DMP title

Project Name Viral-associated pulmonary aspergillosis: new perspectives on pathophysiology to enable host-directed medicine - DMP title

Grant Title 11M6922N

Principal Investigator / Researcher Simon Feys

Project Data Contact Simon Feys

Description Influenza- and COVID-19-associated pulmonary aspergillosis (IAPA/CAPA, together viral-associated pulmonary aspergillosis or VAPA) comprise a severe healthcare burden with high mortality. Knowledge gaps: VAPA-pathophysiology has never been examined before. LC3-associated phagocytosis (LAP) and Pentraxin-3 (PTX3), essential for fungal killing, might be key players in IAPA and VAPA pathogenesis, respectively. Prospective data and clinical risk factors for IAPA are lacking. Approach: we have recently established a zebrafish larvae model for IAPA, which will be used for visualization of the innate immune response and of LC3-associated phagocytosis in IAPA. Human PTX3 single-nucleotide polymorphism (SNP) analysis will be performed to assess whether they predispose to VAPA-development. Single-cell RNA-sequencing (scRNA-seq) is a powerful technique to unravel cellular/molecular mechanisms governing VAPA-pathogenesis, which will be used on broncho-alveolar lavage fluid and post-mortem biopsies of severe influenza and COVID-19 patients with or without VAPA. We will analyze data of a prospective international multicenter trial on IAPA. Expected outcome: New insights in VAPA-pathogenesis, with identification of diagnostic/prognostic biomarkers and potential immunomodulatory therapeutical targets. Generation of prospective data on IAPA epidemiology and clinical risk factors, allowing identification of patients-at-risk for development of IAPA.

Institution KU Leuven

1. General Information

Name applicant

Simon Feys

FWO Project Number & Title

11M6922N: Viral-associated pulmonary aspergillosis: new perspectives on the pathophysiological and clinical aspects to enable host-directed medicine

Affiliation

- KU Leuven

2. Data description

Will you generate/collect new data and/or make use of existing data?

- Generate new data
- Reuse existing data

Describe in detail the origin, type and format of the data (per dataset) and its (estimated) volume. This may be easiest in a table (see example) or as a data flow and per WP or objective of the project. If you reuse existing data, specify the source of these data. Distinguish data types (the kind of content) from data formats (the technical format).

Work package	Type of data	Format	Volume	How created
WP1.1	SNP-results (RT-qPCR data)	.xls	max 100 MB	SNP-analysis of blood and bronchoalveolar lavage fluid samples from patients with severe influenza or COVID-19 with or without aspergillosis.

WP1.1	Observational pseudonymized clinical patient data	online eCRF format (REDcap, Castor), .xls	max 20MB	Observational data derived from clinical patient records in a prospective and retrospective study (Contagious, PIAS, Variomic study), used to link with SNP-analyses.
WP1.2	Microscopy images	.tif, .lif	100-200GB	High-resolution fluorescence microscopy of zebrafish larvae infected with influenza virus, *Aspergillus* or both, or sham-injected.
WP1.2	RT-qPCR results	.xls	max 10MB	RT-qPCR results of zebrafish larvae infected with influenza virus.
WP1.2	Observational numeric data of zebrafish larvae	.xls	max 10MB	Observational results from zebrafish larvae experiments.
WP2	scRNA-seq results	.fastq and .xls	+/- 550 GB (scRNA-seq from +/- 55 patients at 10 GB per patient)	Results obtained from scRNA-sequencing bronchoalveolar lavage fluid of patients with severe influenza or COVID-19 with or without aspergillosis.
WP2	Observational pseudonymized clinical patient data	online eCRF format (REDcap), .xls	max 5MB	Observational data derived from clinical patient records in a prospective study (Contagious study), used to link with scRNA-seq data.
WP3	Observational pseudonymized clinical patient data	online eCRF format (Castor), .xls	max 100MB	Observational data derived from clinical patient records in a prospective study (IAPAFLU study).
WP1,2,3	Informed consent form	text, printed paper	NA	

WP1,2,3	Patient sample collection (blood, bronchoalveolar lavage fluid, nasal/oral/anal swabs)	biologic samples kept at -20°C or -80°C	NA	Directly collected from the patient

3. Legal and ethical issues

Will you use personal data? If so, shortly describe the kind of personal data you will use. Add the reference to your file in KU Leuven's Register of Data Processing for Research and Public Service Purposes (PRET application). Be aware that registering the fact that you process personal data is a legal obligation.

- Yes

EC Research S-numbers: S63881, S62072, S65588, S64259

Privacy compliance S-numbers: S63381, S65588, S64259

Short description of the kind of personal data that will be used: clinical data of patients admitted to ICU with severe influenza or severe COVID-19, with or without aspergillosis. Data consists of demographic data, medical history before admission, clinical parameters and disease history at ICU admission, laboratory and radiographical parameters, and clinical outcome parameters.

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, add the reference to the formal approval by the relevant ethical review committee(s)

- Yes

EC Research S-numbers: S63881, S62072, S65588, S64259

ECD P-number: P070/2021

Does your work possibly result in research data with potential for tech transfer and valorisation? Will IP restrictions be claimed for the data you created? If so, for what data and which restrictions will be asserted?

- No

Do existing 3rd party agreements restrict dissemination or exploitation of the data you (re)use? If so, to what data do they relate and what restrictions are in place?

- No

4. Documentation and metadata

What documentation will be provided to enable reuse of the data collected/generated in this project?

All data with relation to patients will be coded.

WP1.1:

The information contains the date the SNP-analysis was performed, the study design, methodology, the protocol (or a link to the protocol), reagents, and sampling. The lab notebooks also contain links to the electronic files that contain the raw data, the processed results or other relevant data. Encoded patient data is stored in Redcap or in Castor eCRFs and in excel exports of these data.

WP1.2:

The information contains the date the experiment was performed, the study design, methodology, the protocol (or a link to the protocol), reagents, and sampling. The lab notebooks also contain links to the electronic files that contain the raw data (e.g. of RT-qPCR …), the processed results or other relevant data.

Protocols are digitally available in Word documents and research results are available in Excel documents collected in specific folders. Data files will be logically grouped in folders (according to sub-parts of the project). The description of the experiments will contain all information such that another analyst or scientist can repeat the experiments.

WP2:

Documentation will consist of notes in the Electronic Laboratory Notebook that refers to specific datasets. These notes will describe the biological/clinical samples used, experimental setup and protocols used, sequences generated, links to the specific computer location and the specific names of the respective datasets. Metadata sheets are maintained with the connection between lab samples, sample IDs and files in the data storage so that lab samples, data files and experimental notes remain properly linked to the corresponding samples IDs.

Research methods and practices (SOPs) are fully documented. When wet lab techniques, scripts, algorithms and software tools are finalized, they are additionally described in manuscripts and/or on GitHub.

Raw sequencing data (.fastq files; each named with corresponding sampleID) is collected per sequencing run, including an .xlsx file with the sample sheet information containing the sample IDs sequenced in that run and the sequencing run information per sample ID (Illumina sequencer, lane and index information). The name of the folder will contain the date of the sequencing run and the Illumina sequencer used. When data are published, raw and processed sequencing data will be uploaded on a public repository (e.g. EGA) with appropriate access control if required, to enable sharing and long-term validity of the data.

WP3:

Data generated in this work package is managed by Radboudumc as part of the H2020 project HDM-FUN. In line with Radboudumc policy, (meta)data that are suitable for reuse will be available to other researchers upon request using the DANS EASY repository that is certified (CoreTrustSeal/ nestor Seal 2016). DANS uses Digital Object Identifiers (DOIs). Each dataset stored in EASY has a unique DOI, and new datasets are automatically assigned a DOI upon deposition. You can use this DOI when citing the associated dataset. Each dataset also contains a set of instructions in “Cite as” format to facilitate data citation by secondary users using the DOI. The deposit in the DANS EASY archive contains metadata from the Dublin Core standard, enriched with DataCite metadata fields. The metadata fields in DANS comply with the guidelines of the Dublin Core standard/DataCite and include keywords. Any transformations, restructuring and analysis are performed through scripts/syntax files and/or documentation. Version control will be applied that tracks changes in documents, files, syntaxes. Data will be collected using Castor-EDC. This is a GCP-compliant EDC. Castor-EDC also enables data managers to add metadata to fields. To make the data Interoperable standard data names and types (ontology) will be used, such as SNOMED, MedDRA. When research data is completed and ready for storage, it will be uploaded to partners institutional repository or to Zenodo (https://www.zenodo.org/), when a partner has not access to an institutional repository. A DOI will be assigned to datasets for effective and persistent citation when uploaded in a repository. This DOI can be used in any relevant publications to direct readers to the underlying dataset. Data from each experiment is saved in a word or excel file and each word or excel file is recorded in a spreadsheet with the date and title of experiment. Search keywords will be provided when the dataset is uploaded to the institutional repository and/or to Zenodo which will optimise possibilities for re-used.

Will a metadata standard be used? If so, describe in detail which standard will be used. If no, state in detail which metadata will be created to make the data easy/easier to find and reuse.

- Yes
- No

WP1.1:

Metadata from SNP-analyses (performed in a RT-qPCR-system) are inherently stored in exported files (including all RT-qPCR settings).

WP1.2:

Metadata from RT-qPCR files are inherently stored in exported files (including all RT-qPCR settings). Metadata related to microscopy images generated during the work package will be added to the title of each .lif-file and .tif image (timepoint, microscope settings, and experiment number which refers to an additional file containing experiment metadata), but most metadata are also inherently stored in the files created by the instrument (.lif).

WP2:

Sequencing data types require specific metadata when submitted to public repositories such as EGA, ArrayExpress, GEO or ENA. Data documentation will be tailored to their ultimate deposition in public repositories, with spreadsheet headers corresponding to fields required by

these public repositories. Technical and analytical methods used to generate the data will be documented in sufficient detail to allow for independent reproduction. These will include analysis package version numbers, analysis kit, disease status, treatment type and duration, organism, genome build…. For single-cell experiments, each droplet barcode will also be retained alongside the associated single-cell quality metrics. When depositing data in a repository, the final dataset will be accompanied by this information in the file format that the repository provides. This will allow the data to be understood by other members of the laboratory and add context to the dataset for future reuse.

WP3:

The deposit in the DANS EASY archive contains metadata from the Dublin Core standard, enriched with DataCite metadata fields. The metadata fields in DANS comply with the guidelines of the Dublin Core standard/DataCite and include keywords. Any transformations, restructuring and analysis are performed through scripts/syntax files and/or documentation. Version control will be applied that tracks changes in documents, files, syntaxes. Data will be collected using Castor-EDC. This is a GCP-compliant EDC. Castor-EDC also enables data managers to add metadata to fields.

To make the data Interoperable standard data names and types (ontology) will be used, such as SNOMED, MedDRA. For labdata this is LOINC. When research data is completed and ready for storage, it will be uploaded to partners institutional repository or to Zenodo (https://www.zenodo.org/), when a partner has not access to an institutional repository. A DOI will be assigned to datasets for effective and persistent citation when uploaded in a repository. This DOI can be used in any relevant publications to direct readers to the underlying dataset. Data from each experiment is saved in a word or excel file and each word or excel file is recorded in a spreadsheet with the date and title of experiment.

HDM-FUN naming convention for project datasets will comprise the following:

- A unique chronological number of the datasets
- The title of the dataset
- Each new version of a dataset will be named with a version number (e.g., v1.0, v1.1, v1.2 etc)
- A prefix “HDM-FUN” indicating a project dataset
- A unique identifier number linking with the dataset WP and deliverable (e.g., WP1_D1.1”)

Example: **01_ TITLE OF DATASET_v1.0_HDM-FUN_WP1_D1.1.xlsx**

Search keywords will be provided when the dataset is uploaded to the institutional repository and/or to Zenodo which will optimise possibilities for re-use.

5. Data storage and backup during the FWO project

Where will the data be stored?

Electronic data

The electronic data generated during the SNP work package (WP1.1) will be stored in secured, password-protected and back-up servers of UZ Leuven.

All electronical data collected and generated during the scRNA-seq work package (WP2) and the zebrafish work package (WP1.2) will be processed and (temporarily) stored on secured, password-protected and backed up servers of VIB-KU Leuven and KU Leuven respectively (managed by ICT of the Biomedical Sciences Group).

The sequencing data generated during the scRNA-seq work package (WP2) will either be stored on VIB-KU Leuven servers or on the Flemish Supercomputer Centre (VSC), initially in the staging and archive area, and later only in the archive area (archive is mirrored).

The electronic data generated during the observational study work package (WP3) will be stored centrally at Radboudumc (Nijmegen, the Netherlands) as Radboudumc is the sponsor of this study, in Digital Research Environment (DRE), which is a cloud-based dedicated and secure workspace. The DRE consists of workspaces, from within tools can be used which enable us to import, merge, optimize, store, analyze, archive and share clinical and research data. Each workspace is completely secure and fully scalable. DRE provides the necessary security, ICT infrastructure and compliance with international laws and regulations.

Samples

For the SNP work package (WP1.1), all patient samples will be stored in UZ Leuven in labeled tubes in -20°C or -80°C freezers purchased by own funding. The samples will be registered and handled according to the UZ Leuven Biobank guidelines.

For the zebrafish work package (WP1.2), all samples generated during experiments will be stored

in labeled tubes in the Rega Institute (KU Leuven) in -20°C or -80°C freezers purchased by own funding.Samples will be registered in the FreezerPro (the sample handling system of the Rega Institute).

For the scRNA-seq work package (WP2), all patient samples, ˜single-cell suspensions and sequence library preparations will be stored in labeled tubes or SBS plates in -20°C or -80°C freezers purchased by our own funding. The samples will be registered and handled according to the UZ Leuven Biobank guidelines.

For the observational study work package (WP3), all patient samples are sent to the biobank of Radboudumc Nijmegen for centrally-managed storage.

How is backup of the data provided?

KU/UZ Leuven drives are backed-up automatically on a daily basis using KU/UZ Leuven services. Radboudumc drives are backed-up automatically. All sequencing data stored on the Flemish Supercomputer Centre (VSC) will be regularly transferred to the archive area that is mirrored.

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

There is sufficient storage and back-up capacity on all described servers. For VIB/KU Leuven servers (which will hold the majority of data in this project) specifically:

- The “L-drive” is an easily scalable system, built from General Parallel File System (GPFS) cluster with NetApp eseries storage systems, and a CTDB samba cluster in the front-end.

- The “J-drive” is based on a cluster of NetApp FAS8040 controllers with an Ontap 9.1P9 operating system.

- The Staging and Archive on VSC are also sufficiently scalable (petabyte scale)

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

The total estimated cost of data storage during the 4 years of this FWO project is +/-1100 EUR. This estimation is based on the following costs:

- The costs of digital data storage are as follows: €868,9/5 TB/Year for the “L-drive” and €519/TB/Year for the “J-drive”.
- The cost of VSC archive is €70/TB/Year, and staging €130/TB/Year.
- We expect costs to drop slightly during the coming four years.

For the observational study with data storage by Radboudumc Nijmegen in the Castor environment, no budgeting is necessary as this is a free service by the Radboudumc Nijmegen.

All costs for data storage will be covered by own funding.

Data security: how will you ensure that the data are securely stored and not accessed or modified by unauthorized persons?

Observational clinical patient information as well as sequencing data and associated pseudonymized patient/clinical information is considered sensitive information and will be handled as such.

The data generated in this project will be processed and stored on the VIB-KU Leuven and UZ Leuven IT infrastructure or Radboudumc/Castor infrastructure which are protected by a genuine user authentication system relying on username and password. Access to the data as well as the access level will be limited on a project need and individual basis. Only the researchers working on the project have access to these data. Due to the sample labelling as protective measure, the researchers are not able to decipher the identity of the donor.

No personal data will be stored on the VSC nor local drives, except for the nucleic acid sequences. The coding key to patient information of linked pseudonymized data does not carry any personal identifiers and all records containing the identity of each participant will be kept private and confidential. The coding key will be kept by the PI, ICU physician prof. dr. Joost Wauters.

6. Data preservation after the FWO project

Which data will be retained for the expected 5 year period after the end of the project? In case only a selection of the data can/will be preserved, clearly state the reasons for this (legal or contractual restrictions, physical preservation issues, ...).

All electronical data collected in the two first work packages of this FWO project will be retained for the expected 5 year period after the end of the project. All (remaining) biological samples are preserved for 50 years, in accordance with the guidelines of Biobank UZ/KU Leuven. All samples taken during the observational study will be stored in the Radboudumc biobank for a minimum of 10 years after end of the study.

Where will the data be archived (= stored for the longer 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.

Long term storage will be ensured as follows for the first two work packages:

- Large sequencing data will be stored on VSC archive
- Small digital files, including TIFF files, will be stored on the “L-drive”.
- Developed algorithms and software will be stored on VSC archive and/or L-drive, as well on public repositories such as Github.com

For the third work package: all data will be archived by Radboudumc Nijmegen in the Znodo data sharing repository.

All biological samples obtained during the first two work packages are registered and stored at the Biobank UZ/KU Leuven, in accordance with their guidelines. All samples taken during the observational study will be stored in the Radboudumc biobank for a minimum of 10 years after end of the study.

What are the expected costs for data preservation during the retention period of 5 years? How will the costs be covered?

The total estimated cost of data storage for 5 years after the end of the project is +/- €700 (main costs approximately 200GB on KU Leuven L-drive and approximately 550GB on VSC).

All costs for data preservation will be covered by our own funding.

7. Data sharing and reuse

Are there any factors restricting or preventing the sharing of (some of) the data (e.g. as defined in an agreement with a 3rd party, legal restrictions)?

- No

Which data will be made available after the end of the project?

WP1:

Data resulting in publication will be made available as required, other data upon reasonable request.

WP2:

The promotor (and co-promotors) of this project are committed to publishing scientific research in order to communicate results both to peers and a wider audience. All research outputs supporting publications will be made openly accessible, at the latest, at the time of publication (or preprint deposition) via the required link in the publication or upon reasonable request and after an embargo period after publication.

Data that will be made available include:

- Double-coded raw sequencing data.
- Personal data will be double coded and no reference to subject name will be made.
- Scripts, algorithms and software tools.

Results will be published as Open Access in peer reviewed journal.

Upon reasonable request, scRNA-seq data will be reused by transfer through Belnet Filesender or secure copy.

WP3:

Data will be shared through Zenodo.

Where/how will the data be made available for reuse?

- In an Open Access repository
- Other (specify):

WP1

Whenever possible, datasets and appropriate metadata will be made publicly available through repositories that support FAIR data sharing. Personal data will be double coded and no reference to subject name will be made. Data will be made available upon reasonable request by e-mail.

WP2:

Whenever possible, datasets and appropriate metadata will be made publicly available through repositories that support FAIR data sharing. Personal data will be double coded and no reference to subject name will be made.

Sharing policies for specific research outputs are detailed below:

- Double-coded raw sequencing data (linked to double-coded patient data) will be deposited in open access repositories with restricted access control such as the EBI European Genome-phenome Archive (EGA). The EGA is a repository for personally identifiable genetic and phenotypic data. Sequencing data at EGA will only be available upon reasonable request via our institutional data access committee and if necessary a material transfer agreement will be concluded with the beneficiaries in order to describe the types of reuse that are permitted. The double-coded read count data matrix (linked to double-coded patient data) will be available on an interactive webserver (http://blueprint.lambrechtslab.org).
- Double-coded patient data: Upon publication, all double-coded patient details supporting a manuscript will be made publicly available as supplemental information.
- 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 (raw data) deposited in the E-Notebook are accessible to the PI and the research staff, and will be made available upon request.

Manuscripts: All scientific publications will be shared openly.

For the scRNA-seq work package, at the time of publication, research results will be summarized on the co-promoters' websites (https://gbiomed.kuleuven.be/english/research/50488876, https://www.vibcancer.be/diether-lambrechts) and post-print 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 post-print is not allowed due to copyright agreements, a pre-print version of the manuscript will be made available. (Pre-print) publications will also be automatically added to our institutional repository, Lirias 2.0, based on the authors name and ORCID ID.

- Algorithms, scripts and software: All the relevant algorithms, scripts and software toosls driving the project will be described in manuscripts and/or on GitHub (https://github.com).
- Data that do not support publication will be either deposited in an open access repository or made available upon request by email. Data will be reused by transfer via Belnet Filesender or secure copy.

WP3:

Data will be shared through Zenodo.

When will the data be made available?

- Upon publication of the research results

All research outputs will be made openly accessible, at the latest, at the time of publication (or preprint deposition). 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.

Who will be able to access the data and under what conditions?

WP1:

Data will be available on demand. Access will be considered upon reasonable request.

WP2:

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 be conform to community norms. These repositories clearly describe their conditions of use (typically under a Creative Commons CC0 1.0 Universal (CC0 1.0) Public Domain Dedication or an ODC Public Domain Dedication and Licence, 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. A CC-BY license will be opted for when possible. For data shared directly by the PI (and approval of the 3rd party if necessary), 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.

For KU Leuven data submitted to the EBI European Genome-phenome Archive (EGA), which operates under controlled access, the data access/submission requests will be received by the Genomics Data Access Committee (DAC) of KU Leuven (https://homes.esat.kuleuven.be/~bioiuser/dac/) and processed in consultation with the copromotors produced data. The DAC will provide general guidance in terms of policies and will be referred to in handling controversial cases.

WP3:

The dataset will be uploaded in a cvs format in Zenodo as an open access dataset under a CC-BY license. Therefore, it will be available to anyone for any purpose, provided that they give appropriate credit to the creators.

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

It is the intention to minimize data management costs by implementing standard operating procedures (SOPs) e.g. for metadata collection and file storage and organization from the start of the project, and by using free-to-use data repositories and dissemination facilities whenever possible.

All data management costs will be covered by own funding.

8. Responsibilities

Who will be responsible for data documentation & metadata?

(Meta)data will be documented by the research and technical staff at the time of data collection and analysis, by taking careful notes in the E-notebook that refer to specific datasets. The staff includes the PhD students and study nurses involved in the SNP-project (WP1.1); the PhD student(s), master thesis students, lab assistants involved in the zebrafish project (WP1.2); PhD student(s), technical assistants and bio-informaticians directly involved with the scRNA-seq research project (WP2); myself, study nurses and promotor involved in the clinical observational trial (WP3).

Who will be responsible for data storage & back up during the project?

The staff will ensure data storage and back up, with support from ICTS, gbiomed-IT staff, and UZ-IT staff. For WP3, Radboudumc is responsible for data storage and back-up. More specifically for the scRNA-seq work package, Gino Philips, a junior computer scientist will handle storage and back-up of the sequencing data, under supervision of senior computer scientist Bram Boeckx who has extensive experience in data handling and use of the Flemish Super Computer (VSC) environment.

Final responsibility for data storage & back-up lies with promotor and co-promotors of this project, supported by ICTS, HPC, gbiomed-IT staff and UZ-IT staff. For WP3, final responsibility lies with the promotor and with prof. Frank Van De Veerdonk (Radboudumc).

Who will be responsible for ensuring data preservation and reuse ?

The staff will ensure data storage and back up, with support from ICTS, gbiomed-IT staff, and UZ-IT staff. For WP3, Radboudumc is responsible for data storage and back-up. More specifically for the scRNA-seq work package, Gino Philips, a junior computer scientist will handle storage and back-up of the sequencing data, under supervision of senior computer scientist Bram Boeckx who has extensive experience in data handling and use of the Flemish Super Computer (VSC) environment.

Final responsibility for data storage & back-up lies with promotor and co-promotors of this project, supported by ICTS, HPC, gbiomed-IT staff and UZ-IT staff. For WP3, final responsibility

lies with the promotor and with prof. Frank Van De Veerdonk (Radboudumc).

Who bears the end responsibility for updating & implementing this DMP?
The PI bears the end responsibility of updating & implementing this DMP.