**Summarise for *Acinetobacter baumannii* AB5075 by genome-scale metabolic modelling**

In the study of elucidating the mechanism of polymyxin killing and resistance in *Acinetobacter baumannii* AB5075 by genome-scale metabolic modelling, the first stage is constructing the GSMM for AB5075 with the genome annotation and biochemical data from databases. The large quantity of information featured in public databases (MetaCyc, ModelSEED, KEGG), like details about genomes, pathways, enzymes and proteins have been collected. From the MetaCyc, reactions and compounds were collected via the smart table and exported to two spreadsheets. Data from ModelSEED was collected using the genome of *Acinetobacter baumannii* AB5075. All candidate metabolic genes and their potential reactions have been collected and the reactions and metabolites which collected from MetaCyc and ModelSEED have been gathered in the same spreadsheet. In the spreadsheet, neutral formula, Genes locus, Equation and the pathways have been readily obtained from BioCyc and ModelSEED, duplicates from different databases in the spreadsheet have also been removed. This spreadsheet will serve as a starting point for the manual curation process of the draft reconstruction.