	2026-1					2026-2				2026-3				2026-4					2026-5				2026-6				
		2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	
Genetics factors associated with resistance to (...)																											
Upload gVCFs and VCFS																											
Update so far and way forward																											
Identification of biomarkers in keloids and folliculitis (...)		**Identification of biomarkers in keloids and folliculitis keloidalis nuchae (FKN)**																									
Uploading of data																											
Testing pipeline on subset of data																											
Proteomics raw data uploaded to Blackburn (...)																											
Uploading new data from BGI																											
Renaming all files according to the experiments																											
Full run on ilifu of RNA seq pipeline																											
Preliminary analysis of Proteome identification (...)		**Resolved 0%**																									
MaxQuant run of raw proteomics data		**Resolved 0%**																									
Analyze keloid proteomics data with mqmetaproteomics (...)		**Resolved 0%**																									
QC of aligned reads																											
Differential expression analysis																											
Improve normalization and imputaiton of tissue (...)																											
Time seres analysis																											
Secondary analysis: Transcription factor (...)																											
Median group intensity added to output for (...)		**Resolved 0%**																									
Summary table of mRNA and proteomics analysis (...)		**Resolved 0%**																									
Lactobacillus iners MAGs: Genital inflammation (...)																											
Adding Adijat to the project																											
M. smegmatis variant calling pipeline																											
QC of files																											
Preparation of the reusable pipeline																											
Variant calling																											
Metagenomic sequencing of CSF samples		**Metagenomic sequencing of CSF samples**																									
10 February 2022 meeting update and way forward																											

- Confirmation of the analysis to be conducted (...)

New 0%

- Metaproteome functional and taxonomic profiling (...)
  - Infant stool metaproteome analysis
    - Taxonomic profiling using BLAST of identified (...)
- Pathogen outbreak study - Pseudomonas single isolate (...)
  - Implement/adapt Tychus Nextflow pipeline
- Setting up a portable 16S rDNA pipeline for CBIO
  - Cleaning up current pipeline outputs for (...)
  - Setup a decontamination pipeline for Mark's (...)
  - DADA2 workflow as an additional option for (...)
- Setting up a portable metagenome assembly pipeline (...)
  - Quality trimming with Trimmomatic
  - How to download SRA files to hex
  - Read binning with CONCOCT
  - What we already know and have setup
  - Validate binning using single copy core genes
  - Setup Nextflow metagenomics pipeline YAMP (...)
- Setting up a portable RNA-Seq pipeline for CBIO
  - Setting up the NGI-RNAseq pipeline on UCT (...)
    - Configure NGI-RNAseq pipeline to run (...)
      - Update Nextflow to version 0.27.6
- Setting up the BST helpdesk
  - Add more info in knowledge base categories
  - Add page describing different types of collaboration
  - Adding time tracking to the tickets
  - Add ticket type
  - Add captcha on ticket sumbission
- Testing human WGS alignment, calling and joint (...)
  - Test the DRAGEN GATK best practice workflow (...)
  - Get pipeline details for getting data in (...)
- Testing Redmine project features
  - Support ticket 1
  - Bug ticket 1
  - Bug ticket 2

Support ticket 2	
Testing adding image inline	
Testing category assignment	
Testing mail sending	
Testing time records	
The effect of tadpole-tail blastema extract on (...)	
Perform proteomics differential abundance (...)	
Pathway analysis	
The impact of aSTI on the foreskin: spatial transcriptome (...)	The impact of aSTI on the foreskin: spatial transcriptome and ex vivo HIV-1 infection
Understanding the Slide seq data and analysis (...)	New 100%
Data exploration	New 100%
Adding Nyaradzo Chigorimbo-Tsikiwa on Redmine	
Gene expression levels	New 0%
Cell type identification (manual) and annotation	New 0%
Transcriptomic approach on the early development (...)	Transcriptomic approach on the early development of severe asthma
Adding Nontobeko and the Sabelo on Redmine	New 0%
Creating the project folder on ilifu	
Variant calling: detecting SNPs in WGS data relative (...)	Variant calling: detecting SNPs in WGS data relative to H37Rv
Project for Mthawelanga on Redmine	
Debugging the bacterial variant calling pipeline	New 100%
Follow up on the feedback of the 17 November (...)	New 100%
Meeting: Results and discussion for 91_S91 (...)	New 100%