

Developing a proprietary platform for DNA-based antibody therapeutics through sequence engineering and immunomodulation

FWO DMP (Flemish Standard DMP)

1. Research Data Summary

	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
1. Plasmid and transgene (antibody/protein) DNA sequences (all WPs)	(Annotated) plasmid DNA sequences, and DNA sequences of transgenes/antibodies to be cloned in the plasmids. Some of the sequences will be generated using a neural network. Sequences will be processed and adapted with CLC Main Workbench software (Qiagen). Details of plasmid design/construction will be stored in the electronic lab notebook. Plasmids will be sequence verified (performed at LGC Genomics (.abi files) and stored in SnapGene and/or CLC Workbench (together with the engineered digital maps of the respective plasmids).	<input checked="" type="checkbox"/> Generate new data <input checked="" type="checkbox"/> Reuse existing data	<input checked="" type="checkbox"/> Digital <input type="checkbox"/> Physical	<input type="checkbox"/> Observational <input checked="" type="checkbox"/> Experimental <input type="checkbox"/> Compiled/aggregated data <input type="checkbox"/> Simulation data <input type="checkbox"/> Software <input checked="" type="checkbox"/> Other <input type="checkbox"/> NA	<input type="checkbox"/> .por <input type="checkbox"/> .xml <input type="checkbox"/> .tab <input type="checkbox"/> .csv <input type="checkbox"/> .pdf <input checked="" type="checkbox"/> .txt <input type="checkbox"/> .rtf <input type="checkbox"/> .dwg <input type="checkbox"/> .tab <input type="checkbox"/> .gml <input checked="" type="checkbox"/> other: .clc, .gbk, .dna, .fasta, .tiff, .abi <input type="checkbox"/> NA	<input type="checkbox"/> < 100 MB <input type="checkbox"/> < 1 GB <input checked="" type="checkbox"/> < 100 GB <input type="checkbox"/> < 1 TB <input type="checkbox"/> < 5 TB <input type="checkbox"/> < 10 TB <input type="checkbox"/> < 50 TB <input type="checkbox"/> > 50 TB <input type="checkbox"/> NA	NA
2. <i>In silico</i> design of antibody mutants (SolubiS) (WP1)	PDB structures of wildtype and mutant antibodies with predicted improved aggregation resistance and stability.	<input checked="" type="checkbox"/> Generate new data <input checked="" type="checkbox"/> Reuse existing data	<input checked="" type="checkbox"/> Digital <input type="checkbox"/> Physical	<input type="checkbox"/> Observational <input type="checkbox"/> Experimental <input checked="" type="checkbox"/> Compiled/aggregated data <input checked="" type="checkbox"/> Simulation data <input checked="" type="checkbox"/> Software <input checked="" type="checkbox"/> Other <input type="checkbox"/> NA	<input type="checkbox"/> .por <input type="checkbox"/> .xml <input type="checkbox"/> .tab <input type="checkbox"/> .csv <input type="checkbox"/> .pdf <input checked="" type="checkbox"/> .txt <input type="checkbox"/> .rtf <input type="checkbox"/> .dwg <input type="checkbox"/> .tab <input type="checkbox"/> .gml <input checked="" type="checkbox"/> other: .pdb <input type="checkbox"/> NA	<input type="checkbox"/> < 100 MB <input type="checkbox"/> < 1 GB <input checked="" type="checkbox"/> < 100 GB <input type="checkbox"/> < 1 TB <input type="checkbox"/> < 5 TB <input type="checkbox"/> < 10 TB <input type="checkbox"/> < 50 TB <input type="checkbox"/> > 50 TB <input type="checkbox"/> NA	NA
3. Plasmid DNA (all WPs)	Plasmid DNA, stored either as purified plasmid DNA (-20°C) or as frozen glycerol stocks of transformed bacteria (-80°C).	<input checked="" type="checkbox"/> Generate new data <input checked="" type="checkbox"/> Reuse existing data	<input type="checkbox"/> Digital <input checked="" type="checkbox"/> Physical	NA	NA	NA	50 vials (2mL) in -80°C freezer, 200 vials (1.5 or 2 mL) in -20°C freezer.
4. Purified antibodies/proteins (all WPs)	<i>In vitro</i> transfection experiments for expression of antibodies/proteins. Harvested cell culture medium containing the produced antibody/protein, and purified antibodies/proteins will be stored at -20°C.	<input checked="" type="checkbox"/> Generate new data <input checked="" type="checkbox"/> Reuse existing data	<input type="checkbox"/> Digital <input checked="" type="checkbox"/> Physical	NA	NA	NA	200 vials/tubes of 1 to 10 mL in -20°C freezer.
5. Cell lines (all WPs)	Different types of cell lines from mammalian origin (mouse, hamster and human), used for <i>in vitro</i> cell transfection experiments, reporter cell lines, screening of shRNA/miRNA,...	<input checked="" type="checkbox"/> Generate new data <input checked="" type="checkbox"/> Reuse existing data	<input type="checkbox"/> Digital <input checked="" type="checkbox"/> Physical	NA	NA	NA	100 vials/tubes of 1.5 or 2 mL in liquid nitrogen.

6. viral vectors (WP2)	Different viral vectors (LV) will be generated to transduce target cells of interest. Vectors will be stored in a -80°C freezer at KU Leuven Viral Vector Core and monitored in dedicated databases (.xls file, KUL servers)	<input checked="" type="checkbox"/> Generate new data <input checked="" type="checkbox"/> Reuse existing data	<input checked="" type="checkbox"/> Digital <input checked="" type="checkbox"/> Physical	<input checked="" type="checkbox"/> Observational <input checked="" type="checkbox"/> Experimental <input type="checkbox"/> Compiled/aggregated data <input type="checkbox"/> Simulation data <input type="checkbox"/> Software <input type="checkbox"/> Other <input type="checkbox"/> NA	<input type="checkbox"/> .por <input type="checkbox"/> .xml <input type="checkbox"/> .tab <input type="checkbox"/> .csv <input checked="" type="checkbox"/> .pdf <input type="checkbox"/> .txt <input type="checkbox"/> .rtf <input type="checkbox"/> .dwg <input type="checkbox"/> .tab <input type="checkbox"/> .gml <input checked="" type="checkbox"/> other: .xlsx <input type="checkbox"/> NA	<input type="checkbox"/> < 100 MB <input checked="" type="checkbox"/> < 1 GB <input type="checkbox"/> < 100 GB <input type="checkbox"/> < 1 TB <input type="checkbox"/> < 5 TB <input type="checkbox"/> < 10 TB <input type="checkbox"/> < 50 TB <input type="checkbox"/> > 50 TB <input type="checkbox"/> NA	20 eppendorf vials/tubes of 1,5 mL, each containing 50 µl of vector per prep, in -80°C freezer
7. Physical samples from <i>in vitro</i> experiments (all WPs)	Physical samples from <i>in vitro</i> experiments (e.g. cell medium after cell transfection)	<input checked="" type="checkbox"/> Generate new data <input type="checkbox"/> Reuse existing data	<input type="checkbox"/> Digital <input checked="" type="checkbox"/> Physical	NA	NA	NA	300 vials of 1,5 mL in -20 freezer.
8. Knock-out mice (all WPs)	Knock-out mouse strains are kept in the animal facility of KU Leuven. List of mice used for experiments is available in the LAIS system.	<input checked="" type="checkbox"/> Generate new data <input checked="" type="checkbox"/> Reuse existing data	<input checked="" type="checkbox"/> Digital <input type="checkbox"/> Physical	NA	NA	NA	Live mice in animal facility.
9. <i>In vivo</i> experimental data (all WPs)	Experimental details (treatment parameters, animal handling, observations...) will be written down in electronic lab notebook (eLabJournal, eLabNext, Eppendorf Group), raw data (e.g. body weight vs. time) will be stored as Excel files.	<input checked="" type="checkbox"/> Generate new data <input checked="" type="checkbox"/> Reuse existing data	<input checked="" type="checkbox"/> Digital <input type="checkbox"/> Physical	<input checked="" type="checkbox"/> Observational <input checked="" type="checkbox"/> Experimental <input type="checkbox"/> Compiled/aggregated data <input type="checkbox"/> Simulation data <input type="checkbox"/> Software <input type="checkbox"/> Other <input type="checkbox"/> NA	<input type="checkbox"/> .por <input type="checkbox"/> .xml <input type="checkbox"/> .tab <input type="checkbox"/> .csv <input checked="" type="checkbox"/> .pdf <input type="checkbox"/> .txt <input type="checkbox"/> .rtf <input type="checkbox"/> .dwg <input type="checkbox"/> .tab <input type="checkbox"/> .gml <input checked="" type="checkbox"/> other: .xlsx <input type="checkbox"/> NA	<input checked="" type="checkbox"/> < 100 MB <input type="checkbox"/> < 1 GB <input type="checkbox"/> < 100 GB <input type="checkbox"/> < 1 TB <input type="checkbox"/> < 5 TB <input type="checkbox"/> < 10 TB <input type="checkbox"/> < 50 TB <input type="checkbox"/> > 50 TB <input type="checkbox"/> NA	NA
10. Mouse plasma samples (all WPs)	Plasma samples collected at different timepoints during <i>in vivo</i> gene transfer experiments in mice.	<input checked="" type="checkbox"/> Generate new data <input type="checkbox"/> Reuse existing data	<input type="checkbox"/> Digital <input checked="" type="checkbox"/> Physical	NA	NA	NA	1000 vials/tubes of 1,5 mL in -20°C freezer.
11. ELISA data (all WPs)	Enzyme-linked immunosorbent assays performed on different sample types (e.g. medium of <i>in vitro</i> transfected cells, plasma of treated mice) for quantification of transgene expression. Readout in excel files and data analysis in GraphPad prism.	<input checked="" type="checkbox"/> Generate new data <input type="checkbox"/> Reuse existing data	<input checked="" type="checkbox"/> Digital <input type="checkbox"/> Physical	<input type="checkbox"/> Observational <input checked="" type="checkbox"/> Experimental <input checked="" type="checkbox"/> Compiled/aggregated data <input type="checkbox"/> Simulation data <input type="checkbox"/> Software <input type="checkbox"/> Other <input type="checkbox"/> NA	<input type="checkbox"/> .por <input type="checkbox"/> .xml <input type="checkbox"/> .tab <input type="checkbox"/> .csv <input type="checkbox"/> .pdf <input type="checkbox"/> .txt <input type="checkbox"/> .rtf <input type="checkbox"/> .dwg <input type="checkbox"/> .tab <input type="checkbox"/> .gml <input checked="" type="checkbox"/> other: .pzf, .xlsx <input type="checkbox"/> NA	<input type="checkbox"/> < 100 MB <input checked="" type="checkbox"/> < 1 GB <input type="checkbox"/> < 100 GB <input type="checkbox"/> < 1 TB <input type="checkbox"/> < 5 TB <input type="checkbox"/> < 10 TB <input type="checkbox"/> < 50 TB <input type="checkbox"/> > 50 TB <input type="checkbox"/> NA	NA
12. Muscle samples (WP2)	Mouse muscle samples collected after <i>in vivo</i> gene transfer.	<input checked="" type="checkbox"/> Generate new data <input type="checkbox"/> Reuse existing data	<input type="checkbox"/> Digital <input checked="" type="checkbox"/> Physical	NA	NA	NA	300 vials/tubes of 1,5 mL in -80°C freezer.
13. mRNA and cDNA samples (WP2)	mRNA will be extracted from different cell lines and conditions, and stored at -80°C. cDNA samples generated by reverse transcription of mRNA of <i>in vitro</i> cultured cells. cDNA will also be generated from mRNA from <i>in vivo</i> targeted tissue.	<input checked="" type="checkbox"/> Generate new data <input type="checkbox"/> Reuse existing data	<input type="checkbox"/> Digital <input checked="" type="checkbox"/> Physical	NA	NA	NA	100 vials/tubes of 1,5 mL in -80°C freezer. 100 vials/tubes of 200 µL in -20°C freezer.

14. Gene expression data (WP2)	Evaluation of transgene expression or target gene silencing in cell culture and <i>in vivo</i> in targeted tissue cells by (RT-)qPCR.	<input checked="" type="checkbox"/> Generate new data <input type="checkbox"/> Reuse existing data	<input checked="" type="checkbox"/> Digital <input type="checkbox"/> Physical	<input type="checkbox"/> Observational <input checked="" type="checkbox"/> Experimental <input checked="" type="checkbox"/> Compiled/aggregated data <input type="checkbox"/> Simulation data <input type="checkbox"/> Software <input type="checkbox"/> Other <input type="checkbox"/> NA	<input type="checkbox"/> .por <input type="checkbox"/> .xml <input type="checkbox"/> .tab <input checked="" type="checkbox"/> .csv <input type="checkbox"/> .pdf <input type="checkbox"/> .txt <input type="checkbox"/> .rtf <input type="checkbox"/> .dwg <input type="checkbox"/> .tab <input type="checkbox"/> .gml <input checked="" type="checkbox"/> other: .pzf, .xlsx <input type="checkbox"/> NA	<input type="checkbox"/> < 100 MB <input type="checkbox"/> < 1 GB <input checked="" type="checkbox"/> < 100 GB <input type="checkbox"/> < 1 TB <input type="checkbox"/> < 5 TB <input type="checkbox"/> < 10 TB <input type="checkbox"/> < 50 TB <input type="checkbox"/> > 50 TB <input type="checkbox"/> NA	NA
15. Reporter assay data (WP2)	Reporter assay data performed on different sample types (e.g. medium of <i>in vitro</i> transfected cells, plasma of treated mice) for quantification of the Type I IFN and NFkB pathway. Readout in Excel files and data analysis in GraphPad prism.	<input checked="" type="checkbox"/> Generate new data <input type="checkbox"/> Reuse existing data	<input checked="" type="checkbox"/> Digital <input type="checkbox"/> Physical	<input type="checkbox"/> Observational <input checked="" type="checkbox"/> Experimental <input checked="" type="checkbox"/> Compiled/aggregated data <input type="checkbox"/> Simulation data <input type="checkbox"/> Software <input type="checkbox"/> Other <input type="checkbox"/> NA	<input type="checkbox"/> .por <input type="checkbox"/> .xml <input type="checkbox"/> .tab <input checked="" type="checkbox"/> .csv <input type="checkbox"/> .pdf <input type="checkbox"/> .txt <input type="checkbox"/> .rtf <input type="checkbox"/> .dwg <input type="checkbox"/> .tab <input type="checkbox"/> .gml <input checked="" type="checkbox"/> other: .pzf, .xlsx <input type="checkbox"/> NA	<input checked="" type="checkbox"/> < 100 MB <input type="checkbox"/> < 1 GB <input type="checkbox"/> < 100 GB <input type="checkbox"/> < 1 TB <input type="checkbox"/> < 5 TB <input type="checkbox"/> < 10 TB <input type="checkbox"/> < 50 TB <input type="checkbox"/> > 50 TB <input type="checkbox"/> NA	NA
16. Cytokine array data (WP2)	Cytokine array data performed on different sample types (e.g. medium of <i>in vitro</i> transfected cells, plasma of treated mice) for quantification of different secreted cytokines. Images (.scn) and quantifications in Excel files and data analysis in GraphPad prism.	<input checked="" type="checkbox"/> Generate new data <input type="checkbox"/> Reuse existing data	<input checked="" type="checkbox"/> Digital <input type="checkbox"/> Physical	<input type="checkbox"/> Observational <input checked="" type="checkbox"/> Experimental <input checked="" type="checkbox"/> Compiled/aggregated data <input type="checkbox"/> Simulation data <input type="checkbox"/> Software <input type="checkbox"/> Other <input type="checkbox"/> NA	<input type="checkbox"/> .por <input type="checkbox"/> .xml <input type="checkbox"/> .tab <input checked="" type="checkbox"/> .csv <input type="checkbox"/> .pdf <input type="checkbox"/> .txt <input type="checkbox"/> .rtf <input type="checkbox"/> .dwg <input type="checkbox"/> .tab <input type="checkbox"/> .gml <input checked="" type="checkbox"/> other: .scn, .xlsx, .pzf <input type="checkbox"/> NA	<input checked="" type="checkbox"/> < 100 MB <input type="checkbox"/> < 1 GB <input type="checkbox"/> < 100 GB <input type="checkbox"/> < 1 TB <input type="checkbox"/> < 5 TB <input type="checkbox"/> < 10 TB <input type="checkbox"/> < 50 TB <input type="checkbox"/> > 50 TB <input type="checkbox"/> NA	NA
17. Flow cytometry data (WP2)	Raw data of single cell phenotypes generated by flow cytometry (.fcs) or analysed via FlowJo (.wsp) and GraphPad prism.	<input checked="" type="checkbox"/> Generate new data <input type="checkbox"/> Reuse existing data	<input checked="" type="checkbox"/> Digital <input type="checkbox"/> Physical	<input type="checkbox"/> Observational <input checked="" type="checkbox"/> Experimental <input checked="" type="checkbox"/> Compiled/aggregated data <input type="checkbox"/> Simulation data <input type="checkbox"/> Software <input type="checkbox"/> Other <input type="checkbox"/> NA	<input type="checkbox"/> .por <input type="checkbox"/> .xml <input type="checkbox"/> .tab <input checked="" type="checkbox"/> .csv <input type="checkbox"/> .pdf <input type="checkbox"/> .txt <input type="checkbox"/> .rtf <input type="checkbox"/> .dwg <input type="checkbox"/> .tab <input type="checkbox"/> .gml <input checked="" type="checkbox"/> other: .fcs, .wsp, .pzf <input checked="" type="checkbox"/> NA	<input checked="" type="checkbox"/> < 100 MB <input type="checkbox"/> < 1 GB <input type="checkbox"/> < 100 GB <input type="checkbox"/> < 1 TB <input type="checkbox"/> < 5 TB <input type="checkbox"/> < 10 TB <input type="checkbox"/> < 50 TB <input type="checkbox"/> > 50 TB <input type="checkbox"/> NA	NA
18. Analyzed data, figures and statistical analyses (all WPs)	Analysis of raw data (excel data sheets with quantitative data and summary data), visualization of data in Excel and GraphPad Prism, and statistical analyses in GraphPad Prism. Presentation slides summarizing key findings of the project will be generated in Powerpoint.	<input checked="" type="checkbox"/> Generate new data <input type="checkbox"/> Reuse existing data	<input checked="" type="checkbox"/> Digital <input type="checkbox"/> Physical	<input type="checkbox"/> Observational <input checked="" type="checkbox"/> Experimental <input checked="" type="checkbox"/> Compiled/aggregated data <input type="checkbox"/> Simulation data <input type="checkbox"/> Software <input type="checkbox"/> Other <input type="checkbox"/> NA	<input type="checkbox"/> .por <input type="checkbox"/> .xml <input type="checkbox"/> .tab <input checked="" type="checkbox"/> .csv <input checked="" type="checkbox"/> .pdf <input type="checkbox"/> .txt <input type="checkbox"/> .rtf <input type="checkbox"/> .dwg <input type="checkbox"/> .tab <input type="checkbox"/> .gml <input checked="" type="checkbox"/> other: .pzf, .xlsx, .pdf, .tiff <input type="checkbox"/> NA	<input checked="" type="checkbox"/> < 100 MB <input type="checkbox"/> < 1 GB <input type="checkbox"/> < 100 GB <input type="checkbox"/> < 1 TB <input type="checkbox"/> < 5 TB <input type="checkbox"/> < 10 TB <input type="checkbox"/> < 50 TB <input type="checkbox"/> > 50 TB <input type="checkbox"/> NA	NA

19. Protocols, experimental documentation, metadata, and manuscripts (all WPs)	Experimental protocols, details related to data collection/processing, and data collection/analysis particularities, will be stored in the electronic lab notebook (LTDA/PharmAbs), or Word (.docx) or Excel (.xlsx) files (LCSI), or Word and Excel files linked in an electronic lab notebook in OneNote LMVGT).	<input checked="" type="checkbox"/> Generate new data <input checked="" type="checkbox"/> Reuse existing data	<input checked="" type="checkbox"/> Digital <input type="checkbox"/> Physical	<input checked="" type="checkbox"/> Observational <input checked="" type="checkbox"/> Experimental <input checked="" type="checkbox"/> Compiled/aggregated data <input type="checkbox"/> Simulation data <input type="checkbox"/> Software <input type="checkbox"/> Other <input type="checkbox"/> NA	<input type="checkbox"/> .por <input type="checkbox"/> .xml <input type="checkbox"/> .tab <input type="checkbox"/> .csv <input checked="" type="checkbox"/> .pdf <input type="checkbox"/> .txt <input type="checkbox"/> .rtf <input type="checkbox"/> .dwg <input type="checkbox"/> .tab <input type="checkbox"/> .gml <input checked="" type="checkbox"/> other: .docx, .xlsx, .pdf, .one <input type="checkbox"/> NA	<input checked="" type="checkbox"/> < 100 MB <input type="checkbox"/> < 1 GB <input type="checkbox"/> < 100 GB <input type="checkbox"/> < 1 TB <input type="checkbox"/> < 5 TB <input type="checkbox"/> < 10 TB <input type="checkbox"/> < 50 TB <input type="checkbox"/> > 50 TB <input type="checkbox"/> NA	NA
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Existing data that will be reused are the following: protocols, DNA sequences of plasmids and transgenes (antibody/protein) and plasmid DNA (physical samples). All these data were previously generated in the labs of the PI and co-PIs, and are therefore available from this source (no external sources).

- Yes, animal data

All experiments in animals (mice) are approved by the Animal Ethics Committee of KU Leuven (project number P149/2022). Guidelines and rules from the HSE (Health, Safety and Environment) Department and the Animal Ethics Committee of KU Leuven will be followed.

- No

NA

- Yes

The research data that will be generated in this project hold great potential for tech transfer and valorization. The potential for commercial valorization will be continuously monitored and evaluated by the PharmAbs consortium IOF manager (Dr. Nick Geukens), together with KU Leuven Research & Development (LRD) and the VIB Tech Transfer Office (TTO), and further steps in the valorization process will be done in close collaboration with KU Leuven LRD and the VIB TTO. In this regard, all datasets generated within the current project will be reserved for at least 2 years after the end of the project for the launch of a spin-off company. Upon the launch of the spin-off company, KU Leuven and VIB will license commercial exploitation rights on the available proprietary knowledge and patent applications enabled by the results obtained in the current project to the spin-off company, and will provide access to relevant background IP and know-how to maximize the value of the spin-off company.

- No

Currently, there are no 3rd party agreements that restrict exploitation or dissemination of the data we (re)use, but this can/will probably change during the course of the project.

- No

Currently, there are no other legal issues, such as IP rights and ownership, to be managed related to the data we (re)use, but this can/will probably change during the course of the project.

2. Documentation and Metadata

Detailed experimental protocols, the research progress and clear descriptions of obtained data, what they represent and how they were generated, will be collected in an electronic lab notebook (eLabJournal, eLabNext, Eppendorf Group or Excel at PharmAbs; OneNote at LMVGT; E-notebook at Switch) and/or in hard copy lab notebooks that refer to specific datasets. Here, folders are provided for all subtasks of the project (folder structure: Project group > Project > Study > Experiment). In each folder, a new file will be made for each experiment, named with the data and subject, and including information on the responsible person (i.e. the person who created the file) as well as version tracking. Each experimental file will contain a section on the subject, objective and experimental design, used protocols, used and generated samples, results (a description of results and observation rather than all raw and analysed data) and conclusion. For each experiment, all raw and analysed data files, supplemented with a .pdf transcript of the experiment in the electronic lab notebook, will be stored in a folder on the shared server, using the same hierarchical folder structure as the electronic lab notebook. By using the same structure on the server and in the electronic lab notebook, contextual information on the experimentally obtained data can be easily searched and reused by a secondary analyst via the electronic lab notebook.

For each peer-reviewed article, a separate folder will be made on the server, containing the latest word version and all raw and processed data used in the article. In addition, a separate file will be made in the electronic lab notebook for each article, containing clickable links to all metadata files of data that were used in that article, to facilitate tracing back of protocols, results and conclusions

A physical sample inventory will be stored in freezers and all samples will be added to a digital inventory in the electronic lab notebook (with links to the experiments in which the samples are generated/used, and a link to the sample details).

- No

No uniform metadata standard is available for all different aspects of this project. Therefore, we will create a uniform system ourselves to enhance the use of secondary data. We will use the electronic lab notebook in which a number of predetermined topics have to be described for each experiment (Title/subject, Objective, protocol, results and conclusion). The electronic lab notebook facilitates searching for particular metadata through a search engine. By mimicking the folder structure of the electronic lab notebook in the server-based folder with the experimental data, linking of the metadata to the actual data will be facilitated. Folder names will be descriptive, and file names will have a clear meaning which include: date/date range of the experiment, project or experiment name/number, initials of author of the file, type of data and version number of the file.

For certain datasets, a metadata standard will be used:

- Nucleotide sequence files (vectors and sequencing): GenBank Sequence Format (<https://fairsharing.org/FAIRsharing.rq2vmt/>)
- Proteomics data: Proteomics IDentifications database (PRIDE, <https://www.ebi.ac.uk/pride/>)

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

The time-stamped digital data will be stored in a project folder on the KU Leuven shared J-drive (all involved research groups) or in shared laboratory folders of an off-site online backup service (VIB Switch lab). The time-stamped digital (meta)data will be stored on the server of the electronic lab notebook, and a .pdf export of the electronic lab notebook experimental documentation will be made upon completion of the experiment to be saved in the project folder on the shared drive. This folder will be open for the lab members participating in this project, and is secured and backed-up by the ICTS service of KU Leuven. The researchers working on the project will have copies of the data files, as well as of the derived and compiled data stored on their personal computers. Paper lab notebooks (in LMVGT) are only used and kept in the L2 lab of the co-PI.

The Switch Lab has a professional subscription to an off-site online backup service with unlimited space, version control and roll-back capability, which will be used for storage during the project and after. There is also a secondary on-campus physical backup of the online storage which synchronizes with the online content with a one-day delay.

All the relevant algorithms, scripts and software code driving the project will be stored in a private online git repository from the GitHub account of the department (<https://github.com/vibcbd>).

Regarding the data pertaining to publications, the first author is responsible for storing all raw and processed data, and metadata, of the paper concerned in a subfolder on the KU Leuven shared J-drive. Next to this, all data underlying analyses/figures of the paper concerned will be stored together with the analysed data, tables, figures in the project folder in the electronic lab notebook together with a detailed description of the performed analyses.

The physical samples will be stored in the freezers of the labs of the PI and co-PIs. A digital overview of all stored samples will be available (either in an Excel file or in the sample inventory system of the electronic lab notebook).

The digital data (saved on KU Leuven J-drive) will be stored on the university's central servers with automatic hourly back-up procedures (PharmAbs, LMVGT). Backup copies will be made on hard drives and on a local RAID storage available in the office (LCSI).

The data stored in the electronic lab notebook (eLabJournal, eLabNext, Eppendorf group) is replicated to 3 different data centers in real-time. Additionally, a full back-up of all data files is made every 24 hours. Data back-ups are stored as fully encrypted files to an external vault in case of an emergency and the necessity of a full recovery.

The Switch Lab has a professional subscription to an off-site online backup service with unlimited space, version control and roll-back capability, which will be used for storage during the project and after. There is also a secondary on-campus physical backup of the online storage which synchronizes with the online content with a one-day delay.

Physical samples will be kept for 10 years post-project in the freezers of the project collaborators, with 2 vials of each crucial sample being stored in different freezers as back-up.

- Yes

KU Leuven provides sufficient storage and back-up capacity during and after the project. If necessary, the volume of the KU Leuven shared J-drive can be expanded with blocks of 100 GB at any time, for which budget is available.

Sufficient freezer capacity is available in the different labs.

The Switch Lab has a professional subscription to an off-site online backup service with unlimited space, which will be used for storage during the project and after.

Only lab members actively working on the project will have access to the KU Leuven J-drive (access is granted by the PI).

In the electronic lab notebook (eLabJournal, eLabNext, Eppendorf group), only the people actively working on the project will be granted access to the experimental data of the project (settings by administrators for each individual lab member). Furthermore, after completion, experiments will be signed and locked into a read-only mode, which prevents further data modification, and a digital signature including time stamp is added to the experiment. Access to all digital data saved on servers is u-number and password controlled. All notebooks and physical data are stored in the labs. Secure storage of physical samples and paper notebooks is enabled by locking the laboratory doors when researchers are out of the office. Additionally, only people working in the respective labs can access the lab by using a personnel card reader system and/or a key, which only allows people working in the lab to enter.

Data storage on the KU Leuven J-drive with backup will cost 519€ per Tb per year. Each eLabJournal Cloud license seat costs approximately 150€ per year. The Switch Lab has a yearly subscription to an off-site online backup service which costs 5500€ per year. This costs includes unlimited data storage, not only the data belonging to the present project. Costs will be covered by the general laboratory costs or project consumables budget.

4. Data preservation after the end of the research project

All generated research data (physical and digital; raw and processed) will be preserved for at least 10 years after the end of the project conform the FWO RDM policy. The PI and co-PIs will decide on which research data will be kept past this timeframe.

Exception: for biological samples it is not always possible to keep them for 10 years because of stability issues or because of expensive storage at very low temperatures. The PI and co-PIs will decide on which samples are considered valuable, difficult to obtain, likely to be reused and stable, and will preserve those biological samples. Samples that are easy to reproduce and those that are unstable will be discarded, but documentation and metadata related to these samples will be retained, and it will be indicated why these samples were discarded.

For the KU Leuven groups (PharmAbs, LCSI, LMVGT): The digital data will be stored on the university's central servers (with automatic backup procedures) and paper lab notebooks will be kept in locked cabinets in the lab of the PIs concerned for at least 10 years, conform the KU Leuven RDM policy.

The physical data will be stored in freezers in the labs of the PI and co-PIs for up to 10 years after the project (exception: see point 5.1).

For the VIB group (Switch): Digital datasets will be stored on storage space of an online data-backup service. The physical data will be stored in freezers in the labs of the PI and co-PIs for up to 10 years after the project (exception: see point 5.1).

For the KU Leuven groups (PharmAbs, LCSI, LMVGT): Data storage on the KU Leuven J-drive with backup costs 519€ per Tb per year (current fee). Costs will be covered by the laboratory budget.

For the VIB group (Switch): The cost of the laboratory's professional subscription to the online data backup service is 5500€ per year. This cost includes unlimited data storage, not only the data belonging to the present project. Data storage and backup costs are included in general lab costs.

5. Data sharing and reuse

- Other, please specify:

The key findings of the project and their interpretation will be made available through publication of journal articles in established, peer-reviewed academic journals. Relevant data will be made available after publication upon reasonable request by email. These published data contain the results of processed data presented in tables.

Data with valuable IP will be protected prior to publication. Unpublished data will be used for future grant applications/publications, and as such, can only be communicated privately to selected colleagues for as long as the IP potential has not been cleared by LRD and/or VIB TTO. This is a precautionary measure to avoid compromising the IP potential of the work.

Since the research data that will be generated in this project hold great potential for tech transfer and valorization, the datasets generated within the current project will be reserved for at least 2 years after the end of the project for the launch of a spin-off company. Upon the launch of the spin-off company, KU Leuven and VIB will license commercial exploitation rights on the available proprietary knowledge and patent applications enabled by the results obtained in the current project to the spin-off company, and will provide access to relevant background IP and know-how to maximize the value of the spin-off company.

Access to data, concerning ongoing, unpublished research, will be restricted to the researchers participating in the specific project as long as they are affiliated with the project's research groups. Once published, data will be accessible to all, either through reading the relevant paper, or upon reasonable request to the authors by email. For data shared directly by the PIs, a material/data 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 (usually under a CC BY-NC reuse license). Commercial-based requests will be navigated in coordination between the involved (co-)PI(s) and KU Leuven LRD and/or VIB TTO.

- Yes, Intellectual Property Rights

The research data that will be generated in this project hold great potential for tech transfer and valorization. In this regard, datasets generated within the current project will be reserved for at least 2 years after the end of the project for the launch of a spin-off company. Upon the launch of the spin-off company, KU Leuven and VIB TTO will license commercial exploitation rights on the available proprietary knowledge and patent applications enabled by the results obtained in the current project to the spin-off company, and will provide access to relevant background IP and know-how to maximize the value of the spin-off company.

All digital data will be stored and be available for lab members using shared network drives (see above). In addition, the relevant data will be made available to external people upon reasonable request by email. In case of data sharing outside KU Leuven/VIB, the universities' privacy and legal experts will be consulted prior to data sharing to regulate the data sharing process (e.g. data/material transfer agreement, non-disclosure agreement).

Data will only made available to other researchers after publication of the research results. No embargo will be foreseen unless imposed e.g. by pending publications, potential IP requirements (note: patent application filing will be planned so that publications need not to be delayed) or ongoing projects requiring data confidentiality. In those cases, datasets will be made available as soon as the embargo is lifted.

Additional, non-published data can be made available for external researchers upon reasonable request (based on contract or material/data transfer agreement).

Furthermore, data with IP (potential) will be reserved and thus not shared for at least 2 years after the end of the project for the launch of a spin-off company.

For data shared directly by the PIs, a material/data 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, usually under a CC BY-NC reuse licence so that users can only share the work (while giving credit to the original data creators) but not change it or use it commercially.

Commercial-based requests will be navigated in coordination between the involved (co-)PI and KU Leuven LRD, but since the research data that will be generated in this project hold great potential for tech transfer and valorization, the datasets generated within the current project will be reserved for at least 2 years after the end of the project for the launch of a spin-off company. Upon the launch of the spin-off company, KU Leuven will license commercial exploitation rights on the available proprietary knowledge and patent applications enabled by the results obtained in the current project to the spin-off company, and will provide access to relevant background IP and know-how to maximize the value of the spin-off company.

- No

NA

We will minimize data management costs by implementing standard procedures e.g. for (meta)data collection, and file/sample storage and organization from the start of the project. The expected data management/sharing costs will therefore be minimal and will be covered by the laboratory budget of the project. For sharing physical samples, costs for sharing will be discussed with the receiving party on a case-by-case basis. Publication costs (open access) will be covered by the consumables budget of the project.

6. Responsibilities

Post-docs, PhDs and technicians will have the daily responsibility of record keeping of all data (digital, paper and physical samples). They will also be responsible for a correct and accurate data entry and recording of metadata.

Post-docs, PhDs and technicians will have the daily responsibility for managing data storage and backing up of all data (digital, paper and physical samples). They will also be responsible for a correct and accurate data entry and recording of metadata.

The PI (Prof. Karen Vanhoorelbeke (PharmAbs)) and the co-PIs (Prof. Abhishek Garg (LCSI), Prof. Rik Gijssbers (LMVGT), and Prof. Joost Schymkowitz and Prof. Frederic

Rousseau (Switch lab)) will be responsible for data preservation and eventual reuse of obtained data, with support from the research and technical staff involved in the project.

The PI (Prof. Karen Vanhoorelbeke (PharmAbs)) bears the end responsibility of updating and implementing this DMP.