Iteration Number: Description: Experiment Name: 1 Computational Requirements for Bayesian Optimization ☐ Generate samples using Sobol sampling Generate the layout for **Opentrons II robot** transfer, generate a tick box list for the manual mixes, and the automated csv file for the Triple Quadrupole mass spectrometer This will generate 5 files: A master table with the run information, a Opentrons II robot script, an QqQ csy table for mass spec run, a diagram with the microplate and the corresponding condition, and a table with the microplate layout and the colors. Generate tables for the microtubes mixes Pause! ☐ Dataset prepared and preprocessed for the optimization task ☐ Give new recommendations using the acquisition function This will give files: Come back to the second step in a new sheet, all the boxes should be ticked 2 Opentrons II Robot Preparation Test the programmed protocol with water and dummy plates On the preparation day! Check the stock solutions that are needed for the experiment. Prepare fresh ones when required. Keep it fridged. Filter-sterilise when it's possible, specially with concentrated solutions. Prepare the necessary mixes and keep in the fridge ☐ Calibration of the robot (very important) Loading of necessary labware (pipette tips, plates, etc.) Programming the experimental protocol (it's given before) Loading of samples and reagents ☐ Run the programmed protocol After samples are collected

Run the programmed protocol to make the QC pool

3	Plate Reader Preparation
	Prepare agar plate with the bacteria (one day before)
	Prepare complete media for pre-cultures
	Prepare precultures (5ml complete media)
	Calibration of the plate reader (Currently not done by user)
	Setting up the main script with the correct parameters (wavelength, time, temperature, etc.)
	Book the slot for the plater reader in the building system
	On the day of the experiment!
	Setting up the software with the preheating programme (15 minutes before)
	Preparing and loading the sample plate (Come from Opentrons II robot
	Verifying the functioning and cleanliness of the reading chamber (Currently not done by user)
	Running the plate
	On between!
	Prepare ice before taking off the plates
	Weight and label every tube that will be used After 24 / 36 / 48 hrs
	Take off the plate from the reader
	Put the plate on ice, mix the wells with the tip, and move 500 ul to the tubes (that are on ice Keep the plates for biofilm assay)
	Quenching with cold methanol/water, the ratio should be
	Centrifuge the tubes in a cold centrifuge
	Take 400ul of the tubes into new ones cold, remove the rest of supernatant, keep everything on ice Weight the pellet quickly
	Move the tubes to the -80 freezer
4	Triple Quadrupole Mass Spectrometer Preparation
	Calibration of the mass spectrometer(Currently not done by user)
	Cleaning and verifying the ion source and detector Has to be done once a while
	Open csv for the sequence list, create new sequence from this file
	Check that there's enough mobile phase solvent for the run and miliQ water for the seal wash
	Check the status of the mass spec by looking at the parameters, and if they are in range
	Run a few blanks, plus system suitability sample, plus a few blanks
	Preparing and loading the samples from the experiment
	Perform the run