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## Introduction

*E. faecalis* is a gram-positive bacterium that is getting more attention due to its "two-face" behavior. This natural inhabitant of the mammalian gastrointestinal tract is also an opportunistic pathogen responsible for urinary tract infections, nosocomial infections, bacteremia and infective endocarditis. Its intrinsic physiological properties such as inherent antibiotic resistance and exceptional ability to adapt to harsh conditions provide this organism with an enormous advantage in the infection processes.

## Methods

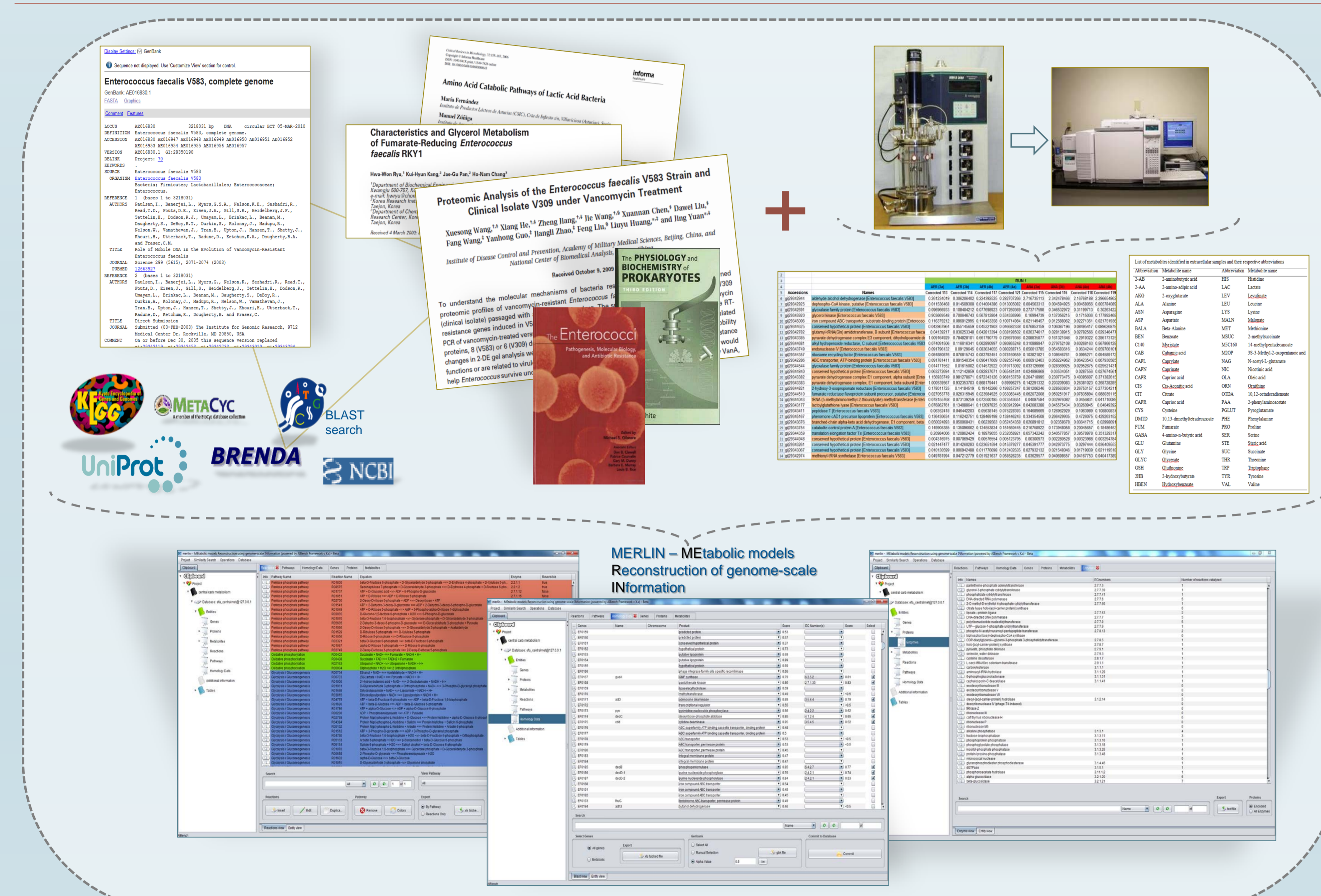


Figure 1: Data integration of different levels of information.

## Objectives

We propose to reconstruct the genome scale metabolic network of the central carbon metabolism of *E. faecalis*. The model will support the interpretation and better understanding of the metabolomic and proteomic data. The reconstruction will be based initially on the genome sequencing information available as well as online databases and literature research.

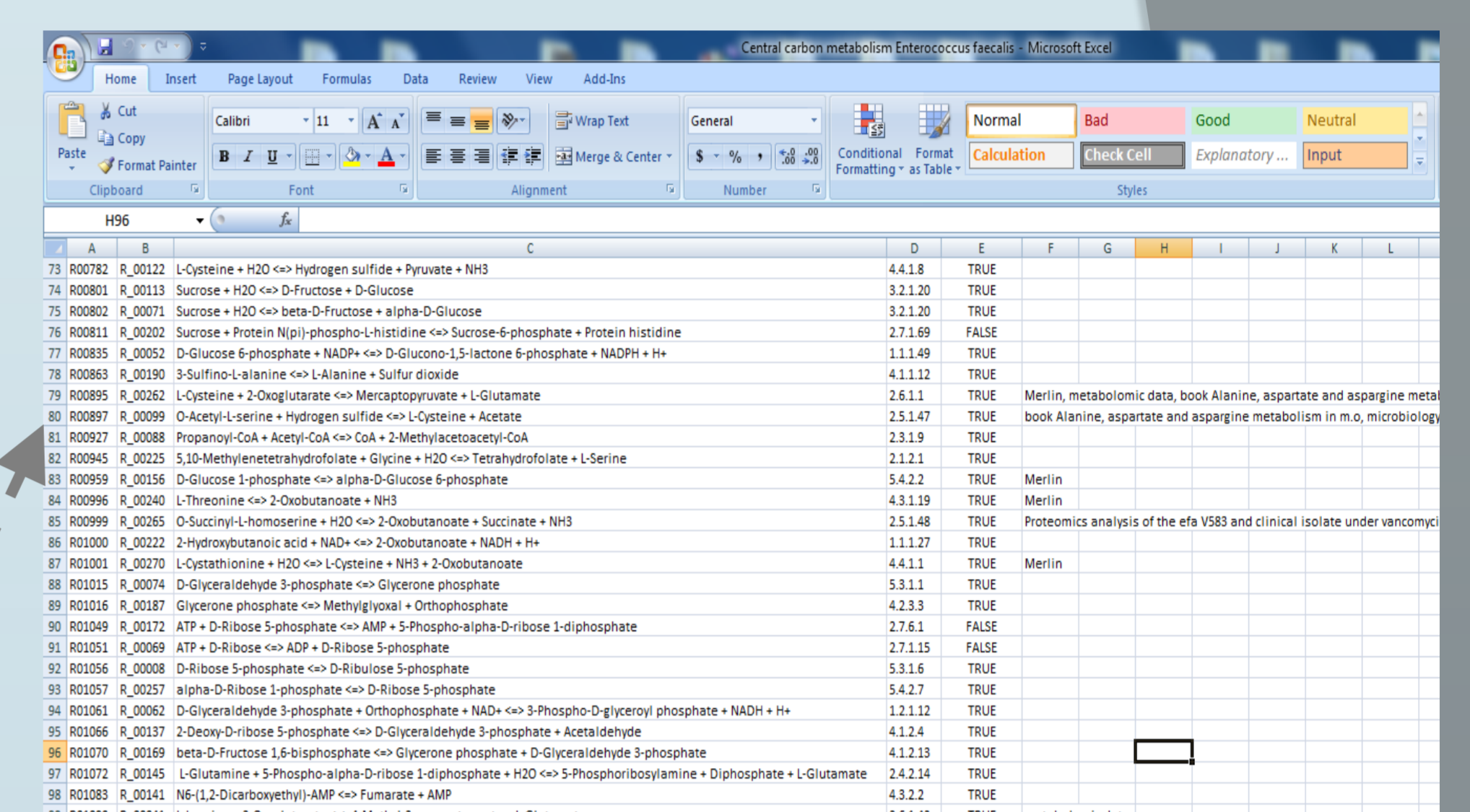


Figure 2: Metabolic network of the central carbon metabolism in an Excel spreadsheet

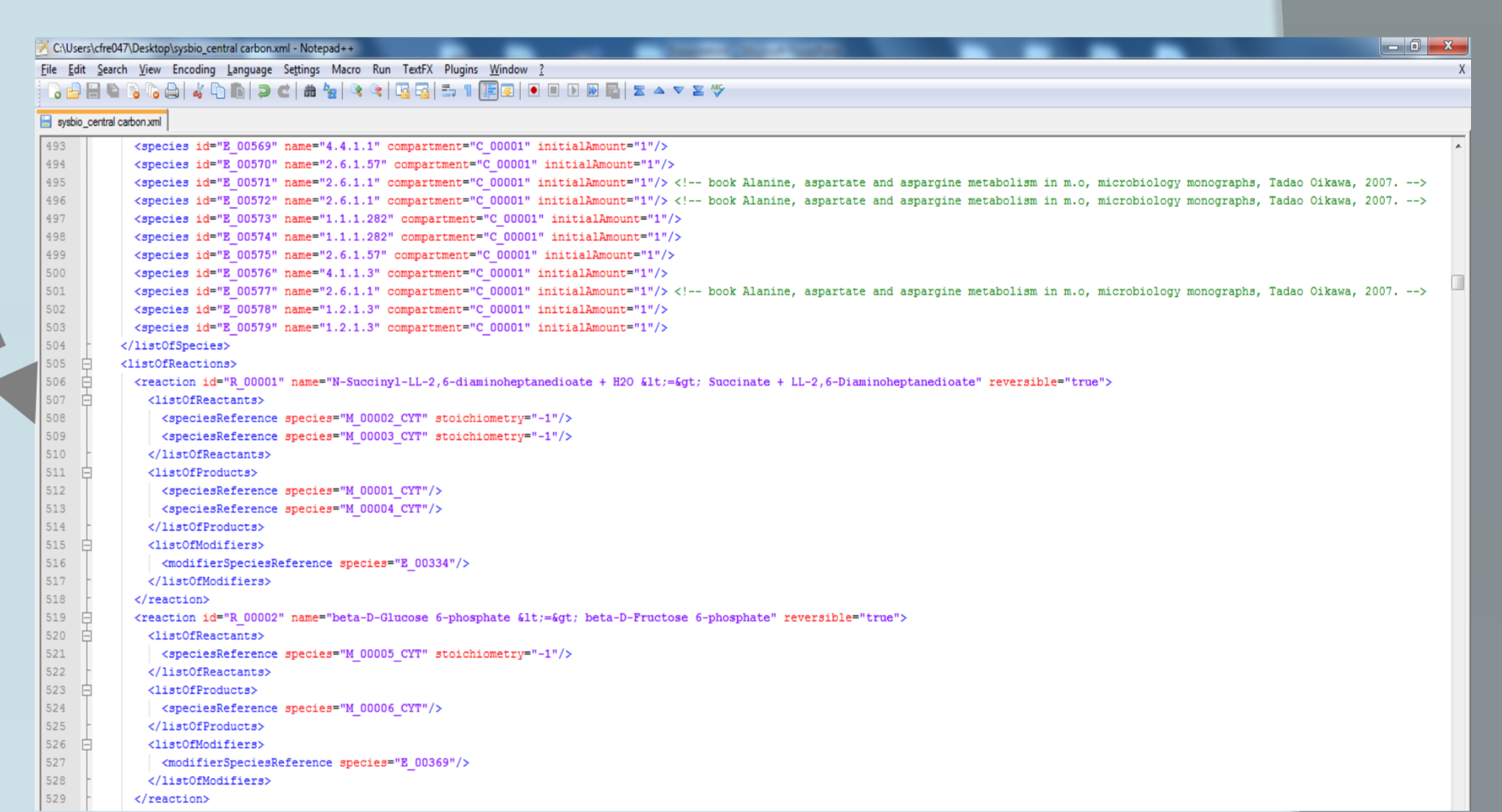


Figure 3: Metabolic network of the central carbon metabolism in an XML formal - SBML

## Results

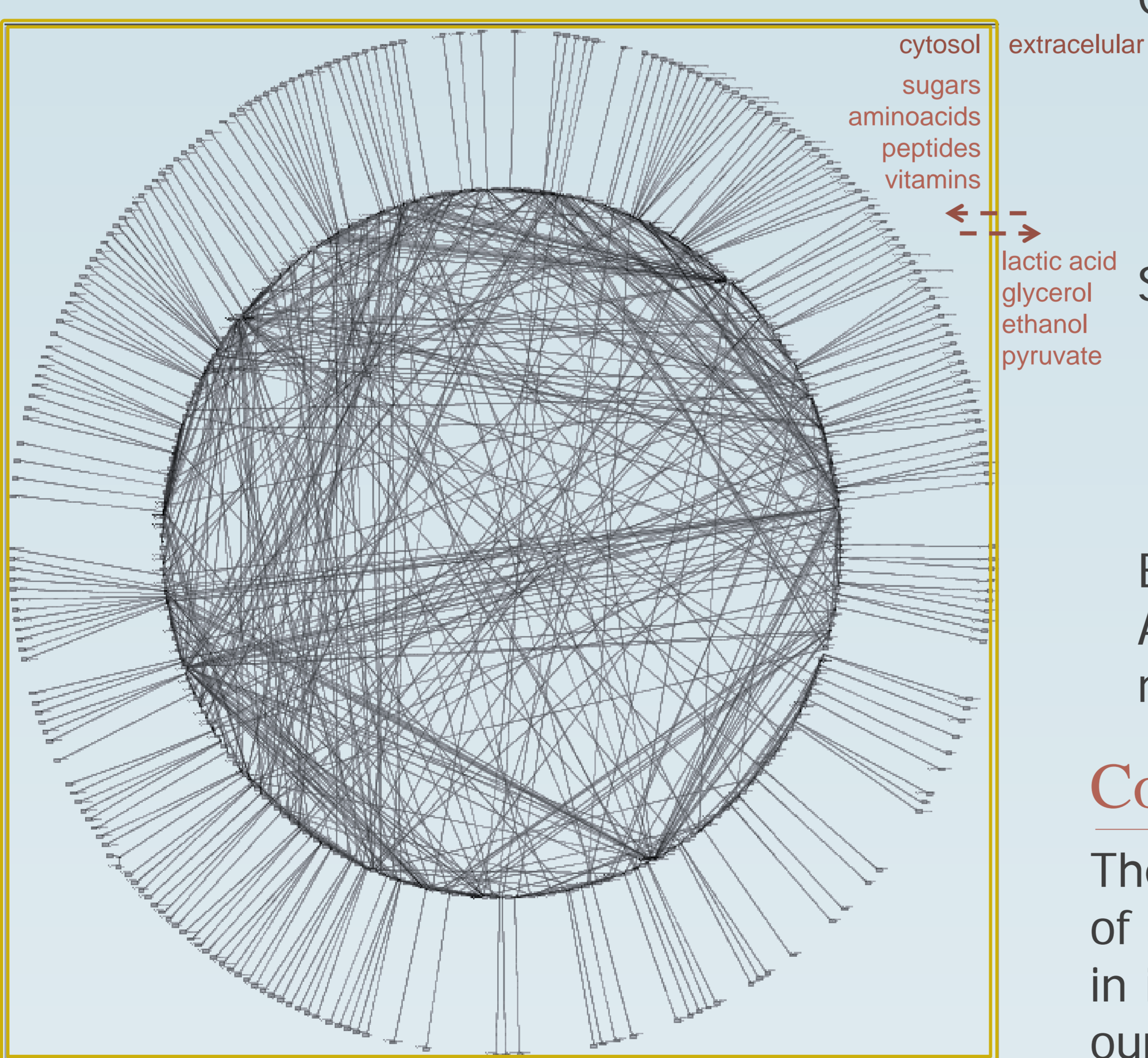


Figure 4: Graphical representation of the central carbon metabolism of *Enterococcus faecalis* metabolic network - Cell designer

## Future directions

On-going activities are the addition of:

- ❖ Membrane transport reactions (of extracellular compounds to the inside of the cell)
- ❖ Metabolism products (that are secreted by the cell)
- ❖ Biomass equation

Simulations:

- ❖ Optimization of growth
- ❖ Minimal nutrient requirements
- ❖ Gene deletion

Extend model for full metabolic network

A metabolic network reconstruction is practically an endless process that may lead to even more accurate predictions of cell metabolism.



## Conclusions

The metabolic model generated for this bacterium will allow the correlation of metabolite levels and fluxes, enabling identification of key control points in its metabolism. Additionally, the metabolomic data already generated by our group allowed the identification of key compounds/reactions in *E. faecalis* metabolism that were still unclear. As it has been previously shown for other organisms, the metabolic network reconstruction may serve as a valuable tool to predict the phenotypic behaviour under various genetic and environmental conditions as well as to perform metabolic engineering simulations (e.g. gene deletion experiments).

## Acknowledgements

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