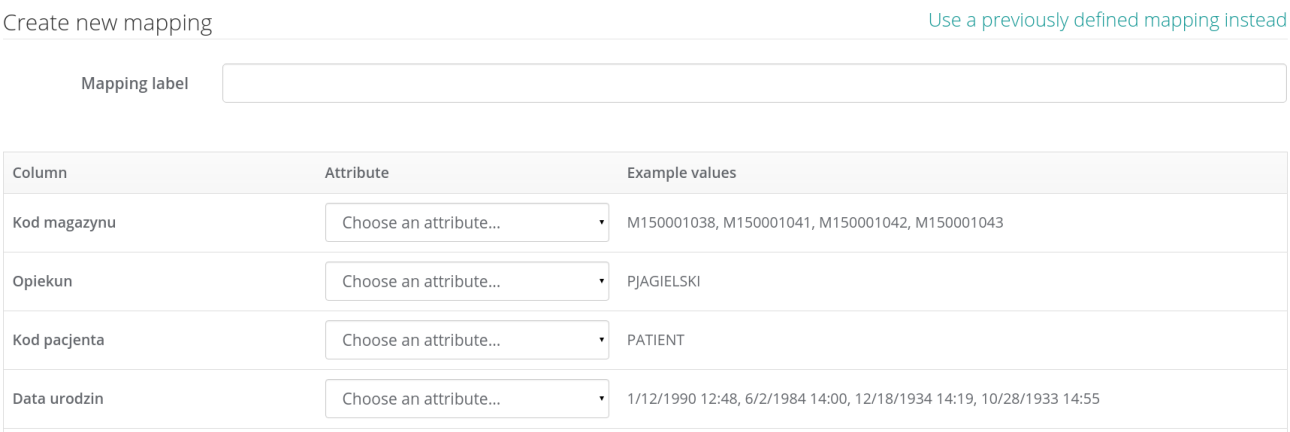
```
Kod,Opiekun,Kod pacjenta,Pe,Wiek,Materia,Temperatura,Pobrane dane
M150004247,JSMITH,p031,Female,25,DNA,-20,4/30/2015 13:07
M150004248,JSMITH,p032,Female,30,DNA,-20,4/30/2015 16:55
```

In this case the file contains a header row followed by a set of data rows, each of which contains a description of an individual sample.

We are aware that not exports are created equal and may include different types of data regarding samples (expressed as individual columns in your CSV file). In order to enable your data to be imported in a meaningful fashion, MetaBiobank asks you - as the second step in the import process - to specify a *mapping* between CSV columns and metadata terms specified by the MIABIS biobank description standard. Clicking **Upload** will validate your file and take you to the next step in the import process where you can specify an existing mapping, as shown in the following image:



...or, alternatively, create and save a new mapping for later use by clicking the **Create a new mapping instead** option:



A mapping is a collection of *column*/*term* assignments where *column* is one of the data columns in your CSV file while *term* is one of the available MIABIS terms. For example, if you assign column named '*Data pobrania*' to the MIABIS term *Sampled date*, the MetaBiobank service will assume that all values of this column in the CSV file indicate the dates on which each sample was taken.

Note that while MetaBiobank will do its best to analyze and properly parse the data present in your CSV file, we cannot guarantee that a sensible match for a meaningful MIABIS value can be made in each case (for example - the date field may be blank or formatted in a way which the MetaBiobank service does not understand). In all such cases the 'problematic' data items will be copied to a separate field in the sample description. We have named this field **Comments** and it can later be used to retrieve data which the data import facility could not appropriately parse.

Also note that in order to be usable, a mapping must, at the very least, include mapping items for the following MIABIS terms:

- **Sample ID** - column which contains a unique identifier of each sample

- **Material type** - column which lists the type of biological material represented by each sample
- **Storage temperature** - column which lists the temperature at which each sample was stored.

Failure to specify mappings for any of these fields will make the mapping unusable until such time as the missing data is provided.

How to contact authors

In case of further questions or if you are interested in cooperation with our team, please contact us by e-mail. If you wish to file a bug report or describe a feature request, please use the PL-Grid Helpdesk system. The MetaBiobank service is developed, delivered and maintained by ACC Cyfronet AGH and LifeScience Kraków Cluster.