The astrocyte-specific proteome in inhibitory tripartite synapse formation and function in the context of Autism Spectrum Disorder - FWO 11M4323N DMP

A Data Management Plan created using DMPonline.be

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Project abstract:

The neurobiology underlying Autism Spectrum Disorder (ASD) remains elusive. Results from largescale genetic studies strongly implicate abnormal synaptic organization and inhibitory signaling in the pathophysiology of ASD. To date, the research on ASD has been neuron-centric. However, astrocytes, a type of glial cell, closely interact with neurons and play a critical role in the formation and function of synapses. Recent work suggests that excitatory and inhibitory synapse formation and function are differentially regulated by astrocytes. My goal is to gain fundamental knowledge on the composition and function of the inhibitory synapse and the role this may play in ASD. For this, I will use a novel proximity biotinylation-based approach to identify astrocyte proteins, previously linked with ASD, which are present at the inhibitory synapse. I will then assess the role of these proteins using a loss-of-function approach combined with testing for structural and functional effects on synapse formation, and by performing extensive in vivo behavioral phenotyping for ASD. Establishing a key role for astrocytes in controlling synapse-specific wiring and function would constitute a novel important finding that would spark intensive research in the ASD field, with important consequences for human disease research.

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Application DMP

Questionnaire

Describe the datatypes (surveys, sequences, manuscripts, objects …) the research will collect and/or generate and /or (re)use. (use up to 700 characters)

This question and the following 4 questions constitute the RDM section that was part of the FWO grant application. As my project/fellowship (11M4323N) has already started and is currently granted by the FWO, I don't have to fill and submit this section (5 questions of the application) again. As per guidance provided, please refer directly to the full FWO DMP (Flemish standard DMP) in the next sections of this file.

Specify in which way the following provisions are in place in order to preserve the data during and at least 5 years after the end of the research? Motivate your answer. (use up to 700 characters)

Please refer to the note above.

What's the reason why you wish to deviate from the principle of preservation of data and of the minimum preservation term of 5 years? (max. 700 characters)

Please refer to the note above.

Are there issues concerning research data indicated in the ethics questionnaire of this application form? Which specific security measures do those data require? (use up to 700 characters)

Please refer to the note above.

Which other issues related to the data management are relevant to mention? (use up to 700 characters)

Please refer to the note above.

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DPIA

DPIA

Have you performed a DPIA for the personal data processing activities for this project?

- Not applicable

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GDPR

GDPR

Have you registered personal data processing activities for this project?

- Not applicable

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FWO DMP (Flemish Standard DMP)

1. Research Data Summary

List and describe all datasets or research materials that you plan to generate/collect or reuse during your research project. For each dataset or data type (observational, experimental etc.), provide a short name & description (sufficient for yourself to know what data it is about), indicate whether the data are newly generated/collected or reused, digital or physical, also indicate the type of the data (the kind of content), its technical format (file extension), and an estimate of the upper limit of the volume of the data.

				Only for digital data	Only for digital data	Only for digital data	Only for physical data
Dataset Name	**Description**	**New or reused**	**Digital or Physical**	**Digital Data Type**	**Digital Data format**	**Digital data volume (MB/GB/TB)**	**Physical volume**
		Please choose from the following options: • Generate new data • Reuse existing data	*Please choose from the following options:* • Digital • Physical	*Please choose from the following options:* • Observational • Experimental • Compiled/aggregated data • Simulation data • Software • Other • NA	*Please choose from the following options:* • .por, .xml, .tab, .cvs,.pdf, .txt, .rtf, .dwg, .gml, … • NA	*Please choose from the following options:* • <100MB • <1GB • <100GB • <1TB • <5TB • <10TB • <50TB • >50TB • NA	
Analysis of confocal images	Numerical data. Analysis of confocal image data (performed using ImageJ, CellProfiler, QuPath, or proprietary image analysis software), in Microsoft Excel and GraphPad Prism files.	Generate new data	Digital	Analysis data	.xls, .csv, .pzfx	50-200MB	NA
Analysis of Western blot images	Numerical data. Analysis of Western blot images (performed using imageJ or proprietary image analysis software), in Microsoft Excel and GraphPad Prism files.	Generate new data	Digital	Analysis data	.xls, .csv, .pzfx	50-200MB	NA
Confocal images of mouse brain tissue	Confocal microscopy images of stained mouse brain tissue acquired using a ZEISS or a LEICA confocal microscope.	Generate new data	Digital	Experimental	.czi, .lif, .tif, .tiff, .ome.tif, .ome.tiff, ome.tf2, ome.tf8, ome.btf	100-500GB	NA
Western blot images	Images of chemiluminiscent, fluorescent or colorimetric signal from WB gels. Images are acquired using various imaging instruments.	Generate new data	Digital	Experimental	.gel, .ome.tiff, .ome.tif, .tif, .tiff	500-1000MB	NA
Mounted microscopy slides	Glass microscopy slides of stained mouse brain tissue or cells used for imaging, following immunohistochemistry, immunocytochemistry and immunofluorescence protocols.	Generate new data	Physical	Experimental	NA	NA	250-500 glass microscopy slides, stored in fridges or freezers using appropriate cryoprotectants.
Nucleic acid vectors	Tubes of liquid containing DNA plasmids produced during the project, derived from existing DNA plasmids provided by commercial and non-commercial suppliers.	Generate new data	Physical	Experimental	NA	NA	Storage box containing tubes with several microliters of purified constructs.
Plasmid maps	In silico processing and editing of plasmid sequences from papers and online databases, to create new plasmid vectors.	Generate new data	Digital	Experimental	.dna	10-50MB	NA

DNA sequencing files	Sequencing of plasmids, sequencing of PCR products.	Generate new data	Digital	Experimental	.abi	200-500MB	NA
PCR gel images	Images of UV-irradiated DNA samples run on agarose gels containing Midori Green or GelRed dyes. Images are acquired using various gel imaging systems.	Generate new data	Digital	Experimental	.gel, .ome.tiff, .ome.tif, .tif, .tiff	10-50MB	NA
Recombinant AAV vectors	Genetically engineered viral vectors derived from adeno-associated viruses (AAVs) carrying transgenes of interest for the conditional expression of enzymes and reporter proteins.	Generate new data	Physical	Experimental	NA	NA	Storage box containing tubes with several microliters of recombinant AAVs.
Analysis of mass spectrometry data	Statistical analysis lists of identified protein targets in mass spectrometry experiments.	Generate new data	Digital	Analysis data	.xls, .csv, .pzfx	50-200MB	NA
Mass spectrometry - raw data	Data readable as LC chromatograms, mass spectra, or identified protein lists produced using the MaxQuant quantitative proteomics software package.	Generate new data	Digital	Experimental	.raw, .mzID	10-1000GB	NA
Protein samples	Samples of denatured or undenatured proteins extracted from tissue or cells using detergents.	Generate new data	Physical	Experimental	NA	NA	Storage box containing tubes of tissue extracts containing protein, stored at very low temperatures.
Analysis of behavioral data	Numerical data. Analysis of mouse behavioral data, in Microsoft Excel and GraphPad Prism files.	Generate new data	Digital	Analysis data	.xls, .csv, .pzfx	50-200MB	NA
Behavioral data - raw data	Recording of count data from mouse behavioral assays	Generate new data	Digital	Experimental	.raw, .csv	5-10GB	NA
Transgenic mouse lines	2 transgenic mouse lines generated via microinjection of DNA into mouse oocytes or embryos as work from previous labs, and 1 line generated in our animal facility as cross of the 2 above.	Reuse existing data, Generate new data	Physical	Experimental	NA	NA	3 mouse lines, kept as ongoing breeding in the animal facility or cryopreserved.
Standard Operating Procedures (SOPs)	Written operating procedures for experimental workflows performed within the lab and animal facility.	Generate new data	Digital	Descriptive	docx, .pdf	50-200MB	NA
Risk assessments	Written risk assessments associated with carrying out experimental procedures performed within the lab and animal facility.	Generate new data	Digital	Descriptive	docx, .pdf	50-200MB	NA
Lab notebooks	Dated written notes associated with carrying out experimental procedures and project progress observations.	Generate new data	Digital (Electronic lab notebook using OneNote) + Physical (paper notes)	Experimental	.one, .onetoc2, .docx, .pdf (for digital notes)	5 lab books + 2GB	NA

If you reuse existing data, please specify the source, preferably by using a persistent identifier (e.g. DOI, Handle, URL etc.) per dataset or data type:

We currently use 2 mouse strains that were generated previously by other labs. These are:

1. The **B6;CBA-Tg(Fgfr3-icre/ERT2)4-2Wdr/J** mouse strain (please see: Rivers LE, Young KM, Rizzi M, et al. PDGFRA/NG2 glia generate myelinating oligodendrocytes and piriform projection neurons in adult mice. *Nat Neurosci*. 2008;11(12):1392-1401. doi:10.1038/nn.2220). RRID identifier --> IMSR_JAX:025809; JAX stock #025809 and MGI identifier --> MGI:3832576
2. The **B6;129-Gt(ROSA)26Sortm1(CAG-cas9*,-EGFP)Fezh/J** mouse strain (please see: Platt RJ, Chen S, Zhou Y, et al. CRISPR-Cas9 knockin mice for genome editing and cancer modeling. Cell. 2014;159(2):440-455. doi:10.1016/j.cell.2014.09.014). RRID identifier --> IMSR_JAX:024857; JAX stock #024857 and MGI identifier --> MGI:5583839

Are there any ethical issues concerning the creation and/or use of the data (e.g. experiments on humans or animals, dual use)? Describe these issues in the comment section. Please refer to specific datasets or data types when appropriate.

- Yes, animal data

I am currently in the process of obtaining ethical approval.

Will you process personal data? If so, briefly describe the kind of personal data you will use in the comment section. Please refer to specific datasets or data types when appropriate.

- No

Does your work have potential for commercial valorization (e.g. tech transfer, for example spin-offs, commercial exploitation, …)? If so, please comment per dataset or data type where appropriate.

- No

Do existing 3rd party agreements restrict exploitation or dissemination of the data you (re)use (e.g. Material/Data transfer agreements/ research collaboration agreements)? If so, please explain in the comment section to what data they relate and what restrictions are in place.

- No

Are there any other legal issues, such as intellectual property rights and ownership, to be managed related to the data you (re)use? If so, please explain in the comment section to what data they relate and which restrictions will be asserted.

- Yes

Discovery downstream of the mass spectrometry experiments may lead to *potential* IP requirements, but the concrete possibility of this will determined later in the project when targets are identified. Should the opportunity arise, discussion with the KU Leuven Research & Development - Tech Transfer Office about intellectual property rights and ownership will be started and patent application filing will be planned accordingly.

2. Documentation and Metadata

Clearly describe what approach will be followed to capture the accompanying information necessary to keep data understandable and usable, for yourself and others, now and in the future (e.g., in terms of documentation levels and types required, procedures used, Electronic Lab Notebooks, README.txt files, Codebook.tsv etc. where this information is recorded).

Dataset Name	Associated Documentation
Analysis of confocal images	ROIs drawn in images will be saved as metadata attached to TIFFs of images and stored with image analysis files.
Analysis of Western blot images	Names of analyzed images will be stored as part of the image analysis in the Excel files.
Confocal images of mouse brain tissue	For microscopy images the following information will be noted: image dimensions, image type, bit-depth, pixel size, and microscope acquisition settings. The methodology and protocol will be described in detail in the lab notebooks (digital/physical). A README.txt file for the image collection will be written.
Western blot images	The following metadata will be noted: image dimensions, image type, bit-depth, pixel size. The methodology and protocol will be described in detail in the lab notebooks (digital/physical).
Mounted microscopy slides	Location of stored glass microscopy slides, date of their creation, and tissue sample types will be noted in the lab notebooks (digital/physical).
Nucleic acid vectors	Sequence of plasmids will be stored digitally on the storage servers. Location of stored plasmid will be noted in the lab notebooks (digital/physical).
Plasmid maps	Notes on design and generation of the sequences will be described in the lab notebooks (digital/physical).
DNA sequencing files	Sequencing files will be stored with associated plasmid sequences on the storage servers. Details of dates of sequencing will be recorded in the lab notebooks (digital/physical).
PCR gel images	The following metadata will be noted: image dimensions, image type, bit-depth, pixel size. The methodology and protocol will be described in detail in the lab notebooks (digital/physical).
Recombinant AAV vectors	Location and information on stored batches of recombinant AAVs will be noted in the lab notebooks (digital/physical).
Analysis of mass spectrometry data	Analyzed data will be stored with a README.txt file.
Mass spectrometry - raw data	Raw data will be associated with the related analyzed data indicated above.
Protein samples	Information on date of protein extraction, sample sources, and concentration will be described in detail in the lab notebooks (digital/physical).
Analysis of behavioral data	Analyzed data will be stored with a README.txt file. All additional information including genotype and sex will be stored as a separate tab in the Excel files.
Behavioral data - raw data	Raw data will be associated with the related analyzed data indicated above.
Transgenic mouse lines	Information on date of surgical procedures, type and doses of injected AAVs, and follow-up observations will be stored in the lab notebooks (digital/physical). An Excel list of mouse breeding pairs and stocks for each mouse line will be created and stored on the storage servers.
Lab notebooks, Standard Operating Procedures (SOPs), and Risk assessments	Lab notebooks and paper notes (physical) will be stored in an agreed location in the lab. Electronic lab notebook using OneNote (digital) including scans of physical lab notebooks, as well as files of Standard Operating Procedures (SOPs) and Risk assessments will be stored on the storage servers.

Will a metadata standard be used to make it easier to find and reuse the data? If so, please specify (where appropriate per dataset or data type) which metadata standard will be used. If not, please specify (where appropriate per dataset or data type) which metadata will be created to make the data easier to find and reuse.

- Yes

Where available, accepted metadata standards will be employed as in the table below:

Type of Data	Metadata standard
Confocal images of mouse brain tissue	OME-TIFF
Fluorescent imaging files	OME-TIFF
Immunohistochemistry images	OME-TIFF
PCR gel images	OME-TIFF
Western blot images	OME-TIFF
Mass spectrometry raw data	mzML

Where no metadata standard exists, metadata will be stored based on *the Dublin Core standard*. The following information will be stored:

- Title: free text
- Creator: Last name, first name, organization
- Date and time reference
- Subject: Choice of keywords and classifications
- Description: Text explaining the content of the data set and other contextual information needed for the correct interpretation of the data, the software(s) (including version number) used to produce and to read the data, the purpose of the experiment, etc.
- Format: Details of the file format
- Resource Type: data set, image, audio, etc.
- Identifier: DOI (when applicable)
- Access rights: closed access, embargoed access, restricted access, open access.

The final dataset will be accompanied by this information under the form of a

README.txt or .docx document file. This file will be located in the top level directory of the dataset and will also list the contents of the other files and outline the file-naming convention used. This will allow the data to be understood by other members of the laboratory and add contextual value to the dataset for future reuse.

3. Data storage & back-up during the research project

Where will the data be stored?

All electronic files (text documents, images, sequences) will be stored on KU Leuven servers, with hourly on-site backup and mirroring or stored on a cloud-based service offered by KU Leuven (OneDrive). In addition data will be regularly backed-up and stored on an external hard drive.
All physical samples will be stored as appropriate:
Nucleic acids, viral vectors, protein samples will be stored at -80°C with appropriate backup copies of the stock in the PI lab at KU Leuven.
Vectors: as a general rule at least two independently obtained clones will be preserved for each vector, both under the form of purified DNA (in -20°C freezer). All published vectors and the associated sequences will be sent to the non-profit plasmid repository Addgene, which will take care of vector storage and shipping upon request.
Other biological and chemical samples: storage at 4°C and/or as frozen samples in cryovials as appropriate.

How will the data be backed up?

Use of standard back-up provided by KU Leuven ICTS: data will be stored on the OneDrive for Business cloud storage, which is synced approximately every 10 minutes. KU Leuven servers have hourly on-site backup and mirroring.
Additionally, backup to external hard drives will be performed once every 3 months.

Is there currently sufficient storage & backup capacity during the project? If yes, specify concisely.
If no or insufficient storage or backup capacities are available, then explain how this will be taken care of.

- Yes

The OneDrive for Business cloud storage provided by KU Leuven ICTS provides 2TB of storage data, which should be sufficient for the data generated in the project.

How will you ensure that the data are securely stored and not accessed or modified by unauthorized persons?

Both the “L-drive” (Large Volume Storage) and “J-drive” (Shared Network Drive) servers by KU Leuven ICTS are accessible only by laboratory members, and are mirrored in the second ICTS datacenter for business continuity and disaster recovery, so that a copy of the data can be recovered within an hour.
The project does not involve the use of sensitive personal data.

What are the expected costs for data storage and backup during the research project? How will these costs be covered?

The total amount of digital data associated with the project is expected to be around 2TB. The cost for storage of 1TB data per year on the KU Leuven ICTS “L-drive” (Large Volume Storage) server is approximately € 104,42 / TB / year.
The PI and the lab manager if applicable are responsible for the preservation of the mouse lines, as well as administrative and experimental data.
The mouse lines used in the project will be cryopreserved after the end of the project (Mouse Expertise Unit of VIB-KU Leuven: exact costs are to be determined, but usually they range from a few hundred to several thousand euros). All published lines will be preserved for the remainder of the PI’s research career. All unpublished lines will be preserved for a minimum of 5 years after the end of the project.

4. Data preservation after the end of the research project

Which data will be retained for at least five years (or longer, in agreement with other retention policies that are applicable) after the end of the project? In case some data cannot be preserved, clearly state the reasons for this (e.g. legal or contractual restrictions, storage/budget issues, institutional policies...).

The minimum preservation period of 5 years after the end of the project will be applied to all datasets.

Where will these data be archived (stored and curated for the long-term)?

As a general rule, datasets will be made openly accessible, whenever possible via existing platforms that support FAIR data sharing (www.fairsharing.org), at the latest at the time of publication.
For all other datasets, long term storage will be ensured as follows:

- Digital datasets: files will be stored on the “L-drive” (Large Volume Storage) server of KU Leuven ICTS;
- Used or Novel transgenic mouse lines will be kept locally in the animal facility or cryopreserved;
- Biological samples (protein, DNA samples, etc.) will be stored locally in the laboratory freezers;
- Immunohistochemistry and immunofluorescence stained samples (on mounted slides) will be stored locally in the laboratory fridges -or freezers using appropriate cryoprotectants-;
- Tissue samples will be stored locally in the laboratory freezers/fridges;
- Omics data: datasets will be stored on the “L-drive” (Large Volume Storage) server of KU Leuven ICTS;
- Nucleic acid vectors: As a general rule, at least two independently obtained clones will be preserved for each vector in the form of purified DNA (in -20°C freezer);
- Other biological and chemical samples: storage at 4°C and/or as frozen samples in cryovials locally in the laboratory freezers as appropriate.

What are the expected costs for data preservation during the expected retention period? How will these costs be covered?

The costs of the storage of 1-2 TB data for 5 years on KU Leuven servers are maximally €1500. The cost of storage of cryopreserved mouse lines is estimated to be around €2000 euros over 5 years. These costs will be met partially by the bench fee provided by the FWO and partially by existing lab grants.

5. Data sharing and reuse

Will the data (or part of the data) be made available for reuse after/during the project? In the comment section please explain per dataset or data type which data will be made available.

- Yes, in an Open Access repository

Participants to the present project are committed to publish research results to communicate them to peers and to a wider audience. All research outputs supporting publications will be made openly accessible. Depending on their nature, some data may be made available prior to publication, either on an individual basis to interested researchers and/or potential new collaborators, or publicly via repositories. Clearly, metadata will be openly available, as is typically the case for metadata access.

If access is restricted, please specify who will be able to access the data and under what conditions.

For data managed and shared directly by the PI, a material transfer agreement (and a non-disclosure agreement if applicable) will be concluded with the beneficiaries in order to clearly describe the types of data access and reuse that are permitted.

Are there any factors that restrict or prevent the sharing of (some of) the data (e.g. as defined in an agreement with a 3rd party, legal restrictions)? Please explain in the comment section per dataset or data type where appropriate.

- No

Where will the data be made available? If already known, please provide a repository per dataset or data type.

The data will be made available:

- In an Open Access repository
- Upon request by mail
- Other (specified here):

As a general rule, datasets will be made openly accessible via existing platforms that support FAIR data sharing (www.fairsharing.org). Sharing policies for specific research outputs are detailed here below:

- Omics datasets: These will be deposited in open access repositories such as the PRIDE Archive for proteomics data.
- Vectors: Upon publication, all vectors supporting a manuscript will be made publicly available via the non-profit plasmid repository Addgene, along with the corresponding DNA sequences. Addgene in turns performs quality control on the DNA, curates the plasmids online with all relevant information (maps, sequences), and for a minimal cost (typically $65) ships the vectors upon simple request and signature of a material transfer agreement (MTA). The MTA will be prepared before depositing the vectors with the help of the KU Leuven Research & Development - Tech Transfer Office. For transfer between nonprofit or academic institutions, Addgene typically uses the Uniform Biological Material Transfer Agreement (https://www.addgene.org/terms/1047/). All non-published vectors and the associated documentation will be shared by the PI upon request and after signature of a material transfer agreement, at no cost except the cost of shipment.
- Genetically modified organisms: All genetically modified mouse lines used in publications will be made available to researchers upon request at the time of publication. Transgenic mouse lines will be kept locally in the animal facility or cryopreserved, and samples will be sent to requesting researchers for a nominal processing fee.
- Other digital datasets that support publications (including image, video or audio files, electrophysiology data, spectroscopy data, behavioral data) will be made publicly available via an open research data platform such as Mendeley Data or Zenodo.
- Antibodies, synthetic and recombinant compounds: Samples will be stored as appropriate in the laboratory. Within availability, they will be shared with interested researchers upon request.
- Research documentation: All protocols used to generate published data will be described in the corresponding manuscript(s), and the related documentation will be included as supplementary information. These data and all other documents (daily logs, raw data) are accessible to the PI and the research staff, and will be made available upon request.
- Manuscripts: All scientific publications will be shared openly. Manuscripts submitted for publication will be deposited in a preprint server such as bioRxiv, arXiv, or ASAPbio. At the time of publication, research results will be summarized on the PI's website and postprint pdf versions of publications will be made available there if allowed by copyright agreements, possibly after an embargo as determined by the publisher. Before the end of the embargo or in cases where sharing the postprint is not allowed due to copyright agreements, a preprint version of the manuscript will be made available. Publications will also be automatically listed in the institutional academic database of the KU Leuven Association, Lirias 2.0, based on the authors name and ORCID ID.
- Data that do not support publication: These will be either deposited in an open access repository or made available upon request by email.

When will the data be made available?

The data will be made available:

- Immediately after the end of the project
- After an embargo period, if necessary
- Upon publication of the research results

As a general rule, all research outputs will be made openly accessible at the latest at the time of publication. No embargo will be foreseen unless imposed, e.g. by pending publications, potential IP requirements – note that patent application filing will be planned so that publications need not be delayed - or ongoing projects requiring confidential data. In those cases, datasets will be made publicly available as soon as the embargo date is reached.

Which data usage licenses are you going to provide? If none, please explain why.

Whenever possible, datasets and the appropriate metadata will be made publicly available through repositories that support FAIR data sharing. As detailed above, metadata will contain sufficient information to support data interpretation and reuse, and will conform to community norms. These repositories clearly describe their conditions of use (typically under a Creative Commons CC0 1.0 Universal Public Domain Dedication (CC0), a Creative Commons Attribution (CC-BY), or an ODC Public Domain Dedication and License (PDDL), with a material transfer agreement when applicable). Interested parties will thereby be allowed to access data directly, and they will give credit to the authors for the data used by citing the corresponding DOI. For data shared directly by the PI, a material transfer agreement (and a non-disclosure agreement if applicable) will be concluded with the beneficiaries in order to clearly describe the types of reuse that are permitted.

Do you intend to add a PID/DOI/accession number to your dataset(s)? If already available, you have the option to provide it in the comment section.

- Yes

As stated above, interested parties will be allowed to access data directly, and they will give credit to the authors for the data used by citing the corresponding DOI.

What are the expected costs for data sharing? How will these costs be covered?

From the start of the project, data management costs will be minimized by implementing standard procedures, e.g. for metadata collection and file storage and organization, and by using free-to-use data repositories and dissemination facilities whenever possible. When sharing and shipping physical data, substantial costs will be paid by the researcher colleagues requesting the materials. The laboratory budget will cover the costs associated with general data management and sharing.

6. Responsibilities

Who will manage data documentation and metadata during the research project?

Metadata will be documented by the research and technical staff at the time of data collection and analysis, by taking careful notes in the laboratory notebook that refer to specific datasets, and additionally compiling applicable metadata along with the data in the manner described above.

Who will manage data storage and backup during the research project?

The research and technical staff will ensure data storage and backup, with support from technical staff and IT administrators for the KU Leuven drives.

Who will manage data preservation and sharing?

The PI is responsible for long-term data preservation and sharing, with support from the research and technical staff involved in the project, and from technical stuff and IT administrators for the KU Leuven drives.

Who will update and implement this DMP?

The PI bears the end responsibility of updating and implementing this DMP.