**How to do:**

1. Please fill in the form and send it by email to jinalB@nicd.ac.za and thabom@nicd.ac.za for approval
2. When the form has been signed and approved by the reference centre, you can send your isolate/sample(s) together with this delivery note.

**Project description for WGS samples to reference centre**

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| --- |
| **Information about the sender** |
| **Institution/laboratory** | Name:  |
| Address:  |
| **Contact person** | Name: |
| Phone number: |
| Email: |
| **Information about the isolate or isolate set or samples** |
| **What is the purpose of sequencing the isolate/samples(s)? What question do you expect to be answered by the sequencing and analysis?** |  |
| **Please give a short description of the project/program to which the isolates/samples belong.** |  |
| **With which public health institute(s) are the isolates/samples associated or should the data be shared with?** |  |
| **Are other institutes/stakeholders involved in the project?** **If yes, list the institutes and the contact persons.** |  |
| **Is the bacterial species known?** | Yes – Please state the species and how identified:NoNot applicable (if sending samples for SARS-CoV-2 WGS) |
| **Number of isolates/samples** |  |
| **Please give details of any other isolates / sequences related to this project (e.g. accession numbers for isolates from published studies, sample identifier for isolates already sent to us)** |  |
| **What material are you sending?** | Bacterial isolates – for extraction and sequencingDNA – for QC and sequencingRNA – for SARS-CoV-2 sequencingRespiratory sample – for SARS-CoV-2 sequencingSample type (e.g. nasal, nasopharageal swab etc): |
| **What processing / analysis do you want performed on the isolates/samples?** **(tick all that apply)** |  None – I just want the raw reads (FASTQ files)Mapped genomes (please specify if you have a preferred reference genome)Assembled genomesReport on presence / absence of resistance genes / mutationsPhylogenetic analysis (please indicate if you have other isolates / sequences that you want to compare with)Other – please specifyI don’t know, please contact me to discuss**Please give further details:**  |
| **Metadata for the isolate(s)**Please feel free to supply this in an excel-sheet, if more convenient *(required for SARS-CoV-2 WGS*). Please included the information listed here as a minimum. PLEASE NOTE THAT IDENTIFYING INFORMATION MUST NOT BE SUPPLIED | Date of isolation (DD/MM/YYYY):Location (City/Country/e.g. GPS):Host (human/ animal species):Source (blood, faeces, urine etc.): |
| **Will the data be part of a publication?**If yes, the Fleming Fund should be acknowledged in the manner that will be specified to you.We also recommend you to offer co-authorship to staff involved at the WGS reference centre.  |  |
| **Other comments** |  |
|  |
| **Signature by sender**By signing this you agree that the metadata can be shared, and that the genome/metadata can be submitted to ENA/NCBI of SEQAFRICA and open-source genomic analysis platforms such EnteroBase and BIGSdb |  |
| **Decision on this enquiry for WGS** | Yes, the samples can be sequenced. Approximate timing for the sequencing: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_No, the samples cannot be sequenced in this project due to (please state why):  |
| **Signature by reference centre**For approval and justification |  |