** UNIVERSITY OF CAPE TOWN COMPUTATIONAL BIOLOGY DIVISION**

**Bioinformatics Support Request**

Please provide us with more information on your request for support. Complete the form as comprehensively as possible, and please indicate where there is still uncertainty.

**Please note, the earlier we are involved the better – for example, it would be better for us to be involved during the study design and even grant application stage**.

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| **CONTACT DETAILS** |
| Date of request | **26 – October – 2021** |
| Name | **Mthawelanga Ndengane** |
| Email address | **NDNMTH001@myuct.ac.za** |
| Research Group/Department | **CIDRI-AFRICA/ IDM** |
| Faculty | **Health Sciences**  |
| IF student, name & email of supervisor | **Dr Anna Coussens** coussens.a@wehi.edu.au  |

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| **PROJECT DETAILS** |
| 1. What is the scientific question? |
| Two clinical *Mtb* strains with a SNP predicted to be under HIV-1 positive directional selection were subjected to mutagenesis by electroporation to revert the SNP to match H37Rv in that position. H37Rv was also subjected to mutation to mimic the SNPs found in the strains.  |
| 2. Who are the partners on the project? |
| The project is carried out as part of my PhD research hosted by CIDRI-AFRICA supervised by A/Prof Anna Coussens and co-supervised by Prof Robert Wilkinson and Dr Anastasia Koch (MMRU). The partners include Dr Apoorva Bhatt from Birmingham University who did the lipid analysis for the strains, and the WEHI Medical Research Institute who conducted the whole genome sequencing of all strains post electroporation.  |
| 3. What type of collaboration with CBIO is expected? For a project that is done as collaboration or for a fee, we will put the agreement in writing. |
| We would elect to do this project via a collaborative agreement. |
| 4. Are there any ethical issues we should be aware of? |
| There are not ethical issues.  |
| 5. How much work is expected from CBIO and when? |
| We request that CBIO complete data access (from WEHI’s FTP server), mapping and alignment, SNP-calling, and detection of SNPs (relative to H37Rv) in WGS for 6 strains. Thesis submission will be Dec 2021 and we hope to include WGS analysis in the thesis.  |
| 6. What type of data will be generated (e.g. sequencing, genotyping, expression, etc.) and what technology platform will be used? |
| Whole genome sequencing data of Mtb clinical isolates. We would take guidance from CBIO on the appropriate tools to use for analysis. Data would have been generated via an Illumina platform.  |
| 7. When do you expect the data? Does it need to be transferred from somewhere else? |
| The data will be available from WEHI in the week of January 17th. The data will need to be transferred from the WEHI database to UCT.  |
| 8. How large will the data be? How long does it need to stored for, and have you made arrangements for storage?  |
| The data will contain whole genome sequences from 6 strains of *Mtb* and would like to be 50GB in size. The data may be stored only during analysis and until transferred to me for long term storage  |
| 9. What bioinformatics analysis needs to be done? Which tools are required? |
| Alignment of sequences between a wild-type and mutant strains to check for additional mutations in the mutant strains that may be a result of electroporation. Please advise on the tools required to achieve this aim.  |
| 10. If a collaborative model is being used, what papers are envisaged and who will the authors be? |
| The PhD is expected to generate a paper on the role of *Mtb* SNP in HIV-1 replication *in vivo*. The authors: M Ndengane (PhD student) Dr Anna Coussens (PI) Dr Anastasia Koch (Supervisor) Dr Nashied Peton (Supervisor) Dr Joana Evans (Supervisor) Prof. Robert Wilkinson (Supervisor) Dr Apoorva Bhatt (Collaborator) And suggested CBIO collaborators.  |

**PLEASE FORWARD THE COMPLETED FORM TO:**

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