Plan Overview

A Data Management Plan created using DMPonline

Title: SECURED: Safe and Efficient CUres for RarE Diseases

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Funder: Netherlands Organisation for Scientific Research (NWO)

Template: Data Management Plan NWO (September 2020)

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Project abstract:

Novel technologies enable us to make precise edits to the DNA, promising a cure for genetic diseases. This is particularly good news for patients with rare genetic disorders, because alternative therapies are seldomly available. However, cell delivery and safety need to drastically improve before therapeutic application is possible. Here I propose to create virus-inspired particles that act as Trojan horses for efficient and safe delivery of the DNA-editing tools to cells. As proof of principle, I will apply this method to correct a gene that causes severe intestinal inflammation in young children.

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SECURED: Safe and Efficient CUres for RarE Diseases

General Information

Name applicant and project number

Name applicant: Ewart Kuijk
Project Number: OCENW.XS22.2.065

Name of data management support staff consulted during the preparation of this plan and date of consultation.

NA

1. What data will be collected or produced, and what existing data will be re-used?

1.1 Will you re-use existing data for this research?

If yes: explain which existing data you will re-use and under which terms of use.

- No

1.2 If new data will be produced: describe the data you expect your research will generate and the format and volumes to be collected or produced.

The data that will be generated will consist of:

1. PCR gels
2. Sanger sequencing of plasmids and genomic DNA
3. Microscopy images of cells
4. FACS counting
5. Western blot

1.3. How much data storage will your project require in total?

- 0 – 10 GB

2. What metadata and documentation will accompany the data?

2.1 Indicate what documentation will accompany the data.

Documentation will involve:
Plasmid names and maps
Cloning design strategies (in silico cloning)
Cell types, numbers used for transductions
Production details for virus / Virus Like Particles (plasmid types and concentration of plasmids, dates of transfection and harvesting)

2.2 Indicate which metadata will be provided to help others identify and discover the data.

Cell type
Plasmid type

3. How will data and metadata be stored and backed up during the research?

3.1 Describe where the data and metadata will be stored and backed up during the project.

- Other (please specify)

Institution networked research storage and Benchling

3.2 How will data security and protection of sensitive data be taken care of during the research?

- Not applicable (no sensitive data)

4. How will you handle issues regarding the processing of personal information and intellectual property rights and ownership?

4.1 Will you process and/or store personal data during your project?

If yes, how will compliance with legislation and (institutional) regulation on personal data be ensured?

- No

4.2 How will ownership of the data and intellectual property rights to the data be managed?

The generated data will be owned by the UMC. Data will be stored on institution networked research storage and on Benchling, which is only accessible if access is granted by the project leader (Ewart Kuijk)

5. How and when will data be shared and preserved for the long term?

5.1 How will data be selected for long-term preservation?

- All data resulting from the project will be preserved for at least 10 years

All the data that from this project will be retained long-term (>10 years) on Benchling and in future publications.

5.2 Are there any (legal, IP, privacy related, security related) reasons to restrict access to the data once made publicly available, to limit which data will be made publicly available, or to not make part of the data publicly available?

If yes, please explain.

- No

5.3 What data will be made available for re-use?

- Other (please specify)

It is uncommon for the types of data that will be generated to be reused (unlike for example sequencing or proteomics data). All data that support our main findings (sequencing traces, western blots, pcr gels) will become part of the open access manuscript, where it will be annotated in the figures and figure legends and will be accessible through Benchling.

5.4 When will the data be available for re-use, and for how long will the data be available?

- Data available as soon as article is published

Data will also become available during the project on Benchling

5.5 In which repository will the data be archived and made available for re-use, and under which license?

The manuscript will be published on Biorxiv just prior to the first submission under CC BY license. Data will also be stored on Benchling under CC BY license.

5.6 Describe your strategy for publishing the analysis software that will be generated in this project.

NA

6. Data management costs

6.1 What resources (for example financial and time) will be dedicated to data management and ensuring that data will be FAIR (Findable, Accessible, Interoperable, Re-usable)?

Data will be stored on Benchling
Findability
Benchling assigns each registered entity (such as a cell line or protein) its own unique ID, with a URL link that serves as the unique and persistent identifier. Every entity can be associated with critical metadata, which not only describes it, but also provides useful context.
Data and metadata are stored and indexed in Benchling's searchable cloud application, and can be accessed and discovered through the UI, through REST APIs, or through the data warehouse.
Accessibility
Benchling makes data more accessible through its SaaS-based structure, which enables entries to be accessed by authorized personnel using the unique identifier and HTTP URL (internet link). Benchling also conforms to the openAPI standard, which allows computational systems to discover and understand the capabilities of the service without access to source code or documentation.
Interoperability
Benchling's configurable data model is built with standard vocabulary and ontologies that are agreed upon prior to implementation, and can map to any scientific process.
In Benchling, meaningful "smart links" are created between data and metadata resources These links provide qualified references between the (meta)data, enriching researchers' contextual knowledge about each piece of information. Users can click on any single element and instantly view the whole picture — author, antibody chain info, number of antibody lots, plasmid preps info, etc.
Reusability
Benchling's unified informatics platform makes data points reusable, by making it easy for organizations to link them to the context under which they were originally generated — such as the materials used, protocol used, date of generation, and experimental parameters.
Benchling has adopted the HELM standard to deal with many subtleties of biologics (antibodies, antibody fragments, oligos, etc.).

This standard aligns with the frameworks of many scientific communities, allowing information to be easily shared among scientists and organizations across multiple disciplines.