FWO DMP Template - Flemish Standard Data Management Plan

Project supervisors (from application round 2018 onwards) and fellows (from application round 2020 onwards) will, upon being awarded their project or fellowship, be invited to develop their answers to the data management related questions into a DMP. The FWO expects a **completed DMP no later than 6 months after the official start date** of the project or fellowship. The DMP should not be submitted to FWO but to the research co-ordination office of the host institute; FWO may request the DMP in a random check.

At the end of the project, the **final version of the DMP** has to be added to the final report of the project; this should be submitted to FWO by the supervisor-spokesperson through FWO's e-portal. This DMP may of course have been updated since its first version. The DMP is an element in the final evaluation of the project by the relevant expert panel. Both the DMP submitted within the first 6 months after the start date and the final DMP may use this template.

The DMP template used by the Research Foundation Flanders (FWO) corresponds with the Flemish Standard Data Management Plan. This Flemish Standard DMP was developed by the Flemish Research Data Network (FRDN) Task Force DMP which comprises representatives of all Flemish funders and research institutions. This is a standardized DMP template based on the previous FWO template that contains the core requirements for data management planning. To increase understanding and facilitate completion of the DMP, a standardized **glossary** of definitions and abbreviations is available via the following link.

1. General Project Information	
Name Grant Holder & ORCID	Margot Vanoppen, ORCID ID: 0000-0002-7041-2620
Contributor name(s) (+ ORCID) & roles	Patrick Matthys, ORCID ID: 0000-0002-9685-6836 (promotor of the project)
Project number[1] & title	
Funder(s) GrantID[2]	198669
Affiliation(s)	☐ KU Leuven ☐ Universiteit Antwerpen ☐ Universiteit Gent ☐ Universiteit Hasselt ☐ Vrije Universiteit Brussel ☐ Other: Provide ROR[3] identifier when possible:

[1] "Project number" refers to the institutional project number. This question is optional since not every institution has an internal project number different from the GrantID. Applicants can only provide one project number.

[2] Funder(s) GrantID refers to the number of the DMP at the funder(s), here one can specify multiple GrantIDs if multiple funding sources were used.

[3] Research Organization Registry Community. https://ror.org/

Please provide a short project description	Granulomas are aggregates of immune cells that can be found in both infectious and non-infectious diseases. The core of granulomas consists of Langhans giant cells, which are multinucleated giant cells originating from macrophage fusion. Although Langhans giant cells occur in multiple diseases, little is known about their functioning and immunological activities, especially in diseases without apparent infection. Blau syndrome and sarcoidosis are two inflammatory granulomatous disorders of interest since they are characterized by Langhans giant cell-containing granulomas in various organs. In these diseases, it is unclear why and how granulomas and Langhans giant cells are formed and to what extent they contribute to the disease pathogenesis. In this project, we hypothesize that Langhans giant cells are key in granuloma development and disease control. Starting from in vitro generated Langhans giant cells and from granulomatous tissue biopsies from Blau syndrome and sarcoidosis patients, we will uncover the formation, cell functions and immunological features of Langhans giant cells and granulomas. For this, we will use cutting-edge technologies, including single-nucleus and single-cell sequencing, spatial transcriptomics and in vitro technologies. Since Langhans giant cell-containing granulomas occur in a myriad of diseases, we are convinced that this project can be regarded as a pioneer work to study the role of these multinucleated cells and granulomas in other diseases.

2. 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[4].

				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
Image-based sort (BD FacVulcan™)	Image-based sort of LGCs based on their number of nuclei in 96-well plates for single-cell RNA sequencing	☒ Generate new data ☐ Reuse existing data	☒ Digital ☒ Physical	☐ Observational ☒ Experimental ☐ Compiled/ aggregated data ☐ Simulation data ☐ Software ☐ Other ☐ NA	☐ .por ☐ .xml ☐ .tab ☐ .csv ☒ .pdf ☐ .txt ☐ .rtf ☐ .dwg ☐ .tab ☐ .gml ☒ other: .tif, .fcs ☐ NA	☐ < 100 MB ☐ < 1 GB ☐ < 100 GB ☒ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	96-well plates containing cells (RNA) will be stored in the biobank at -80 °C, this will take approximately 15 boxes
Single-cell RNA sequencing	Smart-seq[2] Single-cell RNA sequencing at different stages of LGC fusion (Day 0, 3 and 7)	☒ Generate new data ☐ Reuse existing data	☒ Digital ☐ Physical	☐ Observational ☒ Experimental ☐ Compiled/ aggregated data ☐ Simulation data	☐ .por ☐ .xml ☐ .tab ☒ .csv ☐ .pdf ☐ .txt	☐ < 100 MB ☐ < 1 GB ☒ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB	None

[4] Add rows for each dataset you want to describe.

				☐ Software ☐ Other ☐ NA	☐ .rtf ☐ .dwg ☐ .tab ☐ .gml ☒ other: .fastq, .count, .sam, .bam, .bai, .tif., .xls ☐ NA	☐ < 50 TB ☐ > 50 TB ☐ NA	
Single-nucleus ATAC-plus-RNA sequencing	Single-nucleus ATAC-plus-RNA sequencing on isolated nuclei of LGCs to identify different transcriptional states among nuclei	☒ Generate new data ☐ Reuse existing data	☒ Digital ☐ Physical	☐ Observational ☒ Experimental ☐ Compiled/ aggregated data ☐ Simulation data ☐ Software ☐ Other ☐ NA	☐ .por ☐ .xml ☐ .tab ☒ .csv ☐ .pdf ☐ .txt ☐ .rtf ☐ .dwg ☐ .tab ☐ .gml ☒ other: .fastq, .count, .sam, .bam, .bai, .tsv, .tbi, .bed, .tif, .xls ☐ NA	☐ < 100 MB ☐ < 1 GB ☒ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	None
MERFISH LGCs	MERFISH on LGC cultures in order to visualize heterogenous RNA sequencing	☒ Generate new data ☐ Reuse existing data	☒ Digital ☐ Physical	☐ Observational ☒ Experimental ☐ Compiled/ aggregated data ☐ Simulation	☐ .por ☐ .xml ☐ .tab ☒ .csv ☐ .pdf	☐ < 100 MB ☐ < 1 GB ☐ < 100 GB	None

	among nuclei in the same cell			data ☐ Software ☐ Other ☐ NA	☐ .txt ☐ .rtf ☐ .dwg ☐ .tab ☐ .gml ☒ other: .tif ☐ NA	☒ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	
Nuclei isolation and sorting	Isolation and sorting of LGC nuclei required for single-nucleus ATAC-plus-RNA sequencing	☒ Generate new data ☐ Reuse existing data	☒ Digital ☐ Physical	☐ Observational ☒ Experimental ☐ Compiled/ aggregated data ☐ Simulation data ☐ Software ☐ Other ☐ NA	☐ .por ☐ .xml ☐ .tab ☒ .csv ☐ .pdf ☐ .txt ☐ .rtf ☐ .dwg ☐ .tab ☐ .gml ☒ other: .fcs, tif. ☐ NA	☐ < 100 MB ☐ < 1 GB ☒ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	None
Fusion experiments (qPCR)	qPCR of LGCs transfected with siRNA targeting candidate fusion regulators to check for siRNA effectivity	☒ Generate new data ☐ Reuse existing data	☒ Digital ☒ Physical	☐ Observational ☒ Experimental ☐ Compiled/ aggregated data ☐ Simulation data ☐ Software ☐ Other ☐ NA	☐ .por ☐ .xml ☐ .tab ☒ .csv ☐ .pdf ☐ .txt ☐ .rtf ☐ .dwg ☐ .tab ☐ .gml ☐ other:	☒ < 100 MB ☐ < 1 GB ☐ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	Cell lysates (to release total RNA) and isolated mRNA will be stored in the biobank at -80 °C, this will take approximately 5 boxes

					☐ NA		
Fusion experiments (microscopy)	Bright field microscopy of Langhans giant cell cultures to identify fusion regulators	☒ Generate new data ☐ Reuse existing data	☒ Digital ☐ Physical	☐ Observational ☒ Experimental ☐ Compiled/ aggregated data ☐ Simulation data ☐ Software ☐ Other ☐ NA	☐ .por ☐ .xml ☐ .tab ☒ .csv ☐ .pdf ☐ .txt ☐ .rtf ☐ .dwg ☐ .tab ☐ .gml ☒ other: .tif ☐ NA	☐ < 100 MB ☐ < 1 GB ☒ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	None
ImageStream experiments	ImageStream analysis of Langhans giant cell cultures (with focus on characterisation of proteins involved in antigen presentation)	☒ Generate new data ☐ Reuse existing data	☒ Digital ☐ Physical	☐ Observational ☒ Experimental ☐ Compiled/ aggregated data ☐ Simulation data ☐ Software ☐ Other ☐ NA	☐ .por ☐ .xml ☐ .tab ☒ .csv ☐ .pdf ☐ .txt ☐ .rtf ☐ .dwg ☐ .tab ☐ .gml ☒ other: .daf, .ctm, . rif, .cif ☐ NA	☐ < 100 MB ☐ < 1 GB ☐ < 100 GB ☒ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	None
Chemotaxis assay	Chemotaxis assays (Boyden chamber and	☒ Generate new data ☐ Reuse existing	☒ Digital ☐ Physical	☐ Observational ☒ Experimental ☐ Compiled/	☐ .por	☐ < 100 MB	None

	ibidi µ slide) to investigate the potential of Langhans giant cells to attract T cells	data		aggregated data ☐ Simulation data ☐ Software ☐ Other ☐ NA	☐ .xml ☐ .tab ☒ .csv ☐ .pdf ☐ .txt ☐ .rtf ☐ .dwg ☐ .tab ☐ .gml ☐ other: .tif ☐ NA	☐ < 1 GB ☒ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	
MSD experiments	Measurement of cytokines and chemokines in supernatant of LGC cultures using MSD inflammatory cytokine panel	☒ Generate new data ☐ Reuse existing data	☒ Digital ☒ Physical	☐ Observational ☒ Experimental ☐ Compiled/ aggregated data ☐ Simulation data ☐ Software ☐ Other ☐ NA	☐ .por ☐ .xml ☐ .tab ☒ .csv ☐ .pdf ☐ .txt ☐ .rtf ☐ .dwg ☐ .tab ☐ .gml ☒ other: .xls ☐ NA	☒ < 100 MB ☐ < 1 GB ☐ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	Supernatant will be stored in the biobank at -80°C, this will take approximately 1 box
Spatial transcriptomics (tissue)	Spatial transcriptomics of granulomatous and non-granulomatous	☒ Generate new data ☐ Reuse existing data	☒ Digital ☐ Physical	☐ Observational ☒ Experimental ☐ Compiled/ aggregated data ☐ Simulation data	☐ .por ☐ .xml ☐ .tab ☒ .csv ☐ .pdf ☐ .txt	☐ < 100 MB ☐ < 1 GB ☒ < 100 GB	Tissue samples will be stored in the biobank in liquid nitrogen

	tissue of Blau syndrome and sarcoidosis patients			☐ Software ☐ Other ☐ NA	☐ .rtf ☐ .dwg ☐ .tab ☐ .gml ☐ other: .fastq, .count, .sam, .bam, .bai, .tif, .xls ☐ NA	☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	
Single-nucleus RNA sequencing (tissue)	Single-nucleus RNA sequencing of granulomatous and non-granulomatous tissue of Blau syndrome and sarcoidosis patients	☒ Generate new data ☐ Reuse existing data	☒ Digital ☐ Physical	☐ Observational ☒ Experimental ☐ Compiled/ aggregated data ☐ Simulation data ☐ Software ☐ Other ☐ NA	☐ .por ☐ .xml ☐ .tab ☒ .csv ☐ .pdf ☐ .txt ☐ .rtf ☐ .dwg ☐ .tab ☐ .gml ☐ other: .fastq, .count, .sam, .bam, .bai, .tif, .xls ☐ NA	☐ < 100 MB ☐ < 1 GB ☒ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	Tissue samples will be stored in the biobank in liquid nitrogen

Guidance: *Data can be digital or physical (for example biobank, biological samples, …). Data type: Data are often grouped by type (observational, experimental etc.), format and/or collection/generation method.* *Examples of data types: observational (e.g. survey results, sensor readings, sensory observations); experimental (e.g. microscopy, spectroscopy, chromatograms, gene sequences); compiled/aggregated data[5] (e.g. text & data mining, derived variables, 3D modelling); simulation data (e.g. climate models); software, etc.* *Examples of data formats: tabular data (.por,. spss, structured text or mark-up file XML, .tab, .csv), textual data (.rtf, .xml, .txt), geospatial data (.dwg,. GML, ..), image data, audio data, video data, documentation & computational script.* *digital data volume: Please estimate the upper limit of the volume of the data per dataset or data type.* *physical volume: Please estimate the physical volume of the research materials (for example the number of relevant biological samples that need to be stored and preserved during the project and/or after).*	
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 will not reuse existing data for this project.
Are there any ethical issues concerning the creation and/or use of the data (e.g. experiments on humans or animals, dual use)? If so, please describe these issues further and refer to specific datasets or data types when appropriate.	☒ Yes, human subject data ☐ Yes, animal data ☐ Yes, dual use ☐ No If yes, please describe: For the use of human derived Langhans giant cell cultures and tissue biopsies approval of the ethical committee is and already granted (S65230). For collection and use of samples from healthy control and Blau syndrome patients ethical approval has already been granted (S65230). For the use of sarcoidosis samples, we will apply an amendment at the responsible ethical committee.

[5] These data are generated by combining multiple existing datasets.

Will you process personal data[6]? If so, briefly describe the kind of personal data you will use. Please refer to specific datasets or data types when appropriate. If available, add the reference to your file in your host institution's privacy register.	☒ Yes ☐ No If yes: The personal data Blau syndrome and sarcoidosis patients will be collected. This includes 'regular' personal data such as age and gender but also 'sensitive' data such as health (in order to better select samples for sequencing). The privacy of patients will be guaranteed through data anonymization and storage within the secured database of the UZ Leuven. The treating physicians that participate in this study, possess a personal account and password to access the patients' data. For Blau syndrome patients, ethical approval has already been granted (S65230). For sarcoidosis patients, an amendment will be applied.
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.	☐ Yes ☒ No If yes, please comment:
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 to what data they relate and what restrictions are in place.	☐ Yes ☒ No If yes, please explain:
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 to what data they relate and which restrictions will be asserted.	☐ Yes ☒ No If yes, please explain:

[6] See Glossary Flemish Standard Data Management Plan

3. 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).	The protocols of all experiments will be described in detail in Word or Excel files and stored on a shared drive (J-drive). Experimental results will also be stored at the shared drive. Every experiment has an experiment number enabling to link all resulting data files to the correct experiment. Only members from the team will have access to these folders. Informed consents (physical data) will be safely stored behind lock and key by the primary investigator (Margot Vanoppen), only she will have access to these documents.

Will a metadata standard be used to make it easier to **find and reuse the data**? If so, please specify which metadata standard will be used. If not, please specify which metadata will be created to make the data easier to find and reuse. *Repositories could ask to deliver metadata in a certain format, with specified ontologies and vocabularies, i.e. standard lists with unique identifiers.*	☐ Yes ☒ No If yes, please specify (where appropriate per dataset or data type) which metadata standard will be used: If no, please specify (where appropriate per dataset or data type) which metadata will be created: Metadata standards are typically not used within our lab group. However, we ensure possibility to interpret and reuse the data when necessary and permitted. Every member of our lab has a folder on the shared J-drive where he/she can safe his/her data. All data regarding one experiment will be kept on the J-drive in one folder with experiment number, title, type of data and file size to ensure all information on a single experiment is kept together. In the protocols, we will describe all the reagents and kits used in the corresponding experiment as well as the patient and healthy control numbers. For microscopy experiments, every picture will be labelled with healthy control/patient number, experimental stimulus, and the magnification. Analyses, either in excel or R (for sequencing data) will be made available in the shared drive within the corresponding folder of the experiment. All patient information (age, gender, disease) will be registered in an anonymized way in the file containing all collected samples and every patient will receive an identification number.

4. Data Storage & Back-up during the Research Project	
Where will the data be stored?	- All data will be electronically saved on the KU Leuven OneDrive and a shared network drive (J-drive). Only members of the lab group that have permission to access the files have ICT permission. - Biological samples (blood and tissue) will be stored in the biobank. µ - Cell lysates (for total RNA isolation) and isolated RNA (for qPCR), cell supernatant (for MSD multiplex), and 96-well plates containing cells for Smart-seq2 will be stored in -80 °C in the biobank.

How will the data be backed up? *What storage and backup procedures will be in place to prevent data loss? Describe the locations, storage media and procedures that will be used for storing and backing up digital and non-digital data during research.*[7] *Refer to institution-specific policies regarding backup procedures when appropriate.*	Backup is secured daily by KU Leuven ICTS.
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 ☐ No If yes, please specify concisely: The OneDrive has a limitation in storage capacity (2 TB) which will be sufficient for this project. If no, please specify:
How will you ensure that the data are securely stored and not accessed or modified by unauthorized persons? *Clearly describe the measures (in terms of physical security, network security, and security of computer systems and files) that will be taken to ensure that stored and transferred data are safe.* [7]	All the above-mentioned protocols, raw data and analyzed data are stored at a shared Rega drive which is IP protected. In order to secure our data, the shared Rega drive is exclusively accessible through a login connected to your personal KU Leuven account and password. The privacy of patients will be guaranteed through data anonymization and storage within the secured database of the UZ Leuven. The treating physicians that participate in this study, possess a personal account and password to access the patients' data. Informed consents (physical data) will be safely stored behind lock and key by the primary investigator (Margot Vanoppen), only she will have access to these documents.
What are the expected costs for data storage and backup during the research project? How will these costs be covered?	The OneDrive (2TB) comes without charge, and should be enough for completion of this project. The FWO bench fee could be used to pay for extra storage capacity.

[7] Source: Ghent University Generic DMP Evaluation Rubric: https://osf.io/2z5g3/

5. 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...).	All data generated and biopsies (blood tissue) will be retained for minimally 10 years after ending the FWO project. This is because of the possibility of reuse of samples or data for new research projects. The informed consent includes a clause that permits later reuse of the obtained data. The cell cultures obtained will not be stored since this is biologically not possible.
Where will these data be archived (stored and curated for the long-term)?	Data will be stored at the KU Leuven OneDrive for at least 10 years, conform the KU Leuven RDM policy.
What are the expected costs for data preservation during the expected retention period? How will these costs be covered?	The OneDrive (2TB) comes without charge, and should be enough for completion of this project. The FWO bench fee could be used to pay for extra storage capacity.

6. Data Sharing and Reuse	
Will the data (or part of the data) be made available for reuse after/during the project? Please explain per dataset or data type which data will be made available. *NOTE THAT 'AVAILABLE' DOES NOT NECESSARILY MEAN THAT THE DATA SET BECOMES OPENLY AVAILABLE, CONDITIONS FOR ACCESS AND USE MAY APPLY. AVAILABILITY IN THIS QUESTION THUS ENTAILS BOTH OPEN & RESTRICTED ACCESS. FOR MORE INFORMATION: HTTPS://WIKI.SURFNET.NL/DISPLAY/STANDARDS/INFO-EU-REPO/#INFOEUREPO-ACCESSRIGHTS*	☐ Yes, in an Open Access repository ☒ Yes, in a restricted access repository (after approval, institutional access only, …) ☐ No (closed access) ☐ Other, please specify: Only published data will be available in the form of publications or other dissemination of scientific work. All data will be anonymised when disseminated. More data can be made available or shared after permission of the responsible person (Prof. Patrick Matthys). Non-published data will remain confidential until a final decision on publication of the data has been taken.
If access is restricted, please specify who will be able to access the data and under what conditions.	Data could be reused by other members of the Prof. Patrick Matthys team. Data can possibly be accessed by a third party after signing a data sharing agreement and approval of Patrick Matthys. Exchange of an e-mail address will be required (in order to keep in touch with people requesting our data) to access the data and an appropriate DTA and/or MTA will be in place. Costs for shipment are to be covered by the requesting party. Access will be considered after a request is submitted explaining the planned reuse. Only uses for research purposes will be allowed and commercial reuse will be excluded. Exceptions are to be submitted to the head of our lab group (Prof. Patrick Matthys).

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 per dataset or data type where appropriate.	☒ Yes, privacy aspects ☐ Yes, intellectual property rights ☐ Yes, ethical aspects ☐ Yes, aspects of dual use ☐ Yes, other ☐ No If yes, please specify: Privacy aspects of our patients need to be protected. Therefore, data will only be accessible after anonymization.
Where will the data be made available? If already known, please provide a repository per dataset or data type.	A specific repository will be chosen after the publication strategy is known as some journal request specific repositories.
When will the data be made available? *This could be a specific date (dd/mm/yyyy) or an indication such as 'upon publication of research results'.*	Upon publication of research results in peer-reviewed journals

Which data usage licenses are you going to provide? If none, please explain why. *A data usage license indicates whether the data can be reused or not and under what conditions. If no licence is granted, the data are in a grey zone and cannot be legally reused. Do note that you may only release data under a licence chosen by yourself if it does not already fall under another licence that might prohibit that.* *Example Answer: E.g. "Data from the project that can be shared will be made available under a Creative Commons Attribution license (CC-BY 4.0), so that users have to give credit to the original data creators."* [8]	Data usage licences will be discussed with LRD before any licences are granted.
Do you intend to add a PID/DOI/accession number to your dataset(s)? If already available, please provide it here. *Indicate whether you intend to add a persistent and unique identifier in order to identify and retrieve the data.*	☒ Yes ☐ No If yes: Depending on the data repository and the type of data that would be made available, a unique identifier will be added to the data set.
What are the expected costs for data sharing? How will these costs be covered?	In case we will need to pay for reposition of our data, costs will be covered by the bench. fee. Costs for shipment of data or material to a third party will be paid by the researcher/lab requesting the data or material.

7. Responsibilities	
Who will manage data documentation and metadata during the research project?	PhD researcher (Margot Vanoppen) and PI (Patrick Matthys)

[8] Source: Ghent University Generic DMP Evaluation Rubric: https://osf.io/2z5g3/

Who will manage data storage and backup during the research project?	PhD researcher (Margot Vanoppen) and PI (Patrick Matthys)
Who will manage data preservation and sharing?	PI (Patrick Matthys)
Who will update and implement this DMP?	PhD researcher (Margot Vanoppen) and PI (Patrick Matthys)