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	**Louwagie Sofie 0000-0002-2471-4046**
Contributor name(s) (+ ORCID) & roles	**Michiels Jan (promotor) 0000-0001-5829-0897** **Verstraeten Natalie (co-promotor) 0000-0002-9548-4647**
Project number[1] & title	3E220831 Deciphering persister awakening in uropathogenic Escherichia coli through CRISPRi screening
Funder(s) GrantID[2]	1101023N
Affiliation(s)	✓ KU Leuven ☐ Universiteit Antwerpen ☐ Universiteit Gent ☐ Universiteit Hasselt ☐ Vrije Universiteit Brussel ✓ Other: VIB Provide ROR[3] identifier when possible: https://ror.org/02bpp8r91 (VIB - KU Leuven Center for Microbiology)

[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	Urinary tract infections (UTIs) are a worldwide health concern and are mainly caused by uropathogenic Escherichia coli (UPEC). Antibiotic therapy failure and the chronic nature of UTIs can be attributed to a small fraction of transiently non-growing, antibiotic-tolerant cells called persisters. An innovative method to cure chronic UTIs would be to induce growth resumption in UPEC persisters, thereby re-sensitizing them to conventional antibiotics. However, our current understanding of persister recovery is far from complete, hampering the development of anti-persister drugs. The aim of this project is to gain mechanistic insight in persister recovery in UPEC. First, we will identify genetic factors contributing to persister recovery in a high-throughput way by screening of pooled CRISPRi libraries containing thousands of cells that are each silencing a specific gene. Identified awakening determinants will be subjected to extensive functional and biochemical examination, which will contribute immensely to our understanding of persister recovery. Finally, we will develop and implement cellular model systems for persistence to validate our findings in vivo. This project will lead to novel insights in persister recovery and will pave the way for the development of diagnostic tests for persistence as well as anti-persister drugs to effectively clear UTIs.

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
WP 1: Screening of a pooled CRISPRi library							
Persister recovery genes (amplicon sequencing results from CRISPRi screening)	Next-generation sequencing of sgRNAs resulting from the pooled CRISPRi screening performed during persister recovery with samples taken at different time points prior to and during recovery	☒ 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 ☐ NA	☐ < 100 MB ☐ < 1 GB ☐ < 100 GB ☒ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	
CRISPRi sgRNA libraries of *E. coli* UTI89	sgRNA library of *E. coli* UTI89 created with custom R scripts. sgRNAs will be cloned	☒ 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	2 mL cryotubes (approx. 10)

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

	into backbone vector and transformed into strain carrying an inducible dCas9			☐ Software ☐ Other ☐ NA	☐ .rtf ☐ .dwg ☐ .tab ☐ .gml ☐ other: ☐ NA	☐ < 50 TB ☐ > 50 TB ☐ NA	
CRISPRi sgRNA libraries of *E. coli* CFT073	sgRNA library of *E. coli* CFT073	☐ 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: ☐ NA	☐ < 100 MB ☐ < 1 GB ☐ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	2 mL cryotubes (approx. 10)
dCas9 pooled CRISPRi library	Images of DNA gels	☒ 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	☐ < 100 MB ☒ < 1 GB ☐ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	

					☒ other: .tiff ☐ NA		
sgRNA read counts persister recovery	Log fold changes in sgRNA abundances	☒ 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: .xslx ☐ NA:	☐ < 100 MB ☐ < 1 GB ☒ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	
MIC	The MIC for the pooled UPEC population in different conditions	☒ 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: .xlsx, .pzfx ☐ NA	☐ < 100 MB ☒ < 1 GB ☐ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	

GO enrichment analysis	GO enrichment analysis on identified hits from CRISPRi screening to differentiate between genes based on function	☒ 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: .xlsx ☐ NA	☐ < 100 MB ☒ < 1 GB ☐ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	
PheNetic analysis	PheNetic analysis on identified hits from CRISPRi screening to differentiate between genes based on interactions	☒ 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: .sif, .tab, .svg, .png ☐ NA	☐ < 100 MB ☒ < 1 GB ☐ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	
Knockout mutants persister	Knockout mutants in UPEC or lab strain of	☒ Generate new data	☐ Digital ☒ Physical	☐ Observational ☐ Experimental	☐ .por ☐ .xml ☐ .tab	☐ < 100 MB ☐ < 1 GB ☐ < 100 GB	2 mL cryotubes (with an estimated maximum of 100 for different genes)

recovery genes	persister recovery genes identified in CRISPRi screening	☐ Reuse existing data		☐ Compiled/ aggregated data ☐ Simulation data ☐ Software ☐ Other ☐ NA	☐ .csv ☐ .pdf ☐ .txt ☐ .rtf ☐ .dwg ☐ .tab ☐ .gml ☐ other: ☐ NA	☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	
Sequencing knockout mutants	Sequencing of knockout mutants after PCR to validate knockout	☒ 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: .fasta ☐ NA	☐ < 100 MB ☒ < 1 GB ☐ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	
Gel knockout mutants	Images of DNA gels after PCR to validate knockout mutant	☒ Generate new data ☐ Reuse existing data	☒ Digital ☐ Physical	☐ Observational ☒ Experimental ☐ Compiled/ aggregated data ☐ Simulation data ☐ Software	☐ .por ☐ .xml ☐ .tab ☐ .csv ☐ .pdf ☐ .txt ☐ .rtf	☐ < 100 MB ☒ < 1 GB ☐ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB	

				☐ Other ☐ NA	☐ .dwg ☐ .tab ☐ .gml ☒ other: .tiff ☐ NA	☐ > 50 TB ☐ NA	
Persister recovery mutants validation population level	Read counts during persister recovery of knockout mutants to validate on population level	☒ 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: .xlsx, .pzfx ☐ NA	☐ < 100 MB ☐ < 1 GB ☒ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	
Persister recovery mutants validation single-cell level	Microscopic images of time lapses to observe single-cell level persister recovery of knockout mutants	☒ 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	☐ < 100 MB ☐ < 1 GB ☐ < 100 GB ☒ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	

					☒ other: .nd2, .tiff ☐ NA		
WP 2: Elucidation of regulatory mechanisms underlying persister awakening (the experiments in this WP depend on the findings of WP 1, the datasets listed below are possible or probable datasets)							
Characterization awakening effectors	Unknown at this point but likely will involve flow cytometry data for the characterization of identified awakening effectors using reporters	☒ 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 ☐ NA	☐ < 100 MB ☐ < 1 GB ☒ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	
Characterization awakening effectors	Unknown at this point but likely will involve microscopy data for the characterization of identified awakening effectors using reporters	☒ 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	☐ < 100 MB ☐ < 1 GB ☒ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	

					☒ other: .nd2, .tiff ☐ NA		
Mutant and/or reporter strains validation awakening effectors	Unknown at this point but we will likely generate knockout/ overexpression mutant for the characterization of identified awakening effectors	☒ 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: .nd2, .tiff ☐ NA	☐ < 100 MB ☐ < 1 GB ☐ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	2 mL cryotubes (with an estimated maximum of 100 for different genes)
Validation awakening effector	Unknown at this point: other phenotypic analyses for the characterization of identified awakening effectors	☒ 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: .pzfx ☐ NA	☐ < 100 MB ☐ < 1 GB ☒ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	

WP 3: Persister awakening in an intracellular model of infection							
Survival analysis	Read counts of UPEC strain (wt and mutant) infecting epithelial cells	☒ 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: .xlsx, .pzfx, .nd2 ☐ NA	☐ < 100 MB ☐ < 1 GB ☒ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	
UPEC mutants with fluorescent reporter	UPECs mutants from WP 1 with a fluorescent reporter (pTIMER or GFP) inserted to track cell division of UPECs infecting epithelial cells	☒ 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: .nd2, .tiff ☐ NA	☐ < 100 MB ☐ < 1 GB ☐ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	2 mL cryotubes (with an estimated maximum of 100 for different genes)

Awakening kinetics UPEC infections	Time lapse microscopy of epithelial cells infected by UPEC strains (wt and mutants)	☒ 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: .nd2, .tiff ☐ NA	☐ < 100 MB ☐ < 1 GB ☐ < 100 GB ☒ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	
Dynamics in hollow fiber model	Read counts of UPECs infecting epithelial cells in hollow fiber model mimicking antibiotic treatment	☒ 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: .xlsx, .pzfx ☐ NA	☐ < 100 MB ☐ < 1 GB ☒ < 100 GB ☐ < 1 TB ☐ < 5 TB ☐ < 10 TB ☐ < 50 TB ☐ > 50 TB ☐ NA	

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.	CRISPRi library CFT073 from research group Christoph Dehio (University of Basel, Switzerland). The article still has to be published so no DOI is available as of yet.
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:

[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: - Short description of the kind of personal data that will be used: - Privacy Registry Reference:
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: The project is performed in the context of an EOS project in collaboration with Wim Versées (Vrije Universiteit Brussel), Steven Ballet (Vrije Univeristeit Brussel), Françoise Van Bambeke (Université Catholique de Louvain), Régis Hallez (Université de Namur) and Jörg Vogel (University of Würzburg). Potential tech transfer will be discussed with the research and development offices of KU Leuven, Vrije Universiteit Brussel, Université Catholique de Louvain, Université de Namur, University of Würzburg and VIB. Ownership of the generated data has been stipulated in a Consortium Agreement. In addition, potential tech transfer will be discussed with the research and development offices of KU Leuven and VIB. Ownership of the generated data has been stipulated in a Cooperation Agreement.
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:

[6] See Glossary Flemish Standard Data Management Plan

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: In regards to WP2, materials (e.g. reporters) may be requested from other labs that might require MTAs. This will be done in consultation with our host institutions' legal departments to minimize restrictions on the use of these materials. Overall, copyright of the generated data belongs to Jan Michiels. Ownership of the generated data belongs to VIB and KU Leuven in accordance with the framework agreement between both institutes.

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).	**Biological material** Cryotubes will possess a reference number that can be found in our Microsoft Access Database which can be accessed from the central server to which all people involved in the project have access. Any relevant information (growth conditions, origin, vectors, genotype, year) will also be provided in the database. **Experimental data** All protocols will be stored as OneNote/Word files in a shared environment. All experimental digital data is named as following: YYYYMMDD_shortdescription and will be provided with the protocols thereof in the same file/environment. Analyses performed in R will contain comments detailing the different steps of the script. In addition, a digital notebook will be kept detailing the daily activities.

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: For certain assays (*e.g.*, the CRISPRi screening, persister assays), I will specify the strains (parental strain, mutations, vectors) and conditions (concentration, duration, treatment) that were used in the same file as the results. Moreover, all strains and conditions will also be specified in the digital notebook. If no, please specify (where appropriate per dataset or data type) which metadata will be created: For remaining data sets for which there is no formally acknowledged metadata standard specific to our discipline, Dublin Core Metadata will be used. Additionally, MIBBI (Minimum Information for Biological and Biomedical Investigations) will be closely monitored for metadata standards that are more specific to our data.

4. Data Storage & Back-up during the Research Project

Where will the data be stored?	**Biological material** 2 mL cryotubes will be stored in -80 °C freezers present in Jan Michiels lab. Strains, vectors, enzymes, dyes… used on short-term will be stored in 4°C and -18°C freezers present in Jan Michiels lab **Experimental data** All data will be stored on two or more locations. Datasets of limited volume will be stored on the device where data was generated (computer linked to the device generating the data, *e.g.*, flow cytometry data) or on my personal tablet (*e.g.*, read counts) and on my personal laptop in a drive accessible through the KU Leuven server and on Onedrive/Sharepoint. Large datasets (*e.g.*, timelapse microscopy images) will be stored on the computer linked to the microscope and accessible on a large storage drive through the KU Leuven server. Regular back-ups will be made on the external password-locked hard drive of all datasets.
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.*	**Biological material** For selected strains, a 2 mL backup cryotube will be stored in a -80° freezer at a different physical location (Kevin Verstrepen lab). **Experimental data** Data will be stored on secure university servers with built-in backup and versioning. Files on Onedrive/Sharepoint are backed up in the cloud and on the KU Leuven network. Password-protected hard drives equipped with anti-virus programs will be used as backup

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

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: Onedrive provides up to 5 TB per user. Furthermore, my external hard drive provides 1 TB space which is sufficient for the foreseeable future. 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]	**Biological material** Unauthorized people do not have access. **Experimental data** The university provides a secure network for long term storage after finalization. The files on Onedrive/sharepoint are linked to my KU Leuven account which is protected by a two factor authorization. The external hard drive is password protected and is stored safe at my home.
What are the expected costs for data storage and backup during the research project? How will these costs be covered?	**Biological material** Cost are covered by general lab expenses. **Experimental data** The data stored on Onedrive/Sharepoint and the central server are covered by lab expenses (€51.9 per year per person) .

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...).	**Biological material** All strains will be stored for at least 5 more years (and longer, complying with the 10 year data preservation rule of KU Leuven) after the end of the project. **Experimental data** All data will be stored for at least 5 more years (and longer, complying with the 10 year data preservation rule of KU Leuven) after the end of the project, conform to the KU Leuven RDM policy. Costs are covered by general lab expenses.
Where will these data be archived (stored and curated for the long-term)?	**Biological material** The strains in cryotubes are stored in -80° C freezers present in the Michiels lab. A backup of selected strains will be stored in -80 °C freezers present in a different physical location (Kevin Verstrepen lab, Heverlee). Unauthorized people do not have access to the strains. **Experimental data** Data will be stored on secure university servers with built-in backup and versioning
What are the expected costs for data preservation during the expected retention period? How will these costs be covered?	**Biological material** Costs of storage in -80 °C freezers are covered by general lab expenses **Experimental data** Estimated cost of storage on the univeristy's central servers is €100/year, covered by general lab expenses.

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:
If access is restricted, please specify who will be able to access the data and under what conditions.	Unpublished and important data will be available to (future) lab members.
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:

Where will the data be made available? If already known, please provide a repository per dataset or data type.	**Biological material** Biological material from published research will be shared upon request. **Experimental data** Published data will be made available in an open access repository or restricted access repository depending on the requirements imposed by the journal.
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, the published data will be made available. Biological material can be shared upon request. The unpublished data will remain restricted access according to a 5 year embargo.
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]	Open Access publications in scientific, peer-reviewed journals are typically covered by a Creative Commons Attribution Licence (CC-BY). The Research Data Repository allows to share data using CC-BY.

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

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: This is standard procedure. Manuscripts will be assigned a unique DOI upon publication and datasets will receive a PID upon deposit in an online platform
What are the expected costs for data sharing? How will these costs be covered?	**Biological material** Shipping fees will be covered by the requesting party. **Experimental data** Publication costs will be covered by general lab expenses. Preferably, a free of charge online repository is chosen. Furthermore, network storage at KU Leuven costs €100/1TB/year and is covered by the lab.

7. Responsibilities	
Who will manage data documentation and metadata during the research project?	Sofie Louwagie
Who will manage data storage and backup during the research project?	Sofie Louwagie
Who will manage data preservation and sharing?	Jan Michiels, Natalie Verstraeten
Who will update and implement this DMP?	Jan Michiels