# LM-GlycoRepo Ver.1.0

**Last update: Feb/2025**

## Data list

As the “embargo” system, after the registrant-specified release date, the submitted files and metadata are made visible on a data list of the LM-GlycoRepo homepage. Other users can access and download the deposited resources as they were submitted from the “Detail page”, where all deposited files and metadata are available, allowing for users to review the details of the source and experimental procedures and to re-analyze offline.

A key feature of LM-GlycoRepo is the visualization of deposited data on LM-GlycomeAtlas by API data sharing. To this end, each entry in the data list of LM-GlycoRepo contains a direct link to the LM-GlycomeAtlas, allowing users to visually explore the data using the web-based tools provided on the GlyCosmos Portal.

Upon public release, LM-GlycoRepo Version 1.0 contains four projects linked to previously published articles, denoted as References 1–4. These tissue glycome mapping datasets were obtained from 14 tissues of normal and diseased mice using laser microdissection (LMD)-assisted lectin microarray (LMA) with 45 lectins. The glycomic profiles obtained from normal C57BL/6J male mice in Reference 1 and Reference 2 are useful for an overview of site- and tissue-specific tissue glycosylations. Reference 3 contains a data set of cardiac tissues from the DCM model and age-matched normal mice used to elucidate glycosylation changes associated with cardiac fibrosis in failing hearts. Reference 4 is a data set of cardiac tissues obtained from normal C57BL6/N female mice at three different ages, providing insight into region-specific glycosylation and its age-related changes.

## How to log-in the submission system

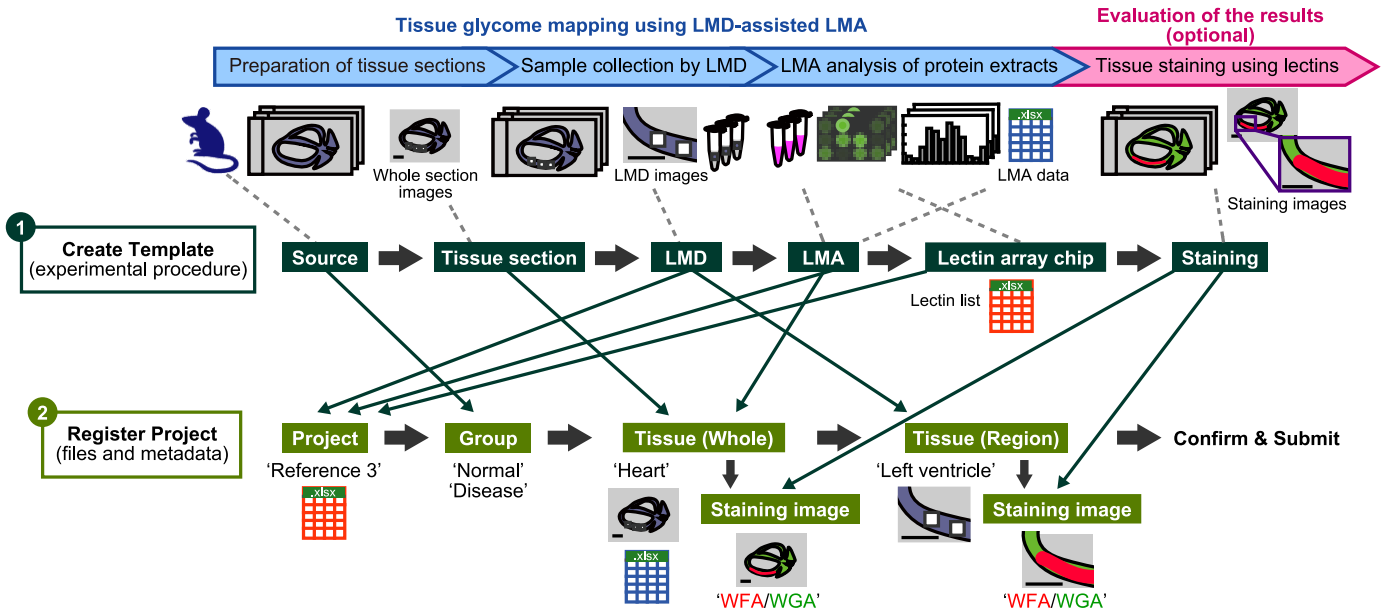
If you would like to deposit data, please log in from the homepage. If you are using the site for the first time, please create an account from “Sign Up”.

## Submission

### How to submit data

Data deposition on LM-GlycoRepo involves two main steps: “Create Template” and “Register Project”. In the first step, users access the “Create Template” section to set up templates detailing the experimental procedures, including tissue section preparation, laser microdissection (LMD)-assisted sample collection, and subsequent lectin microarray (LMA). These templates are then used

in the “Register Project” section to simplify the entry of metadata associated with the uploaded data files. Once created, the templates can be reused with modification (if necessary) for future projects with similar experimental procedures.




The “Create Template” section contains six subsections: (1) Source, (2) Tissue sections, (3) LMD, (4) LMA, (5) Lectin array chip, and (6) Staining.

The “Register Project” section comprises four subsections: (1) Project, (2) Group, (3) Tissue (Whole), and (4) Tissue (Region). Steps 3 and 4 include a module for registering the staining images. After providing all the required information, users can review the uploaded files and metadata before finalizing the submission. As an "embargo" system, when finalizing the submission, registrants can determine when the deposited data will be released to the public.

Details of these subsections are described below.

## Create Template

### Source

This subsection describes the creation of templates containing information on biological sources including species, strain, age, and sex. In version 1.0, only the mouse data can be registered.

### Tissue section

This subsection describes all aspects of tissue section preparation, including the section type (e.g., FFPE), fixation method (e.g., 4% paraformaldehyde), section thickness, slide glass type (e.g., PEN), and LMD staining method (e.g., hematoxylin). Detailed staining methods follow the format of the Experimental Procedures section of the research paper.

**LMD**

This subsection describes the creation of templates describing laser microdissection (LMD) procedures, including the supplier and instrument name of the LMD system, and the type of observation (e.g., bright field). The detailed LMD procedures are also described in the Experimental Procedures section of a research paper.

**LMA**

This subsection covers all aspects of the lectin microarray (LMA) procedures, except for the lectin array chip, which is described in the following subsection. Information such as the supplier and instrument name of the LMA system and the image analysis software for the LMA scans should be included. The detailed LMA procedures, including sample preparation, data acquisition, processing, and statistical analysis, are also described as in the Experimental Procedures section of a research paper.

**Lectin Array Chip**

This subsection describes detailed information regarding lectin array chips. The information entered was used directly for project registration without modification. Because the items to be registered varies depending on whether the chips are custom-made or commercial, users first select the chip type.

For custom-made chips, details should be provided according to the MIRAGE guidelines for LMA, covering sections such as “immobilization surface” and “array production,” which includes the details of quality control.

For commercial chips, the inclusion of array fabrication details is optional (except for the number of lectin replicates, e.g., three spots). Instead, product identification details, including name, supplier, catalog number, and website URL, should be provided, allowing for users to access to the information about the chip including the quality control that has been performed by the supplier.

A list of lectins used in the array panel should also be provided and formatted as a template (.xlsx), including lectin names and their identifiers (i.e., UniProt ID or GlyCosmos Lectin No.). It is recommended to use lectin names provided by the supplier be used for consistency, especially for commercial chips. The identifiers are used for automatically making a direct link to the lectin’s detail page of the GlyCosmos Lectins (https://glycosmos.org/lectins) on the main page of the LM-GlycomeAtlas. For custom-made chips, additional information is required to comply with the MIRAGE guidelines, including the vender, type of source (i.e., natural or recombinant), modification, and a lot of lectins used for the fabrication of LMA, allowing for users to check the details of the array used for analysis.

**Staining**

This subsection describes all aspects of the tissue staining procedures that may accompany tissue glycome mapping experiments. This can include conventional methods, such as hematoxylin and eosin (HE) staining for morphological observation or histochemical staining using lectins.

Information such as the method name (e.g., HE) or lectin name (e.g., AAL), along with the supplier and product details of the microscopy system used for imaging, should be included. Detailed staining protocols and microscopic methods are also described as in the Experimental Procedures section of a research paper.

## Register Project

### Project

In this subsection, users define a project name that serves as the primary identifier in the data list displayed on the LM-GlycoRepo homepage. Users also register the details about the LMD and LMA procedures and the lectin array chip used for the project, using templates created in the “Create Template” section. Since this system allows only one setting for these details, the data set obtained using a different experimental procedure and lectin array chip should be registered as a different project.

### Group

In this subsection, users define the sample groups to be compared (e.g., “Normal” and “Disease”). Users can select a preset “Source” template to autofill in the biological source information, such as strain, age, and sex. Additionally, the number of individuals used for the analysis should be provided.

### Tissue (Whole)

This subsection is for registering information about tissue sections analyzed in a project, allowing users to autofill details using the “Tissue Section” template. Users must upload a whole-section image file (in .png format), in which the regions used for tissue collection are labeled. An LMA data file (in .xlsx format) should also be uploaded for each tissue, ensuring that all LMA data registered within a single project are comparable (i.e., array format and chip lot should be identical). As an option, users can register staining images for whole tissue sections and the associated metadata by using a “Staining” template.

### Tissue (Region)

In this subsection, users upload a composite image file that summarizes multiple LMD images for a single tissue region (e.g., the left ventricle of the heart). This section also allows users to register detailed information and files for magnified tissue staining images for a single region, similar to the “Tissue (Whole)” section.